Table S6. Differentially regulated genes (up and down regulated) in the control compared with THyPRP silenced plants in FAZ at 16 h along with their expression values, fold changes, annotations, GO ids and terms.

Worksheet 2 & 3

Set5					
Line	Array	Details	Time	Treated vs. Con	Set
Control – New Yorker	254331010027_1_1	16h_9_AZ	16h	Control	Set 5
Control – New Yorker	254331010027_1_2	16h_10_AZ	16h		
TAPG + TPRP	254331010036_1_1	16h_45_AZ	16h	Treated	
TAPG + TPRP	254331010036_1_2	16h_46_AZ	16h		

Note:

Fold change expression values are provided as logbase 2

Flagging Criteria:

Compromised: If the gProcessedSignal value is less than the background intensity
Detected: If the gProcessedSignal value is above background intensity

Column Header	Description
ProbeName	Unique probe identifier
GeneName	GeneSymbol
Fold	Fold change calculated is log base 2
Flag	Detected or Compromised
GeomeanFold	Average Fold change for the replicates calculated is log base 2
p-Value	t-test p- value
gProcessedSigna	Background substracted signal intensity

Cut off used to filter up and down regulated genes

Upregulated

For filtering upregulation we consider flag should be Detected in the treated sample and can be Compromised or Detected in the control sample and fold>=0.8 in the individual replicates and fold>=1 in the Geomean of treated samples.

Downregulated

For filtering downregulation we consider flag can be Detected or Compromised in the treated sample and should be Detected in the control sample and fold<=-0.8 in the individual replicates and fold<=-1 in the Geomean of treated samples.

Differentially Regulated Probes

Sample	Up	Down
16h_TPRP_ AZ vs. 16h_Control_AZ_Sense	2408	2491
16h_TPRP_ AZ vs. 16h_Control_AZ_Antisense	1483	895

Worksheet 4 & 5

This file contains the fold change for all the spots in the array

GO ID

Gene Ontology ID

GO ACCESSION

Gene Ontology Function name

p-value :

The probability of obtaining the specified GO accession number from a list of random entities. Less the p-value more significant is the GO accession number.

Significant pvalue<0.05

Count in Selection :

This refers to the number of genes in the selected entity (for example, from T-test) list which have that particular GO term.

%Count in Selection :

This refers to the percentage of genes in the input entity list which have that GO term.

Count in Total :

This refers to the number of genes in All Entities which have that GO term.

%Count in Total :

This refers to the percentage of genes in the All Entities list which have that GO term.

		16h_AZ_Control					16h_AZ_TAPG + TPRP vs. 16h_AZ_Control									
ProbeNar	Orientatic	Fold 16h	Flag 16h	Fold 16h	Flag 16h	Geomean	Fold 16h	Flag 16h	Fold 16h	Flag 16h	Geomean	P-value	ProbeNar	GeneNar	Systemat	Descripti
A 96 P0	Sense	0.462	Detected	-0.462	Detected	0.000	2.830	Detected	1.913	Detected	2.372	0.068	A 96 P0	A 96 P0	A 96 P0	Unknown
A 96 P0	Sense	0.070	Detected	-0.070	Detected	0.000	1.421	Detected	0.920	Detected	1.171	0.046	A 96 P0	AK32048	AK32048	Solanum
A 96 P01	Sense	0.509	Detected	-0.509	Detected	0.000	1.753	Detected	0.950	Detected	1.352	0.172	A 96 P01	AK32373	AK32373	Solanum
A 96 P01	Sense	0.994	Detected	-0.994	Detected	0.000	4.888	Detected	3.934	Detected	4.411	0.057	A 96 P01	AW94475	AW94475	EST3368
A 96 P01	Sense	0.133	Detected	-0.133	Detected	0.000	3.916	Detected	3.084	Detected	3.500	0.015	A 96 P01	BI933034	BI933034	EST5529
A 96 P01	Sense	0.171	Detected	-0.171	Detected	0.000	1.990	Detected	2.294	Detected	2.142	0.011	A 96 P01	AW73822	AW73822	EST3396
A 96 P01	Sense	0.379	Detected	-0.379	Detected	0.000	2.247	Detected	1.247	Detected	1.747	0.108	A 96 P01	LOC5440	NM 0012	Solanum
A 96 P01	Sense	-0.089	Detected	0.089	Detected	0.000	2.318	Detected	1.667	Detected	1.993	0.028	A 96 P01	LOX1.1	NM 0012	Solanum
A 96 P01	Sense	-0.197	Detected	0.197	Detected	0.000	1.931	Detected	1.885	Detected	1.908	0.011	A 96 P01	LOC5438	NM 0012	Solanum
A 96 P01	Sense	-0.167	Detected	0.167	Detected	0.000	1.043	Detected	1.014	Detected	1.028	0.026	A 96 P01	PPCK2	NM 0012	Solanum
A 96 P01	Sense	0.762	Detected	-0.762	Comprom	0.000	4.293	Detected	3.368	Detected	3.830	0.050	A 96 P01	wus	NM 0012	Solanum
A 96 P01	Sense	-0.180	Detected	0.180	Detected	0.000	1.915	Detected	1.441	Detected	1.678	0.030	A 96 P01	TA37803	TA37803	Rep: Chr
A 96 P03	Sense	0.486	Detected	-0.486	Detected	0.000	1.858	Detected	1.088	Detected	1.473	0.141	A 96 P03	Td	M61914	L.esculer
A 96 P03	Sense	-0.006	Detected	0.006	Detected	0.000	1.275	Detected	0.917	Detected	1.096	0.026	A 96 P03	AK32134	AK32134	Solanum
A 96 P05	Sense	-0.056	Detected	0.056	Detected	0.000	2.737	Detected	1.903	Detected	2.320	0.031	A 96 P05	GO37623	GO37623	ctsd3j1 T
A 96 P05	Sense	-0.030	Detected	0.030	Detected	0.000	1.494	Detected	0.891	Detected	1.193	0.059	A 96 P05	LOC7783	NM 0012	Solanum
A 96 P05	Sense	0.077	Detected	-0.077	Detected	0.000	0.993	Detected	1.173	Detected	1.083	0.012	A 96 P05	AI483528	AI483528	EST2493
A 96 P05	Sense	0.681	Detected	-0.681	Detected	0.000	4.678	Detected	2.944	Detected	3.811	0.074	A 96 P05	LOC1001	Z75519	L.esculer
A 96 P05	Sense	0.386	Detected	-0.386	Detected	0.000	2.099	Detected	1.306	Detected	1.702	0.091	A 96 P05	AK32258	AK32258	Solanum
A 96 P05	Sense	0.152	Detected	-0.152	Detected	0.000	1.712	Detected	0.805	Detected	1.258	0.119	A 96 P05	DB69307	DB69307	DB69307
A 96 P06	Sense	-0.372	Detected	0.372	Detected	0.000	1.365	Detected	1.029	Detected	1.197	0.100	A 96 P06	AK32477	AK32477	Solanum
A 96 P06	Sense	-0.008	Detected	0.008	Detected	0.000	4.087	Detected	2.170	Detected	3.129	0.082	A 96 P06	DB69309	DB69309	DB69309
A 96 P06	Sense	0.486	Detected	-0.486	Detected	0.000	1.317	Detected	1.919	Detected	1.618	0.106	A 96 P06	AK31923	AK31923	Solanum
A 96 P06	Sense	-0.381	Detected	0.381	Detected	0.000	5.397	Detected	3.110	Detected	4.253	0.072	A 96 P06	AK22483	AK22483	Solanum
A 96 P07	Sense	-0.289	Detected	0.289	Detected	0.000	1.744	Detected	1.166	Detected	1.455	0.070	A 96 P07	DB71124	DB71124	DB71124
A 96 P07	Sense	0.020	Detected	-0.020	Detected	0.000	1.213	Detected	1.568	Detected	1.390	0.016	A 96 P07	DB70200	DB70200	DB70200
A 96 P07	Sense	0.868	Detected	-0.868	Detected	0.000	2.284	Detected	1.397	Detected	1.841	0.200	A 96 P07	LOC5439	AK24724	Solanum
A 96 P07	Sense	1.091	Detected	-1.091	Detected	0.000	3.876	Detected	2.490	Detected	3.183	0.133	A 96 P07	LOC5440	NM 0012	Solanum
A 96 P07	Sense	-0.497	Detected	0.497	Detected	0.000	1.337	Detected	3.236	Detected	2.287	0.166	A 96 P07	ADH2	NM 0012	Solanum
A 96 P07	Sense	0.547	Detected	-0.547	Detected	0.000	2.227	Detected	0.943	Detected	1.585	0.201	A 96 P07	LOC5442	NM 0012	Solanum
A 96 P07	Sense	-0.247	Detected	0.247	Detected	0.000	1.291	Detected	1.633	Detected	1.462	0.040	A 96 P07	TA36339	TA36339	Unknown
A 96 P08	Sense	-0.146	Detected	0.146	Detected	0.000	1.388	Detected	1.147	Detected	1.267	0.022	A 96 P08	EG55367	EG55367	to00628 T
A 96 P08	Sense	-0.146	Comprom	0.146	Comprom	0.000	2.994	Detected	2.525	Detected	2.759	0.010	A 96 P08	BG12915	BG12915	EST4748
A 96 P08	Sense	0.207	Detected	-0.207	Detected	0.000	1.477	Detected	0.843	Detected	1.160	0.092	A 96 P08	TA35649	TA35649	Unknown
A 96 P08	Sense	-0.173	Detected	0.173	Detected	0.000	1.042	Detected	0.960	Detected	1.001	0.030	A 96 P08	TA35693	TA35693	Rep: Sec
A 96 P08	Sense	-0.280	Detected	0.280	Detected	0.000	5.425	Detected	3.148	Detected	4.287	0.067	A 96 P08	AK22483	AK22483	Solanum
A 96 P08	Sense	0.302	Detected	-0.302	Detected	0.000	4.204	Detected	3.029	Detected	3.616	0.032	A 96 P08	TA36105	TA36105	Rep: Carl
A 96 P08	Sense	-0.312	Detected	0.312	Detected	0.000	1.299	Detected	1.619	Detected	1.459	0.053	A 96 P08	TA36340	TA36340	Rep: Hist
A 96 P08	Sense	-0.406	Detected	0.406	Detected	0.000	0.923	Detected	3.039	Detected	1.981	0.223	A 96 P08	ADH2	NM 0012	Solanum
A 96 P08	Sense	-0.464	Detected	0.464	Detected	0.000	1.174	Detected	3.070	Detected	2.122	0.182	A 96 P08	ADH2	NM 0012	Solanum
A 96 P09	Sense	0.797	Detected	-0.797	Detected	0.000	2.432	Detected	1.534	Detected	1.983	0.162	A 96 P09	TA38240	TA38240	Rep: Wou
A 96 P10	Sense	-0.359	Detected	0.359	Detected	0.000	2.809	Detected	2.746	Detected	2.777	0.016	A 96 P10	TA44511	TA44511	Rep: Wou
A 96 P10	Sense	-0.087	Comprom	0.087	Comprom	0.000	5.534	Detected	3.049	Detected	4.291	0.075	A 96 P10	BG12974	BG12974	EST4753
A 96 P11	Sense	0.113	Detected	-0.113	Detected	0.000	1.232	Detected	1.639	Detected	1.435	0.025	A 96 P11	AK32107	AK32107	Solanum
A 96 P11	Sense	-0.065	Comprom	0.065	Comprom	0.000	1.465	Detected	1.501	Detected	1.483	0.002	A 96 P11	TA53569	TA53569	Unknown
A 96 P11	Sense	-0.370	Comprom	0.370	Detected	0.000	4.862	Detected	2.865	Detected	3.864	0.068	A 96 P11	AK32877	AK32877	Solanum
A 96 P11	Sense	-0.371	Detected	0.371	Detected	0.000	2.028	Detected	1.532	Detected	1.780	0.057	A 96 P11	TA54138	TA54138	Rep: Clas
A 96 P12	Sense	0.359	Detected	-0.359	Detected	0.000	2.134	Detected	1.505	Detected	1.820	0.062	A 96 P12	AK32258	AK32258	Solanum
A 96 P12	Sense	-0.782	Comprom	0.782	Detected	0.000	2.774	Detected	1.953	Detected	2.363	0.116	A 96 P12	TA56320	TA56320	Rep: Gibb
A 96 P12	Sense	0.193	Detected	-0.193	Detected	0.000	1.592	Detected	1.079	Detected	1.335	0.053	A 96 P12	NP00006	NP00006	GB
A 96 P12	Sense	-0.254	Detected	0.254	Detected	0.000	1.196	Detected	1.891	Detected	1.543	0.070	A 96 P12	NP23285	NP23285	GB
A 96 P12	Sense	-0.474	Comprom	0.474	Detected	0.000	1.026	Detected	1.009	Detected	1.017	0.165	A 96 P12	NP92874	NP92874	GB
A 96 P12	Sense	0.163	Comprom	-0.163	Comprom	0.000	2.173	Detected	3.718	Detected	2.946	0.065	A 96 P12	NP92878	NP92878	GB
A 96 P12	Sense	-0.002	Detected	0.002	Detected	0.000	1.876	Detected	1.257	Detected	1.566	0.037	A 96 P12	AK32048	AK32048	Solanum
A 96 P12	Sense	0.347	Comprom	-0.347	Comprom	0.000	1.276	Detected	1.808	Detected	1.542	0.072	A 96 P12	NP92874	NP92874	GB
A 96 P13	Sense	0.249	Detected	-0.249	Detected	0.000	2.178	Detected	1.154	Detected	1.666	0.100	A 96 P13	AI485885	AI485885	Unknown
A 96 P13	Sense	-0.238	Detected	0.238	Detected	0.000	4.757	Detected	3.712	Detected	4.234	0.018	A 96 P13	LOC5440	BI931665	EST5515
A 96 P13	Sense	0.480	Detected	-0.480	Detected	0.000	2.440	Detected	1.760	Detected	2.100	0.070	A 96 P13	AI487256	AI487256	Unknown
A 96 P13	Sense	0.386	Detected	-0.386	Detected	0.000	2.990	Detected	1.459	Detected	2.225	0.122	A 96 P13	systemin	M84801	Lycopers
A 96 P13	Sense	0.917	Detected	-0.917	Detected	0.000	2.848	Detected	1.958	Detected	2.403	0.142	A 96 P13	TA38240	TA38240	Rep: Wou
A 96 P13	Sense	0.019	Detected	-0.019	Detected	0.000	2.280	Detected	1.568	Detected	1.924	0.033	A 96 P13	ca2	NM 0012	Solanum
A 96 P13	Sense	-0.047	Detected	0.047	Detected	0.000	0.965	Detected	1.068	Detected	1.017	0.005	A 96 P13	AI778706	AI778706	Unknown
A 96 P14	Sense	-0.468	Detected	0.468	Detected	0.000	1.320	Detected	3.152	Detected	2.236	0.162	A 96 P14	ADH2	NM 0012	Solanum
A 96 P14	Sense	-0.507	Detected	0.507	Detected	0.000	5.166	Detected	2.977	Detected	4.071	0.078	A 96 P14	AK22483	AK22483	Solanum
A 96 P15	Sense	-0.131	Detected	0.131	Detected	0.000	1.656	Detected	1.162	Detected	1.409	0.037	A 96 P15	AK32048	AK32048	Solanum
A 96 P15	Sense	0.119	Detected	-0.119	Detected	0.000	2.734	Detected	1.672	Detected	2.203	0.056	A 96 P15	ca2	NM 0012	Solanum
A 96 P15	Sense	-0.006	Detected	0.006	Detected	0.000	2.403	Detected	1.563	Detected	1.983	0.042	A 96 P15	ca2	NM 0012	Solanum
A 96 P15	Sense	0.084	Detected	-0.084	Detected	0.000	2.645	Detected	1.541	Detected	2.093	0.064	A 96 P15	ca2	NM 0012	Solanum
A 96 P15	Sense	0.210	Detected	-0.210	Detected	0.000	3.623	Detected	2.580	Detected	3.101	0.031	A 96 P15	AW09412	AW09412	Rep: Carl
A 96 P15	Sense	0.341	Detected	-0.341	Detected	0.000	1.399	Detected	0.838	Detected	1.118	0.127	A 96 P15	AK32511	AK32511	Solanum
A 96 P15	Sense	-0.323	Comprom	0.323	Detected	0.000	1.614	Detected	2.725	Detected	2.169	0.078	A 96 P15	AW22169	AW22169	Unknown
A 96 P15	Sense	-0.725	Detected	0.725	Detected	0.000	1.833	Detected	1.576	Detected	1.705	0.147	A 96 P15	AW22440	AW22440	Unknown
A 96 P15	Sense	-0.123	Detected	0.123	Detected	0.000	0.908	Detected	1.452	Detected	1.180	0.059	A 96 P15	AW62135	AW62135	Rep: Chr
A 96 P15	Sense	-0.452	Detected	0.452	Detected	0.000	1.237	Detected	0.850	Detected	1.044	0.168	A 96 P15	AK32097	AK32097	Solanum
A 96 P16	Sense	-0.122	Detected	0.122	Detected	0.000	2.553	Detected	2.145	Detected	2.349	0.010	A 96 P16	AW65032	AW65032	Unknown
A 96 P16	Sense	0.325	Detected	-0.325	Detected	0.000	1.881	Detected	1.068	Detected	1.475	0.105	A 96 P16	TA36834	TA36834	Rep: Wou
A 96 P16	Sense	-0.178	Detected	0.178	Detected	0.000	2.048	Detected	1.069	Detected	1.558	0.096	A 96 P16	LOX1.1	NM 0012	Solanum
A 96 P16	Sense	0.606	Comprom	-0.606	Comprom	0.000	3.658	Detected	2.701	Detected	3.179	0.054	A 96 P16	TA40055	TA40055	Unknown
A 96 P16	Sense	0.346	Detected	-0.346	Comprom	0.000	3.411	Detected	2.624	Detected	3.018	0.029	A 96 P16	AW93434	AW93434	Unknown
A 96 P17	Sense	0.574	Detected	-0.574	Detected	0.000	1.852	Detected	0.816	Detected	1.334	0.227	A 96 P17	Td	M61914	L.esculer
A 96 P17	Sense	0.397	Detected	-0.397	Comprom	0.000	0.835	Detected	2.341	Detected	1.588	0.203	A 96 P17	BE43531	BE43531	Rep: Cati
A 96 P17	Sense	0.170	Detected	-0.170	Detected	0.000	3.221	Detected	1.531	Detected	2.376	0.110	A 96 P17	systemin	M84801	Lycopers
A 96 P17	Sense	-0.459	Detected	0.459	Detected	0.000	5.364	Detected	2.967	Detected	4.165	0.083	A 96 P17	AK22483	AK22483	Solanum
A 96 P17	Sense	0.162	Detected	-0.162	Detected	0.000	1.249	Detected	2.209	Detected	1.729	0.076	A 96 P17	ADH2	NM 0012	Solanum
A 96 P17	Sense	0.285	Detected	-0.285	Detected	0.000	1.873	Detected	1.174	Detected	1.523	0.078	A 96 P17	TA36834	TA36834	Unknown
A 96 P18	Sense	0.184	Detected	-0.184	Detected	0.000	1.051	Detected	1.344	Detected	1.198	0.036	A 96 P18	BF11392	BF11392	Unknown
A 96 P18	Sense	0.148	Comprom	-0.148	Comprom	0.000	1.562	Detected	1.997	Detected	1.780	0.021	A 96 P18	BF11394	BF11394	Unknown
A 96 P18	Sense	-0.080	Detected	0.080	Detected	0.000	1.396	Detected	1.139	Detected	1.268	0.014	A 96 P18	GO37247	GO37247	ctsb1n5 T
A 96 P18	Sense	0.020	Detected	-0.020	Detected	0.000	1.787	Detected	1.520	Detected	1.653	0.007	A 96 P18	BG13364	BG13364	Unknown
A 96 P19	Sense	0.303	Comprom	-0.303	Comprom	0.000	2.004	Detected	2.083	Detected	2.043	0.022	A 96 P19	BG13505	BG13505	Rep: Chr
A 96 P19	Sense	0.310	Detected	-0.310	Detected	0.000	2.269	Detected	1.344	Detected	1.807	0.083	A 96 P19	TA36834	TA36834	Unknown
A 96 P19	Sense	0.561	Detected	-0.561	Detected	0.000	2.656	Detected	1.831	Detected	2.244	0.084	A 96 P19	TA36834	TA36834	Rep: Wou
A 96 P19	Sense	-0.186	Detected	0.186	Detected	0.000	1.093	Detected	1.028	Detected	1.060	0.030	A 96 P19	BG73500	BG73500	Unknown
A 96 P19	Sense	-0.329	Detected	0.329	Detected	0.000	1.559	Detected	1.911	Detected	1.735	0.043	A 96 P19	BI203257	BI203257	Unknown
A 96 P20	Sense	-0.955	Comprom	0.955	Comprom	0.000	3.813	Detected	2.720	Detected	3.267	0.097	A 96 P20	BI925055	BI925055	Unknown
A 96 P20	Sense	0.805	Detected	-0.805	Detected	0.000	2.484	Detected	1.569	Detected	2.026	0.160	A 96 P20	TA38240	TA38240	Rep: Wou
A 96 P20	Sense	-0.067	Detected	0.067	Detected	0.000	1.261	Detected	0.861	Detected	1.061	0.037	A 96 P20	BI933909	BI933909	Unknown
A 96 P21	Sense	0.022	Detected	-0.022	Detected	0.000	1.805	Detected	0.974	Detected	1.389	0.079	A 96 P21	AK32806	AK32806	Solanum
A 96 P21	Sense	-0.100	Comprom	0.100	Comprom	0.000	2.967	Detected	3.059	Detected	3.013	0.001	A 96 P21	TA36591	TA36591	Unknown
A 96 P21	Sense	-0.344	Detected	0.344	Detected	0.000	1.675	Detected	1.637	Detected	1.656	0.041	A 96 P21	BP89517	BP89517	Unknown
A 96 P21	Sense	0.250	Detected	-0.250	Detected	0.000	3.789	Detected	2.610	Detected	3.200	0.038	A 96 P21	BP90263	BP90263	Rep: Carl
A 96 P22	Sense	0.083	Detected	-0.083	Detected	0.000	1.378	Detected	1.648	Detected	1.513	0.011	A 96 P22	BP90794	BP90794	Unknown
A 96 P22	Sense	-0.716	Detected	0.716	Detected	0.000	2.109	Detected	1.800	Detected	1.955	0.116	A 96 P22	AK32160	AK32160	Solanum
A 96 P22	Sense	0.201	Detected	-0.201	Detected	0.000	1.141	Detected	1.120	Detected	1.130	0.030	A 96 P22	CD00230	CD00230	Unknown
A 96 P22	Sense	0.220	Detected	-0.220	Detected	0.000	3.576	Detected	2.427	Detected	3.001	0.039	A 96 P22	TA36105	TA36105	Unknown
A 96 P22	Sense	-0.162	Detected	0.162	Detected	0.000	1.095	Detected	0.930	Detected	1.012	0.031	A 96 P22	AK31970	AK31970	Solanum
A 96 P22	Sense	0.441	Detected	-0.441	Comprom	0.000	2.132	Detected	0.891	Detected	1.512	0.186	A 96 P22	AK32017	AK32017	Solanum
A 96 P22	Sense	-0.161	Detected	0.161	Detected	0.000	2.273	Detected	1.608	Detected	1.941	0.034	A 96 P22	DB68495	DB68495	Unknown
A 96 P23	Sense	0.007	Detected	-0.007	Detected	0.000	2.285	Detected	1.265	Detected	1.775	0.074	A 96 P23	ca2	NM 0012	Solanum
A 96 P24	Sense	-0.535	Comprom	0.535	Comprom	0.000	1.762	Detected	1.486	Detected	1.624	0.099	A 96 P24	AK32806	AK32806	Solanum
A 96 P24	Sense	-0.264	Comprom	0.264	Detected	0.000	2.818	Detected	2.052	Detected	2.435	0.035	A 96 P24	GO37623	GO37623	ctsd3j1 T
A 96 P24	Sense	0.541	Detected	-0.541	Detected	0.000	1.724	Detected	1.265	Detected	1.495	0.126	A 96 P24	TA37203	TA37203	Unknown
A 96 P25	Sense	0.071	Detected	-0.071	Detected	0.000	1.514	Detected	1.439	Detected	1.476	0.003	A 96 P25	TC23209	TC23209	Rep: 13 k
A 96 P25	Sense	0.323	Detected	-0.323	Detected	0.000	2.152	Detected	1.192	Detected	1.672	0.102	A 96 P25	LOC5440	NM 0012	Solanum
A 96 P25	Sense	0.037	Detected	-0.037	Detected	0.000	4.793	Detected	2.450	Detected	3.621	0.091	A 96 P25	GO37623	GO37623	ctsd3j1 T
A 96 P25	Sense	-0.041	Detected	0.041	Detected	0.000	1.284	Detected	1.026	Detected	1.155	0.013	A 96 P25	TC24016	TC24016	Rep: Chr
A 96 P26	Sense	1.136	Detected	-1.136	Detected	0.000	3.966	Detected	2.376	Detected	3.171	0.150	A 96 P26	LOC5440	NM 0012	Solanum
GT Sense	Sense	-0.280	Comprom	0.280	Detected	0.000	1.401	Detected	1.006	Detected	1.204	0.072	GT Sens	AT1G178	AT1G178	putative a
GT Sense	Sense	0.162	Detected	-0.162	Comprom	0.000	1.343	Detected	1.568	Detected	1.455	0.018	GT Sens	AT4G009	AT4G009	Ca2+-trar
GT Sense	Sense	-0.116	Detected	0.116	Detected	0.000	1.564	Detected	0.994	Detected	1.279	0.053	GT Sens	contig100	contig100	Unknown
GT Sense	Sense	0.143	Detected	-0.143	Detected	0.000	1.526	Detected	1.230	Detected	1.378	0.021	GT Sens	contig100	contig100	Heat sho
GT Sense	Sense	-0.065	Detected	0.065	Detected	0.000	1.158	Detected	0.875	Detected	1.017	0.023	GT Sens	contig100	contig100	Unknown
GT Sense	Sense	-0.359	Detected	0.359	Detected	0.000	2.046	Detected	1.851	Detected	1.948	0.035	GT Sens	contig100	contig100	Cystathio
GT Sense	Sense	0.062	Detected	-0.062	Detected	0.000	1.427	Detected	2.328	Detected	1.878	0.054	GT Sens	contig100	contig100	Zinc-finge
GT Sense	Sense	-0.220	Detected	0.220	Detected	0.000	1.266	Detected	0.943	Detected	1.105	0.056	GT Sens	contig100	contig100	Programm
GT Sense	Sense	-0.003	Detected	0.003	Detected	0.000	1.229	Detected	0.971	Detected	1.100	0.013	GT Sens	contig101	contig101	Protein ty
GT Sense	Sense	0.602	Detected	-0.602	Detected	0.000	2.590	Detected	1.535	Detected	2.062	0.123	GT Sens	contig101	contig101	Unknown
GT Sense	Sense	-0.017	Detected	0.017	Detected	0.000	1.250	Detected	0.886	Detected	1.068	0.028	GT Sens	contig101	contig101	RING fing
GT Sense	Sense	-0.016	Detected	0.016	Detected	0.000	1.377	Detected	0.982	Detected	1.180	0.027	GT Sens	contig102	contig102	Cation ca
GT Sense	Sense	-0.128	Detected	0.128	Detected	0.000	1.877	Detected	1.072	Detected	1.475	0.073	GT Sens	contig102	contig102	Myb tran
GT Sense	Sense	0.024	Detected	-0.024	Detected	0.000	1.851	Detected	0.894	Detected	1.372	0.103	GT Sens	contig102	contig102	Multidrug
GT Sense	Sense	-0.287	Detected	0.287	Detected	0.000	1.689	Detected	1.677	Detected	1.683	0.028	GT Sens	contig102	contig102	Unknown
GT Sense	Sense	0.005	Detected	-0.005	Detected	0.000	1.212	Detected	0.808	Detected	1.010	0.038	GT Sens	contig103	contig103	Jp18 (AH
GT Sense	Sense	-0.324	Detected	0.324	Detected	0.000	1.431	Detected	1.157	Detected	1.294	0.067	GT Sens	contig103	contig103	Peptide tr
GT Sense	Sense	-0.262	Detected	0.262	Detected	0.000	1.668	Detected	1.444	Detected	1.556	0.032	GT Sens	contig103	contig103	Unknown
GT Sense	Sense	-0.139	Detected	0.139	Detected	0.000	1.498	Detected	0.935	Detected	1.216	0.061	GT Sens	contig103	contig103	Unknown
GT Sense	Sense	0.598	Detected	-0.598	Comprom	0.000	1.565	Detected	1.335	Detected	1.450	0.140	GT Sens	contig103	contig103	PAP fibril
GT Sense	Sense	0.004	Detected	-0.004	Detected	0.000	1.239	Detected	0.936	Detected	1.087	0.019	GT Sens	contig103	contig103	Unknown
GT Sense	Sense	0.443	Detected	-0.443	Detected	0.000	2.044	Detected	2.259	Detected	2.152	0.042	GT Sens	contig103	contig103	Unknown
GT Sense	Sense	-0.120	Detected	0.120	Detected	0.000	1.245	Detected	0.906	Detected	1.076	0.035	GT Sens	contig104	contig104	Uncharac
GT Sense	Sense	-0.064	Comprom	0.064	Comprom	0.000	2.275	Detected	1.973	Detected	2.124	0.006	GT Sens	contig104	contig104	Receptor-
GT Sense	Sense	0.182	Detected	-0.182	Detected	0.000	2.026	Detected	1.261	Detected	1.643	0.060	GT Sens	contig104	contig104	Unknown
GT Sense	Sense	0.040	Detected	-0.040	Detected	0.000	1.640	Detected	1.433	Detected	1.537	0.005	GT Sens	contig104	contig104	Unknown
GT Sense	Sense	-0.247	Comprom	0.247	Detected	0.000	1.404	Detected	1.089	Detected	1.247	0.051	GT Sens	contig104	contig104	Unknown
GT Sense	Sense	0.000	Comprom	0.000	Comprom	0.000	2.033	Detected	1.883	Detected	1.958	0.001	GT Sens	contig104	contig104	Unknown
GT Sense	Sense	0.323	Detected	-0.323	Detected	0.000	0.945	Detected	1.116	Detected	1.031	0.091	GT Sens	contig105	contig105	NAD(P)H-
GT Sense	Sense	0.290	Comprom	-0.290	Comprom	0.000	1.451	Detected	1.859	Detected	1.655	0.043	GT Sens	contig105	contig105	MADS-bo
GT Sense	Sense	-0.183	Detected	0.183	Detected	0.000	1.545	Detected	0.957	Detected	1.251	0.069	GT Sens	contig105	contig105	Kinase in
GT Sense	Sense	0.207	Comprom	-0.207	Comprom	0.000	2.174	Detected	2.171	Detected	2.172	0.009	GT Sens	contig105	contig105	Long-cha
GT Sense	Sense	-0.195	Detected	0.195	Detected	0.000	1.696	Detected	1.103	Detected	1.399	0.059	GT Sens	contig106	contig106	1-aminoc
GT Sense	Sense	-0.761	Detected	0.761	Detected	0.000	1.560	Detected	0.820	Detected	1.190	0.295	GT Sens	contig106	contig106	Fasciclin-
GT Sense	Sense	-0.002	Detected	0.002	Detected	0.000	1.033	Detected	1.663	Detected	1.348	0.051	GT Sens	contig106	contig106	Beta-gluc
GT Sense	Sense	-0.638	Comprom	0.638	Comprom	0.000	2.466	Detected	2.397	Detected	2.432	0.063	GT Sens	contig106	contig106	Aspartyl p
GT Sense	Sense	-0.047	Detected	0.047	Detected	0.000	1.127	Detected	0.922	Detected	1.025	0.012	GT Sens	contig106	contig106	ATP-depe
GT Sense	Sense	-0.233	Detected	0.233	Detected	0.000	1.904	Detected	1.101	Detected	1.503	0.084	GT Sens	contig106	contig106	Serine/thr
GT Sense	Sense	0.113	Detected	-0.113	Detected	0.000	1.443	Detected	0.973	Detected	1.208	0.044	GT Sens	contig106	contig106	Phycoery
GT Sense	Sense	-0.159	Detected	0.159	Detected	0.000	2.821	Detected	1.708	Detected	2.264	0.060	GT Sens	contig106	contig106	Cation dif
GT Sense	Sense	-0.355	Detected	0.355	Detected	0.000	2.925	Detected	2.909	Detected	2.917	0.015	GT Sens	contig107	contig107	Plant vira
GT Sense	Sense	-0.222	Detected	0.222	Detected	0.000	2.275	Detected	1.378	Detected	1.826	0.068	GT Sens	contig107	contig107	High affin
GT Sense	Sense	0.272	Detected	-0.272	Detected	0.000	2.303	Detected	1.668	Detected	1.986	0.042	GT Sens	contig108	contig108	MtN3-like
GT Sense	Sense	-0.129	Detected	0.129	Detected	0.000	1.826	Detected	1.423	Detected	1.625	0.021	GT Sens	contig109	contig109	Coenzym
GT Sense	Sense	0.230	Detected	-0.230	Detected	0.000	2.257	Detected	1.692	Detected	1.974	0.032	GT Sens	contig109	contig109	UPF0497
GT Sense	Sense	0.110	Detected	-0.110	Detected	0.000	1.472	Detected	1.313	Detected	1.393	0.009	GT Sens	contig109	contig109	Carbonyl
GT Sense	Sense	0.228	Detected	-0.228	Detected	0.000	1.104	Detected	0.907	Detected	1.006	0.056	GT Sens	contig109	contig109	Unknown
GT Sense	Sense	-0.170	Detected	0.170	Detected	0.000	1.493	Detected	1.126	Detected	1.310	0.035	GT Sens	contig109	contig109	Transduc
GT Sense	Sense	-0.793	Comprom	0.793	Detected	0.000	3.732	Detected	1.464	Detected	2.598	0.201	GT Sens	contig109	contig109	Receptor-
GT Sense	Sense	-0.452	Detected	0.452	Detected	0.000	1.735	Detected	1.023	Detected	1.379	0.139	GT Sens	contig110	contig110	Short inte
GT Sense	Sense	-0.199	Comprom	0.199	Comprom	0.000	1.543	Detected	1.132	Detected	1.338	0.043	GT Sens	contig110	contig110	Late emb
GT Sense	Sense	0.108	Detected	-0.108	Detected	0.000	1.269	Detected	0.928	Detected	1.099	0.032	GT Sens	contig110	contig110	F-box/kel
GT Sense	Sense	0.585	Detected	-0.585	Comprom	0.000	0.891	Detected	1.958	Detected	1.425	0.214	GT Sens	contig110	contig110	Unknown
GT Sense	Sense	0.313	Comprom	-0.313	Comprom	0.000	3.933	Detected	2.357	Detected	3.145	0.066	GT Sens	contig110	contig110	Glutared
GT Sense	Sense	-0.252	Detected	0.252	Detected	0.000	1.859	Detected	0.906	Detected	1.383	0.124	GT Sens	contig110	contig110	Interferor
GT Sense	Sense	-0.815	Detected	0.815	Detected	0.000	1.999	Detected	0.831	Detected	1.415	0.294	GT Sens	contig111	contig111	Unknown
GT Sense	Sense	-0.035	Detected	0.035	Detected	0.000	2.297	Detected	1.084	Detected	1.691	0.109	GT Sens	contig111	contig111	Unknown
GT Sense	Sense	-0.153	Detected	0.153	Detected	0.000	1.234	Detected	0.842	Detected	1.038	0.053	GT Sens	contig112	contig112	Dynamin-
GT Sense	Sense	0.995	Detected	-0.995	Comprom	0.000	4.040	Detected	2.771	Detected	3.406	0.102	GT Sens	contig112	contig112	Genomic
GT Sense	Sense	-0.123	Detected	0.123	Detected	0.000	2.373	Detected	2.178	Detected	2.275	0.005	GT Sens	contig112	contig112	EPF-type
GT Sense	Sense	-0.037	Detected	0.037	Detected	0.000	2.401	Detected	1.916	Detected	2.158	0.013	GT Sens	contig112	contig112	Gibberelli
GT Sense	Sense	0.059	Detected	-0.059	Detected	0.000	1.594	Detected	0.810	Detected	1.202	0.094	GT Sens	contig112	contig112	Microtub
GT Sense	Sense	-0.214	Detected	0.214	Detected	0.000	2.026	Detected	1.097	Detected	1.562	0.093	GT Sens	contig112	contig112	Unknown
GT Sense	Sense	-0.316	Detected	0.316	Detected	0.000	1.214	Detected	1.119	Detected	1.167	0.067	GT Sens	contig112	contig112	Pyruvate
GT Sense	Sense	-0.093	Detected	0.093	Detected	0.000	1.880	Detected	1.598	Detected	1.739	0.009	GT Sens	contig112	contig112	Chloroph
GT Sense	Sense	-0.231	Comprom	0.231	Comprom	0.000	3.629	Detected	2.614	Detected	3.121	0.030	GT Sens	contig112	contig112	F-box fan
GT Sense	Sense	0.301	Detected	-0.301	Detected	0.000	1.423	Detected	1.013	Detected	1.218	0.079	GT Sens	contig112	contig112	ATP-bind
GT Sense	Sense	0.260	Detected	-0.260	Detected	0.000	2.024	Detected	1.742	Detected	1.883	0.024	GT Sens	contig113	contig113	Apyrase
GT Sense	Sense	-0.287	Detected	0.287	Detected	0.000	1.638	Detected	1.363	Detected	1.500	0.042	GT Sens	contig113	contig113	Chloroph
GT Sense	Sense	-0.608	Comprom	0.608	Comprom	0.000	1.208	Detected	1.477	Detected	1.342	0.164	GT Sens	contig113	contig113	Pentatric
GT Sense	Sense	-0.083	Detected	0.083	Detected	0.000	1.839	Detected	1.060	Detected	1.450	0.068	GT Sens	contig114	contig114	Zinc finge
GT Sense	Sense	-0.375	Comprom	0.375	Comprom	0.000	0.944	Detected	1.356	Detected	1.150	0.115	GT Sens	contig114	contig114	Myb (AHF
GT Sense	Sense	0.652	Comprom	-0.652	Comprom	0.000	1.829	Detected	1.914	Detected	1.872	0.103	GT Sens	contig115	contig115	Ethylene-
GT Sense	Sense	0.044	Comprom	-0.044	Comprom	0.000	1.217	Detected	1.198	Detected	1.207	0.001	GT Sens	contig115	contig115	Unknown
GT Sense	Sense	0.196	Detected	-0.196	Detected	0.000	1.603	Detected	1.519	Detected	1.561	0.016	GT Sens	contig115	contig115	Cellulose
GT Sense	Sense	-0.413	Comprom	0.413	Detected	0.000	1.393	Detected	1.282	Detected	1.337	0.085	GT Sens	contig115	contig115	Oligopep
GT Sense	Sense	-0.624	Comprom	0.624	Comprom	0.000	0.977	Detected	1.424	Detected	1.201	0.212	GT Sens	contig115	contig115	Gag-Pol p
GT Sense	Sense	-0.793	Detected	0.793	Detected	0.000	2.851	Detected	1.905	Detected	2.378	0.123	GT Sens	contig115	contig115	Calcium i
GT Sense	Sense	-0.092	Detected	0.092	Detected	0.000	2.335	Detected	1.578	Detected	1.956	0.037	GT Sens	contig115	contig115	Conserve
GT Sense	Sense	-0.209	Detected	0.209	Detected	0.000	1.093	Detected	1.006	Detected	1.050	0.039	GT Sens	contig116	contig116	photosys
GT Sense	Sense	0.252	Comprom	-0.252	Comprom	0.000	1.124	Detected	1.438	Detected	1.281	0.050	GT Sens	contig116	contig116	AT5g069
GT Sense	Sense	0.462	Detected	-0.462	Comprom	0.000	0.944	Detected	1.845	Detected	1.394	0.163	GT Sens	contig116	contig116	BEL1-like
GT Sense	Sense	-0.150	Detected	0.150	Detected	0.000	1.955	Detected	1.233	Detected	1.594	0.055	GT Sens	contig116	contig116	Transcrip
GT Sense	Sense	-0.391	Detected	0.391	Detected	0.000	1.432	Detected	2.536	Detected	1.984	0.099	GT Sens	contig117	contig117	Unknown
GT Sense	Sense	-0.008	Detected	0.008	Detected	0.000	1.689	Detected	1.074	Detected	1.381	0.046	GT Sens	contig117	contig117	Respons
GT Sense	Sense	-0.208	Detected	0.208	Detected	0.000	1.166	Detected	1.041	Detected	1.104	0.037	GT Sens	contig117	contig117	Late elon
GT Sense	Sense	-0.067	Detected	0.067	Detected	0.000	1.101	Detected	0.980	Detected	1.040	0.007	GT Sens	contig117	contig117	Mitochon
GT Sense	Sense	-0.106	Detected	0.106	Detected	0.000	1.057	Detected	1.135	Detected	1.096	0.011	GT Sens	contig117	contig117	Copper c
GT Sense	Sense	0.644	Detected	-0.644	Detected	0.000	3.185	Detected	2.310	Detected	2.748	0.072	GT Sens	contig117	contig117	Patatin-lik
GT Sense	Sense	-0.130	Comprom	0.130	Comprom	0.000	1.323	Detected	1.561	Detected	1.442	0.015	GT Sens	contig117	contig117	Unknown
GT Sense	Sense	-0.124	Detected	0.124	Detected	0.000	2.597	Detected	0.872	Detected	1.735	0.185	GT Sens	contig117	contig117	Sodium/c
GT Sense	Sense	-0.457	Detected	0.457	Detected	0.000	2.556	Detected	1.976	Detected	2.266	0.053	GT Sens	contig118	contig118	Auxin res
GT Sense	Sense	0.116	Detected	-0.116	Detected	0.000	1.553	Detected	1.703	Detected	1.628	0.007	GT Sens	contig118	contig118	HAT famil
GT Sense	Sense	0.115	Detected	-0.115	Detected	0.000	1.708	Detected	1.075	Detected	1.392	0.054	GT Sens	contig118	contig118	Peptidyl-
GT Sense	Sense	-0.155	Detected	0.155	Detected	0.000	1.218	Detected	0.868	Detected	1.043	0.047	GT Sens	contig119	contig119	Auxin-ind
GT Sense	Sense	0.046	Detected	-0.046	Detected	0.000	1.194	Detected	1.017	Detected	1.105	0.008	GT Sens	contig119	contig119	Inactivate
GT Sense	Sense	-0.268	Detected	0.268	Detected	0.000	1.277	Detected	1.350	Detected	1.314	0.040	GT Sens	contig119	contig119	E3 ubiqui
GT Sense	Sense	-0.673	Detected	0.673	Detected	0.000	2.102	Detected	1.301	Detected	1.701	0.162	GT Sens	contig119	contig119	Unknown
GT Sense	Sense	-0.279	Comprom	0.279	Comprom	0.000	2.033	Detected	2.802	Detected	2.417	0.037	GT Sens	contig119	contig119	Unknown
GT Sense	Sense	0.672	Detected	-0.672	Comprom	0.000	1.439	Detected	1.643	Detected	1.541	0.151	GT Sens	contig119	contig119	Mutator-li
GT Sense	Sense	-0.034	Detected	0.034	Detected	0.000	1.824	Detected	0.884	Detected	1.354	0.103	GT Sens	contig119	contig119	Cinnamo
GT Sense	Sense	-0.522	Comprom	0.522	Comprom	0.000	1.562	Detected	5.185	Detected	3.374	0.215	GT Sens	contig121	contig121	Flavopro
GT Sense	Sense	0.587	Detected	-0.587	Detected	0.000	2.665	Detected	1.627	Detected	2.146	0.111	GT Sens	contig121	contig121	Unknown
GT Sense	Sense	0.163	Detected	-0.163	Detected	0.000	2.219	Detected	2.254	Detected	2.236	0.005	GT Sens	contig122	contig122	BTB/POZ
GT Sense	Sense	-0.062	Comprom	0.062	Comprom	0.000	2.957	Detected	2.272	Detected	2.614	0.017	GT Sens	contig122	contig122	Germin-li
GT Sense	Sense	-0.270	Detected	0.270	Detected	0.000	2.059	Detected	1.523	Detected	1.791	0.042	GT Sens	contig122	contig122	Disease r
GT Sense	Sense	0.096	Detected	-0.096	Comprom	0.000	2.502	Detected	1.776	Detected	2.139	0.029	GT Sens	contig122	contig122	cDNA clo
GT Sense	Sense	-0.158	Detected	0.158	Detected	0.000	1.084	Detected	1.283	Detected	1.184	0.024	GT Sens	contig123	contig123	Os01g04
GT Sense	Sense	-0.333	Detected	0.333	Detected	0.000	1.880	Detected	2.247	Detected	2.064	0.032	GT Sens	contig123	contig123	Nodulin-li
GT Sense	Sense	0.179	Detected	-0.179	Detected	0.000	2.203	Detected	1.825	Detected	2.014	0.016	GT Sens	contig123	contig123	Cellulose
GT Sense	Sense	-0.353	Detected	0.353	Detected	0.000	1.346	Detected	1.567	Detected	1.456	0.059	GT Sens	contig123	contig123	Myb famil
GT Sense	Sense	-0.314	Detected	0.314	Detected	0.000	2.675	Detected	1.220	Detected	1.947	0.133	GT Sens	contig123	contig123	Histidine
GT Sense	Sense	0.274	Detected	-0.274	Detected	0.000	1.100	Detected	0.953	Detected	1.026	0.068	GT Sens	contig123	contig123	Binding p
GT Sense	Sense	-0.101	Comprom	0.101	Comprom	0.000	2.430	Detected	1.513	Detected	1.972	0.052	GT Sens	contig123	contig123	Transcrip
GT Sense	Sense	-0.512	Detected	0.512	Detected	0.000	1.496	Detected	1.410	Detected	1.453	0.106	GT Sens	contig123	contig123	MADS bo
GT Sense	Sense	-0.079	Detected	0.079	Detected	0.000	1.397	Detected	1.029	Detected	1.213	0.026	GT Sens	contig124	contig124	EPIDERM
GT Sense	Sense	-0.226	Comprom	0.226	Comprom	0.000	1.635	Detected	1.622	Detected	1.629	0.019	GT Sens	contig124	contig124	MADS-bo
GT Sense	Sense	-0.165	Detected	0.165	Detected	0.000	1.129	Detected	1.073	Detected	1.101	0.022	GT Sens	contig124	contig124	Unknown
GT Sense	Sense	-0.068	Detected	0.068	Detected	0.000	1.340	Detected	1.315	Detected	1.328	0.003	GT Sens	contig124	contig124	Unknown
GT Sense	Sense	0.141	Detected	-0.141	Detected	0.000	1.941	Detected	0.902	Detected	1.422	0.118	GT Sens	contig125	contig125	Cytochro
GT Sense	Sense	-0.094	Detected	0.094	Detected	0.000	1.402	Detected	0.857	Detected	1.130	0.059	GT Sens	contig125	contig125	Growth-r
GT Sense	Sense	0.420	Comprom	-0.420	Comprom	0.000	4.596	Detected	2.343	Detected	3.469	0.102	GT Sens	contig125	contig125	BHLH tra
GT Sense	Sense	-0.826	Comprom	0.826	Comprom	0.000	1.203	Detected	1.704	Detected	1.454	0.234	GT Sens	contig125	contig125	Unknown
GT Sense	Sense	0.159	Detected	-0.159	Detected	0.000	1.846	Detected	1.018	Detected	1.432	0.084	GT Sens	contig125	contig125	Dof zinc f
GT Sense	Sense	-0.101	Comprom	0.101	Comprom	0.000	1.980	Detected	1.782	Detected	1.881	0.006	GT Sens	contig125	contig125	Os03g02

GT	Sens	Sense	-0.648	Comprom	0.648	Detected	0.000	1.571	Detected	1.207	Detected	1.389	0.175	GT	Sens	contig125	contig125	Acidic ch	ATAGCA
GT	Sens	Sense	-0.217	Detected	0.217	Detected	0.000	1.169	Detected	1.048	Detected	1.108	0.039	GT	Sens	contig125	contig125	Ubiquitin-	TAAAGA
GT	Sens	Sense	0.026	Detected	-0.026	Detected	0.000	0.997	Detected	1.011	Detected	1.004	0.001	GT	Sens	contig125	contig125	Reverse t	GTCCGG
GT	Sens	Sense	-0.685	Comprom	0.685	Comprom	0.000	1.499	Detected	1.492	Detected	1.495	0.161	GT	Sens	contig126	contig126	CER1 pro	ATAAAC
GT	Sens	Sense	-0.225	Detected	0.225	Detected	0.000	1.349	Detected	1.082	Detected	1.216	0.043	GT	Sens	contig126	contig126	Chaperon	CTGACG
GT	Sens	Sense	-0.216	Detected	0.216	Detected	0.000	1.539	Detected	1.233	Detected	1.386	0.035	GT	Sens	contig126	contig126	C2H2L do	TTGGAG
GT	Sens	Sense	-0.305	Detected	0.305	Detected	0.000	1.396	Detected	0.866	Detected	1.131	0.108	GT	Sens	contig127	contig127	Glutathio	CGTGTA
GT	Sens	Sense	-0.074	Detected	0.074	Detected	0.000	1.295	Detected	0.942	Detected	1.119	0.028	GT	Sens	contig127	contig127	Dehydrog	ACCAAT
GT	Sens	Sense	-0.316	Detected	0.316	Detected	0.000	2.074	Detected	1.215	Detected	1.644	0.091	GT	Sens	contig127	contig127	Glycine-ri	ATTGGA
GT	Sens	Sense	-0.349	Detected	0.349	Detected	0.000	3.298	Detected	2.245	Detected	2.772	0.048	GT	Sens	contig127	contig127	Acyl-CoA	GTAAAG
GT	Sens	Sense	0.348	Detected	-0.348	Detected	0.000	3.009	Detected	2.115	Detected	2.562	0.046	GT	Sens	contig128	contig128	Beta-Amy	TTGGTG
GT	Sens	Sense	0.025	Comprom	-0.025	Comprom	0.000	1.070	Detected	1.180	Detected	1.125	0.003	GT	Sens	contig128	contig128	Unknown	TCGTAC
GT	Sens	Sense	0.707	Comprom	-0.707	Comprom	0.000	3.152	Detected	1.788	Detected	2.470	0.129	GT	Sens	contig128	contig128	Heat stres	AGAGGA
GT	Sens	Sense	0.539	Comprom	-0.539	Comprom	0.000	1.607	Detected	1.980	Detected	1.793	0.088	GT	Sens	contig128	contig128	Gibberelli	GCTGTT
GT	Sens	Sense	0.240	Detected	-0.240	Detected	0.000	1.463	Detected	1.509	Detected	1.486	0.025	GT	Sens	contig129	contig129	Ulp1 prot	TAAAAA
GT	Sens	Sense	-0.851	Comprom	0.851	Detected	0.000	1.847	Detected	2.189	Detected	2.018	0.146	GT	Sens	contig129	contig129	Unknown	CGTGAA
GT	Sens	Sense	-0.045	Detected	0.045	Detected	0.000	1.118	Detected	0.971	Detected	1.045	0.007	GT	Sens	contig129	contig129	Unknown	CAAAAT
GT	Sens	Sense	0.283	Comprom	-0.283	Comprom	0.000	1.713	Detected	1.562	Detected	1.637	0.031	GT	Sens	contig129	contig129	Unknown	ATGCAA
GT	Sens	Sense	-0.221	Comprom	0.221	Comprom	0.000	2.641	Detected	2.218	Detected	2.430	0.015	GT	Sens	contig129	contig129	Wax synt	TTTATG
GT	Sens	Sense	-0.580	Comprom	0.580	Detected	0.000	1.272	Detected	1.032	Detected	1.152	0.191	GT	Sens	contig129	contig129	Cyclin B-l	ACACTG
GT	Sens	Sense	-0.860	Comprom	0.860	Comprom	0.000	5.541	Detected	5.337	Detected	5.439	0.024	GT	Sens	contig129	contig129	Plant-spe	GGGGAT
GT	Sens	Sense	0.186	Detected	-0.186	Detected	0.000	1.470	Detected	1.287	Detected	1.378	0.022	GT	Sens	contig129	contig129	Senescen	ATCTGG
GT	Sens	Sense	0.777	Comprom	-0.777	Comprom	0.000	1.674	Detected	1.555	Detected	1.614	0.174	GT	Sens	contig129	contig129	Gag non-	TCTTCA
GT	Sens	Sense	0.135	Detected	-0.135	Detected	0.000	2.002	Detected	1.737	Detected	1.870	0.010	GT	Sens	contig130	contig130	Myb-relat	GGAGGG
GT	Sens	Sense	0.314	Detected	-0.314	Detected	0.000	2.776	Detected	1.852	Detected	2.314	0.054	GT	Sens	contig130	contig130	Peptide tr	GCTGCC
GT	Sens	Sense	0.584	Detected	-0.584	Comprom	0.000	1.758	Detected	1.916	Detected	1.837	0.089	GT	Sens	contig130	contig130	Oxalate o	AATTCA
GT	Sens	Sense	-0.135	Comprom	0.135	Comprom	0.000	1.690	Detected	1.177	Detected	1.434	0.038	GT	Sens	contig130	contig130	Genomic	TAAGCC
GT	Sens	Sense	-0.318	Comprom	0.318	Comprom	0.000	1.247	Detected	1.003	Detected	1.125	0.081	GT	Sens	contig130	contig130	Cathepsi	AATGCA
GT	Sens	Sense	-0.358	Detected	0.358	Detected	0.000	2.094	Detected	1.665	Detected	1.879	0.046	GT	Sens	contig130	contig130	Ch-cobra	TTTCAA
GT	Sens	Sense	-0.032	Detected	0.032	Detected	0.000	1.600	Detected	1.032	Detected	1.316	0.044	GT	Sens	contig130	contig130	1-aminoc	TGCCAC
GT	Sens	Sense	0.282	Detected	-0.282	Detected	0.000	2.325	Detected	1.367	Detected	1.846	0.080	GT	Sens	contig131	contig131	Kunitz try	CTTGCA
GT	Sens	Sense	-0.208	Detected	0.208	Detected	0.000	1.665	Detected	1.360	Detected	1.513	0.028	GT	Sens	contig131	contig131	GDU1 (AH	GTCTCG
GT	Sens	Sense	0.072	Detected	-0.072	Detected	0.000	0.894	Detected	1.215	Detected	1.055	0.027	GT	Sens	contig132	contig132	GIGANTE	GCTGAT
GT	Sens	Sense	-0.200	Detected	0.200	Detected	0.000	1.427	Detected	1.123	Detected	1.275	0.037	GT	Sens	contig132	contig132	Ribonucle	GAAGAC
GT	Sens	Sense	-0.224	Detected	0.224	Detected	0.000	1.356	Detected	0.914	Detected	1.135	0.069	GT	Sens	contig132	contig132	Thioredo	AATCCA
GT	Sens	Sense	0.184	Comprom	-0.184	Comprom	0.000	1.920	Detected	3.320	Detected	2.620	0.069	GT	Sens	contig132	contig132	Dihydrofl	ACTGCA
GT	Sens	Sense	-0.056	Detected	0.056	Detected	0.000	3.676	Detected	2.934	Detected	3.305	0.013	GT	Sens	contig132	contig132	Unknown	ACAAAT
GT	Sens	Sense	-0.562	Comprom	0.562	Detected	0.000	1.139	Detected	1.033	Detected	1.086	0.194	GT	Sens	contig132	contig132	Unknown	CCTCGA
GT	Sens	Sense	0.067	Detected	-0.067	Detected	0.000	1.195	Detected	1.316	Detected	1.255	0.005	GT	Sens	contig133	contig133	MADS-bo	TGAAAG
GT	Sens	Sense	-0.249	Detected	0.249	Detected	0.000	1.143	Detected	1.051	Detected	1.097	0.049	GT	Sens	contig133	contig133	Hv711N16	TGCTTA
GT	Sens	Sense	0.028	Detected	-0.028	Detected	0.000	3.827	Detected	1.922	Detected	2.874	0.095	GT	Sens	contig133	contig133	Os07g06	AGGGTT
GT	Sens	Sense	0.190	Detected	-0.190	Detected	0.000	1.262	Detected	0.923	Detected	1.092	0.050	GT	Sens	contig133	contig133	Glucan en	ACAGAT
GT	Sens	Sense	1.031	Detected	-1.031	Comprom	0.000	2.218	Detected	1.720	Detected	1.969	0.205	GT	Sens	contig134	contig134	Zinc trans	CATAGT
GT	Sens	Sense	0.060	Detected	-0.060	Detected	0.000	1.785	Detected	1.255	Detected	1.520	0.031	GT	Sens	contig134	contig134	DNA prim	CCGAAA
GT	Sens	Sense	0.173	Detected	-0.173	Detected	0.000	1.692	Detected	1.303	Detected	1.497	0.029	GT	Sens	contig134	contig134	BEL1-like	CCAAAA
GT	Sens	Sense	-0.200	Detected	0.200	Detected	0.000	1.144	Detected	1.058	Detected	1.101	0.033	GT	Sens	contig135	contig135	Unknown	AATTCA
GT	Sens	Sense	-0.717	Comprom	0.717	Detected	0.000	1.614	Detected	1.271	Detected	1.442	0.189	GT	Sens	contig135	contig135	Phototrop	AAGAAA
GT	Sens	Sense	-0.397	Detected	0.397	Detected	0.000	1.541	Detected	1.515	Detected	1.528	0.061	GT	Sens	contig135	contig135	BZIP tran	CCTTTG
GT	Sens	Sense	-0.103	Comprom	0.103	Comprom	0.000	1.567	Detected	1.964	Detected	1.765	0.016	GT	Sens	contig135	contig135	Ring H2 fi	ATATCA
GT	Sens	Sense	0.050	Detected	-0.050	Detected	0.000	1.687	Detected	1.049	Detected	1.368	0.051	GT	Sens	contig135	contig135	Genome s	ATTCTT
GT	Sens	Sense	0.057	Detected	-0.057	Detected	0.000	1.855	Detected	1.136	Detected	1.496	0.055	GT	Sens	contig135	contig135	Lipase (F	GATATT
GT	Sens	Sense	-0.192	Detected	0.192	Detected	0.000	1.217	Detected	0.959	Detected	1.088	0.042	GT	Sens	contig135	contig135	Transcrip	TACTGC
GT	Sens	Sense	-0.309	Comprom	0.309	Comprom	0.000	2.952	Detected	3.534	Detected	3.243	0.017	GT	Sens	contig136	contig136	Receptor-	ATTGAT
GT	Sens	Sense	-0.125	Comprom	0.125	Comprom	0.000	1.651	Detected	1.271	Detected	1.461	0.023	GT	Sens	contig136	contig136	Unknown	AGAAGA
GT	Sens	Sense	-0.564	Detected	0.564	Detected	0.000	1.476	Detected	1.125	Detected	1.301	0.159	GT	Sens	contig137	contig137	Protein T	GGTTCT
GT	Sens	Sense	0.004	Comprom	-0.004	Comprom	0.000	5.012	Detected	5.238	Detected	5.125	0.000	GT	Sens	contig137	contig137	Beta-1 3-	TACTTA
GT	Sens	Sense	0.189	Detected	-0.189	Detected	0.000	2.956	Detected	1.989	Detected	2.472	0.041	GT	Sens	contig137	contig137	GDSL est	CACTGA
GT	Sens	Sense	-0.677	Detected	0.677	Detected	0.000	2.475	Detected	2.067	Detected	2.271	0.085	GT	Sens	contig137	contig137	Squamos	TCCATT
GT	Sens	Sense	-0.243	Comprom	0.243	Comprom	0.000	2.372	Detected	2.099	Detected	2.236	0.015	GT	Sens	contig137	contig137	Reverse t	CCCATT
GT	Sens	Sense	0.096	Detected	-0.096	Detected	0.000	1.230	Detected	0.929	Detected	1.079	0.026	GT	Sens	contig137	contig137	Unknown	GCAAAT
GT	Sens	Sense	-1.253	Comprom	1.253	Detected	0.000	2.639	Detected	1.243	Detected	1.941	0.309	GT	Sens	contig137	contig137	Cyclin-de	TTGGAG
GT	Sens	Sense	0.160	Detected	-0.160	Comprom	0.000	1.331	Detected	1.236	Detected	1.284	0.016	GT	Sens	contig138	contig138	Unknown	TTAGGA
GT	Sens	Sense	0.044	Detected	-0.044	Detected	0.000	0.984	Detected	1.157	Detected	1.071	0.008	GT	Sens	contig138	contig138	Unknown	TGCAAG
GT	Sens	Sense	0.031	Detected	-0.031	Detected	0.000	2.216	Detected	1.732	Detected	1.974	0.015	GT	Sens	contig138	contig138	cDNA clo	TCTATA
GT	Sens	Sense	-0.481	Detected	0.481	Detected	0.000	3.094	Detected	2.292	Detected	2.693	0.050	GT	Sens	contig138	contig138	Unknown	CAAGCA
GT	Sens	Sense	-0.561	Comprom	0.561	Comprom	0.000	1.583	Detected	2.179	Detected	1.881	0.098	GT	Sens	contig138	contig138	Ripening-	TATATC
GT	Sens	Sense	-0.498	Detected	0.498	Detected	0.000	1.499	Detected	1.153	Detected	1.326	0.128	GT	Sens	contig139	contig139	Peptide tr	TGTAAT
GT	Sens	Sense	-0.334	Detected	0.334	Detected	0.000	1.177	Detected	0.966	Detected	1.071	0.092	GT	Sens	contig139	contig139	Mate efflu	AGATTA
GT	Sens	Sense	0.467	Detected	-0.467	Comprom	0.000	1.034	Detected	1.708	Detected	1.371	0.140	GT	Sens	contig140	contig140	Epoxide h	GCTAGA
GT	Sens	Sense	0.006	Detected	-0.006	Detected	0.000	4.178	Detected	3.089	Detected	3.634	0.022	GT	Sens	contig140	contig140	Unknown	GAAACT
GT	Sens	Sense	0.537	Comprom	-0.537	Comprom	0.000	2.818	Detected	1.659	Detected	2.239	0.105	GT	Sens	contig140	contig140	Ulp1 prot	GAGAAG
GT	Sens	Sense	-0.153	Detected	0.153	Detected	0.000	3.195	Detected	1.685	Detected	2.440	0.087	GT	Sens	contig140	contig140	Unknown	GTTTGC
GT	Sens	Sense	-0.022	Detected	0.022	Detected	0.000	2.169	Detected	2.097	Detected	2.133	0.000	GT	Sens	contig140	contig140	Dihydrofl	GGGATG
GT	Sens	Sense	-0.124	Detected	0.124	Detected	0.000	2.134	Detected	1.459	Detected	1.796	0.038	GT	Sens	contig141	contig141	Polygalac	TCTGAA
GT	Sens	Sense	-0.340	Detected	0.340	Detected	0.000	1.983	Detected	1.629	Detected	1.806	0.042	GT	Sens	contig141	contig141	Methanol	ATAGGT
GT	Sens	Sense	0.192	Detected	-0.192	Detected	0.000	0.926	Detected	1.267	Detected	1.096	0.051	GT	Sens	contig141	contig141	Glucan en	AAGCAT
GT	Sens	Sense	-0.029	Detected	0.029	Detected	0.000	1.246	Detected	0.881	Detected	1.063	0.029	GT	Sens	contig141	contig141	Glucan en	ATGCTT
GT	Sens	Sense	0.171	Detected	-0.171	Detected	0.000	1.810	Detected	1.108	Detected	1.459	0.065	GT	Sens	contig142	contig142	ABC trans	GTTGCA
GT	Sens	Sense	-0.185	Detected	0.185	Detected	0.000	1.404	Detected	1.076	Detected	1.240	0.038	GT	Sens	contig142	contig142	Unknown	ATAATG
GT	Sens	Sense	-0.333	Detected	0.333	Detected	0.000	2.169	Detected	1.763	Detected	1.966	0.037	GT	Sens	contig142	contig142	Ring fing	CTCCCT
GT	Sens	Sense	0.025	Detected	-0.025	Detected	0.000	2.675	Detected	3.083	Detected	2.879	0.005	GT	Sens	contig142	contig142	BZIP tran	ATTTGA
GT	Sens	Sense	0.126	Detected	-0.126	Detected	0.000	1.555	Detected	0.916	Detected	1.235	0.069	GT	Sens	contig142	contig142	Unknown	ATACAG
GT	Sens	Sense	-0.080	Detected	0.080	Detected	0.000	1.651	Detected	0.948	Detected	1.300	0.069	GT	Sens	contig142	contig142	Peptidase	AAAGGA
GT	Sens	Sense	-0.940	Comprom	0.940	Comprom	0.000	1.652	Detected	1.495	Detected	1.573	0.237	GT	Sens	contig142	contig142	Os01g07	AAGAGA
GT	Sens	Sense	-0.048	Detected	0.048	Detected	0.000	1.175	Detected	1.022	Detected	1.098	0.007	GT	Sens	contig143	contig143	Alpha-tax	AAACAG
GT	Sens	Sense	0.081	Detected	-0.081	Detected	0.000	1.138	Detected	1.106	Detected	1.122	0.005	GT	Sens	contig143	contig143	BHLH tra	TGAGGA
GT	Sens	Sense	-0.066	Detected	0.066	Detected	0.000	1.146	Detected	1.173	Detected	1.159	0.003	GT	Sens	contig143	contig143	Unknown	ATGATA
GT	Sens	Sense	0.099	Detected	-0.099	Detected	0.000	2.063	Detected	1.310	Detected	1.687	0.049	GT	Sens	contig143	contig143	Peptidyl-p	CCTCCA
GT	Sens	Sense	0.255	Comprom	-0.255	Comprom	0.000	1.726	Detected	1.685	Detected	1.705	0.022	GT	Sens	contig144	contig144	Ulp1 prot	GTTCTT
GT	Sens	Sense	0.230	Detected	-0.230	Detected	0.000	1.518	Detected	1.013	Detected	1.265	0.066	GT	Sens	contig144	contig144	Stress res	GAAGAC
GT	Sens	Sense	0.245	Comprom	-0.245	Comprom	0.000	2.890	Detected	2.359	Detected	2.624	0.018	GT	Sens	contig144	contig144	Inositol 1	ATTCTG
GT	Sens	Sense	-0.259	Detected	0.259	Detected	0.000	1.210	Detected	0.843	Detected	1.027	0.084	GT	Sens	contig144	contig144	Serine ca	GGAAGA
GT	Sens	Sense	0.163	Detected	-0.163	Detected	0.000	2.896	Detected	3.043	Detected	2.970	0.004	GT	Sens	contig144	contig144	Ulp1 prot	AGTATT
GT	Sens	Sense	-0.008	Detected	0.008	Detected	0.000	1.248	Detected	1.279	Detected	1.263	0.000	GT	Sens	contig144	contig144	Pseudo re	AAATGT
GT	Sens	Sense	-0.636	Comprom	0.636	Detected	0.000	1.129	Detected	1.603	Detected	1.366	0.182	GT	Sens	contig144	contig144	Ethylene	CCCAGA
GT	Sens	Sense	0.157	Detected	-0.157	Detected	0.000	1.704	Detected	1.424	Detected	1.564	0.018	GT	Sens	contig144	contig144	Unknown	CCAGGA
GT	Sens	Sense	-0.120	Detected	0.120	Detected	0.000	1.082	Detected	0.963	Detected	1.023	0.017	GT	Sens	contig145	contig145	Peptidase	ACACTG
GT	Sens	Sense	-0.017	Detected	0.017	Detected	0.000	1.860	Detected	0.969	Detected	1.415	0.087	GT	Sens	contig145	contig145	Unknown	GCAGAA
GT	Sens	Sense	0.259	Detected	-0.259	Detected	0.000	1.704	Detected	0.900	Detected	1.302	0.113	GT	Sens	contig146	contig146	Unknown	CAAGTC
GT	Sens	Sense	-0.131	Detected	0.131	Detected	0.000	1.039	Detected	1.031	Detected	1.035	0.016	GT	Sens	contig146	contig146	Palmitoyl	TTTTTT
GT	Sens	Sense	-0.098	Detected	0.098	Detected	0.000	1.010	Detected	1.030	Detected	1.020	0.009	GT	Sens	contig146	contig146	Oxidored	ATTGTG
GT	Sens	Sense	0.662	Detected	-0.662	Detected	0.000	2.756	Detected	1.421	Detected	2.088	0.156	GT	Sens	contig146	contig146	Metalloca	TGTTGG
GT	Sens	Sense	0.060	Detected	-0.060	Detected	0.000	1.448	Detected	0.994	Detected	1.221	0.035	GT	Sens	contig146	contig146	Proton an	TTGTTG
GT	Sens	Sense	-0.060	Detected	0.060	Detected	0.000	1.095	Detected	0.950	Detected	1.022	0.008	GT	Sens	contig146	contig146	Serine/thr	TGCGTG
GT	Sens	Sense	0.195	Detected	-0.195	Detected	0.000	1.272	Detected	0.805	Detected	1.039	0.076	GT	Sens	contig146	contig146	RING fing	GATACA
GT	Sens	Sense	0.550	Detected	-0.550	Detected	0.000	0.919	Detected	2.380	Detected	1.650	0.213	GT	Sens	contig147	contig147	Lipoxyge	GAGCTG
GT	Sens	Sense	-0.432	Comprom	0.432	Comprom	0.000	1.925	Detected	1.623	Detected	1.774	0.060	GT	Sens	contig147	contig147	Glutathio	AGTTTA
GT	Sens	Sense	-0.002	Detected	0.002	Detected	0.000	1.179	Detected	0.946	Detected	1.063	0.012	GT	Sens	contig147	contig147	Unknown	CCATGA
GT	Sens	Sense	-0.143	Detected	0.143	Detected	0.000	2.437	Detected	1.620	Detected	2.029	0.043	GT	Sens	contig148	contig148	Heat shoc	CAAATG
GT	Sens	Sense	-0.252	Detected	0.252	Detected	0.000	1.179	Detected	1.189	Detected	1.184	0.042	GT	Sens	contig148	contig148	Unknown	ACACTT
GT	Sens	Sense	-0.324	Detected	0.324	Detected	0.000	1.655	Detected	1.051	Detected	1.353	0.093	GT	Sens	contig148	contig148	Unknown	TGGCAA
GT	Sens	Sense	-0.240	Detected	0.240	Detected	0.000	0.933	Detected	1.305	Detected	1.119	0.066	GT	Sens	contig148	contig148	Mutator-li	ACAGCC
GT	Sens	Sense	0.329	Detected	-0.329	Detected	0.000	3.377	Detected	2.171	Detected	2.774	0.056	GT	Sens	contig148	contig148	Glutaredo	GAGTTT
GT	Sens	Sense	-0.462	Detected	0.462	Detected	0.000	1.011	Detected	1.028	Detected	1.019	0.158	GT	Sens	contig149	contig149	Blue copp	AGGTCA
GT	Sens	Sense	-0.148	Detected	0.148	Detected	0.000	1.808	Detected	1.174	Detected	1.491	0.051	GT	Sens	contig149	contig149	Primary a	ACAGGG
GT	Sens	Sense	-0.317	Comprom	0.317	Comprom	0.000	1.989	Detected	1.742	Detected	1.865	0.032	GT	Sens	contig149	contig149	B-like cyc	AGTTCA
GT	Sens	Sense	0.095	Comprom	-0.095	Comprom	0.000	1.631	Detected	0.949	Detected	1.290	0.068	GT	Sens	contig150	contig150	Receptor-	CTAGTT
GT	Sens	Sense	-0.190	Detected	0.190	Detected	0.000	1.290	Detected	1.002	Detected	1.146	0.041	GT	Sens	contig150	contig150	Serine/thr	TCCAAC
GT	Sens	Sense	0.090	Detected	-0.090	Detected	0.000	2.646	Detected	1.793	Detected	2.219	0.036	GT	Sens	contig150	contig150	Pre-mRNA	GCGGAC
GT	Sens	Sense	0.104	Detected	-0.104	Detected	0.000	1.986	Detected	1.390	Detected	1.688	0.033	GT	Sens	contig150	contig150	Exostosin	ATATAT
GT	Sens	Sense	0.134	Detected	-0.134	Detected	0.000	1.664	Detected	1.571	Detected	1.617	0.008	GT	Sens	contig151	contig151	Dehydrog	AGGGTC
GT	Sens	Sense	0.015	Detected	-0.015	Detected	0.000	1.346	Detected	1.252	Detected	1.299	0.001	GT	Sens	contig151	contig151	Acetyltran	CTACTC
GT	Sens	Sense	-0.211	Detected	0.211	Detected	0.000	1.405	Detected	1.170	Detected	1.287	0.033	GT	Sens	contig151	contig151	Cystine tr	AAATCA
GT	Sens	Sense	-0.146	Detected	0.146	Detected	0.000	2.347	Detected	1.795	Detected	2.071	0.022	GT	Sens	contig151	contig151	LOB dom	ATCCTA
GT	Sens	Sense	-0.150	Detected	0.150	Detected	0.000	1.606	Detected	1.013	Detected	1.309	0.059	GT	Sens	contig152	contig152	Acetyl-co	GCTGCT
GT	Sens	Sense	-0.188	Detected	0.188	Detected	0.000	1.086	Detected	1.148	Detected	1.117	0.028	GT	Sens	contig152	contig152	Homolog	AATGAT
GT	Sens	Sense	-0.043	Detected	0.043	Detected	0.000	2.912	Detected	2.016	Detected	2.464	0.032	GT	Sens	contig152	contig152	EPIDERM	ATGGCT
GT	Sens	Sense	0.183	Detected	-0.183	Detected	0.000	3.131	Detected	1.936	Detected	2.533	0.056	GT	Sens	contig153	contig153	Formamid	AGGTCA
GT	Sens	Sense	-0.276	Detected	0.276	Detected	0.000	2.259	Detected	1.720	Detected	1.990	0.036	GT	Sens	contig153	contig153	MYB tran	GAGACT
GT	Sens	Sense	0.050	Detected	-0.050	Comprom	0.000	2.873	Detected	2.025	Detected	2.449	0.029	GT	Sens	contig153	contig153	Spermidi	TTCTTC
GT	Sens	Sense	0.206	Comprom	-0.206	Comprom	0.000	1.521	Detected	2.520	Detected	2.021	0.065	GT	Sens	contig154	contig154	Unknown	ATTGAA
GT	Sens	Sense	-0.104	Detected	0.104	Detected	0.000	3.642	Detected	2.039	Detected	2.841	0.072	GT	Sens	contig154	contig154	MtN3-like	CGCAAA
GT	Sens	Sense	0.865	Detected	-0.865	Detected	0.000	3.366	Detected	2.079	Detected	2.722	0.128	GT	Sens	contig154	contig154	Proteinas	ATGATT
GT	Sens	Sense	0.111	Detected	-0.111	Detected	0.000	1.634	Detected	1.375	Detected	1.505	0.013	GT	Sens	contig155	contig155	Unknown	ATACCT
GT	Sens	Sense	-0.064	Detected	0.064	Detected	0.000	1.632	Detected	0.997	Detected	1.315	0.056	GT	Sens	contig155	contig155	Unknown	AACAAG
GT	Sens	Sense	0.267	Detected	-0.267	Detected	0.000	1.235	Detected	0.817	Detected	1.026	0.094	GT	Sens	contig156	contig156	Unknown	ATTTCT
GT	Sens	Sense	-0.072	Detected	0.072	Detected	0.000	2.922	Detected	1.496	Detected	2.209	0.091	GT	Sens	contig156	contig156	Lysine/his	TAGCTA
GT	Sens	Sense	0.361	Detected	-0.361	Detected	0.000	1.673	Detected	0.811	Detected	1.242	0.158	GT	Sens	contig156	contig156	Hypersen	ATAAAG
GT	Sens	Sense	0.553	Detected	-0.553	Detected	0.000	5.371	Detected	3.006	Detected	4.188	0.085	GT	Sens	contig156	contig156	MtN3-like	GGAGTT
GT	Sens	Sense	-0.475	Detected	0.475	Detected	0.000	1.541	Detected	1.362	Detected	1.451	0.095	GT	Sens	contig156	contig156	Chloroph	GCACTT
GT	Sens	Sense	-0.274	Detected	0.274	Detected	0.000	1.353	Detected	0.842	Detected	1.098	0.099	GT	Sens	contig157	contig157	BHLH tra	ACAAGT
GT	Sens	Sense	-0.165	Detected	0.165	Detected	0.000	1.443	Detected	1.338	Detected	1.390	0.015	GT	Sens	contig157	contig157	Zinc finge	TTTTGC
GT	Sens	Sense	-0.447	Detected	0.447	Detected	0.000	1.093	Detected	1.060	Detected	1.077	0.138	GT	Sens	contig157	contig157	Oxidored	TTTTAT
GT	Sens	Sense	0.112	Detected	-0.112	Detected	0.000	1.200	Detected	1.538	Detected	1.369	0.021	GT	Sens	contig158	contig158	Plant cell	GGGGGA
GT	Sens	Sense	-0.154	Detected	0.154	Detected	0.000	2.012	Detected	1.814	Detected	1.913	0.009	GT	Sens	contig158	contig158	Chloroph	AAACCT
GT	Sens	Sense	-0.359	Comprom	0.359	Comprom	0.000	2.136	Detected	2.125	Detected	2.131	0.027	GT	Sens	contig158	contig158	Unknown	CGTTGT
GT	Sens	Sense	-0.264	Comprom	0.264	Detected	0.000	1.574	Detected	1.071	Detected	1.322	0.068	GT	Sens	contig158	contig158	Unknown	ATATTT
GT	Sens	Sense	-0.305	Detected	0.305	Detected	0.000	1.579	Detected	1.147	Detected	1.363	0.067	GT	Sens	contig158	contig158	Superoxi	AGAACC
GT	Sens	Sense	-0.596	Comprom	0.596	Comprom	0.000	1.546	Detected	1.188	Detected	1.367	0.159	GT	Sens	contig159	contig159	Unknown	GAAGAA
GT	Sens	Sense	0.031	Detected	-0.031	Detected	0.000	1.159	Detected	1.592	Detected	1.375	0.024	GT	Sens	contig159	contig159	Cytochro	CGAATA
GT	Sens	Sense	0.020	Comprom	-0.020	Comprom	0.000	2.836	Detected	1.722	Detected	2.279	0.055	GT	Sens	contig159	contig159	Unknown	CAAAAC
GT	Sens	Sense	-0.101	Detected	0.101	Detected	0.000	1.277	Detected	1.058	Detected	1.168	0.016	GT	Sens	contig159	contig159	NADH ubi	TTGAGG
GT	Sens	Sense	-0.211	Comprom	0.211	Comprom	0.000	2.344	Detected	1.675	Detected	2.010	0.037	GT	Sens	contig159	contig159	Shugoshi	CAAGGA
GT	Sens	Sense	-0.247	Detected	0.247	Detected	0.000	1.294	Detected	1.297	Detected	1.295	0.035	GT	Sens	contig160	contig160	Chloroph	TGTCCG
GT	Sens	Sense	-0.207	Detected	0.207	Detected	0.000	1.547	Detected	1.197	Detected	1.372	0.037	GT	Sens	contig160	contig160	Chloroph	GGGGTT
GT	Sens	Sense	0.164	Comprom	-0.164	Comprom	0.000	1.540	Detected	4.138	Detected	2.839	0.162	GT	Sens	contig160	contig160	Unknown	GATAAT
GT	Sens	Sense	0.394	Detected	-0.394	Detected	0.000	2.205	Detected	1.715	Detected	1.960	0.052	GT	Sens	contig161	contig161	Galactino	TACAAT
GT	Sens	Sense	-0.339	Detected	0.339	Detected	0.000	2.568	Detected	2.055	Detected	2.311	0.032	GT	Sens	contig161	contig161	Regulator	ACAAGT
GT	Sens	Sense	-0.117	Comprom	0.117	Comprom	0.000	2.459	Detected	2.195	Detected	2.327	0.006	GT	Sens	contig161	contig161	Nodulin-li	GCCATT
GT	Sens	Sense	-0.109	Comprom	0.109	Comprom	0.000	1.348	Detected	0.915	Detected	1.132	0.043	GT	Sens	contig161	contig161	cDNA clo	TTTGAA
GT	Sens	Sense	0.198	Detected	-0.198	Detected	0.000	1.184	Detected	1.401	Detected	1.293	0.029	GT	Sens	contig161	contig161	AT-hook	TCATCA
GT	Sens	Sense	-0.626	Detected	0.626	Detected	0.000	1.006	Detected	2.363	Detected	1.685	0.210	GT	Sens	contig162	contig162	GDSL est	AATGCA
GT	Sens	Sense	0.105	Comprom	-0.105	Comprom	0.000	1.473	Detected	2.436	Detected	1.955	0.058	GT	Sens	contig162	contig162	UDP-gluc	GCCAAT
GT	Sens	Sense	-0.286	Comprom	0.286	Comprom	0.000	1.583	Detected	1.826	Detected	1.704	0.032	GT	Sens	contig163	contig163	Alcohol d	ATTACT
GT	Sens	Sense	0.332	Detected	-0.332	Detected	0.000	1.752	Detected	1.142	Detected	1.447	0.085	GT	Sens	contig163	contig163	Branched	CTGTAG
GT	Sens	Sense	0.208	Comprom	-0.208	Comprom	0.000	2.584	Detected	2.009	Detected	2.296	0.023	GT	Sens	contig164	contig164	NAC dom	CATAAT
GT	Sens	Sense	-0.202	Detected	0.202	Detected	0.000	1.261	Detected	0.880	Detected	1.070	0.061	GT	Sens	contig165	contig165	Conserve	TATAAG
GT	Sens	Sense	-0.204	Detected	0.204	Detected	0.000	1.355	Detected	1.029	Detected	1.192	0.045	GT	Sens	contig165	contig165	PAP fibril	AGACAC
GT	Sens	Sense	0.237	Detected	-0.237	Detected	0.000	1.310	Detected	0.894	Detected	1.102	0.073	GT	Sens	contig165	contig165	Unknown	ACTGGA
GT	Sens	Sense	-0.433	Detected	0.433	Detected	0.000	2.837	Detected	1.532	Detected	2.185	0.108	GT	Sens	contig165	contig165	Unknown	AATTAT
GT	Sens	Sense	-0.009	Detected	0.009	Detected	0.000	1.129	Detected	1.163	Detected	1.146	0.000	GT	Sens	contig166	contig166	3-phenyl	GCTAAT
GT	Sens	Sense	-0.759	Comprom	0.759	Detected	0.000	1.882	Detected	1.019	Detected	1.450	0.239	GT	Sens	contig166	contig166	Unknown	AAGAAA
GT	Sens	Sense	0.007	Comprom	-0.007	Comprom	0.000	2.474	Detected	2.598	Detected	2.536	0.001	GT	Sens	contig166	contig166	WRKY tra	TCGACG
GT	Sens	Sense	-0.755	Detected	0.755	Detected	0.000	1.423	Detected	0.853	Detected	1.138	0.294	GT	Sens	contig166	contig166	Endo-1 4-	TAATTC
GT	Sens	Sense	-0.071	Detected	0.071	Detected	0.000	1.167	Detected	1.009	Detected	1.088	0.009	GT	Sens	contig166	contig166	Unknown	GACCAT
GT	Sens	Sense	0.143	Detected	-0.143	Comprom	0.000	1.933	Detected	1.334	Detected	1.633	0.039	GT	Sens	contig167	contig167	BAH-PHD	ACTGGT
GT	Sens	Sense	-0.184	Detected	0.184	Detected	0.000	1.002	Detected	1.195	Detected	1.098	0.034	GT	Sens	contig167	contig167	Pentatric	TGTTTT
GT	Sens	Sense	0.187	Detected	-0.187	Detected	0.000	1.013	Detected	1.078	Detected	1.045	0.031	GT	Sens	contig167	contig167	C2 domai	TGCATC
GT	Sens	Sense	-0.132	Detected	0.132	Detected	0.000	1.621	Detected	1.052	Detected	1.336	0.051	GT	Sens	contig167	contig167	ClpB cha	AGGGCT
GT	Sens	Sense	-0.068	Detected	0.068	Detected	0.000	1.414	Detected	2.218	Detected	1.816	0.047	GT	Sens	contig167	contig167	UDP-gluc	TCCACG
GT	Sens	Sense	-0.609	Comprom	0.609	Comprom	0.000	1.453	Detected	1.596	Detected	1.524	0.131	GT	Sens	contig167	contig167	Proton-de	GAGAAT
GT	Sens	Sense	-0.010	Detected	0.010	Detected	0.000	1.945	Detected	0.856	Detected	1.400	0.124	GT	Sens	contig167	contig167	Unknown	GGTTAT
GT	Sens	Sense	0.296	Detected	-0.296	Detected	0.000	1.312	Detected	1.190	Detected	1.251	0.054	GT	Sens	contig167	contig167	30S ribos	TCGCGG
GT	Sens	Sense	0.505	Detected	-0.505	Comprom	0.000	1.622	Detected	1.607	Detected	1.614	0.086	GT	Sens	contig168	contig168	Unknown	CTCGAG
GT	Sens	Sense	-0.243	Detected	0.243	Detected	0.000	1.576	Detected	1.420	Detected	1.498	0.028	GT	Sens	contig168	contig168	Long-cha	ATAACA
GT	Sens	Sense	-0.123	Detected	0.123	Detected	0.000	1.163	Detected	0.863	Detected	1.013	0.035	GT	Sens	contig168	contig168	U-box do	TTGTAC
GT	Sens	Sense	-0.303	Comprom	0.303	Comprom	0.000	2.223	Detected	2.090	Detected	2.156	0.020	GT	Sens	contig168	contig168	Cytokinin	CCCAGC
GT	Sens	Sense	-0.214	Detected	0.214	Detected	0.000	1.979	Detected	1.559	Detected	1.769	0.028	GT	Sens	contig168	contig168	Serine ca	TCTCCT
GT	Sens	Sense	-0.504	Comprom	0.504	Comprom	0.000	2.501	Detected	2.091	Detected	2.296	0.052	GT	Sens	contig168	contig168	Unknown	CATTAG
GT	Sens	Sense	0.444	Detected	-0.444	Detected	0.000	1.482	Detected	1.756	Detected	1.619	0.073	GT	Sens	contig169	contig169	40S ribos	TGATGT
GT	Sens	Sense	0.431	Detected	-0.431	Detected	0.000	1.784	Detected	1.083	Detected	1.434	0.123	GT	Sens	contig169	contig169	Threonin	GTTGGA
GT	Sens	Sense	-0.277	Detected	0.277	Detected	0.000	1.325	Detected	0.897	Detected	1.111	0.087	GT	Sens	contig169	contig169	Os03g02	ATAGCA
GT	Sens	Sense	-0.142	Detected	0.142	Detected	0.000	1.134	Detected	0.911	Detected	1.022	0.030	GT	Sens	contig169	contig169	ATP-depe	TGATAA
GT	Sens	Sense	-0.210	Detected	0.210	Detected	0.000	2.874	Detected	2.416	Detected	2.645	0.014	GT	Sens	contig169	contig169	Genomic	GGATGA
GT	Sens	Sense	-0.528	Detected	0.528	Detected	0.000	1.997	Detected	1.824	Detected	1.911	0.070	GT	Sens	contig169	contig169	Nitrate tra	AGTATC
GT	Sens	Sense	-0.666	Comprom	0.666	Detected	0.000	2.095	Detected	0.846	Detected	1.471	0.249	GT	Sens	contig170	contig170	Zinc finge	ATAGCC
GT	Sens	Sense	0.186	Detected	-0.186	Detected	0.000	1.895	Detected	1.065	Detected	1.480	0.083	GT	Sens	contig170	contig170	Nodulin-li	GGTTGG
GT	Sens	Sense	0.102	Detected	-0.102	Detected	0.000	2.688	Detected	1.007	Detected	1.848	0.161	GT	Sens	contig170	contig170	Ectonucle	TACACT
GT	Sens	Sense	-0.040	Detected	0.040	Detected	0.000	2.567	Detected	1.395	Detected	1.981	0.078	GT	Sens	contig171	contig171	Subtilisin	GGTGCA
GT	Sens	Sense	-0.305	Detected	0.305	Detected	0.000	1.187	Detected	0.834	Detected	1.011	0.103	GT	Sens	contig171	contig171	Genomic	TCAAAT
GT	Sens	Sense	0.417	Comprom	-0.417	Comprom	0.000	2.039	Detected	1.924	Detected	1.981	0.042	GT	Sens	contig172	contig172	Lysine-sp	AAGTTT
GT	Sens	Sense	-0.105	Detected	0.105	Detected	0.000	1.146	Detected	0.918	Detected	1.032	0.022	GT	Sens	contig172	contig172	Gamma-g	AGATGT
GT	Sens	Sense	0.192	Detected	-0.192	Detected	0.000	1.471	Detected	1.151	Detected	1.311	0.035	GT	Sens	contig172	contig172	Norcoclau	CATCTT
GT	Sens	Sense	-0.208	Comprom	0.208	Comprom	0.000	3.373	Detected	2.403	Detected	2.888	0.032	GT	Sens	contig172	contig172	Proteinas	GCCCAG
GT	Sens	Sense	-0.117	Detected	0.117	Detected	0.000	1.165	Detected	0.836	Detected	1.000	0.038	GT	Sens	contig172	contig172	2%2C3-bi	TTATCG
GT	Sens	Sense	0.078	Detected	-0.078	Detected	0.000	1.460	Detected	1.009	Detected	1.235	0.035	GT	Sens	contig173	contig173	Zinc finge	ATAGAT
GT	Sens	Sense	-0.207	Detected	0.207	Detected	0.000	1.499	Detected	0.927	Detected	1.213	0.075	GT	Sens	contig173	contig173	EPF-type	ACCAAT
GT	Sens	Sense	0.595	Detected	-0.595	Detected	0.000	2.189	Detected	0.905	Detected	1.547	0.219	GT	Sens	contig173	contig173	Cysteine-	TAAGTT
GT	Sens	Sense	0.001	Detected	-0.001	Detected	0.000	1.508	Detected	0.905	Detected	1.207	0.057	GT	Sens	contig173	contig173	Homeobo	TTGAAA
GT	Sens	Sense	0.035	Detected	-0.035	Detected	0.000	1.735	Detected	1.587	Detected	1.661	0.002	GT	Sens	contig173	contig173	Unknown	AATTTC
GT	Sens	Sense	-0.638	Comprom	0.638	Comprom	0.000	0.843	Detected	1.215	Detected	1.029	0.261	GT	Sens	contig174	contig174	Unknown	AACGTA
GT	Sens	Sense	-0.206	Comprom	0.206	Comprom	0.000	1.934	Detected	1.864	Detected	1.899	0.012	GT	Sens	contig174	contig174	2-oxoglut	GGTATG
GT	Sens	Sense	-0.116	Detected	0.116	Detected	0.000	2.601	Detected	1.134	Detected	1.868	0.128	GT	Sens	contig174	contig174	MazG nuc	GAACTT
GT	Sens	Sense	0.100	Detected	-0.100	Detected	0.000	2.418	Detected	2.129	Detected	2.273	0.006	GT	Sens	contig174	contig174	Unknown	TTTTCT
GT	Sens	Sense	0.228	Detected	-0.228	Detected	0.000	0.830	Detected	1.283	Detected	1.057	0.081	GT	Sens	contig174	contig174	Ferredox	CTCGTG
GT	Sens	Sense	0.193	Detected	-0.193	Detected	0.000	1.400	Detected	1.477	Detected	1.438	0.018	GT	Sens	contig175	contig175	ATP-bind	GTGATT
GT	Sens	Sense	-0.489	Detected	0.489	Detected	0.000	1.968	Detected	1.523	Detected	1.746	0.083	GT	Sens	contig175	contig175	Unknown	TCAATA
GT	Sens	Sense	-0.079	Detected	0.079	Detected	0.000	2.399	Detected	1.161	Detected	1.780	0.104	GT	Sens	contig175	contig175	Genomic	TCATGC
GT	Sens	Sense	0.086	Detected	-0.086	Detected	0.000	1.941	Detected	1.482	Detected	1.711	0.020	GT	Sens	contig175	contig175	Magnesiu	TGGTAT
GT	Sens	Sense	0.327	Detected	-0.327	Detected	0.000	1.733	Detected	0.878	Detected	1.305	0.136	GT	Sens	contig176	contig176	Diacylglyc	TCAAAC
GT	Sens	Sense	-0.059	Detected	0.059	Detected	0.000	1.815	Detected	1.555	Detected	1.685	0.007	GT	Sens	contig176	contig176	Genomic	TGAACA
GT	Sens	Sense	-0.122	Detected	0.122	Detected	0.000	1.219	Detected	0.827	Detected	1.023	0.048	GT	Sens	contig177	contig177	Dienelact	GCAGAT
GT	Sens	Sense	0.234	Detected	-0.234	Detected	0.000	1.320	Detected	1.022	Detected	1.171	0.052	GT	Sens	contig177	contig177	L-tyrosin	GGTATT
GT	Sens	Sense	0.177	Detected	-0.177	Detected	0.000	1.270	Detected	1.024	Detected	1.147	0.034	GT	Sens	contig177	contig177	Mutator-li	TAGAAA
GT	Sens	Sense	-0.134	Detected	0.134	Detected	0.000	1.421	Detected	1.048	Detected	1.234	0.033	GT	Sens	contig177	contig177	C1orf93 h	CAAGGA
GT	Sens	Sense	-0.048	Detected	0.048	Detected	0.000	1.146	Detected	0.958	Detected	1.052	0.010	GT	Sens	contig178	contig178	1-aminoc	GGTATA
GT	Sens	Sense	-0.449	Comprom	0.449	Detected	0.000	2.593	Detected	2.021	Detected	2.307	0.049	GT	Sens	contig179	contig179	LINE-type	ACAAGA
GT	Sens	Sense	0.189	Detected	-0.189	Detected	0.000	1.306	Detected	0.902	Detected	1.104	0.057	GT	Sens	contig179	contig179	Fructose-	TCAGGA
GT	Sens	Sense	0.274	Detected	-0.274	Detected	0.000	1.642	Detected	1.984	Detected	1.813	0.030	GT	Sens	contig179	contig179	ATP-depe	GAGAAC
GT	Sens	Sense	-0.134	Detected	0.134	Detected	0.000	1.814	Detected	1.701	Detected	1.758	0.007	GT	Sens	contig179	contig179	BURP dor	ATGATT
GT	Sens	Sense	0.129	Detected	-0.129	Detected	0.000	1.263	Detected	0.830	Detected	1.046	0.053	GT	Sens	contig179	contig179	Cc-nbs-lr	GGTCCC
GT	Sens	Sense	-0.663	Detected	0.663	Detected	0.000	3.890	Detected	2.744	Detected	3.317	0.063	GT	Sens	contig179	contig179	Myb trans	TCCGAC
GT	Sens	Sense	0.086	Detected	-0.086	Detected	0.000	1.229	Detected	1.526	Detected	1.377	0.015	GT	Sens	contig179	contig179	Protein ki	GGGTAA
GT	Sens	Sense	0.007	Detected	-0.007	Detected	0.000	1.376	Detected	1.109	Detected	1.242	0.011	GT	Sens	contig180	contig180	WRKY far	CAGGAG
GT	Sens	Sense	-0.147	Comprom	0.147	Comprom	0.000	1.961	Detected	2.797	Detected	2.379	0.033	GT	Sens	contig180	contig180	Unknown	TGCAAA
GT	Sens	Sense	-0.400	Detected	0.400	Detected	0.000	1.569	Detected	1.532	Detected	1.550	0.061	GT	Sens	contig180	contig180	Early nod	CAAAAT
GT	Sens	Sense	-0.251	Detected	0.251	Detected	0.000	1.630	Detected	1.122	Detected	1.376	0.061	GT	Sens	contig180	contig180	Unknown	TCCAAA
GT	Sens	Sense	-0.150	Comprom	0.150	Comprom	0.000	1.800	Detected	1.348	Detected	1.574	0.028	GT	Sens	contig180	contig180	Uncharac	TCTAAT
GT	Sens	Sense	-0.120	Detected	0.120	Detected	0.000	1.531	Detected	1.199	Detected	1.365	0.022	GT	Sens	contig180	contig180	Ulp1 prot	TCAAGA
GT	Sens	Sense	-0.226	Detected	0.226	Detected	0.000	1.771	Detected	2.210	Detected	1.990	0.024	GT	Sens	contig180	contig180	Histidine	CCAAGA
GT	Sens	Sense	0.135	Detected	-0.135	Detected	0.000	1.400	Detected	0.880	Detected	1.140	0.060	GT	Sens	contig181	contig181	Amino ac	AAGGGG
GT	Sens	Sense	-1.032	Comprom	1.032	Detected	0.000	5.856	Detected	4.446	Detected	5.151	0.054	GT	Sens	contig181	contig181	Nitrate tra	ACTCGG
GT	Sens	Sense	-0.110	Detected	0.110	Detected	0.000	1.189	Detected	1.582	Detected	1.385	0.025	GT	Sens	contig181	contig181	Myb famil	CTAACG
GT	Sens	Sense	0.141	Detected	-0.141	Detected	0.000	1.567	Detected	0.812	Detected	1.189	0.098	GT	Sens	contig182	contig182	Os02g05	CACTAG

GT	Sense	Sense	0.369	Detected	-0.369	Comprom	0.000	2.519	Detected	2.311	Detected	2.415	0.024	GT	Sens	contig182	contig182	Unknown	GTGTAT	contig182	Solyc11g
GT	Sense	Sense	-0.693	Comprom	0.693	Comprom	0.000	1.982	Detected	2.101	Detected	2.041	0.099	GT	Sens	contig182	contig182	Auxin Effl	AGTGAC	contig182	Solyc01g
GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	1.153	Detected	0.891	Detected	1.022	0.039	GT	Sens	contig182	contig182	Unknown	CAATAT	contig182	Solyc07g
GT	Sense	Sense	-0.136	Detected	0.136	Detected	0.000	1.230	Detected	1.121	Detected	1.176	0.015	GT	Sens	contig182	contig182	Uncharac	TTTGAC	contig182	Solyc08g
GT	Sense	Sense	0.619	Detected	-0.619	Detected	0.000	1.466	Detected	1.161	Detected	1.314	0.175	GT	Sens	contig182	contig182	Cytochro	ACTGAA	contig182	Solyc03g
GT	Sense	Sense	-0.133	Detected	0.133	Detected	0.000	1.294	Detected	0.881	Detected	1.087	0.047	GT	Sens	contig182	contig182	Catalase	TTTATG	contig182	Solyc02g
GT	Sense	Sense	-0.248	Detected	0.248	Detected	0.000	2.037	Detected	1.516	Detected	1.776	0.039	GT	Sens	contig183	contig183	Auxin-rer	ATGTGT	contig183	Solyc03g
GT	Sense	Sense	-0.262	Detected	0.262	Detected	0.000	1.719	Detected	1.312	Detected	1.516	0.045	GT	Sens	contig183	contig183	Photosys	ATGGAA	contig183	Solyc06g
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	1.600	Detected	1.198	Detected	1.399	0.022	GT	Sens	contig183	contig183	Unknown	GAACAA	contig183	Solyc10g
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	1.366	Detected	1.308	Detected	1.337	0.015	GT	Sens	contig183	contig183	Lipase (A	GGTCAT	contig183	Solyc11g
GT	Sense	Sense	-0.108	Detected	0.108	Detected	0.000	2.139	Detected	0.956	Detected	1.547	0.124	GT	Sens	contig184	contig184	LRR rece	CTAGTG	contig184	Solyc01g
GT	Sense	Sense	0.429	Comprom	-0.429	Comprom	0.000	2.888	Detected	2.618	Detected	2.753	0.026	GT	Sens	contig184	contig184	Abc trans	CTGTTA	contig184	Solyc10g
GT	Sense	Sense	0.090	Comprom	-0.090	Comprom	0.000	2.907	Detected	2.038	Detected	2.472	0.031	GT	Sens	contig184	contig184	Aspartic	TACTGG	contig184	Solyc06g
GT	Sense	Sense	-0.020	Comprom	0.020	Comprom	0.000	4.435	Detected	3.770	Detected	4.103	0.007	GT	Sens	contig184	contig184	Leucine-r	GTGTGG	contig184	Solyc01g
GT	Sense	Sense	-0.186	Detected	0.186	Detected	0.000	1.623	Detected	1.129	Detected	1.376	0.047	GT	Sens	contig185	contig185	Serine/th	GATGCT	contig185	Solyc05g
GT	Sense	Sense	-0.081	Comprom	0.081	Comprom	0.000	1.201	Detected	1.476	Detected	1.339	0.014	GT	Sens	contig185	contig185	Gag-Pol	CAAAAA	contig185	Solyc10g
GT	Sense	Sense	0.258	Detected	-0.258	Detected	0.000	1.802	Detected	1.448	Detected	1.625	0.035	GT	Sens	contig185	contig185	Glycosyl	CCCAAT	contig185	Solyc03g
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	1.175	Detected	1.342	Detected	1.258	0.005	GT	Sens	contig185	contig185	Unknown	TTCTTT	contig185	Solyc05g
GT	Sense	Sense	-0.182	Detected	0.182	Detected	0.000	1.113	Detected	1.166	Detected	1.139	0.025	GT	Sens	contig185	contig185	Nbs-lrr re	CAGATG	contig185	Solyc07g
GT	Sense	Sense	-0.457	Detected	0.457	Detected	0.000	1.523	Detected	1.366	Detected	1.444	0.089	GT	Sens	contig185	contig185	Amino ac	CCTCTC	contig185	Solyc08g
GT	Sense	Sense	1.126	Detected	-1.126	Comprom	0.000	3.278	Detected	2.540	Detected	2.909	0.133	GT	Sens	contig185	contig185	GDSL est	GAGCTA	contig185	Solyc01g
GT	Sense	Sense	-0.659	Comprom	0.659	Detected	0.000	1.093	Detected	1.283	Detected	1.188	0.216	GT	Sens	contig185	contig185	Serine/th	TAACAG	contig185	Solyc02g
GT	Sense	Sense	-0.294	Detected	0.294	Detected	0.000	2.211	Detected	1.371	Detected	1.791	0.073	GT	Sens	contig186	contig186	Light-dep	AGGTTG	contig186	Solyc02g
GT	Sense	Sense	-0.345	Detected	0.345	Detected	0.000	1.372	Detected	1.210	Detected	1.291	0.068	GT	Sens	contig186	contig186	Gibberelli	GTTTTG	contig186	Solyc02g
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	1.363	Detected	0.815	Detected	1.089	0.067	GT	Sens	contig186	contig186	PPPDE p	ACCACT	contig186	Solyc02g
GT	Sense	Sense	0.179	Detected	-0.179	Detected	0.000	0.985	Detected	1.680	Detected	1.333	0.076	GT	Sens	contig186	contig186	1-aminoc	GTCCTG	contig186	Solyc09g
GT	Sense	Sense	-0.046	Detected	0.046	Detected	0.000	0.804	Detected	1.343	Detected	1.073	0.059	GT	Sens	contig186	contig186	Glutathio	GAAGCT	contig186	Solyc09g
GT	Sense	Sense	-0.308	Detected	0.308	Detected	0.000	1.379	Detected	1.078	Detected	1.229	0.070	GT	Sens	contig187	contig187	Transme	ATTATG	contig187	Solyc10g
GT	Sense	Sense	-0.222	Detected	0.222	Detected	0.000	1.272	Detected	1.073	Detected	1.172	0.041	GT	Sens	contig187	contig187	Unknown	TGGAGA	contig187	Solyc11g
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	1.242	Detected	0.940	Detected	1.091	0.021	GT	Sens	contig187	contig187	Glyoxylat	GTTCTG	contig187	Solyc01g
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	0.861	Detected	1.147	Detected	1.004	0.036	GT	Sens	contig187	contig187	Cullin 1-li	TTGTTG	contig187	Solyc01g
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	1.472	Detected	1.108	Detected	1.290	0.024	GT	Sens	contig187	contig187	Ring H2 fi	GAGCAA	contig187	Solyc06g
GT	Sense	Sense	-0.031	Detected	0.031	Detected	0.000	1.069	Detected	0.935	Detected	1.002	0.005	GT	Sens	contig187	contig187	Zeaxanth	CATCCA	contig187	Solyc02g
GT	Sense	Sense	-0.271	Comprom	0.271	Comprom	0.000	1.427	Detected	1.662	Detected	1.545	0.035	GT	Sens	contig188	contig188	cDNA clo	TGAGTT	contig188	Solyc06g
GT	Sense	Sense	-0.483	Detected	0.483	Detected	0.000	1.354	Detected	0.968	Detected	1.161	0.155	GT	Sens	contig189	contig189	Receptor	AATTAG	contig189	Solyc07g
GT	Sense	Sense	-0.850	Comprom	0.850	Detected	0.000	4.852	Detected	3.031	Detected	3.942	0.087	GT	Sens	contig189	contig189	Cytochro	GTTGCA	contig189	Solyc01g
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	1.649	Detected	0.808	Detected	1.229	0.112	GT	Sens	contig189	contig189	Heat shoc	TGATGA	contig189	Solyc11g
GT	Sense	Sense	-0.071	Detected	0.071	Detected	0.000	2.853	Detected	1.541	Detected	2.197	0.080	GT	Sens	contig189	contig189	Seed spe	ATCATC	contig189	Solyc06g
GT	Sense	Sense	0.361	Comprom	-0.361	Comprom	0.000	1.764	Detected	1.155	Detected	1.459	0.091	GT	Sens	contig190	contig190	Mutator-li	GTCCGT	contig190	Solyc10g
GT	Sense	Sense	0.312	Detected	-0.312	Detected	0.000	2.698	Detected	1.368	Detected	2.033	0.110	GT	Sens	contig190	contig190	Serine ca	TCAACA	contig190	Solyc06g
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	1.432	Detected	1.163	Detected	1.298	0.012	GT	Sens	contig190	contig190	Aspartic	TCGGAG	contig190	Solyc08g
GT	Sense	Sense	-0.531	Comprom	0.531	Comprom	0.000	2.364	Detected	1.715	Detected	2.039	0.082	GT	Sens	contig190	contig190	Os04g04	GCTTTT	contig190	Solyc06g
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	3.696	Detected	2.818	Detected	3.257	0.019	GT	Sens	contig191	contig191	Kunitz-ty	TATTTG	contig191	Solyc03g
GT	Sense	Sense	0.038	Comprom	-0.038	Comprom	0.000	2.075	Detected	1.629	Detected	1.852	0.015	GT	Sens	contig191	contig191	Non-race	TGTGAG	contig191	Solyc01g
GT	Sense	Sense	1.093	Detected	-1.093	Comprom	0.000	1.082	Detected	1.137	Detected	1.110	0.417	GT	Sens	contig191	contig191	Unknown	CAAAGA	contig191	Solyc02g
GT	Sense	Sense	-0.425	Detected	0.425	Detected	0.000	1.255	Detected	0.990	Detected	1.123	0.128	GT	Sens	contig191	contig191	CHCH do	ATTCAA	contig191	Solyc10g
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	1.993	Detected	0.973	Detected	1.483	0.101	GT	Sens	contig191	contig191	C2 domai	GAGAGT	contig191	Solyc12g
GT	Sense	Sense	0.202	Detected	-0.202	Detected	0.000	1.097	Detected	1.232	Detected	1.165	0.032	GT	Sens	contig191	contig191	Polyprote	ACCTTA	contig191	Solyc07g
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	2.636	Detected	2.278	Detected	2.457	0.010	GT	Sens	contig192	contig192	Genomic	ATGTTT	contig192	Solyc11g

GT	Sense	Sense	0.204	Detected	-0.204	Detected	0.000	1.152	Detected	0.988	Detected	1.070	0.040	GT	Sens	contig235	contig235	Endo-1 3-	GTTTGT	contig235	Solyc03g	Solyc03g	Endo-1 3-	GO:0016	GO:0016	contig235	Solyc03g	Endo-1 3-	GO:0016	SL2.40ch	AT1G18310.1		glycosyl	chr1:630	176.204	125.03	217.608	236.475	351.778	313.054
GT	Sense	Sense	0.259	Comprom	-0.259	Comprom	0.000	2.499	Detected	2.220	Detected	2.360	0.015	GT	Sens	contig235	contig235	Serine ca	GTGATC	contig235	Solyc05g	Solyc05g	Serine ca	GO:0006	GO:0006	contig235	Solyc05g	Serine ca	GO:0016	SL2.40ch	AT2G23000.1				3.52002	2.31327	5.95051	10.3707	17.207	14.135
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	1.359	Detected	0.815	Detected	1.087	0.082	GT	Sens	contig236	contig236	Sulfate tr	TGGGTC	contig236	Solyc10g	Solyc10g	Sulfate tr	GO:0016	GO:0016	contig236	Solyc10g	Sulfate tr	GO:0016	SL2.40ch	AT2G256	MOT1	MOT1 (m	chr2:109	844.932	608.804	1593.92	1135.3	1961.88	1341.77
GT	Sense	Sense	-0.400	Detected	0.400	Detected	0.000	1.120	Detected	0.896	Detected	1.008	0.136	GT	Sens	contig236	contig236	HAT famil	GGTCAT	contig236	Solyc12g	Solyc12g	HAT family dimerisation doma			contig236	Solyc12g	HAT family dimerisa		SL2.40ch	AT3G10970.3		haloacid	chr3:343	20.2323	33.158	39.8464	35.2544	60.0198	51.2419
GT	Sense	Sense	-0.150	Detected	0.150	Detected	0.000	1.193	Detected	0.833	Detected	1.013	0.049	GT	Sens	contig236	contig236	Unknown	CAGCCT	contig236	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig236	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G24890.1		unknown	chr5:855	63.2144	73.2427	107.932	92.8787	165.879	128.915
GT	Sense	Sense	-0.157	Comprom	0.157	Comprom	0.000	1.636	Detected	1.689	Detected	1.663	0.009	GT	Sens	contig237	contig237	Proline-ri	TTATTCA	contig237	Solyc10g	Solyc10g	Proline-rich protein (AHRD V1			contig237	Solyc10g	Proline-rich protein		SL2.40ch	AT5G042	KTF1	KTF1 (K	chr5:119	4.28762	5.01716	3.75933	12.1759	15.3746	15.8975
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	1.330	Detected	0.804	Detected	1.067	0.065	GT	Sens	contig237	contig237	Oligoribo	GGAAAT	contig237	Solyc06g	Solyc06g	Oligoribo	GO:0000	GO:0000	contig237	Solyc06g	Oligoribo	GO:0000	SL2.40ch	AT2G26970.2		exonucle	chr2:115	116.146	128.081	147.943	127.338	327.003	226.364
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	1.619	Detected	1.188	Detected	1.403	0.023	GT	Sens	contig237	contig237	Wound-in	AGTATT	contig237	Solyc09g	Solyc09g	Wound-induced protein 1 (AHF			contig237	Solyc09g	Wound-induced pro		SL2.40ch	AT4G13360.1		catalytic	chr4:777	7727.77	7385.22	16737.4	15511	24750.3	18294.6
GT	Sense	Sense	-0.189	Comprom	0.189	Comprom	0.000	1.242	Detected	0.867	Detected	1.055	0.058	GT	Sens	contig237	contig237	RING fing	GAAAAA	contig237	Solyc04g	Solyc04g	RING fing	GO:0008	GO:0008	contig237	Solyc09g	RING fing	GO:0008	SL2.40ch	AT2G18938.1				5.1899	6.34251	5.24302	2.44786	14.4715	11.1271
GT	Sense	Sense	-0.181	Detected	0.181	Detected	0.000	1.514	Detected	0.847	Detected	1.180	0.090	GT	Sens	contig238	contig238	Calcium-r	TCATCA	contig238	Solyc04g	Solyc04g	Calcium-responsive transactiv			contig238	Solyc04g	Calcium-responsive		SL2.40ch	AT5G286	AN3, GIF,	AN3 (AN	chr5:106	14.8534	17.9574	29.3736	24.0781	49.7307	31.2238
GT	Sense	Sense	0.866	Detected	-0.866	Comprom	0.000	2.199	Detected	1.001	Detected	1.600	0.268	GT	Sens	contig238	contig238	Ulp1 prot	GTGAGA	contig238	Solyc09g	Solyc09g	Ulp1 prot	GO:0006	GO:0006	contig238	Solyc09g	Ulp1 prot	GO:0006	SL2.40ch	AT2G45590.1		protein k	chr2:187	11.3633	3.21749	6.32316	11.7081	29.6021	12.8672
GT	Sense	Sense	-0.202	Detected	0.202	Detected	0.000	2.175	Detected	1.385	Detected	1.780	0.057	GT	Sens	contig238	contig238	Lipoxyge	GAGGAA	contig238	Solyc08g	Solyc08g	Lipoxyge	GO:0016	GO:0016	contig238	Solyc08g	Lipoxyge	GO:0016	SL2.40ch	AT3G224	LOX5	LOX5: el	chr3:792	2781.36	3460.5	2495.12	2139.5	14941	8612.01
GT	Sense	Sense	-0.141	Detected	0.141	Detected	0.000	2.219	Detected	1.048	Detected	1.633	0.113	GT	Sens	contig238	contig238	Genomic	TATCCA	contig238	Solyc01g	Solyc01g	Genomic DNA chromosome 5			contig238	Solyc01g	Genomic DNA chror		SL2.40ch	AT3G24600.1		INVOLVE	chr3:897	16.0813	18.4066	46.5914	25.0289	85.393	37.8307
GT	Sense	Sense	-0.765	Comprom	0.765	Comprom	0.000	2.436	Detected	1.985	Detected	2.210	0.109	GT	Sens	contig238	contig238	Unknown	CAAAGC	contig238	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig238	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G08430.1		SWIB co	chr5:271	2.14457	5.82665	4.05495	12.081	20.3987	14.877
GT	Sense	Sense	-0.151	Detected	0.151	Detected	0.000	1.619	Detected	1.651	Detected	1.635	0.009	GT	Sens	contig238	contig238	Invertase	GCTAGT	contig238	Solyc12g	Solyc12g	Invertase	GO:0046	GO:0046	contig238	Solyc12g	Invertase	GO:0046	SL2.40ch	AT1G25320.1		leucine-r	chr1:887	190.493	221.026	383.839	313.576	672.006	685.156
GT	Sense	Sense	0.854	Detected	-0.854	Detected	0.000	3.673	Detected	2.520	Detected	3.096	0.095	GT	Sens	contig238	contig238	Patatin-lik	GGCTCA	contig238	Solyc04g	Solyc04g	Patatin-lil	GO:0008	GO:0008	contig238	Solyc04g	Patatin-lik	GO:0008	SL2.40ch	AT1G341	ARF13	transcrip	chr1:124	83.0947	23.9415	202.178	104.447	606.704	271.97
GT	Sense	Sense	-0.111	Comprom	0.111	Comprom	0.000	1.304	Detected	1.418	Detected	1.361	0.008	GT	Sens	contig238	contig238	CW-type	GGGAAA	contig238	Solyc12g	Solyc12g	CW-type	GO:0008	GO:0008	contig238	Solyc12g	CW-type	GO:0008	SL2.40ch	AT2G15640.1		F-box far	chr2:681	4.91095	5.38624	4.78562	2.53879	13.541	14.6083
GT	Sense	Sense	-0.239	Detected	0.239	Detected	0.000	2.386	Detected	1.294	Detected	1.840	0.091	GT	Sens	contig239	contig239	Phototro	GGGCAA	contig239	Solyc09g	Solyc09g	Phototro	GO:0009	GO:0009	contig239	Solyc09g	Phototro	GO:0005	SL2.40ch	AT5G48800.1		phototro	chr5:197	21.1719	27.7367	63.9633	46.7889	135.11	63.1803
GT	Sense	Sense	-0.107	Comprom	0.107	Comprom	0.000	1.377	Detected	1.411	Detected	1.394	0.006	GT	Sens	contig239	contig239	WD repea	CCATAT	contig239	Solyc09g	Solyc09g	WD repea	GO:0005	GO:0005	contig239	Solyc09g	WD repea	GO:0005	SL2.40ch	AT5G587	DDB2	DDB2 (da	chr5:237	4.66163	5.09047	6.0208	4.24463	13.4949	13.7687
GT	Sense	Sense	-0.160	Detected	0.160	Detected	0.000	1.034	Detected	1.228	Detected	1.131	0.026	GT	Sens	contig239	contig239	Ethylene	TGCAAT	contig239	Solyc09g	Solyc09g	Ethylene	GO:0051	GO:0051	contig239	Solyc09g	Ethylene	GO:0051	SL2.40ch	AT3G045	EIN4	EIN4 (ET	chr3:123	33.999	39.9092	49.6885	91.0183	80.4313	91.7401
GT	Sense	Sense	-0.100	Detected	0.100	Detected	0.000	1.585	Detected	1.059	Detected	1.322	0.042	GT	Sens	contig239	contig239	Alpha-am	CATGAA	contig239	Solyc09g	Solyc09g	Alpha-am	GO:0030	GO:0030	contig239	Solyc09g	Alpha-am	GO:0030	SL2.40ch	AT2G205	RPN1A, A	RPN1A (2	chr2:885	626.772	677.562	1487.47	638.57	2084.85	1443.37
GT	Sense	Sense	-0.661	Detected	0.661	Detected	0.000	1.466	Detected	1.388	Detected	1.427	0.164	GT	Sens	contig239	contig239	Cellulose	CATTGT	contig239	Solyc07g	Solyc07g	Cellulose	GO:0016	GO:0016	contig239	Solyc07g	Cellulose	GO:0016	SL2.40ch	AT5G174	IRX3, CES	IRX3 (IRR	chr5:573	25.5342	60.0918	65.1364	68.6966	115.417	109.014
GT	Sense	Sense	-0.164	Detected	0.164	Detected	0.000	2.634	Detected	1.622	Detected	2.128	0.057	GT	Sens	contig239	contig239	Malate de	TAAATA	contig239	Solyc03g	Solyc03g	Malate de	GO:0030	GO:0030	contig239	Solyc03g	Malate de	GO:0030	SL2.40ch	AT5G58330.1		malate d	chr5:235	17.6397	20.8475	133.952	31.693	126.947	62.7385
GT	Sense	Sense	0.226	Detected	-0.226	Detected	0.000	0.804	Detected	1.248	Detected	1.026	0.083	GT	Sens	contig239	contig239	Unknown	TCTTAG	contig239	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig239	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G50540.1		unknown	chr5:205	71.6579	49.2961	96.4179	157.585	110.674	150.046
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	1.672	Detected	1.145	Detected	1.408	0.034	GT	Sens	contig239	contig239	Anthocya	GCCTGC	contig239	Solyc10g	Solyc10g	Anthocya	GO:0055	GO:0055	contig239	Solyc10g	Anthocya	GO:0016	SL2.40ch	AT3G55970.1		oxidored	chr3:207	2964.31	2899.64	5523.37	3314.34	9963.66	6891.51
GT	Sense	Sense	-0.162	Detected	0.162	Detected	0.000	1.408	Detected	1.259	Detected	1.334	0.017	GT	Sens	contig240	contig240	Photosys	CTTTAC	contig240	Solyc08g	Solyc08g	Photosys	GO:0042	GO:0042	contig240	Solyc08g	Photosys	GO:0005	SL2.40ch	AT5G640	PSAN	PSAN: ca	chr5:256	4652.21	5479.85	15231	7604.68	14286.8	12850.3
GT	Sense	Sense	-0.183	Comprom	0.183	Comprom	0.000	2.095	Detected	2.211	Detected	2.153	0.008	GT	Sens	contig240	contig240	Harpin-in	GATTAG	contig240	Solyc11g	Solyc11g	Harpin-induced 1 (AHRD V1 ***			contig240	Solyc11g	Harpin-induced 1 (A		SL2.40ch	AT5G16870.1		aminoac	chr5:554	2.2552	2.73396	4.09501	7.44319	11.315	12.2188
GT	Sense	Sense	-0.509	Comprom	0.509	Comprom	0.000	1.991	Detected	2.293	Detected	2.142	0.056	GT	Sens	contig240	contig240	Unknown	TTGTAC	contig240	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig240	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G256	ACD1-LIK	ACD1-LIK	chr4:130	2.82806	5.38872	11.8317	13.6267	16.5483	20.335
GT	Sense	Sense	-0.381	Detected	0.381	Detected	0.000	2.547	Detected	1.924	Detected	2.236	0.045	GT	Sens	contig240	contig240	AT2G453	TTTGCA	contig240	Solyc01g	Solyc01g	AT2G45380 protein (Fragment			contig240	Solyc01g	AT2G45380 protein		SL2.40ch	AT5G35960.1		protein k	chr5:141	726.428	1159.08	1168.05	861.259	5719.48	3702.32
GT	Sense	Sense	-0.281	Comprom	0.281	Detected	0.000	2.003	Detected	1.112	Detected	1.558	0.098	GT	Sens	contig240	contig240	Unknown	ATATGT	contig240	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig240	Solyc06g	Unknown Protein (A		SL2.40ch	AT4G290	PAP2, IAA	PAP2 (PH	chr4:143	9.86758	13.6985	12.284	11.4444	49.7015	26.7195
GT	Sense	Sense	1.043	Detected	-1.043	Comprom	0.000	3.654	Detected	3.165	Detected	3.410	0.086	GT	Sens	contig241	contig241	Unknown	AGCTCA	contig241	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig241	Solyc05g	Unknown Protein (A		SL2.40ch	AT3G52700.1		unknown	chr3:195	20.3036	4.50062	45.2161	3.96167	128.341	91.1861
GT	Sense	Sense	-0.402	Detected	0.402	Detected	0.000	2.052	Detected	1.440	Detected	1.746	0.075	GT	Sens	contig241	contig241	Unknown	ATATGC	contig241	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig241	Solyc09g	Unknown Protein (A		SL2.40ch	AT3G073	ATCSLC	ATCSLC	chr3:233	52.26	85.902	262.943	135.086	296.248	193.272
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	2.030	Detected	1.533	Detected	1.781	0.020	GT	Sens	contig241	contig241	Tubulin b	TGCAGT	contig241	Solyc06g	Solyc06g	Tubulin b	GO:0043	GO:0043	contig241	Solyc06g	Tubulin b	GO:0005	SL2.40ch	AT2G295	TUB7	TUB7: st	chr2:126	74.3243	65.2051	145.793	79.7362	303.199	214.178
GT	Sense	Sense	-0.176	Detected	0.176	Detected	0.000	1.416	Detected	0.977	Detected	1.197	0.051	GT	Sens	contig241	contig241	Chromos	GAGAAA	contig241	Solyc09g	Solyc09g	Chromosome 04 contig 1 DNA			contig241	Solyc09g	Chromosome 04 co		SL2.40ch	AT1G05385.1		photosys	chr1:158	137.39	164.915	277.018	140.13	428.227	315.109
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	1.596	Detected	1.450	Detected	1.523	0.011	GT	Sens	contig241	contig241	cDNA clo	TCTGAT	contig241	Solyc10g	Solyc10g	cDNA clone J013057C16 full in			contig241	Solyc10g	cDNA clone J01305		SL2.40ch	AT3G20730.1		pentatric	chr3:724	697.135	535.871	1355.77	873.652	1970.36	1775.22
GT	Sense	Sense	-0.093	Detected	0.093	Detected	0.000	1.288	Detected	1.060	Detected	1.174	0.015	GT	Sens	contig242	contig242	Protease	CATGCT	contig242	Solyc11g	Solyc11g	Protease (AHRD V1 ***- C8TDY			contig242	Solyc11g	Protease (AHRD V1		SL2.40ch	AT2G388	HTA8	HTA8 (HI	chr2:162	185.159	198.262	229.863	194.021	498.844	424.85
GT	Sense	Sense	-0.355	Detected	0.355	Detected	0.000	1.734	Detected	1.499	Detected	1.617	0.050	GT	Sens	contig242	contig242	YABBY-lil	TCTACA	contig242	Solyc06g	Solyc06g	YABBY-lil	GO:0003	GO:0003	contig242	Solyc06g	YABBY-lil	GO:0003	SL2.40ch	AT1G084	YAB2	YAB2 (Y	chr1:267	154.014	237.152	301.833	238.752	677.891	574.485
GT	Sense	Sense	-0.335	Detected	0.335	Detected	0.000	1.330	Detected	1.057	Detected	1.194	0.081	GT	Sens	contig242	contig242	NPR1-like	CTCTTC	contig242	Solyc04g	Solyc04g	NPR1-like	GO:0005	GO:0005	contig242	Solyc04g	NPR1-like	GO:0005	SL2.40ch	AT2G413	BOP2	BOP2 (B	chr2:172	105.265	157.698	176.255	89.613	345.466	285.035
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	1.545	Detected	1.267	Detected	1.406	0.011	GT	Sens	contig242	contig242	Glucan sy	TTAGCT	contig242	Solyc07g	Solyc07g	Glucan sy	GO:0016	GO:0016	contig242	Solyc07g	Glucan sy	GO:0016	SL2.40ch	AT3G145	ATGSL04	ATGSL0	chr3:489	799.288	796.689	1304.13	1206.61	2483.35	2041.19
GT	Sense	Sense	-0.080	Comprom	0.080	Comprom	0.000	1.843	Detected	1.792	Detected	1.817	0.002	GT	Sens	contig242	contig242	Unknown	AGGCAA	contig242	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig242	Solyc04g	Unknown Protein (A		SL2.40ch	AT4G34330.1		unknown	chr4:164	3.62556	3.8092	13.0947	5.73447	14.2176	13.6821
GT	Sense	Sense	-0.226	Detected	0.226	Detected	0.000	1.628	Detected	1.564	Detected	1.596	0.020	GT	Sens	contig243	contig243	RAG1-act	CCCAAG	contig243	Solyc01g	Solyc01g	RAG1-act	GO:0016	GO:0016	contig243	Solyc01g	RAG1-act	GO:0016	SL2.40ch	AT5G236	MTN3	MTN3 (A	chr5:797	557.436	717.612	960.057	953.572	2084.65	1987.79
GT	Sense	Sense	-0.222	Detected	0.222	Detected	0.000	2.077	Detected	1.387	Detected	1.732	0.052	GT	Sens	contig243	contig243	Receptor	CAAGTT	contig243	Solyc10g	Solyc10g	Receptor	GO:0006	GO:0006	contig243	Solyc10g	Receptor	GO:0005	SL2.40ch	AT3G03770.1		leucine-r	chr3:945	59.3311	75.9833	139.635	81.312	302.115	186.715
GT	Sense	Sense	-0.204	Detected	0.204	Detected	0.000	1.607	Detected	1.123	Detected	1.365	0.050	GT	Sens	contig243	contig243	Nuclear t	TTGATG	contig243	Solyc01g	Solyc01g	Nuclear t	GO:0003	GO:0003	contig243	Solyc01g	Nuclear t	GO:0003	SL2.40ch	AT1G090	NF-YB4	NF-YB4 (	chr1:290	41.8785	52.2829	76.4652	102.911	151.949	108.323
GT	Sense	Sense	-0.205	Detected	0.205	Detected	0.000	1.225	Detected	1.013	Detected	1.119	0.040	GT	Sens	contig243	contig243	Ubiquitin-	GATGAC	contig243	Solyc01g	Solyc01g	Ubiquitin-	GO:0005	GO:0005	contig243	Solyc01g	Ubiquitin-	GO:0005	SL2.40ch	AT4G06599.1		ubiquitin	chr4:366	385.012	481.243	698.927	467.163	1072.97	923.623
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	1.652	Detected	1.172	Detected	1.412	0.029	GT	Sens	contig243	contig243	Unknown	TTGAAG	contig243	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig243	Solyc02g	Unknown Protein (A		SL2.40ch	AT2G236	YCF37	YCF37 (A	chr2:100	5549.11	5576.31	11961.6	6807.03	18644.3	13324.6
GT	Sense	Sense	-0.336	Comprom	0.336	Comprom	0.000	1.913	Detected	7.638	Detected	4.776	0.239	GT	Sens	contig243	contig243	Unknown	CTTGGA	contig243	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig243	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G238	AAP7	AAP7: an	chr5:802	2.16558	3.24681	4.8341	20.3597	10.6505	561.744
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	1.154	Detected	1.622	Detected	1.388	0.034	GT	Sens	contig244	contig244	HAT famil	CAAGAG	contig244	Solyc11g	Solyc11g	HAT famil	GO:0003	GO:0003	contig244	Solyc11g	HAT famil	GO:0003	SL2.40ch	AT2G42450.1		lipase cla	chr2:176	15.9184	12.703	26.1917	42.3838	33.7518	46.5274
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	1.287	Detected	1.021	Detected	1.154	0.014	GT	Sens	contig244	contig244	Potassiu	GTTCGC	contig244	Solyc07g	Solyc07g	Potassiu	GO:0016	GO:0016	contig244	Solyc07g	Potassiu	GO:0030	SL2.40ch	AT4G301	HMA2	HMA2: ca	chr4:147	4135.73	4044.06	5619.17	5256.33	10639.5	8823.85
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	1.428	Detected	0.999	Detected	1.214	0.046	GT	Sens	contig244	contig244	Lipase (A	AGTGCA	contig244	Solyc09g	Solyc09g	Lipase (A	GO:0006	GO:0006	contig244	Solyc09g	Lipase (A	GO:0006	SL2.40ch	AT4G13550.1		triacylgly	chr4:787	244.21	288.757	482.342	218.482	762.212	564.29
GT	Sense	Sense	-0.060	Detected	0.060	Detected	0.000	1.227	Detected	1.204	Detected	1.215	0.003	GT	Sens	contig244	contig244	NHL repe	CAAGAA	contig244	Solyc02g	Solyc02g	NHL repeat-containing protein			contig244	Solyc02g	NHL repeat-containi		SL2.40ch	AT1G23880.1		NHL repe	chr1:843	335.412	342.915	539.869	667.726	846.36	830.82
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	1.844	Detected	0.996	Detected	1.420	0.080	GT	Sens	contig244	contig244	Ribonucl	TTTTGT	contig244	Solyc10g	Solyc10g	Ribonucleoside hydrolase 1 (A			contig244	Solyc10g	Ribonucleoside hyd		SL2.40ch	AT2G363	URH1	URH1 (U	chr2:152	26.1131	26.091	25.9105	21.6377	99.9425	55.3317
GT	Sense	Sense	-0.297	Detected	0.297	Detected	0.000	1.724	Detected	1.269	Detected	1.497	0.057	GT	Sens	contig245	contig245	Carboxyl	CCATTT	contig245	Solyc02g	Solyc02g	Carboxyl	GO:0008	GO:0008	contig245	Solyc02g	Carboxyl	GO:0008	SL2.40ch	AT4G36470.1		S-adeno	chr4:172	5210.96	7404.47	14934.9	9735.51	21883.9	15919.8
GT	Sense	Sense	0.012	Comprom	-0.012	Comprom	0.000	2.484	Detected	2.058	Detected	2.271	0.009	GT	Sens	contig245	contig245	F-box fan	ATTTCAT	contig245	Solyc03g	Solyc03g	F-box family protein (AHRD V1			contig245	Solyc03g	F-box family protein		SL2.40ch	AT1G51720.1		glutamat	chr1:191	7.88322	7.29734	43.6924	26.095	45.2416	33.5782
GT	Sense	Sense	-0.047	Comprom	0.047	Comprom	0.000	2.837	Detected	2.750	Detected	2.794	0.001	GT	Sens	contig245	contig245	Unknown	AGGATT	contig245	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)%			contig245	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G129	CLE40	CLE40 (C	chr5:410	2.18736	2.19705	9.51591	5.03958	16.7049	15.6812
GT	Sense	Sense	0.157	Detected	-0.157	Detected	0.000	1.691	Detected	1.721	Detected	1.706	0.008	GT	Sens	contig245	contig245	Plant vira	TGAGTA	contig245	Solyc01g	Solyc01g	Plant viral-response family pro			contig245	Solyc01g	Plant viral-response		SL2.40ch	AT1G55230.1		unknown	chr1:206	298.722	226.041	453.944	318.031	894.958	910.518
GT	Sense	Sense	-0.092	Comprom	0.092	Comprom	0.000	2.542	Detected	4.784	Detected	3.663	0.083	GT	Sens	contig245	contig245	Laccase-	AGAGAT	contig245	Solyc01g	Solyc01g	Laccase-	GO:0055	GO:0055	contig245	Solyc01g	Laccase-	GO:0055	SL2.40ch	AT1G55560.1				2.05066	2.19323	9.57614	3.67606	13.1671	62.1139
GT	Sense	Sense	0.394	Detected	-0.394	Detected	0.000	1.711	Detected	1.280	Detected	1.496	0.079	GT	Sens	contig245	contig245	Fructose-	AGAGGC	contig245	Solyc07g	Solyc07g	Fructose-	GO:0006	GO:0006	contig245	Solyc07g	Fructose-	GO:0005	SL2.40ch	AT4G26530.2		fructose-	chr4:133	520.418	283.658	1893.86	739.068	1341.49	992.2
GT	Sense	Sense	0.072	Comprom	-0.072	Comprom	0.000	0.973	Detected	1.409	Detected	1.191	0.035	GT	Sens	contig245	contig245	Retrotran	AAATCA	contig245	Solyc04g	Solyc04g	Retrotransposon gag protein (			contig245	Solyc04g	Retrotransposon ga		SL2.40ch	AT1G56230.1		unknown	chr1:210	6.31299	5.3753	4.19296	10.6574	12.1958	16.4476
GT	Sense	Sense	-0.805	Comprom	0.805	Detected	0.000	1.550	Detected	1.310	Detected	1.430	0.221	GT	Sens	contig245	contig245	Growth-r	TCACCA	contig245	Solyc07g	Solyc07g	Growth-r	GO:0005	GO:0005	contig245	Solyc07g	Growth-r	GO:0005	SL2.40ch	AT3G139	AtGRF5	AtGRF5 (	chr3:460	7.54083	21.6567	13.5572	19.4922	39.9085	33.6949
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	1.047	Detected	1.018	Detected	1.033	0.012	GT	Sens	contig246	contig246	Unknown	GATGTG	contig246	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig246	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G11390.1		unknown	chr5:363	60.6913	48.6679	63.4507	57.0791	119.735	117.052
GT	Sense	Sense	-0.286	Detected	0.286	Detected	0.000	1.536	Detected	1.443	Detected	1.489	0.036	GT	Sens	contig246	contig246	Unknown	CAAGGC	contig246	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig246	Solyc10g	Unknown Protein (A		SL2.40ch	AT1G07050.1		CONSTA	chr1:216	97.3521	136.184	259.157	163.101	355.946	332.76
GT	Sense	Sense	0.320	Detected	-0.320	Detected	0.000	2.122	Detected	1.283	Detected	1.702	0.084	GT	Sens	contig246	contig246	Unknown	GATGAG	contig246	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig246	Solyc10g	Unknown Protein (A		SL2.40ch	AT3G63300.2		phospho	chr3:233	729.531	440.247	1701.67	781.465	2630.43	1465.77
GT	Sense	Sense	-0.227	Detected	0.227	Detected	0.000	1.512	Detected	1.339	Detected	1.425	0.028	GT	Sens	contig246	contig246	Glucose t	ACATTC	contig246	Solyc01g	Solyc01g	Glucose t	GO:0016	GO:0016	contig246	Solyc01g	Glucose t	GO:0016	SL2.40ch	AT3G20460.1		sugar tra	chr3:713	3044.87	3925.55	6715.78	4834.56	10512.9	9299.64
GT	Sense	Sense	0.691	Comprom	-0.691	Comprom	0.000	2.663	Detected	1.922	Detected	2.293	0.100	GT	Sens	contig247	contig247	Unknown	AAGCTT	contig247	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig247	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G12900.1		unknown	chr5:407	6.69114	2.41464	14.1556	11.2061	27.1476	16.1994
GT	Sense	Sense	-0.213	Comprom	0.213	Comprom	0.000	1.727	Detected	3.201	Detected	2.464	0.085	GT	Sens	contig247	contig247	Pectinest	TATGAA	contig247	Solyc01g	Solyc01g	Pectinest	GO:0030	GO:0030	contig247	Solyc01g	Pectinest	GO:0005	SL2.40ch	AT5G49180.1		pectines	chr5:199	5.36879	6.78582	5.28253	2.75911	21.3046	58.9988
GT	Sense	Sense	-0.263	Detected	0.263	Detected	0.000	1.590	Detected	1.402	Detected	1.496	0.033	GT	Sens	contig248	contig248	REF-like s	GTGTTG	contig248	Solyc05g	Solyc05g	REF-like stress related protein			contig248	Solyc05g	REF-like stress relat		SL2.40ch	AT1G67360.1		rubber e	chr1:252	3750.05	5080.62	7845.95	5960.97	14012.3	12266.1
GT	Sense	Sense	0.076	Detected	-0.076	Detected	0.000	1.056	Detected	1.002	Detected	1.029	0.006	GT	Sens	contig248	contig248	Unknown	CATGGG	contig248	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig248	Solyc08g	Unknown Protein (A		SL2.40ch	AT4G19840.1				98.2798	83.2258	160.51	133.25	200.548	192.585
GT	Sense	Sense	-0.067	Detected	0.067	Detected	0.000	1.053	Detected	1.042	Detected	1.047	0.004	GT	Sens	contig248	contig248	Telomere	AAGTGA	contig248	Solyc06g	Solyc06g	Telomere	GO:0003	GO:0003	contig248	Solyc06g	Telomere	GO:0003	SL2.40ch	AT1G075	TRFL2	TRFL2 (T	chr1:231	18.9731	19.5897	15.4994	24.5145	42.6451	42.216
GT	Sense	Sense	-0.179	Detected	0.179	Detected	0.000	1.103	Detected	1.265	Detected	1.184	0.026	GT	Sens	contig249	contig249	NPR1-like	GTGTAT	contig249	Solyc10g	Solyc10g	NPR1-like	GO:0005	GO:0005	contig249	Solyc10g	NPR1-like	GO:0005	SL2.40ch	AT2G413	BOP2	BOP2 (B	chr2:172	1626.56	1961.87	2598.6	2986.75	4092.41	4565.86
GT	Sense	Sense	-0.590	Detected	0.590	Detected	0.000	1.297	Detected	1.081	Detected	1.189	0.186	GT	Sens	contig249	contig249	Cellulose	TGTGCT	contig249	Solyc02g	Solyc02g	Cellulose	GO:0016	GO:0016	contig249	Solyc02g	Cellulose	GO:0016	SL2.40ch	AT4G187	CESA8, IF	IRX1 (IRR	chr4:103	81.823	174.395	199.716	136.36	313.107	268.643
GT	Sense	Sense	0.226	Comprom	-0.226	Comprom	0.000	2.174	Detected	3.364	Detected	2.769	0.049	GT	Sens	contig249	contig249	Leucine-r	ACTATT	contig249	Solyc03g	Solyc03g	Leucine-rich repeat receptor-li			contig249	Solyc11g	Retrograde Golgi tra		SL2.40ch	AT3G01260.1				4.43142	3.04787	2.72602	2.75194	17.6854	40.2291
GT	Sense	Sense	-0.483	Comprom	0.483	Comprom	0.000	2.074	Detected	1.761	Detected	1.917	0.063	GT	Sens	contig250	contig250	Unknown	AAGTGT	contig250	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig250	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G01850.1		protein k	chr5:332	3.07536	5.65125	12.2794	14.04	18.7134	15.0217
GT	Sense	Sense	-0.205	Detected	0.205	Detected	0.000	1.477	Detected	0.954	Detected	1.215	0.067	GT	Sens	contig250	contig250	Cellulose	GTCAAG	contig250	Solyc03g	Solyc03g	Cellulose	GO:0016	GO:0016	contig250	Solyc03g	Cellulose	GO:0016	SL2.40ch	AT1G654	GTB1	GTB1: RI	chr1:243	1183.97	1480.86	2853.91	2027.27	3930.48	2726.36
GT	Sense	Sense	0.473	Detected	-0.473	Comprom	0.000	3.946	Detected	3.749	Detected	3.847	0.015	GT	Sens	contig250	contig250	Unknown	GAAAAA	contig250	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig250	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G30320.1		unknown	chr3:119	12.685	6.19602	48.7065	46.6864	145.665	126.732
GT	Sense	Sense	1.010	Comprom	-1.010	Comprom	0.000	1.303	Detected	2.006	Detected	1.655	0.262	GT	Sens	contig250	contig250	Ethylene	GTAAAA	contig250	Solyc03g	Solyc03g	Ethylene	GO:0003	GO:0003	contig250	Solyc03g	Ethylene	GO:0016	SL2.40ch	AT3G232	ERF1, AT	ERF1 (ET	chr3:829	9.43623	2.19012	16.0821	11.7643	11.9643	19.4114
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	1.295	Detected	0.834	Detected	1.064	0.044	GT	Sens	contig250	contig250	Plastoqui	CCTGCA	contig250	Solyc01g	Solyc01g	Plastoqui	GO:0009	GO:0009	contig250	Solyc01g	Plastoqui	GO:0009	SL2.40ch	AT2G26500.1		cytochro	chr2:112	1709.4	1573.5	5080.28	2380.91	4291.29	3108.06
GT	Sense	Sense	0.107	Detected	-0.107	Detected	0.000	2.813	Detected	1.758	Detected	2.286	0.051	GT	Sens	contig250	contig250	Carbonic	TGTGAA	contig250	Solyc02g	Solyc02g	Carbonic	GO:0005	GO:0005	contig250	Solyc02g	Carbonic	GO:0005	SL2.40ch	AT5G147	CA2, CA1	CA2 (CA	chr5:475	788.681	639.648	5291.87	2268.97	5323.16	2553.95
GT	Sense	Sense	-0.025	Detected	0.025	Detected	0.000	1.974	Detected	2.235	Detected	2.104	0.004	GT	Sens	contig251	contig251	Light regu	TGTCTAT	contig251	Solyc09g	Solyc09g	Light regulated protein-like pro			contig251	Solyc09g	Light regulated prot		SL2.40ch	AT3G267	CCL	CCL (CC	chr3:982	13.4585	13.1132	98.5101	26.8098	55.6416	66.4741
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	1.846	Detected	1.205	Detected	1.525	0.043	GT	Sens	contig251	contig251	Fatty acid	TAGATG	contig251	Solyc05g	Solyc05g	Fatty acid	GO:0009	GO:0009	contig251	Solyc05g	Fatty acid	GO:0009	SL2.40ch	AT1G685	CUT1, PO	KCS6 (3-	chr1:257	37.7599	32.4169	64.8034	57.9344	134.084	85.755
GT	Sense	Sense	0.250	Detected	-0.250	Detected	0.000	1.109	Detected	0.993	Detected	1.051	0.055	GT	Sens	contig251	contig251	Movemen	GGATGC	contig251	Solyc09g	Solyc09g	Movemen	GO:0006	GO:0006	contig251	Solyc09g015550.1.1				AT5G60430.2		antiporte	chr5:243	258.333	171.877	228.442	244.183	484.593	445.92
GT	Sense	Sense	0.112	Detected	-0.112	Detected	0.000	1.853	Detected	0.894	Detected	1.374	0.108	GT	Sens	contig251	contig251	Transcrip	GATCAT	contig251	Solyc10g	Solyc10g	Transcrip	GO:0003	GO:0003	contig251	Solyc10g	Transcrip	GO:0003	SL2.40ch	AT2G41130.1		basic hel	chr2:171	20.9689	16.8984	29.7794	21.1404	72.5225	37.1917
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	1.287	Detected	1.227	Detected	1.257	0.011	GT	Sens	contig251	contig251	Unknown	GGACGA	contig251	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig251	Solyc07g	Unknown Protein (A		SL2.40ch	AT4G00300.1		fringe-re	chr4:126	138.841	109.447	274.513	201.479	320.75	306.862
GT	Sense	Sense	-0.738	Comprom	0.738	Detected	0.000	1.122	Detected	1.035	Detected	1.078	0.282	GT	Sens	contig251	contig251	GDSL est	TAATATT	contig251	Solyc01g	Solyc01g	GDSL est	GO:0006	GO:0006	contig251	Solyc01g	GDSL est	GO:0004	SL2.40ch	#N/A	#N/A	#N/A	#N/A	4.34283	11.3663	7.90027	10.9693	16.3068	15.304
GT	Sense	Sense	-0.386	Detected	0.386	Detected	0.000	1.145	Detected	0.880	Detected	1.013	0.131	GT	Sens	contig252	contig252	Unknown	TTATCG	contig252	Solyc03g	Solyc03g	Unknown Protein (AHRD V1):O			contig252	Solyc03g	Unknown	GO:0005	SL2.40ch	AT2G454	LBD19	LBD19 (L	chr2:187	484.829	778.478	920.046	777.357	1449.02	1202.13
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	1.257	Detected	1.036	Detected	1.146	0.020	GT	Sens	contig252	contig252	Unknown	GGCAGC	contig252	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig252	Solyc06g	Unknown Protein (A		SL2.40ch	AT2G297	UGT71C1	UGT71C	chr2:127	30.3467	33.7953	54.0391	49.0186	81.6318	69.8007
GT	Sense	Sense	0.348	Detected	-0.348	Detected	0.000	2.001	Detected	0.869	Detected	1.435	0.163	GT	Sens	contig252	contig252	Lipoxyge	CCACTG	contig252	Solyc01g	Solyc01g	Lipoxyge	GO:0016	GO:0016	contig252	Solyc01g	Lipoxyge	GO:0016	SL2.40ch	AT1G550	LOX1	LOX1: lir	chr1:205	28.6207	16.6302	32.1657	25.6567	93.0997	42.3685
GT	Sense	Sense	-0.208	Detected	0.208	Detected	0.000	1.022	Detected	1.115	Detected	1.068	0.037	GT	Sens	contig252	contig252	Glutaredo	TGAGAT	contig252	Solyc11g	Solyc11g	Glutaredo	GO:0045	GO:0045	contig252	Solyc11g	Glutaredo	GO:0045	SL2.40ch	AT5G11930.1		glutared	chr5:384	2036.49	2555.96	3529.92	3092.3	4941.41	5253.06
GT	Sense	Sense	-0.123	Detected	0.123	Detected	0.000	1.255	Detected	1.061	Detected	1.158	0.018	GT	Sens	contig253	contig253	Unknown	TGCAGC	contig253	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)%			contig253	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G44180.1		homeob	chr5:177	1019.96	1138.2	1776.38	1351.89	2742.88	2389.79
GT	Sense	Sense	0.182	Comprom	-0.182	Comprom	0.000	3.207	Detected	1.472	Detected	2.340	0.119	GT	Sens	contig253	contig253	SNF2 dor	GGATGA	contig253	Solyc03g	Solyc03g	SNF2 domain-containing prote			contig253	Solyc03g	SNF2 domain-conta		SL2.40ch	AT1G44120.1		C2 doma	chr1:167	6.19883	4.53024	10.8076	7.95654	52.1888	15.6299
GT	Sense	Sense	-0.691	Detected	0.691	Detected	0.000	3.478	Detected	1.639	Detected	2.558	0.156	GT	Sens	contig253	contig253	NHL1 (Fra	TGGGTT	contig253	Solyc03g	Solyc03g	NHL1 (Fragment) (AHRD V1 **-			contig253	Solyc03g	NHL1 (Fragment) (A		SL2.40ch	AT1G03060.1		WD-40 re	chr1:712	15.3099	37.5561	115.501	28.3527	284.992	79.3805
GT	Sense	Sense	0.236	Comprom	-0.236	Comprom	0.000	2.062	Detected	2.037	Detected	2.050	0.013	GT	Sens	contig253	contig253	Unknown	GTATGG	contig253	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig253	Solyc09g	Unknown Protein (A		SL2.40ch	AT2G43970.2		La doma	chr2:182	3.25538	2.20853	7.73165	2.90871	11.9424	11.6995
GT	Sense	Sense	0.109	Comprom	-0.109	Comprom	0.000	5.456	Detected	2.537	Detected	3.997	0.112	GT	Sens	contig253	contig253	RING fing	ATTGAT	contig253	Solyc12g	Solyc12g	RING fing	GO:0008	GO:0008	contig253	Solyc12g	RING fing	GO:0008	SL2.40ch	AT4G35510.1		unknown	chr4:168	2.71707	2.19912	3.85968	2.40083	114.434	15.087
GT	Sense	Sense	0.632	Comprom	-0.632	Comprom	0.000	2.230	Detected	2.954	Detected	2.592	0.071	GT	Sens	contig253	contig253	IFA bindi	TTTGGT	contig253	Solyc12g	Solyc12g	IFA binding protein (AHRD V1			contig253	Solyc12g	IFA binding protein		SL2.40ch	ATCG007	PETD	A chloro	chrC:764	5.82734	2.28184	14.9439	13.707	18.2373	30.0437
GT	Sense	Sense	-0.431	Comprom	0.431	Detected	0.000	1.819	Detected	1.474	Detected	1.646	0.071	GT	Sens	contig253	contig253	Ulp1 prot	TCTGCT	contig253	Solyc07g	Solyc07g	Ulp1 protease family C-termina			contig253	Solyc07g	Ulp1 protease family		SL2.40ch	AT1G49530.1				7.24249	12.3915	21.5658	22.1124	35.6424	27.981
GT	Sense	Sense	0.073	Comprom	-0.073	Comprom	0.000	1.996	Detected	1.299	Detected	1.647	0.044	GT	Sens	contig253	contig253	Ycf2 (AHF	GCGTTT	contig253	Solyc12g	Solyc12g	Ycf2 (AHF	GO:0009	GO:0009	contig253	Solyc12g035980.1.1				AT3G53560.1		chloropla	chr3:198	8.39396	7.1402	15.4162	11.1059	32.9231	20.2544
GT	Sense	Sense	-0.364	Detected	0.364	Detected	0.000	1.115	Detected	1.168	Detected	1.141	0.089	GT	Sens	contig253	contig253	Purple ac	GTTAAA	contig253	Solyc12g	Solyc12g	Purple ac	GO:0046	GO:0046	contig253	Solyc12g	Purple ac	GO:0016	SL2.40ch	AT5G348	ATPAP26	PAP26 (F	chr5:131	1314.9	2048.3	3366.92	2541.07	3789.74	3920.58
GT	Sense	Sense	-0.195	Detected	0.195	Detected	0.000	1.820	Detected	1.312	Detected	1.566	0.039	GT	Sens	contig254	contig254	Receptor	ACTAAA	contig254	Solyc07g	Solyc07g	Receptor	GO:0005	GO:0005	contig254	Solyc07g	Receptor	GO:0001	SL2.40ch	AT4G30520.1		leucine-r	chr4:149	142.126	175.195	313.807	205.76	594.191	416.563
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	1.283	Detected	1.018	Detected	1.151	0.037	GT	Sens	contig254	contig254	Glucosyl	ATTTATT	contig254	Solyc01g	Solyc01g	Glucosyl	GO:0010	GO:0010	contig254	Solyc01g	Glucosyl	GO:0010	SL2.40ch	AT1G67270.1		FUNCTIO	chr1:251	32.7553	23.7903	49.3362	25.6411	72.4543	60.0956
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	2.289	Detected	1.438	Detected	1.864	0.050	GT	Sens	contig254	contig254	LRR rece	TCGAAA	contig254	Solyc05g	Solyc05g	LRR rece	GO:0004	GO:0004	contig254	Solyc05g	Pto-like, S	GO:0004	SL2.40ch	AT1G67720.1		leucine-r	chr1:253	204.383	217.018	485.077	356.981	1097.73	606.882
GT	Sense	Sense	-0.505	Detected	0.505	Detected	0.000	2.616	Detected	2.349	Detected	2.483	0.041	GT	Sens	contig255	contig255	Metal ion	AGCACT	contig255	Solyc02g	Solyc02g	Metal ion	GO:0046	GO:0046	contig255	Solyc02g	Metal ion	GO:0046	SL2.40ch	AT1G312	ZIP10	ZIP10 (ZI	chr1:111	17.5137	33.1766	47.134	62.0035	157.626	130.611
GT	Sense	Sense	0.588	Detected	-0.588	Detected	0.000	2.395	Detected	1.205	Detected	1.800	0.164	GT	Sens	contig255	contig255	LRR rece	GGTAAT	contig255	Solyc07g	Solyc07g	LRR rece	GO:0004	GO:0004	contig255	Solyc07g	LRR rece	GO:0004	SL2.40ch	AT5G18610.1		protein k	chr5:619	128.653	53.5417	151.461	128.525	465.497	203.455
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	1.708	Detected	1.200	Detected	1.454	0.029	GT	Sens	contig255	contig255	Myb famil	CCTTCT	contig255	Solyc08g	Solyc08g	Myb fami	GO:0045449		contig255	Solyc08g	Myb famil	GO:0045	SL2.40ch	AT1G322	KAN2	KAN2 (K	chr1:116	110.112	102.015	287.191	186.77	369.129	258.896
GT	Sense	Sense	-0.174	Detected	0.174	Detected	0.000	1.969	Detected	2.105	Detected	2.037	0.008	GT	Sens	contig255	contig255	Peptide tr	ACATTT	contig255	Solyc02g	Solyc02g	Peptide tr	GO:0080	GO:0080	contig255	Solyc02g	Peptide tr	GO:0080	SL2.40ch	AT3G01350.1		proton-d	chr3:135	1008.99	1208.67	2759.24	3552.25	4610.01	5049.54
GT	Sense	Sense	0.048	Comprom	-0.048	Comprom	0.000	1.826	Detected	1.591	Detected	1.709	0.005	GT	Sens	contig256	contig256	Unknown	GAGAAG	contig256	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig256	Solyc07g	Unknown Protein (A		SL2.40ch	AT1G563	CRT1	CRT1 (C	chr1:210	9.83845	8.66576	25.3005	19.1837	34.923	29.5694
GT	Sense	Sense	-0.108	Comprom	0.108	Comprom	0.000	5.250	Detected	5.608	Detected	5.429	0.001	GT	Sens	contig256	contig256	1-aminoc	TGACAA	contig256	Solyc09g	Solyc09g	1-aminoc	GO:0016	GO:0016	contig256	Solyc09g	1-aminoc	GO:0009	SL2.40ch	AT1G78550.1		oxidored	chr1:295	2.05843	2.24934	114.339	84.5272	87.3008	111.613
GT	Sense	Sense	-0.070	Detected	0.070	Detected	0.000	1.644	Detected	0.885	Detected	1.265	0.082	GT	Sens	contig256	contig256	Genomic	GCTAAA	contig256	Solyc06g	Solyc06g	Genomic DNA chromosome 5			contig256	Solyc06g	Genomic DNA chror		SL2.40ch	AT2G20330.1		transduc	chr2:877	129.588	134.42	172.552	160.965	439.897	259.143
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	1.287	Detected	0.851	Detected	1.069	0.039	GT	Sens	contig257	contig257	MADS-bo	TGGTAG	contig257	Solyc04g	Solyc04g	MADS-bo	GO:0005	GO:0005	contig257	Solyc04g	MADS-bo	GO:0017	SL2.40ch	AT4G36590.1		MADS-bo	chr4:172	154.901	146.61	145.106	189.749	392.256	288.968
GT	Sense	Sense	0.267	Detected	-0.267	Detected	0.000	1.594	Detected	1.015	Detected	1.305	0.080	GT	Sens	contig257	contig257	Gibberell	AGCTTT	contig257	Solyc07g	Solyc07g	Gibberell	GO:0016	GO:0016	contig257	Solyc07g	Gibberelli	GO:0004	SL2.40ch	AT1G784	ATGA2OX	ATGA2O	chr1:295	917.284	595.858	2087.61	1175.67	2380.55	1588.84
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	1.533	Detected	1.088	Detected	1.310	0.028	GT	Sens	contig257	contig257	WD-repea	ATGTCA	contig257	Solyc06g	Solyc06g	WD-repea	GO:0004	GO:0004	contig257	Solyc06g	WD-repea	GO:0004	SL2.40ch	AT5G138	FZR3	FZR3 (FI	chr5:446	13.9384	12.6637	15.4825	15.7879	41.0099	30.0191
GT	Sense	Sense	-0.175	Comprom	0.175	Comprom	0.000	3.288	Detected	2.387	Detected	2.838	0.028	GT	Sens	contig258	contig258	Receptor	GTGTGA	contig258	Solyc02g	Solyc02g	Receptor	GO:0006	GO:0006	contig258	Solyc02g	Receptor	GO:0006	SL2.40ch	AT1G56120.1		kinase	chr1:209	3.14482	3.77262	6.94669	10.2386	35.8847	19.1552
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	1.839	Detected	1.348	Detected	1.593	0.025	GT	Sens	contig258	contig258	Peptidyl-p	ACTTCT	contig258	Solyc03g	Solyc03g	Peptidyl-p	GO:0006	GO:0006	contig258	Solyc03g	Peptidyl-p	GO:0006	SL2.40ch	AT1G74070.1		peptidyl-	chr1:278	174.187	147.278	538.937	284.164	610.859	433.436
GT	Sense	Sense	-0.319	Detected	0.319	Detected	0.000	1.230	Detected	1.550	Detected	1.390	0.060	GT	Sens	contig258	contig258	Unknown	CAAAGC	contig258	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig258	Solyc08g	Unknown Protein (A		SL2.40ch	AT4G027	SULTR3:	SULTR3:	chr4:118	5777.34	8463.57	13839.2	10844	17489.7	21769.5
GT	Sense	Sense	-0.346	Comprom	0.346	Detected	0.000	1.487	Detected	1.258	Detected	1.372	0.064	GT	Sens	contig258	contig258	Auxin effl	AATTGT	contig258	Solyc10g	Solyc10g	Auxin effl	GO:0016	GO:0016	contig258	Solyc10g	Auxin effl	GO:0016	SL2.40ch	AT1G230	PIN7	PIN7 (PIN	chr1:818	8.36358	12.7212	12.7611	14.9582	30.8263	26.2276
GT	Sense	Sense	0.190	Detected	-0.190	Detected	0.000	1.116	Detected	1.077	Detected	1.097	0.029	GT	Sens	contig258	contig258	BHLH tra	GGAGCT	contig258	Solyc07g	Solyc07g	BHLH trai	GO:0045449		contig258	Solyc07g	BHLH trai	GO:0005	SL2.40ch	AT3G20640.1		ethylene-	chr3:721	27.0017	19.5333	18.2399	14.4847	53.0757	51.5201
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	1.141	Detected	1.213	Detected	1.177	0.014	GT	Sens	contig259	contig259	HAT famil	ATGTTG	contig259	Solyc07g	Solyc07g	HAT family dimerisation doma			contig259	Solyc04g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	153.245	118.97	159.147	195.269	317.588	332.867
GT	Sense	Sense	0.269	Comprom	-0.269	Comprom	0.000	1.411	Detected	1.238	Detected	1.325	0.043	GT	Sens	contig259	contig259	Ribosoma	CGTTTT	contig259	Solyc08g	Solyc08g	Ribosomal protein-like (AHRD			contig259	Solyc08g	Ribosomal protein-li		SL2.40ch	AT3G31402.1		FUNCTIO	chr3:127	6.08678	3.94449	11.0828	6.2986	13.8938	12.2898
GT	Sense	Sense	-0.547	Detected	0.547	Detected	0.000	2.136	Detected	2.211	Detected	2.173	0.058	GT	Sens	contig259	contig259	ARGONA	TCACGT	contig259	Solyc12g	Solyc12g	ARGONA	GO:0003	GO:0003	contig259	Solyc12g	ARGONA	GO:0019	SL2.40ch	AT5G438	ZLL, PNH	ZLL (ZWI	chr5:176	115.032	230.977	272.567	348.016	763.806	802.138
GT	Sense	Sense	0.130	Detected	-0.130	Detected	0.000	1.385	Detected	0.888	Detected	1.137	0.056	GT	Sens	contig259	contig259	Auxin-res	ATGCTT	contig259	Solyc10g	Solyc10g	Auxin-responsive protein (AHF			contig259	Solyc10g	Auxin-responsive p		SL2.40ch	AT5G41750.2		disease	chr5:166	22.4745	17.6715	44.3715	35.2163	55.5075	39.2125
GT	Sense	Sense	-0.092	Detected	0.092	Detected	0.000	1.836	Detected	1.487	Detected	1.662	0.014	GT	Sens	contig259	contig259	Meiosis 5	AAGAGG	contig259	Solyc07g	Solyc07g	Meiosis 5 (AHRD V1 *-*- B6T5X			contig259	Solyc07g	Meiosis 5 (AHRD V1		SL2.40ch	AT2G428	PDF1	PDF1 (PF	chr2:178	45.9774	49.116	68.6519	110.831	180.96	141.64
GT	Sense	Sense	-0.005	Detected	0.005	Detected	0.000	1.543	Detected	1.107	Detected	1.325	0.026	GT	Sens	contig260	contig260	MYB tran	TGATTTA	contig260	Solyc01g	Solyc01g	MYB tran	GO:0003	GO:0003	contig260	Solyc01g	MYB tran	GO:0003	SL2.40ch	AT4G094	ATMYB6	ATMYB6	chr4:599	1290.01	1222.26	2709.84	1566.27	3901.36	2875.3
GT	Sense	Sense	-0.086	Detected	0.086	Detected	0.000	1.098	Detected	1.185	Detected	1.141	0.007	GT	Sens	contig260	contig260	Unknown	GCCAGC	contig260	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)%			contig260	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G49070.1		unknown	chr3:181	2131.94	2259.9	4038.89	4106.33	5010.99	5304.44
GT	Sense	Sense	-0.246	Detected	0.246	Detected	0.000	1.188	Detected	1.193	Detected	1.190	0.040	GT	Sens	contig260	contig260	UDP-gluc	CAAAGA	contig260	Solyc03g	Solyc03g	UDP-gluc	GO:0008	GO:0008	contig260	Solyc03g	UDP-gluc	GO:0008	SL2.40ch	AT1G15890.1		disease	chr1:546	74.0812	97.9912	119.825	115.914	207	207.084
GT	Sense	Sense	-0.223	Comprom	0.223	Comprom	0.000	1.909	Detected	1.743	Detected	1.826	0.017	GT	Sens	contig260	contig260	Calmodul	ATGAAA	contig260	Solyc04g	Solyc04g	Calmodul	GO:0008	GO:0008	contig260	Solyc04g	Calmodul	GO:0008	SL2.40ch	AT5G14770.1		pentatric	chr5:477	6.22399	7.97476	20.0699	13.6827	28.218	25.0754
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	2.912	Detected	1.381	Detected	2.147	0.107	GT	Sens	contig260	contig260	Lysosom	GAAGGT	contig260	Solyc09g	Solyc09g	Lysosom	GO:0004	GO:0004	contig260	Solyc09g	Lysosom	GO:0004	SL2.40ch	AT5G65760.1		serine ca	chr5:263	21.3978	19.4149	27.0382	7.86495	163.606	56.4399
GT	Sense	Sense	-0.337	Detected	0.337	Detected	0.000	1.325	Detected	1.254	Detected	1.290	0.063	GT	Sens	contig260	contig260	Receptor	TAAAAT	contig260	Solyc08g	Solyc08g	Receptor	GO:0004	GO:0004	contig260	Solyc08g	Receptor	GO:0004	SL2.40ch	AT1G17230.1		ATP bind	chr1:589	82.5727	124.031	243.562	96.2092	270.387	256.682
GT	Sense	Sense	-0.335	Comprom	0.335	Comprom	0.000	0.865	Detected	1.308	Detected	1.086	0.114	GT	Sens	contig261	contig261	Leucine-r	CAAACA	contig261	Solyc05g	Solyc05g	Leucine-r	GO:0016	GO:0016	contig261	Solyc05g	LRR rece	GO:0016	SL2.40ch	AT3G21220.1				5.34327	7.99717	12.0005	9.08803	12.6941	17.2059
GT	Sense	Sense	-0.294	Comprom	0.294	Comprom	0.000	2.393	Detected	2.561	Detected	2.477	0.015	GT	Sens	contig261	contig261	Cysteine-	TCAACA	contig261	Solyc01g	Solyc01g	Cysteine-rich extensin-like pro			contig261	Solyc01g	Cysteine-rich exten		SL2.40ch	AT4G15160.2		lipid bind	chr4:864	2.26868	3.2081	2.36261	1.96408	15.1074	16.9277
GT	Sense	Sense	-0.056	Detected	0.056	Detected	0.000	1.111	Detected	1.140	Detected	1.126	0.003	GT	Sens	contig261	contig261	Calmodul	TTGTTT	contig261	Solyc09g	Solyc09g	Calmodulin protein kinase (Fra			contig261	Solyc04g	Synapton	GO:0005	SL2.40ch	#N/A	#N/A	#N/A	#N/A	599.489	609.946	607.586	574.196	1392.74	1416.99
GT	Sense	Sense	0.179	Comprom	-0.179	Comprom	0.000	1.916	Detected	1.739	Detected	1.827	0.012	GT	Sens	contig262	contig262	Purple ac	CGCGCA	contig262	Solyc04g	Solyc04g	Purple acid phosphatase 22 (A			contig262	Solyc07g	Purple ac	GO:0004	SL2.40ch	AT5G504	ATPAP27	PAP27 (F	chr5:205	4.80929	3.53018	8.25026	5.80751	16.5776	14.6224
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	1.343	Detected	1.321	Detected	1.332	0.045	GT	Sens	contig262	contig262	Glutaredo	ATTCTT	contig262	Solyc09g	Solyc09g	Glutaredo	GO:0045	GO:0045	contig262	Solyc09g	Glutaredo	GO:0008	SL2.40ch	AT2G30540.1		glutared	chr2:130	331.071	208.162	498.844	320.659	709.919	697.112
GT	Sense	Sense	-0.202	Detected	0.202	Detected	0.000	2.826	Detected	1.903	Detected	2.364	0.043	GT	Sens	contig262	contig262	Receptor	CTTGTC	contig262	Solyc11g	Solyc11g	Receptor	GO:0006	GO:0006	contig262	Solyc11g	Receptor	GO:0004	SL2.40ch	AT1G72180.1		leucine-r	chr1:271	538.775	670.407	1971.21	1293.56	4545.88	2389.05
GT	Sense	Sense	-0.334	Detected	0.334	Detected	0.000	3.123	Detected	1.801	Detected	2.462	0.080	GT	Sens	contig262	contig262	Myrosina	GAAACT	contig262	Solyc03g	Solyc03g	Myrosinase-binding protein 2			contig262	Solyc03g	Myrosinase-binding		SL2.40ch	AT5G531	FTSH11	FTSH11	chr5:215	98.1698	146.807	563.324	255.414	1115.37	444.78
GT	Sense	Sense	-0.585	Comprom	0.585	Comprom	0.000	1.904	Detected	1.725	Detected	1.814	0.092	GT	Sens	contig262	contig262	DNA-3-me	TCCATG	contig262	Solyc05g	Solyc05g	DNA-3-me	GO:0006	GO:0006	contig262	Solyc05g	DNA-3-me	GO:0006	SL2.40ch	AT3G52700.1		unknown	chr3:195	2.93899	6.22495	27.1837	19.6587	17.0686	15.0324
GT	Sense	Sense	0.362	Detected	-0.362	Detected	0.000	2.302	Detected	1.310	Detected	1.806	0.099	GT	Sens	contig263	contig263	Cinnamyl	AGACAT	contig263	Solyc05g	Solyc05g	Cinnamyl alcohol dehydrogen			contig263	Solyc11g	Alcohol d	GO:0008	SL2.40ch	AT1G02330.1		FUNCTIO	chr1:462	26.1941	14.9224	22.1612	21.9422	103.997	52.1034
GT	Sense	Sense	0.180	Detected	-0.180	Detected	0.000	1.316	Detected	0.826	Detected	1.071	0.072	GT	Sens	contig263	contig263	Accelerat	TAACAT	contig263	Solyc05g	Solyc05g	Accelerated cell death 6 (Frag			contig263	Solyc05g	Accelerated cell dea		SL2.40ch	AT4G242	MLO13, A	MLO13 (I	chr4:125	17.0548	12.5097	17.7828	16.3507	38.7674	27.5398
GT	Sense	Sense	0.708	Detected	-0.708	Comprom	0.000	2.006	Detected	1.891	Detected	1.948	0.111	GT	Sens	contig263	contig263	Unknown	ATCTTG	contig263	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig263	Solyc11g	Unknown Protein (A		SL2.40ch	AT1G60200.1		splicing	chr1:222	14.3733	5.06738	23.5757	18.9087	36.5449	33.6483
GT	Sense	Sense	-0.114	Comprom	0.114	Comprom	0.000	2.253	Detected	1.292	Detected	1.773	0.070	GT	Sens	contig263	contig263	Os11g01	AGTTGA	contig263	Solyc08g	Solyc08g	Os11g0198100 protein (Fragm			contig263	Solyc08g	Os11g0198100 prot		SL2.40ch	AT5G46220.1		unknown	chr5:187	5.20793	5.74301	14.6904	3.83088	27.8014	14.2425
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	2.079	Detected	1.396	Detected	1.738	0.039	GT	Sens	contig263	contig263	Sugar tra	CCTGGA	contig263	Solyc02g	Solyc02g	Sugar tra	GO:0055	GO:0055	contig263	Solyc02g	Sugar tra	GO:0005	SL2.40ch	AT1G08900.3		carbohy	chr1:285	188.843	200.981	406.258	214.407	877.825	545.293
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	1.945	Detected	1.517	Detected	1.731	0.015	GT	Sens	contig263	contig263	Plant-spe	CCATGG	contig263	Solyc11g	Solyc11g	Plant-specific domain TIGR01			contig263	Solyc11g	Plant-specific doma		SL2.40ch	AT3G29060.1		LOCATE	chr3:110	46.6621	43.076	183.119	100.735	184.142	136.383
GT	Sense	Sense	1.067	Detected	-1.067	Comprom	0.000	1.545	Detected	1.428	Detected	1.487	0.299	GT	Sens	contig264	contig264	Hypotheti	AAGTTG	contig264	Solyc10g	Solyc10g	Hypothetical chloroplast RF1 (			contig264	Solyc10g	Hypothetical chloro		SL2.40ch	AT4G04790.1		FUNCTIO	chr4:243	15.1763	3.25356	14.8624	13.3033	21.8686	20.104
GT	Sense	Sense	0.032	Detected	-0.032	Detected	0.000	3.854	Detected	2.656	Detected	3.255	0.032	GT	Sens	contig264	contig264	Auxin effl	GGATCA	contig264	Solyc02g	Solyc02g	Auxin effl	GO:0009	GO:0009	contig264	Solyc02g	Auxin effl	GO:0009	SL2.40ch	AT1G76520.2		auxin effl	chr1:287	437.697	393.74	1295	440.722	6403.44	2781.61
GT	Sense	Sense	-0.484	Detected	0.484	Detected	0.000	1.681	Detected	1.125	Detected	1.403	0.128	GT	Sens	contig264	contig264	ARGONA	ATTTGT	contig264	Solyc01g	Solyc01g	ARGONA	GO:0003	GO:0003	contig264	Solyc01g	ARGONA	GO:0019	SL2.40ch	AT1G694	AGO7, ZI	AGO7 (A	chr1:261	22.2077	40.8722	44.6256	30.3982	103.027	69.8676
GT	Sense	Sense	-0.557	Comprom	0.557	Comprom	0.000	1.019	Detected	1.788	Detected	1.404	0.174	GT	Sens	contig264	contig264	Unknown	AAGAAG	contig264	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig264	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G491	SUS2, SS	SUS2 (S	chr5:199	3.57634	7.27858	17.9467	11.6463	11.0268	18.7371
GT	Sense	Sense	0.559	Detected	-0.559	Detected	0.000	1.529	Detected	1.940	Detected	1.734	0.100	GT	Sens	contig265	contig265	Rhomboi	GGAATG	contig265	Solyc02g	Solyc02g	Rhomboi	GO:0016	GO:0016	contig265	Solyc02g	Rhomboi	GO:0016	SL2.40ch	AT5G38510.2		rhomboi	chr5:154	255.056	110.643	651.911	270.961	516.987	685.229
GT	Sense	Sense	0.264	Comprom	-0.264	Comprom	0.000	1.296	Detected	1.191	Detected	1.244	0.044	GT	Sens	contig265	contig265	Unknown	CGTGGA	contig265	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig265	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G11385.1		DC1 dom	chr3:356	8.64623	5.64151	5.08142	3.37361	18.2883	16.9557
GT	Sense	Sense	-0.272	Detected	0.272	Detected	0.000	1.381	Detected	0.880	Detected	1.131	0.092	GT	Sens	contig265	contig265	LOB dom	CAAATT	contig265	Solyc04g	Solyc04g	LOB domain protein 38 (AHRD			contig265	Solyc04g	LOB domain protei		SL2.40ch	AT4G375	LBD39	LBD39 (L	chr4:176	385.225	528.819	719.767	537.353	1253.34	883.337
GT	Sense	Sense	-0.056	Detected	0.056	Detected	0.000	1.393	Detected	1.059	Detected	1.226	0.020	GT	Sens	contig265	contig265	Protein ki	CTTGCA	contig265	Solyc12g	Solyc12g	Protein ki	GO:0006	GO:0006	contig265	Solyc12g	Protein ki	GO:0006	SL2.40ch	AT1G688	STN7	STN7 (St	chr1:258	1083.74	1101.86	1971.49	1276.96	3060.83	2421.05
GT	Sense	Sense	-0.133	Comprom	0.133	Comprom	0.000	1.406	Detected	1.332	Detected	1.369	0.010	GT	Sens	contig265	contig265	Desiccati	TCATAT	contig265	Solyc01g	Solyc01g	Desiccation-related protein PC			contig265	Solyc01g099150.2.1				AT1G14590.1		FUNCTIO	chr1:499	4.11273	4.65046	5.63065	11.4921	12.3556	11.7029
GT	Sense	Sense	-0.659	Comprom	0.659	Comprom	0.000	3.651	Detected	1.888	Detected	2.770	0.128	GT	Sens	contig265	contig265	RAG1-act	GTTATG	contig265	Solyc01g	Solyc01g	RAG1-act	GO:0016	GO:0016	contig265	Solyc01g	RAG1-act	GO:0016	SL2.40ch	AT3G16690.1		nodulin	chr3:568	2.43971	5.72022	29.0105	13.4211	50.0415	14.7045
GT	Sense	Sense	-0.234	Detected	0.234	Detected	0.000	1.698	Detected	1.139	Detected	1.418	0.060	GT	Sens	contig265	contig265	Arabidop	CCCACG	contig265	Solyc02g	Solyc02g	Arabidopsis thaliana genomic			contig265	Solyc02g	Arabidopsis thalian		SL2.40ch	AT4G04630.1		unknown	chr4:233	6841.13	8903.6	17003.2	8975	27002.3	18273.7
GT	Sense	Sense	0.644	Comprom	-0.644	Comprom	0.000	1.390	Detected	3.488	Detected	2.439	0.186	GT	Sens	contig265	contig265	Nitrilase-a	ATTACT	contig265	Solyc08g	Solyc08g	Nitrilase-associated protein (A			contig265	Solyc08g	Nitrilase-associated		SL2.40ch	AT5G19350.2		RNA-bind	chr5:651	6.70473	2.58262	1.84589	2.44429	11.6334	49.6324
GT	Sense	Sense	-0.266	Detected	0.266	Detected	0.000	2.150	Detected	1.044	Detected	1.597	0.121	GT	Sens	contig265	contig265	AE family	AAGCAT	contig265	Solyc01g	Solyc01g	AE family	GO:0005	GO:0005	contig265	Solyc01g	AE family	GO:0005	SL2.40ch	AT3G62270.1		anion ex	chr3:230	15.4752	21.0639	44.9424	31.5917	85.4659	39.5696
GT	Sense	Sense	-0.746	Comprom	0.746	Comprom	0.000	2.080	Detected	1.713	Detected	1.897	0.132	GT	Sens	contig265	contig265	Os03g02	GGAGGC	contig265	Solyc09g	Solyc09g	Os03g0291800 protein (Fragm			contig265	Solyc09g	Os03g0291800 prot		SL2.40ch	AT2G38320.1		unknown	chr2:160	2.00494	5.30548	12.0617	4.24671	14.7084	11.3686
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	1.112	Detected	1.024	Detected	1.068	0.012	GT	Sens	contig266	contig266	Receptor	CCACAA	contig266	Solyc10g	Solyc10g	Receptor	GO:0031	GO:0031	contig266	Solyc10g	Receptor	GO:0031	SL2.40ch	AT2G428	HVA22F	HVA22F	chr2:178	67.1657	54.2493	68.021	93.7658	139.1	130.49
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	2.458	Detected	1.432	Detected	1.945	0.063	GT	Sens	contig266	contig266	Bcl-2-ass	CACAAA	contig266	Solyc06g	Solyc06g	Bcl-2-ass	GO:0006	GO:0006	contig266	Solyc06g	Bcl-2-ass	GO:0006	SL2.40ch	AT5G53440.1		unknown	chr5:216	265.478	264.627	461.25	303.789	1553.14	760.559
GT	Sense	Sense	-0.360	Detected	0.360	Comprom	0.000	2.713	Detected	1.809	Detected	2.261	0.060	GT	Sens	contig266	contig266	MuDR far	AGTATG	contig266	Solyc08g	Solyc08g	MuDR family transposase con			contig266	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	2.76151	4.28153	4.73946	3.41488	24.0447	12.8136
GT	Sense	Sense	0.262	Detected	-0.262	Comprom	0.000	2.015	Detected	1.736	Detected	1.876	0.024	GT	Sens	contig266	contig266	Reverse t	ATATGA	contig266	Solyc06g	Solyc06g	Reverse t	GO:0006	GO:0006	contig266	Solyc03g013430.1.1				AT1G10370.1				11.0482	7.22495	12.2573	5.99501	38.5105	31.6506
GT	Sense	Sense	0.396	Detected	-0.396	Detected	0.000	1.336	Detected	1.452	Detected	1.394	0.074	GT	Sens	contig266	contig266	Myb-like	GGGACT	contig266	Solyc05g	Solyc05g	Myb-like	GO:0003	GO:0003	contig266	Solyc05g	Myb-like	GO:0003	SL2.40ch	AT4G31900.1		chromati	chr4:154	100.642	54.6609	141.521	52.2552	199.619	215.689
GT	Sense	Sense	-0.305	Detected	0.305	Detected	0.000	1.612	Detected	0.908	Detected	1.260	0.114	GT	Sens	contig266	contig266	heat shoc	AAGAAG	contig266	Solyc04g	Solyc04g	heat shoc	GO:0005	GO:0005	contig266	Solyc04g	heat shoc	GO:0051	SL2.40ch	AT3G125	HSP70	HSP70 (h	chr3:399	3288.64	4722.52	3167.39	3962.05	12847.9	7864.45
GT	Sense	Sense	0.236	Detected	-0.236	Detected	0.000	3.846	Detected	1.779	Detected	2.813	0.117	GT	Sens	contig266	contig266	Carbonic	CAATAT	contig266	Solyc09g	Solyc09g	Carbonic	GO:0004	GO:0004	contig266	Solyc09g	Carbonic	GO:0004	SL2.40ch	AT3G527	ATACA1,	ACA1 (A	chr3:195	11.7551	7.97985	16.0897	8.59779	148.526	35.3504
GT	Sense	Sense	1.787	Detected	-1.787	Comprom	0.000	1.287	Detected	0.953	Detected	1.120	0.596	GT	Sens	contig266	contig266	GDSL est	GTCCTT	contig266	Solyc10g	Solyc10g	GDSL est	GO:0016	GO:0016	contig266	Solyc10g	GDSL est	GO:0016	SL2.40ch	AT1G62150.1		mitochon	chr1:229	29.2421	2.30922	6.47277	5.14512	21.3903	16.9115
GT	Sense	Sense	0.255	Detected	-0.255	Detected	0.000	1.224	Detected	1.196	Detected	1.210	0.042	GT	Sens	contig267	contig267	Ulp1 prot	ATAAAC	contig267	Solyc11g	Solyc11g	Ulp1 protease family C-termina			contig267	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	20.5264	13.5697	9.56449	14.4106	41.5602	40.6461
GT	Sense	Sense	-0.474	Detected	0.474	Detected	0.000	1.265	Detected	1.622	Detected	1.444	0.104	GT	Sens	contig267	contig267	Glycosyl	TAAGAG	contig267	Solyc10g	Solyc10g	Glycosyl	GO:0004	GO:0004	contig267	Solyc10g	Glycosyl	GO:0004	SL2.40ch	AT5G546	GAUT12,	GAUT12	chr5:222	14.2973	25.9649	29.8639	22.0954	49.3847	63.0739
GT	Sense	Sense	-0.027	Comprom	0.027	Comprom	0.000	1.994	Detected	1.493	Detected	1.744	0.020	GT	Sens	contig268	contig268	Unknown	CTCCAA	contig268	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig268	Solyc06g	Unknown Protein (A		SL2.40ch	AT5G04885.1		glycosyl	chr5:142	4.47221	4.37012	5.71278	8.83351	18.7777	13.2333
GT	Sense	Sense	-1.003	Comprom	1.003	Detected	0.000	1.915	Detected	1.473	Detected	1.694	0.241	GT	Sens	contig268	contig268	COBRA-li	CAGAAA	contig268	Solyc03g	Solyc03g	COBRA-like protein (AHRD V1			contig268	Solyc03g	COBRA-like protein		SL2.40ch	AT5G156	COBL4, II	IRX6	chr5:508	3.05595	11.5487	12.4525	3.58854	23.8875	17.5373
GT	Sense	Sense	0.449	Detected	-0.449	Comprom	0.000	2.093	Detected	1.066	Detected	1.580	0.146	GT	Sens	contig268	contig268	Male ster	ACCACC	contig268	Solyc09g	Solyc09g	Male ster	GO:0005	GO:0005	contig268	Solyc09g	Male ster	GO:0005	SL2.40ch	AT1G04770.1		male ste	chr1:133	15.7501	7.95455	31.2603	17.9411	50.9266	24.9206
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	1.147	Detected	0.878	Detected	1.013	0.017	GT	Sens	contig268	contig268	Homolog	CTACGA	contig268	Solyc05g	Solyc05g	Homology to unknown gene (A			contig268	Solyc05g	Homology to unkno		SL2.40ch	AT3G17930.1		unknown	chr3:614	722.774	665.023	1444.26	937.821	1637.36	1355.08
GT	Sense	Sense	0.257	Comprom	-0.257	Comprom	0.000	2.018	Detected	1.663	Detected	1.840	0.028	GT	Sens	contig268	contig268	Acetyl es	GCTGCT	contig268	Solyc06g	Solyc06g	Acetyl es	GO:0004	GO:0004	contig268	Solyc06g	Acetyl es	GO:0004	SL2.40ch	AT1G05520.1		transpor	chr1:163	4.49809	2.9634	4.4389	7.03669	15.7693	12.2892
GT	Sense	Sense	-0.106	Comprom	0.106	Comprom	0.000	3.279	Detected	4.587	Detected	3.933	0.027	GT	Sens	contig269	contig269	Laccase	AAACTT	contig269	Solyc02g	Solyc02g	Laccase	GO:0055	GO:0055	contig269	Solyc02g	Laccase	GO:0055	SL2.40ch	AT5G58750.1		wound-re	chr5:237	2.05219	2.23795	1.71589	3.06814	22.1817	54.7693
GT	Sense	Sense	-0.246	Detected	0.246	Detected	0.000	1.587	Detected	1.120	Detected	1.353	0.057	GT	Sens	contig269	contig269	Uncharac	TACATT	contig269	Solyc03g	Solyc03g	Uncharacterized conserved pr			contig269	Solyc03g	Uncharacterized co		SL2.40ch	AT3G221	IOD5	IOD5 (IO-	chr3:783	94.5719	125.155	245.014	166.46	348.504	251.419
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	1.558	Detected	1.227	Detected	1.392	0.020	GT	Sens	contig269	contig269	Methyltra	ATAGTT	contig269	Solyc07g	Solyc07g	Methyltra	GO:0008	GO:0008	contig269	Solyc07g	Methyltra	GO:0008	SL2.40ch	AT4G29590.1		methyltra	chr4:145	364.85	401.173	502.196	343.793	1200.88	951.88
GT	Sense	Sense	0.168	Detected	-0.168	Detected	0.000	1.350	Detected	1.184	Detected	1.267	0.021	GT	Sens	contig269	contig269	Cytochro	TCCTTTA	contig269	Solyc03g	Solyc03g	Cytochro	GO:0019	GO:0019	contig269	Solyc03g	Cytochro	GO:0019	SL2.40ch	AT4G133	CYP71A2	CYP71A2	chr4:775	79.0713	58.9235	44.5585	39.9838	185.603	164.919
GT	Sense	Sense	-0.243	Detected	0.243	Detected	0.000	2.593	Detected	1.576	Detected	2.084	0.066	GT	Sens	contig270	contig270	Ring H2 fi	GAAGAA	contig270	Solyc08g	Solyc08g	Ring H2 fi	GO:0008	GO:0008	contig270	Solyc08g	Ring H2 fi	GO:0008	SL2.40ch	AT4G24015.1		zinc fing	chr4:124	60.8689	80.2599	251.285	71.2098	449.558	221.532
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	1.936	Detected	1.085	Detected	1.511	0.076	GT	Sens	contig270	contig270	Os04g04	GTCTCC	contig270	Solyc01g	Solyc01g	Os04g04	GO:0019	GO:0019	contig270	Solyc01g	Os04g04	GO:0019	SL2.40ch	AT5G57710.1		heat sho	chr5:233	104.507	83.4785	171.909	88.1209	381.038	210.727
GT	Sense	Sense	0.336	Detected	-0.336	Detected	0.000	1.698	Detected	0.982	Detected	1.340	0.112	GT	Sens	contig271	contig271	CBL-inter	CAGGGG	contig271	Solyc02g	Solyc02g	CBL-inter	GO:0004	GO:0004	contig271	Solyc02g	CBL-inter	GO:0004	SL2.40ch	AT5G583	CIPK10, F	SIP1 (SO	chr5:235	407.152	240.341	335.093	251.651	1082.55	656.967
GT	Sense	Sense	-0.330	Detected	0.330	Detected	0.000	1.680	Detected	1.155	Detected	1.417	0.078	GT	Sens	contig271	contig271	Peptidyl-p	GTTATG	contig271	Solyc12g	Solyc12g	Peptidyl-p	GO:0005	GO:0005	contig271	Solyc12g	Peptidyl-p	GO:0003	SL2.40ch	AT5G67410.1		unknown	chr5:268	23.4731	34.8943	41.0993	41.9086	97.7675	67.7545
GT	Sense	Sense	-0.079	Detected	0.079	Detected	0.000	2.101	Detected	1.000	Detected	1.551	0.108	GT	Sens	contig271	contig271	Calmodul	AGCTTC	contig271	Solyc08g	Solyc08g	Calmodul	GO:0005	GO:0005	contig271	Solyc08g	Calmodul	GO:0005	SL2.40ch	AT1G011	IOD18	IOD18 (IC	chr1:522	37.7552	39.6533	59.78	61.1501	177.063	82.2576
GT	Sense	Sense	-0.098	Detected	0.098	Detected	0.000	1.538	Detected	1.136	Detected	1.337	0.027	GT	Sens	contig271	contig271	Peptidase	ACTTGG	contig271	Solyc01g	Solyc01g	Peptidase M50 family (AHRD V			contig271	Solyc01g	Peptidase M50 fami		SL2.40ch	AT1G178	ATEGY3,	EGY3 (E	chr1:615	1441.51	1554.7	3609.64	2217.46	4636.64	3498.79
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	1.186	Detected	0.868	Detected	1.027	0.038	GT	Sens	contig271	contig271	Integrato	ATTCAT	contig271	Solyc03g	Solyc03g	Integrator complex subunit 9 (			contig271	Solyc03g	Integrator complex		SL2.40ch	AT3G07530.1		unknown	chr3:240	990.539	1119.36	1516.55	1125.09	2555.49	2043.5
GT	Sense	Sense	-0.108	Comprom	0.108	Comprom	0.000	2.684	Detected	2.760	Detected	2.722	0.002	GT	Sens	contig272	contig272	Unknown	CATCTT	contig272	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig272	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G38040.1		UDP-gluc	chr5:151	2.04432	2.23305	6.67389	1.92927	14.6459	15.3874
GT	Sense	Sense	-0.006	Detected	0.006	Detected	0.000	1.303	Detected	1.051	Detected	1.177	0.011	GT	Sens	contig272	contig272	Ycf33 pro	GGGCTG	contig272	Solyc11g	Solyc11g	Ycf33 protein (AHRD V1 *-*- O8			contig272	Solyc11g	Ycf33 protein (AHRD		SL2.40ch	AT3G46880.1		unknown	chr3:172	175.348	166.46	543.834	214.619	449.609	376.325
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	1.973	Detected	1.455	Detected	1.714	0.024	GT	Sens	contig272	contig272	Nuclear t	AGGAAG	contig272	Solyc10g	Solyc10g	Nuclear t	GO:0005	GO:0005	contig272	Solyc10g	Nuclear t	GO:0005	SL2.40ch	AT5G065	NF-YA10	NF-YA10	chr5:198	33.9585	28.5105	54.5069	38.277	130.269	90.7206
GT	Sense	Sense	-0.714	Comprom	0.714	Detected	0.000	2.631	Detected	1.789	Detected	2.210	0.117	GT	Sens	contig273	contig273	Zinc finge	AGCAAT	contig273	Solyc08g	Solyc08g	Zinc finge	GO:0003	GO:0003	contig273	Solyc08g	Zinc finge	GO:0003	SL2.40ch	AT1G325	LOL1	LOL1 (LS	chr1:117	5.67968	14.3861	28.6426	14.7069	59.7058	33.2127
GT	Sense	Sense	-0.072	Comprom	0.072	Comprom	0.000	1.271	Detected	1.104	Detected	1.188	0.009	GT	Sens	contig273	contig273	Glycosyl	CCTGTT	contig273	Solyc12g	Solyc12g	Glycosyltransferase-like prote			contig273	Solyc12g	Glycosyltransferase		SL2.40ch	AT4G23490.1		fringe-re	chr4:122	5.52748	5.75014	2.01062	2.61435	14.5125	12.8848
GT	Sense	Sense	-0.800	Detected	0.800	Detected	0.000	1.931	Detected	1.589	Detected	1.760	0.165	GT	Sens	contig274	contig274	Urea acti	CTGAAT	contig274	Solyc08g	Solyc08g	Urea acti	GO:0015	GO:0015	contig274	Solyc08g	Urea acti	GO:0015	SL2.40ch	AT5G453	ATDUR3,	sodium:s	chr5:183	12.3238	35.1764	157.161	128.836	84.6381	66.6112
GT	Sense	Sense	-0.901	Comprom	0.901	Comprom	0.000	0.972	Detected	1.264	Detected	1.118	0.345	GT	Sens	contig274	contig274	BOP/NPR	TCTCAA	contig274	Solyc05g	Solyc05g	BOP/NPR	GO:0005	GO:0005	contig274	Solyc10g	NPR1-like	GO:0005	SL2.40ch	AT3G571	BOP1	BOP1 (B	chr3:211	3.81216	12.5131	2.5773	2.87725	14.4517	17.6344
GT	Sense	Sense	-0.117	Comprom	0.117	Comprom	0.000	1.756	Detected	1.630	Detected	1.693	0.006	GT	Sens	contig275	contig275	MADS bo	CTTGAG	contig275	Solyc06g	Solyc06g	MADS bo	GO:0005	GO:0005	contig275	Solyc06g	MADS bo	GO:0003	SL2.40ch	AT5G202	PI	PI (PISTI	chr5:682	3.72594	4.12427	3.0377	4.81884	14.1194	12.9011
GT	Sense	Sense	0.120	Detected	-0.120	Detected	0.000	0.952	Detected	1.190	Detected	1.071	0.024	GT	Sens	contig275	contig275	Unknown	AAGTTG	contig275	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig275	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G09770.1		meprin a	chr4:615	95.0053	75.6792	127.375	167.113	174.891	205.617
GT	Sense	Sense	-0.095	Comprom	0.095	Comprom	0.000	1.413	Detected	1.406	Detected	1.410	0.004	GT	Sens	contig275	contig275	Unknown	CTAGGA	contig275	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)%			contig275	Solyc03g	Unknown Protein (A		SL2.40ch	AT2G474	CP12-1, C	CP12-1	chr2:194	4.01727	4.3094	9.44881	10.0466	11.8169	11.7245
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	2.580	Detected	2.149	Detected	2.364	0.010	GT	Sens	contig275	contig275	Unknown	ATGTTA	contig275	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig275	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G07680.1		unknown	chr1:237	1045.27	849.052	3349.35	2676.82	6005.05	4441.63
GT	Sense	Sense	0.040	Comprom	-0.040	Comprom	0.000	5.378	Detected	1.797	Detected	3.588	0.183	GT	Sens	contig275	contig275	B3 domai	AAACCA	contig275	Solyc08g	Solyc08g	B3 domai	GO:0006	GO:0006	contig275	Solyc08g	B3 domai	GO:0006	SL2.40ch	AT3G20730.1		pentatric	chr3:724	4.00455	3.56718	10.0807	2.91209	167.633	13.9661
GT	Sense	Sense	-0.507	Comprom	0.507	Comprom	0.000	2.066	Detected	1.935	Detected	2.001	0.060	GT	Sens	contig275	contig275	ATP bind	AGGAGC	contig275	Solyc02g	Solyc02g	ATP bind	GO:0005	GO:0005	contig275	Solyc02g	ATP bind	GO:0005	SL2.40ch	AT5G48740.1		leucine-r	chr5:197	2.45415	4.66503	2.108	1.97571	15.1106	13.7551
GT	Sense	Sense	-0.381	Detected	0.381	Detected	0.000	1.380	Detected	1.271	Detected	1.326	0.075	GT	Sens	contig276	contig276	Genomic	GCTCCC	contig276	Solyc12g	Solyc12g	Genomic DNA chromosome 5			contig276	Solyc12g	Genomic DNA chror		SL2.40ch	AT5G43720.1		unknown	chr5:175	1287.5	2054.87	4337.06	2635.58	4515.9	4174.5
GT	Sense	Sense	-0.281	Detected	0.281	Detected	0.000	1.508	Detected	1.011	Detected	1.259	0.079	GT	Sens	contig276	contig276	Serine-th	CAAAAA	contig276	Solyc11g	Solyc11g	Serine-th	GO:0006	GO:0006	contig276	Solyc11g	Serine-th	GO:0006	SL2.40ch	AT1G78290.3		serine/th	chr1:294	42.3057	58.7934	71.6671	42.9567	151.242	106.854
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	1.024	Detected	1.049	Detected	1.037	0.017	GT	Sens	contig276	contig276	Receptor	GAAGTT	contig276	Solyc12g	Solyc12g	Receptor	GO:0005	GO:0005	contig276	Solyc12g	Receptor	GO:0005	SL2.40ch	AT5G204	EFR	EFR (EF-	chr5:692	344.383	268.606	860.523	893.045	659.734	669.193
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	1.239	Detected	1.008	Detected	1.123	0.011	GT	Sens	contig277	contig277	Unknown	TGTGAA	contig277	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig277	Solyc02g	Unknown Protein (A		SL2.40ch	AT2G04690.2		cellular r	chr2:164	14.952	13.5798	34.0031	26.2	35.8638	30.458
GT	Sense	Sense	-0.419	Comprom	0.419	Detected	0.000	1.917	Detected	1.186	Detected	1.552	0.108	GT	Sens	contig277	contig277	MYB tran	GTGCAG	contig277	Solyc11g	Solyc11g	MYB transcription factor (AHR			contig277	Solyc11g	MYB transcription f		SL2.40ch	AT5G251	CYP71B1	CYP71B1	chr5:867	7.35473	12.3766	17.3413	14.5061	38.4139	23.0866
GT	Sense	Sense	0.450	Detected	-0.450	Detected	0.000	2.244	Detected	1.473	Detected	1.859	0.088	GT	Sens	contig277	contig277	Proteinas	GTGCTG	contig277	Solyc09g	Solyc09g	Proteinas	GO:0009	GO:0009	contig277	Solyc09g	Proteinas	GO:0009	SL2.40ch	AT2G364	AtGRF3	AtGRF3 (	chr2:152	4933.39	2487.24	1933.43	1556.63	17692.1	10340.5
GT	Sense	Sense	0.259	Detected	-0.259	Detected	0.000	1.379	Detected	0.825	Detected	1.102	0.101	GT	Sens	contig277	contig277	NADH del	GGACCT	contig277	Solyc06g	Solyc06g	NADH del	GO:0008	GO:0008	contig277	Solyc06g	NADH del	GO:0008	SL2.40ch	AT1G071	ATNDI1, N	NDA1 (A	chr1:220	241.451	158.697	678.292	248.487	542.887	368.739
GT	Sense	Sense	-0.296	Comprom	0.296	Comprom	0.000	4.196	Detected	3.696	Detected	3.946	0.010	GT	Sens	contig278	contig278	Ribose-pl	CAAAAA	contig278	Solyc06g	Solyc06g	Ribose-pl	GO:0009	GO:0009	contig278	Solyc06g	Ribose-pl	GO:0042	SL2.40ch	AT1G32380.1		ribose-pl	chr1:116	2.06942	2.93629	14.2148	9.68899	48.1953	33.9601
GT	Sense	Sense	0.141	Comprom	-0.141	Comprom	0.000	2.732	Detected	2.527	Detected	2.630	0.004	GT	Sens	contig278	contig278	Patatin-lik	CTGCTG	contig278	Solyc10g	Solyc10g	Patatin-lik	GO:0006	GO:0006	contig278	Solyc10g	Patatin-lik	GO:0006	SL2.40ch	AT2G392	PLP6, PL	PLP6 (PA	chr2:163	2.8947	2.24048	5.0565	11.4748	18.0376	15.6111
GT	Sense	Sense	-0.146	Detected	0.146	Detected	0.000	1.743	Detected	1.789	Detected	1.766	0.007	GT	Sens	contig278	contig278	Prenyltra	CAAAAA	contig278	Solyc04g	Solyc04g	Prenyltra	GO:0008	GO:0008	contig278	Solyc04g	Prenyltra	GO:0008	SL2.40ch	AT1G213	ATEXT3,	ATEXT3	chr1:745	33.6814	38.7782	33.5235	23.1273	128.983	132.822
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	2.561	Detected	1.705	Detected	2.133	0.040	GT	Sens	contig279	contig279	Receptor	GAGTGG	contig279	Solyc05g	Solyc05g	Receptor	GO:0004	GO:0004	contig279	Solyc05g	Receptor	GO:0001	SL2.40ch	AT5G63710.1		leucine-r	chr5:254	160.006	132.925	449.434	225.226	917.544	505.441
GT	Sense	Sense	-0.482	Comprom	0.482	Comprom	0.000	1.692	Detected	2.499	Detected	2.095	0.079	GT	Sens	contig279	contig279	Fatty acid	TTGGAG	contig279	Solyc02g	Solyc02g	Fatty acid	GO:0005	GO:0005	contig279	Solyc02g	Fatty acid	GO:0005	SL2.40ch	AT4G208	FAH2, AT	FAH2 (FA	chr4:111	9.16676	16.8356	21.3558	22.3185	42.8005	74.6383
GT	Sense	Sense	0.697	Detected	-0.697	Comprom	0.000	2.946	Detected	2.336	Detected	2.641	0.074	GT	Sens	contig281	contig281	Proteinas	GTAACT	contig281	Solyc09g	Solyc09g	Proteinas	GO:0009	GO:0009	contig281	Solyc09g	Proteinas	GO:0009	SL2.40ch	AT3G08947.1		binding /	chr3:272	4717.08	1689.34	3801.86	2369.77	23194.8	15149.2
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	1.114	Detected	0.914	Detected	1.014	0.010	GT	Sens	contig281	contig281	Cytochro	GTGTTT	contig281	Solyc07g	Solyc07g	Cytochro	GO:0019	GO:0019	contig281	Solyc07g	Cytochro	GO:0019	SL2.40ch	AT3G261	CYP71B1	CYP71B1	chr3:957	4012.3	3937.25	5321.54	4325.09	9171.24	7964.69
GT	Sense	Sense	-0.253	Comprom	0.253	Comprom	0.000	3.017	Detected	1.845	Detected	2.431	0.063	GT	Sens	contig281	contig281	Dihydrofl	TCCGAG	contig281	Solyc03g	Solyc03g	Dihydrofl	GO:0004	GO:0004	contig281	Solyc03g	Dihydrofl	GO:0004	SL2.40ch	AT5G414	BEL1	BEL1 (BE	chr5:165	3.11394	4.15825	25.9146	12.6063	31.0623	13.7436
GT	Sense	Sense	-0.151	Detected	0.151	Detected	0.000	1.617	Detected	1.078	Detected	1.347	0.049	GT	Sens	contig281	contig281	Hydrolase	AATAACA	contig281	Solyc01g	Solyc01g	Hydrolase	GO:0003	GO:0003	contig281	Solyc01g	Hydrolase	GO:0003	SL2.40ch	AT1G54570.1		esterase	chr1:203	382.489	443.483	688.145	633.226	1346.78	924.549
GT	Sense	Sense	-0.400	Detected	0.400	Detected	0.000	2.034	Detected	1.794	Detected	1.914	0.045	GT	Sens	contig281	contig281	26S prote	GAGCAA	contig281	Solyc02g	Solyc02g	26S prote	GO:0005	GO:0005	contig281	Solyc02g	26S prote	GO:0016	SL2.40ch	AT2G18193.1		AAA-type	chr2:791	590.414	967.546	1934.69	1525.84	3300.59	2785.93
GT	Sense	Sense	-0.249	Detected	0.249	Detected	0.000	2.246	Detected	1.666	Detected	1.956	0.036	GT	Sens	contig282	contig282	Subtilisin	TCAACC	contig282	Solyc03g	Solyc03g	Subtilisin	GO:0004	GO:0004	contig282	Solyc03g	Subtilisin	GO:0004	SL2.40ch	AT4G21630.1		subtilase	chr4:114	303.084	402.871	847.197	622.488	1767.48	1179.03
GT	Sense	Sense	-0.283	Comprom	0.283	Comprom	0.000	4.146	Detected	2.233	Detected	3.189	0.085	GT	Sens	contig282	contig282	Light-dep	GCTATT	contig282	Solyc04g	Solyc04g	Light-dependent short hypocc			contig282	Solyc04g	Light-dependent sh		SL2.40ch	AT3G045	LSH2	LSH2 (LI	chr3:121	4.32853	6.02823	26.1936	15.3199	96.4399	25.5255
GT	Sense	Sense	0.850	Detected	-0.850	Comprom	0.000	2.391	Detected	1.331	Detected	1.861	0.204	GT	Sens	contig282	contig282	Cortical c	CTATGT	contig282	Solyc01g	Solyc01g	Cortical c	GO:0008	GO:0008	contig282	Solyc01g	Cortical c	GO:0008	SL2.40ch	AT1G520	MBP2, MI	MBP2 (M	chr1:193	11.5786	3.35316	42.1315	15.6144	34.8478	16.6663
GT	Sense	Sense	-0.543	Comprom	0.543	Comprom	0.000	1.171	Detected	1.209	Detected	1.190	0.160	GT	Sens	contig282	contig282	RAG1-act	CAATAT	contig282	Solyc06g	Solyc06g	RAG1-act	GO:0016	GO:0016	contig282	Solyc06g	RAG1-act	GO:0016	SL2.40ch	AT1G21460.1		nodulin	chr1:751	3.93348	7.86059	10.5895	10.7717	13.3545	13.6671
GT	Sense	Sense	0.144	Detected	-0.144	Detected	0.000	1.496	Detected	0.852	Detected	1.174	0.080	GT	Sens	contig283	contig283	UDP flavo	TGTGTA	contig283	Solyc07g	Solyc07g	UDP flavo	GO:0080	GO:0080	contig283	Solyc01g	LRR rece	GO:0004	SL2.40ch	AT4G244	GWD3, P	PWD (PH	chr4:126	4735.47	3648.59	7468.57	4186.99	12499.9	7976.64
GT	Sense	Sense	0.042	Comprom	-0.042	Comprom	0.000	2.768	Detected	1.607	Detected	2.188	0.064	GT	Sens	contig283	contig283	Homeobo	ACATTC	contig283	Solyc08g	Solyc08g	Homeobo	GO:0043	GO:0043	contig283	Solyc08g	Homeobo	GO:0043	SL2.40ch	AT4G174	HAT1	HAT1: DI	chr4:973	6.18997	5.49802	9.30655	6.58285	42.3723	18.897
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	1.589	Detected	1.174	Detected	1.382	0.024	GT	Sens	contig283	contig283	NAD(P)H-	CGTATA	contig283	Solyc11g	Solyc11g	NAD(P)H-quinone oxidoreduct			contig283	Solyc11g	NAD(P)H-quinone o		SL2.40ch	AT1G748	NDH-O	NDH-O (N	chr1:281	611.242	524.554	1530.29	729.18	1816.16	1358.83
GT	Sense	Sense	0.577	Comprom	-0.577	Comprom	0.000	1.105	Detected	1.450	Detected	1.277	0.168	GT	Sens	contig283	contig283	Unknown	GCAACA	contig283	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig283	Solyc11g	Unknown Protein (A		SL2.40ch	AT4G16610.1		zinc fing	chr4:935	7.73461	3.26887	4.49382	5.5485	11.5341	14.6011
GT	Sense	Sense	-0.975	Comprom	0.975	Comprom	0.000	1.726	Detected	1.458	Detected	1.592	0.247	GT	Sens	contig283	contig283	Subtilisin	TATGGA	contig283	Solyc01g	Solyc01g	Subtilisin-like protease (AHRD			contig283	Solyc01g	Subtilisin-like protea		SL2.40ch	AT1G71370.1		DEAD/DE	chr1:268	2.01489	7.32505	13.483	4.79698	13.5514	11.2248
GT	Sense	Sense	0.481	Comprom	-0.481	Comprom	0.000	3.397	Detected	3.094	Detected	3.246	0.023	GT	Sens	contig283	contig283	DNA-dire	CAGATA	contig283	Solyc01g	Solyc01g	DNA-dire	GO:0006350		contig283	Solyc01g	DNA-dire	GO:0006	SL2.40ch	ATCG007	RPOA	RNA poly	chrC:779	6.61211	3.19238	20.0839	13.2276	51.6135	41.7196
GT	Sense	Sense	-0.486	Detected	0.486	Detected	0.000	2.520	Detected	1.455	Detected	1.987	0.110	GT	Sens	contig284	contig284	LOB dom	GGTTTT	contig284	Solyc03g	Solyc03g	LOB domain protein 1 (AHRD \			contig284	Solyc03g	LOB domain protei		SL2.40ch	AT5G630	LOB	LOB (LAT	chr5:253	79.0403	145.8	141.451	82.9354	656.49	312.86
GT	Sense	Sense	-0.016	Detected	0.016	Detected	0.000	1.604	Detected	1.204	Detected	1.404	0.020	GT	Sens	contig284	contig284	FAD depe	ATGCGG	contig284	Solyc02g	Solyc02g	FAD depe	GO:0016	GO:0016	contig284	Solyc02g	FAD depe	GO:0016	SL2.40ch	AT5G49555.1		amine ox	chr5:201	108.853	104.793	170.905	157.647	346.26	261.604
GT	Sense	Sense	0.328	Detected	-0.328	Detected	0.000	1.076	Detected	2.375	Detected	1.726	0.141	GT	Sens	contig284	contig284	F-box fan	GATGTA	contig284	Solyc08g	Solyc08g	F-box family protein (AHRD V1			contig284	Solyc08g	F-box family protein		SL2.40ch	AT3G47150.1		F-box far	chr3:173	30.2033	18.0439	281.016	274.231	52.4773	128.791
GT	Sense	Sense	0.259	Detected	-0.259	Detected	0.000	2.354	Detected	1.570	Detected	1.962	0.053	GT	Sens	contig284	contig284	Genomic	AGGACT	contig284	Solyc05g	Solyc05g	Genomic DNA chromosome 5			contig284	Solyc05g	Genomic DNA chror		SL2.40ch	AT3G190	TAF1, TA	HAF2 (HI	chr3:656	25.8508	16.9798	33.6379	41.6881	114.207	66.1155
GT	Sense	Sense	-0.220	Detected	0.220	Detected	0.000	1.023	Detected	1.738	Detected	1.381	0.081	GT	Sens	contig284	contig284	Unknown	TGTGTT	contig284	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig284	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G37220.1		zinc fing	chr5:147	191.297	244.167	313.507	400.886	468.424	766.487
GT	Sense	Sense	-0.227	Comprom	0.227	Comprom	0.000	1.416	Detected	1.697	Detected	1.556	0.028	GT	Sens	contig284	contig284	Unknown	TTATGA	contig284	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig284	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G66170.2		FUNCTIO	chr5:264	3.97355	5.12415	6.1832	13.433	12.8374	15.5528
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	1.956	Detected	1.302	Detected	1.629	0.040	GT	Sens	contig285	contig285	WW doma	GGTCAC	contig285	Solyc04g	Solyc04g	WW doma	GO:0005	GO:0005	contig285	Solyc04g	WW doma	GO:0005	SL2.40ch	AT5G10410.1		epsin N-t	chr5:327	27.4589	28.9867	101.314	76.2705	116.766	73.9613
GT	Sense	Sense	0.076	Detected	-0.076	Detected	0.000	1.342	Detected	1.409	Detected	1.376	0.004	GT	Sens	contig285	contig285	Unknown	TGAAAT	contig285	Solyc02g	Solyc02g	Unknown	GO:0016	GO:0016	contig285	Solyc03g	SPFH domain/band		SL2.40ch	AT5G22550.2		unknown	chr5:748	15.1833	12.8586	17.389	12.3156	37.7731	39.4587
GT	Sense	Sense	0.050	Detected	-0.050	Detected	0.000	0.973	Detected	1.363	Detected	1.168	0.028	GT	Sens	contig285	contig285	BZIP tran	GCACAT	contig285	Solyc02g	Solyc02g	BZIP tran	GO:0005	GO:0005	contig285	Solyc02g	BZIP tran	GO:0005	SL2.40ch	AT2G362	ABI5, GIA	ABI5 (AB	chr2:152	22.5979	19.8258	18.849	13.0464	44.3187	57.8869
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	2.539	Detected	1.026	Detected	1.782	0.146	GT	Sens	contig285	contig285	Alpha-dio	CAAACA	contig285	Solyc03g	Solyc03g	Alpha-dio	GO:0055	GO:0055	contig285	Solyc03g	Alpha-dio	GO:0016	SL2.40ch	AT1G73680.1		pathoge	chr1:277	814.431	637.515	1427.18	552.603	4465	1559.69
GT	Sense	Sense	-0.272	Detected	0.272	Detected	0.000	1.140	Detected	1.313	Detected	1.227	0.050	GT	Sens	contig286	contig286	Phospho	AATACA	contig286	Solyc07g	Solyc07g	Phospho	GO:0005	GO:0005	contig286	Solyc07g	Phospho	GO:0005	SL2.40ch	AT3G149	ATPPC3	ATPPC3	chr3:502	216.758	297.57	442.349	309.802	597.049	670.801
GT	Sense	Sense	-0.296	Detected	0.296	Detected	0.000	1.055	Detected	1.057	Detected	1.056	0.071	GT	Sens	contig286	contig286	Glutamat	TGCGAT	contig286	Solyc11g	Solyc11g	Glutamate carboxypeptidase 2			contig286	Solyc11g	Glutamate carboxyp		SL2.40ch	AT3G10550.1		phospha	chr3:329	348.747	494.893	587.687	327.502	920.177	918.956
GT	Sense	Sense	0.195	Comprom	-0.195	Comprom	0.000	1.320	Detected	1.301	Detected	1.311	0.021	GT	Sens	contig286	contig286	Unknown	TGTCTT	contig286	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig286	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G541	ATOMT1,	ATOMT1	chr5:219	5.43427	3.90472	3.48232	6.95128	12.2631	12.0713
GT	Sense	Sense	0.265	Detected	-0.265	Detected	0.000	2.951	Detected	1.178	Detected	2.064	0.155	GT	Sens	contig286	contig286	High affin	GTTCCA	contig286	Solyc06g	Solyc06g	High affin	GO:0015	GO:0015	contig286	Solyc06g	High affin	GO:0015	SL2.40ch	AT4G027	SULTR3:	SULTR3:	chr4:118	76.8329	50.0981	95.493	49.2453	511.55	149.248
GT	Sense	Sense	-0.344	Comprom	0.344	Detected	0.000	2.788	Detected	1.842	Detected	2.315	0.058	GT	Sens	contig286	contig286	Nuclear t	GGGATT	contig286	Solyc10g	Solyc10g	Nuclear t	GO:0005	GO:0005	contig286	Solyc10g	Nuclear t	GO:0005	SL2.40ch	AT5G036	PTL	PTL (PET	chr5:957	8.848	13.4118	17.5551	2.17751	80.2408	41.5317
GT	Sense	Sense	-0.423	Comprom	0.423	Detected	0.000	0.826	Detected	2.044	Detected	1.435	0.193	GT	Sens	contig287	contig287	Unknown	GGGGGG	contig287	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig287	Solyc02g	Unknown Protein (A		SL2.40ch	AT1G72900.1				6.57042	11.1129	16.9078	19.7695	16.151	37.4681
GT	Sense	Sense	-0.062	Comprom	0.062	Comprom	0.000	2.260	Detected	2.013	Detected	2.136	0.004	GT	Sens	contig287	contig287	Unknown	CATCTT	contig287	Solyc11g	Solyc11g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.134	Comprom	0.134	Comprom	0.000	2.133	Detected	2.179	Detected	2.156	0.004	GT	Sens	contig287	contig287	Ycf2 (AHF	TGGTTA	contig287	Solyc11g	Solyc11g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	1.052	Detected	0.954	Detected	1.003	0.004	GT	Sens	contig288	contig288	UDP-gluc	AGACAT	contig288	Solyc11g	Solyc11g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.226	Detected	0.226	Detected	0.000	1.617	Detected	0.965	Detected	1.291	0.083	GT	Sens	contig288	contig288	Sterol red	ACATCT	contig288	Solyc06g	Solyc06g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.303	Detected	-0.303	Detected	0.000	2.121	Detected	1.290	Detected	1.706	0.080	GT	Sens	contig288	contig288	Sodium/c	TTACTAT	contig288	Solyc09g	Solyc09g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.314	Detected	0.314	Detected	0.000	1.408	Detected	0.991	Detected	1.199	0.086	GT	Sens	contig288	contig288	Genomic	GAAACT	contig288	Solyc10g	Solyc10g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.288	Detected	0.288	Detected	0.000	2.573	Detected	1.029	Detected	1.801	0.160	GT	Sens	contig289	contig289	At1g6705	TTGAAG	contig289	Solyc02g	Solyc02g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.546	Comprom	-0.546	Comprom	0.000	1.975	Detected	1.398	Detected	1.687	0.112	GT	Sens	contig289	contig289	Heat shoc	CTTGTC	contig289	Solyc03g	Solyc03g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.331	Comprom	0.331	Comprom	0.000	5.493	Detected	4.126	Detected	4.810	0.024	GT	Sens	contig289	contig289	Unknown	GGGTCC	contig289	Solyc06g	Solyc06g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

GT	Sens	Sense	-0.212	Detected	0.212	Detected	0.000	1.413	Detected	1.075	Detected	1.244	0.044	GT	Sens	contig289	contig289	NHL repe
GT	Sens	Sense	-0.745	Comprom	0.745	Comprom	0.000	3.288	Detected	2.983	Detected	3.136	0.054	GT	Sens	contig290	contig290	Expresse
GT	Sens	Sense	0.338	Detected	-0.338	Detected	0.000	2.087	Detected	1.956	Detected	2.022	0.028	GT	Sens	contig290	contig290	Unknown
GT	Sens	Sense	0.741	Detected	-0.741	Comprom	0.000	2.371	Detected	2.365	Detected	2.368	0.086	GT	Sens	contig290	contig290	Unknown
GT	Sens	Sense	0.476	Detected	-0.476	Comprom	0.000	1.479	Detected	2.296	Detected	1.888	0.095	GT	Sens	contig290	contig290	ABA indu
GT	Sens	Sense	0.927	Detected	-0.927	Detected	0.000	0.812	Detected	1.625	Detected	1.218	0.352	GT	Sens	contig290	contig290	9-cis-epo
GT	Sens	Sense	-0.110	Detected	0.110	Detected	0.000	1.400	Detected	0.963	Detected	1.181	0.040	GT	Sens	contig290	contig290	Cytochro
GT	Sens	Sense	0.238	Detected	-0.238	Detected	0.000	1.908	Detected	2.221	Detected	2.065	0.019	GT	Sens	contig290	contig290	Kunitz try
GT	Sens	Sense	-0.127	Detected	0.127	Detected	0.000	1.328	Detected	0.882	Detected	1.105	0.050	GT	Sens	contig290	contig290	Os04g05
GT	Sens	Sense	-0.089	Detected	0.089	Detected	0.000	1.633	Detected	1.126	Detected	1.380	0.036	GT	Sens	contig290	contig290	Carbohy
GT	Sens	Sense	0.387	Detected	-0.387	Detected	0.000	1.464	Detected	1.070	Detected	1.267	0.100	GT	Sens	contig291	contig291	Protease
GT	Sens	Sense	-0.152	Detected	0.152	Detected	0.000	1.181	Detected	0.832	Detected	1.007	0.049	GT	Sens	contig291	contig291	DNA misr
GT	Sens	Sense	-0.404	Detected	0.404	Detected	0.000	2.891	Detected	2.235	Detected	2.563	0.039	GT	Sens	contig291	contig291	Cytochro
GT	Sens	Sense	0.066	Detected	-0.066	Detected	0.000	1.313	Detected	1.428	Detected	1.370	0.004	GT	Sens	contig292	contig292	Zinc finge
GT	Sens	Sense	-0.336	Detected	0.336	Detected	0.000	1.754	Detected	0.992	Detected	1.373	0.114	GT	Sens	contig292	contig292	Transcrip
GT	Sens	Sense	-0.180	Detected	0.180	Detected	0.000	1.480	Detected	0.847	Detected	1.163	0.086	GT	Sens	contig292	contig292	GATA tra
GT	Sens	Sense	0.055	Comprom	-0.055	Comprom	0.000	0.961	Detected	1.362	Detected	1.162	0.030	GT	Sens	contig292	contig292	Ankyrin r
GT	Sens	Sense	-0.412	Detected	0.412	Detected	0.000	2.556	Detected	1.518	Detected	2.037	0.092	GT	Sens	contig292	contig292	Receptor-
GT	Sens	Sense	-0.109	Detected	0.109	Detected	0.000	1.247	Detected	1.091	Detected	1.169	0.013	GT	Sens	contig292	contig292	Low mole
GT	Sens	Sense	-0.223	Detected	0.223	Detected	0.000	1.157	Detected	1.104	Detected	1.130	0.037	GT	Sens	contig292	contig292	Unknown
GT	Sens	Sense	-0.110	Detected	0.110	Detected	0.000	1.285	Detected	0.858	Detected	1.071	0.047	GT	Sens	contig292	contig292	Leucine-r
GT	Sens	Sense	0.092	Detected	-0.092	Detected	0.000	1.797	Detected	1.238	Detected	1.518	0.036	GT	Sens	contig293	contig293	Unknown
GT	Sens	Sense	0.109	Detected	-0.109	Detected	0.000	3.083	Detected	1.617	Detected	2.350	0.087	GT	Sens	contig293	contig293	Squamos
GT	Sens	Sense	-0.406	Detected	0.406	Detected	0.000	1.264	Detected	0.936	Detected	1.100	0.129	GT	Sens	contig293	contig293	Fimbrin-li
GT	Sens	Sense	0.168	Detected	-0.168	Detected	0.000	2.151	Detected	2.055	Detected	2.103	0.007	GT	Sens	contig293	contig293	Potassiu
GT	Sens	Sense	0.140	Detected	-0.140	Detected	0.000	1.768	Detected	1.219	Detected	1.493	0.040	GT	Sens	contig293	contig293	Heavy me
GT	Sens	Sense	0.083	Detected	-0.083	Detected	0.000	1.867	Detected	0.908	Detected	1.387	0.104	GT	Sens	contig293	contig293	AT5g4758
GT	Sens	Sense	-0.002	Comprom	0.002	Comprom	0.000	1.339	Detected	0.903	Detected	1.121	0.036	GT	Sens	contig294	contig294	Nucleore
GT	Sens	Sense	-0.081	Detected	0.081	Detected	0.000	1.575	Detected	1.501	Detected	1.538	0.003	GT	Sens	contig294	contig294	Genomic
GT	Sens	Sense	-0.159	Detected	0.159	Detected	0.000	3.281	Detected	1.588	Detected	2.435	0.106	GT	Sens	contig294	contig294	Alpha-gal
GT	Sens	Sense	-0.682	Detected	0.682	Detected	0.000	2.443	Detected	2.475	Detected	2.459	0.069	GT	Sens	contig294	contig294	B3 domai
GT	Sens	Sense	-0.022	Detected	0.022	Detected	0.000	1.403	Detected	1.004	Detected	1.204	0.027	GT	Sens	contig294	contig294	Pseudo-r
GT	Sens	Sense	-0.241	Detected	0.241	Detected	0.000	1.867	Detected	1.317	Detected	1.592	0.049	GT	Sens	contig294	contig294	Receptor-
GT	Sens	Sense	-0.281	Detected	0.281	Detected	0.000	2.875	Detected	2.533	Detected	2.704	0.015	GT	Sens	contig294	contig294	High affin
GT	Sens	Sense	0.406	Detected	-0.406	Detected	0.000	1.965	Detected	2.335	Detected	2.150	0.041	GT	Sens	contig295	contig295	UDP-gluc
GT	Sens	Sense	0.161	Detected	-0.161	Detected	0.000	1.542	Detected	0.825	Detected	1.184	0.095	GT	Sens	contig295	contig295	RAG1-act
GT	Sens	Sense	0.185	Comprom	-0.185	Comprom	0.000	1.206	Detected	0.926	Detected	1.066	0.044	GT	Sens	contig295	contig295	Unknown
GT	Sens	Sense	-0.062	Detected	0.062	Detected	0.000	1.230	Detected	0.960	Detected	1.095	0.018	GT	Sens	contig295	contig295	Dihydrofl
GT	Sens	Sense	-0.239	Detected	0.239	Detected	0.000	1.165	Detected	0.869	Detected	1.017	0.069	GT	Sens	contig295	contig295	Nodulin M
GT	Sens	Sense	0.604	Detected	-0.604	Comprom	0.000	1.462	Detected	1.445	Detected	1.453	0.138	GT	Sens	contig295	contig295	Unknown
GT	Sens	Sense	-0.010	Detected	0.010	Detected	0.000	1.630	Detected	1.628	Detected	1.629	0.000	GT	Sens	contig295	contig295	Unknown
GT	Sens	Sense	-0.131	Detected	0.131	Detected	0.000	1.174	Detected	0.906	Detected	1.040	0.031	GT	Sens	contig295	contig295	Atozi1 (Fr
GT	Sens	Sense	-0.509	Detected	0.509	Detected	0.000	1.602	Detected	1.339	Detected	1.470	0.108	GT	Sens	contig295	contig295	Unknown
GT	Sens	Sense	-0.780	Detected	0.780	Detected	0.000	2.605	Detected	1.694	Detected	2.149	0.140	GT	Sens	contig296	contig296	Pistil exte
GT	Sens	Sense	0.132	Detected	-0.132	Comprom	0.000	1.687	Detected	1.383	Detected	1.535	0.017	GT	Sens	contig296	contig296	HAT famil
GT	Sens	Sense	-0.246	Detected	0.246	Detected	0.000	1.205	Detected	0.862	Detected	1.033	0.075	GT	Sens	contig296	contig296	Monooxy
GT	Sens	Sense	-0.127	Detected	0.127	Detected	0.000	1.841	Detected	1.181	Detected	1.511	0.051	GT	Sens	contig296	contig296	Transcrip
GT	Sens	Sense	-0.393	Comprom	0.393	Comprom	0.000	1.807	Detected	2.111	Detected	1.959	0.043	GT	Sens	contig297	contig297	Unknown
GT	Sens	Sense	-0.025	Detected	0.025	Detected	0.000	2.321	Detected	1.648	Detected	1.985	0.028	GT	Sens	contig297	contig297	Unknown
GT	Sens	Sense	0.118	Detected	-0.118	Comprom	0.000	1.515	Detected	1.088	Detected	1.301	0.033	GT	Sens	contig297	contig297	Transcrip
GT	Sens	Sense	-0.199	Detected	0.199	Detected	0.000	1.935	Detected	1.654	Detected	1.795	0.018	GT	Sens	contig297	contig297	Cellular r
GT	Sens	Sense	-0.048	Comprom	0.048	Comprom	0.000	4.071	Detected	3.142	Detected	3.607	0.016	GT	Sens	contig297	contig297	Unknown
GT	Sens	Sense	0.170	Detected	-0.170	Detected	0.000	1.165	Detected	1.431	Detected	1.298	0.027	GT	Sens	contig297	contig297	Transpos
GT	Sens	Sense	-0.316	Comprom	0.316	Comprom	0.000	1.401	Detected	1.355	Detected	1.378	0.049	GT	Sens	contig297	contig297	Unknown
GT	Sens	Sense	-0.039	Detected	0.039	Detected	0.000	1.856	Detected	1.004	Detected	1.430	0.079	GT	Sens	contig297	contig297	Homeobo
GT	Sens	Sense	-0.207	Detected	0.207	Detected	0.000	1.315	Detected	0.851	Detected	1.083	0.074	GT	Sens	contig297	contig297	CRABS C
GT	Sens	Sense	-0.041	Detected	0.041	Detected	0.000	1.630	Detected	0.921	Detected	1.275	0.070	GT	Sens	contig297	contig297	Unknown
GT	Sens	Sense	0.129	Detected	-0.129	Detected	0.000	2.538	Detected	1.201	Detected	1.870	0.111	GT	Sens	contig297	contig297	Multidrug
GT	Sens	Sense	-0.007	Comprom	0.007	Comprom	0.000	3.145	Detected	2.070	Detected	2.608	0.040	GT	Sens	contig298	contig298	Caffeoyl-
GT	Sens	Sense	0.876	Detected	-0.876	Comprom	0.000	2.975	Detected	1.280	Detected	2.127	0.223	GT	Sens	contig298	contig298	Sulfate tr
GT	Sens	Sense	-0.574	Comprom	0.574	Comprom	0.000	1.659	Detected	1.682	Detected	1.670	0.101	GT	Sens	contig298	contig298	Unknown
GT	Sens	Sense	0.447	Detected	-0.447	Comprom	0.000	3.511	Detected	1.777	Detected	2.644	0.113	GT	Sens	contig298	contig298	MtN3-like
GT	Sens	Sense	-0.248	Detected	0.248	Detected	0.000	0.853	Detected	2.634	Detected	1.744	0.200	GT	Sens	contig298	contig298	Unknown
GT	Sens	Sense	-0.248	Detected	0.248	Detected	0.000	1.243	Detected	0.807	Detected	1.025	0.090	GT	Sens	contig299	contig299	Speckle-t
GT	Sens	Sense	0.288	Detected	-0.288	Comprom	0.000	2.095	Detected	1.128	Detected	1.611	0.103	GT	Sens	contig299	contig299	Cationic a
GT	Sens	Sense	0.174	Detected	-0.174	Detected	0.000	3.189	Detected	1.544	Detected	2.367	0.106	GT	Sens	contig299	contig299	Prosyste
GT	Sens	Sense	0.069	Detected	-0.069	Detected	0.000	1.681	Detected	1.886	Detected	1.784	0.005	GT	Sens	contig300	contig300	Unknown
GT	Sens	Sense	-0.047	Detected	0.047	Detected	0.000	1.494	Detected	1.318	Detected	1.406	0.005	GT	Sens	contig300	contig300	Ulp1 prot
GT	Sens	Sense	0.019	Comprom	-0.019	Comprom	0.000	1.605	Detected	0.931	Detected	1.268	0.064	GT	Sens	contig300	contig300	Endo-1 4-
GT	Sens	Sense	-0.181	Detected	0.181	Detected	0.000	1.912	Detected	1.501	Detected	1.706	0.025	GT	Sens	contig300	contig300	Unknown
GT	Sens	Sense	-0.010	Detected	0.010	Detected	0.000	1.087	Detected	1.347	Detected	1.217	0.011	GT	Sens	contig300	contig300	Unknown
GT	Sens	Sense	0.016	Detected	-0.016	Detected	0.000	1.394	Detected	1.139	Detected	1.267	0.010	GT	Sens	contig300	contig300	Dopamine
GT	Sens	Sense	0.022	Detected	-0.022	Detected	0.000	1.047	Detected	0.974	Detected	1.011	0.002	GT	Sens	contig300	contig300	Homeobo
GT	Sens	Sense	-0.065	Detected	0.065	Detected	0.000	1.274	Detected	0.908	Detected	1.091	0.030	GT	Sens	contig300	contig300	Strictosid
GT	Sens	Sense	0.220	Detected	-0.220	Detected	0.000	1.450	Detected	1.698	Detected	1.574	0.025	GT	Sens	contig300	contig300	Unknown
GT	Sens	Sense	-0.319	Detected	0.319	Detected	0.000	2.044	Detected	1.702	Detected	1.873	0.035	GT	Sens	contig301	contig301	Dihydrofl
GT	Sens	Sense	-0.487	Comprom	0.487	Detected	0.000	1.607	Detected	1.378	Detected	1.492	0.096	GT	Sens	contig301	contig301	Galactosy
GT	Sens	Sense	-0.306	Detected	0.306	Detected	0.000	2.189	Detected	1.479	Detected	1.834	0.060	GT	Sens	contig301	contig301	Zinc finge
GT	Sens	Sense	0.486	Comprom	-0.486	Comprom	0.000	1.512	Detected	1.728	Detected	1.620	0.083	GT	Sens	contig301	contig301	Kelch-like
GT	Sens	Sense	-0.246	Detected	0.246	Detected	0.000	3.352	Detected	2.741	Detected	3.046	0.016	GT	Sens	contig302	contig302	Subtilisin
GT	Sens	Sense	0.062	Detected	-0.062	Detected	0.000	2.398	Detected	1.466	Detected	1.932	0.054	GT	Sens	contig302	contig302	UDP-gluc
GT	Sens	Sense	-0.144	Comprom	0.144	Comprom	0.000	2.519	Detected	2.158	Detected	2.338	0.010	GT	Sens	contig302	contig302	Unknown
GT	Sens	Sense	-0.207	Comprom	0.207	Comprom	0.000	3.106	Detected	2.839	Detected	2.973	0.007	GT	Sens	contig302	contig302	Unknown
GT	Sens	Sense	-0.105	Detected	0.105	Detected	0.000	1.406	Detected	1.349	Detected	1.378	0.006	GT	Sens	contig302	contig302	Unknown
GT	Sens	Sense	0.505	Detected	-0.505	Detected	0.000	1.399	Detected	1.248	Detected	1.324	0.122	GT	Sens	contig303	contig303	Ve resista
GT	Sens	Sense	-0.180	Detected	0.180	Detected	0.000	2.826	Detected	2.739	Detected	2.783	0.004	GT	Sens	contig303	contig303	BZip tran
GT	Sens	Sense	0.090	Comprom	-0.090	Comprom	0.000	2.051	Detected	2.037	Detected	2.044	0.002	GT	Sens	contig303	contig303	Short-cha
GT	Sens	Sense	-0.276	Detected	0.276	Detected	0.000	1.221	Detected	0.900	Detected	1.061	0.080	GT	Sens	contig304	contig304	Yippee fa
GT	Sens	Sense	0.403	Comprom	-0.403	Comprom	0.000	1.395	Detected	0.850	Detected	1.123	0.147	GT	Sens	contig305	contig305	Protein F
GT	Sens	Sense	-0.235	Detected	0.235	Detected	0.000	2.550	Detected	2.769	Detected	2.659	0.009	GT	Sens	contig305	contig305	At5g2428
GT	Sens	Sense	-0.541	Comprom	0.541	Comprom	0.000	2.646	Detected	2.307	Detected	2.477	0.049	GT	Sens	contig305	contig305	Unknown
GT	Sens	Sense	-0.093	Detected	0.093	Detected	0.000	1.254	Detected	0.805	Detected	1.030	0.052	GT	Sens	contig305	contig305	Unknown
GT	Sens	Sense	-0.008	Detected	0.008	Detected	0.000	1.181	Detected	1.266	Detected	1.224	0.001	GT	Sens	contig305	contig305	Calmodul
GT	Sens	Sense	0.246	Detected	-0.246	Comprom	0.000	3.508	Detected	2.063	Detected	2.785	0.068	GT	Sens	contig305	contig305	class IV h
GT	Sens	Sense	-0.130	Detected	0.130	Detected	0.000	1.873	Detected	1.395	Detected	1.634	0.027	GT	Sens	contig306	contig306	Unknown
GT	Sens	Sense	-0.125	Detected	0.125	Detected	0.000	1.208	Detected	0.853	Detected	1.030	0.042	GT	Sens	contig306	contig306	Peptide m
GT	Sens	Sense	-0.247	Detected	0.247	Detected	0.000	1.799	Detected	1.572	Detected	1.686	0.025	GT	Sens	contig306	contig306	Myrosina
GT	Sens	Sense	0.303	Comprom	-0.303	Comprom	0.000	0.945	Detected	1.105	Detected	1.025	0.082	GT	Sens	contig306	contig306	Ulp1 prot
GT	Sens	Sense	-0.566	Comprom	0.566	Comprom	0.000	2.580	Detected	2.336	Detected	2.458	0.051	GT	Sens	contig306	contig306	Glucan e
GT	Sens	Sense	-0.315	Detected	0.315	Detected	0.000	1.472	Detected	1.473	Detected	1.472	0.043	GT	Sens	contig306	contig306	Leucine-r
GT	Sens	Sense	0.229	Detected	-0.229	Detected	0.000	1.272	Detected	1.212	Detected	1.242	0.033	GT	Sens	contig306	contig306	NAC dom
GT	Sens	Sense	-0.050	Comprom	0.050	Comprom	0.000	2.215	Detected	2.102	Detected	2.159	0.001	GT	Sens	contig306	contig306	RNA poly
GT	Sens	Sense	0.010	Detected	-0.010	Detected	0.000	1.184	Detected	0.828	Detected	1.006	0.030	GT	Sens	contig307	contig307	Red chlor
GT	Sens	Sense	0.271	Detected	-0.271	Detected	0.000	1.531	Detected	1.102	Detected	1.317	0.062	GT	Sens	contig307	contig307	Unknown
GT	Sens	Sense	-0.770	Comprom	0.770	Comprom	0.000	1.161	Detected	1.774	Detected	1.467	0.219	GT	Sens	contig307	contig307	Nucleopo
GT	Sens	Sense	-0.366	Detected	0.366	Detected	0.000	1.480	Detected	1.349	Detected	1.414	0.063	GT	Sens	contig307	contig307	Metal ion
GT	Sens	Sense	-0.170	Detected	0.170	Detected	0.000	1.113	Detected	0.895	Detected	1.004	0.038	GT	Sens	contig309	contig309	Ycf36 pro
GT	Sens	Sense	0.177	Detected	-0.177	Detected	0.000	3.461	Detected	3.457	Detected	3.459	0.003	GT	Sens	contig309	contig309	Unknown
GT	Sens	Sense	0.532	Detected	-0.532	Detected	0.000	2.165	Detected	1.299	Detected	1.732	0.128	GT	Sens	contig309	contig309	Kunitz-ty
GT	Sens	Sense	-0.093	Comprom	0.093	Comprom	0.000	3.625	Detected	2.791	Detected	3.208	0.017	GT	Sens	contig309	contig309	Pentatric
GT	Sens	Sense	-0.273	Detected	0.273	Detected	0.000	1.327	Detected	0.998	Detected	1.162	0.068	GT	Sens	contig309	contig309	DNA-3-me
GT	Sens	Sense	-0.097	Comprom	0.097	Comprom	0.000	1.170	Detected	1.050	Detected	1.110	0.010	GT	Sens	contig310	contig310	Os01g06
GT	Sens	Sense	0.198	Detected	-0.198	Detected	0.000	1.193	Detected	1.012	Detected	1.102	0.037	GT	Sens	contig310	contig310	Glucan e
GT	Sens	Sense	-0.086	Detected	0.086	Detected	0.000	1.348	Detected	1.567	Detected	1.457	0.009	GT	Sens	contig310	contig310	NBS-LRR
GT	Sens	Sense	-0.286	Comprom	0.286	Comprom	0.000	2.066	Detected	1.873	Detected	1.969	0.023	GT	Sens	contig310	contig310	Unknown
GT	Sens	Sense	0.034	Detected	-0.034	Detected	0.000	1.134	Detected	1.492	Detected	1.313	0.019	GT	Sens	contig311	contig311	Xylogluca
GT	Sens	Sense	-0.131	Detected	0.131	Detected	0.000	1.261	Detected	0.962	Detected	1.112	0.031	GT	Sens	contig311	contig311	Glyoxalas
GT	Sens	Sense	0.070	Comprom	-0.070	Comprom	0.000	1.739	Detected	2.315	Detected	2.027	0.021	GT	Sens	contig311	contig311	Glucan e
GT	Sens	Sense	0.063	Comprom	-0.063	Comprom	0.000	1.482	Detected	1.349	Detected	1.416	0.004	GT	Sens	contig311	contig311	Plasma m
GT	Sens	Sense	-0.673	Detected	0.673	Detected	0.000	3.681	Detected	3.682	Detected	3.681	0.032	GT	Sens	contig312	contig312	Plant-spe
GT	Sens	Sense	-0.072	Comprom	0.072	Comprom	0.000	2.606	Detected	2.743	Detected	2.674	0.001	GT	Sens	contig312	contig312	Unknown
GT	Sens	Sense	-0.104	Detected	0.104	Detected	0.000	1.200	Detected	0.866	Detected	1.033	0.034	GT	Sens	contig313	contig313	Malate de
GT	Sens	Sense	0.404	Detected	-0.404	Detected	0.000	1.375	Detected	1.198	Detected	1.286	0.090	GT	Sens	contig313	contig313	Unannota
GT	Sens	Sense	0.433	Comprom	-0.433	Comprom	0.000	2.746	Detected	2.950	Detected	2.848	0.024	GT	Sens	contig313	contig313	Unannota
GT	Sens	Sense	-0.562	Comprom	0.562	Comprom	0.000	1.566	Detected	1.875	Detected	1.721	0.098	GT	Sens	contig313	contig313	Unannota
GT	Sens	Sense	-0.087	Comprom	0.087	Comprom	0.000	3.710	Detected	2.798	Detected	3.254	0.020	GT	Sens	contig313	contig313	Unannota
GT	Sens	Sense	-0.206	Comprom	0.206	Comprom	0.000	1.381	Detected	1.664	Detected	1.523	0.026	GT	Sens	contig314	contig314	Unannota
GT	Sens	Sense	-1.017	Comprom	1.017	Detected	0.000	1.176	Detected	1.428	Detected	1.302	0.332	GT	Sens	contig314	contig314	Unannota
GT	Sens	Sense	-0.502	Comprom	0.502	Comprom	0.000	2.010	Detected	2.017	Detected	2.014	0.057	GT	Sens	contig314	contig314	Unannota
GT	Sens	Sense	-0.488	Comprom	0.488	Comprom	0.000	2.264	Detected	1.924	Detected	2.094	0.056	GT	Sens	contig314	contig314	Unannota
GT	Sens	Sense	0.742	Detected	-0.742	Comprom	0.000	0.903	Detected	1.145	Detected	1.024	0.306	GT	Sens	contig314	contig314	Unannota
GT	Sens	Sense	0.321	Comprom	-0.321	Comprom	0.000	2.161	Detected	1.039	Detected	1.600	0.132	GT	Sens	contig314	contig314	Unannota
GT	Sens	Sense	-0.349	Comprom	0.349	Detected	0.000	1.497	Detected	0.881	Detected	1.189	0.125	GT	Sens	contig314	contig314	Unannota
GT	Sens	Sense	0.725	Detected	-0.725	Comprom	0.000	1.102	Detected	1.206	Detected	1.154	0.253	GT	Sens	contig314	contig314	Unannota
GT	Sens	Sense	-0.231	Comprom	0.231	Comprom	0.000	1.184	Detected	1.984	Detected	1.584	0.075	GT	Sens	contig315	contig315	Unannota
GT	Sens	Sense	-0.254	Comprom	0.254	Comprom	0.000	1.351	Detected	1.251	Detected	1.301	0.037	GT	Sens	contig315	contig315	Unannota
GT	Sens	Sense	-0.862	Comprom	0.862	Detected	0.000	2.345	Detected	1.382	Detected	1.863	0.200	GT	Sens	contig315	contig315	Unannota
GT	Sens	Sense	0.094	Comprom	-0.094	Comprom	0.000	1.622	Detected	2.165	Detected	1.893	0.022	GT	Sens	contig315	contig315	Unannota
GT	Sens	Sense	-0.312	Comprom	0.312	Comprom	0.000	1.412	Detected	1.971	Detected	1.692	0.056	GT	Sens	contig315	contig315	Unannota
GT	Sens	Sense	-0.763	Detected	0.763	Detected	0.000	3.788	Detected	3.169	Detected	3.479	0.052	GT	Sens	contig315	contig315	Transcrip
GT	Sens	Sense	0.120	Detected	-0.120	Detected	0.000	1.787	Detected	0.821	Detected	1.304	0.120	GT	Sens	contig315	contig315	Unannota
GT	Sens	Sense	0.280	Detected	-0.280	Comprom	0.000	1.252	Detected	0.884	Detected	1.068	0.086	GT	Sens	contig316	contig316	Unannota
GT	Sens	Sense	-0.108	Detected	0.108	Detected	0.000	1.388	Detected	1.421	Detected	1.405	0.006	GT	Sens	contig316	contig316	Unannota
GT	Sens	Sense	-0.170	Detected	0.170	Detected	0.000	1.381	Detected	1.300	Detected	1.341	0.016	GT	Sens	contig316	contig316	Unannota
GT	Sens	Sense	0.268	Detected	-0.268	Detected	0.000	1.419	Detected	1.211	Detected	1.315	0.045	GT	Sens	contig317	contig317	Unannota
GT	Sens	Sense	-0.188	Comprom	0.188	Comprom	0.000	1.628	Detected	1.541	Detected	1.584	0.014	GT	Sens	contig317	contig317	Unannota
GT	Sens	Sense	-0.199	Comprom	0.199	Comprom	0.000	0.934	Detected	1.687	Detected	1.311	0.091	GT	Sens	contig317	contig317	Unannota
GT	Sens	Sense	-0.176	Comprom	0.176	Comprom	0.000	0.963	Detected	1.236	Detected	1.100	0.039	GT	Sens	contig317	contig317	Unannota
GT	Sens	Sense	0.380	Comprom	-0.380	Comprom	0.000	1.415	Detected	1.486	Detected	1.450	0.063	GT	Sens	contig317	contig317	Unannota
GT	Sens	Sense	0.076	Detected	-0.076	Detected	0.000	1.509	Detected	1.411	Detected	1.460	0.004	GT	Sens	contig317	contig317	Unannota
GT	Sens	Sense	-0.269	Detected	0.269	Detected	0.000	3.875	Detected	3.559	Detected	3.717	0.007	GT	Sens	contig317	contig317	DUF599 f
GT	Sens	Sense	0.267	Comprom	-0.267	Comprom	0.000	1.200	Detected	0.991	Detected	1.096	0.062	GT	Sens	contig318	contig318	Unannota
GT	Sens	Sense	0.440	Comprom	-0.440	Comprom	0.000	1.514	Detected	1.730	Detected	1.622	0.070	GT	Sens	contig318	contig318	Unannota
GT	Sens	Sense	-0.180	Comprom	0.180	Comprom	0.000	2.245	Detected	0.921	Detected	1.583	0.147	GT	Sens	contig318	contig318	Unannota
GT	Sens	Sense	-0.034	Detected	0.034	Detected	0.000	1.511	Detected	1.377	Detected	1.444	0.003	GT	Sens	contig318	contig318	Unannota
GT	Sens	Sense	-0.087	Detected	0.087	Detected	0.000	1.096	Detected	1.183	Detected	1.139	0.007	GT	Sens	contig318	contig318	Unannota
GT	Sens	Sense	-0.298	Comprom	0.298	Comprom	0.000	2.001	Detected	2.076	Detected	2.038	0.021	GT	Sens	contig319	contig319	Unannota
GT	Sens	Sense	0.607	Detected	-0.607	Comprom	0.000	2.499	Detected	2.194	Detected	2.346	0.064	GT	Sens	contig319	contig319	Calcium-
GT	Sens	Sense	-0.478	Comprom	0.478	Comprom	0.000	1.389	Detected	1.515	Detected	1.452	0.095	GT	Sens	contig319	contig319	Unannota
GT	Sens	Sense	-0.101	Comprom	0.101	Comprom	0.000	1.270	Detected	1.179	Detected	1.225	0.008	GT	Sens	contig319	contig319	Unannota
GT	Sens	Sense	-0.490	Comprom	0.490	Comprom	0.000	2.158	Detected	2.436	Detected	2.297	0.046	GT	Sens	contig319	contig319	Unannota
GT	Sens	Sense	0.227	Comprom	-0.227	Comprom	0.000	1.172	Detected	0.965	Detected	1.069	0.050	GT	Sens	contig320	contig320	Unannota
GT	Sens	Sense	-0.064	Comprom	0.064	Comprom	0.000	1.437	Detected	1.522	Detected	1.480	0.003	GT	Sens	contig320	contig320	Unannota
GT	Sens	Sense	-0.292	Detected	0.292	Detected	0.000	1.795	Detected	1.411	Detected	1.603	0.044	GT	Sens	contig320	contig320	Unannota
GT	Sens	Sense	-0.212	Detected	0.212	Detected	0.000	1.800	Detected	1.307	Detected	1.554	0.041	GT	Sens	contig320	contig320	Unannota
GT	Sens	Sense	0.150	Detected	-0.150	Detected	0.000	1.114	Detected	1.164	Detected	1.139	0.017	GT	Sens	contig320	contig320	Unannota
GT	Sens	Sense	0.072	Detected	-0.072	Detected	0.000	1.162	Detected	0.870	Detected	1.016	0.025	GT	Sens	contig320	contig320	Unannota
GT	Sens	Sense	0.070	Detected	-0.070	Detected	0.000	1.119	Detected	1.497	Detected	1.308	0.023	GT	Sens	contig321	contig321	Transpos
GT	Sens	Sense	-0.397	Comprom	0.397	Comprom	0.000	2.007	Detected	1.719	Detected	1.863	0.048	GT	Sens	contig321	contig321	NHL1 (Fra
GT	Sens	Sense	-0.322	Comprom	0.322	Comprom	0.000	1.640	Detected	1.756	Detected	1.698	0.035	GT	Sens	contig321	contig321	Unknown
GT	Sens	Sense	-0.448	Detected	0.448	Detected	0.000	2.769	Detected	2.172	Detected	2.470	0.044	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	-0.424	Detected	0.424	Detected	0.000	2.497	Detected	1.989	Detected	2.243	0.045	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	-0.640	Comprom	0.640	Detected	0.000	1.043	Detected	0.973	Detected	1.008	0.256	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	0.696	Comprom	-0.696	Comprom	0.000	1.299	Detected	2.125	Detected	1.712	0.169	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	0.420	Detected	-0.420	Detected	0.000	1.162	Detected	1.132	Detected	1.147	0.112	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	0.101	Detected	-0.101	Detected	0.000	1.223	Detected	1.027	Detected	1.125	0.015	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	0.340	Detected	-0.340	Detected	0.000	2.377	Detected	2.535	Detected	2.456	0.020	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	0.084	Detected	-0.084	Detected	0.000	1.489	Detected	0.936	Detected	1.213	0.052	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	-0.091	Detected	0.091	Detected	0.000	1.428	Detected	0.891	Detected	1.160	0.055	GT	Sens	contig321	contig321	Unannota
GT	Sens	Sense	0.888	Comprom	-0.888	Comprom	0.000	1.136	Detected	1.596	Detected	1.366	0.275	GT	Sens	contig322	contig322	Unannota
GT	Sens	Sense	0.098	Comprom	-0.098	Comprom	0.000	4.132	Detected	1.229	Detected	2.681	0.207	GT	Sens	contig322	contig322	Unannota
GT	Sens	Sense	-0.318	Comprom	0.318	Comprom	0.000	3.203	Detected	2.661	Detected	2.932	0.020	GT	Sens	contig322	contig322	Hydroxy
GT	Sens	Sense	0.431	Detected	-0.431	Comprom	0.000	1.678	Detected	1.671	Detected	1.674	0.060	GT	Sens	contig323	contig323	Ycf2 (AHF
GT	Sens	Sense	-0.325	Detected	0.325	Detected	0.000	1.300	Detected	0.801	Detected	1.051	0.125	GT	Sens	contig323	contig323	Unannota
GT	Sens	Sense	-0.272	Detected	0.272	Detected	0.000	1.301	Detected	0.834	Detected	1.068	0.097	GT	Sens	contig323	contig323	Unannota
GT	Sens	Sense	0.309	Comprom	-0.309	Comprom	0.000	2.012	Detected	1.973	Detected	1.992	0.023	GT	Sens	contig323	contig323	Unannota
GT	Sens	Sense	0.231	Comprom	-0.231	Comprom	0.000	1.488	Detected	2.827	Detected	2.158	0.093	GT	Sens	contig323	contig323	Unannota
GT	Sens	Sense	-0.068	Comprom	0.068	Comprom	0.000	1.593	Detected	0.995	Detected	1.294	0.052	GT	Sens	contig323	contig323	Unknown
GT	Sens	Sense	-0.017	Detected	0.017	Detected	0.000	1.269	Detected	0.855	Detected	1.062	0.036	GT	Sens	contig324	contig324	Unannota
GT	Sens	Sense	0.302	Detected	-0.302	Detected	0.000	0.910	Detected	1.178	Detected	1.044	0.087	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	-0.014	Detected	0.014	Detected	0.000	1.302	Detected	1.573	Detected	1.438	0.009	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	-0.397	Comprom	0.397	Comprom	0.000	2.018	Detected	1.567	Detected	1.793	0.059	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	-0.374	Comprom	0.374	Comprom	0.000	2.140	Detected	2.284	Detected	2.212	0.028	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	0.067	Comprom	-0.067	Comprom	0.000	1.396	Detected	1.231	Detected	1.314	0.006	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	-0.149	Detected	0.149	Detected	0.000	1.991	Detected	0.907	Detected	1.449	0.123	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	-0.215	Detected	0.215	Detected	0.000	2.012	Detected	1.044	Detected	1.528	0.102	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	-0.061	Comprom	0.061	Comprom	0.000	1.159	Detected	0.906	Detected	1.032	0.018	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	-0.602	Comprom	0.602	Comprom	0.000	1.648	Detected	2.991	Detected	2.319	0.124	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	0.148	Comprom	-0.148	Comprom	0.000	1.833	Detected	1.507	Detected	1.670	0.017	GT	Sens	contig325	contig325	Unannota
GT	Sens	Sense	0.214	Detected	-0.214	Detected	0.000	1.248	Detected	0.803	Detected	1.026	0.080	GT	Sens	contig326	contig326	Unannota
GT	Sens	Sense	-0.099	Comprom	0.099	Comprom	0.000	1.323	Detected	1.585	Detected	1.454	0.013	GT	Sens	contig326	contig326	Unannota
GT	Sens	Sense	-0.197	Detected	0.197	Detected	0.000	2.261	Detected	1.410	Detected	1.835	0.060	GT	Sens	contig326	contig326	Receptor
GT	Sens	Sense	-0.103	Comprom	0.103	Comprom	0.000	1.605	Detected	1.802	Detected	1.703	0.007	GT	Sens	contig326	contig326	Unannota
GT	Sens	Sense	-0.564	Comprom	0.564	Comprom	0.000	6.946	Detected	2.064	Detected	4.505	0.214	GT	Sens	contig327	contig327	Unannota
GT	Sens	Sense	0.126	Detected	-0.126	Detected	0.000	1.514	Detected	1.307	Detected	1.410	0.013	GT	Sens	contig328	contig328	Unannota
GT	Sens	Sense	-0.521	Comprom	0.521	Comprom	0.000	1.861	Detected	2.199	Detected	2.030	0.066	GT	Sens	contig328	contig328	Unannota
GT	Sens	Sense	-0.453	Comprom	0.453	Comprom	0.000	1.367	Detected	0.866	Detected	1.117	0.164	GT	Sens	contig328	contig328	Unannota
GT	Sens	Sense	0.563	Detected	-0.563	Comprom	0.000	1.195	Detected	0.922	Detected	1.059	0.209	GT	Sens	contig329	contig329	Unannota
GT	Sens	Sense	-0.154	Detected	0.154	Detected	0.000	2.048	Detected	2.467	Detected	2.258	0.013	GT	Sens	contig329	contig329	Unannota
GT	Sens	Sense	-0.220	Detected	0.220	Detected	0.000	1.229	Detected	1.694	Detected	1.461	0.045	GT	Sens	contig329	contig329	Unannota
GT	Sens	Sense	0.349	Comprom	-0.349	Comprom	0.000	1.308	Detected	2.132	Detected	1.720	0.086	GT	Sens	contig329	contig329	Unannota
GT	Sens	Sense	-0.116	Detected	0.116	Detected	0.000	1.102	Detected	1.182	Detected	1.142	0.011	GT	Sens	contig329	contig329	Unannota
GT	Sens	Sense	-0.177	Detected	0.177	Detected	0.000	1.052	Detected	1.012	Detected	1.032	0.029	GT	Sens	contig329	contig329	Unannota
GT	Sens	Sense	-0.626	Comprom	0.626	Detected	0.000	1.188	Detected	1.029	Detected	1.108	0.221	GT	Sens	contig329	contig329	Unannota
GT	Sens	Sense	0.277	Comprom	-0.277	Comprom	0.000	1.671	Detected	1.156	Detected	1.414	0.065	GT	Sens	contig330	contig330	Unannota
GT	Sens	Sense	-0.642	Comprom	0.642	Comprom	0.000	2.133	Detected	1.526	Detected	1.829	0.123	GT	Sens	contig330	contig330	Unannota
GT	Sens	Sense	-0.338	Comprom	0.338	Comprom	0.000	0.849	Detected	4.302	Detected	2.576	0.281	GT	Sens	contig330	contig330	Unannota
GT	Sens	Sense	0.302	Detected	-0.302	Detected	0.000	1.156	Detected	1.201	Detected	1.178	0.060	GT	Sens	contig330	contig330	Unannota
GT	Sens	Sense	-0.227	Detected	0.227	Detected	0.000	1.247	Detected	1.459	Detected	1.353	0.033	GT	Sens	contig330	contig330	Unannota
GT	Sens	Sense	-1.079	Comprom	1.079	Detected	0.000	1.761	Detected	0.827	Detected	1.294	0.386	GT	Sens	contig331	contig331	Unannota
GT	Sens	Sense	-0.185	Detected	0.185	Detected	0.000	0.960	Detected	1.055	Detected	1.008	0.034	GT	Sens	contig331	contig331	Unannota
GT	Sens	Sense	-0.071	Detected	0.071	Detected	0.000	1.274	Detected	0.878	Detected	1.076	0.036	GT	Sens	contig331	contig331	Unannota
GT	Sens	Sense	0.058	Detected	-0.058	Detected	0.000	1.388	Detected	1.097	Detected	1.242	0.016	GT	Sens	contig331	contig331	Unannota
GT	Sens	Sense	-0.266	Detected	0.266	Detected	0.000	0.985	Detected	1.028	Detected	1.007	0.064	GT	Sens	contig331	contig331	Unannota
GT	Sens	Sense	0.016	Comprom	-0.016	Comprom	0.000	1.015	Detected	1.129	Detected	1.072	0.003	GT	Sens	contig332	contig332	Unannota
GT	Sens	Sense	0.207	Comprom	-0.207	Comprom	0.000	2.046	Detected	1.841	Detected	1.944	0.014	GT	Sens	contig332	contig332	Unannota
GT	Sens	Sense	0.168	Detected	-0.168	Detected	0.000	1.140	Detected	0.978	Detected	1.059	0.030	GT	Sens	contig332	contig332	1-phosph
GT	Sens	Sense	-0.054	Detected	0.054	Detected	0.000	1.571	Detected	1.221	Detected	1.396	0.017	GT	Sens	contig332	contig332	Peptide tr
GT	Sens	Sense	0.244	Detected	-0.244	Detected	0.000	1.011	Detected	1.366	Detected	1.189	0.059	GT	Sens	contig332	contig332	Unannota
GT	Sens	Sense	0.118	Detected	-0.118	Detected	0.000	1.908	Detected	1.958	Detected	1.933	0.004	GT	Sens	contig332	contig332	Unannota
GT	Sens	Sense	0.263	Detected	-0.263	Detected	0.000	2.165	Detected	1.467	Detected	1.816	0.053	GT	Sens	contig333	contig333	Unannota
GT	Sens	Sense	-0.454	Comprom	0.454	Comprom	0.000	3.392	Detected	2.432	Detected	2.912	0.048	GT	Sens	contig333	contig333	Unannota
GT	Sens	Sense	-0.602	Comprom	0.602	Comprom	0.000	1.872	Detected	1.871	Detected	1.872	0.090	GT	Sens	contig333	contig333	Unannota
GT	Sens	Sense	-0.632	Detected	0.632	Detected	0.000	2.712	Detected	2.272	Detected	2.492	0.065	GT	Sens	contig333	contig333	Unannota
GT	Sens	Sense	-0.624	Comprom	0.624	Comprom	0.000	2.764	Detected	2.427	Detected	2.595	0.057	GT	Sens	contig333	contig333	Unannota
GT	Sens	Sense	0.030	Comprom	-0.030	Comprom	0.000	1.991	Detected	2.422	Detected	2.206	0.010	GT	Sens	contig333	contig333	Unannota
GT	Sens	Sense	0.170	Comprom	-0.170	Comprom	0.000	2.195	Detected	4.768	Detected	3.481	0.115	GT	Sens	contig333	contig333	Unannota
GT	Sens	Sense	0.053	Detected	-0.053	Detected	0.000	1.859	Detected	1.216	Detected	1.538	0.042	GT	Sens	contig334	contig334	Unannota
GT	Sens	Sense	0.014	Detected	-0.014	Detected	0.000	1.979	Detected	1.387	Detected	1.683	0.030	GT	Sens	contig334	contig334	Unannota
GT	Sens	Sense	-0.551	Comprom	0.551	Comprom	0.000	1.189	Detected	1.081	Detected	1.135	0.177	GT	Sens	contig334	contig334	Unannota
GT	Sens	Sense	-0.385	Comprom	0.385	Comprom	0.000	2.436	Detected	1.162	Detected	1.799	0.137	GT	Sens	contig334	contig334	Unannota
GT	Sens	Sense	-0.381	Detected	0.381	Detected	0.000	1.058	Detected	1.314	Detected	1.186	0.098	GT	Sens	contig334	contig334	Unannota
GT	Sens	Sense	-0.550	Comprom	0.550	Comprom	0.000	0.945	Detected	1.274	Detected	1.109	0.193	GT	Sens	contig334	contig334	Unannota
GT	Sens	Sense	-1.028	Comprom	1.028	Comprom	0.000	1.996	Detected	1.514	Detected	1.755	0.238	GT	Sens	contig334	contig334	Unannota

GT	Sense	Sense	-0.245	Detected	0.245	Detected	0.000	2.019	Detected	1.520	Detected	1.769	0.037	GT	Sens	SL2.40ch	AT4G01050.1		hydroxy	chr4:455	135.319	178.744	478.077	214.726	671.955	474.192
GT	Sense	Sense	0.029	Comprom	-0.029	Comprom	0.000	1.746	Detected	2.066	Detected	1.906	0.007	GT	Sens	SL2.40ch	AT1G269	AtHB23	AtHB23 (/	chr1:935	4.34805	3.93194	15.1869	14.8928	14.789	18.4112
GT	Sense	Sense	-0.355	Comprom	0.355	Comprom	0.000	1.517	Detected	2.094	Detected	1.805	0.059	GT	Sens	SL2.40ch	AT5G18000.1		transcrip	chr5:596	3.23322	4.97667	8.6001	12.2089	12.2413	18.2019
GT	Sense	Sense	0.255	Detected	-0.255	Comprom	0.000	2.063	Detected	1.310	Detected	1.687	0.066	GT	Sens	SL2.40ch	AT2G386	PECT1	PECT1 (F	chr2:161	12.5323	8.28453	11.4688	9.95621	45.4169	26.8687
GT	Sense	Sense	0.001	Detected	-0.001	Detected	0.000	1.255	Detected	1.441	Detected	1.348	0.005	GT	Sens	SL2.40ch	AT2G386	PECT1	PECT1 (F	chr2:161	14.3503	13.4902	13.5562	13.7271	35.4099	40.1775
GT	Sense	Sense	-0.786	Comprom	0.786	Comprom	0.000	1.350	Detected	1.580	Detected	1.465	0.206	GT	Sens	SL2.40ch	AT5G14440.2		FUNCTIO	chr5:465	2.14464	5.99865	9.01381	3.46388	9.74964	11.3971
GT	Sense	Sense	-0.174	Comprom	0.174	Detected	0.000	1.072	Detected	1.084	Detected	1.078	0.025	GT	Sens		AT1G205	AAE1	AAE1 (AC	chr1:711	9.57015	11.4679	13.493	5.73737	23.4796	23.6125
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	1.345	Detected	1.021	Detected	1.183	0.021	GT	Sens	SL2.40ch	AT5G61940.1		ubiquitin	chr5:248	56.0246	48.0948	76.1747	79.374	140.627	112.024
GT	Sense	Sense	0.374	Comprom	-0.374	Comprom	0.000	1.753	Detected	1.413	Detected	1.583	0.061	GT	Sens	SL2.40ch	AT1G68910.2		unknowr	chr1:259	6.74414	3.7785	11.4673	17.2172	18.1452	14.2956
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	1.263	Detected	0.921	Detected	1.092	0.024	GT	Sens	SL2.40ch	AT3G08960.1		binding /	chr3:273	35.1176	33.6	48.6951	48.9258	87.882	69.1681
GT	Sense	Sense	-0.414	Comprom	0.414	Detected	0.000	0.926	Detected	1.089	Detected	1.007	0.140	GT	Sens	SL2.40ch	AT3G256	CHUP1	CHUP1 (C	chr3:935	7.60709	12.7071	19.7467	29.5984	19.9197	22.2361
GT	Sense	Sense	0.383	Detected	-0.383	Detected	0.000	1.224	Detected	1.445	Detected	1.335	0.079	GT	Sens	SL2.40ch	AT3G51690.1				23.6258	13.0688	26.1521	52.0646	43.7678	50.8809
GT	Sense	Sense	-0.198	Comprom	0.198	Comprom	0.000	0.830	Detected	1.212	Detected	1.021	0.065	GT	Sens	SL2.40ch	AT3G08660.1		phototro	chr3:263	5.30211	6.56357	9.04505	8.72417	11.1859	14.533
GT	Sense	Sense	-0.203	Detected	0.203	Detected	0.000	0.939	Detected	1.249	Detected	1.094	0.051	GT	Sens	SL2.40ch	AT3G52700.1		unknowr	chr3:195	223.139	278.317	440.861	334.871	509.441	629.819
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	1.033	Detected	1.188	Detected	1.111	0.066	GT	Sens	SL2.40ch	AT4G303	ATDGK7	ATDGK7	chr4:148	50.7812	31.921	66.5845	122.468	87.8653	97.539
GT	Sense	Sense	-0.178	Detected	0.178	Detected	0.000	1.508	Detected	1.411	Detected	1.459	0.016	GT	Sens	SL2.40ch	AT1G68490.1		unknowr	chr1:256	118.481	142.623	136.915	181.584	394.276	367.497
GT	Sense	Sense	-0.254	Comprom	0.254	Comprom	0.000	1.456	Detected	1.407	Detected	1.431	0.030	GT	Sens	SL2.40ch	AT1G01650.2		aspartic-	chr1:233	3.53554	4.73121	11.5985	7.85447	11.966	11.5286
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	1.206	Detected	1.133	Detected	1.170	0.012	GT	Sens	SL2.40ch	AT5G24450.1		unknowr	chr5:834	24.3198	19.2102	18.9263	42.7521	53.1924	50.4055
GT	Sense	Sense	-0.095	Comprom	0.095	Comprom	0.000	0.937	Detected	1.162	Detected	1.049	0.019	GT	Sens	SL2.40ch	AT1G12810.2				6.32795	6.79665	9.04121	6.17912	13.3897	15.5986
GT	Sense	Sense	-0.034	Comprom	0.034	Comprom	0.000	1.433	Detected	1.432	Detected	1.432	0.001	GT	Sens	SL2.40ch	ATCG011	YCF1.2	hypothet	chrC:123	4.05143	3.99457	8.94125	4.18821	11.5831	11.5395
GT	Sense	Sense	-0.492	Comprom	0.492	Comprom	0.000	3.186	Detected	4.816	Detected	4.001	0.052	GT	Sens	SL2.40ch	AT4G376	BT5	BT5 (BTE	chr4:176	2.45817	4.57384	3.27905	6.295	32.5393	100.421
GT	Sense	Sense	-0.634	Comprom	0.634	Comprom	0.000	2.080	Detected	2.177	Detected	2.128	0.079	GT	Sens		AT4G32610.1		unknowr	chr4:157	3.04131	6.89605	31.5413	23.1655	20.6428	22.0201
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	1.294	Detected	1.227	Detected	1.260	0.001	GT	Sens	SL2.40ch	AT5G22240.1				118.311	112.62	138.343	141.078	301.753	287.218
GT	Sense	Sense	0.535	Comprom	-0.535	Comprom	0.000	0.851	Detected	1.859	Detected	1.355	0.207	GT	Sens	SL2.40ch	AT5G25440.1				8.53761	3.8258	11.4011	15.602	10.9916	22.0434
GT	Sense	Sense	-0.044	Comprom	0.044	Comprom	0.000	1.385	Detected	1.353	Detected	1.369	0.001	GT	Sens	SL2.40ch	AT4G14920.1		DNA binc	chr4:853	4.78911	4.78967	12.1632	11.19	13.3369	13.0066
GT	Sense	Sense	-0.111	Detected	0.111	Detected	0.000	1.233	Detected	1.160	Detected	1.197	0.009	GT	Sens	SL2.40ch	AT5G57200.1		epsin N-t	chr5:231	249.325	273.489	391.1	288.81	654.562	620.432
GT	Sense	Sense	-0.015	Comprom	0.015	Comprom	0.000	1.239	Detected	1.212	Detected	1.226	0.000	GT	Sens	SL2.40ch	AT3G19080.1				6.93873	6.66935	17.3532	17.6324	17.1215	16.7589
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	1.157	Detected	1.039	Detected	1.098	0.020	GT	Sens	SL2.40ch	AT5G178	CSA1	CSA1 (cc	chr5:590	157.523	121.127	242.165	244.84	328.518	301.768
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	1.776	Detected	1.746	Detected	1.761	0.000	GT	Sens	SL2.40ch	AT5G62270.1		FUNCTIO	chr5:250	20.6881	18.9322	13.8534	17.5648	72.2626	70.5767
GT	Sense	Sense	-0.131	Comprom	0.131	Comprom	0.000	1.098	Detected	0.926	Detected	1.012	0.023	GT	Sens	SL2.40ch	ATCG011	YCF1.2	hypothet	chrC:123	7.81026	8.81109	17.8906	11.7247	18.9332	16.7634
GT	Sense	Sense	-0.311	Detected	0.311	Detected	0.000	3.081	Detected	1.002	Detected	2.042	0.201	GT	Sens	SL2.40ch	AT5G65460.1		kinesin n	chr5:261	24.1212	34.9505	58.9131	104.48	262.011	61.8399
GT	Sense	Sense	-0.053	Detected	0.053	Detected	0.000	1.481	Detected	0.972	Detected	1.227	0.042	GT	Sens	SL2.40ch	AT3G125	TRFL9. A	TRFL9 (T	chr3:398	39.5708	40.0874	56.1007	46.5816	118.538	83.0806
GT	Sense	Sense	-0.123	Detected	0.123	Detected	0.000	1.551	Detected	0.992	Detected	1.271	0.053	GT	Sens	SL2.40ch	AT3G125	TRFL9. A	TRFL9 (T	chr3:398	58.3906	65.1564	85.2173	75.1451	192.748	130.397
GT	Sense	Sense	0.144	Comprom	-0.144	Comprom	0.000	0.829	Detected	1.193	Detected	1.011	0.049	GT	Sens	SL2.40ch	AT3G02710.1		nuclear a	chr3:583	7.58776	5.85064	14.0172	16.1876	12.6263	16.1928
GT	Sense	Sense	-0.098	Detected	0.098	Detected	0.000	1.700	Detected	1.072	Detected	1.386	0.052	GT	Sens	SL2.40ch	AT3G02710.1		nuclear a	chr3:583	12.8628	13.87	13.9513	17.0775	46.276	29.8641
GT	Sense	Sense	0.605	Comprom	-0.605	Comprom	0.000	1.504	Detected	1.763	Detected	1.633	0.118	GT	Sens	SL2.40ch	AT3G518	ATG2	ATG2: ar	chr3:192	6.08777	2.47604	11.7245	6.56072	11.7443	14.0064
GT	Sense	Sense	-0.449	Comprom	0.449	Comprom	0.000	2.271	Detected	2.270	Detected	2.270	0.037	GT	Sens	SL2.40ch	AT4G34100.2		protein b	chr4:163	2.6778	4.69854	11.9687	12.0636	18.2544	18.1888
GT	Sense	Sense	-0.010	Detected	0.010	Detected	0.000	1.150	Detected	0.875	Detected	1.013	0.018	GT	Sens	SL2.40ch	AT5G43570.1		serine-tv	chr5:175	65.1595	62.1696	138.414	100.9	150.645	124.102
GT	Sense	Sense	0.223	Detected	-0.223	Detected	0.000	1.278	Detected	0.914	Detected	1.096	0.063	GT	Sens	SL2.40ch	AT5G43570.1		serine-tv	chr5:175	34.8358	24.0508	59.0467	40.9604	74.8281	57.9982
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	1.415	Detected	0.807	Detected	1.111	0.086	GT	Sens	SL2.40ch	AT5G036	SBE2.2	SBE2.2 (:	chr5:931	25.8034	19.1235	43.5842	25.0875	63.1679	41.3324
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	1.339	Detected	0.940	Detected	1.140	0.029	GT	Sens	SL2.40ch	AT5G036	SBE2.2	SBE2.2 (:	chr5:931	258.473	247.052	576.102	401.761	681.689	515.606
GT	Sense	Sense	0.185	Comprom	-0.185	Comprom	0.000	2.288	Detected	2.694	Detected	2.491	0.012	GT	Sens	SL2.40ch	AT2G21050.1		amino ac	chr2:903	12.4809	9.09033	32.5404	32.0725	55.4913	73.2607
GT	Sense	Sense	-0.157	Comprom	0.157	Comprom	0.000	0.901	Detected	1.647	Detected	1.274	0.088	GT	Sens	SL2.40ch	AT3G037	RIF10	RIF10 (re	chr3:919	5.54947	6.48725	8.36061	6.96517	11.952	19.9771
GT	Sense	Sense	-0.151	Comprom	0.151	Comprom	0.000	2.021	Detected	1.670	Detected	1.846	0.015	GT	Sens	SL2.40ch	AT5G41620.1		FUNCTIO	chr5:166	3.65518	4.23852	6.4409	4.17511	17.035	13.3192
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	1.313	Detected	0.955	Detected	1.134	0.038	GT	Sens	SL2.40ch	AT4G119	PGRL1B	PGRL1B	chr4:717	1088.9	1247.91	2420.59	1326.56	3089.29	2403.36
GT	Sense	Sense	-0.610	Comprom	0.610	Comprom	0.000	1.351	Detected	1.345	Detected	1.348	0.158	GT	Sens	SL2.40ch	AT1G144	UBC1. AT	UBC1 (UE	chr1:492	4.05056	8.88394	22.5085	4.53217	16.3222	16.2061
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	2.134	Detected	1.730	Detected	1.932	0.012	GT	Sens	SL2.40ch	AT1G31050.1				35.3732	36.8715	90.2283	54.9955	169.045	127.398
GT	Sense	Sense	-0.246	Comprom	0.246	Comprom	0.000	1.312	Detected	1.620	Detected	1.466	0.037	GT	Sens	SL2.40ch	AT5G467	MSP2	MSP2 (m	chr5:189	5.32287	7.04258	2.4656	6.52726	16.2062	20.0062
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	1.232	Detected	0.979	Detected	1.106	0.016	GT	Sens	SL2.40ch	AT5G550	ATMYB1	MYB120	chr5:223	291.665	299.104	692.476	746.29	739.999	619.189
GT	Sense	Sense	0.243	Comprom	-0.243	Comprom	0.000	2.825	Detected	2.655	Detected	2.740	0.009	GT	Sens	SL2.40ch	AT5G550	ATMYB1	MYB120	chr5:223	3.3856	2.27479	9.38644	6.74957	20.9723	18.58
GT	Sense	Sense	0.269	Comprom	-0.269	Comprom	0.000	2.245	Detected	1.746	Detected	1.995	0.032	GT	Sens	SL2.40ch	AT4G37550.2		formamic	chr4:176	4.23441	2.74292	10.5859	7.64766	17.2234	12.1567
GT	Sense	Sense	0.412	Comprom	-0.412	Comprom	0.000	1.556	Detected	1.398	Detected	1.477	0.072	GT	Sens	SL2.40ch	AT4G37550.2		formamic	chr4:176	6.09295	3.23778	11.1763	5.14667	13.9237	12.4409
GT	Sense	Sense	-0.625	Comprom	0.625	Comprom	0.000	0.900	Detected	1.370	Detected	1.135	0.231	GT	Sens		AT1G61490.1				4.14718	9.28565	7.67301	10.8608	12.346	17.0558
GT	Sense	Sense	0.216	Comprom	-0.216	Comprom	0.000	1.246	Detected	1.400	Detected	1.323	0.029	GT	Sens	SL2.40ch	AT5G38350.1		disease r	chr5:153	5.80288	4.049	4.21491	6.14598	12.262	13.6044
GT	Sense	Sense	0.178	Detected	-0.178	Detected	0.000	1.316	Detected	1.432	Detected	1.374	0.018	GT	Sens	SL2.40ch	AT5G39820.1				1569.6	1153.68	2492.5	2793.29	3571.75	3860.44
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	1.556	Detected	1.646	Detected	1.601	0.013	GT	Sens	SL2.40ch	AT5G39820.1				826.084	609.493	1380.4	1611.57	2225	2361.77
GT	Sense	Sense	0.672	Comprom	-0.672	Comprom	0.000	1.911	Detected	3.650	Detected	2.780	0.127	GT	Sens		AT1G14540.1		anionic p	chr1:497	5.98378	2.21674	11.0352	6.9813	14.6038	48.5972
GT	Sense	Sense	-0.257	Detected	0.257	Detected	0.000	1.216	Detected	1.651	Detected	1.433	0.051	GT	Sens	SL2.40ch	AT2G28620.1				12.2647	16.4793	22.2961	17.0784	35.2211	47.4553
GT	Sense	Sense	-0.201	Detected	0.201	Detected	0.000	0.881	Detected	1.168	Detected	1.024	0.053	GT	Sens	SL2.40ch	AT2G28620.1				31.0284	38.5663	33.1177	38.982	67.9347	82.6201
GT	Sense	Sense	-0.318	Detected	0.318	Detected	0.000	2.001	Detected	1.301	Detected	1.651	0.073	GT	Sens	SL2.40ch	AT4G03110.2		RNA-binc	chr4:137	21.7261	31.7907	76.2762	45.1968	112.197	68.8458
GT	Sense	Sense	-0.374	Detected	0.374	Detected	0.000	2.030	Detected	1.318	Detected	1.674	0.083	GT	Sens	SL2.40ch	AT4G03110.2		RNA-binc	chr4:137	19.3612	30.5795	75.3844	46.9398	105.966	64.4864
GT	Sense	Sense	0.496	Comprom	-0.496	Comprom	0.000	1.868	Detected	2.069	Detected	1.968	0.060	GT	Sens	SL2.40ch	AT5G57120.1		FUNCTIO	chr5:231	4.61275	2.18371	47.5993	33.8405	12.3503	14.1615
GT	Sense	Sense	-0.598	Comprom	0.598	Comprom	0.000	1.659	Detected	1.797	Detected	1.728	0.103	GT	Sens	SL2.40ch	AT1G535	MAP3KA.	MAP3KA	chr1:199	4.50006	9.70607	17.6784	18.8544	22.2612	24.4166
GT	Sense	Sense	0.314	Comprom	-0.314	Comprom	0.000	1.900	Detected	2.166	Detected	2.033	0.027	GT	Sens	SL2.40ch	AT2G391	ATATH8	ATATH8:	chr2:163	3.83216	2.33473	24.4552	3.87155	11.9047	14.2704
GT	Sense	Sense	-0.606	Comprom	0.606	Comprom	0.000	0.976	Detected	4.384	Detected	2.680	0.277	GT	Sens	SL2.40ch	AT1G48140.1				3.31334	7.22275	6.85971	8.94577	10.2615	108.582
GT	Sense	Sense	-0.006	Comprom	0.006	Comprom	0.000	1.005	Detected	1.055	Detected	1.030	0.001	GT	Sens	SL2.40ch	AT5G52900.1				8.14932	7.73345	21.1859	24.672	16.9877	17.54
GT	Sense	Sense	0.211	Detected	-0.211	Detected	0.000	1.444	Detected	1.435	Detected	1.439	0.021	GT	Sens	SL2.40ch	AT1G69980.1		unknowr	chr1:263	726.239	509.7	1402.8	877.535	1765	1748.42
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	1.313	Detected	0.927	Detected	1.120	0.029	GT	Sens	SL2.40ch	AT1G707	CRR23	CRR23 ((	chr1:266	468.059	458.2	1196.7	581.917	1227.38	935.874
GT	Sense	Sense	0.149	Detected	-0.149	Detected	0.000	3.247	Detected	2.183	Detected	2.715	0.039	GT	Sens	SL2.40ch	AT1G13420.1				33.8029	25.8686	155.373	43.0462	299.323	142.767
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	3.239	Detected	2.290	Detected	2.765	0.031	GT	Sens	SL2.40ch	AT1G13420.1				88.0633	65.9471	367.889	115.205	767.092	396.343
GT	Sense	Sense	0.355	Comprom	-0.355	Comprom	0.000	5.002	Detected	4.251	Detected	4.626	0.012	GT	Sens	SL2.40ch	AT1G50140.2		ATP bind	chr1:185	3.92898	2.26059	37.6134	4.24135	101.816	60.3294
GT	Sense	Sense	-0.986	Comprom	0.986	Detected	0.000	1.063	Detected	1.026	Detected	1.044	0.401	GT	Sens	SL2.40ch	AT3G127	ZIP1	ZIP1 (ZIN	chr3:405	4.54346	16.7782	11.4523	6.40764	19.4468	18.9011
GT	Sense	Sense	-0.633	Comprom	0.633	Comprom	0.000	1.537	Detected	1.696	Detected	1.617	0.127	GT	Sens	SL2.40ch	AT5G666	DAR5	DAR5 (D/	chr5:265	3.57524	8.09489	5.83271	11.4851	16.6515	18.5359
GT	Sense	Sense	0.091	Comprom	-0.091	Comprom	0.000	2.464	Detected	2.028	Detected	2.246	0.011	GT	Sens	SL2.40ch	AT3G52700.1		unknowr	chr3:195	2.9666	2.45972	15.712	12.064	15.8926	11.713
GT	Sense	Sense	-0.090	Comprom	0.090	Comprom	0.000	5.030	Detected	2.452	Detected	3.741	0.101	GT	Sens		AT5G06400.1		pentatric	chr5:195	2.08872	2.22789	1.71118	1.92721	75.149	12.5518
GT	Sense	Sense	-0.209	Comprom	0.209	Comprom	0.000	1.046	Detected	1.348	Detected	1.197	0.044	GT	Sens	SL2.40ch	AT2G21990.1				4.64802	5.8473	9.27674	4.67528	11.4803	14.11
GT	Sense	Sense	0.253	Comprom	-0.253	Comprom	0.000	1.898	Detected	1.980	Detected	1.939	0.017	GT	Sens	SL2.40ch	AT5G35430.1		binding	chr5:136	3.29687	2.18547	6.94103	4.63927	10.6655	11.2605
GT	Sense	Sense	0.639	Detected	-0.639	Comprom	0.000	0.950	Detected	1.058	Detected	1.004	0.258	GT	Sens	SL2.40ch	AT5G35430.1		binding	chr5:136	11.5445	4.4781	5.58086	11.9201	14.8087	15.917
GT	Sense	Sense	-1.329	Comprom	1.329	Detected	0.000	2.559	Detected	1.716	Detected	2.137	0.265	GT	Sens	SL2.40ch	AT5G35180.4		phospho	chr5:134	2.05377	12.203	13.5691	2.68967	31.4673	17.4803
GT	Sense	Sense	-0.229	Detected	0.229	Detected	0.000	1.167	Detected	1.096	Detected	1.132	0.040	GT	Sens	SL2.40ch	AT1G649	GTG1	GTG1 (G	chr1:241	10.4111	13.4628	35.8904	38.2993	28.3526	26.9147
GT	Sense	Sense	-0.441	Detected	0.441	Detected	0.000	1.534	Detected	1.077	Detected	1.305	0.119	GT	Sens	SL2.40ch	AT1G649	GTG1	GTG1 (G	chr1:241	15.5285	26.9104	56.4053	54.6784	63.1235	45.8506
GT	Sense	Sense	-1.173	Comprom	1.173	Detected	0.000	0.864	Detected	3.567	Detected	2.215	0.341	GT	Sens	SL2.40ch	AT3G15130.1		pentatric	chr3:509	3.11242	14.896	13.6301	13.4385	13.2112	85.8242
GT	Sense	Sense	0.405	Detected	-0.405	Detected	0.000	2.283	Detected	1.205	Detected	1.744	0.123	GT	Sens	SL2.40ch	AT3G153	SPA3	SPA3 (SF	chr3:516	104.401	56.0506	177.562	73.2492	397.016	187.503
GT	Sense	Sense	0.303	Detected	-0.303	Detected	0.000	1.867	Detected	0.921	Detected	1.394	0.131	GT	Sens	SL2.40ch	AT3G153	SPA3	SPA3 (SF	chr3:516	294.814	182.144	429.79	201.076	901.268	466.369
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	1.556	Detected	1.380	Detected	1.468	0.008	GT	Sens	SL2.40ch	AT1G700	SNL4	SNL4 (SI	chr1:263	86.4013	70.5493	174.602	110.891	244.837	216.044
GT	Sense	Sense	-0.790	Comprom	0.790	Comprom	0.000	2.351	Detected	1.844	Detected	2.097	0.127	GT	Sens		AT3G43400.1				2.1884	6.15327	22.8096	23.8383	19.9573	14.0109
GT	Sense	Sense	0.897	Detected	-0.897	Comprom	0.000	1.220	Detected	1.959	Detected	1.589	0.243	GT	Sens	SL2.40ch	AT5G54030.1		DC1 dom	chr5:219	11.0614	3.00291	11.7991	15.6465	14.3188	23.8201
GT	Sense	Sense	0.963	Detected	-0.963	Detected	0.000	3.032	Detected	2.115	Detected	2.574	0.137	GT	Sens	SL2.40ch	AT5G07080.1		transfera	chr5:220	10254.1	2537.97	7415.14	2340.41	44500.2	23498.7
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	1.640	Detected	1.254	Detected	1.447	0.019	GT	Sens	SL2.40ch	AT5G35810.1		FUNCTIO	chr5:139	471.287	483.286	1050.15	746.696	1586.16	1210.3
GT	Sense	Sense	-0.183	Comprom	0.183	Comprom	0.000	1.094	Detected	1.760	Detected	1.427	0.064	GT	Sens	SL2.40ch	AT5G16570.1				4.69754	5.69539	11.7745	12.1092	11.7784	18.6324
GT	Sense	Sense	-0.118	Detected	0.118	Detected	0.000	2.125	Detected	0.893	Detected	1.509	0.138	GT	Sens	SL2.40ch	AT1G60160.1		potassiu	chr1:221	10.6087	11.7556	10.4683	5.56647	51.9352	22.0418
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	2.231	Detected	1.761	Detected	1.996	0.015	GT	Sens	SL2.40ch	AT1G29560.2				121.927	104.55	199.661	199.387	565.071	406.845
GT	Sense	Sense	-0.188	Comprom	0.188	Comprom	0.000	2.373	Detected	1.961	Detected	2.167	0.016	GT	Sens	SL2.40ch	AT1G29560.2				4.85611	5.93377	8.20575	11.7054	29.6465	22.213
GT	Sense	Sense	-0.211	Detected	0.211	Detected	0.000	1.037	Detected	1.075	Detected	1.056	0.038	GT	Sens	SL2.40ch	AT5G036	PTL	PTL (PET	chr5:957	31.9124	40.204	47.7876	25.5514	78.3844	80.238
GT	Sense	Sense	0.008	Detected	-0.008	Detected	0.000	0.860	Detected	1.286	Detected	1.073	0.037	GT	Sens	SL2.40ch	AT5G18840.1		sugar tra	chr5:628	15.1839	14.1203	37.8469	34.8076	28.3353	37.9681
GT	Sense	Sense	-0.229	Detected	0.229	Detected	0.000	1.374	Detected	1.439	Detected	1.406	0.026	GT	Sens		AT5G34930.1		arogenat	chr5:132	35.4839	45.8503	59.5033	79.5717	111.456	116.257
GT	Sense	Sense	-0.205	Detected	0.205	Detected	0.000	1.018	Detected	1.055	Detected	1.037	0.037	GT	Sens		AT5G34930.1		arogenat	chr5:132	150.093	187.536	252.514	328.858	362.409	370.597
GT	Sense	Sense	0.212	Detected	-0.212	Detected	0.000	1.090	Detected	0.952	Detected	1.021	0.044	GT	Sens	SL2.40ch	AT1G530	UBC26. P	UBC26 (U	chr1:197	70.8225	49.6791	91.9392	50.9516	134.675	122.002
GT	Sense	Sense	-0.474	Detected	0.474	Detected	0.000	1.259	Detected	1.013	Detected	1.136	0.146	GT	Sens	SL2.40ch	AT3G22670.1		pentatric	chr3:801	19.1705	34.7799	33.06	34.6846	65.9019	55.4002
GT	Sense	Sense	0.138	Detected	-0.138	Detected	0.000	1.533	Detected	1.488	Detected	1.511	0.008	GT	Sens	SL2.40ch	AT2G271	POL2B. T	TIL2 (TIL	chr2:115	235.384	182.842	597.077	378.739	640.344	618.676
GT	Sense	Sense	-0.356	Comprom	0.356	Comprom	0.000	3.285	Detected	2.937	Detected	3.111	0.016	GT	Sens	SL2.40ch	AT3G16160.1				2.04964	3.15865	2.60187	4.13687	26.4398	20.7124
GT	Sense	Sense	-0.477	Comprom	0.477	Comprom	0.000	0.831	Detected	1.261	Detected	1.046	0.184	GT	Sens	SL2.40ch	AT3G27110.2		peptidas	chr3:999	4.76964	8.69367	13.236	11.5431	12.2161	16.4083
GT	Sense	Sense	-0.522	Comprom	0.522	Comprom	0.000	1.359	Detected	1.295	Detected	1.327	0.126	GT	Sens	SL2.40ch	AT3G27110.2		peptidas	chr3:999	4.59466	8.91144	14.9569	10.3789	17.5025	16.6978
GT	Sense	Sense	-0.215	Comprom	0.215	Comprom	0.000	1.652	Detected	1.263	Detected	1.457	0.037	GT	Sens	SL2.40ch	AT2G362	ABI5. GIA	ABI5 (AB	chr2:152	4.50591	5.71021	12.0126	11.9498	16.9954	12.9451
GT	Sense	Sense	0.899	Detected	-0.899	Comprom	0.000	3.663	Detected	1.628	Detected	2.645	0.191	GT	Sens	SL2.40ch	AT4G319	CYP82C2	CYP82C2	chr4:154	13.3125	3.60158	22.7949	11.1874	93.5168	22.7513
GT	Sense	Sense	-0.473	Detected	0.473	Detected	0.000	1.737	Detected	2.084	Detected	1.911	0.063	GT	Sens	SL2.40ch	AT3G543	ATVAMP	ATVAMP	chr3:201	61.6181	111.705	196.787	192.468	294.936	374.091
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	0.906	Detected	1.246	Detected	1.076	0.031	GT	Sens	SL2.40ch	AT3G543	ATVAMP	ATVAMP	chr3:201	53.7743	57.6712	68.1639	86.6192	111.247	140.461
GT	Sense	Sense	-0.392	Comprom	0.392	Detected	0.000	2.985	Detected	1.615	Detected	2.300	0.100	GT	Sens	SL2.40ch	AT3G52700.1		unknowr	chr3:195	6.87293	11.1341	23.6045	5.33027	73.8317	28.4859
GT	Sense	Sense	-0.206	Detected	0.206	Detected	0.000	2.615	Detected	1.309	Detected	1.962	0.103	GT	Sens	SL2.40ch	AT3G52700.1		unknowr	chr3:195	714.885	895.187	2434.34	830.857	5226.41	2107.65
GT	Sense	Sense	0.282	Comprom	-0.282	Comprom	0.000	1.120	Detected	1.555	Detected	1.338	0.064	GT	Sens	SL2.40ch	AT4G139	AtRLP50	AtRLP50	chr4:804	5.82681	3.71004	15.6964	14.6925	10.7765	14.5269
GT	Sense	Sense	-0.397	Comprom	0.397	Comprom	0.000	1.061	Detected	1.417	Detected	1.239	0.104	GT	Sens	SL2.40ch	ATCG010	NDHF	Chloropl	chrC:110	4.73114	7.71911	11.5007	14.1855	13.4487	17.1615
GT	Sense	Sense	-0.019	Comprom	0.019	Comprom	0.000	5.926	Detected	4.681	Detected	5.303	0.014	GT	Sens	SL2.40ch	AT2G17650.1		AMP-dep	chr2:767	2.75756	2.66376	2.08271	1.90658	175.696	73.9224
GT	Sense	Sense	-1.054	Comprom	1.054	Comprom	0.000	1.376	Detected	1.935	Detected	1.656	0.268	GT	Sens	SL2.40ch	AT2G22610.1		kinesin n	chr2:959	2.08114	8.4393	16.1893	10.0756	11.6017	17.0352
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	1.123	Detected	0.951	Detected	1.037	0.007	GT	Sens	SL2.40ch	AT3G209	NF-YA9	NF-YA9 (	chr3:732	265.435	256.293	554.903	401.315	605.982	536.214
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	0.837	Detected	2.434	Detected	1.636	0.177	GT	Sens	SL2.40ch	AT1G74450.1		unknowr	chr1:279	15.7045	15.6085	13.8418	18.2125	29.8329	89.9338
GT	Sense	Sense	0.208	Detected	-0.208	Detected	0.000	1.186	Detected	1.272	Detected	1.229	0.028	GT	Sens		AT3G58060.1		cation ef	chr3:214	29.9738	21.1522	40.9119	68.901	61.0908	64.6334
GT	Sense	Sense	-0.106	Comprom	0.106	Comprom	0.000	6.303	Detected	3.321	Detected	4.812	0.084	GT	Sens	SL2.40ch	AT3G15980.3		coatome	chr3:541	2.00876	2.18885	1.67424	13.8747	176.505	22.2732
GT	Sense	Sense	-0.407	Comprom	0.407	Comprom	0.000	3.271	Detected	1.227	Detected	2.249	0.178	GT	Sens	SL2.40ch	AT5G16110.1		unknowr	chr5:526	3.9259	6.49292	15.3611	10.9317	51.975	12.5624
GT	Sense	Sense	0.123	Comprom	-0.123	Comprom	0.000	1.684	Detected	2.265	Detected	1.975	0.025	GT	Sens	SL2.40ch	AT5G478	AMK2	AMK2 (A	chr5:193	3.39917	2.69822	2.78785	3.37477	10.3782	15.4754
GT	Sense	Sense	-0.266	Detected	0.266	Detected	0.000	1.062	Detected	1.140	Detected	1.101	0.055	GT	Sens	SL2.40ch	AT5G067	HAT14	HAT14 (H	chr5:206	35.5946	48.4567	67.9943	87.3346	92.4763	97.3279
GT	Sense	Sense	-0.358	Comprom	0.358	Comprom	0.000	3.093	Detected	1.631	Detected	2.362	0.101	GT	Sens	SL2.40ch	AT5G57670.2		protein k	chr5:233	3.16273	4.88652	7.89842	20.364	35.7768	12.9471
GT	Sense	Sense	-0.303	Comprom	0.303	Comprom	0.000	1.275	Detected	2.008	Detected	1.642	0.075	GT	Sens	SL2.40ch	AT2G31130.1		unknowr	chr2:132	3.70959	5.31403	16.1989	11.5852	11.4572	18.9896
GT	Sense	Sense	-0.456	Detected	0.456	Detected	0.000	1.141	Detected	1.934	Detected	1.538	0.126	GT	Sens	SL2.40ch	AT3G03290.1		universa	chr3:766	256.785	454.553	562.998	507.42	803.74	1387.88
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	1.411	Detected	0.965	Detected	1.188	0.045	GT	Sens	SL2.40ch	AT2G17670.1		pentatric	chr2:767	61.1767	69.3586	118.68	93.9788	184.725	135.147
GT	Sense	Sense	0.050	Detected	-0.050	Detected	0.000	1.565	Detected	1.030	Detected	1.298	0.041	GT	Sens	SL2.40ch	AT2G17670.1		pentatric	chr2:767	68.5036	60.1109	132.998	92.0704	202.518	139.308
GT	Sense	Sense	-0.393	Comprom	0.393	Comprom	0.000	1.658	Detected	1.973	Detected	1.815	0.050	GT	Sens	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:145	3.7895	6.1478	12.3123	20.8184	16.2378	20.1416
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	1.618	Detected	1.295	Detected	1.456	0.016	GT	Sens	SL2.40ch	AT2G27830.1		FUNCTIO	chr2:118	104.227	110.933	262.574	192.109	351.921	280.43
GT	Sense	Sense	-0.326	Comprom	0.326	Comprom	0.000	1.420	Detected	2.438	Detected	1.929	0.086	GT	Sens	SL2.40ch	AT3G04150.1		germin-li	chr3:108	4.05477	5.99497	19.3405	19.8389	14.0733	28.4
GT	Sense	Sense	-0.070	Comprom	0.070	Comprom	0.000	2.544	Detected	2.234	Detected	2.389	0.005	GT	Sens	SL2.40ch	AT3G14550.1				2.22678	2.30828	3.135	14.257	14.1037	11.3406
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	1.401	Detected	1.002	Detected	1.202	0.027	GT	Sens	SL2.40ch	AT2G263	ER. ORP1	ER (ERE(	chr2:112	17.997	16.1715	25.8132	22.2019	48.0421	36.3377
GT	Sense	Sense	-0.645	Comprom	0.645	Comprom	0.000	1.623	Detected	1.462	Detected	1.543	0.141	GT	Sens	SL2.40ch	AT5G28630.1		glycine-r	chr5:106	3.01837	6.94298	12.6339	15.6169	15.0406	13.4079
GT	Sense	Sense	-0.279	Detected	0.279	Detected	0.000	1.594	Detected	1.048	Detected	1.321	0.077	GT	Sens	SL2.40ch	AT1G554	CPN60B.	CPN60B	chr1:207	451.563	625.233	1251.8	554.8	1710.14	1168.43
GT	Sense	Sense	-0.239	Detected	0.239	Detected	0.000	1.610	Detected	1.775	Detected	1.692	0.022	GT	Sens	SL2.40ch	AT4G191	ERD3	ERD3 (ea	chr4:104	34.3064	44.9787	121.543	95.9752	127.831	142.898
GT	Sense	Sense	0.077	Comprom	-0.077	Comprom	0.000	1.517	Detected	1.500	Detected	1.509	0.003	GT	Sens	SL2.40ch	AT4G191	ERD3	ERD3 (ea	chr4:104	6.57099	5.55614	10.7253	5.86362	18.4385	18.1754
GT	Sense	Sense	0.167	Comprom	-0.167	Comprom	0.000	1.217	Detected	2.028	Detected	1.622	0.066	GT	Sens		AT3G19480.1		D-3-phos	chr3:675	4.6817	3.49404	1.73005	3.76038	10.0247	17.5334
GT	Sense	Sense	-0.483	Detected	0.483	Detected	0.000	1.640	Detected	1.422	Detected	1.531	0.091	GT	Sens	SL2.40ch	AT2G321	HSP70T-2	HSP70T-	chr2:136	43.1283	79.3017	82.9039	65.7565	194.371	166.615
GT	Sense	Sense	-1.295	Comprom	1.295	Detected	0.000	1.427	Detected	1.351	Detected	1.389	0.396	GT	Sens	SL2.40ch	AT5G60210.1		LOCATE	chr5:242	4.16005	23.5753	22.3214	15.2404	28.3914	26.8534
GT	Sense	Sense	-0.160	Comprom	0.160	Comprom	0.000	1.454	Detected	1.408	Detected	1.431	0.012	GT	Sens	SL2.40ch	AT5G378	NIP4:2. NI	NIP4:2 (N	chr5:150	6.951	8.16023	13.2651	12.9455	22.0029	21.2483
GT	Sense	Sense	-0.148	Comprom	0.148	Comprom	0.000	1.643	Detected	1.542	Detected	1.592	0.010	GT	Sens	SL2.40ch	AT3G27570.1		FUNCTIO	chr3:102	5.14004	5.93884	7.60145	10.3285	18.3946	17.102
GT	Sense	Sense	-0.604	Detected	0.604	Detected	0.000	1.378	Detected	1.373	Detected	1.375	0.151	GT	Sens	SL2.40ch	AT4G359	MCA1	MCA1 (m	chr4:170	13.4009	29.1378	39.0974	39.8357	54.7572	54.4177
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	1.846	Detected	1.694	Detected	1.770	0.006	GT	Sens	SL2.40ch	AT1G49890.1		unknowr	chr1:184	214.551	171.527	284.59	327.34	735.223	659.885
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	1.407	Detected	1.210	Detected	1.309	0.006	GT	Sens	SL2.40ch	ATMG001	CCB452	cytochro	chrM:51	118.461	114.891	165.207	167.761	329.941	286.983
GT	Sense	Sense	-0.125	Detected	0.125	Detected	0.000	1.217	Detected	1.049	Detected	1.133	0.017	GT	Sens	SL2.40ch	ATMG001	CCB452	cytochro	chrM:51	348.665	390.114	452.848	497.305	914.099	811.267
GT	Sense	Sense	-0.699	Comprom	0.699	Comprom	0.000	1.522	Detected	1.749	Detected	1.636	0.147	GT	Sens	SL2.40ch	AT5G63620.2		oxidored	chr5:254	2.42011	6.00491	6.56534	5.45579	11.6783	13.6245
GT	Sense	Sense	-0.192	Detected	0.192	Detected	0.000	1.358	Detected	1.040	Detected	1.199	0.041	GT	Sens	SL2.40ch	AT4G07675.1				13.3997	16.4594	27.9989	19.0465	40.5983	32.467
GT	Sense	Sense	-0.195	Comprom	0.195	Comprom	0.000	3.616	Detected	2.480	Detected	3.048	0.037	GT	Sens	SL2.40ch	AT4G07675.1				2.03065	2.50505	10.023	5.08585	29.4816	13.3811
GT	Sense	Sense	0.511	Detected	-0.511	Comprom	0.000	0.911	Detected	1.223	Detected	1.067	0.184	GT	Sens		AT3G231	AtRLP37	AtRLP37	chr3:822	10.3331	4.78874	9.97589	11.6644	14.1042	17.4633
GT	Sense	Sense	0.519	Comprom	-0.519	Comprom	0.000	1.125	Detected	1.658	Detected	1.391	0.140	GT	Sens		AT3G231	AtRLP37	AtRLP37	chr3:822	6.11956	2.80316	3.59566	7.06063	9.63218	13.8936
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	1.317	Detected	1.171	Detected	1.244	0.009	GT	Sens	SL2.40ch	AT4G16670.1		phospho	chr4:938	37.3928	40.1622	38.8172	38.4262	102.96	92.7493
GT	Sense	Sense	-0.100	Comprom	0.100	Comprom	0.000	2.504	Detected	2.828	Detected	2.666	0.005	GT	Sens	SL2.40ch	AT2G34970.1		eIF4-gam	chr2:147	2.08061	2.2489	1.71677	2.80264	13.0881	16.3307
GT	Sense	Sense	0.874	Comprom	-0.874	Comprom	0.000	1.594	Detected	1.642	Detected	1.618	0.206	GT	Sens	SL2.40ch	AT3G050	HST. HST	HST (HAS	chr3:140	8.12409	2.27474	11.7434	23.5528	13.8376	14.2689
GT	Sense	Sense	-0.190	Detected	0.190	Detected	0.000	1.332	Detected	0.942	Detected	1.137	0.053	GT	Sens	SL2.40ch	AT3G01100.2				123.548	151.23	242.678	210.491	366.852	279.19
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	1.311	Detected	0.992	Detected	1.152	0.019	GT	Sens	SL2.40ch	AT3G01100.2				171.599	163.971	366.826	313.497	443.886	354.712
GT	Sense	Sense	0.216	Detected	-0.216	Detected	0.000	0.976	Detected	1.038	Detected	1.007	0.044	GT	Sens	SL2.40ch	AT1G05910.1		cell divis	chr1:179	19.0421	13.2811	32.5217	44.5464	33.3533	34.7244
GT	Sense	Sense	0.317	Comprom	-0.317	Comprom	0.000	2.229	Detected	1.962	Detected	2.095	0.026	GT	Sens	SL2.40ch	AT5G47690.3		binding	chr5:193	3.82461	2.31994	17.218	14.2462	14.8933	12.3348
GT	Sense	Sense	-0.456	Comprom	0.456	Comprom	0.000	2.014	Detected	1.689	Detected	1.851	0.062	GT	Sens	SL2.40ch	AT5G40450.2		unknowr	chr5:161	5.269	9.33532	29.7688	36.5909	30.2049	24.0376
GT	Sense	Sense	0.559	Comprom	-0.559	Comprom	0.000	3.415	Detected	1.272	Detected	2.343	0.192	GT	Sens	SL2.40ch	AT5G238	AAP7	AAP7: ar	chr5:802	7.54002	3.27056	3.1497	11.6937	56.4723	12.7489
GT	Sense	Sense	-0.946	Comprom	0.946	Comprom	0.000	1.460	Detected	1.441	Detected	1.451	0.265	GT	Sens	SL2.40ch	AT3G52700.1		unknowr	chr3:195	2.02514	7.07167	3.94809	1.94217	11.1032	10.9252
GT	Sense	Sense	-0.186	Comprom	0.186	Comprom	0.000	1.676	Detected	1.452	Detected	1.564	0.019	GT	Sens	SL2.40ch	AT5G39830.2				5.25074	6.39746	7.57626	11.2608	19.7472	16.8588
GT	Sense	Sense	-0.166	Comprom	0.166	Comprom	0.000	1.363	Detected	3.734	Detected	2.549	0.167	GT	Sens	SL2.40ch	AT2G346	AIR9	AIR9: prc	chr2:146	5.01294	5.93458	4.62631	2.44925	14.9619	77.1652
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	1.182	Detected	1.568	Detected	1.375	0.019	GT	Sens	SL2.40ch	AT1G20380.1				62.1439	60.0667	47.8014	51.1224	147.849	192.608
GT	Sense	Sense	-0.261	Detected	0.261	Detected	0.000	0.877	Detected	1.133	Detected	1.005	0.074	GT	Sens	SL2.40ch	AT1G20380.1				97.5676	131.774	72.6742	61.8732	222.012	264.327
GT	Sense	Sense	1.224	Detected	-1.224	Comprom	0.000	1.071	Detected	1.169	Detected	1.120	0.457	GT	Sens	SL2.40ch	AT3G088	RAPTOR1	RAPTOR	chr3:268	13.9134	2.39877	3.80862	13.5295	12.9454	13.815
GT	Sense	Sense	-1.329	Comprom	1.329	Detected	0.000	1.396	Detected	1.155	Detected	1.275	0.440	GT	Sens	SL2.40ch	AT2G44420.1		protein N	chr2:183	2.22959	13.2385	10.3459	14.0403	15.2465	12.8609
GT	Sense	Sense	0.261	Comprom	-0.261	Comprom	0.000	1.261	Detected	1.480	Detected	1.371	0.040	GT	Sens	SL2.40ch	AT2G444	BGLU29	BGLU29	chr2:183	5.66808	3.71407	4.48002	15.9849	11.7269	13.6079
GT	Sense	Sense	-0.222	Comprom	0.222	Comprom	0.000	1.345	Detected	1.459	Detected	1.402	0.026	GT	Sens	SL2.40ch	AT1G631	UGE3	UGE3 (UI	chr1:234	4.51664	5.78074	17.7031	19.2637	13.8403	14.9356
GT	Sense	Sense	-0.251	Comprom	0.251	Comprom	0.000	1.619	Detected	1.896	Detected	1.757	0.026	GT	Sens	SL2.40ch	AT3G31402.1		FUNCTIO	chr3:127	4.52571	6.028	16.3196	24.8442	17.1117	20.6626
GT	Sense	Sense	-0.505	Comprom	0.505	Detected	0.000	1.255	Detected	1.258	Detected	1.256	0.131	GT	Sens	SL2.40ch	AT1G74780.1		nodulin f	chr1:280	6.51413	12.3513	17.6452	11.7334	22.8333	22.8008
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	1.583	Detected	0.994	Detected	1.289	0.057	GT	Sens	SL2.40ch	AT5G172	PSY	phytoene	chr5:565	7154.32	8083.61	12664.1	9654.96	24302.4	16100.1
GT	Sense	Sense	-0.190	Detected	0.190	Detected	0.000	1.306	Detected	1.291	Detected	1.299	0.021	GT	Sens	SL2.40ch	AT5G63550.2		EXPRES	chr5:254	15.9801	19.5776	49.4164	26.465	46.6324	46.0294
GT	Sense	Sense	0.127	Comprom	-0.127	Comprom	0.000	1.827	Detected	1.830	Detected	1.829	0.005	GT	Sens	SL2.40ch	AT5G63550.2		EXPRES	chr5:254	3.73969	2.95271	14.0479	6.26083	12.5724	12.5638
GT	Sense	Sense	-0.212	Detected	0.212	Detected	0.000	1.355	Detected	1.029	Detected	1.192	0.047	GT	Sens	SL2.40ch	AT1G62160.1		serine-tv	chr1:229	470.82	594.45	1009.17	948.61	1443.4	1147.46
GT	Sense	Sense	-0.081	Comprom	0.081	Comprom	0.000	3.583	Detected	2.378	Detected	2.980	0.039	GT	Sens	SL2.40ch	AT2G465	LAC6	LAC6 (la	chr2:191	2.20853	2.32478	1.82041	2.554	28.9579	12.5195
GT	Sense	Sense	-0.071	Comprom	0.071	Comprom	0.000	1.167	Detected	1.064	Detected	1.115	0.006	GT	Sens	SL2.40ch	AT3G514	ATGLR3.	ATGLR3.	chr3:191	4.8424	5.02783	13.2719	5.49907	11.8147	10.9676
GT	Sense	Sense	-0.788	Comprom	0.788	Comprom	0.000	1.539	Detected	1.585	Detected	1.562	0.186	GT	Sens	SL2.40ch	AT4G18270.1				3.27226	9.18167	10.4461	9.97184	16.984	17.4801
GT	Sense	Sense	-0.253	Detected	0.253	Detected	0.000	1.653	Detected	1.002	Detected	1.328	0.084	GT	Sens	SL2.40ch	AT2G02380.1				12.8599	17.1852	15.3179	23.3647	49.8619	31.6579
GT	Sense	Sense	-0.148	Detected	0.148	Detected	0.000	1.088	Detected	0.988	Detected	1.038	0.022	GT	Sens	SL2.40ch	AT4G30350.1		heat sho	chr4:148	29.6608	34.2646	32.9397	31.5133	72.2749	67.2348
GT	Sense	Sense	-0.585	Detected	0.585	Detected	0.000	0.906	Detected	2.343	Detected	1.625	0.222	GT	Sens	SL2.40ch	AT5G54950.1				1177.54	2491.65	3677.49	4153.72	3423.06	9241.36
GT	Sense	Sense	-0.453	Detected	0.453	Detected	0.000	0.948	Detected	2.289	Detected	1.618	0.184	GT	Sens	SL2.40ch	AT5G54950.1				951.122	1676.8	2867.76	3227.07	2597.36	6561.95
GT	Sense	Sense	-0.004	Comprom	0.004	Comprom	0.000	1.364	Detected	1.803	Detected	1.583	0.019	GT	Sens	SL2.40ch	AT3G58560.1		endonuc	chr3:216	4.09788	3.87808	6.67626	16.8894	10.9392	14.7873
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	1.151	Detected	1.107	Detected	1.129	0.001	GT	Sens	SL2.40ch	AT1G025	MEA. EMI	MEA (ME	chr1:544	20.9156	20.1526	29.6169	18.7518	48.6065	47.0229
GT	Sense	Sense	-0.434	Comprom	0.434	Detected	0.000	0.921	Detected	1.089	Detected	1.005	0.151	GT	Sens	SL2.40ch	AT4G38750.1		unknowr	chr4:180	10.2014	17.5116	17.6821	22.2001	26.9834	30.2372
GT	Sense	Sense	-0.157	Comprom	0.157	Comprom	0.000	1.121	Detected	1.227	Detected	1.174	0.019	GT	Sens	SL2.40ch	AT2G019	VH1. BRL	BRL2 (BF	chr2:440	7.42169	8.68562	14.5941	20.0268	18.6175	19.9797
GT	Sense	Sense	-0.122	Comprom	0.122	Comprom	0.000	1.482	Detected	1.867	Detected	1.675	0.018	GT	Sens	SL2.40ch	AT2G019	VH1. BRL	BRL2 (BF	chr2:440	4.18636	4.6677	18.5121	23.1274	13.1704	17.1418
GT	Sense	Sense	-0.245	Detected	0.245	Detected	0.000	1.403	Detected	1.035	Detected	1.219	0.058	GT	Sens	SL2.40ch	AT1G03070.1		glutamat	chr1:730	82.8455	109.51	130.131	101.451	268.556	207.5
GT	Sense	Sense	0.262	Detected	-0.262	Detected	0.000	2.386	Detected	1.833	Detected	2.110	0.031	GT	Sens		AT5G41630.1		F-box far	chr5:166	20.7161	13.5611	38.3655	26.6655	93.4531	63.4992
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	2.449	Detected	1.707	Detected	2.078	0.031	GT	Sens		AT5G41630.1		F-box far	chr5:166	16.0998	16.189	43.8384	26.3442	94.0083	56.05
GT	Sense	Sense	-0.331	Detected	0.331	Detected	0.000	1.218	Detected	0.999	Detected	1.109	0.086	GT	Sens	SL2.40ch	AT5G50540.1		unknowr	chr5:205	11.2428	16.7405	40.6866	28.505	34.0404	29.1523
GT	Sense	Sense	-0.379	Comprom	0.379	Comprom	0.000	1.420	Detected	1.799	Detected	1.609	0.063	GT	Sens	SL2.40ch	AT4G18160.1				4.14328	6.59437	2.56176	3.59931	14.9114	19.3331
GT	Sense	Sense	-0.127	Comprom	0.127	Comprom	0.000	1.161	Detected	1.537	Detected	1.349	0.027	GT	Sens	SL2.40ch	AT2G25737.1		unknowr	chr2:109	4.80948	5.3942	13.3623	3.65117	12.1491	15.7168
GT	Sense	Sense	-0.061	Comprom	0.061	Comprom	0.000	2.680	Detected	2.980	Detected	2.830	0.003	GT	Sens	SL2.40ch	AT5G20660.1		24 kDa v	chr5:698	2.16241	2.21363	1.71262	1.91337	14.9517	18.3589
GT	Sense	Sense	-0.224	Comprom	0.224	Comprom	0.000	1.143	Detected	0.968	Detected	1.055	0.048	GT	Sens	SL2.40ch	AT3G52700.1		unknowr	chr3:195	5.26532	6.75793	12.9407	13.6891	14.0463	12.4025
GT	Sense	Sense	-0.136	Detected	0.136	Detected	0.000	1.138	Detected	1.014	Detected	1.076	0.019	GT	Sens	SL2.40ch	AT3G10190.1		calmodu	chr3:315	212.857	241.865	249.9	289.135	532.638	487.114
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	1.317	Detected	1.092	Detected	1.205	0.017	GT	Sens	SL2.40ch	AT3G10190.1		calmodu	chr3:315	366.808	404.172	443.019	514.074	1022.77	872.914
GT	Sense	Sense	0.265	Comprom	-0.265	Comprom	0.000	2.479	Detected	1.497	Detected	1.988	0.071	GT	Sens	SL2.40ch	AT3G52700.1		unknowr	chr3:195	6.59625	4.29551	11.9226	15.082	31.6562	15.9727
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	1.240	Detected	1.094	Detected	1.167	0.008	GT	Sens	SL2.40ch	AT5G56560.1				14.4752	15.1723	15.4538	21.6072	37.3264	33.6363
GT	Sense	Sense	0.269	Detected	-0.269	Detected	0.000	1.417	Detected	0.982	Detected	1.200	0.074	GT	Sens	SL2.40ch	AT4G22370.1		unknowr	chr4:118	53.868	34.8891	77.0074	81.0776	123.456	91.0607
GT	Sense	Sense	-0.935	Comprom	0.935	Comprom	0.000	1.096	Detected	1.274	Detected	1.185	0.334	GT	Sens	SL2.40ch	AT4G16563.1		aspartyl	chr4:932	3.13707	10.7949	7.37849	8.44033	13.2677	14.9648
GT	Sense	Sense	-0.120	Comprom	0.120	Comprom	0.000	1.719	Detected	1.628	Detected	1.674	0.006	GT	Sens	SL2.40ch	AT5G66005.3		Expresse	chr5:263	3.79682	4.22133	14.451	19.2877	14.0549	13.1561
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	1.227	Detected	0.861	Detected	1.044	0.030	GT	Sens	SL2.40ch	AT3G553	PGP20	PGP20 (F	chr3:205	15.6432	14.2334	19.7617	17.1109	37.2422	28.8061
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	1.657	Detected	0.885	Detected	1.271	0.089	GT	Sens	SL2.40ch	AT5G19420.1		Ran GTP	chr5:654	182.185	142.818	301.724	215.453	542.445	316.725
GT	Sense	Sense	-0.291	Comprom	0.291	Comprom	0.000	1.451	Detected	1.772	Detected	1.612	0.040	GT	Sens	SL2.40ch	AT1G13520.1				3.37508	4.75657	5.31161	11.1902	11.682	14.5503
GT	Sense	Sense	0.281	Comprom	-0.281	Comprom	0.000	1.688	Detected	1.915	Detected	1.801	0.027	GT	Sens	SL2.40ch	AT4G199	FRS1	FRS1 (FA	chr4:108	4.80324	3.06186	8.37136	11.4935	13.1768	15.3751
GT	Sense	Sense	-0.131	Comprom	0.131	Comprom	0.000	2.158	Detected	2.217	Detected	2.187	0.004	GT	Sens	SL2.40ch	AT3G502	KICP-02	KICP-02:	chr3:186	2.49792	2.81757	4.5774	3.59554	12.6225	13.113
GT	Sense	Sense	-0.297	Detected	0.297	Detected	0.000	1.394	Detected	1.032	Detected	1.213	0.073	GT	Sens	SL2.40ch	AT4G10265.1		wound-re	chr4:637	318.662	452.465	979.69	544.572	1064.33	825.805
GT	Sense	Sense	-0.981	Comprom	0.981	Comprom	0.000	1.925	Detected	1.463	Detected	1.694	0.235	GT	Sens	SL2.40ch	AT3G544	SRS6	SRS6 (SH	chr3:201	2.07443	7.60287	6.53275	7.50946	16.0869	11.6402
GT	Sense	Sense	-0.153	Comprom	0.153	Comprom	0.000	1.881	Detected	3.569	Detected	2.725	0.086	GT	Sens	SL2.40ch	AT5G58787.1				4.62414	5.37582	6.75533	8.56066	19.5797	62.8918
GT	Sense	Sense	-0.286	Comprom	0.286	Comprom	0.000	1.257	Detected	1.660	Detected	1.458	0.053	GT	Sens	SL2.40ch	AT2G27285.1		unknowr	chr2:116	3.84223	5.37238	9.75791	7.25221	11.5763	15.2689
GT	Sense	Sense	-0.158	Detected	0.158	Detected	0.000	1.266	Detected	0.987	Detected	1.127	0.033	GT	Sens	SL2.40ch	AT3G15000.1		LOCATE	chr3:505	1275.03	1492.8	3222.39	2102.68	3538.09	2907.9
GT	Sense	Sense	-0.255	Comprom	0.255	Comprom	0.000	1.261	Detected	1.777	Detected	1.519	0.053	GT	Sens		AT5G44180.1		homeobo	chr5:177	3.8619	5.17638	3.92099	3.57181	11.4239	16.2956
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	1.060	Detected	1.108	Detected	1.084	0.004	GT	Sens	SL2.40ch	AT3G26200.1				344.771	295.069	442.851	468.537	708.901	730.921
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	1.153	Detected	1.269	Detected	1.211	0.003	GT	Sens	SL2.40ch	AT3G26200.1				318.255	289.108	458.517	423.599	719.41	777.254
GT	Sense	Sense	-0.039	Comprom	0.039	Comprom	0.000	1.581	Detected	1.620	Detected	1.601	0.001	GT	Sens	SL2.40ch	AT2G34770.1				4.22664	4.19897	13.535	9.37125	13.4383	13.772
GT	Sense	Sense	0.520	Comprom	-0.520	Comprom	0.000	1.512	Detected	1.075	Detected	1.293	0.149	GT	Sens	SL2.40ch	AT2G34770.1				7.85446	3.59418	11.105	8.28548	16.1567	11.898
GT	Sense	Sense	0.683	Detected	-0.683	Comprom	0.000	1.070	Detected	1.467	Detected	1.268	0.216	GT	Sens	SL2.40ch	AT1G04200.1		unknowr	chr1:110	11.122	4.05939	11.9377	30.4034	15.045	19.7448
GT	Sense	Sense	0.018	Detected	-0.018	Detected	0.000	1.058	Detected	1.177	Detected	1.117	0.003	GT	Sens	SL2.40ch	AT3G05620.1		pectines	chr3:162	39.1506	35.9548	57.2422	62.1102	83.2949	90.1901
GT	Sense	Sense	0.149	Detected	-0.149	Detected	0.000	0.927	Detected	1.191	Detected	1.059	0.034	GT	Sens	SL2.40ch	AT3G05620.1		pectines	chr3:162	106.869	81.7522	117.416	170.245	189.505	226.841
GT	Sense	Sense	-0.840	Comprom	0.840	Comprom	0.000	1.426	Detected	1.336	Detected	1.381	0.242	GT	Sens	SL2.40ch	AT5G16010.1				2.43996	7.35948	10.9876	12.7893	12.1417	11.3741
GT	Sense	Sense	0.456	Detected	-0.456	Detected	0.000	1.796	Detected	1.303	Detected	1.550	0.096	GT	Sens		AT2G28830.1				248.723	124.434	510.253	392.886	651.446	461.673
GT	Sense	Sense	0.556	Detected	-0.556	Detected	0.000	2.555	Detected	2.087	Detected	2.321	0.061	GT	Sens		AT2G28830.1				77.1647	33.5722	214.897	179.605	318.983	229.896
GT	Sense	Sense	-0.340	Detected	0.340	Detected	0.000	1.136	Detected	1.204	Detected	1.170	0.076	GT	Sens	SL2.40ch	AT2G42000.1				594.925	896.459	705.736	489.454	1711.94	1788.15
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	1.539	Detected	1.775	Detected	1.657	0.007	GT	Sens	SL2.40ch	AT2G42000.1				68.7074	59.0132	99.8095	70.0806	197.347	231.623
GT	Sense	Sense	0.462	Detected	-0.462	Comprom	0.000	0.859	Detected	1.186	Detected	1.022	0.173	GT	Sens	SL2.40ch	AT5G168	ATTERT	ATTERT	chr5:553	14.7177	7.29413	15.6316	13.4974	20.0346	25.0693
GT	Sense	Sense	-0.915	Comprom	0.915	Comprom	0.000	2.180	Detected	1.934	Detected	2.057	0.156	GT	Sens	SL2.40ch	AT4G30825.1		pentatric	chr4:150	2.36724	7.91522	8.87778	13.0165	20.9245	17.5894
GT	Sense	Sense	0.048	Comprom	-0.048	Comprom	0.000	2.033	Detected	1.684	Detected	1.858	0.009	GT	Sens	SL2.40ch	AT4G01810.1		protein tr	chr4:776	4.51702	3.97646	12.1975	13.3824	18.4992	14.4754
GT	Sense	Sense	0.688	Comprom	-0.688	Comprom	0.000	1.510	Detected	1.647	Detected	1.578	0.150	GT	Sens	SL2.40ch	AT2G400	ATATH9	ATATH9:	chr2:167	6.28472	2.27868	8.81432	11.7502	11.49	12.5974
GT	Sense	Sense	-1.223	Comprom	1.223	Detected	0.000	2.116	Detected	1.595	Detected	1.856	0.276	GT	Sens	SL2.40ch	AT1G55545.1		unknowr	chr1:207	3.98716	20.4295	10.8873	31.1843	41.7142	28.9941
GT	Sense	Sense	0.385	Detected	-0.385	Detected	0.000	0.904	Detected	1.153	Detected	1.028	0.126	GT	Sens	SL2.40ch	AT5G55660.1		LOCATE	chr5:225	106.74	58.904	96.7167	90	158.193	187.503
GT	Sense	Sense	0.142	Comprom	-0.142	Comprom	0.000	1.126	Detected	1.294	Detected	1.210	0.018	GT	Sens	SL2.40ch	AT3G17920.1				5.64657	4.36304	9.06502	4.30489	11.554	12.9411
GT	Sense	Sense	-0.154	Detected	0.154	Detected	0.000	1.375	Detected	1.194	Detected	1.285	0.019	GT	Sens	SL2.40ch	AT5G107	AHK5. CK	AHK5 (AF	chr5:338	525.717	612.072	790.305	664.561	1569.12	1380.17
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	1.573	Detected	1.370	Detected	1.472	0.011	GT	Sens	SL2.40ch	AT5G107	AHK5. CK	AHK5 (AF	chr5:338	119.043	131.175	212.58	157.775	396.591	343.516
GT	Sense	Sense	-0.214	Comprom	0.214	Comprom	0.000	1.599	Detected	2.031	Detected	1.815	0.027	GT	Sens	SL2.40ch	AT2G19210.1				2.80352	3.55099	10.1318	4.05674	10.1953	13.7057
GT	Sense	Sense	-0.304	Comprom	0.304	Comprom	0.000	1.324	Detected	1.211	Detected	1.268	0.055	GT	Sens	SL2.40ch	AT2G331	SAR1. VA	SAR1 (SY	chr2:140	4.06313	5.82988	4.31492	10.2626	12.996	11.9775
GT	Sense	Sense	-0.091	Detected	0.091	Detected	0.000	1.499	Detected	1.355	Detected	1.427	0.007	GT	Sens	SL2.40ch	AT5G61390.1		exonucle	chr5:246	14.2687	15.2281	38.505	28.1136	44.442	40.0779
GT	Sense	Sense	-0.398	Detected	0.398	Detected	0.000	0.987	Detected	1.343	Detected	1.165	0.116	GT	Sens		AT5G47300.1		F-box far	chr5:191	58.7233	95.9297	103.178	134.532	158.66	202.455
GT	Sense	Sense	-0.267	Detected	0.267	Detected	0.000	0.887	Detected	1.294	Detected	1.091	0.083	GT	Sens		AT5G47300.1		F-box far	chr5:191	382.894	521.812	583.922	760.554	881.591	1165.33
GT	Sense	Sense	-0.355	Detected	0.355	Detected	0.000	0.930	Detected	1.243	Detected	1.087	0.107	GT	Sens		AT5G61550.1		protein k	chr5:247	26.1143	40.1791	50.8411	52.5067	65.8342	81.5217
GT	Sense	Sense	-0.594	Comprom	0.594	Comprom	0.000	1.957	Detected	1.960	Detected	1.959	0.081	GT	Sens	SL2.40ch	AT4G21850.2				3.30114	7.08113	29.8852	34.6699	20.0152	20.0048
GT	Sense	Sense	-0.606	Comprom	0.606	Detected	0.000	1.822	Detected	1.705	Detected	1.764	0.101	GT	Sens	SL2.40ch	AT1G135	LAG13	LAG13 (L	chr1:464	6.07716	13.2379	18.2255	32.5093	33.8289	31.0914
GT	Sense	Sense	-0.146	Comprom	0.146	Comprom	0.000	2.460	Detected	2.334	Detected	2.397	0.004	GT	Sens	SL2.40ch	AT1G135	LAG13	LAG13 (L	chr1:464	4.9	5.64331	20.5224	20.6615	30.8601	28.1836
GT	Sense	Sense	0.256	Comprom	-0.256	Comprom	0.000	1.601	Detected	2.322	Detected	1.961	0.047	GT	Sens	SL2.40ch	AT5G22480.1		zinc fing	chr5:745	8.65846	5.71483	10.7404	5.10332	22.7479	37.4082
GT	Sense	Sense	0.254	Detected	-0.254	Detected	0.000	1.274	Detected	0.941	Detected	1.108	0.068	GT	Sens	SL2.40ch	AT4G34480.1				599.165	396.555	932.561	780.592	1257.24	994.982
GT	Sense	Sense	0.446	Comprom	-0.446	Comprom	0.000	1.539	Detected	1.826	Detected	1.683	0.070	GT	Sens	SL2.40ch	AT5G42390.1		metalloe	chr5:169	6.94358	3.52105	5.91844	12.3717	15.3229	18.6401
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	1.249	Detected	0.983	Detected	1.116	0.019	GT	Sens	SL2.40ch	AT2G430	CPuORF1	CPuORF	chr2:178	3238.78	3418.42	3129.82	2093.51	8433.64	6990.55

GT	Sense	Sense	0.759	Comprom	-0.759	Comprom	0.000	1.480	Detected	2.255	Detected	1.867	0.160	GT	Sens	contig378	contig378	Unannota
GT	Sense	Sense	0.403	Detected	-0.403	Detected	0.000	1.534	Detected	0.915	Detected	1.224	0.138	GT	Sens	contig378	contig378	Unannota
GT	Sense	Sense	-0.523	Comprom	0.523	Comprom	0.000	2.036	Detected	1.828	Detected	1.932	0.068	GT	Sens	contig379	contig379	Unannota
GT	Sense	Sense	-0.108	Detected	0.108	Detected	0.000	1.360	Detected	1.120	Detected	1.240	0.017	GT	Sens	contig379	contig379	Unannota
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	1.308	Detected	1.034	Detected	1.171	0.014	GT	Sens	contig379	contig379	Unannota
GT	Sense	Sense	-0.252	Comprom	0.252	Comprom	0.000	1.043	Detected	1.415	Detected	1.229	0.059	GT	Sens	contig379	contig379	Unannota
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	1.253	Detected	1.014	Detected	1.134	0.040	GT	Sens	contig379	contig379	Unannota
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	1.503	Detected	1.215	Detected	1.359	0.018	GT	Sens	contig380	contig380	Unannota
GT	Sense	Sense	-0.137	Detected	0.137	Detected	0.000	1.406	Detected	1.550	Detected	1.478	0.011	GT	Sens	contig381	contig381	Unannota
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	1.256	Detected	1.181	Detected	1.218	0.007	GT	Sens	contig381	contig381	Unannota
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	1.748	Detected	1.492	Detected	1.620	0.006	GT	Sens	contig381	contig381	Unannota
GT	Sense	Sense	0.851	Detected	-0.851	Comprom	0.000	1.649	Detected	2.592	Detected	2.121	0.161	GT	Sens	contig381	contig381	Receptor
GT	Sense	Sense	-0.069	Comprom	0.069	Comprom	0.000	2.667	Detected	3.618	Detected	3.143	0.023	GT	Sens	contig381	contig381	Unannota
GT	Sense	Sense	0.169	Detected	-0.169	Detected	0.000	2.468	Detected	2.001	Detected	2.234	0.016	GT	Sens	contig382	contig382	Unannota
GT	Sense	Sense	0.107	Detected	-0.107	Detected	0.000	2.493	Detected	1.993	Detected	2.243	0.014	GT	Sens	contig382	contig382	Unannota
GT	Sense	Sense	-0.071	Comprom	0.071	Comprom	0.000	1.606	Detected	1.168	Detected	1.387	0.026	GT	Sens	contig382	contig382	Unannota
GT	Sense	Sense	-0.042	Comprom	0.042	Comprom	0.000	3.251	Detected	2.912	Detected	3.081	0.003	GT	Sens	contig382	contig382	Unannota
GT	Sense	Sense	0.247	Comprom	-0.247	Comprom	0.000	2.256	Detected	2.182	Detected	2.219	0.012	GT	Sens	contig382	contig382	Unannota
GT	Sense	Sense	0.091	Detected	-0.091	Detected	0.000	1.872	Detected	1.710	Detected	1.791	0.005	GT	Sens	contig382	contig382	Unannota
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	1.217	Detected	0.930	Detected	1.074	0.025	GT	Sens	contig382	contig382	Unannota
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	1.045	Detected	1.104	Detected	1.074	0.007	GT	Sens	contig383	contig383	Unannota
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	1.053	Detected	1.071	Detected	1.062	0.022	GT	Sens	contig383	contig383	Unannota
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	2.394	Detected	1.268	Detected	1.831	0.089	GT	Sens	contig383	contig383	Peptide t
GT	Sense	Sense	-0.748	Comprom	0.748	Comprom	0.000	1.413	Detected	1.889	Detected	1.651	0.170	GT	Sens	contig384	contig384	Unannota
GT	Sense	Sense	-0.267	Comprom	0.267	Detected	0.000	1.906	Detected	2.386	Detected	2.146	0.027	GT	Sens	contig384	contig384	Unannota
GT	Sense	Sense	0.195	Comprom	-0.195	Comprom	0.000	2.816	Detected	2.588	Detected	2.702	0.007	GT	Sens	contig384	contig384	Unannota
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	1.283	Detected	0.959	Detected	1.121	0.034	GT	Sens	contig384	contig384	Unannota
GT	Sense	Sense	-0.304	Detected	0.304	Detected	0.000	3.197	Detected	2.181	Detected	2.689	0.045	GT	Sens	contig384	contig384	Unannota
GT	Sense	Sense	-0.627	Detected	0.627	Detected	0.000	2.487	Detected	1.597	Detected	2.042	0.117	GT	Sens	contig384	contig384	Unannota
GT	Sense	Sense	-0.026	Detected	0.026	Detected	0.000	0.927	Detected	1.142	Detected	1.035	0.011	GT	Sens	contig384	contig384	Unannota
GT	Sense	Sense	-0.180	Detected	0.180	Detected	0.000	1.019	Detected	0.989	Detected	1.004	0.031	GT	Sens	contig386	contig386	Unannota
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	1.136	Detected	0.963	Detected	1.050	0.018	GT	Sens	contig386	contig386	Unannota
GT	Sense	Sense	-0.422	Comprom	0.422	Detected	0.000	2.443	Detected	1.505	Detected	1.974	0.089	GT	Sens	contig387	contig387	Unknown
GT	Sense	Sense	0.300	Comprom	-0.300	Comprom	0.000	1.138	Detected	1.504	Detected	1.321	0.064	GT	Sens	contig387	contig387	Unannota
GT	Sense	Sense	-0.136	Comprom	0.136	Comprom	0.000	0.902	Detected	1.549	Detected	1.225	0.073	GT	Sens	contig387	contig387	Unannota
GT	Sense	Sense	0.325	Detected	-0.325	Comprom	0.000	2.121	Detected	1.113	Detected	1.617	0.114	GT	Sens	contig387	contig387	Unannota
GT	Sense	Sense	-0.325	Detected	0.325	Detected	0.000	1.380	Detected	1.250	Detected	1.315	0.058	GT	Sens	contig387	contig387	Unannota
GT	Sense	Sense	-0.157	Detected	0.157	Detected	0.000	2.254	Detected	1.771	Detected	2.013	0.020	GT	Sens	contig387	contig387	Unannota
GT	Sense	Sense	-0.115	Detected	0.115	Detected	0.000	2.210	Detected	1.737	Detected	1.974	0.017	GT	Sens	contig387	contig387	Unannota
GT	Sense	Sense	0.311	Comprom	-0.311	Comprom	0.000	1.309	Detected	1.576	Detected	1.442	0.051	GT	Sens	contig388	contig388	Unannota
GT	Sense	Sense	0.738	Detected	-0.738	Comprom	0.000	1.638	Detected	1.302	Detected	1.470	0.192	GT	Sens	contig388	contig388	Unannota
GT	Sense	Sense	0.329	Detected	-0.329	Detected	0.000	1.891	Detected	1.662	Detected	1.777	0.036	GT	Sens	contig388	contig388	Unannota
GT	Sense	Sense	-0.694	Comprom	0.694	Comprom	0.000	0.991	Detected	1.679	Detected	1.335	0.227	GT	Sens	contig388	contig388	Unannota
GT	Sense	Sense	-0.993	Comprom	0.993	Detected	0.000	1.440	Detected	1.058	Detected	1.249	0.342	GT	Sens	contig389	contig389	Unannota
GT	Sense	Sense	-0.033	Detected	0.033	Detected	0.000	1.117	Detected	0.929	Detected	1.023	0.009	GT	Sens	contig389	contig389	Unannota
GT	Sense	Sense	-0.363	Detected	0.363	Detected	0.000	1.921	Detected	1.792	Detected	1.856	0.037	GT	Sens	contig389	contig389	Unannota
GT	Sense	Sense	-0.267	Detected	0.267	Detected	0.000	1.945	Detected	1.960	Detected	1.952	0.018	GT	Sens	contig389	contig389	Unannota
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	0.832	Detected	1.671	Detected	1.252	0.096	GT	Sens	contig389	contig389	Receptor
GT	Sense	Sense	-0.013	Comprom	0.013	Comprom	0.000	1.364	Detected	1.258	Detected	1.311	0.002	GT	Sens	contig389	contig389	Unannota
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	1.108	Detected	1.066	Detected	1.087	0.000	GT	Sens	contig390	contig390	Unannota
GT	Sense	Sense	0.053	Comprom	-0.053	Comprom	0.000	1.828	Detected	0.830	Detected	1.329	0.118	GT	Sens	contig390	contig390	Unannota
GT	Sense	Sense	-0.254	Comprom	0.254	Comprom	0.000	2.022	Detected	1.016	Detected	1.519	0.114	GT	Sens	contig390	contig390	Unannota
GT	Sense	Sense	0.421	Detected	-0.421	Detected	0.000	0.993	Detected	1.026	Detected	1.010	0.139	GT	Sens	contig390	contig390	Unannota
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	1.353	Detected	1.072	Detected	1.212	0.014	GT	Sens	contig391	contig391	Unannota
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	1.397	Detected	0.961	Detected	1.179	0.047	GT	Sens	contig391	contig391	Unannota
GT	Sense	Sense	-0.075	Comprom	0.075	Comprom	0.000	1.888	Detected	1.903	Detected	1.896	0.002	GT	Sens	contig391	contig391	Unannota
GT	Sense	Sense	0.137	Comprom	-0.137	Comprom	0.000	1.790	Detected	1.641	Detected	1.715	0.008	GT	Sens	contig391	contig391	Unannota
GT	Sense	Sense	-0.205	Detected	0.205	Detected	0.000	0.828	Detected	1.441	Detected	1.135	0.091	GT	Sens	contig392	contig392	Unannota
GT	Sense	Sense	0.717	Comprom	-0.717	Comprom	0.000	3.335	Detected	3.212	Detected	3.273	0.045	GT	Sens	contig392	contig392	Unannota
GT	Sense	Sense	0.350	Detected	-0.350	Detected	0.000	1.174	Detected	1.043	Detected	1.109	0.089	GT	Sens	contig392	contig392	Unannota
GT	Sense	Sense	0.258	Detected	-0.258	Detected	0.000	1.080	Detected	1.000	Detected	1.040	0.058	GT	Sens	contig392	contig392	Unannota
GT	Sense	Sense	-0.264	Detected	0.264	Detected	0.000	2.131	Detected	2.665	Detected	2.398	0.024	GT	Sens	contig392	contig392	Unannota
GT	Sense	Sense	-0.292	Detected	0.292	Detected	0.000	1.258	Detected	1.866	Detected	1.562	0.066	GT	Sens	contig392	contig392	Unannota
GT	Sense	Sense	-0.128	Detected	0.128	Detected	0.000	1.149	Detected	1.453	Detected	1.301	0.023	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	-0.086	Detected	0.086	Detected	0.000	0.994	Detected	1.266	Detected	1.130	0.020	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	-1.030	Comprom	1.030	Detected	0.000	2.612	Detected	2.019	Detected	2.315	0.163	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	-1.013	Comprom	1.013	Detected	0.000	2.224	Detected	1.965	Detected	2.094	0.177	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	-0.125	Comprom	0.125	Comprom	0.000	2.187	Detected	1.046	Detected	1.616	0.110	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	0.262	Detected	-0.262	Detected	0.000	1.327	Detected	1.117	Detected	1.222	0.049	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	1.062	Detected	1.033	Detected	1.048	0.001	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	0.059	Comprom	-0.059	Comprom	0.000	1.482	Detected	1.358	Detected	1.420	0.004	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	-0.430	Detected	0.430	Detected	0.000	1.263	Detected	1.124	Detected	1.194	0.111	GT	Sens	contig393	contig393	HEAT rep
GT	Sense	Sense	0.587	Comprom	-0.587	Comprom	0.000	1.410	Detected	1.288	Detected	1.349	0.149	GT	Sens	contig393	contig393	Unannota
GT	Sense	Sense	-0.387	Comprom	0.387	Comprom	0.000	1.620	Detected	1.649	Detected	1.634	0.052	GT	Sens	contig394	contig394	Unannota
GT	Sense	Sense	0.147	Detected	-0.147	Detected	0.000	1.335	Detected	1.330	Detected	1.333	0.012	GT	Sens	contig394	contig394	Unannota
GT	Sense	Sense	-0.274	Detected	0.274	Detected	0.000	1.224	Detected	1.051	Detected	1.138	0.058	GT	Sens	contig395	contig395	Unannota
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	1.253	Detected	1.325	Detected	1.289	0.001	GT	Sens	contig395	contig395	Unannota
GT	Sense	Sense	1.174	Detected	-1.174	Comprom	0.000	2.323	Detected	1.857	Detected	2.090	0.223	GT	Sens	contig395	contig395	Unannota
GT	Sense	Sense	-0.192	Comprom	0.192	Comprom	0.000	2.852	Detected	2.175	Detected	2.514	0.023	GT	Sens	contig395	contig395	Unannota
GT	Sense	Sense	-0.732	Comprom	0.732	Detected	0.000	1.135	Detected	1.152	Detected	1.144	0.259	GT	Sens	contig395	contig395	Unannota
GT	Sense	Sense	0.582	Detected	-0.582	Comprom	0.000	0.826	Detected	1.421	Detected	1.124	0.228	GT	Sens	contig396	contig396	Unannota
GT	Sense	Sense	-0.214	Detected	0.214	Detected	0.000	1.913	Detected	1.484	Detected	1.699	0.030	GT	Sens	contig396	contig396	Unannota
GT	Sense	Sense	-0.102	Detected	0.102	Detected	0.000	1.140	Detected	1.119	Detected	1.130	0.008	GT	Sens	contig396	contig396	Unannota
GT	Sense	Sense	-0.323	Detected	0.323	Detected	0.000	1.133	Detected	1.201	Detected	1.167	0.069	GT	Sens	contig396	contig396	Unannota
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	2.063	Detected	0.868	Detected	1.465	0.139	GT	Sens	contig397	contig397	Unannota
GT	Sense	Sense	-0.300	Detected	0.300	Detected	0.000	1.282	Detected	1.309	Detected	1.295	0.050	GT	Sens	contig397	contig397	Unannota
GT	Sense	Sense	-0.267	Comprom	0.267	Comprom	0.000	1.898	Detected	1.081	Detected	1.489	0.092	GT	Sens	contig397	contig397	Unannota
GT	Sense	Sense	-0.590	Comprom	0.590	Comprom	0.000	2.166	Detected	1.667	Detected	1.916	0.096	GT	Sens	contig397	contig397	Unannota
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	4.553	Detected	4.206	Detected	4.380	0.002	GT	Sens	contig397	contig397	Unknown
GT	Sense	Sense	-0.380	Comprom	0.380	Comprom	0.000	1.902	Detected	1.673	Detected	1.787	0.046	GT	Sens	contig397	contig397	Unannota
GT	Sense	Sense	1.400	Detected	-1.400	Comprom	0.000	4.171	Detected	1.348	Detected	2.759	0.300	GT	Sens	contig397	contig397	Unannota
GT	Sense	Sense	-0.435	Comprom	0.435	Comprom	0.000	1.225	Detected	1.433	Detected	1.329	0.097	GT	Sens	contig397	contig397	Unannota
GT	Sense	Sense	-0.260	Detected	0.260	Detected	0.000	1.661	Detected	1.069	Detected	1.365	0.074	GT	Sens	contig397	contig397	LTRGag-
GT	Sense	Sense	-0.804	Comprom	0.804	Detected	0.000	1.487	Detected	1.041	Detected	1.264	0.269	GT	Sens	contig397	contig397	Unannota
GT	Sense	Sense	-0.170	Detected	0.170	Detected	0.000	0.817	Detected	1.231	Detected	1.024	0.062	GT	Sens	contig398	contig398	Unannota
GT	Sense	Sense	-0.031	Comprom	0.031	Comprom	0.000	1.208	Detected	0.906	Detected	1.057	0.021	GT	Sens	contig399	contig399	Unannota
GT	Sense	Sense	-0.508	Comprom	0.508	Comprom	0.000	1.582	Detected	1.312	Detected	1.447	0.110	GT	Sens	contig399	contig399	Unannota
GT	Sense	Sense	-1.019	Comprom	1.019	Detected	0.000	1.206	Detected	0.907	Detected	1.056	0.413	GT	Sens	contig399	contig399	Unannota
GT	Sense	Sense	0.201	Detected	-0.201	Detected	0.000	1.667	Detected	0.819	Detected	1.243	0.118	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	1.894	Detected	1.248	Detected	1.571	0.040	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	-0.164	Detected	0.164	Detected	0.000	1.302	Detected	1.310	Detected	1.306	0.015	GT	Sens	contig400	contig400	Ninia-fam
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	1.107	Detected	0.924	Detected	1.015	0.015	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	-0.047	Comprom	0.047	Comprom	0.000	1.959	Detected	2.022	Detected	1.991	0.001	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	-0.092	Comprom	0.092	Comprom	0.000	2.198	Detected	1.229	Detected	1.713	0.074	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	0.274	Detected	-0.274	Detected	0.000	1.277	Detected	1.489	Detected	1.383	0.042	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	-0.108	Detected	0.108	Detected	0.000	1.303	Detected	1.233	Detected	1.268	0.008	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	1.155	Detected	1.095	Detected	1.125	0.002	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	-0.058	Comprom	0.058	Comprom	0.000	2.010	Detected	2.124	Detected	2.067	0.002	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	-0.159	Detected	0.159	Detected	0.000	1.009	Detected	1.063	Detected	1.036	0.023	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	0.548	Detected	-0.548	Comprom	0.000	2.417	Detected	1.733	Detected	2.075	0.085	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	0.027	Comprom	-0.027	Comprom	0.000	1.668	Detected	1.475	Detected	1.572	0.004	GT	Sens	contig400	contig400	Unannota
GT	Sense	Sense	0.216	Detected	-0.216	Detected	0.000	1.251	Detected	0.986	Detected	1.119	0.048	GT	Sens	contig401	contig401	Unannota
GT	Sense	Sense	-0.154	Comprom	0.154	Comprom	0.000	1.318	Detected	1.364	Detected	1.341	0.013	GT	Sens	contig401	contig401	Unannota
GT	Sense	Sense	-0.250	Detected	0.250	Detected	0.000	1.228	Detected	0.950	Detected	1.089	0.063	GT	Sens	contig401	contig401	Unannota
GT	Sense	Sense	-0.579	Comprom	0.579	Comprom	0.000	1.631	Detected	1.236	Detected	1.434	0.144	GT	Sens	contig401	contig401	Unannota
GT	Sense	Sense	-0.003	Comprom	0.003	Comprom	0.000	1.315	Detected	1.376	Detected	1.346	0.001	GT	Sens	contig401	contig401	Unannota
GT	Sense	Sense	-0.432	Comprom	0.432	Comprom	0.000	1.078	Detected	1.880	Detected	1.479	0.129	GT	Sens	contig401	contig401	Unannota
GT	Sense	Sense	-0.285	Detected	0.285	Detected	0.000	2.236	Detected	1.594	Detected	1.915	0.047	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	-0.076	Detected	0.076	Detected	0.000	1.905	Detected	1.269	Detected	1.587	0.040	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	0.251	Detected	-0.251	Detected	0.000	1.349	Detected	1.509	Detected	1.429	0.032	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	-0.900	Comprom	0.900	Detected	0.000	1.706	Detected	0.924	Detected	1.315	0.312	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	-0.385	Detected	0.385	Detected	0.000	1.603	Detected	1.363	Detected	1.483	0.067	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	0.044	Detected	-0.044	Detected	0.000	0.968	Detected	1.074	Detected	1.021	0.005	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	1.279	Detected	1.054	Detected	1.166	0.037	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	-0.099	Detected	0.099	Detected	0.000	1.423	Detected	1.160	Detected	1.291	0.016	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	1.568	Detected	1.290	Detected	1.429	0.023	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	1.641	Detected	1.343	Detected	1.492	0.022	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	-0.146	Comprom	0.146	Comprom	0.000	3.001	Detected	1.421	Detected	2.211	0.110	GT	Sens	contig402	contig402	Unannota
GT	Sense	Sense	0.210	Detected	-0.210	Comprom	0.000	0.876	Detected	1.196	Detected	1.036	0.059	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	-0.128	Comprom	0.128	Comprom	0.000	2.568	Detected	2.460	Detected	2.514	0.003	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	-0.315	Comprom	0.315	Comprom	0.000	1.229	Detected	1.073	Detected	1.151	0.071	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	1.087	Detected	1.188	Detected	1.138	0.014	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	1.689	Detected	1.604	Detected	1.647	0.004	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	1.865	Detected	1.466	Detected	1.666	0.014	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	0.279	Comprom	-0.279	Comprom	0.000	1.988	Detected	2.086	Detected	2.037	0.019	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	0.083	Detected	-0.083	Detected	0.000	1.421	Detected	1.287	Detected	1.354	0.006	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	-0.682	Comprom	0.682	Comprom	0.000	0.924	Detected	2.012	Detected	1.468	0.234	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	-0.217	Comprom	0.217	Comprom	0.000	2.232	Detected	2.284	Detected	2.258	0.009	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	0.155	Comprom	-0.155	Comprom	0.000	4.414	Detected	1.205	Detected	2.809	0.223	GT	Sens	contig403	contig403	Unannota
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	1.281	Detected	0.879	Detected	1.080	0.033	GT	Sens	contig404	contig404	Unannota
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	1.103	Detected	1.278	Detected	1.190	0.006	GT	Sens	contig404	contig404	Unannota
GT	Sense	Sense	0.207	Comprom	-0.207	Comprom	0.000	1.549	Detected	1.701	Detected	1.625	0.018	GT	Sens	contig404	contig404	Unannota
GT	Sense	Sense	0.484	Comprom	-0.484	Comprom	0.000	1.126	Detected	0.959	Detected	1.043	0.168	GT	Sens	contig404	contig404	Unannota
GT	Sense	Sense	-0.507	Comprom	0.507	Detected	0.000	0.897	Detected	1.309	Detected	1.103	0.181	GT	Sens	contig404	contig404	Unannota
GT	Sense	Sense	-0.682	Comprom	0.682	Comprom	0.000	1.784	Detected	1.812	Detected	1.798	0.119	GT	Sens	contig404	contig404	Unannota
GT	Sense	Sense	-0.338	Detected	0.338	Detected	0.000	1.599	Detected	0.831	Detected	1.215	0.141	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	1.995	Detected	0.954	Detected	1.475	0.105	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	1.450	Detected	0.964	Detected	1.207	0.048	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	-0.237	Comprom	0.237	Comprom	0.000	1.387	Detected	1.582	Detected	1.484	0.029	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.227	Detected	-0.227	Detected	0.000	1.051	Detected	1.615	Detected	1.333	0.067	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.236	Detected	-0.236	Detected	0.000	0.867	Detected	1.416	Detected	1.142	0.088	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	0.900	Detected	1.147	Detected	1.023	0.048	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.122	Comprom	-0.122	Comprom	0.000	2.320	Detected	2.028	Detected	2.174	0.008	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	-0.323	Comprom	0.323	Detected	0.000	1.407	Detected	1.262	Detected	1.334	0.056	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	0.927	Detected	1.106	Detected	1.017	0.008	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.090	Detected	-0.090	Comprom	0.000	0.946	Detected	1.421	Detected	1.183	0.043	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	0.929	Detected	-0.929	Comprom	0.000	0.827	Detected	1.226	Detected	1.026	0.393	GT	Sens	contig405	contig405	Unannota
GT	Sense	Sense	-0.041	Comprom	0.041	Comprom	0.000	1.220	Detected	1.351	Detected	1.286	0.004	GT	Sens	contig406	contig406	Unannota
GT	Sense	Sense	-0.203	Comprom	0.203	Comprom	0.000	1.698	Detected	1.842	Detected	1.770	0.015	GT	Sens	contig406	contig406	Unannota
GT	Sense	Sense	-0.049	Comprom	0.049	Comprom	0.000	1.179	Detected	1.458	Detected	1.319	0.012	GT	Sens	contig406	contig406	Unannota
GT	Sense	Sense	0.160	Detected	-0.160	Detected	0.000	0.865	Detected	1.300	Detected	1.083	0.057	GT	Sens	contig406	contig406	Unannota
GT	Sense	Sense	0.262	Comprom	-0.262	Comprom	0.000	1.599	Detected	1.304	Detected	1.451	0.040	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	-1.164	Comprom	1.164	Detected	0.000	1.138	Detected	1.519	Detected	1.328	0.377	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	0.085	Detected	-0.085	Detected	0.000	1.520	Detected	1.168	Detected	1.344	0.020	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	0.183	Comprom	-0.183	Comprom	0.000	1.721	Detected	1.208	Detected	1.464	0.043	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	0.826	Detected	-0.826	Comprom	0.000	1.231	Detected	1.386	Detected	1.309	0.256	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	0.827	Detected	1.377	Detected	1.102	0.065	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	-0.207	Detected	0.207	Detected	0.000	1.749	Detected	0.981	Detected	1.365	0.089	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	0.277	Detected	-0.277	Detected	0.000	0.859	Detected	1.378	Detected	1.118	0.098	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	1.183	Detected	0.923	Detected	1.053	0.016	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	-0.038	Detected	0.038	Detected	0.000	1.537	Detected	1.151	Detected	1.344	0.021	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	-0.433	Comprom	0.433	Comprom	0.000	2.181	Detected	1.703	Detected	1.942	0.059	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	-0.121	Detected	0.121	Detected	0.000	1.447	Detected	1.105	Detected	1.276	0.026	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	-0.670	Comprom	0.670	Comprom	0.000	1.532	Detected	2.793	Detected	2.162	0.143	GT	Sens	contig407	contig407	Beta-ocin
GT	Sense	Sense	0.226	Detected	-0.226	Detected	0.000	1.384	Detected	1.737	Detected	1.560	0.032	GT	Sens	contig407	contig407	Unannota
GT	Sense	Sense	-0.868	Detected	0.868	Detected	0.000	1.341	Detected	1.059	Detected	1.200	0.306	GT	Sens	contig408	contig408	Unannota
GT	Sense	Sense	-0.207	Detected	0.207	Detected	0.000	0.897	Detected	1.120	Detected	1.008	0.050	GT	Sens	contig408	contig408	Unannota
GT	Sense	Sense	-0.101	Comprom	0.101	Comprom	0.000	1.615	Detected	1.583	Detected	1.599	0.004	GT	Sens	contig408	contig408	Unannota
GT	Sense	Sense	-0.087	Comprom	0.087	Comprom	0.000	1.197	Detected	0.880	Detected	1.039	0.029	GT	Sens	contig408	contig408	Unannota
GT	Sense	Sense	0.351	Detected	-0.351	Comprom	0.000	1.053	Detected	1.417	Detected	1.235	0.089	GT	Sens	contig408	contig408	Unannota
GT	Sense	Sense	-0.747	Comprom	0.747	Comprom	0.000	1.122	Detected	1.109	Detected	1.115	0.274	GT	Sens	contig408	contig408	Unannota
GT	Sense	Sense	0.624	Detected	-0.624	Comprom	0.000	1.951	Detected	2.091	Detected	2.021	0.085	GT	Sens	contig408	contig408	Unannota
GT	Sense	Sense	0.221	Detected	-0.221	Detected	0.000	1.403	Detected	1.253	Detected	1.328	0.029	GT	Sens	contig408	contig408	Unannota
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	1.333	Detected	1.282	Detected	1.308	0.007	GT	Sens	contig409	contig409	Unannota
GT	Sense	Sense	0.074	Comprom	-0.074	Comprom	0.000	1.299	Detected	1.028	Detected	1.164	0.017	GT	Sens	contig409	contig409	Unannota
GT	Sense	Sense	0.520	Detected	-0.520	Detected	0.000	1.616	Detected	1.508	Detected	1.562	0.096	GT	Sens	contig409	contig409	Unannota
GT	Sense	Sense	0.247	Detected	-0.247	Comprom	0.000	1.303	Detected	1.242	Detected	1.272	0.036	GT	Sens	contig410	contig410	Unannota
GT	Sense	Sense	0.293	Detected	-0.293	Detected	0.000	1.207	Detected	0.884	Detected	1.046	0.089	GT	Sens	contig410	contig410	Unknown
GT	Sense	Sense	-0.868	Comprom	0.868	Comprom	0.000	1.577	Detected	1.411	Detected	1.494	0.229	GT	Sens	contig410	contig410	Unannota
GT	Sense	Sense	-0.269	Comprom	0.269	Comprom	0.000	1.187	Detected	1.180	Detected	1.183	0.048	GT	Sens	contig410	contig410	Unannota
GT	Sense	Sense	0.407	Detected	-0.407	Comprom	0.000	2.219	Detected	2.023	Detected	2.121	0.037	GT	Sens	contig410	contig410	Unannota
GT	Sense	Sense	-0.026	Detected	0.026	Detected	0.000	1.341	Detected	1.139	Detected	1.240	0.007	GT	Sens	contig411	contig411	Unannota
GT	Sense	Sense	-0.467	Detected	0.467	Detected	0.000	3.225	Detected	2.308	Detected	2.767	0.052	GT	Sens	contig411	contig411	Genomic
GT	Sense	Sense	0.262	Detected	-0.262	Detected	0.000	1.970	Detected	1.279	Detected	1.625	0.064	GT	Sens	contig411	contig411	Unannota
GT	Sense	Sense	-0.200	Detected	0.200	Detected	0.000	0.877	Detected	1.167	Detected	1.022	0.054	GT	Sens	contig411	contig411	LOB dom
GT	Sense	Sense	-0.319	Detected	0.319	Detected	0.000	1.485	Detected	1.163	Detected	1.324	0.066	GT	Sens	contig411	contig411	Unannota
GT	Sense	Sense	-0.203	Detected	0.203	Detected	0.000	1.429	Detected	1.037	Detected	1.233	0.049	GT	Sens	contig411	contig411	Unannota
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	1.348	Detected	0.883	Detected	1.116	0.055	GT	Sens	contig411	contig411	Unannota
GT	Sense	Sense	-0.065	Detected	0.065	Detected	0.000	2.091	Detected	1.916	Detected	2.003	0.003	GT	Sens	contig411	contig411	Unannota
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	1.855	Detected	1.683	Detected	1.769	0.002	GT	Sens	contig411	contig411	Unannota
GT	Sense	Sense	0.248	Detected	-0.248	Detected	0.000	1.705	Detected	1.050	Detected	1.378	0.079	GT	Sens	contig411	contig411	Unannota
GT	Sense	Sense	0.244	Comprom	-0.244	Comprom	0.000	4.927	Detected	2.856	Detected	3.892	0.067	GT	Sens	contig412	contig412	Unannota
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	1.378	Detected	1.409	Detected	1.394	0.000	GT	Sens	contig412	contig412	Unannota
GT	Sense	Sense	-0.134	Comprom	0.134	Comprom	0.000	1.205	Detected	1.585	Detected	1.395	0.027	GT	Sens	contig412	contig412	Unannota
GT	Sense	Sense	0.394	Detected	-0.394	Comprom	0.000	0.959	Detected	1.142	Detected	1.051	0.122	GT	Sens	contig413	contig413	Unannota
GT	Sense	Sense	-0.055	Detected	0.055	Detected	0.000	1.293	Detected	1.302	Detected	1.297	0.002	GT	Sens	contig413	contig413	Unannota
GT	Sense	Sense	-0.320	Comprom	0.320	Comprom	0.000	1.272	Detected	1.480	Detected	1.376	0.055	GT	Sens	contig413	contig413	Unannota
GT	Sense	Sense	-0.743	Comprom	0.743	Comprom	0.000	1.582	Detected	1.411	Detected	1.496	0.184	GT	Sens	contig414	contig414	Unannota
GT	Sense	Sense	0.763	Comprom	-0.763	Comprom	0.000	2.427	Detected	1.657	Detected	2.042	0.139	GT	Sens	contig414	contig414	Unannota
GT	Sense	Sense	-0.233	Comprom	0.233	Comprom	0.000	1.895	Detected	1.307	Detected	1.601	0.051	GT	Sens	contig414	contig414	Unannota
GT	Sense	Sense	0.830	Detected	-0.830	Comprom	0.000	1.219	Detected	1.554	Detected	1.386	0.243	GT	Sens	contig414	contig414	Unannota
GT	Sense	Sense	-0.513	Comprom	0.513	Comprom	0.000	0.940	Detected	1.619	Detected	1.279	0.173	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	0.558	Detected	-0.558	Comprom	0.000	2.360	Detected	2.760	Detected	2.560	0.050	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	0.092	Detected	-0.092	Detected	0.000	1.656	Detected	2.042	Detected	1.849	0.013	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	0.583	Detected	-0.583	Detected	0.000	2.344	Detected	1.123	Detected	1.733	0.176	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	1.215	Detected	0.995	Detected	1.105	0.016	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	-0.282	Detected	0.282	Detected	0.000	0.928	Detected	1.142	Detected	1.035	0.076	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	-0.182	Detected	0.182	Detected	0.000	1.038	Detected	1.245	Detected	1.142	0.032	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	0.022	Detected	-0.022	Detected	0.000	1.265	Detected	1.348	Detected	1.307	0.001	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	-0.275	Comprom	0.275	Comprom	0.000	2.059	Detected	2.067	Detected	2.063	0.017	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	-0.126	Detected	0.126	Detected	0.000	1.033	Detected	0.999	Detected	1.016	0.015	GT	Sens	contig415	contig415	Ternary c
GT	Sense	Sense	-0.302	Detected	0.302	Detected	0.000	1.700	Detected	1.507	Detected	1.603	0.037	GT	Sens	contig415	contig415	Unknown
GT	Sense	Sense	0.186	Comprom	-0.186	Comprom	0.000	2.252	Detected	2.773	Detected	2.512	0.016	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	0.153	Detected	-0.153	Detected	0.000	1.568	Detected	1.066	Detected	1.317	0.046	GT	Sens	contig415	contig415	Unannota
GT	Sense	Sense	0.147	Detected	-0.147	Detected	0.000	1.217	Detected	0.907	Detected	1.062	0.038	GT	Sens	contig416	contig416	Unannota
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	1.116	Detected	0.953	Detected	1.034	0.010	GT	Sens	contig416	contig416	Unannota
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	1.698	Detected	1.324	Detected	1.511	0.017	GT	Sens	contig416	contig416	Deoxyrib
GT	Sense	Sense	0.225	Detected	-0.225	Comprom	0.000	0.937	Detected	1.271	Detected	1.104	0.059	GT	Sens	contig416	contig416	Unannota
GT	Sense	Sense	0.219	Detected	-0.219	Comprom	0.000	1.284	Detected	1.476	Detected	1.380	0.029	GT	Sens	contig416	contig416	Unannota
GT	Sense	Sense	-0.445	Comprom	0.445	Comprom	0.000	1.687	Detected	2.076	Detected	1.882	0.061	GT	Sens	contig417	contig417	Unannota
GT	Sense	Sense	-0.660	Comprom	0.660	Comprom	0.000	1.282	Detected	0.853	Detected	1.068	0.264	GT	Sens	contig417	contig417	Unannota
GT	Sense	Sense	-0.358	Comprom	0.358	Comprom	0.000	1.054	Detected	1.761	Detected	1.407	0.108	GT	Sens	contig417	contig417	Unannota
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	1.317	Detected	1.163	Detected	1.240	0.007	GT	Sens	contig417	contig417	Unannota
GT	Sense	Sense	-0.732	Comprom	0.732	Comprom	0.000	2.024	Detected	2.184	Detected	2.104	0.104	GT	Sens	contig417	contig417	Unannota
GT	Sense	Sense	0.174	Comprom	-0.174	Comprom	0.000	1.904	Detected	7.106	Detected	4.505	0.226	GT	Sens	contig417	contig417	Unannota
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	1.102	Detected	0.911	Detected	1.007	0.010	GT	Sens	contig417	contig417	Unannota
GT	Sense	Sense	0.891	Detected	-0.891	Comprom	0.000	2.227	Detected	2.476	Detected	2.351	0.121	GT	Sens	contig418	contig418	Unannota
GT	Sense	Sense	0.369	Comprom	-0.369	Comprom	0.000	1.079	Detected	1.168	Detected	1.123	0.094	GT	Sens	contig418	contig418	Unannota
GT	Sense	Sense	0.227	Detected	-0.227	Detected	0.000	1.988	Detected	1.755	Detected	1.871	0.018	GT	Sens	contig418	contig418	Unannota
GT	Sense	Sense	1.002	Detected	-1.002	Comprom	0.000	1.491	Detected	2.104	Detected	1.798	0.228	GT	Sens	contig418	contig418	Unannota
GT	Sense	Sense	0.034	Comprom	-0.034	Comprom	0.000	1.125	Detected	1.429	Detected	1.277	0.015	GT	Sens	contig418	contig418	Unannota
GT	Sense	Sense	-0.044	Detected	0.044	Detected	0.000	1.394	Detected	0.901	Detected	1.148	0.044	GT	Sens	contig418	contig418	Unannota
GT	Sense	Sense	-0.432	Comprom	0.432	Comprom	0.000	1.090	Detected	1.037	Detected	1.064	0.133	GT	Sens	contig419	contig419	Unannota
GT	Sense	Sense	-0.694	Detected	0.694	Detected	0.000	2.188	Detected	1.970	Detected	2.079	0.098	GT	Sens	contig419	contig419	Vacuolar

GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	1.810	Detected	1.472	Detected	1.641	0.017	GT	Sens	contig419	contig419	Unannota	GAAGTTTTATTCTGGCTAATTTCTAAAGTATTTAATTTAAAATCATAAAG	contig419	Solyc03g	Potassiur	GO:0005	SL2.40ch	AT3G53235.1		unknown	chr3:197	208.957	235.832	589.394	407.815	829.926	654.673
GT	Sense	Sense	-0.169	Detected	0.169	Detected	0.000	1.438	Detected	1.206	Detected	1.322	0.023	GT	Sens	contig419	contig419	Unannota	GTCATTAATTGATGTGTGTGTGTACATATAAATTAATTTTCATTTTCGT	contig419	Solyc03g	Potassiur	GO:0005	SL2.40ch	AT3G53235.1		unknown	chr3:197	798.206	949.4	2174.87	1662.83	2514.48	2135.73
GT	Sense	Sense	-0.879	Comprom	0.879	Detected	0.000	1.799	Detected	1.775	Detected	1.787	0.179	GT	Sens	contig420	contig420	Unannota	AAATAGCCTGAGGCCGGATCGTGAACGAACGTATTGATCTTAGCTTGA	contig420	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G67520.1		adenvlvl	chr5:269	4.47674	14.2467	34.2136	22.9675	29.6319	29.0527
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	1.049	Detected	1.077	Detected	1.063	0.005	GT	Sens	contig420	contig420	Unannota	ATTGTAGTCGTCGTGTATCAGAAGGATCAAATTTAGAATTTACTAACGA	contig420	Solyc04g	Alcohol d	GO:0004	SL2.40ch	AT3G256	CHUP1	CHUP1 (C	chr3:935	38.6861	32.7103	101.799	63.0212	78.4675	79.7642
GT	Sense	Sense	-0.143	Detected	0.143	Detected	0.000	1.481	Detected	1.309	Detected	1.395	0.014	GT	Sens	contig420	contig420	Unannota	GAGTTCACGTGTGGCTCAGCCACTGATTCACATAAGTTTATTTTAATTA	contig420	Solyc04g	Alcohol d	GO:0004	SL2.40ch	AT3G256	CHUP1	CHUP1 (C	chr3:935	24.62	28.2294	74.9513	51.4183	78.4722	69.441
GT	Sense	Sense	-0.437	Comprom	0.437	Comprom	0.000	1.281	Detected	1.968	Detected	1.625	0.100	GT	Sens	contig420	contig420	Unannota	TTCTAGGCTTGAGGGTGTTATTCCAGATGTTGTTGCTCTTGTTTTTTG	contig420	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G24350.1		FUNCTIO	chr5:830	2.83136	4.88345	4.51407	3.03212	9.63907	15.466
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	1.153	Detected	0.942	Detected	1.048	0.010	GT	Sens	contig420	contig420	Unannota	GAGCTAGCTTTTGGGGTTGAGTTACGTTAGACTGGATGTCATATCTTG	contig420	Solyc07g	Carboxyl-	GO:0005	SL2.40ch	AT5G42320.1		metalloc	chr5:169	76.0916	70.297	78.2317	64.0996	173.479	149.405
GT	Sense	Sense	-0.159	Detected	0.159	Detected	0.000	1.568	Detected	1.116	Detected	1.342	0.040	GT	Sens	contig421	contig421	Histidine	TACCCT contig421 Solyc12g Solyc12g Histidine GO:0006 GO:0006	contig421	Solyc12g	Histidine	GO:0006	SL2.40ch	AT3G03210.1		unknown	chr3:740	20.5323	24.0765	32.7169	24.5338	70.3109	51.2397
GT	Sense	Sense	-0.568	Comprom	0.568	Comprom	0.000	0.906	Detected	1.161	Detected	1.034	0.218	GT	Sens	contig421	contig421	Unannota	ATGGAAGAATCAGTCAGAATCCATTAGGTTGCATGCAGCAACATTCAC	contig421	Solyc02g	Transcription factor		SL2.40ch	AT3G483	PIMT1	PIMT1 (P	chr3:178	3.84388	7.94424	16.9845	8.47486	11.0416	13.141
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	1.042	Detected	1.079	Detected	1.061	0.006	GT	Sens	contig421	contig421	Unannota	GGACTCCAACATAATCTACTCATCATGAGTCAACTGTGTGATGTTATAT	contig421	Solyc11g	Kinase family protei		SL2.40ch	AT5G41180.1		leucine-r	chr5:164	60.2354	50.6121	61.9739	66.4323	121.239	124.031
GT	Sense	Sense	-0.190	Detected	0.190	Detected	0.000	1.240	Detected	0.890	Detected	1.065	0.054	GT	Sens	contig421	contig421	Unannota	CGATCGATAAAAATCTAGCTTGGATGCTCTGGTACACTTTTTCAATCTA	contig421	Solyc10g024390.1.1				AT5G47170.1				321.889	394.026	624.294	474.898	897.258	701.874
GT	Sense	Sense	-0.844	Comprom	0.844	Comprom	0.000	1.683	Detected	1.492	Detected	1.588	0.202	GT	Sens	contig421	contig421	Unannota	TAAGCATAAGGTATACTAATTGACTACGAGTGTAATAAGAGCATCAGTC	contig421	Solyc09g	Ycf2 (AHF	GO:0009	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:145	2.94968	8.93974	8.30411	6.64171	17.5883	15.3593
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	1.637	Detected	1.633	Detected	1.635	0.006	GT	Sens	contig421	contig421	Unannota	TATTTTAATATGTACAACATAACTCAAACAAACCAAAAGACAAAAATTCA	contig421	Solyc08g	Polyprote	GO:0006	SL2.40ch	AT5G562	HAP8	HAP8 (HA	chr5:227	85.8762	67.2651	205.258	136.511	251.989	250.643
GT	Sense	Sense	-0.403	Detected	0.403	Detected	0.000	2.893	Detected	3.167	Detected	3.030	0.019	GT	Sens	contig421	contig421	Beta-gluc	AGGGAA contig421 Solyc12g Solyc12g Beta-gluc GO:0005 GO:0005	contig421	Solyc12g	Beta-gluc	GO:0005	SL2.40ch	AT3G180	BGLU43	BGLU43	chr3:618	66.5144	109.481	77.5479	133.038	676.175	814.977
GT	Sense	Sense	0.122	Detected	-0.122	Detected	0.000	1.197	Detected	1.020	Detected	1.108	0.018	GT	Sens	contig421	contig421	Unannota	CCTATGTTCATCGAAAGGTTCATTATGAGACAGTTTTGATATTTGTCTT	contig421	Solyc04g	Glucosylt	GO:0080	SL2.40ch	AT5G496	AAP6	AAP6 (AN	chr5:201	89.4383	71.0625	222.925	125.268	194.845	171.919
GT	Sense	Sense	-0.466	Comprom	0.466	Comprom	0.000	0.904	Detected	1.243	Detected	1.073	0.163	GT	Sens	contig422	contig422	Unannota	GGAATTACCCGAATGAAAGTTCCCCACCTACATTACAATACCTTACTCT	contig422	Solyc11g	ATP synth	GO:0045	SL2.40ch	AT5G27930.2		protein p	chr5:995	5.46033	9.80171	10.0407	15.1109	14.5952	18.404
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	1.626	Detected	1.081	Detected	1.353	0.047	GT	Sens	contig422	contig422	Unannota	TATTCTCCGTCATATTTCTGGGACATTGGTGTCCTTTCCGTTCAAAATC	contig422	Solyc11g	Ribonucle	GO:0006	SL2.40ch	AT5G376	UBO9	UBO9: p	chr5:149	38.0526	42.9204	53.6608	30.1343	133.02	90.8671
GT	Sense	Sense	-0.208	Detected	0.208	Detected	0.000	1.691	Detected	1.138	Detected	1.415	0.055	GT	Sens	contig422	contig422	Unannota	TACCTTTTACTCTGACGGATGACTGAATAGGAGCACATGGCACAATCTT	contig422	Solyc11g	Ribonucle	GO:0006	SL2.40ch	AT5G376	UBO9	UBO9: p	chr5:149	35.5242	44.6039	50.914	25.1218	137.095	93.137
GT	Sense	Sense	-0.579	Comprom	0.579	Comprom	0.000	1.307	Detected	1.767	Detected	1.537	0.132	GT	Sens	contig422	contig422	Unannota	ATCCCAAGGAGTGTCATCAGGACTGCAGGTTACACCAAAACGAAGAGA	contig422	Solyc06g	Ubiquitin-	GO:0004	SL2.40ch	AT1G144	UBC1, AT	UBC1 (UB	chr1:492	2.94606	6.18301	6.83519	8.08457	11.2627	15.4425
GT	Sense	Sense	0.745	Detected	-0.745	Comprom	0.000	1.374	Detected	1.796	Detected	1.585	0.177	GT	Sens	contig422	contig422	Unannota	CCAACATTGAGTTCCTTATAAGTACGAAATGCGGAAGATAAAATATATC	contig422	Solyc12g	Ceramide glucosylt		SL2.40ch	AT4G35470.1		leucine-r	chr4:168	13.86	4.64405	15.9332	23.4136	22.1739	29.6104
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	1.349	Detected	1.128	Detected	1.239	0.026	GT	Sens	contig422	contig422	Unannota	TAGAACTCTTCTCGGATTTTGTTAGCTGTATAGCTTAGGAAGAGGCTA	contig422	Solyc03g	Timing of	GO:0030	SL2.40ch	AT1G44224.1				40.6611	30.1873	42.779	51.0218	95.1766	81.418
GT	Sense	Sense	-0.121	Comprom	0.121	Comprom	0.000	8.256	Detected	4.397	Detected	6.327	0.082	GT	Sens	contig423	contig423	Unannota	GGAAATTGGTTTGAGCTACTAAATTCTGAGATGTTTGATTGAAGAAATC	contig423	Solyc01g	GRAS fan	GO:0003	SL2.40ch	AT5G04020.1		calmodu	chr5:108	2.6814	2.98334	2.55889	3.01527	922.272	63.3414
GT	Sense	Sense	-0.214	Detected	0.214	Detected	0.000	2.184	Detected	2.756	Detected	2.470	0.020	GT	Sens	contig423	contig423	Unannota	TTGCCTTTCGAGATGACCCAGTTTCTGTGCTCCACTTTTGGGACTTGT	contig423	Solyc04g	Beige/BEACH doma		SL2.40ch	AT5G59930.1		DC1 dom	chr5:241	13.9651	17.6816	137.922	143.926	76.1658	112.847
GT	Sense	Sense	0.613	Comprom	-0.613	Comprom	0.000	2.639	Detected	3.190	Detected	2.915	0.049	GT	Sens	contig423	contig423	Unannota	GGGTGAGCACATGGTGTTTTATACAATTTAAGTCTCCATCCATATATAT	contig423	Solyc04g	Beige/BEACH doma		SL2.40ch	AT5G59930.1		DC1 dom	chr5:241	6.56195	2.63996	40.4916	41.1018	27.6529	40.396
GT	Sense	Sense	0.392	Detected	-0.392	Detected	0.000	1.227	Detected	2.809	Detected	2.018	0.150	GT	Sens	contig423	contig423	Unannota	GCCAAAGTTAGGATTGCTGTTATACATTGACCAATGACGCTTATAGAGA	contig423	Solyc10g049240.1.1				AT1G22830.2		pentatric	chr1:807	1025.82	560.61	1268.32	2421.61	1892.38	5651.86
GT	Sense	Sense	0.458	Detected	-0.458	Comprom	0.000	1.958	Detected	3.075	Detected	2.516	0.073	GT	Sens	contig423	contig423	Unannota	TGGTTCTATCTATGTATAAAAGAAAAACTAACTGATTAACAGAGAATGT	contig423	Solyc10g049240.1.1				AT1G22830.2		pentatric	chr1:807	17.6885	8.82684	34.7679	49.336	51.7697	111.946
GT	Sense	Sense	-0.746	Comprom	0.746	Comprom	0.000	2.429	Detected	2.298	Detected	2.364	0.087	GT	Sens	contig424	contig424	Unannota	CAAATAGTCGATGTGCATTATTTCTGCAATGCACTTCTTTTTTATGATG	contig424	Solyc08g	Vacuolar	GO:0004	SL2.40ch	AT3G57630.2		exostosi	chr3:213	2.03401	5.38294	15.7473	16.3598	19.0086	17.3027

GT	Sense	Sense	-0.548	Detected	0.548	Detected	0.000	2.212	Detected	1.970	Detected	2.091	0.065	GT	Sens	contig815	contig815	Phototro	GCCGTA	contig815	Solvc02g	Solvc02g	Phototro	GO:00094	GO:00094	contig815	Solvc02g	Phototro	GO:00055	SL2.40ch	AT5G67385.1		protein b	chr5:268	1110.34	2232.39	3421.75	2205.53	7778.16	6556.56
GT	Sense	Sense	0.425	Detected	-0.425	Comprom	0.000	1.301	Detected	0.893	Detected	1.097	0.145	GT	Sens	contig823	contig823	Calmodul	ACATTG	contig823	Solvc10g	Solvc10g	Calmodulin binding protein (Al			contig823	Solvc10g	Calmodulin binding		SL2.40ch	AT3G522	IOD3	IOD3 (IO-	chr3:193	16.3794	8.54918	24.2237	17.9236	31.0882	23.3692
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	1.318	Detected	1.170	Detected	1.244	0.004	GT	Sens	contig827	contig827	Unknown	CAGTTT	contig827	Solvc05g	Solvc05g	Unknown Protein (AHRD V1)			contig827	Solvc05g	Unknown Protein (A		SL2.40ch	AT5G49680.2		cell expa	chr5:201	19.034	17.2809	20.1883	21.7569	48.2171	43.3739
GT	Sense	Sense	0.089	Comprom	-0.089	Comprom	0.000	1.818	Detected	1.729	Detected	1.774	0.003	GT	Sens	contig829	contig829	Ankyrin r	GTTCAT	contig829	Solvc06g	Solvc06g	Ankyrin r	GO:00055	GO:00055	contig829	Solvc06g	Ankyrin r	GO:00055	SL2.40ch	AT4G346	SOS1. ER	SOS1 (S(	chr4:165	6.47514	5.38546	18.6357	19.3507	22.2064	20.8105
GT	Sense	Sense	-1.273	Comprom	1.273	Detected	0.000	3.754	Detected	3.392	Detected	3.573	0.109	GT	Sens	contig835	contig835	Telomere	TTTCCA	contig835	Solvc11g	Solvc11g	Telomere	GO:00036	GO:00036	contig835	Solvc11g	Telomere	GO:00036	SL2.40ch	AT5G037	TRFL10	TRFL10 (	chr5:999	4.11796	22.6425	18.1126	27.5755	138.88	107.807
GT	Sense	Sense	-0.329	Detected	0.329	Detected	0.000	1.949	Detected	1.881	Detected	1.915	0.029	GT	Sens	contig835	contig835	Unknown	GAATAT	contig835	Solvc01g	Solvc01g	Unknown Protein (AHRD V1)			contig835	Solvc01g	Unknown Protein (A		SL2.40ch	AT3G09950.1		unknowr	chr3:306	1318.57	1957.54	6960.75	4057.78	6613.9	6291.75
GT	Sense	Sense	-0.133	Detected	0.133	Detected	0.000	1.540	Detected	1.136	Detected	1.338	0.031	GT	Sens	contig839	contig839	Strictosid	GATGAT	contig839	Solvc05g	Solvc05g	Strictosid	GO:00040	GO:00040	contig839	Solvc05g	Strictosid	GO:00040	SL2.40ch	AT5G49960.1		binding /	chr5:203	1367.14	1546.02	3468.55	2046.59	4508.4	3397.67
GT	Sense	Sense	-0.053	Detected	0.053	Detected	0.000	1.582	Detected	0.963	Detected	1.272	0.056	GT	Sens	contig843	contig843	Pentatric	GGGTCT	contig843	Solvc03g	Solvc03g	Pentatricopeptide repeat-conta			contig843	Solvc03g	Pentatricopeptide re		SL2.40ch	AT3G48250.1		pentatric	chr3:178	144.477	146.271	404.094	175.562	463.991	301.27
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	1.660	Detected	1.198	Detected	1.429	0.033	GT	Sens	contig844	contig844	Ribonucl	GTCGAT	contig844	Solvc07g	Solvc07g	Ribonucl	GO:00045	GO:00045	contig844	Solvc07g	Ribonucl	GO:00055	SL2.40ch	AT2G260	AtGLDP2	AtGLDP2	chr2:111	700.395	790.362	1513.33	1300.88	2506.78	1814.49
GT	Sense	Sense	-0.218	Comprom	0.218	Comprom	0.000	1.172	Detected	1.257	Detected	1.215	0.032	GT	Sens	contig849	contig849	Sigma fac	CCAAAA	contig849	Solvc03g	Solvc03g	Sigma factor (AHRD V1 *-*- O9			contig849	Solvc03g	Sigma factor (AHRD		SL2.40ch	AT3G61300.1				6.46626	8.23617	4.03625	16.1999	17.5407	18.5417
GT	Sense	Sense	0.527	Detected	-0.527	Comprom	0.000	1.131	Detected	1.334	Detected	1.232	0.149	GT	Sens	contig851	contig851	Unknown	CCAAAT	contig851	Solvc04g	Solvc04g	Unknown Protein (AHRD V1)			contig851	Solvc04g	Unknown Protein (A		SL2.40ch	AT2G433	ATGPX3	ATGPX3	chr2:180	19.7552	8.95265	20.0384	36.6553	31.061	35.6358
GT	Sense	Sense	-0.191	Detected	0.191	Detected	0.000	1.956	Detected	1.413	Detected	1.685	0.037	GT	Sens	contig851	contig851	LRR rece	ACGTAT	contig851	Solvc04g	Solvc04g	LRR rece	GO:00055	GO:00055	contig851	Solvc04g	Receptor	GO:00046	SL2.40ch	AT5G49660.1		leucine-r	chr5:201	1524.78	1868.57	5024.35	2897.38	6985.96	4780.26
GT	Sense	Sense	-0.138	Detected	0.138	Detected	0.000	1.780	Detected	1.442	Detected	1.611	0.018	GT	Sens	contig853	contig853	Zinc finge	GCATCT	contig853	Solvc03g	Solvc03g	Zinc finge	GO:00056	GO:00056	contig853	Solvc03g	Zinc finge	GO:00056	SL2.40ch	AT3G576	NTT	NTT (NO	chr3:213	79.6073	90.6631	251.617	126.532	311.226	245.384
GT	Sense	Sense	-0.140	Comprom	0.140	Comprom	0.000	2.548	Detected	1.806	Detected	2.177	0.032	GT	Sens	contig856	contig856	BURP do	AGTCCA	contig856	Solvc01g	Solvc01g	BURP domain-containing prot			contig856	Solvc01g	BURP domain-conta		SL2.40ch	AT3G59780.1		FUNCTIO	chr3:220	3.36474	3.84203	6.58754	6.78281	22.4154	13.371
GT	Sense	Sense	-0.142	Comprom	0.142	Comprom	0.000	1.139	Detected	1.279	Detected	1.209	0.017	GT	Sens	contig857	contig857	Unknown	GAACCA	contig857	Solvc04g	Solvc04g	Unknown	GO:00055	GO:00055	contig857	Solvc08g	Lysine-sp	GO:00056	SL2.40ch	AT5G47790.1		forkhead	chr5:193	5.77639	6.61941	6.09822	3.22555	14.5174	15.9571
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	1.395	Detected	1.021	Detected	1.208	0.024	GT	Sens	contig857	contig857	Ammoniu	TTGGAA	contig857	Solvc03g	Solvc03g	Ammoniu	GO:00153	GO:00153	contig857	Solvc03g	Ammoniu	GO:00153	SL2.40ch	AT3G243	AMT1:3. /	AMT1:3 (	chr3:880	1079.2	977.478	3783.39	1848.51	2879.46	2216
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	1.075	Detected	0.929	Detected	1.002	0.015	GT	Sens	contig862	contig862	Cysteine-	TTAGTT	contig862	Solvc03g	Solvc03g	Cysteine-rich receptor-like pro			contig862	Solvc08g	Protein s	GO:00163	SL2.40ch	AT4G38950.2				81.8757	66.8815	141.766	114.529	166.249	149.824
GT	Sense	Sense	-0.144	Detected	0.144	Detected	0.000	1.636	Detected	1.385	Detected	1.510	0.016	GT	Sens	contig863	contig863	Ring H2 fi	GGATAT	contig863	Solvc11g	Solvc11g	Ring H2 fi	GO:00082	GO:00082	contig863	Solvc11g	Ring H2 fi	GO:00082	SL2.40ch	AT5G155	LNG1	LNG1 (LO	chr5:506	140.68	161.665	413.25	219.038	499.671	418.822
GT	Sense	Sense	-0.220	Detected	0.220	Detected	0.000	2.115	Detected	1.357	Detected	1.736	0.058	GT	Sens	contig869	contig869	Dof zinc f	CCAAAG	contig869	Solvc06g	Solvc06g	Dof zinc f	GO:0045449		contig869	Solvc06g	Dof zinc f	GO:00454	SL2.40ch	AT5G62940.1		Dof-type	chr5:252	174.347	222.398	363.9	370.989	909.735	536.248
GT	Sense	Sense	-0.210	Detected	0.210	Detected	0.000	1.445	Detected	1.161	Detected	1.303	0.036	GT	Sens	contig869	contig869	Chloroph	TTCTAT	contig869	Solvc06g	Solvc06g	Chloroph	GO:00160	GO:00160	contig869	Solvc06g	Chloroph	GO:00160	SL2.40ch	AT4G103	LHCB5	LHCB5 (L	chr4:640	4635.96	5839.72	10657.2	7053.02	15109.5	12372.4
GT	Sense	Sense	-0.215	Detected	0.215	Detected	0.000	1.550	Detected	1.369	Detected	1.459	0.025	GT	Sens	contig870	contig870	Unknown	GAAATC	contig870	Solvc10g	Solvc10g	Unknown Protein (AHRD V1)			contig870	Solvc10g	Unknown Protein (A		SL2.40ch	AT2G022	ATPSKR1	PSKR1 (F	chr2:584	119.059	150.883	133.529	131.604	418.385	367.959
GT	Sense	Sense	-0.204	Comprom	0.204	Comprom	0.000	1.208	Detected	1.070	Detected	1.139	0.034	GT	Sens	contig872	contig872	Glucose-	GAAGCG	contig872	Solvc03g	Solvc03g	Glucose-I	GO:00085	GO:00085	contig872	Solvc03g	Glucose-I	GO:00085	SL2.40ch	AT5G548	GPT1	GPT1: ar	chr5:222	9.18018	11.4571	6.18333	10.9955	25.2663	22.8868
GT	Sense	Sense	-0.689	Comprom	0.689	Detected	0.000	0.980	Detected	1.185	Detected	1.082	0.260	GT	Sens	contig877	contig877	S-locus r	GACTCA	contig877	Solvc02g	Solvc02g	S-locus r	GO:0005529		contig877	Solvc02g	S-locus r	GO:00055	SL2.40ch	AT1G613	SD1-29	SD1-29 (S	chr1:226	6.06656	14.8301	24.9332	20.7956	19.9464	22.9329
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	1.733	Detected	2.271	Detected	2.002	0.037	GT	Sens	contig878	contig878	1-aminoc	GCCATT	contig878	Solvc01g	Solvc01g	1-aminoc	GO:00166	GO:00166	contig878	Solvc01g	1-aminoc	GO:00167	SL2.40ch	AT3G21420.1		oxidored	chr3:754	25.4171	15.9687	31.3481	8.73078	71.4193	103.393
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	1.158	Detected	0.853	Detected	1.005	0.027	GT	Sens	contig881	contig881	Cathepsi	TTAAAC	contig881	Solvc01g	Solvc01g	Cathepsi	GO:00065	GO:00065	contig881	Solvc01g	Aspartic	GO:00041	SL2.40ch	AT1G11910.1		aspartyl	chr1:401	22235.4	23105.2	27611.4	20289.4	53919.4	43517.6
GT	Sense	Sense	0.396	Comprom	-0.396	Comprom	0.000	1.693	Detected	1.238	Detected	1.466	0.085	GT	Sens	contig884	contig884	Unknown	GAAGCA	contig884	Solvc06g	Solvc06g	Unknown Protein (AHRD V1)%			contig884	Solvc06g	Unknown Protein (A		SL2.40ch	AT5G25840.1		unknowr	chr5:901	8.80665	4.78443	18.2017	1.9078	22.3774	16.2818
GT	Sense	Sense	-0.275	Detected	0.275	Detected	0.000	0.978	Detected	1.076	Detected	1.027	0.067	GT	Sens	contig887	contig887	Chitinase	AGCAAG	contig887	Solvc11g	Solvc11g	Chitinase	GO:00059	GO:00059	contig887	Solvc11g	Chitinase	GO:00059	SL2.40ch	AT5G25840.1		unknowr	chr5:901	347.675	478.826	729.125	770.255	857.273	914.754
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	1.224	Detected	0.881	Detected	1.052	0.026	GT	Sens	contig890	contig890	LRR rece	TAGATG	contig890	Solvc01g	Solvc01g	LRR rece	GO:00046	GO:00046	contig890	Solvc01g	Receptor	GO:00428	SL2.40ch	AT5G49760.1		leucine-r	chr5:202	1132.72	1023.65	2332.39	1592.24	2681.46	2108.85
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	1.132	Detected	0.995	Detected	1.063	0.004	GT	Sens	contig901	contig901	Gamma-g	TTCAAA	contig901	Solvc05g	Solvc05g	Gamma-g	GO:00167	GO:00167	contig901	Solvc05g	Gamma-g	GO:00167	SL2.40ch	AT4G396	GGT1	GGT1 (G	chr4:184	212.235	201.801	380.741	349.334	483.507	438.577
GT	Sense	Sense	-0.477	Detected	0.477	Detected	0.000	1.772	Detected	1.360	Detected	1.566	0.095	GT	Sens	contig902	contig902	cDNA clo	GAAAGA	contig902	Solvc11g	Solvc11g	cDNA clone J033118E13 full in			contig902	Solvc11g	cDNA clone J03311		SL2.40ch	AT3G52900.1		unknowr	chr3:196	28.0423	51.1469	81.8828	54.6594	137.909	103.34
GT	Sense	Sense	-0.170	Detected	0.170	Detected	0.000	1.695	Detected	1.440	Detected	1.568	0.018	GT	Sens	contig904	contig904	Unknown	CGTTGT	contig904	Solvc03g	Solvc03g	Unknown Protein (AHRD V1)			contig904	Solvc03g	Unknown Protein (A		SL2.40ch	AT5G41420.1		unknowr	chr5:165	21.1445	25.1854	50.9988	36.2967	79.6683	66.5764
GT	Sense	Sense	-0.301	Detected	0.301	Detected	0.000	1.092	Detected	1.086	Detected	1.089	0.068	GT	Sens	contig905	contig905	DNA (Cyt	AACCTC	contig905	Solvc04g	Solvc04g	DNA (Cyt	GO:00063	GO:00063	contig905	Solvc04g	DNA (Cyt	GO:00038	SL2.40ch	AT5G441	CRA1. AT	CRA1 (CF	chr5:177	618.509	882.794	1242.2	1076.66	1679.71	1667.29
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	2.601	Detected	2.168	Detected	2.385	0.015	GT	Sens	contig908	contig908	Zinc ion b	AATATC	contig908	Solvc04g	Solvc04g	Zinc ion binding protein (AHRD			contig908	Solvc04g	Zinc ion binding pro		SL2.40ch	AT5G44005.1		unknowr	chr5:177	210.019	148.721	631.76	347.385	1143.78	844.277
GT	Sense	Sense	0.264	Detected	-0.264	Detected	0.000	2.546	Detected	1.091	Detected	1.819	0.143	GT	Sens	contig910	contig910	Unknown	ACTTTC	contig910	Solvc05g	Solvc05g	Unknown Protein (AHRD V1)			contig910	Solvc08g	Pectinace	GO:00040	SL2.40ch	AT1G26976.1				283.294	184.819	661.195	536.051	1425.39	518.174
GT	Sense	Sense	-0.103	Comprom	0.103	Comprom	0.000	2.890	Detected	2.646	Detected	2.768	0.003	GT	Sens	contig910	contig910	RING fing	CTCCGC	contig910	Solvc12g	Solvc12g	RING fing	GO:00082	GO:00082	contig910	Solvc12g	RING fing	GO:00082	SL2.40ch	AT4G26580.1		protein b	chr4:134	2.01502	2.18666	12.9529	4.63217	16.5881	13.9738
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	0.992	Detected	1.559	Detected	1.275	0.046	GT	Sens	contig914	contig914	Dirigent-l	TTCTGT	contig914	Solvc02g	Solvc02g	Dirigent-like protein 1 (AHRD V			contig914	Solvc02g	Dirigent-like protein		SL2.40ch	AT3G10810.1		zinc fing	chr3:338	2339.45	2156.46	3937.87	2548.26	4762.3	7035.68
GT	Sense	Sense	0.253	Detected	-0.253	Detected	0.000	1.304	Detected	1.047	Detected	1.175	0.054	GT	Sens	contig918	contig918	NAD(P)H-	TTTGTA	contig918	Solvc03g	Solvc03g	NAD(P)H-	GO:00551	GO:00551	contig918	Solvc01g	NAD(P)H-	GO:00551	SL2.40ch	ATCG012	NDHB.2	NADH de	chrC:141	20.0289	13.2745	37.9096	26.4768	42.929	35.8215
GT	Sense	Sense	-0.137	Detected	0.137	Detected	0.000	1.423	Detected	1.007	Detected	1.215	0.040	GT	Sens	contig918	contig918	Unknown	ACAGTC	contig918	Solvc07g	Solvc07g	Unknown Protein (AHRD V1)			contig918	Solvc07g	Unknown Protein (A		SL2.40ch	AT3G543	emb1967	emb1967	chr3:201	30.0794	34.2413	47.6032	46.8882	91.7425	68.5714
GT	Sense	Sense	-0.186	Detected	0.186	Detected	0.000	2.663	Detected	1.337	Detected	2.000	0.101	GT	Sens	contig919	contig919	SCAREC	AATGGA	contig919	Solvc10g	Solvc10g	SCARECROW (AHRD V1 *--- O5			contig919	Solvc10g	SCARECROW (AHRD		SL2.40ch	AT3G542	SCR. SGF	SCR (SC	chr3:200	14.5696	17.7388	31.1818	15.81	108.605	43.1847
GT	Sense	Sense	-0.538	Detected	0.538	Detected	0.000	1.859	Detected	1.542	Detected	1.701	0.094	GT	Sens	contig919	contig919	Allantoina	TAGTAT	contig919	Solvc02g	Solvc02g	Allantoina	GO:00041	GO:00041	contig919	Solvc02g	Allantoina	GO:00040	SL2.40ch	AT4G049	ATALN	ATALN (A	chr4:252	7055.93	13999.2	27558.6	19043.6	38444.2	30773.5
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	1.142	Detected	1.089	Detected	1.115	0.002	GT	Sens	contig920	contig920	UPF0497	CATTGC	contig920	Solvc09g	Solvc09g	UPF0497	GO:00055	GO:00055	contig920	Solvc09g	UPF0497	GO:00055	SL2.40ch	AT1G080	ATACA5.	ACA5 (AL	chr1:251	233.777	207.518	481.786	329.795	518.351	498.083
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	1.370	Detected	0.802	Detected	1.086	0.064	GT	Sens	contig920	contig920	Genomic	GCGCGA	contig920	Solvc09g	Solvc09g	Genomic DNA chromosome 5			contig920	Solvc09g	Genomic DNA chror		SL2.40ch	AT5G43750.1		unknowr	chr5:175	609.805	529.816	1855.17	862.632	1566.61	1054
GT	Sense	Sense	-0.566	Comprom	0.566	Comprom	0.000	1.630	Detected	1.293	Detected	1.461	0.132	GT	Sens	contig921	contig921	Calmodul	AACTTA	contig921	Solvc03g	Solvc03g	Calmodul	GO:00055	GO:00055	contig921	Solvc03g	Calmodul	GO:00055	SL2.40ch	AT1G726	igd8	igd8 (IO-(	chr1:273	3.79706	7.82996	10.9575	14.3215	18.0007	14.2014
GT	Sense	Sense	0.306	Comprom	-0.306	Comprom	0.000	1.302	Detected	1.446	Detected	1.374	0.048	GT	Sens	contig924	contig924	Unknown	AGAGGG	contig924	Solvc11g	Solvc11g	Unknown Protein (AHRD V1)			contig924	Solvc11g	Unknown Protein (A		SL2.40ch	ATMG00540.1				6.45757	3.97677	9.39997	8.97436	13.3251	14.6789
GT	Sense	Sense	0.056	Comprom	-0.056	Comprom	0.000	2.589	Detected	2.420	Detected	2.504	0.002	GT	Sens	contig925	contig925	Delta-6 fa	ACACTT	contig925	Solvc05g	Solvc05g	Delta-6 fa	GO:00200	GO:00200	contig925	Solvc05g	Delta-6 fa	GO:00422	SL2.40ch	AT2G46210.1		delta-8 s	chr2:189	2.6358	2.29644	14.7352	4.18729	15.7819	14.0012
GT	Sense	Sense	-0.025	Detected	0.025	Detected	0.000	1.766	Detected	1.108	Detected	1.437	0.049	GT	Sens	contig929	contig929	ABC tran	TGTTTG	contig929	Solvc05g	Solvc05g	ABC tran	GO:00168	GO:00168	contig929	Solvc05g	ABC tran	GO:00171	SL2.40ch	AT1G53270.1		ABC tran	chr1:198	53.8912	52.5169	94.9028	60.8847	192.89	121.903
GT	Sense	Sense	-0.151	Detected	0.151	Detected	0.000	1.609	Detected	1.591	Detected	1.600	0.009	GT	Sens	contig933	contig933	Compone	CAATCT	contig933	Solvc03g	Solvc03g	Component of high affinity nitr			contig933	Solvc03g	Component of high		SL2.40ch	AT1G581	AtRLP9	AtRLP9 (	chr1:215	15.4481	17.9231	33.2248	38.6948	54.1297	53.3092
GT	Sense	Sense	-0.121	Comprom	0.121	Comprom	0.000	1.113	Detected	0.931	Detected	1.022	0.021	GT	Sens	contig936	contig936	Unknown	CCTGCC	contig936	Solvc07g	Solvc07g	Unknown Protein (AHRD V1)			contig936	Solvc07g	Unknown Protein (A		SL2.40ch	AT4G28230.1		unknowr	chr4:139	6.66158	7.4122	5.74891	5.9946	16.2095	14.2419
GT	Sense	Sense	-0.181	Comprom	0.181	Detected	0.000	2.072	Detected	1.017	Detected	1.545	0.109	GT	Sens	contig936	contig936	Cytochro	GATCAA	contig936	Solvc06g	Solvc06g	Cytochro	GO:00198	GO:00198	contig936	Solvc06g	cytochrol	GO:00198	SL2.40ch	AT3G483	CYP71A2	CYP71A2	chr3:178	9.57155	11.5733	12.6673	6.39034	47.1855	22.6508
GT	Sense	Sense	0.263	Comprom	-0.263	Comprom	0.000	3.851	Detected	2.677	Detected	3.264	0.037	GT	Sens	contig938	contig938	Unknown	GTAATG	contig938	Solvc07g	Solvc07g	Unknown Protein (AHRD V1)			contig938	Solvc07g	Unknown Protein (A		SL2.40ch	AT5G38600.1		proline-r	chr5:154	3.65076	2.38442	5.17548	3.97735	45.4086	20.0642
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	1.038	Detected	0.974	Detected	1.006	0.018	GT	Sens	contig941	contig941	GDSL est	AACATA	contig941	Solvc04g	Solvc04g	GDSL est	GO:00040	GO:00040	contig941	Solvc04g	GDSL est	GO:00040	SL2.40ch	AT1G539	GLIP5	GLIP5: c	chr1:201	311.639	352.991	789.564	561.766	726.204	692.64
GT	Sense	Sense	0.541	Detected	-0.541	Detected	0.000	1.832	Detected	1.156	Detected	1.494	0.144	GT	Sens	contig944	contig944	Aldose 1-	GAAAGT	contig944	Solvc03g	Solvc03g	Aldose 1-	GO:00059	GO:00059	contig944	Solvc03g	Aldose 1-	GO:00059	SL2.40ch	AT4G216	CPL1. FR	CPL1 (C-	chr4:115	111.677	49.6468	328.876	127.524	282.709	176.421
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	1.118	Detected	1.327	Detected	1.222	0.008	GT	Sens	contig945	contig945	Cytokinin	TGGAGG	contig945	Solvc01g	Solvc01g	Cytokinin	GO:00191	GO:00191	contig945	Solvc01g	Cytokinin	GO:00191	SL2.40ch	AT3G634	ATCKX6.	CKX6 (C	chr3:234	4711.42	4707.25	8386.7	8664.8	10901.7	12557.9
GT	Sense	Sense	-0.266	Detected	0.266	Detected	0.000	1.374	Detected	0.816	Detected	1.095	0.105	GT	Sens	contig947	contig947	Heat stre	GCATCC	contig947	Solvc04g	Solvc04g	Heat stre	GO:00056	GO:00056	contig947	Solvc04g	Heat stre	GO:00036	SL2.40ch	AT1G462	AT-HSFB	AT-HSFB	chr1:172	20.7365	28.2113	31.5317	18.85	66.8298	45.2813
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	0.965	Detected	1.102	Detected	1.034	0.029	GT	Sens	contig947	contig947	BTB/POZ	CGTGAG	contig947	Solvc07g	Solvc07g	BTB/POZ	GO:00055	GO:00055	contig947	Solvc07g	BTB/POZ	GO:00055	SL2.40ch	AT1G55760.1		BTB/POZ	chr1:208	947.049	1120.1	1470.78	1407.41	2143.68	2350.88
GT	Sense	Sense	-0.051	Detected	0.051	Detected	0.000	1.614	Detected	0.996	Detected	1.305	0.053	GT	Sens	contig95	contig95	Choline d	GGAGGG	contig95	Solvc08g	Solvc08g	Choline d	GO:00506	GO:00506	contig95	Solvc08g	Choline d	GO:00166	SL2.40ch	AT5G51930.1		glucose-	chr5:211	169.841	171.614	422.168	326.112	557.263	361.977
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	2.437	Detected	2.025	Detected	2.231	0.035	GT	Sens	contig951	contig951	Unknown	CCTCGT	contig951	Solvc03g	Solvc03g	Unknown Protein (AHRD V1)			contig951	Solvc03g	Unknown Protein (A		SL2.40ch	AT3G14280.1		unknowr	chr3:476	42.3251	67.1184	115.433	63.5094	307.723	230.568
GT	Sense	Sense	-0.093	Detected	0.093	Detected	0.000	1.725	Detected	1.123	Detected	1.424	0.046	GT	Sens	contig954	contig954	Zinc finge	GCCAAG	contig954	Solvc07g	Solvc07g	Zinc finger family protein (AHR			contig954	Solvc03g	E3 ubiqui	GO:00055	SL2.40ch	AT2G02960.3		zinc fing	chr2:862	567.724	607.883	621.803	646.179	2071.29	1360.2
GT	Sense	Sense	-0.077	Detected	0.077	Detected	0.000	1.313	Detected	0.878	Detected	1.095	0.042	GT	Sens	contig955	contig955	Unknown	TAGCTG	contig955	Solvc10g	Solvc10g	Unknown Protein (AHRD V1)%			contig955	Solvc12g	Yippee family protei		SL2.40ch	AT5G622	MAP65-9	MAP65-9	chr5:250	30.4144	31.8249	59.4418	47.2529	82.4437	60.7727
GT	Sense	Sense	0.219	Detected	-0.219	Detected	0.000	1.289	Detected	0.951	Detected	1.120	0.056	GT	Sens	contig958	contig958	Receptor	CAAGTA	contig958	Solvc01g	Solvc01g	Receptor	GO:00055	GO:00055	contig958	Solvc01g	Receptor	GO:00046	SL2.40ch	AT4G202	BAM3	BAM3 (B	chr4:109	436.572	303.239	637.556	694.933	947.841	747.723
GT	Sense	Sense	-0.315	Detected	0.315	Detected	0.000	1.470	Detected	0.944	Detected	1.207	0.099	GT	Sens	contig958	contig958	Unknown	ATTGAG	contig958	Solvc11g	Solvc11g	Unknown	GO:00065	GO:00065	contig958	Solvc11g	Unknown	GO:00065	SL2.40ch	AT1G35340.1		ATP-dep	chr1:129	78.9533	115.01	208.242	99.849	281.582	194.898
GT	Sense	Sense	-0.199	Detected	0.199	Detected	0.000	1.951	Detected	1.502	Detected	1.726	0.029	GT	Sens	contig961	contig961	Non-spec	AAAGCG	contig961	Solvc08g	Solvc08g	Non-spec	GO:00068	GO:00068	contig961	Solvc08g	Non-spec	GO:00055	SL2.40ch	AT5G57710.1		heat sho	chr5:233	14.6055	18.105	79.3726	53.9688	67.035	48.9562
GT	Sense	Sense	1.107	Detected	-1.107	Comprom	0.000	0.877	Detected	1.289	Detected	1.083	0.438	GT	Sens	contig964	contig964	Pentatric	TAATGG	contig964	Solvc01g	Solvc01g	Pentatric	GO:00045	GO:00045	contig964	Solvc01g	Pentatric	GO:00045	SL2.40ch	AT3G29230.1		pentatric	chr3:111	11.7005	2.37274	2.8862	10.9227	10.3221	13.6928
GT	Sense	Sense	-0.388	Detected	0.388	Detected	0.000	5.815	Detected	3.803	Detected	4.809	0.047	GT	Sens	contig967	contig967	Gibberell	TTTCAT	contig967	Solvc03g	Solvc03g	Gibberell	GO:00167	GO:00167	contig967	Solvc03g	Gibberelli	GO:00167	SL2.40ch	AT4G216	ATGA3OX	GA3OX3	chr4:115	12.6172	20.3294	84.8942	21.733	961.765	237.613
GT	Sense	Sense	0.284	Detected	-0.284	Detected	0.000	2.061	Detected	1.012	Detected	1.536	0.123	GT	Sens	contig968	contig968	Flotillin 1	ATGTTG	contig968	Solvc03g	Solvc03g	Flotillin 1 (AHRD V1 *-*- B3V5K			contig968	Solvc03g	Flotillin 1 (AHRD V1		SL2.40ch	AT5G64870.1		FUNCTIO	chr5:259	450.444	285.868	498.102	418.804	1596.28	769.524
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	1.708	Detected	1.830	Detected	1.769	0.006	GT	Sens	contig969	contig969	ATP-depe	ATTATG	contig969	Solvc01g	Solvc01g	ATP-depe	GO:00056	GO:00056	contig969	Solvc01g	ATP-depe	GO:00056	SL2.40ch	AT5G178	CSA1	CSA1 (cc	chr5:590	15.2852	12.0378	49.5554	33.4432	47.2464	51.261
GT	Sense	Sense	-0.058	Detected	0.058	Detected	0.000	1.074	Detected	1.055	Detected	1.064	0.003	GT	Sens	contig970	contig970	Ubiquitin	AATATC	contig970	Solvc06g	Solvc06g	Ubiquitin	GO:00313	GO:00313	contig970	Solvc06g	Ubiquitin	GO:00313	SL2.40ch	AT3G622	UBO5	UBO5 (ul	chr3:230	3295.73	3361.56	3548.28	3737.55	7470.67	7353.14
GT	Sense	Sense	-0.084	Detected	0.084	Detected	0.000	1.187	Detected	0.902	Detected	1.045	0.024	GT	Sens	contig971	contig971	Unknown	TAAATG	contig971	Solvc05g	Solvc05g	Unknown Protein (AHRD V1)			contig971	Solvc05g	Unknown Protein (A		SL2.40ch	AT5G38010.1		UDP-gluc	chr5:151	2439.07	2579.71	4838.85	3264.58	6091.23	4985.03
GT	Sense	Sense	-0.082	Detected	0.082	Detected	0.000	1.335	Detected	1.105	Detected	1.220	0.013	GT	Sens	contig974	contig974	Magnesiu	AAATAA	contig974	Solvc04g	Solvc04g	Magnesiu	GO:00171	GO:00171	contig974	Solvc04g	Magnesiu	GO:00171	SL2.40ch	AT1G085	PDE166. (	CHLD: A	chr1:269	131.98	139.216	264.827	142.311	364.733	310.074
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	1.098	Detected	1.090	Detected	1.094	0.004	GT	Sens	contig975	contig975	B3 domai	GGAGGA	contig975	Solvc02g	Solvc02g	B3 domai	GO:00063	GO:00063	contig975	Solvc02g026080.1.1				AT3G44440.1				408.913	347.768	412.214	423.722	860.922	853.553
GT	Sense	Sense	-0.081	Comprom	0.081	Comprom	0.000	1.227	Detected	0.924	Detected	1.075	0.025	GT	Sens	contig980	contig980	Trehalos	ATTTTG	contig980	Solvc10g	Solvc10g	Trehalos	GO:00059	GO:00059	contig980	Solvc10g	Trehalos	GO:00059	SL2.40ch	AT2G21520.2		transpor	chr2:921	7.24114	7.62512	13.4686	13.0907	18.5529	14.9857
GT	Sense	Sense	-0.321	Comprom	0.321	Comprom	0.000	1.732	Detected	1.190	Detected	1.461	0.074	GT	Sens	contig981	contig981	NBS-LRR	AAGGGC	contig981	Solvc05g	Solvc05g	NBS-LRR	GO:00069	GO:00069	contig981	Solvc05g	Cc-nbs-lr	GO:00069	SL2.40ch	AT4G32610.1		unknowr	chr4:157	7.49855	11.0096	12.1297	15.194	32.1919	22.0461
GT	Sense	Sense	-0.098	Detected	0.098	Detected	0.000	1.313	Detected	1.520	Detected	1.416	0.010	GT	Sens	contig982	contig982	Unknown	GAGGAT	contig982	Solvc02g	Solvc02g	Unknown Protein (AHRD V1)			contig982	Solvc02g	Unknown Protein (A		SL2.40ch	AT5G53500.1		WD-40 re	chr5:217	228.831	246.693	617.165	511.182	629.299	724.213
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	1.836	Detected	0.960	Detected	1.398	0.087	GT	Sens	contig982	contig982	Proteinas	ACAAAT	contig982	Solvc11g	Solvc11g	Proteinas	GO:00048	GO:00048	contig982	Solvc11g	Proteinas	GO:00048	SL2.40ch	AT5G223	ATTIP49A	RIN1 (RE	chr5:739	930.024	941.085	3045.66	1719.18	3560.97	1935.59
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	1.541	Detected	1.268	Detected	1.404	0.015	GT	Sens	contig986	contig986	Kinesin-li	AAATCA	contig986	Solvc12g	Solvc12g	Kinesin-like calmodulin bindin			contig986	Solvc12g	Kinesin-like calmod		SL2.40ch	AT1G11420.1		agenet d	chr1:384	207.422	168.797	308.227	310.324	580.527	479.173
GT	Sense	Sense	-0.755	Detected	0.755	Detected	0.000	1.723	Detected	2.111	Detected	1.917	0.133	GT	Sens	contig989	contig989	Multidrug	TATCAG	contig989	Solvc11g	Solvc11g	Multidrug	GO:00160	GO:00160	contig989	Solvc11g	Multidrug	GO:00160	SL2.40ch	AT1G71870.1		MATE eff	chr1:270	24.0017	64.3408	125.103	90.2997	138.376	180.493
GT	Sense	Sense	0.227	Detected	-0.227	Detected	0.000	1.884	Detected	1.159	Detected	1.522	0.071	GT	Sens	contig989	contig989	Equilibrat	ATTCTT	contig989	Solvc07g	Solvc07g	Equilibrat	GO:00101	GO:00101	contig989	Solvc07g	Equilibrat	GO:00101	SL2.40ch	AT1G02630.2		equilibra	chr1:561	94.8893	65.1378	373.641	350.265	309.503	186.674
GT	Sense	Sense	-0.090	Detected	0.090	Detected	0.000	1.156	Detected	0.989	Detected	1.072	0.013	GT	Sens	contig990	contig990	Serine-gl	CTTGCT	contig990	Solvc12g	Solvc12g	Serine-gl	GO:00301	GO:00301	contig990	Solvc12g	Serine-gl	GO:00081	SL2.40ch	AT2G133	AGT. AGT	AGT (AL	chr2:553	18853	20086.7	50391.1	26610.8	46228.8	41064.8
GT	Sense	Sense	-0.246	Detected	0.246	Detected	0.000	1.523	Detected	1.030	Detected	1.277	0.067	GT	Sens	contig991	contig991	Superoxi	TACTCG	contig991	Solvc03g	Solvc03g	Superoxi	GO:00047	GO:00047	contig991	Solvc03g	Superoxi	GO:00047	SL2.40ch	AT5G511	FSD2	FSD2 (FE	chr5:207	519.574	688.041	1303.71	794.084	1832.97	1298.08
GT	Sense	Sense	0.006	Comprom	-0.006	Comprom	0.000	6.334	Detected	5.739	Detected	6.036	0.002	GT	Sens	contig996	contig996	Cullin-like	CGCAAA	contig996	Solvc01g	Solvc01g	Cullin-like	GO:00314	GO:00314	contig996	Solvc01g	Cullin-like	GO:00314	SL2.40ch	AT4G025	ATCUL1.	ATCUL1	chr4:112	3.61372	3.3744	4.21502	2.18835	300.334	198.317
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	1.053	Detected	0.995	Detected	1.024	0.008	GT	Sens	contig996	contig996	O-methyl	TTATTA	contig996	Solvc09g	Solvc09g	O-methyl	GO:00081	GO:00081	contig996	Solvc09g	O-methyl	GO:00081	SL2.40ch	AT5G16520.1		unknowr	chr5:539	427.001	355.497	630.703	591.86	862.054	825.47
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	1.496	Detected	1.390	Detected	1.443	0.001	GT	Sens	contig997	contig997	Zinc finge	AAGTCT	contig997	Solvc08g	Solvc08g	Zinc finge	GO:00056	GO:00056	contig997	Solvc08g	Zinc finge	GO:00056	SL2.40ch	AT3G15680.1		zinc fing	chr3:531	248.228	232.548	493.701	551.759	722.58	669.516
GT	Sense	Sense	0.136	Detected	-0.136	Detected	0.000	1.573	Detected	1.066	Detected	1.319	0.044	GT	Sens	contig999	contig999	Violaxant	CGAAGG	contig999	Solvc04g	Solvc04g	Violaxant	GO:00095	GO:00095	contig999	Solvc04g	Violaxant	GO:00464	SL2.40ch	AT1G085	NPQ1. AV	NPQ1 (N	chr1:270	315.461	245.701	729.907	363.531	883.035	619.717
GT	Sense	Sense	-0.560	Detected	0.560	Detected	0.000	1.494	Detected	1.280	Detected	1.387	0.136	GT	Sens	contig999	contig999	DVL13 (A	CAAAGG	contig999	Solvc06g	Solvc06g	DVL13 (AHRD V1 *-*- O8L7D0			contig999	Solvc06g	DVL13 (AHRD V1 *-*		SL2.40ch	AT5G56380.1		F-box far	chr5:228	80.8801	165.472	307.204	373.198	347.536	298.716
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	1.307	Detected	1.017	Detected	1.162	0.016	GT	Sens	contig999	contig999	Peptide m	TTGGAG	contig999	Solvc02g	Solvc02g	Peptide m	GO:00081	GO:00081	contig999	Solvc02g	Peptide m	GO:00081	SL2.40ch	AT4G35380.1		guanine	chr4:168	8732.6	7844.81	9748.28	9999.03	21841	17812
GT	Sense	Sense	0.394	Comprom	-0.394	Comprom	0.000	1.076	Detected	1.216	Detected	1.146	0.103	GT	Sens	DQ34025	DQ34025	SlARF2	TGAATCTGGTCAAGCAGAATCTTAGGATCACGAATTCTGGATCCGATACGTAACGCGTCT																6.69283	3.64899	2.57363	3.14649	11.1132	12.2018
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	2.489	Detected	2.265	Detected	2.377	0.004	GT	Sens	HM00452	HM00452	ZmARF5	ACAATCATGGTCCATGTTGTGCGAAGTGTTGCCTGTGGTGGTTGTTGTGAAGAACTGAAT																1119.57	917.306	1707.79	1505.88	6066.44	5180.28
GT	Sense	Sense	-0.238	Detected	0.238	Detected	0.000	1.224	Detected	1.511	Detected	1.368	0.039	GT	Sens	X67238	X67238	18S rRNA	ATGTATTCAACGAGCTTATAGCCTTGGCCGACAGGCCCGGGTAATCTTTGAAATTTCATC																28597.1	37435.4	141827	107540	81491.4	99160.7
GT	Sense	Sense	-0.250	Detected	0.250	Detected	0.000	1.160	Detected	1.100	Detected	1.130	0.046	GT	Sens	X67238	X67238	18S rRNA	ATTTAGAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATT																2437.93	3245.53	8154.56	7699.96	6702.69	6412.28
GT	Sense	Sense	-0.282	Detected	0.282	Detected	0.000	1.447	Detected	0.840	Detected	1.143	0.110	GT	Sens	contig100	contig100	Heat shoc	AATGGA	contig100	Solvc05g	Solvc05g	Heat shock protein (AHRD V1 *			contig100	Solvc05g	Heat shock protein (		SL2.40ch	AT5G499	emb1441	emb1441	chr5:203	23.3123	32.4469	48.4053	45.5633	79.9419	52.3444
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	1.196	Detected	0.924	Detected	1.060	0.017	GT	Sens	contig103	contig103	Calcitonii	TTCAAG	contig103	Solvc11g	Solvc11g	Calcitonin peptide-receptor co			contig103	Solvc11g	Calcitonin peptide-r		SL2.40ch	AT4G217	NRPB2. E	NRPB2: I	chr4:115	75.3549	67.3474	97.7163	67.0945	174.08	143.713
GT	Sense	Sense	-0.201	Detected	0.201	Detected	0.000	1.699	Detected	1.635	Detected	1.667	0.015	GT	Sens	contig103	contig103	Unknown	TATATC	contig103	Solvc02g	Solvc02g	Unknown Protein (AHRD V1)			contig103	Solvc02g	Unknown Protein (A		SL2.40ch	AT4G015	ANAC068	NTM1 (N	chr4:670	20.4881	25.4735	24.7734	28.3745	79.0821	75.4453
GT	Sense	Sense	-0.202	Detected	0.202	Detected	0.000	1.904	Detected	1.640	Detected	1.772	0.018	GT	Sens	contig103	contig103	Unknown	GCAAAA	contig103	Solvc02g	Solvc02g	Unknown Protein (AHRD V1)			contig103	Solvc02g	Unknown Protein (A		SL2.40ch	AT4G015	ANAC068	NTM1 (N	chr4:670	74.025	92.1495	97.9637	99.8669	329.503	273.748
GT	Sense	Sense	0.144	Detected	-0.144	Detected	0.000	1.313	Detected	1.003	Detected	1.158	0.032	GT	Sens	contig101	contig101	Glutathio	CCTAGA	contig101	Solvc09g	Solvc09g	Glutathio	GO:00043	GO:00043	contig101	Solvc09g	Glutathio	GO:00043	SL2.40ch	AT1G783	ATGSTU2	ATGSTU	chr1:294	3643.92	2808.45	4099.32	6031.93	8477.67	6816.51
GT	Sense	Sense	0.706	Detected	-0.706	Comprom	0.000	1.298	Detected	1.318	Detected	1.308	0.205	GT	Sens	contig101	contig101	Protein F	AGATAA	contig101	Solvc02g	Solvc02g	Protein FAR1-RELATED SEQU			contig101	Solvc02g092170.1.1				AT5G189	FRS12	FRS12 (F	chr5:633	14.4926	5.12369	27.0195	18.7239	22.5969	22.8373
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	1.302	Detected	0.992	Detected	1.147	0.019	GT	Sens	contig101	contig101	Unknown	GTTCCC	contig101	Solvc06g	Solvc06g	Unknown Protein (AHRD V1)			contig101	Solvc06g	Unknown Protein (A		SL2.40ch	AT3G076	IBM1	IBM1 (inc	chr3:242	31.3632	27.8013	93.5242	66.6512	77.6272	62.4224
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	1.967	Detected	1.708	Detected	1.837	0.005	GT	Sens	contig102	contig102	MYB tran	AATATT	contig102	Solvc02g	Solvc02g	MYB tran	GO:0045449		contig102	Solvc02g	MYB tran	GO:00036	SL2.40ch	AT5G403	MYB24. A	MYB24 (	chr5:161	184.541	172.666	118.084	125.751	744.344	619.904
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	1.399	Detected	1.271	Detected	1.335	0.003	GT	Sens	contig104	contig104	Purine pe	TATAAA	contig104	Solvc12g	Solvc12g	Purine pe	GO:00160	GO:00160	contig104	Solvc12g	Purine pe	GO:00160	SL2.40ch	AT1G15120.2		ubiquino	chr1:520	2243.44	2175.33	7109.31	5505.11	6210.79	5670.1
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	1.423	Detected	1.687	Detected	1.555	0.007	GT	Sens	contig104	contig104	Unknown	TACGAT	contig104	Solvc08g	Solvc08g	Unknown Protein (AHRD V1)			contig104	Solvc08g	Unknown Protein (A		SL2.40ch	AT5G14610.1		ATP bind	chr5:471	35.2675	32.0165	54.4357	25.1187	96.1094	115.035
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	2.030	Detected	1.972	Detected	2.001	0.003	GT	Sens	contig104	contig104	MYB tran	ATGTCA	contig104	Solvc08g	Solvc08g	MYB tran	GO:0045449		contig104	Solvc04g	SMP-30/Gluconolac		SL2.40ch	AT5G44690.1		unknowr	chr5:180	2502.15	2058.31	4938.04	5732.09	9884.63	9465.72
GT	Sense	Sense	-0.280	Detected	0.280	Detected	0.000	1.660	Detected	1.303	Detected	1.482	0.047	GT	Sens	contig105	contig105	Serine/th	ACAAGG	contig105	Solvc09g	Solvc09g	Serine/threonine-protein phos			contig105	Solvc10g	Serine/threonine-pr		SL2.40ch	AT3G43710.1				564.868	784.022	2082.52	1312.38	2242.95	1745.94
GT	Sense	Sense	0.631	Comprom	-0.631	Comprom	0.000	1.878	Detected	1.954	Detected	1.916	0.094	GT	Sens	contig106	contig106	Sulfotran	TTACAG	contig106	Solvc04g	Solvc04g	Sulfotran	GO:00081	GO:00081	contig106	Solvc04g	Sulfotran	GO:00081	SL2.40ch	AT1G59680.1				9.85422	3.86535	6.69966	1.9213	24.1837	25.419
GT	Sense	Sense	-0.339	Detected	0.339	Detected	0.000	2.864	Detected	2.666	Detected	2.765	0.016	GT	Sens	contig106	contig106	Wound in	TAGAAG	contig106	Solvc07g	Solvc07g	Wound induced protein (AHRD			contig106	Solvc07g	Wound induced pro		SL2.40ch	AT4G10270.1		wound-r	chr4:637	199.997	300.961	1399.4	694.548	1904.66	1655.55
GT	Sense	Sense	-0.223	Detected	0.223	Detected	0.000	0.908	Detected	1.327	Detected	1.118	0.067	GT	Sens	contig106	contig106	ATP-bind	TGCCCA	contig106	Solvc08g	Solvc08g	ATP-bind	GO:00168	GO:00168	contig106	Solvc08g	ATP-bind	GO:00426	SL2.40ch	AT2G299	PDR3. AT	PDR3 (PL	chr2:127	76.3466	97.8836	85.1779	164.846	173.037	230.642
GT	Sense	Sense	0.233	Detected	-0.233	Detected	0.000	1.937	Detected	1.178	Detected	1.557	0.073	GT	Sens	contig107	contig107	Unknown	AACATC	contig107	Solvc04g	Solvc04g	Unknown Protein (AHRD V1)			contig107	Solvc04g	Unknown Protein (A		SL2.40ch	AT4G20160.1		LOCATE	chr4:108	121.274	82.5976	271.017	138.657	408.538	240.714
GT	Sense	Sense	-0.138	Detected	0.138	Detected	0.000	1.264	Detected	0.872	Detected	1.068	0.047	GT	Sens	contig107	contig107	Catalase	AGATGA	contig107	Solvc01g	Solvc01g	Catalase	GO:00551	GO:00551	contig107	Solvc01g	Catalase	GO:00551	SL2.40ch	AT1G206	CAT1	CAT1 (C/	chr1:714	1223.68	1393.21	1984.07	1004	3344.48	2540.84
GT	Sense	Sense	0.343	Detected	-0.343	Detected	0.000	1.083	Detected	1.284	Detected	1.183	0.080	GT	Sens	contig108	contig108	Unknown	GAATCA	contig108	Solvc09g	Solvc09g	Unknown Protein (AHRD V1)			contig108	Solvc09g014920.1.1				ATCG011	YCF1.2	hypothet	chrC:123	35.2706	20.6391	39.7354	65.1177	60.9499	69.8366
GT	Sense	Sense	1.057	Comprom	-1.057	Comprom	0.000	1.507	Detected	1.406	Detected	1.456	0.302	GT	Sens	contig108	contig108	Ulp1 prot	CAACTG	contig108	Solvc09g	Solvc09g	Ulp1 prot	GO:00065	GO:00065	contig108	Solvc09g	Ulp1 prot	GO:00065	SL2.40ch	AT2G28970.1		leucine-r	chr2:124	10.2903	2.23816	13.5187	7.90773	14.541	13.5247
GT	Sense	Sense	0.273	Detected	-0.273	Detected	0.000	2.161	Detected	1.854	Detected	2.007	0.024	GT	Sens	contig109	contig109	Nodulin-li	TTTTGT	contig109	Solvc01g	Solvc01g	Nodulin-li	GO:00160	GO:00160	contig109	Solvc01g	Nodulin-li	GO:00160	SL2.40ch	AT1G44800.1		nodulin M	chr1:169	225.604	145.306	627.577	413.118	863.229	695.87
GT	Sense	Sense	0.119	Comprom	-0.119	Comprom	0.000	2.544	Detected	2.430	Detected	2.487	0.003	GT	Sens	contig110	contig110	Cytochro	GTGATA	contig110	Solvc03g	Solvc03g	Cytochro	GO:00198	GO:00198	contig110	Solvc03g111990.2.1				AT4G133	CYP71A2	CYP71A2	chr4:775	3.37164	2.68867	8.95905	5.38833	18.7227	17.2561
GT	Sense	Sense	0.088	Comprom	-0.088	Comprom	0.000	1.642	Detected	1.933	Detected	1.787	0.009	GT	Sens	contig111	contig111	Transpos	CCGAAG	contig111	Solvc09g	Solvc09g	Transpos	GO:00150	GO:00150	contig111	Solvc01g	Gag-Pol p	GO:00082	SL2.40ch	AT4G24610.1		unknowr	chr4:127	4.05583	3.37794	1.94299	3.20875	12.3161	15.0222
GT	Sense	Sense	0.134	Comprom	-0.134	Comprom	0.000	1.262	Detected	1.180	Detected	1.221	0.013	GT	Sens	contig111	contig111	SKP1-like	AGGCGA	contig111	Solvc10g	Solvc10g	SKP1-like	GO:00065	GO:00065	contig111	Solvc10g	SKP1-like	GO:00055	SL2.40ch	AT5G55970.2		zinc fing	chr5:226	8.79641	6.87458	9.1464	13.3583	19.8925	18.7315
GT	Sense	Sense	0.054	Detected	-0.054	Detected	0.000	1.234	Detected	1.021	Detected	1.128	0.011	GT	Sens	contig116	contig116	Polyprote	CTCAAA	contig116	Solvc03g	Solvc03g	Polyprotein (AHRD V1 ***- A5J			contig116	Solvc03g	Polyprotein (AHRD V		SL2.40ch	AT5G381	PMI15	PMI15 (p	chr5:152	18.5783	16.2245	30.2493	40.5276	43.5582	37.4568
GT	Sense	Sense	1.105	Detected	-1.105	Comprom	0.000	1.715	Detected	1.941	Detected	1.828	0.242	GT	Sens	contig116	contig116	Mutator-li	CGCTGA	contig116	Solvc09g	Solvc09g	Mutator-li	GO:00082	GO:00082	contig116	Solvc08g	Mutator-li	GO:00082	SL2.40ch	AT2G35880.1		FUNCTIO	chr2:150	10.907	2.21787	15.2133	18.4439	17.2238	20.0794
GT	Sense	Sense	0.347	Detected	-0.347	Detected	0.000	1.017	Detected	1.149	Detected	1.083	0.092	GT	Sens	contig116	contig116	MuDR fan	AAAGAG	contig116	Solvc01g	Solvc01g	MuDR family transposase con			contig116	Solvc08g	MuDR family transp		SL2.40ch	AT5G656	bHLH093	bHLH093	chr5:262	33.6793	19.6001	46.751	60.7464	55.4602	60.5833
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	1.219	Detected	1.160	Detected	1.189	0.002	GT	Sens	contig118	contig118	Chloroph	TCTGCC	contig118	Solvc02g	Solvc02g	Chloroph	GO:00055	GO:00055	contig118	Solvc02g	Chloroph	GO:00055	SL2.40ch	AT1G299	CAB1. AB	CAB1 (CI	chr1:104	289.376	291.184	568.163	349.494	720.669	689.501
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	1.034	Detected	1.036	Detected	1.035	0.006	GT	Sens	contig118	contig118	Chloroph	AAATTT	contig118	Solvc02g	Solvc02g	Chloroph	GO:00055	GO:00055	contig118	Solvc02g	Chloroph	GO:00055	SL2.40ch	AT1G299	CAB3. AB	CAB3 (CI	chr1:104	746.394	782.336	1480.31	836.602	1669.17	1665.49
GT	Sense	Sense	-0.044	Detected	0.044	Detected	0.000	1.100	Detected	0.907	Detected	1.004	0.011	GT	Sens	contig119	contig119	Receptor	CATGGC	contig119	Solvc04g	Solvc04g	Receptor expression-enhancii			contig119	Solvc04g	Receptor expressio		SL2.40ch	AT5G507	ATHVA22	ATHVA22	chr5:206	28.5667	28.5683	40.3853	39.3898	65.2928	56.9702
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	1.940	Detected	1.816	Detected	1.878	0.003	GT	Sens	contig119	contig119	1-aminoc	TTTGAA	contig119	Solvc09g	Solvc09g	1-aminocyclopropane-1-carbo			contig119	Solvc09g089700.2.1				AT3G61400.1		2-oxoglu	chr3:227	29.8389	25.376	183.315	81.2749	112.608	103.011
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	2.129	Detected	1.375	Detected	1.752	0.048	GT	Sens	contig119	contig119	Leucine-r	CAAAAT	contig119	Solvc01g	Solvc01g	Leucine-r	GO:00055	GO:00055	contig119	Solvc01g	LRR rece	GO:00163	SL2.40ch	AT3G053	AtRLP31	AtRLP31	chr3:153	19.481	21.9157	20.2718	7.99592	96.3506	56.9707
GT	Sense	Sense	0.637	Detected	-0.637	Comprom	0.000	2.757	Detected	2.701	Detected	2.729	0.050	GT	Sens	contig120	contig120	Cytochro	GTGATT	contig120	Solvc04g	Solvc04g	Cytochro	GO:00198	GO:00198	contig120	Solvc04g	Cytochro	GO:00198	SL2.40ch	AT5G19640.1		proton-d	chr5:663	27.556	10.7238	25.0037	20.7663	123.944	118.828
GT	Sense	Sense	-0.684	Comprom	0.684	Comprom	0.000	2.606	Detected	1.868	Detected	2.237	0.103	GT	Sens	contig120	contig120	COBRA-li	ACTATT	contig120	Solvc02g	Solvc02g	COBRA-like protein (AHRD V1			contig120	Solvc02g	COBRA-like protein		SL2.40ch	AT5G156	COBL4. II	IRX6	chr5:508	2.35595	5.72374	2.12949	5.02596	23.835	14.2532
GT	Sense	Sense	-0.086	Comprom	0.086	Comprom	0.000	2.003	Detected	1.079	Detected	1.541	0.082	GT	Sens	contig122	contig122	Disease r	GATCGT	contig122	Solvc04g	Solvc04g	Disease r	GO:00055	GO:00055	contig122	Solvc04g	Cc-nbs-lr	GO:00055	SL2.40ch	AT4G153	CYP705A	CYP705A	chr4:876	4.67407	4.95703	4.82184	8.91021	20.5759	10.8125
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	1.275	Detected	0.842	Detected	1.059	0.056	GT	Sens	contig123	contig123	Aquapori	AATTCT	contig123	Solvc10g	Solvc10g	Aquapori	GO:00160	GO:00160	contig123	Solvc10g	Aquapori	GO:00152	SL2.40ch	AT2G168	PIP3B. PI	PIP2:8 (P	chr2:730	167.94	129.199	462.849	261.38	380.142	280.809
GT	Sense	Sense	-0.058	Detected	0.058	Detected	0.000	1.173	Detected	1.231	Detected	1.202	0.003	GT	Sens	contig124	contig124	Solute ca	CTTTTG	contig124	Solvc12g	Solvc12g	Solute ca	GO:00160	GO:00160	contig124	Solvc12g	Solute ca	GO:00160	SL2.40ch	AT2G02020.1		proton-d	chr2:479	670.46	683.23	1114.99	884.605	1627.71	1688.79
GT	Sense	Sense	0.374	Detected	-0.374	Detected	0.000	1.436	Detected	2.030	Detected	1.733	0.068	GT	Sens	contig125	contig125	F-box fan	TGGTGC	contig125	Solvc08g	Solvc08g	F-box family protein (AHRD V1			contig125	Solvc08g015890.1.1				AT3G47150.1		F-box far	chr3:173	52.1963	29.2576	330.205	396.983	112.77	169.697
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	1.851	Detected	1.123	Detected	1.487	0.065	GT	Sens	contig129	contig129	Fructose-	TACCTT	contig129	Solvc10g	Solvc10g	Fructose-	GO:00060	GO:00060	contig129	Solvc10g	Fructose-	GO:00428	SL2.40ch	AT2G01140.1		fructose-	chr2:950	605.83	456.024	1782.91	731.432	2021.72	1217.3
GT	Sense	Sense	0.194	Detected	-0.194	Detected	0.000	3.849	Detected	3.122	Detected	3.485	0.014	GT	Sens	contig129	contig129	Unknown	GTGAAA	contig129	Solvc03g	Solvc03g	Unknown Protein (AHRD V1)			contig129	Solvc08g061470.1.1				AT3G45040.1		phospha	chr3:164	352.931	253.665	1267.87	776.165	4598.53	2768.85
GT	Sense	Sense	0.154	Comprom	-0.154	Comprom	0.000	1.071	Detected	1.097	Detected	1.084	0.020	GT	Sens	contig129	contig129	Serine/th	TTGCGA	contig129	Solvc06g	Solvc06g	Serine/threonine-protein phos			contig129	Solvc10g	Serine/threonine-pr		SL2.40ch	AT1G019	ARK2	armadillo	chr1:325	7.66339	5.82441	11.878	23.881	14.9662	15.1984
GT	Sense	Sense	0.269	Comprom	-0.269	Comprom	0.000	3.678	Detected	2.300	Detected	2.989	0.056	GT	Sens	contig130	contig130	Cysteine	GGAATC	contig130	Solvc04g	Solvc04g	Cysteine synthase (AHRD V1 *			contig130	Solvc04g	Cysteine synthase (		SL2.40ch	AT5G37050.1		FUNCTIO	chr5:146	3.25201	2.10751	5.69301	2.82483	35.7257	13.7088
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	1.207	Detected	1.068	Detected	1.137	0.004	GT	Sens	contig131	contig131	Unknown	GTGTTT	contig131	Solvc02g	Solvc02g	Unknown Protein (AHRD V1)			contig131	Solvc02g	Unknown Protein (A		SL2.40ch	AT5G195	MSL9	MSL9 (M	chr5:658	1376.49	1346.27	3388.45	2357.13	3351.95	3033.54
GT	Sense	Sense	0.261	Detected	-0.261	Comprom	0.000	1.055	Detected	1.852	Detected	1.454	0.093	GT	Sens	contig132	contig132	F-box fan	TATAGT	contig132	Solvc08g	Solvc08g	F-box fan	GO:00048	GO:00048	contig132	Solvc12g	Pistil exte	GO:00096	SL2.40ch	AT5G130	ATGSL12	ATGSL12	chr5:411	14.1463	9.27295	23.7102	12.4191	25.3849	43.9545
GT	Sense	Sense	0.365	Detected	-0.365	Detected	0.000	0.983	Detected	1.381	Detected	1.182	0.105	GT	Sens	contig134	contig134	Ycf2 (AHF	GATACT	contig134	Solvc01g	Solvc01g	Ycf2 (AHRD V1 ***- D2SXY2_9M			contig134	Solvc01g	Ycf2 (AHF	GO:00055	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:145	69.0015	39.1443	106.461	112.741	109.529	143.962
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	1.832	Detected	1.562	Detected	1.697	0.006	GT	Sens	contig135	contig135	Aldehyde	AAACAG	contig135	Solvc11g	Solvc11g	Aldehyde	GO:00551	GO:00551	contig135	Solvc11g	Aldehyde	GO:00551	SL2.40ch	AT3G436	AAO2	AAO2 (Al	chr3:155	137.972	133.798	167.781	147.104	515.762	426.509
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	2.519	Detected	2.155	Detected	2.337	0.007	GT	Sens	contig136	contig136	Unknown	TGCAAA	contig136	Solvc11g	Solvc11g	Unknown Protein (AHRD V1)			contig136	Solvc11g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	438.618	368.64	886.579	1011.85	2458.1	1903.56
GT	Sense	Sense	0.584	Detected	-0.584	Detected	0.000	2.824	Detected	1.181	Detected	2.003	0.185	GT	Sens	contig136	contig136	Unknown	TAAGTC	contig136	Solvc04g	Solvc04g	Unknown Protein (AHRD V1)			contig136	Solvc06g	Unknown Protein (A		SL2.40ch	AT5G229	ATCHX3.	ATCHX3:	chr5:765	27.23	11.3958	20.9735	39.4386	133.046	42.4585
GT	Sense	Sense	0.120	Detected	-0.120	Comprom	0.000	1.542	Detected	1.251	Detected	1.396	0.018	GT	Sens	contig138	contig138	Unknown	ATGTTG	contig138	Solvc10g	Solvc10g	Unknown Protein (AHRD V1)			contig138	Solvc10g	Unknown Protein (A		SL2.40ch	AT5G666	DAR3	DAR3 (D/	chr5:265	12.7815	10.1861	45.9812	63.1803	35.431	28.8693
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	0.945	Detected	1.074	Detected	1.009	0.014	GT	Sens	contig138	contig138	Unknown	ATAGTG	contig138	Solvc12g	Solvc12g	Unknown Protein (AHRD V1)			contig138	Solvc12g	Unknown Protein (A		SL2.40ch	AT2G36080.1		DNA-bind	chr2:151	202.512	165.934	206.426	266.07	376.294	410.356
GT	Sense	Sense	-0.286	Comprom	0.286	Comprom	0.000	1.939	Detected	1.442	Detected	1.691	0.047	GT	Sens	contig139	contig139	Unknown	CTTCGT	contig139	Solvc07g	Solvc07g	Unknown Protein (AHRD V1)			contig139	Solvc09g	Transpos	GO:00063	SL2.40ch	AT5G08490.1		pentatric	chr5:274	3.9085	5.46791	12.1728	16.7262	18.9008	13.3564
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	2.004	Detected	1.658	Detected	1.831	0.009	GT	Sens	contig140	contig140	Methyl ja	GGCCCA	contig140	Solvc03g	Solvc03g	Methyl jasmonate esterase (AH			contig140	Solvc03g	Methyl ja	GO:00800	SL2.40ch	AT4G32350.1		unknowr	chr4:156	56.7501	54.5348	69.1994	86.5963	238.015	186.643
GT	Sense	Sense	-0.783	Comprom	0.783	Comprom	0.000	2.119	Detected	1.932	Detected	2.025	0.124	GT	Sens	contig140	contig140	Unknown	AATGAT	contig140	Solvc09g	Solvc09g	Unknown Protein (AHRD V1)			contig140	Solvc09g	Unknown Protein (A		SL2.40ch	AT2G25270.1		unknowr	chr2:107	2.05974	5.73461	4.52672	6.18664	15.9181	13.9405
GT	Sense	Sense	0.773	Detected	-0.773	Detected	0.000	2.327	Detected	1.491	Detected	1.909	0.162	GT	Sens	contig140	contig140	Proteinas	GTCATC	contig140	Solvc09g	Solvc09g	Proteinas	GO:00096	GO:00096	contig140	Solvc09g	Proteinas	GO:00096	SL2.40ch	AT5G553	EDM2	EDM2: tr	chr5:224	4746.16	1530.37	4583.69	970.528	14423	8051.45
GT	Sense	Sense	-0.178	Detected	0.178	Detected	0.000	1.465	Detected	1.276	Detected	1.370	0.021	GT	Sens	contig140	contig140	Chloroph	TTCTTC	contig140	Solvc01g	Solvc01g	Chloroph	GO:00161	GO:00161	contig140	Solvc01g	Chloroph	GO:00161	SL2.40ch	AT1G158	LHCB6. C	LHCB6 (L	chr1:544	7656.26	9218.82	19990.1	13845.9	24736.9	21624
GT	Sense	Sense	0.227	Detected	-0.227	Detected	0.000	0.920	Detected	1.972	Detected	1.446	0.128	GT	Sens	contig141	contig141	Hydrolas	GCAAAA	contig141	Solvc01g	Solvc01g	Hydrolase alpha/beta fold fami			contig141	Solvc01g	Hydrolase alpha/bet		SL2.40ch	AT2G356	MOR1. GI	MOR1 (M	chr2:149	25.6925	17.6602	21.2279	31.8463	42.9857	88.858
GT	Sense	Sense	-0.124	Detected	0.124	Detected	0.000	0.908	Detected	1.298	Detected	1.103	0.041	GT	Sens	contig141	contig141	Type 2 m	ACGTTT	contig141	Solvc04g	Solvc04g	Type 2 m	GO:00055	GO:00055	contig141	Solvc04g	Type 2 m	GO:00055	SL2.40ch	AT3G093	MT2A. AT	MT2A (M	chr3:288	49.2801	55.0468	117.734	163.318	104.247	136.178
GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	1.392	Detected	1.289	Detected	1.341	0.016	GT	Sens	contig141	contig141	Aldehyde	CTGATG	contig141	Solvc01g	Solvc01g	Aldehyde	GO:00551	GO:00551	contig141	Solvc01g	Aldehyde	GO:00551	SL2.40ch	AT4G362	ALDH3F1	ALDH3F1	chr4:171	43.2761	51.043	65.6569	56.7488	131.565	122.099
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	1.837	Detected	1.914	Detected	1.876	0.004	GT	Sens	contig142	contig142	Plant vira	GGAACT	contig142	Solvc04g	Solvc04g	Plant viral-response family pro			contig142	Solvc04g	Plant viral-response		SL2.40ch	AT1G55230.1		unknowr	chr1:206	16.6723	18.2018	25.6797	15.6366	66.3835	69.7879
GT	Sense	Sense	-1.044	Comprom	1.044	Detected	0.000	2.082	Detected	1.114	Detected	1.598	0.299	GT	Sens	contig143	contig143	Ferric red	CTGGTG	contig143	Solvc01g	Solvc01g	Ferric red	GO:00160	GO:00160	contig143	Solvc01g	Ferric red	GO:00002	SL2.40ch	AT5G497	ATFRO7.	ATFRO7	chr5:202	5.74735	22.9937	16.4668	14.8563	51.8921	26.4591
GT	Sense	Sense	0.277	Detected	-0.277	Detected	0.000	1.213	Detected	0.813	Detected	1.013	0.097	GT	Sens	contig144	contig144	Cytochro	CCTGGA	contig144	Solvc09g	Solvc09g	Cytochro	GO:00198	GO:00198	contig144	Solvc09g	Cytochro	GO:00198	SL2.40ch	AT3G533	CYP71B3	CYP71B3	chr3:197	438.615	281.077	699.22	448.158	868.17	655.803
GT	Sense	Sense	-0.126	Detected	0.126	Detected	0.000	1.255	Detected	1.433	Detected	1.344	0.013	GT	Sens	contig144	contig144	Naringen	GGTATT	contig144	Solvc04g	Solvc04g	Naringen	GO:00164	GO:00164	contig144	Solvc09g	1-aminoc	GO:00098	SL2.40ch	AT3G52140.1		tetratrico	chr3:193	128.108	143.642	394.156	264.335	345.29	389.488
GT	Sense	Sense	-0.569	Detected	0.569	Detected	0.000	3.024	Detected	1.191	Detected	2.107	0.190	GT	Sens	contig146	contig146	Chalcone	CTGGTG	contig146	Solvc05g	Solvc05g	Chalcone	GO:00081	GO:00081	contig146	Solvc05g	Chalcone	GO:00084	SL2.40ch	AT5G139	CHS. TT4	TT4 (TRA	chr5:448	1276.46	2642.05	2668.31	3120.74	15924	4458.87
GT	Sense	Sense	0.579	Detected	-0.579	Detected	0.000	1.956	Detected	0.847	Detected	1.401	0.223	GT	Sens	contig146	contig146	Lipoxyge	ATATAT	contig146	Solvc01g	Solvc01g	Lipoxyge	GO:00161	GO:00161	contig146	Solvc01g	Lipoxyge	GO:00055	SL2.40ch	AT3G451	LOX2. AT	LOX2 (LI	chr3:165	3863.54	1628.34	2205.27	1077.86	10375.8	4797.41
GT	Sense	Sense	0.283	Detected	-0.283	Detected	0.000	1.252	Detected	1.114	Detected	1.183	0.056	GT	Sens	contig148	contig148	Unknown	ATTGAG	contig148	Solvc01g	Solvc01g	Unknown Protein (AHRD V1)%			contig148	Solvc01g	Unknown Protein (A		SL2.40ch	AT4G21600.1				18.1625	11.5412	17.7699	28.0252	36.7794	33.3098
GT	Sense	Sense	-0.192	Detected	0.192	Detected	0.000	1.729	Detected	0.902	Detected	1.315	0.102	GT	Sens	contig149	contig149	Ycf2 (AHF	CTACTA	contig149	Solvc12g	Solvc12g	Ycf2 (AHF	GO:00095	GO:00095	contig149	Solvc12g	Ycf2 (AHF	GO:00095	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:145	33.5023	41.1266	74.2802	59.247	131.236	73.7341
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	1.259	Detected	0.881	Detected	1.070	0.051	GT	Sens	contig149	contig149	MuDR far	GAAGTA	contig149	Solvc08g	Solvc08g	MuDR family transposase con			contig149	Solvc10g	Mutator-li	GO:00082	SL2.40ch	AT2G46360.1		unknowr	chr2:190	24.4328	18.2306	24.8369	26.8254	53.8824	41.3344
GT	Sense	Sense	-0.135	Detected	0.135	Detected	0.000	2.655	Detected	2.085	Detected	2.370	0.017	GT	Sens	contig151	contig151	Photosys	GGCCTA	contig151	Solvc12g	Solvc12g	Photosys	GO:00095	GO:00095	contig151	Solvc12g	Photosys	GO:00095	SL2.40ch	AT1G522	PSAH2. P	PSAH2 (F	chr1:194	75.9841	86.1773	432.258	153.79	543.675	364.909
GT	Sense	Sense	0.067	Comprom	-0.067	Comprom	0.000	1.297	Detected	1.447	Detected	1.372	0.005	GT	Sens	contig154	contig154	Mutator-li	GTTACA	contig154	Solvc11g	Solvc11g	Mutator-li	GO:00082	GO:00082	contig154	Solvc11g	Mutator-li	GO:00082	SL2.40ch	AT5G024	PLL2	PLL2: ca	chr5:513	7.04374	6.04385	21.3382	18.0238	17.0968	18.9153
GT	Sense	Sense	0.390	Detected	-0.390	Detected	0.000	1.268	Detected	1.213	Detected	1.241	0.087	GT	Sens	contig154	contig154	CBL-inter	CCTGCA	contig154	Solvc06g	Solvc06g	CBL-inter	GO:00046	GO:00046	contig154	Solvc06g	CBL-inter	GO:00046	SL2.40ch	AT5G583	CIPK10. F	SIP1 (SO	chr5:235	123.752	67.8334	43.3783	102.262	235.356	225.85
GT	Sense	Sense	-0.337	Detected	0.337	Detected	0.000	1.673	Detected	1.024	Detected	1.349	0.102	GT	Sens	contig157	contig157	Heat shoc	AGTGGT	contig157	Solvc04g	Solvc04g	Heat shock cognate protein 2 (			contig157	Solvc04g	Heat shock cognate		SL2.40ch	AT3G32030.1				4662.43	7003.76	5883.08	7354.44	19432.5	12355.4
GT	Sense	Sense	-0.456	Detected	0.456	Detected	0.000	1.975	Detected	1.459	Detected	1.717	0.082	GT	Sens	contig157	contig157	Acyl-CoA	AGCAAA	contig157	Solvc02g	Solvc02g	Acyl-CoA	GO:00188	GO:00188	contig157	Solvc02g	Acyl-CoA	GO:00188	SL2.40ch	AT1G68270.1		AMP-dep	chr1:255	19.5795	34.656	55.423	62.1812	109.221	76.1484
GT	Sense	Sense	-0.322	Detected	0.322	Detected	0.000	1.151	Detected	1.265	Detected	1.208	0.066	GT	Sens	contig158	contig158	Unknown	TACCAG	contig158	Solvc07g	Solvc07g	Unknown Protein (AHRD V1)			contig158	Solvc06g	Unknown Protein (A		SL2.40ch	AT5G202	PI	PI (PISTI	chr5:682	2625.05	3860.32	14135.2	9530.78	7537.32	8134.07
GT	Sense	Sense	-0.459	Comprom	0.459	Comprom	0.000	2.285	Detected	2.015	Detected	2.150	0.046	GT	Sens	contig158	contig158	Ripening-	TGTAGA	contig158	Solvc03g	Solvc03g	Ripening-related protein 3 (AH			contig158	Solvc03g013300.1.1				AT3G16800.1		protein p	chr3:572	5.78692	10.2945	41.718	75.2628	40.1041	33.1705
GT	Sense	Sense	0.000	Detected	0.000	Detected	0.000	0.956	Detected	1.128	Detected	1.042	0.007	GT	Sens	contig158	contig158	Unknown	GTATCC	contig158	Solvc02g	Solvc02g	Unknown Protein (AHRD V1)			contig158	Solvc09g	Unknown Protein (A		SL2.40ch	AT3G46640.2				47.9781	45.173	62.2004	120.542	96.2925	108.176
GT	Sense	Sense	0.018	Detected	-0.018	Detected	0.000	1.215	Detected	1.350	Detected	1.283	0.003	GT	Sens	contig159	contig159	Unknown	TCTTAA	contig159	Solvc05g	Solvc05g	Unknown Protein (AHRD V1)			contig159	Solvc03g	Threonine endopep		SL2.40ch	AT5G10160.1		beta-hyd	chr5:318	92.0802	84.5461	148.743	126.946	218.434	239.205
GT	Sense	Sense	0.253	Comprom	-0.253	Comprom	0.000	2.342	Detected	2.016	Detected	2.179	0.019	GT	Sens	contig159	contig159	Serine/th	TATAGG	contig159	Solvc00g	Solvc00g	Serine/threonine-protein phos			contig159	Solvc09g	Serine/threonine-pr		SL2.40ch	AT5G04060.1		dehydrat	chr5:109	3.49169	2.31492	5.62432	9.94707	15.3708	12.2248
GT	Sense	Sense	1.295	Detected	-1.295	Comprom	0.000	1.485	Detected	1.302	Detected	1.394	0.395	GT	Sens	contig160	contig160	Unknown	GGCCAA	contig160	Solvc03g	Solvc03g	Unknown Protein (AHRD V1)			contig160	Solvc03g	Unknown Protein (A		SL2.40ch	AT4G19570.1		DNAJ he	chr4:106	14.8347	2.31943	9.82078	10.9094	17.5152	15.3728
GT	Sense	Sense	-0.041	Detected	0.041	Detected	0.000	1.107	Detected	0.936	Detected	1.021	0.009	GT	Sens	contig160	contig160	Susceptil	GAAAAA	contig160	Solvc01g	Solvc01g	Susceptil	GO:00055	GO:00055	contig160	Solvc01g	Susceptil	GO:00055	SL2.40ch	AT5G49600.1		unknowr	chr5:201	396.011	394.519	427.134	408.497	907.663	803.808
GT	Sense	Sense	-0.005	Detected	0.005	Detected	0.000	0.806	Detected	1.634	Detected	1.220	0.098	GT	Sens	contig164	contig164	ARID/BRI	CAGCTG	contig164	Solvc12g	Solvc12g	ARID/BRIGHT DNA binding dor			contig164	Solvc12g	ARID/BRIGHT DNA b		SL2.40ch	AT5G22570.1				77.6276	73.5272	50.5654	83.2953	140.873	249.379
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	1.630	Detected	1.550	Detected	1.590	0.010	GT	Sens	contig164	contig164	Transcrip	TCAGAT	contig164	Solvc06g	Solvc06g	Transcription factor homolog			contig164	Solvc07g	Nascent	GO:00510	SL2.40ch	AT5G25500.1		unknowr	chr5:888	196.863	149.142	192.434	149.008	565.731	533.311
GT	Sense	Sense	-0.260	Detected	0.260	Detected	0.000	1.407	Detected	1.113	Detected	1.260	0.052	GT	Sens	contig165	contig165	LRR rece	ACATTG	contig165	Solvc06g	Solvc06g	LRR rece	GO:00046	GO:00046	contig165	Solvc06g	Receptor	GO:00055	SL2.40ch	AT1G19390.1		wall-ass	chr1:670	18.5873	25.0874	12.9846	11.1549	61.0838	49.6566
GT	Sense	Sense	-1.147	Comprom	1.147	Comprom	0.000	1.739	Detected	1.456	Detected	1.598	0.301	GT	Sens	contig165	contig165	F-box pro	GTCATC	contig165	Solvc10g	Solvc10g	F-box protein interaction doma			contig165	Solvc11g	23S rRNA	GO:00063	SL2.40ch	AT5G22100.1		RNA cycl	chr5:732	2.02267	9.32816	9.4112	5.56909	15.4649	12.6712
GT	Sense	Sense	-0.428	Detected	0.428	Detected	0.000	2.172	Detected	1.243	Detected	1.708	0.114	GT	Sens	contig166	contig166	Glutared	AAGGCA	contig166	Solvc01g	Solvc01g	Glutared	GO:00454	GO:00454	contig166	Solvc01g	Glutared	GO:00454	SL2.40ch	AT5G140	ROXY2	ROXY2:	chr5:454	14.1232	24.0666	28.0492	22.2018	88.6085	46.4073
GT	Sense	Sense	-0.127	Detected	0.127	Detected	0.000	1.473	Detected	0.945	Detected	1.209	0.054	GT	Sens	contig166	contig166	Cytochro	GGCAAT	contig166	Solvc09g	Solvc09g	Cytochro	GO:00198	GO:00198	contig166	Solvc11g	Cytochro	GO:00198	SL2.40ch	AT3G533	CYP71B3	CYP71B3	chr3:197	42.8417	48.0643	76.4764	46.1235	134.327	92.8805
GT	Sense	Sense	-0.228	Detected	0.228	Detected	0.000	1.710	Detected	1.473	Detected	1.592	0.025	GT	Sens	contig166	contig166	Subtilisin	ACGAAA	contig166	Solvc08g	Solvc08g	Subtilisin	GO:00042	GO:00042	contig166	Solvc08g	Subtilisin	GO:00042	SL2.40ch	AT2G05920.1		subtilase	chr2:226	100.564	129.743	243.963	112.535	398.561	337.237
GT	Sense	Sense	0.109	Detected	-0.109	Detected	0.000	1.347	Detected	0.969	Detected	1.158	0.034	GT	Sens	contig167	contig167	Receptor	TAGCGG	contig167	Solvc04g	Solvc04g	Receptor	GO:00064	GO:00064	contig167	Solvc04g	Receptor	GO:00064	SL2.40ch	AT2G43700.1		lectin pro	chr2:181	21.6489	17.5165	34.2092	32.8646	52.8407	40.5271
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	1.053	Detected	0.965	Detected	1.009	0.003	GT	Sens	contig168	contig168	Glutathio	CAAGAG	contig168	Solvc09g	Solvc09g	Glutathio	GO:00043	GO:00043	contig168	Solvc09g	Glutathio	GO:00043	SL2.40ch	AT1G699	ATGSTU1	ATGSTU	chr1:263	12651.5	11428.1	14580.6	19824.2	26608.4	24960.2
GT	Sense	Sense	0.847	Detected	-0.847	Detected	0.000	3.433	Detected	2.397	Detected	2.915	0.099	GT	Sens	contig168	contig168	Proteinas	GGTGTT	contig168	Solvc09g	Solvc09g	Proteinas	GO:00096	GO:00096	contig168	Solvc09g	Proteinas	GO:00096	SL2.40ch	AT5G553	EDM2	EDM2: tr	chr5:224	6209.69	1806.18	8174.47	1720.03	38570.1	18749.2
GT	Sense	Sense	0.100	Comprom	-0.100	Comprom	0.000	1.165	Detected	1.121	Detected	1.143	0.008	GT	Sens	contig169	contig169	Ulp1 prot	AAATGA	contig169	Solvc01g	Solvc01g	Ulp1 protease family C-termina			contig169	Solvc12g	Ulp1 protease family		SL2.40ch	AT3G445	FAR8	FAR8 (FA	chr3:161	10.2695	8.40948	12.2209	15.2255	22.2272	21.4969
GT	Sense	Sense	-0.719	Comprom	0.719	Comprom	0.000	7.189	Detected	9.572	Detected	8.380	0.026	GT	Sens	contig170	contig170	Gag poly	CTGCAT	contig170	Solvc00g	Solvc00g	Gag poly	GO:00082	GO:00082	contig170	Solvc11g	Kinase fa	GO:00064	SL2.40ch	AT5G286	WRKY74.	WRKY74	chr5:106	2.35957	6.01793	6.68857	7.22831	586.238	3049.41
GT	Sense	Sense	0.065	Comprom	-0.065	Comprom	0.000	4.430	Detected	2.496	Detected	3.463	0.070	GT	Sens	contig171	contig171	Acetylorn	TCAGGG	contig171	Solvc08g	Solvc08g	Acetylorn	GO:00081	GO:00081	contig171	Solvc08g	Acetylorn	GO:00167	SL2.40ch	AT4G17830.1		peptidas	chr4:991	8.0772	6.94224	10.4113	1.90245	172.083	44.9036
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	1.246	Detected	1.144	Detected	1.195	0.003	GT	Sens	contig171	contig171	Ulp1 prot	TGCAAC	contig171	Solvc12g	Solvc12g	Ulp1 prot	GO:00065	GO:00065	contig171	Solvc09g	Ulp1 protease family		SL2.40ch	AT4G345	FAE1. KC	KCS18: a	chr4:164	39.477	38.9988	36.599	45.9062	99.255	92.211
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	1.755	Detected	1.461	Detected	1.608	0.009	GT	Sens	contig171	contig171	Ulp1 prot	CTCATA	contig171	Solvc05g	Solvc05g	Ulp1 protease family C-termina			contig171	Solvc11g	Ulp1 protease family		SL2.40ch	AT5G28740.1		transcrip	chr5:107	2373.37	2110.15	4050.19	4469.63	8057.01	6549.48
GT	Sense	Sense	-0.308	Detected	0.308	Detected	0.000	2.044	Detected	2.060	Detected	2.052	0.022	GT	Sens	contig172	contig172	Wound in	CCAAGA	contig172	Solvc07g	Solvc07g	Wound induced protein (AHRD			contig172	Solvc07g	Wound induced pro		SL2.40ch	AT4G10270.1		wound-r	chr4:637	53.8362	77.644	329.903	163.746	284.28	286.602
GT	Sense	Sense	-0.071	Detected	0.071	Detected	0.000	1.269	Detected	0.869	Detected	1.069	0.037	GT	Sens	contig173	contig173	Fructose-	ATCTTA	contig173	Solvc02g	Solvc02g	Fructose-	GO:00060	GO:00060	contig173	Solvc02g	Fructose-	GO:00055	SL2.40ch	AT4G38970.1		fructose-	chr4:181	5951.3	6176.25	13478	7294.53	15578.9	11776
GT	Sense	Sense	0.284	Comprom	-0.284	Comprom	0.000	1.061	Detected	1.197	Detected	1.129	0.061	GT	Sens	contig173	contig173	Glutared	TTTACG	contig173	Solvc04g	Solvc04g	Glutared	GO:00454	GO:00454	contig173	Solvc04g	Glutared	GO:00087	SL2.40ch	AT2G017	ATMAP70	ATMAP7	chr2:328	8.12159	5.15295	16.222	5.11152	14.3896	15.7726
GT	Sense	Sense	-0.002	Detected	0.002	Detected	0.000	1.545	Detected	1.068	Detected	1.306	0.032	GT	Sens	contig174	contig174	Plant syn	ATCGGT	contig174	Solvc10g	Solvc10g	Plant synaptotagmin (AHRD V1			contig174	Solvc10g052520.1.1				AT3G610	NTMC2T	NTMC2T	chr3:225	56.6727	53.4496	55.9793	49.4995	171.232	122.684
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	2.226	Detected	1.805	Detected	2.015	0.015	GT	Sens	contig174	contig174	Photosys	AGTGTC	contig174	Solvc06g	Solvc06g	Photosys	GO:00095	GO:00095	contig174	Solvc06g	Photosys	GO:00095	SL2.40ch	AT1G522	PSAH2. P	PSAH2 (F	chr1:194	60.8886	68.9796	285.336	98.8129	323.248	240.777
GT	Sense	Sense	-0.477	Comprom	0.477	Comprom	0.000	2.446	Detected	2.167	Detected	2.307	0.043	GT	Sens	contig174	contig174	Ulp1 prot	AGGGTG	contig174	Solvc10g	Solvc10g	Ulp1 protease family C-termina			contig174	Solvc02g	Ulp1 protease family		SL2.40ch	AT2G03630.1				2.31871	4.22782	8.01903	8.1678	18.1921	14.9526
GT	Sense	Sense	-0.261	Detected	0.261	Detected	0.000	2.022	Detected	0.867	Detected	1.444	0.150	GT	Sens	contig175	contig175	Multidrug	ACGAAT	contig175	Solvc12g	Solvc12g	Multidrug resistance protein A			contig175	Solvc12g	Multidrug	GO:00171	SL2.40ch	AT3G212	ATMRP6.	ATMRP6	chr3:745	21.8373	29.501	71.8888	38.2163	109.893	49.2092
GT	Sense	Sense	-0.050	Detected	0.050	Detected	0.000	1.974	Detected	1.324	Detected	1.649	0.037	GT	Sens	contig175	contig175	FAM65A	AGGTGG	contig175	Solvc05g	Solvc05g	FAM65A protein related (AHRD			contig175	Solvc05g	FAM65A protein rela		SL2.40ch	AT2G18380.1		transcrip	chr2:798	14.6415	14.7747	89.1058	63.0551	61.5964	39.1597
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	1.540	Detected	1.065	Detected	1.303	0.033	GT	Sens	contig176	contig176	S-phase k	AGACAT	contig176	Solvc10g	Solvc10g	S-phase k	GO:00065	GO:00065	contig176	Solvc10g	S-phase k	GO:00055	SL2.40ch	AT1G759	SKP1. AS	SKP1 (S	chr1:285	93.2442	93.0741	112.339	89.2405	288.926	207.235
GT	Sense	Sense	0.153	Comprom	-0.153	Comprom	0.000	1.079	Detected	1.206	Detected	1.142	0.020	GT	Sens	contig177	contig177	Ulp1 prot	CACCAA	contig177	Solvc02g	Solvc02g	Ulp1 protease family C-termina			contig177	Solvc02g037560.1.1				#N/A	#N/A	#N/A	#N/A	8.19396	6.23671	14.6703	12.328	16.1053	17.533
GT	Sense	Sense	0.557	Detected	-0.557	Comprom	0.000	3.769	Detected	2.794	Detected	3.282	0.047	GT	Sens	contig177	contig177	Patatin-lik	CCTTTT	contig177	Solvc04g	Solvc04g	Patatin-lik	GO:00081	GO:00081	contig177	Solvc04g	Patatin-lik	GO:00066	SL2.40ch	AT4G03165.1		unknowr	chr4:139	15.6321	6.79562	56.2354	30.5068	149.877	75.9822
GT	Sense	Sense	-0.737	Comprom	0.737	Comprom	0.000	1.901	Detected	1.747	Detected	1.824	0.133	GT	Sens	contig179	contig179	UDP-gluc	CAACGC	contig179	Solvc10g	Solvc10g	UDP-gluc	GO:00800	GO:00800	contig179	Solvc10g	UDP-gluc	GO:00800	SL2.40ch	AT2G36970.1		UDP-gluc	chr2:155	3.99685	10.4489	27.9665	12.5766	25.7421	23.0594
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	1.201	Detected	1.120	Detected	1.161	0.001	GT	Sens	contig180	contig180	BZIP dom	ATTTTG	contig180	Solvc02g	Solvc02g	BZIP dom	GO:00055	GO:00055	contig180	Solvc02g	BZIP dom	GO:00055	SL2.40ch	AT5G67385.1		protein b	chr5:268	36.2259	33.8979	52.3649	36.9445	85.9376	80.9625
GT	Sense	Sense	-0.146	Detected	0.146	Detected	0.000	1.780	Detected	1.308	Detected	1.544	0.031	GT	Sens	contig181	contig181	Proton-de	CCCAAA	contig181	Solvc06g	Solvc06g	Proton-de	GO:00160	GO:00160	contig181	Solvc06g	Proton-de	GO:00160	SL2.40ch	AT5G62680.1		proton-d	chr5:251	36.6297	42.2082	115.088	104.819	143.999	103.476
GT	Sense	Sense	0.268	Detected	-0.268	Detected	0.000	1.088	Detected	1.125	Detected	1.107	0.054	GT	Sens	contig181	contig181	Aldehyde	TGTGGC	contig181	Solvc11g	Solvc11g	Aldehyde	GO:00506	GO:00506	contig181	Solvc11g	Aldehyde	GO:00090	SL2.40ch	AT1G045	AAO4. AT	AAO4 (Al	chr1:125	402.035	260.888	356.66	344.431	734.111	751.207
GT	Sense	Sense	0.244	Detected	-0.244	Detected	0.000	2.591	Detected	1.291	Detected	1.941	0.108	GT	Sens	contig182	contig182	Subtilisin	TCAGTA	contig182	Solvc01g	Solvc01g	Subtilisin	GO:00065	GO:00065	contig182	Solvc01g	Subtilisin	GO:00065	SL2.40ch	AT5G67090.1		subtilase	chr5:267	377.212	252.903	836.341	649.73	1984.37	803.371
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	1.593	Detected	1.253	Detected	1.423	0.014	GT	Sens	contig182	contig182	Ubiquitin	TCTACC	contig182	Solvc10g	Solvc10g	Ubiquitin	GO:00064	GO:00064	contig182	Solvc12g	Ubiquitin-	GO:00064	SL2.40ch	AT2G18600.1		RUB1-co	chr2:807	1065.26	1044.36	1279.99	1229.7	3393.48	2673.4
GT	Sense	Sense	-0.123	Detected	0.123	Detected	0.000	1.805	Detected	1.786	Detected	1.796	0.005	GT	Sens	contig183	contig183	Photosys	CCTAGC	contig183	Solvc01g	Solvc01g	Photosys	GO:00300	GO:00300	contig183	Solvc01g097530.1.1				ATCG000	PSBA	Encodes	chrC:383	437.675	488.234	1023.5	793.27	1723.03	1695.07
GT	Sense	Sense	0.000	Detected	0.000	Detected	0.000	1.497	Detected	1.436	Detected	1.467	0.000	GT	Sens	contig184	contig184	MuDR far	TTTGAC	contig184	Solvc08g	Solvc08g	MuDR family transposase con			contig184	Solvc08g	MuDR family transp		SL2.40ch	AT5G132	SOL2. CR	CRN (CO	chr5:425	27.606	25.9785	51.6159	47.9299	80.6173	77.0461
GT	Sense	Sense	-0.323	Detected	0.323	Detected	0.000	1.594	Detected	1.154	Detected	1.374	0.072	GT	Sens	contig185	contig185	Callose s	GCAGAT	contig185	Solvc01g	Solvc01g	Callose synthase 1 (AHRD V1 *			contig185	Solvc01g	Callose synthase 1		SL2.40ch	AT5G130	ATGSL12	ATGSL12	chr5:411	2413.02	3550.49	5047.85	2983.86	9424.09	6924.09
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	1.221	Detected	1.120	Detected	1.170	0.006	GT	Sens	contig185	contig185	Unknown	GGAGTT	contig185	Solvc01g	Solvc01g	Unknown Protein (AHRD V1)			contig185	Solvc01g	Unknown Protein (A		SL2.40ch	AT3G19200.1		unknowr	chr3:664	88.5307	92.4899	151.468	125.609	224.944	209.07
GT	Sense	Sense	0.090	Comprom	-0.090	Comprom	0.000	3.781	Detected	2.302	Detected	3.042	0.055	GT	Sens	contig186	contig186	MYB tran	GAGTTT	contig186	Solvc05g	Solvc05g	MYB tran	GO:0045449		contig186	Solvc05g	MYB tran	GO:00036	SL2.40ch	AT3G138	MYB26	ATMYB2	chr3:457	5.84115	4.85007	22.3684	12.71	78.0381	27.9069
GT	Sense	Sense	0.107	Detected	-0.107	Detected	0.000	1.936	Detected	1.639	Detected	1.788	0.010	GT	Sens	contig186	contig186	Ulp1 prot	GAGAAA	contig186	Solvc10g	Solvc10g	Ulp1 protease family C-termina			contig186	Solvc11g	Ulp1 protease family		SL2.40ch	AT4G020	PRL. MCN	PRL (PR(	chr4:901	709.465	575.632	1233.16	1326.03	2607.31	2116.43
GT	Sense	Sense	0.224	Detected	-0.224	Detected	0.000	1.720	Detected	1.480	Detected	1.600	0.024	GT	Sens	contig186	contig186	Cytochro	GGTGAA	contig186	Solvc03g	Solvc03g	Cytochro	GO:00198	GO:00198	contig186	Solvc03g	Cytochro	GO:00198	SL2.40ch	AT4G20240.1				127.151	87.6509	265.602	129.568	370.912	312.993
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	1.545	Detected	1.646	Detected	1.596	0.016	GT	Sens	contig186	contig186	Oxidored	ATTAAG	contig186	Solvc01g	Solvc01g	Oxidored	GO:00081	GO:00081	contig186	Solvc01g	Oxidored	GO:00081	SL2.40ch	AT5G16990.1		NADP-de	chr5:558	37.853	27.1602	312.714	202.316	99.7632	106.718
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	2.057	Detected	1.792	Detected	1.924	0.008	GT	Sens	contig187	contig187	Unknown	TAAAAA	contig187	Solvc03g	Solvc03g	Unknown Protein (AHRD V1)			contig187	Solvc03g	Unknown Protein (A		SL2.40ch	ATMG005	MATR	hypothet	chrM:14	95.628	103.949	150.812	105.853	442.343	367.009
GT	Sense	Sense	0.353	Detected	-0.353	Detected	0.000	1.411	Detected	1.386	Detected	1.399	0.058	GT	Sens	contig189	contig189	Unknown	TGAATC	contig189	Solvc01g	Solvc01g	Unknown Protein (AHRD V1)%			contig189	Solvc01g	Unknown Protein (A		SL2.40ch	AT4G099	EMB1691	EMB169	chr4:624	24.6828	14.2459	36.2942	50.343	53.188	52.1185
GT	Sense	Sense	-0.517	Comprom	0.517	Detected	0.000	1.232	Detected	0.852	Detected	1.042	0.199	GT	Sens	contig189	contig189	Major late	GTGTGA	contig189	Solvc05g	Solvc05g	Major late	GO:00096	GO:00096	contig189	Solvc05g	Major late	GO:00096	SL2.40ch	AT1G708	MLP34	MLP34 (M	chr1:267	7.21062	13.9001	24.3629	11.8444	25.0777	19.2155
GT	Sense	Sense	0.652	Detected	-0.652	Comprom	0.000	2.448	Detected	2.421	Detected	2.434	0.065	GT	Sens	contig19	contig19	Unknown	ATAGGA	contig19	Solvc07g	Solvc07g	Unknown	GO:0045449		contig19	Solvc10g045250.1.1				AT3G02900.1		unknowr	chr3:645	23.733	9.04561	18.1509	19.4477	85.2345	83.3997
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	1.110	Detected	1.190	Detected	1.150	0.002	GT	Sens	contig190	contig190	Ubiquitin-	GATAAA	contig190	Solvc02g	Solvc02g	Ubiquitin-	GO:00436	GO:00436	contig190	Solvc02g	Ubiquitin-	GO:00436	SL2.40ch	AT1G642	UBC28	ubiquitin	chr1:238	1585.01	1422.71	2753.19	2638.46	3455.26	3643.11
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	1.107	Detected	1.058	Detected	1.082	0.004	GT	Sens	contig192	contig192	Unknown	GGTGGT	contig192	Solvc10g	Solvc10g	Unknown Protein (AHRD V1)			contig192	Solvc10g	Unknown Protein (A		SL2.40ch	AT4G030	BSL1	kelch rep	chr4:135	999.805	861.121	1103.13	1264.82	2130.71	2053.82
GT	Sense	Sense	0.310	Detected	-0.310	Detected	0.000	1.316	Detected	0.847	Detected	1.082	0.109	GT	Sens	contig194	contig194	Unknown	CTATGA	contig194	Solvc03g	Solvc03g	Unknown Protein (AHRD V1)			contig194	Solvc09g	Unknown Protein (A		SL2.40ch	AT1G79750.1				21.06	12.8986	26.609	33.5134	43.7736	31.5134
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	1.223	Detected	1.517	Detected	1.370	0.012	GT	Sens	contig194	contig194	Unknown	ACGAAC	contig194	Solvc03g	Solvc03g	Unknown Protein (AHRD V1)			contig194	Solvc03g	Unknown Protein (A		SL2.40ch	AT1G02080.1		transcrip	chr1:373	32995.1	32253	136549	120516	81227.5	99286.4
GT	Sense	Sense	0.037	Comprom	-0.037	Comprom	0.000	1.722	Detected	0.846	Detected	1.284	0.100	GT	Sens	contig195	contig195	Genomic	TTATTC	contig195	Solvc02g	Solvc02g	Genomic DNA chromosome 5			contig195	Solvc02g	Genomic DNA chror		SL2.40ch	AT5G66090.1		unknowr	chr5:264	10.6597	9.53187	6.22103	10.7524	35.4523	19.2597
GT	Sense	Sense	1.329	Detected	-1.329	Comprom	0.000	1.068	Detected	1.023	Detected	1.045	0.514	GT	Sens	contig195	contig195	Mutator-li	ACAAAA	contig195	Solvc01g	Solvc01g	Mutator-li	GO:00082	GO:00082	contig195	Solvc04g054620.1.1				AT4G23230.1		protein k	chr4:121	14.1492	2.11031	7.09142	13.5114	12.2127	11.8044
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	1.131	Detected	0.913	Detected	1.022	0.012	GT	Sens	contig196	contig196	Ubiquitin-	GATAGG	contig196	Solvc03g	Solvc03g	Ubiquitin-	GO:00436	GO:00436	contig196	Solvc03g	Ubiquitin-	GO:00436	SL2.40ch	AT1G642	UBC28	ubiquitin	chr1:238	14.2509	12.9247	34.6968	26.702	31.7041	27.1709
GT	Sense	Sense	-0.285	Comprom	0.285	Comprom	0.000	1.922	Detected	2.782	Detected	2.352	0.045	GT	Sens	contig196	contig196	Peroxida	ATTCTA	contig196	Solvc07g	Solvc07g	Peroxida	GO:00055	GO:00055	contig196	Solvc07g	Peroxida	GO:00046	SL2.40ch	AT5G64100.1		peroxida	chr5:256	3.37213	4.7135	23.7851	8.71191	16.1135	29.1473
GT	Sense	Sense	0.230	Detected	-0.230	Detected	0.000	2.084	Detected	1.093	Detected	1.589	0.101	GT	Sens	contig198	contig198	Lipase (F	TGTGAA	contig198	Solvc12g	Solvc12g	Lipase (F	GO:00066	GO:00066	contig198	Solvc12g	Lipase (F	GO:00066	SL2.40ch	AT2G31100.1		triacylgly	chr2:132	429.452	293.796	247.441	123.893	1605.83	805.738
GT	Sense	Sense	0.450	Detected	-0.450	Comprom	0.000	1.967	Detected	1.705	Detected	1.836	0.059	GT	Sens	contig198	contig198	Unknown	ATCAAG	contig198	Solvc03g	Solvc03g	Unknown Protein (AHRD V1)			contig198	Solvc03g	Unknown Protein (A		SL2.40ch	AT3G05470.1		formin h	chr3:157	14.2529	7.18901	18.897	21.7077	42.2117	35.096
GT	Sense	Sense	-0.161	Comprom	0.161	Comprom	0.000	1.519	Detected	1.335	Detected	1.427	0.017	GT	Sens	contig199	contig199	Ulp1 prot	GGAGCA	contig199	Solvc00g	Solvc00g	Ulp1 prot	GO:00065	GO:00065	contig199	Solvc04g	Ulp1 prot	GO:00065	SL2.40ch	AT4G28720.1		flavin-co	chr4:141	5.14551	6.05368	5.29742	9.03096	17.0619	14.9651
GT	Sense	Sense	-0.270	Detected	0.270	Detected	0.000	1.620	Detected	1.658	Detected	1.639	0.026	GT	Sens	contig202	contig202	RING fing	TCGGTT	contig202	Solvc02g	Solvc02g	RING fing	GO:00082	GO:00082	contig202	Solvc02g	RING fing	GO:00082	SL2.40ch	AT4G11900.1		S-locus l	chr4:715	13133.9	17970.6	107849	69211.4	50347.8	51558.7
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	1.223	Detected	1.605	Detected	1.414	0.022	GT	Sens	contig204	contig204	Transcrip	TGTTTC	contig204	Solvc02g	Solvc02g	Transcrip	GO:00056	GO:00056	contig204	Solvc02g	Transcrip	GO:00037	SL2.40ch	AT3G28857.1		transcrip	chr3:108	15.4167	12.7314	16.8037	29.3566	34.8648	45.3219
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	1.914	Detected	1.840	Detected	1.877	0.003	GT	Sens	contig205	contig205	Ovate pro	CATTAT	contig205	Solvc02g	Solvc02g	Ovate protein (AHRD V1 **-- O8			contig205	Solvc02g	Ovate protein (AHRD		SL2.40ch	AT5G16290.2		acetolact	chr5:533	333.704	359.257	468.218	438.649	1391.49	1317.78
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	2.724	Detected	1.111	Detected	1.917	0.142	GT	Sens	contig206	contig206	Primary a	AATGAT	contig206	Solvc09g	Solvc09g	Primary a	GO:00551	GO:00551	contig206	Solvc09g	Primary a	GO:00551	SL2.40ch	AT1G62810.1		copper a	chr1:232	84.1575	91.4493	415.318	140.842	617.904	201.435
GT	Sense	Sense	-0.989	Comprom	0.989	Detected	0.000	1.205	Detected	1.265	Detected	1.235	0.338	GT	Sens	contig206	contig206	NBS-LRR	CAAGAT	contig206	Solvc06g	Solvc06g	NBS-LRR resistance protein-lil			contig206	Solvc06g	NBS-LRR resistance		SL2.40ch	AT4G30470.1		cinnamo	chr4:148	3.82506	14.1859	10.6195	12.1867	18.1067	18.8194
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	0.823	Detected	1.570	Detected	1.197	0.089	GT	Sens	contig208	contig208	Sulfotran	ACTCAA	contig208	Solvc05g	Solvc05g	Sulfotran	GO:00081	GO:00081	contig208	Solvc05g	Sulfotran	GO:00081	SL2.40ch	AT2G27570.1		sulfotran	chr2:117	13.2161	14.0747	30.3016	16.8665	25.7356	43.0455

GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	1.767	Detected	1.053	Detected	1.410	0.063	GT Sens
GT	Sense	Sense	-0.156	Detected	0.156	Detected	0.000	1.101	Detected	1.093	Detected	1.097	0.020	GT Sens
GT	Sense	Sense	-0.779	Detected	0.779	Detected	0.000	1.894	Detected	1.626	Detected	1.760	0.156	GT Sens
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	1.692	Detected	1.240	Detected	1.466	0.023	GT Sens
GT	Sense	Sense	-0.342	Comprom	0.342	Comprom	0.000	4.913	Detected	4.368	Detected	4.641	0.009	GT Sens
GT	Sense	Sense	0.588	Detected	-0.588	Detected	0.000	3.835	Detected	2.957	Detected	3.396	0.044	GT Sens
GT	Sense	Sense	0.304	Detected	-0.304	Detected	0.000	1.577	Detected	1.858	Detected	1.718	0.036	GT Sens
GT	Sense	Sense	-0.164	Comprom	0.164	Comprom	0.000	2.174	Detected	1.124	Detected	1.649	0.096	GT Sens
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	2.198	Detected	2.033	Detected	2.115	0.002	GT Sens
GT	Sense	Sense	-0.278	Comprom	0.278	Comprom	0.000	1.285	Detected	1.782	Detected	1.534	0.054	GT Sens
GT	Sense	Sense	0.420	Detected	-0.420	Detected	0.000	3.512	Detected	2.537	Detected	3.025	0.042	GT Sens
GT	Sense	Sense	0.514	Comprom	-0.514	Comprom	0.000	1.613	Detected	2.389	Detected	2.001	0.090	GT Sens
GT	Sense	Sense	-0.240	Detected	0.240	Detected	0.000	1.260	Detected	1.445	Detected	1.352	0.034	GT Sens
GT	Sense	Sense	-0.481	Comprom	0.481	Comprom	0.000	1.949	Detected	1.478	Detected	1.713	0.085	GT Sens
GT	Sense	Sense	0.018	Detected	-0.018	Detected	0.000	1.939	Detected	1.881	Detected	1.910	0.000	GT Sens
GT	Sense	Sense	0.334	Detected	-0.334	Detected	0.000	2.795	Detected	1.163	Detected	1.979	0.154	GT Sens
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	1.385	Detected	1.011	Detected	1.198	0.029	GT Sens
GT	Sense	Sense	0.160	Detected	-0.160	Detected	0.000	1.880	Detected	1.739	Detected	1.809	0.009	GT Sens
GT	Sense	Sense	0.801	Comprom	-0.801	Comprom	0.000	1.547	Detected	1.792	Detected	1.669	0.176	GT Sens
GT	Sense	Sense	-0.176	Detected	0.176	Detected	0.000	2.459	Detected	1.359	Detected	1.909	0.081	GT Sens
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	1.574	Detected	1.170	Detected	1.372	0.028	GT Sens
GT	Sense	Sense	1.150	Detected	-1.150	Detected	0.000	5.399	Detected	4.308	Detected	4.854	0.062	GT Sens
GT	Sense	Sense	-0.427	Comprom	0.427	Comprom	0.000	1.495	Detected	0.853	Detected	1.174	0.159	GT Sens
GT	Sense	Sense	-0.016	Detected	0.016	Detected	0.000	1.793	Detected	1.310	Detected	1.552	0.024	GT Sens
GT	Sense	Sense	0.294	Detected	-0.294	Detected	0.000	1.246	Detected	1.278	Detected	1.262	0.050	GT Sens
GT	Sense	Sense	0.359	Detected	-0.359	Detected	0.000	2.096	Detected	1.274	Detected	1.685	0.091	GT Sens
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	2.184	Detected	2.378	Detected	2.281	0.009	GT Sens
GT	Sense	Sense	0.176	Detected	-0.176	Detected	0.000	1.251	Detected	1.768	Detected	1.510	0.040	GT Sens
GT	Sense	Sense	-0.192	Detected	0.192	Detected	0.000	1.741	Detected	1.997	Detected	1.869	0.015	GT Sens
GT	Sense	Sense	-0.512	Comprom	0.512	Comprom	0.000	2.193	Detected	1.076	Detected	1.634	0.164	GT Sens
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	1.428	Detected	1.155	Detected	1.291	0.011	GT Sens
GT	Sense	Sense	0.721	Detected	-0.721	Detected	0.000	0.929	Detected	1.660	Detected	1.295	0.251	GT Sens

		16h_AZ_Control					16h_AZ_TAPG + TPRP vs. 16h_AZ_Control																															
ProbeNar	Orientatic	Fold 16h	Flag 16h	Fold 16h	Flag 16h	Geomean	Fold 16h	Flag 16h	Fold 16h	Flag 16h	Geomean	P-value	ProbeNar	GeneNam	Systemat	Descripti	Sequence	Contig ID	ITAG ID	Parent Ge	ITAG Des	Ontology	Ontology	Contig ID	Target ID	Functiona	GO term	Transcrip	target ID	Symbols	TAIR Des	TAIR Chr	gProcess	gProcess	gProcess	gProcess	gProcess	gProcessedSignal 16h 46 AZ
A 96 P00	Sense	0.296	Detected	-0.296	Detected	0.000	-2.898	Detected	-1.658	Detected	-2.278	0.080	A 96 P00	Dea1	NM 0012	Solanum	CTTATGAGCAATGTTCAAGTGTGTGGTAACTTCTTGTTTCCTTTGTAGCTTGAAATAAGT																1536.27	959.593	242.724	63.6174	173.729	409.182
A 96 P00	Sense	0.083	Detected	-0.083	Detected	0.000	-1.956	Detected	-1.690	Detected	-1.823	0.007	A 96 P00	BI933507	BI933507	EST5533	GGGTGTCATTGAGGAGTTCCTCAAAGTGATTTACGCTCTATTTCAGATCTCGACTTCACT																9325.9	7824.62	1551.92	2137.89	2347.34	2814.72
A 96 P01	Sense	0.003	Detected	-0.003	Detected	0.000	-3.446	Comprom	-1.396	Comprom	-2.421	0.142	A 96 P01	BG12369	BG12369	EST4693	AATCAAAGCTTGGTGATTGTATGAGAGCTGCTTCGATTCGAAAGGAGCGTTACAGAGGAT																19.4017	18.1902	1.68552	1.92534	1.83772	7.59141
A 96 P01	Sense	0.036	Detected	-0.036	Detected	0.000	-1.352	Detected	-0.884	Detected	-1.118	0.042	A 96 P01	LOC5437	NM 0012	Solanum	AATTATGGAAGATTTGATAGTTGTGTTGGGGGTATGGGGGTTATTGCCAAGTAGATTTTG																17551.1	15700.2	11171.1	9114.45	6933.16	9561.67
A 96 P01	Sense	0.434	Detected	-0.434	Detected	0.000	-1.704	Detected	-1.146	Detected	-1.425	0.110	A 96 P01	XTH9	NM 0012	Solanum	ATTCTAAGAGGTTTCCTCAAGGCTTTTCTGCTGAATGCAAGAGTTCAAGATTTTAATGAA																78177.5	40321.8	15525.9	31887.3	18382.4	26978.1
A 96 P02	Sense	-0.107	Detected	0.107	Detected	0.000	-1.371	Detected	-0.865	Detected	-1.118	0.055	A 96 P02	BI924670	BI924670	EST5445	GAATCAGCAAAGCCAGTACCACTTGATCGCTTGAAAAGCAGATTGATCTTCCATGACGGT																2421.17	2641.44	683.522	815.745	1042.35	1475.94
A 96 P02	Sense	-0.025	Detected	0.025	Detected	0.000	-1.081	Detected	-1.067	Detected	-1.074	0.001	A 96 P02	BM41197	BM41197	EST5863	TATTGGTAATGTTGGAGACTCTAAAGCTGTGCTGGGTACAAGAGGCGAGGATGATTCTCT																1111.79	1082.44	327.546	377.656	552.954	556.809
A 96 P02	Sense	0.222	Detected	-0.222	Detected	0.000	-2.055	Detected	-1.275	Detected	-1.665	0.066	A 96 P02	AK32182	AK32182	Solanum	TGAACAGTCATTAGGAACAATTCATTATGGAAGTGCAAAGTGTTTTGATGGTTTGACAGC																70.4688	48.7089	13.1022	10.1245	15.036	25.7434
A 96 P02	Sense	-0.104	Detected	0.104	Detected	0.000	-1.130	Detected	-1.193	Detected	-1.161	0.009	A 96 P02	BE46252	BE46252	EST3247	CTTTCAGTCCAGGATTTATTGGGATGGGCTTGTCCTATGGTCTTTCCTTAAACATGTCTC																802.139	871.213	217.045	274.911	407.381	388.815
A 96 P02	Sense	0.123	Detected	-0.123	Detected	0.000	-2.197	Detected	-1.819	Detected	-2.008	0.012	A 96 P02	AK32303	AK32303	Solanum	CTCTGTGGTCAACAACTAGTTCAAAGTCAAAGGCAAAGGCTAGCAATTCTAGCTCTCATA																3002.14	2381.61	595.803	798.647	621.878	805.992
A 96 P04	Sense	-0.011	Detected	0.011	Detected	0.000	-1.160	Detected	-1.237	Detected	-1.198	0.001	A 96 P04	BI932208	BI932208	EST5520	CTTTCCTTAGACGACTTCGTGTTACCTCAGTACAGGGAAGTAGGGGTTATATTATGGCGT																3994.65	3813.89	1835.41	1877.55	1863.29	1760.17
A 96 P04	Sense	0.039	Detected	-0.039	Detected	0.000	-1.661	Detected	-1.780	Detected	-1.721	0.002	A 96 P04	BE45061	BE45061	EST4015	GCTGGCATATTTGCTTGCAAAATGGTCTATGATCTATGTCAACTGATCAGCAGTTTTTAC																392.121	349.421	127.182	129.316	124.861	114.556
A 96 P04	Sense	0.143	Detected	-0.143	Detected	0.000	-1.421	Detected	-1.073	Detected	-1.247	0.031	A 96 P04	BI935337	BI935337	EST5552	TATTTCCGACAGTTGTTGAAACCTGTCACGTAGTTTCGTCTTTCTTGGTGGTGCATCTTA																362.482	279.756	68.9735	89.3244	126.822	160.972
A 96 P04	Sense	0.477	Detected	-0.477	Detected	0.000	-3.118	Detected	-3.869	Detected	-3.493	0.029	A 96 P04	AK32045	AK32045	Solanum	TGAAGCAGATGAAATTGATATTGTGATTCATAATCCAGCTGTCGAGAAGGACCCGGCTTG																3080.83	1495.74	95.3953	119.86	263.758	156.242
A 96 P05	Sense	-0.140	Detected	0.140	Detected	0.000	-0.990	Detected	-1.146	Detected	-1.068	0.022	A 96 P05	AK32521	AK32521	Solanum	CAAGTCAAGATCTTAATTTCAGTCCTCCCCATATTTGCTTGCACTATTATTTTCAATACC																431.068	492.454	158.721	252.099	247.432	221.395
A 96 P05	Sense	0.140	Detected	-0.140	Detected	0.000	-1.171	Detected	-0.932	Detected	-1.052	0.029	A 96 P05	AK32096	AK32096	Solanum	AGAAGCGTTTGATGTTTTTGACGAGAACGGGGATGGATTTATATCGGCGAAGGAATTGCA																32126.1	24898.1	9616.27	10433.2	13391	15756.4
A 96 P05	Sense	-0.279	Detected	0.279	Detected	0.000	-1.496	Comprom	-1.438	Comprom	-1.467	0.035	A 96 P05	AI771973	AI771973	EST2530	CAAGTTGACTATCTACTTGGAGATAATCCAAGAGCGACAAGTTACATGGTGGGATACGGT																19.1597	26.5242	5.46508	2.70688	8.52296	8.84683
A 96 P05	Sense	0.033	Detected	-0.033	Detected	0.000	-1.263	Detected	-1.080	Detected	-1.172	0.007	A 96 P05	AK32771	AK32771	Solanum	AGCTGGACAAAGTTAGGGAAATATGCAAGTGCATTCTAATTGGTCTAGATTATTTGCACA																164.417	147.831	57.4673	69.885	69.2503	78.4221
A 96 P05	Sense	0.241	Detected	-0.241	Detected	0.000	-1.614	Detected	-1.434	Detected	-1.524	0.027	A 96 P05	BI922989	BI922989	EST5428	GAAGGAATATTCCGGGTTCAAATGTCAAAGCGGATTAGTAAAAGCCATTGTTGTATACGG																1927.23	1298.95	577.288	738.602	551.395	622.43
A 96 P05	Sense	0.053	Detected	-0.053	Detected	0.000	-1.460	Detected	-1.131	Detected	-1.296	0.017	A 96 P05	TA45520	TA45520	Rep: Indo	TCATGATGTCAGAGTCGGAACCATTGATTCCCATAATTACACCGATCTCTCAATTCGAGA																72.4013	63.3251	23.5524	44.0156	26.248	32.8637
A 96 P06	Sense	-0.025	Detected	0.025	Detected	0.000	-1.269	Detected	-1.377	Detected	-1.323	0.002	A 96 P06	DB67967	DB67967	DB67967	GGTGGGCTGAAGATTTAGCTGAATTGAGCATAGACCTATACTGGAGAAGTATGATAGCTA																128.666	125.284	41.4967	41.1766	56.1665	51.9723
A 96 P06	Sense	0.014	Detected	-0.014	Detected	0.000	-1.186	Detected	-1.127	Detected	-1.156	0.001	A 96 P06	BI931461	BI931461	EST5513	TGGGATTGGAAGATTGTGTTGAGAAAATTGATGCTCAACGCGTTTTTGGGTATGCCCTTT																700.829	646.757	215.398	264.222	315.574	327.853
A 96 P06	Sense	0.194	Detected	-0.194	Detected	0.000	-1.845	Comprom	-0.962	Detected	-1.404	0.101	A 96 P06	AK32951	AK32951	Solanum	CGATCGATACACTAATCCTTGTAAACTTTGCTTATATTTTTGCACGAGTACTGGATATGT																33.4643	24.0789	10.4821	24.3145	8.42373	15.4913
A 96 P06	Sense	-0.025	Detected	0.025	Detected	0.000	-1.476	Detected	-1.852	Detected	-1.664	0.013	A 96 P06	AK32697	AK32697	Solanum	ATTGAGCTTTCTGCTATTTCTATTGCTCAATCAGTCATTGGAACCTTCTCTTTCGGGTTC																521.583	508.237	173.208	214.433	197.343	151.662
A 96 P06	Sense	0.089	Detected	-0.089	Detected	0.000	-1.392	Detected	-1.454	Detected	-1.423	0.004	A 96 P06	AK31928	AK31928	Solanum	GTCTTTGGCTGGTTCAAATAGATTCGATCTTCAACCATCATCGCATAACAATACTCATTC																323.107	268.735	63.1159	78.7218	119.754	114.323
A 96 P06	Sense	0.113	Detected	-0.113	Detected	0.000	-1.686	Detected	-1.671	Detected	-1.678	0.005	A 96 P06	BM40986	BM40986	EST5841	TTGTCGATAGCTTTGAAGGGATCAGTGTACGAGAGGCGAAGACAGAATCCTTCATTGTCA																1689.27	1359.15	443.513	443.897	502.304	506.039
A 96 P06	Sense	0.167	Detected	-0.167	Detected	0.000	-1.221	Detected	-1.348	Detected	-1.284	0.019	A 96 P06	DB68804	DB68804	DB68804	GTGCAAAAGCAACAATAAACGTATGGGAACCATCAATCGAAGTAGTGAACGAGTTTAGTC																578.395	431.571	159.483	163.246	228.568	208.721
A 96 P06	Sense	0.053	Detected	-0.053	Detected	0.000	-2.723	Detected	-2.670	Detected	-2.696	0.000	A 96 P06	AK24748	AK24748	Solanum	TGATGAACTTGAGAGAATTGAGAAATCAGGCGGGAAGGTCATCAATTGGAATGGGCATCG																646.816	565.31	63.1712	60.2045	97.6446	101.043
A 96 P06	Sense	-0.062	Detected	0.062	Detected	0.000	-1.272	Detected	-1.017	Detected	-1.144	0.015	A 96 P06	TA47822	TA47822	Rep: Chr	TTTCAGCCCATGCTTATGTTAGGCATCACAGTTGGTGTTTCTCTCAGTGTTGTTTTCCCC																1535.64	1573.74	691.9	556.26	686.679	816.886
A 96 P06	Sense	0.405	Detected	-0.405	Detected	0.000	-2.520	Comprom	-1.590	Detected	-2.055	0.079	A 96 P06	AK32041	AK32041	Solanum	GTTGGATTTTCGTGCTGATTATATTGCGCCTTCAGTTCAAAAACTCTCCACATTTTGTAC																47.7008	25.5981	5.3194	11.8037	6.4984	12.3442
A 96 P06	Sense	-0.037	Detected	0.037	Detected	0.000	-1.180	Detected	-1.089	Detected	-1.134	0.003	A 96 P06	AK32828	AK32828	Solanum	AGCTATCTGCTTACAAATATGGCTTTTCGGGGCAGTCGACATCATGTTTATCATTGAAGA																418.975	415.002	153.618	141.972	196.313	208.363
A 96 P07	Sense	0.053	Detected	-0.053	Detected	0.000	-1.619	Detected	-1.423	Detected	-1.521	0.005	A 96 P07	AK32120	AK32120	Solanum	TTTCTGTACTATCGGAAGCTAAAGCAGAGGATATGCCAAAAGGAGTTGTTATCCACCCTG																413.874	361.824	106.567	100.407	134.379	153.46
A 96 P07	Sense	0.030	Detected	-0.030	Detected	0.000	-1.940	Detected	-1.712	Detected	-1.826	0.004	A 96 P07	AK32576	AK32576	Solanum	TATTCTGATGGTCCTGAAACAATGTCACCTACCGAATCCTTATCCTTGAACTGCAGTGTC																60.9724	55.052	15.8429	15.0465	16.1052	18.8031
A 96 P07	Sense	0.330	Detected	-0.330	Detected	0.000	-1.169	Detected	-2.282	Detected	-1.726	0.117	A 96 P07	BI925698	BI925698	Unknown	GAGCAGTGCGATCTTATTTTGGCTTCTCATTTACTCTCTTCTTTCCCCGTACTAGATTCT																569.242	338.896	70.7448	114.315	208.318	95.9879
A 96 P07	Sense	0.089	Detected	-0.089	Detected	0.000	-1.284	Detected	-1.335	Detected	-1.309	0.005	A 96 P07	AK32308	AK32308	Solanum	AGATAAGAAGTCGTGGGTCCCAAACATTGAGGGATGTCATTTTGAAGAGTTCAGACGAAG																10618	8826.01	2896.9	3212.21	4238.38	4081.05
A 96 P07	Sense	-0.062	Detected	0.062	Detected	0.000	-1.202	Detected	-1.349	Detected	-1.276	0.006	A 96 P07	AK32709	AK32709	Solanum	GTGGTCTGAGGAAGAGCACAAAAAGTTCCTTGAAGCATTAAAGCTTCATGGTAGGGCATG																1326.45	1360	416.416	421.408	622.537	560.572
A 96 P07	Sense	-0.025	Detected	0.025	Detected	0.000	-1.476	Detected	-1.530	Detected	-1.503	0.001	A 96 P07	TA41489	TA41489	Rep: Chr	CTAATTTTATGATTGGCTCACTTTCACCCAACACTGAGACAGCTGAAGAAAACCAGACCA																312.616	304.501	51.2056	82.8766	118.289	113.599
A 96 P07	Sense	0.037	Detected	-0.037	Detected	0.000	-0.993	Detected	-1.203	Detected	-1.098	0.010	A 96 P07	AML1	NM 0012	Solanum	ATAATGATTGAAGCAATCCATCCTGGTGGTACCAGACGGTTGTCGCAGCAATTTCCTTCT																226.702	202.549	72.7067	107.586	114.777	98.9673
A 96 P08	Sense	0.386	Detected	-0.386	Detected	0.000	-0.937	Detected	-2.317	Detected	-1.627	0.176	A 96 P08	BI935704	BI935704	EST5555	CTTGCCTAGTTACATGGTCAAAAATGGGATCACCATAGAAAGATACCTAACCCGGCTTTT																120.263	66.2956	19.5938	25.9583	49.7426	19.0474
A 96 P08	Sense	0.075	Detected	-0.075	Detected	0.000	-1.161	Detected	-1.181	Detected	-1.171	0.004	A 96 P08	AK31994	AK31994	Solanum	CGCACTGCTTTGGGAGATTGGGATTCTAGCAATGCAGAGTCTTTAATCAGATATACGGGT																212.602	180.201	53.6656	50.2216	93.3286	91.8021
A 96 P08	Sense	0.410	Detected	-0.410	Detected	0.000	-2.703	Detected	-1.878	Detected	-2.290	0.059	A 96 P08	AW62139	AW62139	Unknown	ACACGAGAAATTTGAGCTTGAAGAACAAAAAATGAAACCAGTGCTCATTTCTGTGAAAGC																3159.65	1683.13	624.767	1070.21	377.771	666.923
A 96 P08	Sense	0.129	Detected	-0.129	Detected	0.000	-1.095	Detected	-1.586	Detected	-1.340	0.040	A 96 P08	BT01380	BT01380	Lycopers	TGCATTAGACCTAGCAGTATTTTTGGGCCCTGGTGATAGGTTGCTAGTTCCTTCACTAGT																211.709	166.595	74.7368	70.1916	93.7701	66.5164
A 96 P08	Sense	-0.073	Detected	0.073	Detected	0.000	-1.365	Detected	-1.066	Detected	-1.215	0.018	A 96 P08	BP88147	BP88147	BP88147	ATAATCTGTACACTCCTCTTCCACGAGTACTGTAGGCAAAGGTTTGAACCATTGTTCAAG																130.35	135.715	69.1579	56.8874	55.082	67.555
A 96 P08	Sense	0.211	Detected	-0.211	Detected	0.000	-0.962	Detected	-1.222	Detected	-1.092	0.048	A 96 P08	AK32480	AK32480	Solanum	GATAACAACGGAATTATCACTTTTGAGGAGTGGGAGGGATTTTCTTCTACTCTATCCACA																270.054	189.739	93.6841	68.3903	123.9	103.171
A 96 P08	Sense	0.397	Detected	-0.397	Detected	0.000	-1.103	Detected	-2.368	Detected	-1.735	0.146	A 96 P08	LOC1007	NM 0012	Solanum	GCCTCAAGCCAATGCCTTCATTGATATGTTTGTTACTGGACTTGCTAGTTACAATGGTCA																472.805	256.46	57.646	97.2257	172.907	71.7052
A 96 P09	Sense	0.184	Detected	-0.184	Detected	0.000	-1.071	Detected	-1.016	Detected	-1.044	0.030	A 96 P09	AK32516	AK32516	Solanum	GCATCAACAAGCAAATATAGGGAGTCATTTGGAAATCTCATCTAATACTGAAAGGGATGT																175.308	127.87	46.2926	55.9943	75.9752	78.7182
A 96 P09	Sense	0.162	Detected	-0.162	Detected	0.000	-1.892	Detected	-1.632	Detected	-1.762	0.014	A 96 P09	BI933507	BI933507	EST5533	TAATATTGTCTCGGATAGGCTTGGTTGCAGCGTAAGCTTTTCTGAATGCGGAGGAATTGA																9601.31	7221.21	1554.27	2193.24	2392.12	2855.98
A 96 P09	Sense	0.333	Detected	-0.333	Detected	0.000	-1.906	Detected	-1.250	Detected	-1.578	0.078	A 96 P09	AK32681	AK32681	Solanum	GCAAAGCGTGTAGAAATGTAGATTTTCATTGTATTTGCACCCTCTCTGTAATCATATCAA																14749.5	8748.36	3866.01	5784.78	3232.56	5076.57
A 96 P10	Sense	0.317	Detected	-0.317	Detected	0.000	-2.899	Detected	-2.063	Detected	-2.481	0.042	A 96 P10	TA46353	TA46353	Rep: Aral	GAGAATCACAACAACAACAATGATGCTTTCTCGGAGAATCACAACCCACAACATGATGGG																862.958	523.011	157.168	147.172	96.0384	170.94
A 96 P10	Sense	0.468	Detected	-0.468	Detected	0.000	-1.724	Detected	-1.678	Comprom	-1.701	0.068	A 96 P10	DB67967	DB67967	DB67967	TTCAAGTTAAGGGTAGTAGATATTTGCTTCACAAGTTTCCCCTGCTGTCAAAGTGTTCAA																44.7363	22.0108	13.6397	10.9978	10.1324	10.4263
A 96 P10	Sense	0.462	Detected	-0.462	Detected	0.000	-1.374	Detected	-1.219	Detected	-1.296	0.110	A 96 P10	AK32290	AK32290	Solanum	AAGTCTTAAAGATTCACAAGTGATGGAAATAGCAAAAGGTTTGGAGAAAGCAGGACACCC																177.992	88.2229	48.8401	40.1934	51.5649	57.2275
A 96 P10	Sense	0.080	Detected	-0.080	Detected	0.000	-1.264	Detected	-1.296	Detected	-1.280	0.004	A 96 P10	AK32575	AK32575	Solanum	AGAGGCAAGAAAATGATGATAAAGGAGTTTTGTGTAACAAGTGCAGGCCAAGCAATAGGG																739.593	623.277	259.296	459.522	301.569	293.929
A 96 P10	Sense	-0.148	Detected	0.148	Detected	0.000	-0.926	Detected	-1.107	Detected	-1.016	0.028	A 96 P10	AK24731	AK24731	Solanum	CATAAGTTAAAATTGGCATCCATATTAGAAGCTATCGGCAGTCAAATTCATCGAGAAGAT																22.8759	26.4285	5.75746	7.05022	13.8043	12.1386
A 96 P10	Sense	-0.036	Detected	0.036	Detected	0.000	-1.515	Detected	-1.013	Detected	-1.264	0.038	A 96 P10	AK24716	AK24716	Solanum	CTGAAGTCAGCCATGGATGCAGAATGGAATTTATAGCCATGACCTCATTGCCTGATATTA																307.585	304.397	203.084	171.326	114.142	161.186
A 96 P11	Sense	-0.380	Detected	0.380	Detected	0.000	-1.679	Detected	-1.194	Detected	-1.437	0.086	A 96 P11	AK31970	AK31970	Solanum	TTCCCAAGAAACCCCATTATAAGGCCCATTGAAGCTCTACGCGCTATTTATGGAGATGAA																5604.52	8927.2	3638.7	5670.59	2355.42	3286.02
A 96 P11	Sense	0.001	Detected	-0.001	Detected	0.000	-3.631	Detected	-1.036	Detected	-2.334	0.214	A 96 P11	AK32669	AK32669	Solanum	ACGTCATTTAAGATCGTGCAAAGAGCTTTTGAGGCTCTTTAGTAAAGCTTTATGTTCTTT																210.973	198.152	165.486	76.2036	17.5959	106.016
A 96 P12	Sense	0.185	Detected	-0.185	Detected	0.000	-1.875	Detected	-1.965	Detected	-1.920	0.010	A 96 P12	AK32850	AK32850	Solanum	AAGAGAGATAAAGCATCATTCTTGCTGGAGGTTATCGAATATATTCAATTCCTACAAGAG																618.833	450.827	89.055	114.44	153.556	143.847
A 96 P13	Sense	0.152	Detected	-0.152	Detected	0.000	-1.238	Detected	-1.282	Detected	-1.260	0.015	A 96 P13	LOC1001	NM 0012	Solanum	GGAAACCTGATCAACCAGAGAAGGCACAAATGACCATTTTTTATGGTGGACAAGTCATTG																19416.5	14788.8	4217.88	4405.79	7663.47	7410.34
A 96 P13	Sense	0.347	Detected	-0.347	Detected	0.000	-1.004	Detected	-1.018	Detected	-1.011	0.100	A 96 P13	AI771618	AI771618	Unknown	TGCATTTGGGTGTATACTCATGGCACTTGTAGCAAAGTTGGATTACTTGGTATGGGTAAG																130.339	75.8312	29.8553	46.451	52.8768	52.1857
A 96 P13	Sense	-0.548	Detected	0.548	Detected	0.000	-3.045	Comprom	-1.672	Comprom	-2.359	0.115	A 96 P13	AI772225	AI772225	Unknown	TGTAAATGTTGGCTCAACAGCTTATTGGCTTTCTCTTTTGGTGGAATTTGAGGATGGAGA																13.0099	26.1787	6.41947	1.98015	2.38449	6.1556
A 96 P13	Sense	0.072	Detected	-0.072	Detected	0.000	-1.199	Detected	-0.821	Detected	-1.010	0.038	A 96 P13	AI774692	AI774692	Unknown	GATTTTTTCCCTTATTCAGAAGGGTTTCCACGTAAAATTCTTGGTGTCGTTATTTTCCTA																1948.55	1658.35	987.692	1350.49	834.812	1081.8
A 96 P13	Sense	-0.153	Detected	0.153	Detected	0.000	-2.288	Detected	-1.048	Detected	-1.668	0.121	A 96 P13	AI777414	AI777414	Unknown	TTGCAAGAAGAACCATGGAGAAGAGGAAGTTGAATTGGATGGGAGTTTTGAGTATAGCAA																1216.8	1416.36	426.601	478.568	286.561	675.189
A 96 P13	Sense	0.312	Detected	-0.312	Detected	0.000	-2.690	Detected	-1.585	Detected	-2.137	0.078	A 96 P13	Dea1	NM 0012	Solanum	ACGTCTCATTCCCAAATAAGTTGGGGTCACCTATATGAATGTTCATTCTATCACTACTAT																267.385	163.262	32.7007	8.93059	34.5349	74.0577
A 96 P13	Sense	0.164	Detected	-0.164	Detected	0.000	-1.303	Detected	-1.954	Detected	-1.628	0.047	A 96 P13	AK31995	AK31995	Solanum	TCATATGAGTTGGATGTTTGATACCAACACCCTTACTGAGAGGTGTGGGAAGCCCAATAA																223.002	167.22	45.3953	19.4415	83.4499	52.9993
A 96 P14	Sense	0.334	Detected	-0.334	Detected	0.000	-1.901	Detected	-2.043	Detected	-1.972	0.029	A 96 P14	AI897649	AI897649	Unknown	GGAAGAGCACCTAGAGGTGAAAAAACTAATTGGGTCATGCATGAATATAGATTAGATGGA																1086.94	643.507	238.665	284.344	238.804	215.741
A 96 P14	Sense	0.136	Detected	-0.136	Detected	0.000	-1.396	Detected	-1.537	Detected	-1.466	0.011	A 96 P14	AK32028	AK32028	Solanum	TGATGTGTATCTTTCGTATCTTCCCCTGGCACATATCTTCCATCGAGTGATTGAAGAGTG																1983.17	1545.28	458.016	444.31	709.291	641.582
A 96 P14	Sense	0.385	Detected	-0.385	Detected	0.000	-1.787	Detected	-1.508	Detected	-1.648	0.056	A 96 P14	AK32182	AK32182	Solanum	TGTTATAAATATTCACTGTATGGATCGACCTAAGCTTCTGGTTGACATTGTTTGCACCAT																239.609	132.287	37.0359	35.3189	55.0002	66.5308
A 96 P15	Sense	0.166	Detected	-0.166	Detected	0.000	-1.213	Detected	-0.982	Detected	-1.098	0.032	A 96 P15	AK32845	AK32845	Solanum	CAAAAAACATTCAAAATCGCTTGTATGGGAAGATCCATCGGCGGCTTTAGCCAATGCTCG																4376.41	3269.9	987.381	1271.53	1739.68	2035.99
A 96 P15	Sense	-0.028	Detected	0.028	Detected	0.000	-1.307	Detected	-1.491	Detected	-1.399	0.005	A 96 P15	AW22103	AW22103	Unknown	ACGGAAGCACAGGAAACTACCCCTGTTAATTTATGGAGCAAACAGATCTAACTTATGGAG																246.737	241.309	51.9095	74.2866	105.172	92.27
A 96 P15	Sense	0.050	Detected	-0.050	Detected	0.000	-1.696	Detected	-1.492	Detected	-1.594	0.005	A 96 P15	AW22376	AW22376	Unknown	AACCCTAAATCAATCAGGGGGCAGATCATTGACCAATGCAAGCAGTCTAAAGCTTGCAAG																920.144	807.699	160.084	249.538	283.822	325.906
A 96 P15	Sense	0.160	Detected	-0.160	Detected	0.000	-1.027	Detected	-1.468	Detected	-1.248	0.045	A 96 P15	AW44248	AW44248	Unknown	ACGAGGATAATGTCCCTCCTTCTATTGACTGGAGGAAGAAAGGTGCTGTCACTCCTTATT																6646.45	5007.77	1877.11	3015.32	3019.17	2216.88
A 96 P16	Sense	0.246	Detected	-0.246	Detected	0.000	-1.877	Detected	-2.041	Detected	-1.959	0.017	A 96 P16	AW62565	AW62565	EST3195	GCCCAGTGGACATCGATTGTCTATGGAATTATTGATATAAACATTTAGTGAGGGACTTGG																9830.25	6572.34	2704.25	3205.38	2333.25	2076.06
A 96 P16	Sense	0.125	Detected	-0.125	Detected	0.000	-1.270	Detected	-1.799	Detected	-1.535	0.034	A 96 P16	AW62569	AW62569	Unknown	AAAGGTTGATGGAAAAGGCAACCATCAATAGCCAAGCACCCCACGTTCAAAACATTTAGC																217.827	172.443	35.7135	50.1296	85.6844	59.2195
A 96 P16	Sense	0.075	Detected	-0.075	Detected	0.000	-1.548	Detected	-1.399	Detected	-1.474	0.005	A 96 P16	AK32808	AK32808	Solanum	TGTATGAACTCATGTTTCATTTGCTCTTAAACGCCGTGGCGATGGCGTATTGGGTTTGGA																176.516	149.742	37.0344	56.6911	59.274	65.5515
A 96 P16	Sense	-0.044	Detected	0.044	Detected	0.000	-1.036	Detected	-1.061	Detected	-1.048	0.002	A 96 P16	BT01400	BT01400	Lycopers	TTTAGTGGGGATTCTGAATATAGTGACACTTTTGCTGTCGATCCCAATTATAGGAGGAGG																1259.73	1259.21	321.984	461.414	654.859	642.025
A 96 P16	Sense	0.271	Detected	-0.271	Detected	0.000	-0.967	Detected	-2.080	Detected	-1.524	0.133	A 96 P16	LOC1007	NM 0012	Solanum	TTCAGAAAGAGCAGTGCGATCTTATTTTGGCTTCTCCATTTACTCTTCTTTCCCTTAC																539.379	348.404	69.9536	135.473	236.514	108.993
A 96 P16	Sense	0.023	Detected	-0.023	Detected	0.000	-1.405	Detected	-1.316	Detected	-1.361	0.001	A 96 P16	AW93017	AW93017	Unknown	AGCTTGAATTCTATTCGTCTTCGTCGGATCTTCAATGTGTTCGATAGAAATCACGACTGC																12727.4	11605.7	3110.5	3986.91	4894.81	5188.92
A 96 P16	Sense	0.160	Detected	-0.160	Detected	0.000	-2.090	Detected	-1.797	Detected	-1.944	0.012	A 96 P16	AK32303	AK32303	Solanum	TTATTCTTCAAAGGACTCTAGTATGGATATGAGAAGCTTGCACAGTTTACCGCGTGGTAT																2591.57	1952.64	510.834	675.345	563.277	688.362
A 96 P17	Sense	0.188	Detected	-0.188	Detected	0.000	-3.048	Detected	-1.823	Detected	-2.436	0.063	A 96 P17	Dea1	NM 0012	Solanum	CAAAAAAGCTCCATCTGGCTTTCAATGCCCTAAGTGAACAAACAAACAATAGCTACTACG																653.601	474.061	92.2544	23.8354	71.7681	167.258
A 96 P17	Sense	0.171	Detected	-0.171	Detected	0.000	-1.957	Detected	-1.688	Detected	-1.822	0.014	A 96 P17	AK32303	AK32303	Solanum	CTCTACTATGGATATGAGAAGCTAGCACAGCTTACCGCGTGGTATTATCCAAGCAAGATC																1489.7	1106.57	318.342	388.183	352.739	423.77
A 96 P17	Sense	-0.130	Detected	0.130	Detected	0.000	-1.447	Detected	-0.928	Detected	-1.187	0.055	A 96 P17	LOC5441	NM 0012	Solanum	GATCACAGTCAAGGAACTGGTGTTGCAAACGCCGGTTTACTCTATTTCAATAACCGATTA																234.92	264.837	71.5384	117.196	97.5774	139.407
A 96 P17	Sense	-0.156	Detected	0.156	Detected	0.000	-1.013	Detected	-0.991	Detected	-1.002	0.023	A 96 P17	BT01460	BT01460	Lycopers	GGCAGAAGCTATCATGGCATTGTTTTCTTGAGGAACTTCTCAACTTTGACAGCACCATGT																34.977	40.8341	19.9172	14.7006	19.9756	20.2166
A 96 P18	Sense	0.153	Detected	-0.153	Detected	0.000	-1.594	Detected	-1.226	Detected	-1.410	0.028	A 96 P18	BF09749	BF09749	Unknown	GATAACGAAGCGGTTGTCGTCGATGAGGGATCAGTTTGATGATGAGAAAGTGGTGATTAA																406.175	309.192	83.0361	112.63	125.191	161.103
A 96 P18	Sense	0.115	Detected	-0.115	Detected	0.000	-2.020	Detected	-1.724	Detected	-1.872	0.010	A 96 P18	BI933507	BI933507	EST5533	TCAACAAAGTTGGTTGTAAAGCCTGATATGTTGTTTGGCAAGCGTGGACAGAGTGGACCA																2258.21	1812.01	295.879	410.135	531.931	651.059
A 96 P19	Sense	0.176	Detected	-0.176	Detected	0.000	-2.847	Detected	-1.773	Detected	-2.310	0.055	A 96 P19	Dea1	NM 0012	Solanum	TAAGCCTTCTTCTTAATGTTTGTGGCAAAAAAGCTCCATCTGGCTTTCAATGCCCTAAGT																727.111	536.116	88.9021	26.3121	92.5226	194.186
A 96 P19	Sense	0.138	Detected	-0.138	Detected	0.000	-3.901	Detected	-3.000	Detected	-3.451	0.018	A 96 P19	BI209487	BI209487	Unknown	AAAGGAAGGGGTGTGTGATGAAAGCCTTTAATTTGTTACTCTTGAACTATAGTATGACAA																210.744	163.871	22.3237	16.306	13.2654	24.6926
A 96 P19	Sense	0.476	Detected	-0.476	Detected	0.000	-1.708	Detected	-1.145	Detected	-1.426	0.123	A 96 P19	BI211145	BI211145	Rep: Xylo	GTTTCCCCAAGGCTTTTCTGCTGAATGCAAGAGTTCAAGATTTTAATGAATCAAATAAGT																65730.5	31972.6	12945.7	25788	14967.9	22044.9
A 96 P20	Sense	-0.030	Detected	0.030	Detected	0.000	-1.293	Detected	-1.023	Detected	-1.158	0.014	A 96 P20	LOC5437	NM 0012	Solanum	GCAGCCCAACAAAACAATTTGTTCACCAATAATAACAACAACTTGATGATGATAGCCAAT																1448.31	1420.64	808.727	750.3	624.449	750.415
A 96 P20	Sense	-0.043	Detected	0.043	Detected	0.000	-1.503	Detected	-1.269	Detected	-1.386	0.008	A 96 P20	BI924211	BI924211	Unknown	AGAACGATAGTTCAAGAATTGCTGCTAGGCTCTCTCTGGATGCCAACAATGTTAGGTCAG																634.644	634.232	184.405	211.375	238.705	279.824
A 96 P20	Sense	-0.113	Detected	0.113	Detected	0.000	-1.296	Detected	-1.369	Detected	-1.332	0.008	A 96 P20	BI926044	BI926044	Unknown	GGAGATTTACTTTCCTCCTACTTGTCTTCAGCAAGAAAATTTCTGCGAATAAATTTTGTG																98.6106	108.504	24.0525	23.6952	44.9318	42.5858
A 96 P20	Sense	0.288	Detected	-0.288	Detected	0.000	-2.400	Detected	-1.828	Detected	-2.114	0.035	A 96 P20	BI926779	BI926779	Unknown	CACAACTTCTACTACACGTTAGAAGATGTATTGTTCGATGAAGTATCTAGAAAACAACCC																273.043	172.274	34.0138	54.8993	43.8129	64.9641
A 96 P20	Sense	0.077	Detected	-0.077	Detected	0.000	-1.547	Detected	-1.271	Detected	-1.409	0.012	A 96 P20	BI928574	BI928574	Unknown	CCGATATCCTTATGCAGTCTTATACTACATTCATTCAGAACTTTATGGTATGGGAGCAAG																29117	24640.3	8754.01	8957.47	9774.36	11801.5
A 96 P20	Sense	0.349	Detected	-0.349	Detected	0.000	-1.493	Detected	-2.640	Comprom	-2.067	0.091	A 96 P20	AK32041	AK32041	Solanum	GTTTTCATTTTGAGGTGGAACAACAGGTGAATGGGGTATTCTTGAACTTCTTTGGTTTCA																67.238	38.9787	9.05634	18.0853	19.3999	8.72937
A 96 P20	Sense	-0.234	Detected	0.234	Detected	0.000	-1.163	Detected	-1.251	Detected	-1.207	0.037	A 96 P20	BI934195	BI934195	Rep: 3-hy	TTTACATGTCGTTACGCTTTCTGAATTGGGTGCTATTGTTTCGTTAATTGCTTCTGTCAT																670.342	872.095	339.924	370.197	364.215	341.662
A 96 P20	Sense	0.352	Detected	-0.352	Detected	0.000	-1.367	Detected	-2.307	Detected	-1.837	0.089	A 96 P20	LOC1007	NM 0012	Solanum	ACCAACCCCTCGGATTACAGTAACAGATCCAAAGCTAATAAAAGAAGTGGTGAACAGACA																191.72	110.793	22.6216	45.6295	60.2432	31.3182
A 96 P21	Sense	-0.145	Detected	0.145	Detected	0.000	-1.070	Detected	-0.988	Detected	-1.029	0.021	A 96 P21	BP90134	BP90134	Unknown	GAATTCCGAATTCAAGTCCACTATTTCTGCTAACCCTCTTCAAAATACTCTCTCTCTTAA																22.388	25.7718	12.3455	4.97381	12.2034	12.8742
A 96 P21	Sense	0.141	Detected	-0.141	Detected	0.000	-1.849	Detected	-3.812	Detected	-2.831	0.104	A 96 P21	BP90219	BP90219	Unknown	CGTTCATCTCACGACACCTTCCGATTCAATCGATAAGCGTTTCAGGCAATTTTATACTCC																413.983	320.229	74.7858	54.9563	107.767	27.5587
A 96 P21	Sense	0.079	Detected	-0.079	Detected	0.000	-1.220	Detected	-1.700	Detected	-1.460	0.029	A 96 P21	BP90239	BP90239	Unknown	GTCTCTACCTAACAATAATCGGTGGTTGCGTGCACATCTCCTCCTCCCAACATTTTGATT																1196.18	1008.6	259.132	176.52	502.858	359.401
A 96 P22	Sense	0.058	Detected	-0.058	Detected	0.000	-0.978	Detected	-1.177	Detected	-1.077	0.011	A 96 P22	BP90988	BP90988	Unknown	CTTAACAATGTTGGGGATTTAACAAGCCTTGGCTGGAAAATGGTGGAGTTCCCATTGGAT																203.355	176.654	52.0303	55.9064	102.615	89.1263
A 96 P22	Sense	0.020	Detected	-0.020	Detected	0.000	-1.794	Detected	-1.913	Detected	-1.854	0.001	A 96 P22	PIN3	NM 0012	Solanum	TGTTATGGGGATTCCATTATTGATAGCTATGTATGGTGATTATTCAGGTAGTTTGATGGT																328.975	301.238	124.87	93.5638	96.7879	88.8882
A 96 P22	Sense	0.050	Detected	-0.050	Detected	0.000	-1.623	Detected	-1.312	Detected	-1.467	0.012	A 96 P22	CAS1	NM 0012	Solanum	TGGTTCTGCTTTGAGCTATGTTACTCTGAGATTGCTTGGGGAAGGAGCTAATGATGGAGA																58.731	51.5418	12.8576	9.49757	19.0526	23.5582
A 96 P23	Sense	0.211	Detected	-0.211	Detected	0.000	-1.577	Detected	-1.566	Detected	-1.571	0.018	A 96 P23	TA49869	TA49869	Rep: Chr	AAGTAATGAATATGAGTAAAGTGCAACATTTTATGGAGCCAGTTTTGGAGCCACTTATTC																223.097	156.672	73.3109	70.1414	66.8293	67.1518
A 96 P23	Sense	-0.109	Detected	0.109	Detected	0.000	-1.046	Detected	-1.255	Detected	-1.150	0.017	A 96 P23	Aiv-1	NM 0012	Solanum	TCATGATGCTTTATACCGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACC																433.472	474.447	176.78	189.682	234.23	202.053
A 96 P23	Sense	0.204	Detected	-0.204	Detected	0.000	-1.181	Detected	-1.237	Detected	-1.209	0.028	A 96 P23	BT01358	BT01358	Lycopers	TAAAAAGTTGCTAAATGACAACCCTTTTCTTCTTAATGAACGTAACCCTGTTATGGTGCA																362.496	257.145	90.6881	116.222	143.59	137.729
A 96 P23	Sense	-0.026	Detected	0.026	Detected	0.000	-0.849	Detected	-1.281	Detected	-1.065	0.039	A 96 P23	AK32429	AK32429	Solanum	CCGAGAAGGTATCCGAGTCATGGGGAGGTGTTGGAGTATTTGAATGATTTTGCTGTTGAT																2677.07	2612.78	1079.1	1319.84	1565.31	1157.42
A 96 P23	Sense	0.063	Detected	-0.063	Detected	0.000	-0.854	Detected	-1.242	Detected	-1.048	0.036	A 96 P23	Fad7	NM 0012	Solanum	CTTCCGTTTCTGTTTCCGCCACCAGTTTGAATTTGAGAAGAATTTCACCTTCACCTATAC																1541.73	1329.77	577.985	357.132	844.729	643.624
A 96 P23	Sense	0.172	Detected	-0.172	Detected	0.000	-1.475	Detected	-1.362	Detected	-1.418	0.016	A 96 P23	BT01358	BT01358	Lycopers	GATGAACTAGAAAGCGAATTATCTAAAATAGTGGGGCTAGATGAACTTAAACTGCAACTC																722.819	535.52	140.822	188.343	238.687	257.367
A 96 P24	Sense	0.101	Detected	-0.101	Detected	0.000	-1.104	Detected	-1.017	Detected	-1.061	0.011	A 96 P24	DB71980	DB71980	Unknown	CACAGTTGTAATCTTTTCTTCTTTGGTTTTGCAAAAACCTTTCGTTAGGGTTTTCGTTCA																366.845	299.957	118.163	164.435	164.533	174.279
A 96 P24	Sense	0.135	Detected	-0.135	Detected	0.000	-1.342	Detected	-0.910	Detected	-1.126	0.048	A 96 P24	AK32846	AK32846	Solanum	GGTGATCTTGGATATGCTTCTGAGCTCGGTAATTATACCGAATATAGCGGTGCTCCAAAT																8984.25	7008.01	2261.26	3021.88	3337.97	4490.15
A 96 P24	Sense	0.173	Detected	-0.173	Detected	0.000	-0.958	Detected	-1.226	Detected	-1.092	0.038	A 96 P24	PDH	BT01273	Lycopers	ACGGACCGTTACTAATCTATCGGATTCTGGGTTAAAAGCCATGCTTGATTATGGGGTGGA																387.198	286.572	66.4998	140.188	182.908	151.376
A 96 P24	Sense	0.187	Detected	-0.187	Detected	0.000	-2.256	Detected	-1.722	Detected	-1.989	0.026	A 96 P24	TA42313	TA42313	Rep: Chr	TGCTTGTCAAGAAGCTCCAGACATGTTACCCTGTGTTGTTTCTCACAAATGGAGGTACCT																7565.84	5493.37	1183.28	1872.3	1439.72	2078.32
A 96 P24	Sense	-0.063	Detected	0.063	Detected	0.000	-0.844	Detected	-1.647	Detected	-1.246	0.092	A 96 P24	DY52345	DY52345	Rep: Chr	GACTTGCAAGACGTGCTTAGGCGTTTTGCTTTTGATACAATATGCAAGGTGTCCCTAGGT																103.353	106.129	36.196	21.0464	62.2292	35.544
A 96 P24	Sense	0.138	Detected	-0.138	Detected	0.000	-1.498	Detected	-1.456	Detected	-1.477	0.009	A 96 P24	AK32240	AK32240	Solanum	GCAGTTCATGATTTTAATGGTATCGTGAATATTCTGTTGCATCATCCGTATCATGTTGAC																289.696	225.277	70.5908	76.3451	96.445	98.9973
A 96 P25	Sense	-0.233	Detected	0.233	Detected	0.000	-2.463	Comprom	-2.635	Comprom	-2.549	0.009	A 96 P25	ES89576	ES89576	LET094	TCCATTTTGTCATACACCCCATCTATAGATGCTGATATTAGAACTTGTTCAGATGGACAT																22.0345	28.6392	2.01596	2.25361	4.85771	4.30048
A 96 P25	Sense	0.017	Detected	-0.017	Detected	0.000	-1.427	Detected	-1.401	Detected	-1.414	0.000	A 96 P25	TC22461	TC22461	Rep: Chr	GAATGATGCTGAGCTTTTTTGGAGGGCTTCATTTGTTCCTCAAATGAAAAAATTGCCTTT																189.245	174.007	37.2564	61.4716	71.9536	73.0385
A 96 P25	Sense	-0.672	Detected	0.672	Detected	0.000	-1.131	Detected	-1.414	Detected	-1.273	0.205	A 96 P25	ES89697	ES89697	LET111	CCGTTACCAGAGCTTCATCCCCTCAGATATAAGGATTTACCATTTTATGTCGTCAATAAT																23.9684	57.2848	22.0514	15.6998	18.0387	14.7847
A 96 P25	Sense	0.265	Detected	-0.265	Detected	0.000	-3.057	Detected	-1.935	Detected	-2.496	0.057	A 96 P25	AK24727	AK24727	Solanum	TCACAAATTTTGATGATGTAGAAAAGGAATTACAAGGTGCCCGTTTCAACACGGACGAGT																217.957	142.011	45.8075	40.3338	22.5495	48.9282
A 96 P25	Sense	-0.065	Detected	0.065	Detected	0.000	-1.032	Detected	-1.127	Detected	-1.080	0.005	A 96 P25	AW09319	AW09319	EST2863	TCTCCCGGTAGTGAAGACTTTGATAATGCTTCTATAGACAGTTCCACTAGCAGATTTAGT																375.365	386.393	181.41	127.217	198.587	185.352
A 96 P26	Sense	-0.196	Detected	0.196	Detected	0.000	-1.143	Detected	-1.689	Detected	-1.416	0.052	A 96 P26	TC23812	TC23812	Rep: 3-hy	GAATTTCTATTGAAGGAAGATAGTCGTTGTGGACCTGCAACTACTCTTGGTTGTGCACCA																571.45	705.203	222.025	215.921	306.51	209.283
GT Sense	Sense	0.160	Detected	-0.160	Detected	0.000	-2.721	Detected	-2.220	Detected	-2.471	0.014	GT Sens	AF09829	AF09829	Lycopers	TTTTGATAACGAGGTGTTAGGTTGATAATGTGGAGAAGTCGGAGGAAGAAAGGAGTGAAG																7192.73	5418.21	1394.15	1354.89	1009.54	1424.19
GT Sense	Sense	0.266	Detected	-0.266	Detected	0.000	-2.366	Detected	-1.152	Detected	-1.759	0.117	GT Sens	BI206022	BI206022	TPRP-F1	GTGGAGTATGAATGCTGATTTGATTGTATGAACACGAATGAATGAGGAAAAATCACCTAA																998.388	649.978	410.067	240.416	166.694	385.385
GT Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.407	Detected	-2.113	Detected	-1.760	0.043	GT Sens	contig100	contig100	Amino ac	TCATCA	contig100	Solyc10g	Solyc10g	Amino ac	GO:0016	GO:0016	contig100	Solyc10g	Amino ac	GO:0016	SL2.40ch	AT3G19553.1		amino ac	chr3:679	756.979	592.39	184.348	305.251	269.348	164.551
GT Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.750	Detected	-1.349	Detected	-1.550	0.016	GT Sens	contig100	contig100	Processi	TTGTTG	contig100	Solyc12g	Solyc12g	Processi	GO:0009	GO:0009	contig100	Solyc12g	Processi	GO:0009	SL2.40ch	AT5G204	MGD2, AT	MGD2; 1	chr5:689	65.9739	60.7868	24.8539	19.0765	20.0712	26.4368
GT Sense	Sense	0.018	Detected	-0.018	Detected	0.000	-1.398	Detected	-1.540	Detected	-1.469	0.002	GT Sens	contig100	contig100	3-deoxy-	TCATCT	contig100	Solyc04g	Solyc04g	3-deoxy-7	GO:0005	GO:0005	contig100	Solyc04g	3-deoxy-7	GO:0005	SL2.40ch	AT1G22410.1		2-dehydr	chr1:791	19159.8	17588.9	5995.74	7668	7428.69	6713.51
GT Sense	Sense	-0.079	Detected	0.079	Detected	0.000	-1.216	Detected	-1.135	Detected	-1.175	0.006	GT Sens	contig101	contig101	Nuclear t	TTCAACT	contig101	Solyc12g	Solyc12g	Nuclear t	GO:0016	GO:0016	contig101	Solyc12g	Nuclear t	GO:0005	SL2.40ch	AT3G140	NF-YA6	NF-YA6 (	chr3:464	1464.16	1537.51	245.902	230.148	688.903	726.379
GT Sense	Sense	-0.106	Detected	0.106	Detected	0.000	-1.719	Detected	-1.310	Detected	-1.514	0.022	GT Sens	contig101	contig101	Ethylene-	TGGCAA	contig101	Solyc08g	Solyc08g	Ethylene-	GO:0016	GO:0016	contig101	Solyc08g	Ethylene-	GO:0016	SL2.40ch	AT5G519	CBF4, DR	CBF4 (C-	chr5:211	710.631	774.165	394.919	968.003	240.217	318.136
GT Sense	Sense	0.442	Detected	-0.442	Detected	0.000	-4.516	Detected	-3.775	Detected	-4.145	0.019	GT Sens	contig101	contig101	Catalytic/	TGGGAC	contig101	Solyc03g	Solyc03g	Catalytic/	GO:0003	GO:0003	contig101	Solyc03g	Catalytic/	GO:0004	SL2.40ch	AT5G24940.1		protein p	chr5:859	462.93	235.879	28.6015	47.4749	15.4017	25.6691
GT Sense	Sense	0.285	Detected	-0.285	Detected	0.000	-3.763	Detected	-1.828	Detected	-2.796	0.109	GT Sens	contig102	contig102	Chitinase	TAGAGC	contig102	Solyc04g	Solyc04g	Chitinase	GO:0008	GO:0008	contig102	Solyc04g	Chitinase	GO:0008	SL2.40ch	AT3G544	ATEP3, A	ATEP3; c	chr3:201	4614.11	2923.33	1412.05	1750.58	288.463	1099.55
GT Sense	Sense	0.320	Detected	-0.320	Detected	0.000	-2.108	Detected	-1.664	Detected	-1.886	0.040	GT Sens	contig102	contig102	Unknown	CGCCTT	contig102	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig102	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G18370.1		disease r	chr5:608	54.7622	33.0728	19.2683	45.6525	10.5264	14.2794
GT Sense	Sense	0.166	Detected	-0.166	Detected	0.000	-1.304	Comprom	-0.871	Detected	-1.088	0.058	GT Sens	contig102	contig102	Chromod	TGGCGT	contig102	Solyc01g	Solyc01g	Chromod	GO:0005	GO:0005	contig102	Solyc01g	Chromod	GO:0005	SL2.40ch	AT2G44980.2		transcrip	chr2:185	24.8161	18.5417	5.6913	11.4522	9.26114	12.469
GT Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-1.392	Detected	-1.163	Detected	-1.278	0.008	GT Sens	contig102	contig102	Phospho	GTAGCG	contig102	Solyc05g	Solyc05g	Phosphoglycerate mutase fam			contig102	Solyc05g	Phosphoglycerate r		SL2.40ch	AT3G60420.2		LOCATE	chr3:223	7696.11	7377.67	2977.8	4296.29	3060.83	3578.56
GT Sense	Sense	0.116	Detected	-0.116	Detected	0.000	-1.656	Detected	-1.411	Detected	-1.534	0.012	GT Sens	contig103	contig103	Receptor	GTAGAT	contig103	Solyc06g	Solyc06g	Receptor	GO:0005	GO:0005	contig103	Solyc06g	Receptor-	GO:0005	SL2.40ch	AT4G08875.1		Encodes	chr4:567	1566.98	1255.38	529.948	798.583	474.718	560.615
GT Sense	Sense	-0.100	Detected	0.100	Detected	0.000	-1.070	Detected	-1.024	Detected	-1.047	0.009	GT Sens	contig103	contig103	Cysteine-	TGGTTA	contig103	Solyc03g	Solyc03g	Cysteine-rich repeat secretory			contig103	Solyc03g	Cysteine-rich repea		SL2.40ch	AT1G045	PDLP2	PDLP2 (F	chr1:123	392.007	423.725	226	149.93	207.05	213.069
GT Sense	Sense	0.329	Detected	-0.329	Detected	0.000	-1.265	Detected	-1.655	Comprom	-1.460	0.062	GT Sens	contig103	contig103	Os02g07	TCTTGT	contig103	Solyc01g	Solyc01g	Os02g0794300 protein (Fragm			contig103	Solyc01g	Os02g0794300 prot		SL2.40ch	AT2G441	EDE1	EDE1 (EN	chr2:182	34.6473	20.6689	6.83946	10.8839	11.8771	9.03523
GT Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.213	Detected	-0.967	Detected	-1.090	0.014	GT Sens	contig103	contig103	BY-inesin	GACTTC	contig103	Solyc01g	Solyc01g	BY-inesir	GO:0007	GO:0007	contig103	Solyc01g	BY-inesin	GO:0007	SL2.40ch	AT5G27950.1		kinesin n	chr5:998	2268.91	2001.04	769.185	1231.3	980.054	1159.1
GT Sense	Sense	0.091	Detected	-0.091	Detected	0.000	-1.253	Detected	-0.986	Detected	-1.120	0.020	GT Sens	contig103	contig103	Multidrug	AGGATG	contig103	Solyc03g	Solyc03g	Multidrug	GO:0015	GO:0015	contig103	Solyc03g	Multidrug	GO:0015	SL2.40ch	AT4G23030.1		MATE ef	chr4:120	3501.17	2903.07	1746.34	2582.29	1426.61	1710.84
GT Sense	Sense	0.670	Detected	-0.670	Detected	0.000	-3.116	Detected	-3.070	Detected	-3.093	0.044	GT Sens	contig104	contig104	1-aminoc	TGAGAG	contig104	Solyc01g	Solyc01g	1-aminoc	GO:0016	GO:0016	contig104	Solyc01g	1-aminoc	GO:0016	SL2.40ch	AT4G10490.1		oxidored	chr4:648	293.442	109.115	81.5295	28.0151	22.0104	22.6506
GT Sense	Sense	0.135	Detected	-0.135	Detected	0.000	-1.868	Detected	-1.916	Detected	-1.892	0.005	GT Sens	contig104	contig104	BES1/BZI	ATGATC	contig104	Solyc03g	Solyc03g	BES1/BZI	GO:0030	GO:0030	contig104	Solyc03g	BES1/BZI	GO:0030	SL2.40ch	AT1G78700.1		brassino	chr1:295	439.913	343.171	74.6378	105.117	113.506	109.44
GT Sense	Sense	-0.066	Detected	0.066	Detected	0.000	-1.938	Detected	-1.979	Detected	-1.958	0.001	GT Sens	contig104	contig104	Ribonucl	AATGTA	contig104	Solyc05g	Solyc05g	Ribonucl	GO:0033	GO:0033	contig104	Solyc05g	Ribonucl	GO:0004	SL2.40ch	AT2G029	RNS1, AT	RNS1 (RI	chr2:873	185907	191669	106071	86518.1	52528.6	50923.4
GT Sense	Sense	0.302	Detected	-0.302	Detected	0.000	-3.269	Detected	-3.275	Detected	-3.272	0.008	GT Sens	contig104	contig104	Disease r	CAACAT	contig104	Solyc01g	Solyc01g	Disease resistance response			contig104	Solyc01g	Disease resistance		SL2.40ch	AT1G58170.1		disease r	chr1:215	1399.52	866.457	228.288	141.426	121.794	120.95
GT Sense	Sense	-0.080	Detected	0.080	Detected	0.000	-1.443	Detected	-1.127	Detected	-1.285	0.018	GT Sens	contig104	contig104	Zinc finge	CCCTCG	contig104	Solyc04g	Solyc04g	Zinc finge	GO:0003	GO:0003	contig104	Solyc04g	Zinc finge	GO:0005	SL2.40ch	AT4G39070.1		zinc fing	chr4:182	63.5626	66.8421	50.3287	41.6847	25.5614	31.7202
GT Sense	Sense	0.246	Detected	-0.246	Detected	0.000	-3.433	Detected	-2.472	Detected	-2.952	0.032	GT Sens	contig104	contig104	Zinc finge	TTTAGA	contig104	Solyc09g	Solyc09g	Zinc finger and SCAN domain			contig104	Solyc09g	Zinc finger and SCA		SL2.40ch	AT2G38250.1		DNA-bind	chr2:160	1294.87	866.602	167.738	304.029	104.614	203.051
GT Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-1.116	Detected	-0.888	Detected	-1.002	0.018	GT Sens	contig104	contig104	LRR rece	GAAAGT	contig104	Solyc02g	Solyc02g	LRR rece	GO:0005	GO:0005	contig104	Solyc02g	Receptor	GO:0004	SL2.40ch	AT2G23300.1		leucine-r	chr2:991	3803.87	3216.24	1927.39	1924.41	1720.91	2009.38
GT Sense	Sense	-0.403	Detected	0.403	Detected	0.000	-2.493	Comprom	-0.936	Detected	-1.715	0.190	GT Sens	contig104	contig104	Cullin 1B	CATTGG	contig104	Solyc06g	Solyc06g	Cullin 1B	GO:0030	GO:0030	contig104	Solyc06g	Cullin 1B	GO:0030	SL2.40ch	AT4G025	ATCUL1,	ATCUL1	chr4:112	24.7436	40.7244	14.0164	11.2502	6.01149	17.64
GT Sense	Sense	-0.206	Detected	0.206	Detected	0.000	-1.106	Detected	-1.158	Detected	-1.132	0.032	GT Sens	contig104	contig104	Cytokinin	CCAAAG	contig104	Solyc10g	Solyc10g	Cytokinin	GO:0016	GO:0016	contig104	Solyc10g	Cytokinin	GO:0016	SL2.40ch	AT5G06300.1		carboxy-	chr5:192	85.2894	106.825	39.0574	26.3259	47.3048	45.466
GT Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-1.175	Detected	-1.387	Detected	-1.281	0.010	GT Sens	contig105	contig105	Transcrip	AAATCC	contig105	Solyc02g	Solyc02g	Transcription factor (Fragmen			contig105	Solyc02g	Transcription factor		SL2.40ch	AT3G021	PTF1, TF	PTF1 (PL	chr3:391	5281.67	5514.07	2426.04	1954.19	2549.25	2194.24
GT Sense	Sense	0.483	Detected	-0.483	Detected	0.000	-0.854	Detected	-1.351	Detected	-1.102	0.180	GT Sens	contig105	contig105	60S acidi	GTTGCA	contig105	Solyc09g	Solyc09g	60S acidi	GO:0005	GO:0005	contig105	Solyc09g	60S acidi	GO:0005	SL2.40ch	AT2G40010.1		60S acid	chr2:167	98.8724	47.6163	106.286	199.999	40.491	28.6076
GT Sense	Sense	0.324	Detected	-0.324	Detected	0.000	-1.062	Detected	-1.537	Detected	-1.299	0.084	GT Sens	contig105	contig105	GATA tra	AGAGTT	contig105	Solyc01g	Solyc01g	GATA tra	GO:0031	GO:0031	contig105	Solyc01g	GATA tra	GO:0031	SL2.40ch	AT3G60530.1		zinc fing	chr3:223	65.0656	39.0629	8.85567	7.12069	25.7551	18.4762
GT Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-1.625	Detected	-1.371	Detected	-1.498	0.015	GT Sens	contig105	contig105	Fatty acid	GTAGTT	contig105	Solyc10g	Solyc10g	Fatty acid	GO:0009	GO:0009	contig105	Solyc10g	Fatty acid	GO:0009	SL2.40ch	AT5G437	KCS20	KCS20 (3	chr5:175	56686.4	44462.3	19481.8	24793.2	17353.8	20630.2
GT Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-1.545	Detected	-1.362	Detected	-1.453	0.011	GT Sens	contig106	contig106	Unknown	GAGCTG	contig106	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig106	Solyc07g	Unknown Protein (A		SL2.40ch	AT3G05670.1		PHD fing	chr3:165	3396.77	2709.51	1115.32	1386.99	1108.77	1255.16
GT Sense	Sense	0.187	Detected	-0.187	Detected	0.000	-1.549	Detected	-0.925	Detected	-1.237	0.077	GT Sens	contig106	contig106	Chitinase	CTAACT	contig106	Solyc07g	Solyc07g	Chitinase	GO:0006	GO:0006	contig106	Solyc07g	Chitinase	GO:0008	SL2.40ch	AT5G451	NRPC2	NRPC2;	chr5:182	433.416	314.607	240.745	243.29	134.537	206.825
GT Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.205	Detected	-1.215	Detected	-1.210	0.001	GT Sens	contig106	contig106	Os12g05	TGTGAT	contig106	Solyc07g	Solyc07g	Os12g0554100 protein (Fragm			contig106	Solyc07g	Os12g0554100 prot		SL2.40ch	AT5G20680.3		unknown	chr5:699	984.994	870.209	315.208	416.905	428.118	424.124
GT Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.676	Detected	-1.349	Detected	-1.513	0.012	GT Sens	contig106	contig106	ABC tran	CCAATT	contig106	Solyc04g	Solyc04g	ABC tran	GO:0016	GO:0016	contig106	Solyc04g	ABC tran	GO:0008	SL2.40ch	AT3G55090.1		ATPase,	chr3:204	1087.73	966.353	230.783	567.483	342.045	428.008
GT Sense	Sense	0.177	Detected	-0.177	Detected	0.000	-2.545	Detected	-1.908	Detected	-2.226	0.026	GT Sens	contig106	contig106	Transcrip	CATGTT	contig106	Solyc06g	Solyc06g	Transcrip	GO:0003	GO:0003	contig106	Solyc06g	Transcrip	GO:0003	SL2.40ch	AT3G07340.1		basic hel	chr3:234	3535.08	2603.85	505.61	912.003	554.296	859.772
GT Sense	Sense	0.257	Detected	-0.257	Detected	0.000	-1.402	Detected	-1.472	Detected	-1.437	0.031	GT Sens	contig106	contig106	Unknown	GCAGCA	contig106	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig106	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G27690.1		heavy-m	chr5:980	6943.09	4575.28	1726.18	3727.77	2274.67	2159.78
GT Sense	Sense	0.082	Detected	-0.082	Detected	0.000	-1.226	Detected	-1.188	Detected	-1.207	0.005	GT Sens	contig106	contig106	Organic a	GTATGT	contig106	Solyc02g	Solyc02g	Organic a	GO:0008	GO:0008	contig106	Solyc02g	Organic a	GO:0008	SL2.40ch	AT3G17430.1		phospha	chr3:596	797.775	670.123	300.973	333.025	333.262	341.119
GT Sense	Sense	0.064	Detected	-0.064	Detected	0.000	-1.159	Detected	-1.236	Detected	-1.198	0.004	GT Sens	contig107	contig107	Unknown	GAGGAG	contig107	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig107	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G110	MTSSB	MTSSB (	chr4:675	474.357	408.672	227.985	343.294	210.267	198.708
GT Sense	Sense	0.290	Detected	-0.290	Detected	0.000	-2.023	Detected	-1.480	Detected	-1.752	0.048	GT Sens	contig107	contig107	Inositol o	GGCTTC	contig107	Solyc06g	Solyc06g	Inositol o	GO:0050	GO:0050	contig107	Solyc06g	Inositol o	GO:0050	SL2.40ch	AT5G566	MIOX5	MIOX5; i	chr5:229	1909.6	1202.73	586.017	961.399	397.56	577.523
GT Sense	Sense	0.190	Detected	-0.190	Detected	0.000	-1.211	Detected	-1.034	Detected	-1.122	0.033	GT Sens	contig107	contig107	Ras-relat	GTGAAT	contig107	Solyc05g	Solyc05g	Ras-relat	GO:0005	GO:0005	contig107	Solyc05g	Ras-relate	GO:0015	SL2.40ch	AT5G102	AtRABH1	AtRABH1	chr5:321	7126.29	5156.25	2429.64	3227.53	2791.39	3148.44
GT Sense	Sense	0.127	Detected	-0.127	Detected	0.000	-1.248	Detected	-1.351	Detected	-1.300	0.011	GT Sens	contig107	contig107	Receptor	AATTGG	contig107	Solyc03g	Solyc03g	Receptor	GO:0004	GO:0004	contig107	Solyc03g	Receptor	GO:0004	SL2.40ch	AT5G58300.2		leucine-r	chr5:235	47.9045	37.8032	15.151	11.953	19.1021	17.7338
GT Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-2.926	Detected	-2.152	Detected	-2.539	0.024	GT Sens	contig107	contig107	AP2-like	AACAAC	contig107	Solyc11g	Solyc11g	AP2-like	GO:0006	GO:0006	contig107	Solyc11g	AP2-like	GO:0003	SL2.40ch	AT5G105	AIL6, PLT	AIL6 (AIN	chr5:331	862.556	691.699	92.7969	171.464	108.389	184.824
GT Sense	Sense	0.100	Detected	-0.100	Detected	0.000	-1.621	Detected	-1.302	Detected	-1.462	0.016	GT Sens	contig108	contig108	Transmei	AGTACT	contig108	Solyc06g	Solyc06g	Transmei	GO:0016	GO:0016	contig108	Solyc06g	Transmei	GO:0016	SL2.40ch	AT1G61670.1		FUNCTIO	chr1:227	1708.45	1400.31	432.142	697.412	536.203	666.832
GT Sense	Sense	0.309	Detected	-0.309	Detected	0.000	-1.188	Detected	-1.124	Detected	-1.156	0.065	GT Sens	contig108	contig108	Armadillo	GTGAAA	contig108	Solyc02g	Solyc02g	Armadillo	GO:0005	GO:0005	contig108	Solyc02g	Armadillo	GO:0005	SL2.40ch	AT2G27430.1		binding	chr2:117	2188.88	1342.61	930.804	862.957	802.398	836.546
GT Sense	Sense	0.265	Detected	-0.265	Detected	0.000	-1.007	Detected	-1.393	Detected	-1.200	0.067	GT Sens	contig108	contig108	Cyclic nu	AAACAC	contig108	Solyc08g	Solyc08g	Cyclic nu	GO:0016	GO:0016	contig108	Solyc08g	Cyclic nu	GO:0016	SL2.40ch	AT2G246	ATCNGC	ATCNGC	chr2:104	242.29	157.975	63.8099	81.7207	103.807	79.2124
GT Sense	Sense	0.167	Detected	-0.167	Detected	0.000	-1.948	Detected	-1.291	Detected	-1.620	0.048	GT Sens	contig108	contig108	Cellulose	TTGACA	contig108	Solyc04g	Solyc04g	Cellulose	GO:0016	GO:0016	contig108	Solyc04g	Cellulose	GO:0016	SL2.40ch	AT4G079	ATCSLC1	ATCSLC	chr4:480	945.57	706.129	236.556	490.902	225.785	354.918
GT Sense	Sense	0.313	Detected	-0.313	Detected	0.000	-2.646	Detected	-2.446	Detected	-2.546	0.016	GT Sens	contig108	contig108	FAD-bind	ACATAT	contig108	Solyc02g	Solyc02g	FAD-bind	GO:0050	GO:0050	contig108	Solyc02g	FAD-bind	GO:0050	SL2.40ch	AT5G44360.1		FAD-bind	chr5:178	9156.47	5583.63	1253.49	3039.59	1218.46	1395.15
GT Sense	Sense	0.253	Detected	-0.253	Detected	0.000	-2.136	Detected	-1.354	Detected	-1.745	0.064	GT Sens	contig108	contig108	Acetyl xy	CAGACT	contig108	Solyc04g	Solyc04g	Acetyl xylan esterase A (AHRD			contig108	Solyc04g	Acetyl xylan esteras		SL2.40ch	AT2G28360.1		INVOLVE	chr2:121	1844.01	1222.28	523.076	552.142	364.208	624.418
GT Sense	Sense	0.136	Detected	-0.136	Detected	0.000	-2.611	Detected	-2.026	Detected	-2.318	0.019	GT Sens	contig108	contig108	Laccase-	TTCTGT	contig108	Solyc08g	Solyc08g	Laccase-	GO:0055	GO:0055	contig108	Solyc08g	Laccase-	GO:0055	SL2.40ch	AT4G124	SKU5	SKU5; cc	chr4:734	8475.25	6601.11	1213	3351.33	1305.86	1952.24
GT Sense	Sense	-0.310	Detected	0.310	Detected	0.000	-1.844	Detected	-0.935	Detected	-1.389	0.128	GT Sens	contig109	contig109	ATP bind	TACTCA	contig109	Solyc12g	Solyc12g	ATP bind	GO:0005	GO:0005	contig109	Solyc12g	ATP bind	GO:0005	SL2.40ch	AT2G07180.1		protein k	chr2:298	176.031	254.537	110.802	61.8051	62.8749	117.737
GT Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-2.061	Detected	-2.259	Detected	-2.160	0.004	GT Sens	contig109	contig109	Senescer	GGCTAA	contig109	Solyc08g	Solyc08g	Senescer	GO:0016	GO:0016	contig109	Solyc08g	Senescer	GO:0016	SL2.40ch	AT5G467	TET1, TR	TRN2 (TC	chr5:189	520.908	434.305	218.485	126.584	121.593	105.619
GT Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.346	Detected	-0.848	Detected	-1.097	0.053	GT Sens	contig109	contig109	Laccase-	TTACCA	contig109	Solyc04g	Solyc04g	Laccase-	GO:0055	GO:0055	contig109	Solyc04g	Laccase-	GO:0055	SL2.40ch	AT1G761	sks5	sks5 (SK	chr1:285	23882	19919.4	6677.57	11851	9151.73	12882.7
GT Sense	Sense	0.236	Detected	-0.236	Detected	0.000	-2.786	Detected	-1.715	Detected	-2.251	0.062	GT Sens	contig109	contig109	Transcrip	GGGTAG	contig109	Solyc06g	Solyc06g	Transcrip	GO:0005	GO:0005	contig109	Solyc06g	Transcrip	GO:0005	SL2.40ch	AT1G262	CIB5	CIB5 (CR	chr1:908	3798.88	2575.64	620.425	1314.23	483.536	1013.18
GT Sense	Sense	0.482	Detected	-0.482	Detected	0.000	-1.984	Detected	-1.195	Detected	-1.589	0.125	GT Sens	contig109	contig109	Polygalac	GTCCTG	contig109	Solyc12g	Solyc12g	Polygalac	GO:0005	GO:0005	contig109	Solyc12g	Polygalac	GO:0005	SL2.40ch	AT1G65570.1		polygala	chr1:243	977.65	471.484	71.9551	75.0578	183.067	315.316
GT Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-2.133	Detected	-1.001	Detected	-1.567	0.110	GT Sens	contig109	contig109	IFA bindi	AATACC	contig109	Solyc06g	Solyc06g	IFA binding protein (AHRD V1 *			contig109	Solyc06g	IFA binding protein		SL2.40ch	AT1G18990.1		unknown	chr1:655	51.8128	52.9054	30.6612	47.3685	12.7303	27.8181
GT Sense	Sense	0.215	Detected	-0.215	Detected	0.000	-1.632	Detected	-0.954	Detected	-1.293	0.085	GT Sens	contig109	contig109	Cortical c	GTGGCA	contig109	Solyc12g	Solyc12g	Cortical c	GO:0006	GO:0006	contig109	Solyc12g	Cortical c	GO:0006	SL2.40ch	AT3G22800.1		leucine-r	chr3:806	199.416	139.208	98.3925	135.017	57.3121	91.4667
GT Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-1.567	Detected	-1.356	Detected	-1.461	0.007	GT Sens	contig109	contig109	O-methyl	TTGATT	contig109	Solyc06g	Solyc06g	O-methyl	GO:0033	GO:0033	contig109	Solyc06g	O-methyl	GO:0030	SL2.40ch	AT5G38310.1		unknown	chr5:153	1209.24	1053.81	436.592	492.872	406.328	469.024
GT Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-1.011	Detected	-1.073	Detected	-1.042	0.009	GT Sens	contig110	contig110	Scarecro	ACTACA	contig110	Solyc05g	Solyc05g	Scarecrow-like 1 transcription			contig110	Solyc05g	Scarecrow-like 1 tra		SL2.40ch	AT4G172	SCL13	SCL13 (S	chr4:966	910.948	977.248	346.079	392.197	499.388	476.735
GT Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-2.164	Detected	-1.944	Detected	-2.054	0.004	GT Sens	contig110	contig110	Unknown	GGACCT	contig110	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig110	Solyc10g	Unknown Protein (A		SL2.40ch	ATCG002	PSBC	chloropla	chrC:337	276.657	233.732	61.6109	72.1072	60.4954	70.2816
GT Sense	Sense	-0.358	Detected	0.358	Detected	0.000	-1.477	Detected	-1.747	Detected	-1.612	0.052	GT Sens	contig110	contig110	AP2-like	ATAAAA	contig110	Solyc04g	Solyc04g	AP2-like	GO:0006	GO:0006	contig110	Solyc04g	AP2-like	GO:0003	SL2.40ch	AT4G377	ANT, DRG	ANT (AIN	chr4:177	245.051	378.907	133.591	64.1904	116.75	96.5207
GT Sense	Sense	0.155	Detected	-0.155	Detected	0.000	-1.642	Detected	-1.550	Detected	-1.596	0.010	GT Sens	contig111	contig111	Glycerop	AAGATA	contig111	Solyc07g	Solyc07g	Glycerop	GO:0016	GO:0016	contig111	Solyc07g	Glycerop	GO:0016	SL2.40ch	AT4G266	SHV3, MF	SHV3 (SH	chr4:134	3436.52	2608.34	892.441	1148.11	1022.64	1087.21
GT Sense	Sense	0.031	Detected	-0.031	Detected	0.000	-1.119	Detected	-1.194	Detected	-1.157	0.002	GT Sens	contig111	contig111	MaoC-like	TTATAT	contig111	Solyc06g	Solyc06g	MaoC-like	GO:0008	GO:0008	contig111	Solyc06g	MaoC-like	GO:0008	SL2.40ch	AT5G39250.1		F-box far	chr5:157	138.77	125.025	58.288	70.414	64.6607	61.2028
GT Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-2.073	Detected	-1.876	Detected	-1.974	0.009	GT Sens	contig111	contig111	Unknown	TCGGAG	contig111	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig111	Solyc03g	Unknown Protein (A		SL2.40ch	AT1G24405.1		unknown	chr1:865	212.598	159.309	54.0105	74.6955	46.6458	53.3225
GT Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-2.297	Detected	-1.431	Detected	-1.864	0.051	GT Sens	contig111	contig111	Poly(RC)	CATGCA	contig111	Solyc11g	Solyc11g	Poly(RC)	GO:0003	GO:0003	contig111	Solyc11g	Poly(RC)	GO:0003	SL2.40ch	AT5G044	BTR1, BT	BTR1L (E	chr5:125	327.096	275.82	74.9508	98.8246	65.1753	118.429
GT Sense	Sense	-0.273	Detected	0.273	Detected	0.000	-1.555	Detected	-0.931	Detected	-1.243	0.096	GT Sens	contig111	contig111	Multidrug	AATCCT	contig111	Solyc07g	Solyc07g	Multidrug	GO:0016	GO:0016	contig111	Solyc07g	Multidrug	GO:0016	SL2.40ch	AT3G21690.1		MATE ef	chr3:763	32.4732	44.6288	9.68742	12.5082	13.8161	21.2271
GT Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-1.060	Detected	-1.175	Detected	-1.118	0.011	GT Sens	contig111	contig111	Unknown	TCATTT	contig111	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig111	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G17850.1		cation ex	chr5:589	761.88	623.351	307.868	383.472	352.412	324.436
GT Sense	Sense	0.169	Detected	-0.169	Detected	0.000	-1.321	Detected	-1.123	Detected	-1.222	0.025	GT Sens	contig112	contig112	BAC19.4	TATCTC	contig112	Solyc03g	Solyc03g	BAC19.4 (AHRD V1 ***- Q9FYX			contig112	Solyc03g	BAC19.4 (AHRD V1 *		SL2.40ch	AT4G36660.1		unknown	chr4:172	391.667	291.669	154.021	214.62	144.229	164.974
GT Sense	Sense	-0.157	Detected	0.157	Detected	0.000	-0.903	Detected	-1.435	Detected	-1.169	0.063	GT Sens	contig112	contig112	Folate/bio	ATATGT	contig112	Solyc06g	Solyc06g	Folate/bic	GO:0015	GO:0015	contig112	Solyc06g	Folate/bic	GO:0015	SL2.40ch	AT2G32040.1		integral r	chr2:136	42.273	49.4298	15.0992	25.8057	26.0702	17.973
GT Sense	Sense	0.097	Detected	-0.097	Detected	0.000	-1.249	Detected	-0.854	Detected	-1.051	0.041	GT Sens	contig112	contig112	TO62-3 (F	TATTGG	contig112	Solyc07g	Solyc07g	TO62-3 (Fragment) (AHRD V1 *			contig112	Solyc07g	TO62-3 (Fragment) (		SL2.40ch	AT2G32580.1		unknown	chr2:138	9987.65	8216.46	3465.41	4032.96	4064.7	5328.99
GT Sense	Sense	1.808	Detected	-1.808	Detected	0.000	-1.590	Detected	-1.561	Detected	-1.576	0.475	GT Sens	contig112	contig112	Photosys	CATTCA	contig112	Solyc11g	Solyc11g	Photosys	GO:0016	GO:0016	contig112	Solyc11g	Photosys	GO:0016	SL2.40ch	ATCG002	PSBC	chloropla	chrC:337	585.178	44.894	62.7266	72.3909	57.4067	58.3945
GT Sense	Sense	0.242	Detected	-0.242	Detected	0.000	-2.171	Detected	-1.462	Detected	-1.817	0.052	GT Sens	contig112	contig112	Glycerop	TGTAAG	contig112	Solyc02g	Solyc02g	Glycerop	GO:0006	GO:0006	contig112	Solyc02g	Glycerop	GO:0006	SL2.40ch	AT5G41080.2		glycerop	chr5:164	20118.1	13526	3765.88	6196.18	3906.04	6366.15
GT Sense	Sense	0.129	Detected	-0.129	Detected	0.000	-1.727	Detected	-1.058	Detected	-1.393	0.060	GT Sens	contig112	contig112	Transcrip	ATAGCA	contig112	Solyc07g	Solyc07g	Transcrip	GO:0003	GO:0003	contig112	Solyc07g	Transcrip	GO:0003	SL2.40ch	AT3G150	TCP4	TCP4 (TC	chr3:506	166.996	131.446	36.05	48.7467	47.731	75.6488
GT Sense	Sense	0.062	Detected	-0.062	Detected	0.000	-1.292	Detected	-0.998	Detected	-1.145	0.019	GT Sens	contig112	contig112	Receptor	TCAATC	contig112	Solyc12g	Solyc12g	Receptor	GO:0004	GO:0004	contig112	Solyc12g	Receptor	GO:0004	SL2.40ch	AT1G63430.1		leucine-r	chr1:235	259.839	224.278	136.851	88.8396	105.116	128.468
GT Sense	Sense	0.212	Detected	-0.212	Detected	0.000	-2.973	Comprom	-1.079	Detected	-2.026	0.172	GT Sens	contig112	contig112	Receptor	TGAATG	contig112	Solyc06g	Solyc06g	Receptor	GO:0005	GO:0005	contig112	Solyc06g	Receptor	GO:0005	SL2.40ch	AT5G204	EFR	EFR (EF-	chr5:692	49.8379	34.9567	11.6012	15.583	5.66736	21.0066
GT Sense	Sense	0.278	Detected	-0.278	Detected	0.000	-2.542	Detected	-2.052	Detected	-2.297	0.025	GT Sens	contig113	contig113	Laccase-	GTAGGG	contig113	Solyc07g	Solyc07g	Laccase-	GO:0055	GO:0055	contig113	Solyc07g	Laccase-	GO:0055	SL2.40ch	AT4G220	sks4	sks4 (SK	chr4:116	957.331	612.285	150.27	185.219	140.18	196.296
GT Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-1.078	Detected	-1.266	Detected	-1.172	0.016	GT Sens	contig113	contig113	Unknown	TGTTTG	contig113	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig113	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G58540.2		protein k	chr5:236	738.64	592.622	125.882	200.923	334.215	292.468
GT Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-1.412	Detected	-1.780	Detected	-1.596	0.016	GT Sens	contig113	contig113	Cysteine-	CGTTTG	contig113	Solyc05g	Solyc05g	Cysteine-	GO:0016	GO:0016	contig113	Solyc05g	Cysteine-	GO:0016	SL2.40ch	AT1G80510.1		amino ac	chr1:302	44.9253	47.4206	9.32829	20.2675	18.4933	14.2915
GT Sense	Sense	0.331	Detected	-0.331	Detected	0.000	-2.124	Comprom	-1.069	Detected	-1.596	0.125	GT Sens	contig113	contig113	Clathrin a	TATTCT	contig113	Solyc12g	Solyc12g	Clathrin assembly protein (AH			contig113	Solyc12g	Clathrin assembly p		SL2.40ch	AT3G212	ADOF2	ADOF2; I	chr3:747	29.2855	17.411	4.36843	6.53135	5.52415	11.4472
GT Sense	Sense	0.241	Detected	-0.241	Detected	0.000	-2.325	Detected	-1.801	Detected	-2.063	0.028	GT Sens	contig113	contig113	MYB tran	ACACCT	contig113	Solyc02g	Solyc02g	MYB tran	GO:0003	GO:0003	contig113	Solyc02g	MYB tran	GO:0003	SL2.40ch	AT2G311	ATMYB14	MYB14 (I	chr2:132	203.474	137.142	43.4826	44.335	35.5485	50.9543
GT Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-2.292	Detected	-2.199	Detected	-2.245	0.003	GT Sens	contig113	contig113	Protein T	GATAAA	contig113	Solyc08g	Solyc08g	Protein T	GO:0005	GO:0005	contig113	Solyc08g	Protein T	GO:0005	SL2.40ch	AT1G27850.1		unknown	chr1:969	2919.62	2358.13	450.797	618.583	571.224	607.76
GT Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.332	Detected	-1.391	Detected	-1.362	0.001	GT Sens	contig113	contig113	Malic enz	AAATAT	contig113	Solyc08g	Solyc08g	Malic enz	GO:0004	GO:0004	contig113	Solyc08g	Malic enz	GO:0004	SL2.40ch	AT5G116	ATNADP-	ATNADP-	chr5:375	146.413	130.952	53.0576	61.515	58.6413	56.1236
GT Sense	Sense	-0.029	Detected	0.029	Detected	0.000	-1.020	Detected	-1.311	Detected	-1.166	0.016	GT Sens	contig113	contig113	F-box fan	CCGAGG	contig113	Solyc10g	Solyc10g	F-box family protein (AHRD V1			contig113	Solyc10g	F-box family protein		SL2.40ch	AT4G21510.1		F-box far	chr4:114	3151.07	3086.58	893.735	1801.01	1639.65	1336.19
GT Sense	Sense	-0.033	Detected	0.033	Detected	0.000	-2.121	Detected	-1.490	Detected	-1.805	0.029	GT Sens	contig114	contig114	ATP-bind	GCTCAT	contig114	Solyc03g	Solyc03g	ATP-bind	GO:0016	GO:0016	contig114	Solyc03g	ATP-bind	GO:0016	SL2.40ch	AT3G477	ATATH1,	ATATH1;	chr3:175	3655.37	3601.85	974.067	1800.33	889.711	1373.23
GT Sense	Sense	0.213	Detected	-0.213	Detected	0.000	-2.136	Detected	-1.649	Detected	-1.892	0.028	GT Sens	contig114	contig114	Pentatric	CTTGCT	contig114	Solyc02g	Solyc02g	Pentatric	GO:0034	GO:0034	contig114	Solyc02g	Pentatric	GO:0034	SL2.40ch	AT5G42450.1		pentatric	chr5:169	442.403	309.909	77.5756	105.024	89.8582	125.553
GT Sense	Sense	-0.110	Detected	0.110	Detected	0.000	-2.410	Comprom	-1.891	Comprom	-2.151	0.017	GT Sens	contig114	contig114	Unknown	GGGTCA	contig114	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig114	Solyc08g	Unknown Protein (A		SL2.40ch	AT4G11430.1		hydroxyp	chr4:695	12.8209	14.0477	2.10605	2.94506	2.69233	3.84641
GT Sense	Sense	0.099	Detected	-0.099	Detected	0.000	-1.226	Detected	-1.033	Detected	-1.130	0.015	GT Sens	contig114	contig114	Transcrip	CTAAAA	contig114	Solyc02g	Solyc02g	Transcription factor (AHRD V1			contig114	Solyc02g	Transcription factor		SL2.40ch	AT5G05830.1		zinc fing	chr5:175	976.704	800.87	303.632	513.814	403.122	459.531
GT Sense	Sense	0.514	Detected	-0.514	Detected	0.000	-1.307	Detected	-2.990	Detected	-2.148	0.161	GT Sens	contig115	contig115	Acid phos	CTCATA	contig115	Solyc09g	Solyc09g	Acid phos	GO:0003	GO:0003	contig115	Solyc09g	Acid phos	GO:0003	SL2.40ch	AT4G25150.1		acid pho	chr4:129	247.951	114.454	11.1851	10.565	72.6154	22.5475
GT Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-0.985	Detected	-1.245	Detected	-1.115	0.031	GT Sens	contig115	contig115	F-box fan	AGGATT	contig115	Solyc08g	Solyc08g	F-box fan	GO:0005	GO:0005	contig115	Solyc08g	F-box fan	GO:0005	SL2.40ch	AT5G54590.2		protein k	chr5:221	61.9106	47.2425	21.8937	30.0015	29.143	24.2592
GT Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.198	Detected	-0.929	Detected	-1.064	0.017	GT Sens	contig115	contig115	GPI-anch	ACCATG	contig115	Solyc07g	Solyc07g	GPI-anchored protein (AHRD V			contig115	Solyc07g	GPI-anchored prote		SL2.40ch	AT2G20700.1		unknown	chr2:892	39727.6	35351.5	18521.8	24518.8	17415.3	20924.1
GT Sense	Sense	0.265	Detected	-0.265	Detected	0.000	-2.181	Detected	-1.708	Detected	-1.944	0.032	GT Sens	contig115	contig115	Unknown	CAAGTT	contig115	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig115	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G50620.1		nodulatio	chr3:187	1745.14	1137.76	501.151	580.58	331.468	458.519
GT Sense	Sense	-0.196	Detected	0.196	Detected	0.000	-1.745	Detected	-1.687	Detected	-1.716	0.013	GT Sens	contig116	contig116	Endogluc	TCCAGC	contig116	Solyc12g	Solyc12g	Endogluc	GO:0003	GO:0003	contig116	Solyc12g	Endogluc	GO:0008	SL2.40ch	AT1G643	AtGH9C2	AtGH9C2	chr1:239	126.723	156.569	34.0969	24.2304	44.8248	46.5133
GT Sense	Sense	0.107	Detected	-0.107	Detected	0.000	-1.281	Detected	-1.223	Detected	-1.252	0.008	GT Sens	contig116	contig116	Nicalin (A	AGGCAC	contig116	Solyc11g	Solyc11g	Nicalin (A	GO:0016	GO:0016	contig116	Solyc11g	Nicalin (A	GO:0016	SL2.40ch	AT3G44330.1		INVOLVE	chr3:160	1029.91	836.065	330.297	347.103	407.334	422.689
GT Sense	Sense	0.022	Detected	-0.022	Detected	0.000	-4.356	Comprom	-4.128	Comprom	-4.242	0.001	GT Sens	contig116	contig116	Annexin	GCTAAA	contig116	Solyc01g	Solyc01g	Annexin	GO:0005	GO:0005	contig116	Solyc01g	Annexin	GO:0005	SL2.40ch	AT5G654	UBP17	UBP17 (U	chr5:261	46.1844	42.1247	2.23359	3.05564	2.2962	2.6821
GT Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.416	Detected	-2.388	Comprom	-1.902	0.060	GT Sens	contig116	contig116	Receptor	TCCATG	contig116	Solyc04g	Solyc04g	Receptor	GO:0005	GO:0005	contig116	Solyc04g	Receptor-	GO:0006	SL2.40ch	AT1G68690.1		ATP bind	chr1:257	55.6916	49.6004	12.9983	45.5484	21.0004	10.6723
GT Sense	Sense	0.223	Detected	-0.223	Detected	0.000	-1.383	Detected	-1.066	Detected	-1.224	0.046	GT Sens	contig116	contig116	N-hydrox	TTTGGA	contig116	Solyc01g	Solyc01g	N-hydrox	GO:0016	GO:0016	contig116	Solyc01g	N-hydrox	GO:0016	SL2.40ch	AT5G01210.1		transfera	chr5:845	3732.25	2578.16	961.424	1327.85	1268.74	1574.91
GT Sense	Sense	0.144	Detected	-0.144	Detected	0.000	-1.316	Detected	-1.892	Detected	-1.604	0.038	GT Sens	contig116	contig116	Homeobo	GCCTCA	contig116	Solyc06g	Solyc06g	Homeobo	GO:0005	GO:0005	contig116	Solyc06g	Homeobo	GO:0043	SL2.40ch	AT4G377	HAT22	HAT22; t	chr4:177	233.995	180.372	38.832	47.3695	87.9918	58.8681
GT Sense	Sense	-0.087	Detected	0.087	Detected	0.000	-1.348	Detected	-1.044	Detected	-1.196	0.021	GT Sens	contig117	contig117	T6A9.7 pr	TTTATT	contig117	Solyc01g	Solyc01g	T6A9.7 protein (AHRD V1 *-*- Q			contig117	Solyc01g	T6A9.7 protein (AHR		SL2.40ch	AT3G17120.2		unknown	chr3:584	1272.98	1350.82	431.412	651.237	549.224	675.998
GT Sense	Sense	0.182	Detected	-0.182	Detected	0.000	-3.647	Detected	-1.414	Detected	-2.531	0.155	GT Sens	contig117	contig117	Predicted	ATTGAT	contig117	Solyc04g	Solyc04g	Predicted by genscan and ger			contig117	Solyc04g	Predicted by gensca		SL2.40ch	AT1G15010.1		unknown	chr1:517	1014.41	741.517	201.349	246.366	73.8275	346.043
GT Sense	Sense	0.170	Detected	-0.170	Detected	0.000	-2.407	Detected	-1.811	Detected	-2.109	0.025	GT Sens	contig117	contig117	Receptor	TTCATT	contig117	Solyc09g	Solyc09g	Receptor	GO:0006	GO:0006	contig117	Solyc09g	Receptor-	GO:0006	SL2.40ch	AT5G59010.1		protein k	chr5:238	2006.31	1491.32	394.804	523.43	347.77	523.963
GT Sense	Sense	0.052	Detected	-0.052	Detected	0.000	-2.414	Comprom	-2.503	Comprom	-2.458	0.001	GT Sens	contig117	contig117	Stig1 (Fra	CAACAT	contig117	Solyc05g	Solyc05g	Stig1 (Fra	GO:0055	GO:0055	contig117	Solyc05g	Stig1 (Fra	GO:0055	SL2.40ch	AT4G31805.1				31.0562	27.2004	14.0387	24.3359	5.81608	5.45085
GT Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-1.266	Detected	-1.058	Detected	-1.162	0.015	GT Sens	contig118	contig118	Serine/thr	CCCATC	contig118	Solyc04g	Solyc04g	Serine/thr	GO:0005	GO:0005	contig118	Solyc04g	Serine/thr	GO:0005	SL2.40ch	AT1G20650.1		ATP bind	chr1:715	907.085	741.547	290.099	347.205	363.668	418.691
GT Sense	Sense	0.185	Detected	-0.185	Detected	0.000	-2.732	Detected	-1.983	Detected	-2.358	0.030	GT Sens	contig118	contig118	Beta-fruc	AGGGTT	contig118	Solyc10g	Solyc10g	Beta-fruc	GO:0005	GO:0005	contig118	Solyc10g	Beta-fruc	GO:0005	SL2.40ch	AT1G551	ATFRUCT	ATFRUCT	chr1:205	67177.9	48885.6	14080.3	18534.9	9196.83	15407.8
GT Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-1.080	Detected	-1.118	Detected	-1.099	0.002	GT Sens	contig118	contig118	Unknown	ATGCGT	contig118	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig118	Solyc03g	Unknown Protein (A		SL2.40ch	AT1G128	SCRM2, I	SCRM2 (	chr1:438	298.299	262.431	91.8665	135.505	141.177	137.088
GT Sense	Sense	0.166	Detected	-0.166	Detected	0.000	-1.525	Detected	-1.154	Detected	-1.339	0.033	GT Sens	contig118	contig118	Calcium-	CTCAGC	contig118	Solyc11g	Solyc11g	Calcium-(	GO:0006	GO:0006	contig118	Solyc11g	Calcium-d	GO:0006	SL2.40ch	AT5G194	CDPK19,	CDPK19	chr5:655	1512.6	1130.45	512.906	834.542	484.578	624.751
GT Sense	Sense	0.126	Detected	-0.126	Detected	0.000	-1.459	Detected	-1.158	Detected	-1.309	0.022	GT Sens	contig118	contig118	F-box pro	GAAAAC	contig118	Solyc05g	Solyc05g	F-box protein PP2-B1 (AHRD V			contig118	Solyc05g	F-box pro	GO:0030	SL2.40ch	AT2G022	MEE66	MEE66 (r	chr2:592	3485.88	2755.49	865.939	1257.51	1201.84	1476.41
GT Sense	Sense	-0.125	Detected	0.125	Detected	0.000	-3.804	Comprom	-1.027	Detected	-2.415	0.225	GT Sens	contig118	contig118	Unknown	AAGGAT	contig118	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig118	Solyc06g	Unknown Protein (A		SL2.40ch	AT3G33530.2		transduc	chr3:140	42.8264	47.8914	10.5764	10.6011	3.45813	23.6359
GT Sense	Sense	-0.190	Detected	0.190	Detected	0.000	-1.172	Detected	-2.064	Detected	-1.618	0.079	GT Sens	contig118	contig118	Transcrip	AGTGAA	contig118	Solyc00g	Solyc00g	Transcription factor CYCLOID			contig118	Solyc00g	Transcription factor		SL2.40ch	AT1G54740.1		FUNCTIO	chr1:204	1771.46	2168.18	855.133	314.133	927.769	498.154
GT Sense	Sense	0.095	Detected	-0.095	Detected	0.000	-1.369	Detected	-1.377	Detected	-1.373	0.005	GT Sens	contig119	contig119	Genomic	GGTTCC	contig119	Solyc02g	Solyc02g	Genomic DNA chromosome 5			contig119	Solyc02g	Genomic DNA chrom		SL2.40ch	AT5G39240.1		unknown	chr5:157	905.279	746.948	275.984	410.209	339.433	336.529
GT Sense	Sense	0.389	Detected	-0.389	Detected	0.000	-1.191	Detected	-0.892	Detected	-1.041	0.130	GT Sens	contig119	contig119	Binding p	CCTTTA	contig119	Solyc06g	Solyc06g	Binding p	GO:0005	GO:0005	contig119	Solyc06g	Binding p	GO:0005	SL2.40ch	AT1G07280.3		binding	chr1:223	562.935	308.779	125.706	199.359	194.716	238.917
GT Sense	Sense	0.129	Detected	-0.129	Detected	0.000	-2.251	Detected	-1.898	Detected	-2.075	0.011	GT Sens	contig119	contig119	Sulfotran	AATTGG	contig119	Solyc03g	Solyc03g	Sulfotran	GO:0008	GO:0008	contig119	Solyc03g	Sulfotran	GO:0080	SL2.40ch	AT3G45070.1		sulfotran	chr3:164	334.272	263.186	67.383	120.32	66.4473	84.612
GT Sense	Sense	0.307	Detected	-0.307	Detected	0.000	-1.674	Detected	-1.939	Comprom	-1.807	0.033	GT Sens	contig119	contig119	RING fing	ATGCAG	contig119	Solyc11g	Solyc11g	RING fing	GO:0008	GO:0008	contig119	Solyc11g	RING fing	GO:0008	SL2.40ch	AT1G05930.1		DNA bind	chr1:179	36.9727	22.7238	8.83327	12.708	9.68812	8.03467
GT Sense	Sense	-0.356	Detected	0.356	Detected	0.000	-1.610	Comprom	-2.054	Comprom	-1.832	0.049	GT Sens	contig119	contig119	Peroxida	ATGCTA	contig119	Solyc03g	Solyc03g	Peroxida	GO:0005	GO:0005	contig119	Solyc03g	Peroxida	GO:0004	SL2.40ch	AT1G052	RCI3, RCI	RCI3 (RA	chr1:152	15.0336	23.1701	5.15604	5.19585	6.52039	4.77954
GT Sense	Sense	0.630	Detected	-0.630	Detected	0.000	-3.395	Detected	-4.663	Detected	-4.029	0.046	GT Sens	contig119	contig119	Nodulin-li	TGGTGA	contig119	Solyc05g	Solyc05g	Nodulin-like protein (AHRD V1			contig119	Solyc05g	Nodulin-like protein		SL2.40ch	AT5G61950.1		ubiquitin	chr5:248	467.128	183.529	39.488	50.8816	29.6911	12.2871
GT Sense	Sense	0.128	Detected	-0.128	Detected	0.000	-1.847	Detected	-1.761	Detected	-1.804	0.006	GT Sens	contig120	contig120	Actin (AH	ATTCTT	contig120	Solyc01g	Solyc01g	Actin (AH	GO:0005	GO:0005	contig120	Solyc01g	Actin (AH	GO:0005	SL2.40ch	AT5G098	ACT2, AC	ACT7 (AC	chr5:305	7559.79	5958.72	1522.73	1458.66	1989.04	2106.11
GT Sense	Sense	0.542	Detected	-0.542	Detected	0.000	-2.872	Detected	-2.481	Detected	-2.677	0.043	GT Sens	contig120	contig120	Peroxida	CGTTGG	contig120	Solyc09g	Solyc09g	Peroxida	GO:0005	GO:0005	contig120	Solyc09g	Peroxida	GO:0004	SL2.40ch	AT4G26010.1		peroxida	chr4:132	117.575	52.2018	13.6356	11.7855	11.4085	14.9175
GT Sense	Sense	0.305	Detected	-0.305	Detected	0.000	-3.033	Comprom	-2.849	Comprom	-2.941	0.012	GT Sens	contig120	contig120	Sulfotran	CATTTG	contig120	Solyc05g	Solyc05g	Sulfotran	GO:0008	GO:0008	contig120	Solyc05g	Sulfotran	GO:0080	SL2.40ch	AT3G45070.1		sulfotran	chr3:164	21.6027	13.3265	1.87866	2.08177	2.21006	2.50418
GT Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-2.162	Detected	-1.253	Detected	-1.707	0.066	GT Sens	contig120	contig120	Glyoxala	GCAATT	contig120	Solyc12g	Solyc12g	Glyoxalase/bleomycin resistar			contig120	Solyc12g	Glyoxalase/bleomyc		SL2.40ch	AT1G15380.2		lactoylgl	chr1:529	260.06	216.705	61.311	99.6668	56.5589	105.919
GT Sense	Sense	0.315	Detected	-0.315	Detected	0.000	-2.998	Detected	-2.368	Detected	-2.683	0.026	GT Sens	contig120	contig120	Beta-D-gl	AATCCA	contig120	Solyc04g	Solyc04g	Beta-D-gl	GO:0005	GO:0005	contig120	Solyc04g	Beta-D-gl	GO:0005	SL2.40ch	AT5G04885.1		glycosyl	chr5:142	1162.44	707.102	186.586	185.869	120.979	186.722
GT Sense	Sense	0.473	Detected	-0.473	Detected	0.000	-2.569	Detected	-1.292	Detected	-1.930	0.136	GT Sens	contig120	contig120	Xylogluca	CCTATC	contig120	Solyc02g	Solyc02g	Xylogluca	GO:0005	GO:0005	contig120	Solyc02g	Xylogluca	GO:0016	SL2.40ch	AT5G65730.1		xylogluca	chr5:262	122.008	59.5951	22.9269	41.247	15.3262	37.0207
GT Sense	Sense	0.174	Detected	-0.174	Detected	0.000	-1.947	Detected	-2.020	Detected	-1.984	0.008	GT Sens	contig120	contig120	UDP-gluc	ACGGTG	contig120	Solyc06g	Solyc06g	UDP-gluc	GO:0008	GO:0008	contig120	Solyc06g	UDP-gluc	GO:0080	SL2.40ch	AT2G317	UGT74D1	UGT74D1	chr2:134	103.715	76.6632	14.5952	32.4752	24.6616	23.3689
GT Sense	Sense	-0.076	Detected	0.076	Detected	0.000	-1.188	Detected	-0.930	Detected	-1.059	0.019	GT Sens	contig120	contig120	Mutator-li	TTGTTA	contig120	Solyc03g	Solyc03g	Mutator-like transposase (AHR			contig120	Solyc04g	DNA repa	GO:0005	SL2.40ch	AT3G49040.1		F-box far	chr3:181	3317.11	3467.51	1793.33	1487.67	1587.39	1892.46
GT Sense	Sense	0.176	Detected	-0.176	Detected	0.000	-2.039	Detected	-2.501	Detected	-2.270	0.016	GT Sens	contig120	contig120	tRNA dim	TGCAGA	contig120	Solyc05g	Solyc05g	tRNA dim	GO:0009	GO:0009	contig120	Solyc05g	tRNA dim	GO:0009	SL2.40ch	AT4G10620.1		INVOLVE	chr4:656	98.456	72.588	13.5447	6.60905	21.9343	15.8791
GT Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-1.640	Detected	-1.856	Detected	-1.748	0.005	GT Sens	contig121	contig121	Unknown	ATCTTT	contig121	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig121	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G29540.1		unknown	chr1:103	1569.56	1366.49	476.666	529.429	501.128	430.112

GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-1.157	Detected	-1.748	Detected	-1.452	0.050
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-1.167	Detected	-1.211	Detected	-1.189	0.003
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	-1.624	Detected	-2.290	Comprom	-1.957	0.037
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	-1.260	Detected	-0.878	Detected	-1.069	0.053
GT	Sense	Sense	0.002	Detected	-0.002	Detected	0.000	-1.315	Detected	-1.201	Detected	-1.258	0.002
GT	Sense	Sense	-0.061	Detected	0.061	Detected	0.000	-1.073	Detected	-1.502	Detected	-1.288	0.029
GT	Sense	Sense	-0.146	Detected	0.146	Detected	0.000	-2.575	Comprom	-2.427	Comprom	-2.501	0.004
GT	Sense	Sense	0.238	Detected	-0.238	Detected	0.000	-2.995	Detected	-1.693	Detected	-2.344	0.077
GT	Sense	Sense	0.149	Detected	-0.149	Detected	0.000	-1.638	Detected	-1.463	Detected	-1.550	0.012
GT	Sense	Sense	0.117	Detected	-0.117	Detected	0.000	-2.882	Detected	-2.205	Detected	-2.543	0.019
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-2.027	Detected	-1.925	Detected	-1.976	0.001
GT	Sense	Sense	0.107	Detected	-0.107	Detected	0.000	-1.321	Detected	-0.917	Detected	-1.119	0.039
GT	Sense	Sense	0.258	Detected	-0.258	Detected	0.000	-2.503	Detected	-3.104	Detected	-2.803	0.019
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-1.377	Detected	-1.206	Detected	-1.292	0.011
GT	Sense	Sense	0.499	Detected	-0.499	Detected	0.000	-1.319	Detected	-1.206	Detected	-1.262	0.129
GT	Sense	Sense	0.480	Detected	-0.480	Detected	0.000	-3.538	Comprom	-3.522	Comprom	-3.530	0.018
GT	Sense	Sense	-0.281	Detected	0.281	Detected	0.000	-2.606	Comprom	-1.662	Comprom	-2.134	0.060
GT	Sense	Sense	0.234	Detected	-0.234	Detected	0.000	-1.360	Detected	-1.370	Detected	-1.365	0.028
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-4.032	Detected	-4.005	Detected	-4.019	0.000
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-2.378	Detected	-1.789	Detected	-2.084	0.022
GT	Sense	Sense	0.233	Detected	-0.233	Detected	0.000	-1.381	Detected	-1.398	Detected	-1.390	0.027
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	-1.294	Detected	-1.064	Detected	-1.179	0.010
GT	Sense	Sense	0.592	Detected	-0.592	Detected	0.000	-1.221	Detected	-1.005	Detected	-1.113	0.205
GT	Sense	Sense	0.120	Detected	-0.120	Detected	0.000	-1.827	Detected	-1.076	Detected	-1.452	0.066
GT	Sense	Sense	0.303	Detected	-0.303	Detected	0.000	-1.771	Detected	-1.505	Detected	-1.638	0.038
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-0.830	Detected	-1.517	Detected	-1.173	0.079
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	-2.231	Detected	-2.037	Detected	-2.134	0.010
GT	Sense	Sense	0.493	Detected	-0.493	Detected	0.000	-1.775	Comprom	-2.091	Comprom	-1.933	0.065
GT	Sense	Sense	-0.060	Detected	0.060	Detected	0.000	-1.000	Detected	-1.529	Detected	-1.265	0.043
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	-1.018	Detected	-1.419	Detected	-1.218	0.028
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	-1.483	Detected	-1.360	Detected	-1.422	0.003
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-1.321	Detected	-3.052	Comprom	-2.187	0.127
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	-2.926	Detected	-2.541	Detected	-2.733	0.005
GT	Sense	Sense	0.292	Detected	-0.292	Detected	0.000	-3.447	Comprom	-2.066	Detected	-2.757	0.067
GT	Sense	Sense	0.153	Detected	-0.153	Detected	0.000	-1.318	Detected	-2.406	Comprom	-1.862	0.081
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-1.673	Detected	-1.501	Detected	-1.587	0.005
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	-2.473	Comprom	-0.966	Detected	-1.720	0.150
GT	Sense	Sense	0.328	Detected	-0.328	Detected	0.000	-1.602	Detected	-1.495	Detected	-1.548	0.043
GT	Sense	Sense	0.173	Detected	-0.173	Detected	0.000	-2.507	Detected	-2.254	Detected	-2.380	0.008
GT	Sense	Sense	0.159	Detected	-0.159	Detected	0.000	-1.616	Detected	-1.045	Detected	-1.330	0.055
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.138	Detected	-0.886	Detected	-1.012	0.022
GT	Sense	Sense	-0.382	Detected	0.382	Detected	0.000	-2.622	Comprom	-1.119	Detected	-1.871	0.157
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-1.113	Detected	-1.088	Detected	-1.100	0.007
GT	Sense	Sense	0.031	Detected	-0.031	Detected	0.000	-1.281	Detected	-1.292	Detected	-1.287	0.001
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-1.486	Detected	-1.384	Detected	-1.435	0.002
GT	Sense	Sense	-0.093	Detected	0.093	Detected	0.000	-1.188	Detected	-1.010	Detected	-1.099	0.014
GT	Sense	Sense	-0.103	Detected	0.103	Detected	0.000	-0.989	Detected	-1.214	Detected	-1.101	0.019
GT	Sense	Sense	0.250	Detected	-0.250	Detected	0.000	-2.081	Detected	-1.377	Detected	-1.729	0.057
GT	Sense	Sense	0.608	Detected	-0.608	Detected	0.000	-3.765	Comprom	-5.150	Comprom	-4.458	0.040
GT	Sense	Sense	-0.148	Detected	0.148	Detected	0.000	-0.972	Detected	-1.224	Detected	-1.098	0.030
GT	Sense	Sense	0.170	Detected	-0.170	Detected	0.000	-2.634	Detected	-1.601	Detected	-2.118	0.060
GT	Sense	Sense	0.525	Detected	-0.525	Detected	0.000	-1.800	Comprom	-0.832	Detected	-1.316	0.207
GT	Sense	Sense	0.254	Detected	-0.254	Detected	0.000	-2.808	Detected	-1.051	Detected	-1.929	0.169
GT	Sense	Sense	0.022	Detected	-0.022	Detected	0.000	-1.178	Detected	-1.083	Detected	-1.130	0.002
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-1.685	Detected	-1.718	Detected	-1.701	0.005
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.821	Detected	-1.802	Detected	-1.811	0.000
GT	Sense	Sense	-0.256	Detected	0.256	Detected	0.000	-1.967	Detected	-1.593	Detected	-1.780	0.030
GT	Sense	Sense	0.452	Detected	-0.452	Detected	0.000	-2.762	Detected	-2.163	Detected	-2.463	0.045
GT	Sense	Sense	0.491	Detected	-0.491	Detected	0.000	-4.016	Detected	-2.008	Detected	-3.012	0.115
GT	Sense	Sense	0.300	Detected	-0.300	Detected	0.000	-3.948	Detected	-2.693	Detected	-3.320	0.041
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-1.283	Detected	-0.825	Detected	-1.054	0.063
GT	Sense	Sense	0.546	Detected	-0.546	Detected	0.000	-1.108	Detected	-1.273	Detected	-1.190	0.164
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	-2.236	Detected	-1.435	Detected	-1.836	0.046
GT	Sense	Sense	-0.102	Detected	0.102	Detected	0.000	-1.241	Detected	-3.229	Detected	-2.235	0.155
GT	Sense	Sense	0.264	Detected	-0.264	Detected	0.000	-3.154	Detected	-1.566	Detected	-2.360	0.106
GT	Sense	Sense	-0.167	Detected	0.167	Detected	0.000	-2.201	Detected	-1.772	Detected	-1.986	0.018
GT	Sense	Sense	0.457	Detected	-0.457	Detected	0.000	-1.998	Detected	-1.061	Detected	-1.530	0.145
GT	Sense	Sense	0.186	Detected	-0.186	Detected	0.000	-3.295	Detected	-1.700	Detected	-2.498	0.093
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-1.913	Detected	-1.137	Detected	-1.525	0.065
GT	Sense	Sense	0.943	Detected	-0.943	Detected	0.000	-2.512	Comprom	-2.886	Comprom	-2.699	0.107
GT	Sense	Sense	0.166	Detected	-0.166	Detected	0.000	-1.297	Detected	-1.043	Detected	-1.170	0.030
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.584	Detected	-1.531	Detected	-1.557	0.001
GT	Sense	Sense	-0.010	Detected	0.010	Detected	0.000	-1.380	Detected	-1.022	Detected	-1.201	0.022
GT	Sense	Sense	0.582	Detected	-0.582	Detected	0.000	-3.249	Detected	-2.196	Detected	-2.723	0.074
GT	Sense	Sense	0.583	Detected	-0.583	Detected	0.000	-0.943	Detected	-1.524	Detected	-1.234	0.199
GT	Sense	Sense	0.022	Detected	-0.022	Detected	0.000	-1.224	Detected	-0.863	Detected	-1.043	0.029
GT	Sense	Sense	0.159	Detected	-0.159	Detected	0.000	-1.442	Detected	-1.377	Detected	-1.409	0.013
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	-1.471	Detected	-0.957	Detected	-1.214	0.044
GT	Sense	Sense	0.018	Detected	-0.018	Detected	0.000	-2.464	Detected	-1.367	Detected	-1.916	0.073
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-2.758	Detected	-1.219	Detected	-1.989	0.123
GT	Sense	Sense	0.184	Detected	-0.184	Detected	0.000	-1.086	Detected	-0.924	Detected	-1.005	0.038
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.685	Detected	-1.381	Detected	-1.533	0.010
GT	Sense	Sense	0.256	Detected	-0.256	Detected	0.000	-1.163	Detected	-1.149	Detected	-1.156	0.046
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-2.122	Detected	-1.895	Detected	-2.009	0.007
GT	Sense	Sense	0.316	Detected	-0.316	Detected	0.000	-3.368	Detected	-2.129	Detected	-2.748	0.058
GT	Sense	Sense	0.312	Detected	-0.312	Detected	0.000	-2.106	Detected	-0.968	Detected	-1.537	0.141
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-1.218	Detected	-1.014	Detected	-1.116	0.011
GT	Sense	Sense	0.116	Detected	-0.116	Detected	0.000	-1.868	Detected	-0.816	Detected	-1.342	0.130
GT	Sense	Sense	0.238	Detected	-0.238	Detected	0.000	-1.323	Detected	-0.910	Detected	-1.117	0.071
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-1.803	Detected	-1.415	Detected	-1.609	0.015
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	-2.768	Detected	-1.618	Detected	-2.193	0.065
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.805	Detected	-1.285	Detected	-1.545	0.027
GT	Sense	Sense	0.522	Detected	-0.522	Detected	0.000	-4.992	Detected	-4.504	Detected	-4.748	0.014
GT	Sense	Sense	0.527	Detected	-0.527	Detected	0.000	-4.453	Detected	-1.828	Detected	-3.141	0.157
GT	Sense	Sense	0.315	Detected	-0.315	Detected	0.000	-1.453	Detected	-1.535	Detected	-1.494	0.042
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-1.966	Detected	-2.050	Detected	-2.008	0.006
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-2.177	Detected	-2.109	Detected	-2.143	0.003
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-1.523	Detected	-1.443	Detected	-1.483	0.006
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.284	Detected	-1.425	Detected	-1.354	0.008
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	-1.451	Detected	-0.851	Detected	-1.151	0.065
GT	Sense	Sense	0.108	Detected	-0.108	Detected	0.000	-3.182	Detected	-1.684	Detected	-2.433	0.085
GT	Sense	Sense	-0.241	Detected	0.241	Detected	0.000	-2.212	Detected	-2.716	Comprom	-2.464	0.019
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-1.235	Detected	-0.813	Detected	-1.024	0.041
GT	Sense	Sense	0.208	Detected	-0.208	Detected	0.000	-1.065	Detected	-1.141	Detected	-1.103	0.035
GT	Sense	Sense	-0.382	Detected	0.382	Detected	0.000	-0.981	Detected	-1.503	Detected	-1.242	0.115
GT	Sense	Sense	0.069	Detected	-0.069	Detected	0.000	-1.003	Detected	-1.168	Detected	-1.085	0.010
GT	Sense	Sense	-1.023	Detected	1.023	Detected	0.000	-1.698	Detected	-2.499	Comprom	-2.098	0.196
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-1.155	Detected	-1.016	Detected	-1.085	0.011
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-1.035	Detected	-1.295	Detected	-1.165	0.026
GT	Sense	Sense	0.054	Detected	-0.054	Detected	0.000	-1.875	Detected	-2.509	Comprom	-2.192	0.021
GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-1.278	Detected	-1.940	Detected	-1.609	0.051
GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-1.420	Detected	-1.065	Detected	-1.242	0.034
GT	Sense	Sense	0.208	Detected	-0.208	Detected	0.000	-3.397	Detected	-2.039	Detected	-2.718	0.062
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.146	Detected	-0.984	Detected	-1.065	0.008
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	-1.704	Detected	-1.409	Detected	-1.557	0.013
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-1.630	Detected	-1.486	Detected	-1.558	0.004
GT	Sense	Sense	0.190	Detected	-0.190	Detected	0.000	-2.238	Detected	-2.191	Detected	-2.214	0.007
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.211	Detected	-1.052	Detected	-1.131	0.008
GT	Sense	Sense	0.342	Detected	-0.342	Detected	0.000	-1.031	Detected	-1.282	Detected	-1.156	0.087
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-1.675	Detected	-0.878	Detected	-1.276	0.085
GT	Sense	Sense	0.076	Detected	-0.076	Detected	0.000	-1.193	Detected	-1.261	Detected	-1.227	0.005
GT	Sense	Sense	0.124	Detected	-0.124	Detected	0.000	-1.534	Detected	-1.332	Detected	-1.433	0.012
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.008	Detected	-1.632	Comprom	-1.320	0.052
GT	Sense	Sense	0.398	Detected	-0.398	Detected	0.000	-0.966	Detected	-1.469	Detected	-1.218	0.123
GT	Sense	Sense	-0.041	Detected	0.041	Detected	0.000	-3.494	Detected	-1.483	Detected	-2.488	0.132
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-1.118	Detected	-1.797	Comprom	-1.458	0.050
GT	Sense	Sense	0.022	Detected	-0.022	Detected	0.000	-2.074	Detected	-1.503	Detected	-1.788	0.025
GT	Sense	Sense	0.057	Detected	-0.057	Detected	0.000	-1.849	Detected	-1.574	Detected	-1.711	0.007
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-1.233	Detected	-3.473	Detected	-2.353	0.171
GT	Sense	Sense	0.322	Detected	-0.322	Detected	0.000	-1.931	Detected	-1.691	Detected	-1.811	0.034
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	-1.280	Detected	-1.011	Detected	-1.146	0.014
GT	Sense	Sense	0.207	Detected	-0.207	Detected	0.000	-1.207	Detected	-1.313	Detected	-1.260	0.027
GT	Sense	Sense	0.639	Detected	-0.639	Detected	0.000	-2.419	Detected	-1.777	Detected	-2.098	0.099
GT	Sense	Sense	0.140	Detected	-0.140	Detected	0.000	-1.091	Detected	-0.949	Detected	-1.020	0.023
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	-1.604	Detected	-0.953	Detected	-1.278	0.067
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-1.354	Detected	-1.161	Detected	-1.257	0.007
GT	Sense	Sense	0.215	Detected	-0.215	Detected	0.000	-0.901	Detected	-1.570	Detected	-1.236	0.090
GT	Sense	Sense	-0.010	Detected	0.010	Detected	0.000	-1.393	Detected	-1.186	Detected	-1.290	0.006
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	-1.886	Detected	-0.951	Detected	-1.418	0.122
GT	Sense	Sense	0.303	Detected	-0.303	Detected	0.000	-2.173	Detected	-1.291	Detected	-1.732	0.084
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-1.096	Detected	-0.933	Detected	-1.014	0.007
GT	Sense	Sense	0.120	Detected	-0.120	Detected	0.000	-1.855	Comprom	-0.963	Comprom	-1.409	0.093
GT	Sense	Sense	0.289	Detected	-0.289	Detected	0.000	-4.021	Comprom	-1.459	Detected	-2.740	0.172
GT	Sense	Sense	-0.016	Detected	0.016	Detected	0.000	-2.436	Detected	-1.841	Detected	-2.138	0.019
GT	Sense	Sense	-0.643	Detected	0.643	Detected	0.000	-1.014	Detected	-1.589	Detected	-1.302	0.206
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	-1.562	Detected	-1.160	Detected	-1.361	0.031
GT	Sense	Sense	0.152	Detected	-0.152	Detected	0.000	-2.181	Detected	-1.612	Detected	-1.896	0.028
GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-1.539	Detected	-1.626	Detected	-1.583	0.014
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	-3.178	Detected	-3.363	Detected	-3.270	0.002
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-1.105	Detected	-1.104	Detected	-1.104	0.005
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	-1.326	Detected	-1.024	Detected	-1.175	0.043
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-2.141	Comprom	-1.360	Detected	-1.751	0.055
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	-1.064	Detected	-0.967	Detected	-1.016	0.003
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-1.373	Detected	-1.384	Detected	-1.378	0.003
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-1.016	Detected	-0.989	Detected	-1.003	0.005
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-1.585	Detected	-1.129	Detected	-1.357	0.034
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	-1.106	Detected	-1.028	Detected	-1.067	0.004
GT	Sense	Sense	-0.178	Detected	0.178	Detected	0.000	-2.789	Comprom	-2.047	Comprom	-2.418	0.028
GT	Sense	Sense	-0.465	Detected	0.465	Detected	0.000	-1.491	Comprom	-2.306	Comprom	-1.899	0.092
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	-1.616	Detected	-1.235	Detected	-1.425	0.018
GT	Sense	Sense	1.851	Detected	-1.851	Detected	0.000	-1.691	Detected	-1.809	Detected	-1.750	0.444
GT	Sense	Sense	0.426	Detected	-0.426	Detected	0.000	-2.894	Detected	-2.704	Detected	-2.799	0.023
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-1.198	Detected	-1.216	Detected	-1.207	0.002
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	-3.975	Detected	-3.850	Detected	-3.913	0.006
GT	Sense	Sense	0.366	Detected	-0.366	Detected	0.000	-1.244	Detected	-1.332	Detected	-1.288	0.073
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-1.407	Detected	-0.999	Detected	-1.203	0.029
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-1.668	Detected	-0.860	Detected	-1.264	0.093
GT	Sense	Sense	0.181	Detected	-0.181	Detected	0.000	-1.849	Detected	-1.285	Detected	-1.567	0.043
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	-1.269	Detected	-1.096	Detected	-1.182	0.017
GT	Sense	Sense	0.255	Detected	-0.255	Detected	0.000	-2.215	Detected	-1.574	Detected	-1.895	0.044
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-1.954	Detected	-1.235	Detected	-1.594	0.049
GT	Sense	Sense	0.197	Detected	-0.197	Detected	0.000	-1.454	Detected	-1.090	Detected	-1.272	0.042
GT	Sense	Sense	0.560	Detected	-0.560	Detected	0.000	-1.569	Detected	-1.351	Detected	-1.460	0.125
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	-1.132	Detected	-1.207	Detected	-1.169	0.001
GT	Sense	Sense	-0.138	Detected	0.138	Detected	0.000	-1.641	Detected	-1.010	Detected	-1.325	0.061
GT	Sense	Sense	0.344	Detected	-0.344	Detected	0.000	-1.832	Detected	-1.389	Detected	-1.611	0.059
GT	Sense	Sense	0.120	Detected	-0.120	Detected	0.000	-1.900	Detected	-1.179	Detected	-1.539	0.056
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	-1.155	Detected	-1.064	Detected	-1.110	0.015
GT	Sense	Sense	0.696	Detected	-0.696	Detected	0.000	-1.898	Detected	-1.310	Detected	-1.604	0.168
GT	Sense	Sense	0.409	Detected	-0.409	Detected	0.000	-2.829	Detected	-3.664	Detected	-3.247	0.031
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-1.285	Detected	-0.945	Detected	-1.115	0.024
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-1.310	Detected	-0.945	Detected	-1.127	0.030
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	-0.807	Detected	-1.581	Detected	-1.194	0.091
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-1.738	Detected	-1.362	Detected	-1.550	0.016
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-2.322	Detected	-1.867	Detected	-2.095	0.012
GT	Sense	Sense	0.259	Detected	-0.259	Detected	0.000	-2.940	Comprom	-1.267	Comprom	-2.104	0.138
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	-1.563	Detected	-0.874	Detected	-1.219	0.081
GT	Sense	Sense	-0.021	Detected	0.021	Detected	0.000	-1.584	Detected	-1.321	Detected	-1.453	0.008
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	-1.923	Detected	-1.838	Detected	-1.880	0.011
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-1.779	Detected	-1.070	Detected	-1.424	0.065
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-3.024	Detected	-2.950	Detected	-2.987	0.002
GT	Sense	Sense	0.144	Detected	-0.144	Detected	0.000	-1.281	Detected	-2.132	Comprom	-1.706	0.063
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.439	Detected	-0.982	Detected	-1.210	0.035
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-2.727	Comprom	-1.990	Comprom	-2.359	0.026
GT	Sense	Sense	0.277	Detected	-0.277	Detected	0.000	-3.532	Comprom	-3.580	Comprom	-3.556	0.006
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.042	Detected	-1.577	Detected	-1.309	0.040
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.562	Detected	-1.300	Detected	-1.431	0.009
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	-1.070	Detected	-1.363	Detected	-1.217	0.015
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-1.164	Detected	-1.373	Detected	-1.269	0.011
GT	Sense	Sense	0.399	Detected	-0.399	Detected	0.000	-1.152	Detected	-1.629	Detected	-1.391	0.096
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-1.764	Detected	-1.576	Detected	-1.670	0.004
GT	Sense	Sense	0.354	Detected	-0.354	Detected	0.000	-1.923	Detected	-2.149	Detected	-2.036	0.032
GT	Sense	Sense	0.914	Detected	-0.914	Detected	0.000	-2.598	Comprom	-3.484	Comprom	-3.041	0.096
GT	Sense	Sense	0.339	Detected	-0.339	Detected	0.000	-0.984	Detected	-1.069	Detected	-1.026	0.095
GT	Sense	Sense	0.249	Detected	-0.249	Detected	0.000	-1.316	Detected	-2.389	Detected	-1.852	0.089
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-1.185	Detected	-0.871	Detected	-1.028	0.027
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	-1.114	Detected	-1.054	Detected	-1.084	0.022
GT	Sense	Sense	0.122	Detected	-0.122	Detected	0.000	-0.995	Detected	-1.025	Detected	-1.010	0.015
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-1.059	Detected	-0.968	Detected	-1.013	0.006
GT	Sense	Sense	0.099	Detected	-0.099	Detected	0.000	-1.461	Detected	-1.697	Detected	-1.579	0.009
GT	Sense	Sense	0.050	Detected	-0.050	Detected	0.000	-1.096	Detected	-1.144	Detected	-1.120	0.002
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.673	Detected	-1.032	Detected	-1.352	0.055
GT	Sense	Sense	0.264	Detected	-0.264	Detected	0.000	-1.136	Detected	-1.028	Detected	-1.082	0.057
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-1.202	Detected	-0.961	Detected	-1.081	0.014
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-0.856	Detected	-1.374	Detected	-1.115	0.068
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-2.044	Detected	-1.751	Detected	-1.898	0.009
GT	Sense	Sense	0.307	Detected	-0.307	Detected	0.000	-1.116	Detected	-2.168	Detected	-1.642	0.114
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	-2.194	Detected	-1.832	Detected	-2.013	0.008
GT	Sense	Sense	-0.070	Detected	0.070	Detected	0.000	-2.639	Comprom	-2.991	Comprom	-2.815	0.005
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	-0.952	Detected	-1.364	Detected	-1.158	0.031
GT	Sense	Sense	0.238	Detected	-0.238	Detected	0.000	-1.221	Comprom	-1.385	Comprom	-1.303	0.035
GT	Sense	Sense	0.229	Detected	-0.229	Detected	0.000	-1.643	Detected	-1.063	Detected	-1.353	0.067
GT	Sense	Sense	0.062	Detected	-0.062	Detected	0.000	-2.072	Detected	-1.580	Detected	-1.826	0.019
GT	Sense	Sense	0.170	Detected	-0.170	Detected	0.000	-1.544	Detected	-1.717	Detected	-1.631	0.013
GT	Sense	Sense	0.241	Detected	-0.241	Detected	0.000	-1.408	Detected	-0.948	Detected	-1.178	0.072
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	-1.998	Detected	-1.204	Detected	-1.601	0.058
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.214	Detected	-0.801	Detected	-1.008	0.040
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-2.250	Detected	-1.155	Detected	-1.703	0.093
GT	Sense	Sense	0.314	Detected	-0.314	Detected	0.000	-1.813	Comprom	-1.358	Detected	-1.586	0.055
GT	Sense	Sense	0.277	Detected	-0.277	Detected	0.000	-1.026	Detected	-1.362	Detected	-1.194	0.066
GT	Sense	Sense	0.330	Detected	-0.330	Detected	0.000	-2.701	Detected	-1.920	Detected	-2.311	0.046
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-1.623	Detected	-0.992	Detected	-1.308	0.065
GT	Sense	Sense	0.298	Detected	-0.298	Detected	0.000	-1.897	Detected	-1.067	Detected	-1.482	0.101
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	-2.625	Detected	-1.000	Detected	-1.813	0.162
GT	Sense	Sense	0.201	Detected	-0.201	Detected	0.000	-1.343	Detected	-1.486	Detected	-1.414	0.022
GT	Sense	Sense	0.315	Detected	-0.315	Detected	0.000	-2.384	Detected	-2.389	Detected	-2.387	0.017
GT	Sense	Sense	0.189	Detected	-0.189	Detected	0.000	-1.669	Detected	-1.692	Detected	-1.681	0.012
GT	Sense	Sense	0.326	Detected	-0.326	Detected	0.000	-1.718	Detected	-1.424	Detected	-1.571	0.048
GT	Sense	Sense	-0.342	Detected	0.342	Detected	0.000	-2.037	Comprom	-2.399	Comprom	-2.218	0.029
GT	Sense	Sense	0.192	Detected	-0.192	Detected	0.000	-1.569	Detected	-0.846	Detected	-1.208	0.098
GT	Sense	Sense	0.076	Detected	-0.076	Detected	0.000	-1.583	Detected	-1.032	Detected	-1.308	0.045
GT	Sense	Sense	-0.034	Detected	0.034	Detected	0.000	-1.142	Detected	-1.123	Detected	-1.132	0.001
GT	Sense	Sense	0.340	Detected	-0.340	Detected	0.000	-2.351	Detected	-2.025	Detected	-2.188	0.028
GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-2.538	Detected	-1.728	Detected	-2.133	0.041

GT	Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-1.123	Detected	-0.978	Detected	-1.051	0.014	GT	Sens
GT	Sense	Sense	0.095	Detected	-0.095	Detected	0.000	-2.836	Detected	-2.619	Detected	-2.728	0.003	GT	Sens
GT	Sense	Sense	0.279	Detected	-0.279	Detected	0.000	-1.877	Detected	-1.726	Detected	-1.802	0.025	GT	Sens
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-1.373	Detected	-1.132	Detected	-1.252	0.011	GT	Sens
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	-0.886	Detected	-1.649	Detected	-1.267	0.080	GT	Sens
GT	Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-1.219	Detected	-0.851	Detected	-1.035	0.030	GT	Sens
GT	Sense	Sense	0.378	Detected	-0.378	Detected	0.000	-1.269	Detected	-2.256	Comprom	-1.763	0.105	GT	Sens
GT	Sense	Sense	0.049	Detected	-0.049	Detected	0.000	-1.787	Detected	-1.395	Detected	-1.591	0.016	GT	Sens
GT	Sense	Sense	0.124	Detected	-0.124	Detected	0.000	-2.740	Detected	-1.997	Detected	-2.368	0.026	GT	Sens
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-3.581	Detected	-2.040	Detected	-2.810	0.068	GT	Sens
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-1.843	Detected	-0.959	Detected	-1.401	0.088	GT	Sens
GT	Sense	Sense	-0.010	Detected	0.010	Detected	0.000	-1.496	Detected	-1.502	Detected	-1.499	0.000	GT	Sens
GT	Sense	Sense	0.144	Detected	-0.144	Detected	0.000	-1.155	Detected	-0.968	Detected	-1.062	0.025	GT	Sens
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-1.276	Detected	-0.853	Detected	-1.065	0.042	GT	Sens
GT	Sense	Sense	-0.120	Detected	0.120	Detected	0.000	-1.630	Comprom	-1.865	Comprom	-1.748	0.009	GT	Sens
GT	Sense	Sense	0.109	Detected	-0.109	Detected	0.000	-0.988	Detected	-1.030	Detected	-1.009	0.012	GT	Sens
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	-1.283	Detected	-1.009	Detected	-1.146	0.035	GT	Sens
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	-1.205	Detected	-1.040	Detected	-1.122	0.005	GT	Sens
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-1.276	Detected	-0.815	Detected	-1.045	0.051	GT	Sens
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	-1.037	Detected	-1.288	Detected	-1.163	0.023	GT	Sens
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	-1.567	Detected	-1.005	Detected	-1.286	0.045	GT	Sens
GT	Sense	Sense	-0.169	Detected	0.169	Detected	0.000	-2.967	Detected	-1.945	Detected	-2.456	0.045	GT	Sens
GT	Sense	Sense	0.157	Detected	-0.157	Detected	0.000	-1.327	Detected	-1.168	Detected	-1.248	0.019	GT	Sens
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.600	Detected	-2.425	Detected	-2.013	0.041	GT	Sens
GT	Sense	Sense	0.007	Detected	-0.007	Detected	0.000	-1.158	Detected	-1.127	Detected	-1.142	0.000	GT	Sens
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	-2.067	Detected	-1.199	Detected	-1.633	0.065	GT	Sens
GT	Sense	Sense	0.052	Detected	-0.052	Detected	0.000	-2.556	Detected	-3.100	Detected	-2.828	0.009	GT	Sens
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-2.117	Detected	-1.626	Detected	-1.871	0.024	GT	Sens
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	-1.324	Detected	-1.213	Detected	-1.268	0.012	GT	Sens
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-1.379	Detected	-2.136	Detected	-1.758	0.045	GT	Sens
GT	Sense	Sense	0.275	Detected	-0.275	Detected	0.000	-1.265	Detected	-1.988	Detected	-1.626	0.070	GT	Sens
GT	Sense	Sense	0.624	Detected	-0.624	Detected	0.000	-3.263	Comprom	-3.026	Comprom	-3.145	0.038	GT	Sens
GT	Sense	Sense	0.376	Detected	-0.376	Detected	0.000	-3.204	Detected	-2.978	Detected	-3.091	0.016	GT	Sens
GT	Sense	Sense	0.200	Detected	-0.200	Detected	0.000	-1.612	Detected	-1.267	Detected	-1.439	0.032	GT	Sens
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-1.389	Detected	-1.010	Detected	-1.200	0.030	GT	Sens
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-0.972	Detected	-1.096	Detected	-1.034	0.007	GT	Sens
GT	Sense	Sense	-0.160	Detected	0.160	Detected	0.000	-1.449	Detected	-1.297	Detected	-1.373	0.016	GT	Sens
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-1.364	Detected	-1.203	Detected	-1.283	0.021	GT	Sens
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-2.168	Detected	-0.917	Detected	-1.543	0.133	GT	Sens
GT	Sense	Sense	-0.166	Detected	0.166	Detected	0.000	-1.178	Detected	-1.382	Detected	-1.280	0.022	GT	Sens
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	-1.126	Detected	-1.298	Detected	-1.212	0.019	GT	Sens
GT	Sense	Sense	-0.096	Detected	0.096	Detected	0.000	-2.158	Comprom	-2.355	Comprom	-2.256	0.004	GT	Sens
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	-1.269	Detected	-1.348	Detected	-1.309	0.001	GT	Sens
GT	Sense	Sense	0.170	Detected	-0.170	Detected	0.000	-1.423	Detected	-1.257	Detected	-1.340	0.019	GT	Sens
GT	Sense	Sense	0.409	Detected	-0.409	Detected	0.000	-2.960	Detected	-1.908	Detected	-2.434	0.067	GT	Sens
GT	Sense	Sense	0.324	Detected	-0.324	Detected	0.000	-1.036	Detected	-1.431	Detected	-1.234	0.083	GT	Sens
GT	Sense	Sense	0.237	Detected	-0.237	Detected	0.000	-1.994	Detected	-1.056	Detected	-1.525	0.101	GT	Sens
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	-1.406	Detected	-0.805	Detected	-1.105	0.068	GT	Sens
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	-1.132	Detected	-1.092	Detected	-1.112	0.021	GT	Sens
GT	Sense	Sense	-0.265	Detected	0.265	Detected	0.000	-1.158	Detected	-1.512	Detected	-1.335	0.052	GT	Sens
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-1.261	Detected	-0.933	Detected	-1.097	0.023	GT	Sens
GT	Sense	Sense	-0.311	Detected	0.311	Detected	0.000	-1.055	Comprom	-1.439	Comprom	-1.247	0.076	GT	Sens
GT	Sense	Sense	0.374	Detected	-0.374	Detected	0.000	-1.505	Detected	-1.284	Detected	-1.395	0.070	GT	Sens
GT	Sense	Sense	0.344	Detected	-0.344	Detected	0.000	-1.105	Detected	-1.197	Detected	-1.151	0.080	GT	Sens
GT	Sense	Sense	0.358	Detected	-0.358	Detected	0.000	-4.186	Detected	-1.744	Detected	-2.965	0.145	GT	Sens
GT	Sense	Sense	0.271	Detected	-0.271	Detected	0.000	-2.710	Detected	-1.637	Detected	-2.173	0.069	GT	Sens
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-1.669	Detected	-1.687	Detected	-1.678	0.000	GT	Sens
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	-5.400	Comprom	-2.971	Detected	-4.185	0.075	GT	Sens
GT	Sense	Sense	-0.071	Detected	0.071	Detected	0.000	-2.040	Detected	-1.099	Detected	-1.569	0.081	GT	Sens
GT	Sense	Sense	0.049	Detected	-0.049	Detected	0.000	-1.036	Detected	-1.018	Detected	-1.027	0.002	GT	Sens
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	-1.050	Detected	-1.166	Detected	-1.108	0.004	GT	Sens
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.346	Detected	-1.120	Detected	-1.233	0.009	GT	Sens
GT	Sense	Sense	0.399	Detected	-0.399	Detected	0.000	-3.644	Detected	-3.614	Detected	-3.629	0.012	GT	Sens
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	-1.839	Detected	-1.577	Detected	-1.708	0.015	GT	Sens
GT	Sense	Sense	0.359	Detected	-0.359	Detected	0.000	-1.210	Detected	-1.997	Detected	-1.604	0.095	GT	Sens
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.075	Detected	-1.032	Detected	-1.054	0.002	GT	Sens
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-0.930	Detected	-1.112	Detected	-1.021	0.014	GT	Sens
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	-1.105	Detected	-1.093	Detected	-1.099	0.001	GT	Sens
GT	Sense	Sense	0.241	Detected	-0.241	Detected	0.000	-3.130	Detected	-1.899	Detected	-2.514	0.063	GT	Sens
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	-1.571	Detected	-0.971	Detected	-1.271	0.052	GT	Sens
GT	Sense	Sense	0.248	Detected	-0.248	Detected	0.000	-2.387	Detected	-1.519	Detected	-1.953	0.060	GT	Sens
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	-1.691	Comprom	-1.544	Comprom	-1.617	0.002	GT	Sens
GT	Sense	Sense	-0.058	Detected	0.058	Detected	0.000	-2.827	Detected	-2.444	Detected	-2.636	0.006	GT	Sens
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.697	Detected	-1.179	Detected	-1.438	0.031	GT	Sens
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	-1.785	Detected	-1.526	Detected	-1.656	0.011	GT	Sens
GT	Sense	Sense	0.350	Detected	-0.350	Detected	0.000	-0.916	Comprom	-1.189	Comprom	-1.052	0.107	GT	Sens
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-1.361	Detected	-1.025	Detected	-1.193	0.023	GT	Sens
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-1.194	Detected	-1.076	Detected	-1.135	0.007	GT	Sens
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	-1.199	Detected	-1.010	Detected	-1.104	0.007	GT	Sens
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-1.368	Detected	-1.208	Detected	-1.288	0.021	GT	Sens
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-1.138	Detected	-1.142	Detected	-1.140	0.005	GT	Sens
GT	Sense	Sense	0.468	Detected	-0.468	Detected	0.000	-1.647	Detected	-1.118	Detected	-1.382	0.124	GT	Sens
GT	Sense	Sense	0.181	Detected	-0.181	Detected	0.000	-0.990	Detected	-1.038	Detected	-1.014	0.031	GT	Sens
GT	Sense	Sense	0.007	Detected	-0.007	Detected	0.000	-1.858	Detected	-1.713	Detected	-1.786	0.002	GT	Sens
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	-1.378	Detected	-1.022	Detected	-1.200	0.022	GT	Sens
GT	Sense	Sense	0.441	Detected	-0.441	Detected	0.000	-2.662	Detected	-1.533	Detected	-2.097	0.100	GT	Sens
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	-0.853	Detected	-1.594	Detected	-1.223	0.081	GT	Sens
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	-3.068	Detected	-2.659	Detected	-2.863	0.005	GT	Sens
GT	Sense	Sense	0.234	Detected	-0.234	Detected	0.000	-1.092	Detected	-1.156	Detected	-1.124	0.041	GT	Sens
GT	Sense	Sense	0.249	Detected	-0.249	Detected	0.000	-1.479	Detected	-1.116	Detected	-1.297	0.052	GT	Sens
GT	Sense	Sense	-0.262	Detected	0.262	Detected	0.000	-1.109	Detected	-0.972	Detected	-1.041	0.061	GT	Sens
GT	Sense	Sense	0.230	Detected	-0.230	Detected	0.000	-1.885	Detected	-1.744	Detected	-1.815	0.017	GT	Sens
GT	Sense	Sense	-0.007	Detected	0.007	Detected	0.000	-1.192	Detected	-0.886	Detected	-1.039	0.021	GT	Sens
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	-1.440	Detected	-1.369	Detected	-1.404	0.004	GT	Sens
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-1.686	Detected	-1.458	Detected	-1.572	0.006	GT	Sens
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.135	Detected	-1.051	Detected	-1.093	0.009	GT	Sens
GT	Sense	Sense	0.226	Detected	-0.226	Detected	0.000	-2.293	Detected	-2.510	Detected	-2.402	0.011	GT	Sens
GT	Sense	Sense	-0.271	Detected	0.271	Detected	0.000	-1.638	Detected	-2.023	Detected	-1.830	0.031	GT	Sens
GT	Sense	Sense	0.180	Detected	-0.180	Detected	0.000	-1.496	Detected	-1.173	Detected	-1.335	0.031	GT	Sens
GT	Sense	Sense	-0.423	Detected	0.423	Detected	0.000	-3.236	Comprom	-1.824	Detected	-2.530	0.092	GT	Sens
GT	Sense	Sense	0.152	Detected	-0.152	Detected	0.000	-1.140	Detected	-0.879	Detected	-1.009	0.037	GT	Sens
GT	Sense	Sense	0.230	Detected	-0.230	Detected	0.000	-1.640	Detected	-1.784	Detected	-1.712	0.019	GT	Sens
GT	Sense	Sense	0.080	Detected	-0.080	Detected	0.000	-1.569	Detected	-1.278	Detected	-1.424	0.013	GT	Sens
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-1.753	Detected	-1.291	Detected	-1.522	0.023	GT	Sens
GT	Sense	Sense	-0.106	Detected	0.106	Detected	0.000	-1.405	Detected	-1.082	Detected	-1.243	0.023	GT	Sens
GT	Sense	Sense	-0.031	Detected	0.031	Detected	0.000	-0.932	Detected	-1.467	Detected	-1.199	0.047	GT	Sens
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-1.608	Detected	-1.284	Detected	-1.446	0.017	GT	Sens
GT	Sense	Sense	0.192	Detected	-0.192	Detected	0.000	-3.171	Detected	-2.605	Detected	-2.888	0.014	GT	Sens
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	-1.814	Detected	-1.574	Detected	-1.694	0.012	GT	Sens
GT	Sense	Sense	0.184	Detected	-0.184	Detected	0.000	-1.842	Detected	-1.276	Detected	-1.559	0.044	GT	Sens
GT	Sense	Sense	0.049	Detected	-0.049	Detected	0.000	-3.796	Detected	-2.580	Detected	-3.188	0.035	GT	Sens
GT	Sense	Sense	-0.261	Detected	0.261	Detected	0.000	-2.713	Comprom	-2.122	Comprom	-2.418	0.026	GT	Sens
GT	Sense	Sense	0.515	Detected	-0.515	Detected	0.000	-2.366	Detected	-1.507	Detected	-1.936	0.102	GT	Sens
GT	Sense	Sense	0.325	Detected	-0.325	Detected	0.000	-2.269	Detected	-1.950	Detected	-2.110	0.028	GT	Sens
GT	Sense	Sense	0.286	Detected	-0.286	Detected	0.000	-1.937	Detected	-1.256	Detected	-1.597	0.070	GT	Sens
GT	Sense	Sense	-0.010	Detected	0.010	Detected	0.000	-1.480	Detected	-1.261	Detected	-1.370	0.006	GT	Sens
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	-2.456	Detected	-1.087	Detected	-1.771	0.126	GT	Sens
GT	Sense	Sense	0.189	Detected	-0.189	Detected	0.000	-2.799	Detected	-1.621	Detected	-2.210	0.070	GT	Sens
GT	Sense	Sense	0.136	Detected	-0.136	Detected	0.000	-1.539	Detected	-1.122	Detected	-1.330	0.033	GT	Sens
GT	Sense	Sense	0.107	Detected	-0.107	Detected	0.000	-1.464	Detected	-1.557	Detected	-1.510	0.006	GT	Sens
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	-1.187	Detected	-1.629	Detected	-1.408	0.027	GT	Sens
GT	Sense	Sense	0.252	Detected	-0.252	Detected	0.000	-1.607	Detected	-1.274	Detected	-1.440	0.041	GT	Sens
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-1.188	Detected	-1.082	Detected	-1.135	0.022	GT	Sens
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-1.151	Detected	-0.940	Detected	-1.046	0.013	GT	Sens
GT	Sense	Sense	0.185	Detected	-0.185	Detected	0.000	-1.568	Detected	-1.163	Detected	-1.366	0.038	GT	Sens
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	-2.577	Detected	-2.249	Detected	-2.413	0.009	GT	Sens
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	-1.098	Detected	-1.162	Detected	-1.130	0.013	GT	Sens
GT	Sense	Sense	0.396	Detected	-0.396	Detected	0.000	-1.894	Detected	-1.527	Detected	-1.710	0.059	GT	Sens
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-3.172	Comprom	-3.140	Comprom	-3.156	0.001	GT	Sens
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.635	Detected	-1.111	Detected	-1.373	0.035	GT	Sens
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	-1.084	Detected	-0.927	Detected	-1.006	0.007	GT	Sens
GT	Sense	Sense	-0.194	Detected	0.194	Detected	0.000	-1.925	Detected	-1.364	Detected	-1.644	0.040	GT	Sens
GT	Sense	Sense	-2.119	Detected	2.119	Detected	0.000	-1.014	Detected	-1.773	Detected	-1.393	0.584	GT	Sens
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-1.599	Detected	-1.241	Detected	-1.420	0.021	GT	Sens
GT	Sense	Sense	0.379	Detected	-0.379	Detected	0.000	-2.070	Detected	-2.479	Detected	-2.275	0.034	GT	Sens
GT	Sense	Sense	-0.248	Detected	0.248	Detected	0.000	-2.127	Comprom	-1.433	Comprom	-1.780	0.053	GT	Sens
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	-1.298	Detected	-1.159	Detected	-1.229	0.014	GT	Sens
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-1.585	Detected	-1.475	Detected	-1.530	0.003	GT	Sens
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	-2.945	Detected	-1.752	Detected	-2.349	0.062	GT	Sens
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-1.608	Detected	-1.571	Detected	-1.590	0.000	GT	Sens
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-3.055	Detected	-2.556	Detected	-2.806	0.011	GT	Sens
GT	Sense	Sense	0.364	Detected	-0.364	Detected	0.000	-1.616	Detected	-1.763	Detected	-1.690	0.045	GT	Sens
GT	Sense	Sense	-0.140	Detected	0.140	Detected	0.000	-2.288	Detected	-1.460	Detected	-1.874	0.050	GT	Sens
GT	Sense	Sense	0.227	Detected	-0.227	Detected	0.000	-0.998	Detected	-1.189	Detected	-1.093	0.047	GT	Sens
GT	Sense	Sense	0.287	Detected	-0.287	Detected	0.000	-1.413	Detected	-1.315	Detected	-1.364	0.043	GT	Sens
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-2.837	Detected	-1.906	Detected	-2.371	0.040	GT	Sens
GT	Sense	Sense	0.455	Detected	-0.455	Detected	0.000	-2.584	Comprom	-0.932	Detected	-1.758	0.203	GT	Sens
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-2.411	Detected	-1.599	Detected	-2.005	0.044	GT	Sens
GT	Sense	Sense	-0.174	Detected	0.174	Detected	0.000	-0.910	Detected	-1.134	Detected	-1.022	0.039	GT	Sens
GT	Sense	Sense	0.341	Detected	-0.341	Detected	0.000	-2.624	Detected	-1.800	Detected	-2.212	0.054	GT	Sens
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	-1.164	Detected	-0.963	Detected	-1.063	0.012	GT	Sens
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-1.124	Detected	-0.979	Detected	-1.052	0.007	GT	Sens
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	-1.194	Detected	-1.180	Detected	-1.187	0.010	GT	Sens
GT	Sense	Sense	0.225	Detected	-0.225	Detected	0.000	-2.339	Detected	-1.652	Detected	-1.996	0.040	GT	Sens
GT	Sense	Sense	0.329	Detected	-0.329	Detected	0.000	-3.520	Detected	-1.662	Detected	-2.591	0.119	GT	Sens
GT	Sense	Sense	-0.051	Detected	0.051	Detected	0.000	-1.024	Detected	-1.333	Detected	-1.178	0.019	GT	Sens
GT	Sense	Sense	0.257	Detected	-0.257	Detected	0.000	-0.846	Detected	-1.626	Detected	-1.236	0.118	GT	Sens
GT	Sense	Sense	-0.148	Detected	0.148	Detected	0.000	-1.110	Detected	-0.902	Detected	-1.006	0.031	GT	Sens
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-1.402	Detected	-1.055	Detected	-1.229	0.028	GT	Sens
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-1.413	Detected	-1.376	Detected	-1.395	0.007	GT	Sens
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	-1.320	Detected	-1.369	Detected	-1.344	0.000	GT	Sens
GT	Sense	Sense	0.479	Detected	-0.479	Detected	0.000	-3.016	Detected	-1.994	Detected	-2.505	0.070	GT	Sens
GT	Sense	Sense	0.743	Detected	-0.743	Detected	0.000	-3.450	Detected	-3.874	Detected	-3.662	0.042	GT	Sens
GT	Sense	Sense	0.334	Detected	-0.334	Detected	0.000	-1.117	Detected	-1.132	Detected	-1.124	0.078	GT	Sens
GT	Sense	Sense	0.261	Detected	-0.261	Detected	0.000	-1.760	Detected	-1.746	Detected	-1.753	0.021	GT	Sens
GT	Sense	Sense	-0.007	Detected	0.007	Detected	0.000	-1.025	Detected	-1.151	Detected	-1.088	0.003	GT	Sens
GT	Sense	Sense	-0.081	Detected	0.081	Detected	0.000	-0.947	Detected	-1.172	Detected	-1.059	0.017	GT	Sens
GT	Sense	Sense	-0.102	Detected	0.102	Detected	0.000	-1.859	Detected	-1.955	Detected	-1.907	0.003	GT	Sens
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-1.495	Detected	-1.405	Detected	-1.450	0.012	GT	Sens
GT	Sense	Sense	-0.201	Detected	0.201	Detected	0.000	-2.521	Detected	-2.664	Detected	-2.593	0.007	GT	Sens
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-1.228	Detected	-1.031	Detected	-1.130	0.019	GT	Sens
GT	Sense	Sense	-0.080	Detected	0.080	Detected	0.000	-1.529	Detected	-1.421	Detected	-1.475	0.004	GT	Sens
GT	Sense	Sense	0.214	Detected	-0.214	Detected	0.000	-1.598	Detected	-1.255	Detected	-1.427	0.035	GT	Sens
GT	Sense	Sense	0.186	Detected	-0.186	Detected	0.000	-1.186	Detected	-0.983	Detected	-1.085	0.036	GT	Sens
GT	Sense	Sense	0.108	Detected	-0.108	Detected	0.000	-1.088	Detected	-1.209	Detected	-1.148	0.011	GT	Sens
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	-1.095	Detected	-0.908	Detected	-1.002	0.009	GT	Sens
GT	Sense	Sense	0.116	Detected	-0.116	Detected	0.000	-2.550	Detected	-1.325	Detected	-1.938	0.090	GT	Sens
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-3.298	Detected	-2.759	Detected	-3.028	0.008	GT	Sens
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.262	Detected	-1.546	Detected	-1.404	0.011	GT	Sens
GT	Sense	Sense	0.001	Detected	-0.001	Detected	0.000	-0.904	Detected	-1.677	Detected	-1.291	0.079	GT	Sens
GT	Sense	Sense	-0.227	Detected	0.227	Detected	0.000	-2.238	Comprom	-2.684	Comprom	-2.461	0.016	GT	Sens
GT	Sense	Sense	0.217	Detected	-0.217	Detected	0.000	-0.934	Detected	-1.792	Comprom	-1.363	0.105	GT	Sens
GT	Sense	Sense	-0.058	Detected	0.058	Detected	0.000	-1.977	Detected	-1.267	Detected	-1.622	0.046	GT	Sens
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-0.975	Detected	-1.208	Detected	-1.092	0.013	GT	Sens
GT	Sense	Sense	-0.317	Detected	0.317	Detected	0.000	-1.504	Detected	-0.986	Detected	-1.245	0.093	GT	Sens
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-2.024	Detected	-2.226	Detected	-2.125	0.005	GT	Sens
GT	Sense	Sense	-0.014	Detected	0.014	Detected	0.000	-0.958	Comprom	-2.119	Comprom	-1.538	0.118	GT	Sens
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-1.371	Detected	-1.195	Detected	-1.283	0.007	GT	Sens
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	-2.757	Detected	-1.771	Detected	-2.264	0.044	GT	Sens
GT	Sense	Sense	0.407	Detected	-0.407	Detected	0.000	-0.996	Detected	-1.579	Detected	-1.287	0.124	GT	Sens
GT	Sense	Sense	0.209	Detected	-0.209	Detected	0.000	-0.833	Detected	-1.240	Detected	-1.036	0.071	GT	Sens
GT	Sense	Sense	0.179	Detected	-0.179	Detected	0.000	-2.475	Detected	-1.677	Detected	-2.076	0.042	GT	Sens
GT	Sense	Sense	0.022	Detected	-0.022	Detected	0.000	-1.084	Detected	-0.917	Detected	-1.000	0.007	GT	Sens
GT	Sense	Sense	-0.138	Detected	0.138	Detected	0.000	-2.591	Detected	-2.282	Detected	-2.436	0.007	GT	Sens
GT	Sense	Sense	0.492	Detected	-0.492	Detected	0.000	-3.956	Comprom	-3.740	Comprom	-3.848	0.017	GT	Sens
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-1.511	Detected	-1.067	Detected	-1.289	0.035	GT	Sens
GT	Sense	Sense	0.039	Detected	-0.039	Detected	0.000	-1.424	Detected	-1.774	Detected	-1.599	0.012	GT	Sens
GT	Sense	Sense	-0.021	Detected	0.021	Detected	0.000	-1.151	Detected	-0.891	Detected	-1.021	0.016	GT	Sens
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	-2.304	Detected	-1.750	Detected	-2.027	0.027	GT	Sens
GT	Sense	Sense	0.350	Detected	-0.350	Detected	0.000	-3.328	Comprom	-3.406	Comprom	-3.367	0.011	GT	Sens
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-2.122	Detected	-1.494	Detected	-1.808	0.029	GT	Sens
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	-1.701	Detected	-1.615	Detected	-1.658	0.003	GT	Sens
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	-1.337	Detected	-0.955	Detected	-1.146	0.027	GT	Sens
GT	Sense	Sense	0.209	Detected	-0.209	Detected	0.000	-1.125	Detected	-0.910	Detected	-1.018	0.049	GT	Sens
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	-0.980	Detected	-1.138	Detected	-1.059	0.006	GT	Sens
GT	Sense	Sense	0.299	Detected	-0.299	Detected	0.000	-2.787	Comprom	-1.580	Detected	-2.183	0.083	GT	Sens
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	-1.232	Detected	-1.215	Detected	-1.223	0.000	GT	Sens
GT	Sense	Sense	-0.150	Detected	0.150	Detected	0.000	-1.053	Detected	-1.074	Detected	-1.064	0.020	GT	Sens
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	-1.849	Detected	-1.455	Detected	-1.652	0.022	GT	Sens
GT	Sense	Sense	0.252	Detected	-0.252	Detected	0.000	-1.385	Detected	-1.557	Detected	-1.471	0.031	GT	Sens
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-1.062	Detected	-1.007	Detected	-1.035	0.008	GT	Sens
GT	Sense	Sense	0.207	Detected	-0.207	Detected	0.000	-2.041	Detected	-0.986	Detected	-1.514	0.116	GT	Sens
GT	Sense	Sense	0.513	Detected	-0.513	Detected	0.000	-2.955	Comprom	-1.570	Comprom	-2.263	0.120	GT	Sens
GT	Sense	Sense	0.141	Detected	-0.141	Detected	0.000	-2.394	Detected	-2.279	Detected	-2.336	0.004	GT	Sens
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	-1.129	Detected	-1.134	Detected	-1.132	0.005	GT	Sens
GT	Sense	Sense	0.510	Detected	-0.510	Detected	0.000	-2.794	Detected	-2.731	Detected	-2.762	0.033	GT	Sens
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-1.351	Detected	-1.153	Detected	-1.252	0.013	GT	Sens
GT	Sense	Sense	-0.497	Detected	0.497	Detected	0.000	-1.255	Detected	-1.023	Detected	-1.139	0.155	GT	Sens
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.413	Detected	-1.118	Detected	-1.265	0.018	GT	Sens
GT	Sense	Sense	0.277	Detected	-0.277	Detected	0.000	-3.263	Detected	-1.851	Detected	-2.557	0.078	GT	Sens
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-2.585	Detected	-2.062	Detected	-2.323	0.013	GT	Sens
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.487	Detected	-1.266	Detected	-1.376	0.007	GT	Sens
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.664	Detected	-1.202	Detected	-1.433	0.026	GT	Sens
GT	Sense	Sense	-0.082	Detected	0.082	Detected	0.000	-1.259	Detected	-1.511	Detected	-1.385	0.012	GT	Sens
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-2.051	Detected	-0.940	Detected	-1.495	0.115	GT	Sens
GT	Sense	Sense	0.335	Detected	-0.335	Detected	0.000	-2.079	Detected	-1.143	Detected	-1.611	0.107	GT	Sens
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-1.233	Detected	-0.923	Detected	-1.078	0.026	GT	Sens
GT	Sense	Sense	-0.180	Detected	0.180	Detected	0.000	-1.425	Detected	-1.410	Detected	-1.417	0.016	GT	Sens
GT	Sense	Sense	0.147	Detected	-0.147	Detected	0.000	-1.667	Detected	-0.903	Detected	-1.285	0.088	GT	Sens
GT	Sense	Sense	0.257	Detected	-0.257	Detected	0.000	-2.497	Detected	-1.881	Detected	-2.189	0.032	GT	Sens
GT	Sense	Sense	0.343	Detected	-0.343	Detected	0.000	-1.431	Detected	-0.814	Detected	-1.123	0.135	GT	Sens
GT	Sense	Sense	0.217	Detected	-0.217	Detected	0.000	-1.108	Detected	-1.348	Detected	-1.228	0.038	GT	Sens
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-1.451	Detected	-0.969	Detected	-1.210	0.038	GT	Sens
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	-0.888	Detected	-1.251	Comprom	-1.070	0.029	GT	Sens
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-1.443	Detected	-1.896	Detected	-1.669	0.018	GT	Sens
GT	Sense	Sense	-0.505	Detected	0.505	Detected	0.000	-1.219	Detected	-1.962	Detected	-1.590	0.127	GT	Sens
GT	Sense	Sense	0.044	Detected	-0.044	Detected	0.000	-1.415	Detected	-1.103	Detected	-1.259	0.016	GT	Sens
GT	Sense	Sense	-0.026	Detected	0.026	Detected	0.000	-1.331	Detected	-1.686	Detected	-1.508	0.014	GT	Sens
GT	Sense	Sense	-0.079	Detected	0.079	Detected	0.000	-2.166	Detected	-1.637	Detected	-1.902	0.020	GT	Sens
GT	Sense	Sense	0.454	Detected	-0.454	Detected	0.000	-5.078	Comprom	-3.621	Comprom	-4.350	0.037	GT	Sens
GT	Sense	Sense	0.253	Detected	-0.253	Detected	0.000	-2.148	Detected	-1.131	Detected	-1.640	0.102	GT	Sens
GT	Sense	Sense	0.197	Detected	-0.197	Detected	0.000	-0.943	Detected	-1.466	Detected	-1.204	0.066	GT	Sens
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.186	Detected	-1.120	Detected	-1.153	0.007	GT	Sens
GT	Sense	Sense	0.376	Detected	-0.376	Detected	0.000	-1.215	Detected	-1.153	Detected	-1.184	0.088	GT	Sens

GT	Sens	Sense	0.276	Detected	-0.276	Detected	0.000	-1.408	Detected	-1.182	Detected	-1.295	0.049	GT	Sens	contig21	contig21	Carboxyl-	GTAGTG	contig21	Solyc03g	Solyc03g	Carboxyl-terminal proteinase (			contig21	Solyc03g	Carboxyl-terminal p		SL2.40ch	AT5G50150.1		unknow	chr5:204	6381.46	4095.5	2110.7	2210.51	2054.8	2396.16
GT	Sens	Sense	0.401	Detected	-0.401	Detected	0.000	-2.475	Detected	-3.232	Detected	-2.854	0.035	GT	Sens	contig21	contig21	Calmodul	CAACTG	contig21	Solyc01g	Solyc01g	Calmodul	GO:0005	GO:0005	contig21	Solyc01g	Calmodul	GO:0005	SL2.40ch	AT3G13600.1		calmodu	chr3:444	225.237	121.552	17.4937	27.5607	31.7337	18.7237
GT	Sens	Sense	-0.018	Detected	0.018	Detected	0.000	-1.005	Detected	-1.022	Detected	-1.014	0.000	GT	Sens	contig211	contig211	AT-hook	ATGGTC	contig211	Solyc08g	Solyc08g	AT-hook	GO:0003	GO:0003	contig211	Solyc08g	AT-hook	GO:0003	SL2.40ch	AT2G33620.4		DNA-bind	chr2:142	1988.12	1917.18	702.776	634.439	1037.55	1021.85
GT	Sens	Sense	-0.387	Detected	0.387	Detected	0.000	-0.817	Detected	-1.484	Detected	-1.151	0.153	GT	Sens	contig211	contig211	LRR rece	CCGAAA	contig211	Solyc09g	Solyc09g	LRR rece	GO:0005	GO:0005	contig211	Solyc09g	Receptor	GO:0005	SL2.40ch	AT2G36570.1		leucine-r	chr2:153	41.5647	66.9185	44.2715	17.5706	31.9186	20.0411
GT	Sens	Sense	0.168	Detected	-0.168	Detected	0.000	-2.228	Detected	-1.414	Detected	-1.821	0.054	GT	Sens	contig211	contig211	Serine hy	CTCTTG	contig211	Solyc12g	Solyc12g	Serine hy	GO:0004	GO:0004	contig211	Solyc12g	Serine hy	GO:0004	SL2.40ch	AT4G139	SHM4	SHM4 (se	chr4:804	345.938	257.986	71.827	78.5927	68.0104	119.2
GT	Sens	Sense	0.590	Detected	-0.590	Detected	0.000	-0.822	Detected	-1.260	Detected	-1.041	0.240	GT	Sens	contig211	contig211	BCL-2 bir	GGGGTG	contig211	Solyc02g	Solyc02g	BCL-2 binding anthanogene-1			contig211	Solyc02g	BCL-2 binding antha		SL2.40ch	AT5G14360.1		ubiquitin	chr5:463	159.767	66.3297	16.7027	31.5941	62.1138	45.6901
GT	Sens	Sense	0.512	Detected	-0.512	Detected	0.000	-1.892	Detected	-1.358	Detected	-1.625	0.106	GT	Sens	contig211	contig211	Phloem le	AGTATT	contig211	Solyc00g	Solyc00g	Phloem lectin (AHRD V1 ***- O8			contig211	Solyc00g	Phloem le	GO:0030	SL2.40ch	AT5G170	UGT78D2	UGT78D	chr5:560	973.729	450.491	339.797	837.488	190.327	274.702
GT	Sens	Sense	0.148	Detected	-0.148	Detected	0.000	-1.019	Detected	-1.073	Detected	-1.046	0.020	GT	Sens	contig211	contig211	Pentatric	GTTGAT	contig211	Solyc11g	Solyc11g	Pentatric	GO:0004	GO:0004	contig211	Solyc11g	Pentatric	GO:0004	SL2.40ch	AT5G19020.1		pentatric	chr5:635	25.687	19.6897	10.1773	12.0978	11.8317	11.3691
GT	Sens	Sense	-0.020	Detected	0.020	Detected	0.000	-1.255	Detected	-1.076	Detected	-1.166	0.006	GT	Sens	contig212	contig212	E3 ubiqui	ATGGGG	contig212	Solyc03g	Solyc03g	E3 ubiqui	GO:0005	GO:0005	contig212	Solyc03g	E3 ubiqui	GO:0005	SL2.40ch	AT2G02960.3		zinc fing	chr2:862	4844.77	4684.77	2051.91	2690.91	2128.09	2402.39
GT	Sens	Sense	0.341	Detected	-0.341	Detected	0.000	-2.629	Detected	-1.559	Detected	-2.094	0.081	GT	Sens	contig212	contig212	Ring fing	CGGATG	contig212	Solyc01g	Solyc01g	Ring fing	GO:0008	GO:0008	contig212	Solyc01g	Ring fing	GO:0008	SL2.40ch	AT5G13250.1		unknow	chr5:423	2305.95	1352.12	318.859	396.613	304.498	637.259
GT	Sens	Sense	0.284	Detected	-0.284	Detected	0.000	-3.488	Detected	-2.703	Detected	-3.095	0.024	GT	Sens	contig212	contig212	Dehydrat	CAGAAG	contig212	Solyc08g	Solyc08g	Dehydration-responsive family			contig212	Solyc08g	Dehydration-respon		SL2.40ch	AT4G191	ERD3	ERD3 (ea	chr4:104	990.42	628.302	81.1461	106.33	74.9884	128.812
GT	Sens	Sense	0.334	Detected	-0.334	Detected	0.000	-2.164	Detected	-1.183	Detected	-1.673	0.106	GT	Sens	contig212	contig212	Os07g01	TTGGTT	contig212	Solyc12g	Solyc12g	Os07g0175100 protein (Fragm			contig212	Solyc12g	Os07g017	GO:0016	SL2.40ch	AT5G12010.1		unknow	chr5:387	1661.1	983.763	377.287	599.112	304.248	598.549
GT	Sens	Sense	0.027	Detected	-0.027	Detected	0.000	-3.093	Detected	-2.778	Detected	-2.936	0.003	GT	Sens	contig212	contig212	U-box do	AACTCA	contig212	Solyc05g	Solyc05g	U-box do	GO:0005	GO:0005	contig212	Solyc05g	U-box do	GO:0004	SL2.40ch	AT5G486	ATSMC3.	ATSMC3	chr5:197	310.569	281.567	69.4127	73.7476	36.9481	45.8447
GT	Sens	Sense	0.224	Detected	-0.224	Detected	0.000	-1.702	Detected	-1.333	Detected	-1.518	0.035	GT	Sens	contig212	contig212	FAD-bind	GGTATA	contig212	Solyc02g	Solyc02g	FAD-bind	GO:0009	GO:0009	contig212	Solyc02g	FAD-bind	GO:0009	SL2.40ch	AT1G11770.1		FAD bind	chr1:397	1258.98	868.033	502.06	279.211	342.526	441.184
GT	Sens	Sense	-0.115	Detected	0.115	Detected	0.000	-1.793	Detected	-1.062	Detected	-1.427	0.065	GT	Sens	contig212	contig212	Unknown	TGTAGG	contig212	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig212	Solyc02g	Unknown Protein (A		SL2.40ch	AT1G68780.1		leucine-r	chr1:258	46.2477	51.0163	25.6656	32.5489	14.9508	24.7363
GT	Sens	Sense	0.374	Detected	-0.374	Detected	0.000	-1.415	Detected	-1.330	Detected	-1.372	0.068	GT	Sens	contig213	contig213	Leaf sene	TGGCCC	contig213	Solyc02g	Solyc02g	Leaf senescence protein-like (			contig213	Solyc02g	Leaf senescence pr		SL2.40ch	AT5G15900.1		unknow	chr5:518	2779.89	1558.04	961.026	919.504	832.446	880.143
GT	Sens	Sense	0.032	Detected	-0.032	Detected	0.000	-2.776	Detected	-2.599	Detected	-2.687	0.001	GT	Sens	contig213	contig213	Dynamin-	TCTGAT	contig213	Solyc06g	Solyc06g	Dynamin-related protein 1E (A			contig213	Solyc06g	Dynamin-related pr		SL2.40ch	AT5G636	HEN3. CD	CDKE:1	chr5:254	4870.81	4382.89	1308.72	1508.66	719.202	811.039
GT	Sens	Sense	-0.032	Detected	0.032	Detected	0.000	-2.639	Detected	-2.417	Detected	-2.528	0.002	GT	Sens	contig213	contig213	Serine/th	TTTGGG	contig213	Solyc01g	Solyc01g	Serine/th	GO:0005	GO:0005	contig213	Solyc01g	Receptor	GO:0004	SL2.40ch	AT5G51560.1		leucine-r	chr5:209	398.164	391.397	47.5906	44.1524	67.5847	78.6134
GT	Sens	Sense	0.070	Detected	-0.070	Detected	0.000	-2.708	Comprom	-2.820	Comprom	-2.764	0.001	GT	Sens	contig213	contig213	Harpin-in	AATTTT	contig213	Solyc05g	Solyc05g	Harpin-induced protein-related			contig213	Solyc05g	Harpin-induced pro		SL2.40ch	AT5G23930.1		mitochor	chr5:807	16.0328	13.6906	153.902	3.24733	2.41821	2.23013
GT	Sens	Sense	0.164	Detected	-0.164	Detected	0.000	-1.129	Detected	-1.210	Detected	-1.170	0.020	GT	Sens	contig213	contig213	Potassiu	CTGAAC	contig213	Solyc04g	Solyc04g	Potassiu	GO:0009	GO:0009	contig213	Solyc04g	Potassiu	GO:0009	SL2.40ch	AT1G703	KUP6	KUP6: po	chr1:264	370.774	277.783	79.441	107.716	156.463	147.502
GT	Sens	Sense	0.162	Detected	-0.162	Detected	0.000	-1.208	Detected	-1.005	Detected	-1.107	0.029	GT	Sens	contig213	contig213	Beta-D-gl	GGAGAC	contig213	Solyc06g	Solyc06g	Beta-D-gl	GO:0005	GO:0005	contig213	Solyc06g	Beta-D-gl	GO:0005	SL2.40ch	AT3G47000.1		glycosyl	chr3:173	12460.6	9364.65	3280.97	5224.47	4986.39	5721.03
GT	Sens	Sense	-0.246	Detected	0.246	Detected	0.000	-1.604	Comprom	-1.408	Comprom	-1.506	0.029	GT	Sens	contig213	contig213	Unknown	CCAGCT	contig213	Solyc06g	Solyc06g	Unknown	GO:0005	GO:0005	contig213	Solyc06g	Unknown	GO:0005	SL2.40ch	AT1G71850.1		ubiquitin	chr1:270	12.8557	17.0036	12.1216	3.0585	5.18537	5.92301
GT	Sens	Sense	0.088	Detected	-0.088	Detected	0.000	-2.451	Detected	-2.039	Detected	-2.245	0.010	GT	Sens	contig214	contig214	Hydrolas	ATGTTC	contig214	Solyc08g	Solyc08g	Hydrolase alpha/beta fold fami			contig214	Solyc08g	Hydrolase alpha/be		SL2.40ch	AT4G24140.1		hydrolas	chr4:125	6742.98	5612.51	1364.87	2189.74	1199.41	1591.97
GT	Sens	Sense	0.000	Detected	0.000	Detected	0.000	-1.420	Detected	-1.123	Detected	-1.272	0.013	GT	Sens	contig214	contig214	Proteinas	TGAAGG	contig214	Solyc03g	Solyc03g	Proteinas	GO:0004	GO:0004	contig214	Solyc03g	Proteinas	GO:0004	SL2.40ch	AT5G67385.1		protein b	chr5:268	103898	97706.8	56481.8	49928.4	40142.7	49196
GT	Sens	Sense	0.104	Detected	-0.104	Detected	0.000	-2.232	Detected	-1.593	Detected	-1.913	0.030	GT	Sens	contig214	contig214	Cytochro	TTATGA	contig214	Solyc06g	Solyc06g	Cytochro	GO:0019	GO:0019	contig214	Solyc06g	Cytochro	GO:0019	SL2.40ch	AT4G153	CYP705A	CYP705	chr4:876	7484.53	6096.34	1729.06	2413.96	1533.22	2380.43
GT	Sens	Sense	-0.007	Detected	0.007	Detected	0.000	-3.128	Detected	-1.671	Detected	-2.400	0.081	GT	Sens	contig214	contig214	1-aminoc	GGATTT	contig214	Solyc02g	Solyc02g	1-aminoc	GO:0016	GO:0016	contig214	Solyc02g	1-aminoc	GO:0042	SL2.40ch	AT3G497	ETO3. AC	ACS9 (1-	chr3:184	107.702	102.267	12.1631	19.4829	12.7977	35.0448
GT	Sens	Sense	0.125	Detected	-0.125	Detected	0.000	-1.052	Detected	-1.603	Detected	-1.327	0.048	GT	Sens	contig215	contig215	Pirin-like	TATATA	contig215	Solyc09g	Solyc09g	Pirin-like	GO:0003	GO:0003	contig215	Solyc09g	Pirin-like	GO:0005	SL2.40ch	AT2G43120.1		pirin, put	chr2:179	115.387	91.3035	30.8092	37.607	52.7813	35.9321
GT	Sens	Sense	-0.422	Detected	0.422	Detected	0.000	-1.875	Detected	-1.355	Detected	-1.615	0.083	GT	Sens	contig215	contig215	Peroxida	CCGATC	contig215	Solyc11g	Solyc11g	Peroxida	GO:0055	GO:0055	contig215	Solyc11g	Peroxida	GO:0055	SL2.40ch	AT5G06720.1		peroxida	chr5:207	51.7942	87.5114	32.3226	44.9251	19.5766	27.987
GT	Sens	Sense	0.123	Detected	-0.123	Detected	0.000	-2.514	Detected	-1.935	Detected	-2.225	0.019	GT	Sens	contig215	contig215	Harpin-in	AATTAT	contig215	Solyc02g	Solyc02g	Harpin-induced protein-like (F			contig215	Solyc02g	Harpin-induced pro		SL2.40ch	AT4G267	PPX1. PP	PPX1 (PF	chr4:134	2051.27	1626.74	475.007	824.616	340.97	507.765
GT	Sens	Sense	-0.202	Detected	0.202	Detected	0.000	-1.642	Detected	-1.395	Detected	-1.518	0.024	GT	Sens	contig216	contig216	Pentatric	TCTGGT	contig216	Solyc03g	Solyc03g	Pentatricopeptide repeat-cont			contig216	Solyc03g	Pentatricopeptide r		SL2.40ch	AT4G27980.1		FUNCTIO	chr4:139	167.639	208.797	77.252	101.011	63.9256	75.6605
GT	Sens	Sense	0.104	Detected	-0.104	Detected	0.000	-1.603	Detected	-2.835	Comprom	-2.219	0.071	GT	Sens	contig216	contig216	Cytochro	AAACTT	contig216	Solyc01g	Solyc01g	Cytochro	GO:0019	GO:0019	contig216	Solyc01g	Cytochro	GO:0019	SL2.40ch	AT5G249	CYP71A1	CYP71A1	chr5:859	49.8224	40.5786	15.4853	10.7479	15.7887	6.69921
GT	Sens	Sense	-0.034	Detected	0.034	Detected	0.000	-0.974	Detected	-1.086	Detected	-1.030	0.004	GT	Sens	contig216	contig216	Senescer	GTCAAA	contig216	Solyc07g	Solyc07g	Senescer	GO:0016	GO:0016	contig216	Solyc07g	Senescer	GO:0016	SL2.40ch	AT4G280	TET7	TET7 (TE	chr4:139	39610.8	39091	14555.9	21858.2	21363.4	19705.4
GT	Sens	Sense	0.035	Detected	-0.035	Detected	0.000	-2.949	Detected	-2.322	Detected	-2.636	0.014	GT	Sens	contig216	contig216	Kunitz-ty	CTGCTA	contig216	Solyc03g	Solyc03g	Kunitz-ty	GO:0004	GO:0004	contig216	Solyc03g	Kunitz-ty	GO:0004	SL2.40ch	AT1G17860.1		trypsin a	chr1:614	19495.4	17486.4	5820.64	11081.7	2549.04	3926.33
GT	Sens	Sense	0.082	Detected	-0.082	Detected	0.000	-0.985	Detected	-1.084	Detected	-1.034	0.008	GT	Sens	contig216	contig216	Transme	TTCACA	contig216	Solyc02g	Solyc02g	Transme	GO:0016	GO:0016	contig216	Solyc02g	Transme	GO:0016	SL2.40ch	AT4G19645.2		FUNCTIO	chr4:106	1597.22	1342.3	552.937	632.345	788.8	734.495
GT	Sens	Sense	0.113	Detected	-0.113	Detected	0.000	-2.714	Detected	-1.756	Detected	-2.235	0.045	GT	Sens	contig216	contig216	Late emb	ACTGGA	contig216	Solyc03g	Solyc03g	Late embryogenesis abundan			contig216	Solyc03g	Late embryogenesi		SL2.40ch	AT3G15670.1		late emb	chr3:531	350.279	281.945	48.4932	94.189	51.0604	98.9392
GT	Sens	Sense	-0.742	Detected	0.742	Detected	0.000	-1.446	Detected	-1.305	Detected	-1.375	0.206	GT	Sens	contig216	contig216	Membran	GGGATC	contig216	Solyc11g	Solyc11g	Membrane protein (AHRD V1 *			contig216	Solyc11g	Membrane protein (		SL2.40ch	AT3G25290.2		auxin-res	chr3:920	23.7754	62.5888	19.9066	19.366	15.1029	16.5953
GT	Sens	Sense	0.078	Detected	-0.078	Detected	0.000	-2.766	Detected	-1.745	Detected	-2.255	0.049	GT	Sens	contig216	contig216	Leucine-r	CCAAAT	contig216	Solyc07g	Solyc07g	Leucine-r	GO:0005	GO:0005	contig216	Solyc07g	LRR rece	GO:0004	SL2.40ch	AT5G54350.1		FUNCTIO	chr5:220	2623.2	2215.54	905.185	794.64	378.047	764.786
GT	Sens	Sense	0.258	Detected	-0.258	Detected	0.000	-2.747	Detected	-1.692	Detected	-2.219	0.063	GT	Sens	contig217	contig217	Cytochro	GATTTG	contig217	Solyc11g	Solyc11g	Cytochro	GO:0020	GO:0020	contig217	Solyc11g	Cytochro	GO:0019	SL2.40ch	AT4G137	CYP83A1	CYP83A1	chr4:799	86.6122	56.9951	25.4668	32.0283	11.1646	23.1265
GT	Sens	Sense	0.731	Detected	-0.731	Detected	0.000	-2.516	Detected	-2.722	Detected	-2.619	0.071	GT	Sens	contig217	contig217	Zinc fing	GAATTC	contig217	Solyc03g	Solyc03g	Zinc fing	GO:0003	GO:0003	contig217	Solyc03g	Zinc fing	GO:0003	SL2.40ch	AT1G746	MIF1	MIF1 (MI	chr1:280	2330.77	796.18	109.776	121.028	253.904	219.516
GT	Sens	Sense	0.097	Detected	-0.097	Detected	0.000	-1.560	Detected	-0.886	Detected	-1.223	0.073	GT	Sens	contig218	contig218	Oxidation	TATGCA	contig218	Solyc12g	Solyc12g	Oxidation resistance 1-like pro			contig218	Solyc12g	Oxidation resistanc		SL2.40ch	AT2G05590.2		FUNCTIO	chr2:206	480.775	395.558	208.369	223.357	157.687	250.89
GT	Sens	Sense	0.076	Detected	-0.076	Detected	0.000	-1.995	Detected	-1.560	Detected	-1.777	0.016	GT	Sens	contig219	contig219	Tir-nbs re	TTTTCA	contig219	Solyc08g	Solyc08g	Tir-nbs re	GO:0031	GO:0031	contig219	Solyc08g	Tir-nbs re	GO:0031	SL2.40ch	AT4G23440.1		nucleosi	chr4:122	408.067	345.476	141.945	172.098	100.456	135.411
GT	Sens	Sense	0.013	Detected	-0.013	Detected	0.000	-1.251	Detected	-0.974	Detected	-1.112	0.015	GT	Sens	contig219	contig219	ATP bind	TACCAA	contig219	Solyc05g	Solyc05g	ATP bind	GO:0005	GO:0005	contig219	Solyc05g	ATP bind	GO:0005	SL2.40ch	AT5G15080.1		protein k	chr5:488	15801.2	14603.1	5540.98	6773.23	6806.93	8222.57
GT	Sens	Sense	0.060	Detected	-0.060	Detected	0.000	-1.879	Detected	-1.708	Detected	-1.793	0.003	GT	Sens	contig219	contig219	LRR rece	TGTTCG	contig219	Solyc03g	Solyc03g	LRR rece	GO:0004	GO:0004	contig219	Solyc03g	Receptor	GO:0004	SL2.40ch	AT4G36180.1		leucine-r	chr4:171	65.8681	57.0344	22.7643	12.8051	17.7693	19.9506
GT	Sens	Sense	0.085	Detected	-0.085	Detected	0.000	-1.544	Detected	-1.362	Detected	-1.453	0.007	GT	Sens	contig219	contig219	Genomic	TTCATG	contig219	Solyc08g	Solyc08g	Genomic DNA chromosome 5			contig219	Solyc08g	Genomic DNA chro		SL2.40ch	AT5G47400.1		unknow	chr5:192	1952.4	1632.63	664.568	653.892	652.834	738.493
GT	Sens	Sense	0.117	Detected	-0.117	Detected	0.000	-1.435	Detected	-1.090	Detected	-1.262	0.026	GT	Sens	contig219	contig219	Dehydrat	TATTGA	contig219	Solyc04g	Solyc04g	Dehydration-responsive prote			contig219	Solyc04g	Dehydration-respon		SL2.40ch	AT1G782	TSD2. OL	TSD2 (TL	chr1:294	5920.69	4733.97	1937.72	2397.5	2088.22	2644.96
GT	Sens	Sense	0.084	Detected	-0.084	Detected	0.000	-2.818	Detected	-2.547	Detected	-2.682	0.004	GT	Sens	contig219	contig219	AT5G281	AGAAGA	contig219	Solyc01g	Solyc01g	AT5G28150-like protein (Fragn			contig219	Solyc01g	AT5G28150-like pro		SL2.40ch	AT5G105	GTE2	GTE2 (GI	chr5:333	1581.29	1323.86	267.269	439.72	218.841	263.279
GT	Sens	Sense	0.007	Detected	-0.007	Detected	0.000	-1.229	Detected	-0.940	Detected	-1.084	0.017	GT	Sens	contig219	contig219	Vesicular	AAAGAG	contig219	Solyc12g	Solyc12g	Vesicular	GO:0055	GO:0055	contig219	Solyc12g	Vesicular	GO:0055	SL2.40ch	AT5G443	PHT4:6	PHT4:6 (	chr5:178	2529.92	2357.84	1023.6	1189.61	1111.16	1353.49
GT	Sens	Sense	0.037	Detected	-0.037	Detected	0.000	-1.220	Detected	-1.141	Detected	-1.180	0.002	GT	Sens	contig219	contig219	WRKY tra	TTCAAA	contig219	Solyc08g	Solyc08g	WRKY tra	GO:0045449		contig219	Solyc08g	WRKY tra	GO:0045	SL2.40ch	AT1G640	WRKY56.	WRKY56	chr1:237	328.734	293.678	86.395	182.34	142.267	149.814
GT	Sens	Sense	0.017	Detected	-0.017	Detected	0.000	-2.535	Detected	-1.338	Detected	-1.937	0.084	GT	Sens	contig219	contig219	Laccase-	CAATAT	contig219	Solyc02g	Solyc02g	Laccase-	GO:0055	GO:0055	contig219	Solyc02g	Laccase-	GO:0055	SL2.40ch	AT5G669	sks17	sks17 (SI	chr5:267	10875.4	9995.35	3617.56	5804.11	1918.45	4384.47
GT	Sens	Sense	0.145	Detected	-0.145	Detected	0.000	-1.852	Detected	-1.693	Detected	-1.773	0.009	GT	Sens	contig22	contig22	Thaumati	ATATGA	contig22	Solyc04g	Solyc04g	Thaumatin-like protein (AHRD			contig22	Solyc04g	Thaumatin-like prot		SL2.40ch	AT1G75800.1		pathoger	chr1:284	11454.2	8817.56	2336.91	3638.14	2969.25	3303.65
GT	Sens	Sense	-0.047	Detected	0.047	Detected	0.000	-3.940	Detected	-2.425	Detected	-3.182	0.052	GT	Sens	contig22	contig22	Unknown	ATTAGC	contig22	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig22	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G38880.1		unknow	chr5:155	6748.92	6780.3	1970.46	1985.26	469.956	1339.37
GT	Sens	Sense	0.313	Detected	-0.313	Detected	0.000	-2.035	Detected	-1.679	Detected	-1.857	0.036	GT	Sens	contig22	contig22	1-aminoc	CTGACA	contig22	Solyc02g	Solyc02g	1-aminoc	GO:0016	GO:0016	contig22	Solyc02g	1-aminoc	GO:0016	SL2.40ch	AT1G77330.1		1-aminoc	chr1:290	27898.2	17012.1	4020.4	6735.58	5670.67	7234.74
GT	Sens	Sense	0.144	Detected	-0.144	Detected	0.000	-1.169	Detected	-1.273	Detected	-1.221	0.015	GT	Sens	contig22	contig22	Retinobla	ATGGGG	contig22	Solyc03g	Solyc03g	Retinobla	GO:0005	GO:0005	contig22	Solyc03g	Retinobla	GO:0005	SL2.40ch	AT4G17410.1		zinc ion	chr4:971	493.902	380.536	232.106	333.454	205.558	190.774
GT	Sens	Sense	0.142	Detected	-0.142	Detected	0.000	-1.101	Detected	-0.970	Detected	-1.036	0.022	GT	Sens	contig22	contig22	Starch sy	TCCTCG	contig22	Solyc02g	Solyc02g	Starch synthase V (AHRD V1 *			contig22	Solyc02g	Starch synthase V (		SL2.40ch	AT5G04060.1		dehydrat	chr5:109	35.9436	27.7676	14.0044	25.6805	15.7068	17.1439
GT	Sens	Sense	-0.251	Detected	0.251	Detected	0.000	-2.244	Detected	-2.415	Detected	-2.329	0.013	GT	Sens	contig22	contig22	Unknown	TTAAAC	contig22	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig22	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G12050.1		DNA-bind	chr4:722	354.407	472.091	135.774	146.329	92.0858	81.5506
GT	Sens	Sense	0.175	Detected	-0.175	Detected	0.000	-1.364	Detected	-1.267	Detected	-1.315	0.018	GT	Sens	contig22	contig22	Genomic	CTCTGC	contig22	Solyc12g	Solyc12g	Genomic DNA chromosome 3			contig22	Solyc12g	Genomic DNA chro		SL2.40ch	AT3G23930.1		unknow	chr3:864	833.287	615.582	248.561	203.977	296.763	316.413
GT	Sens	Sense	-0.150	Detected	0.150	Detected	0.000	-1.267	Detected	-1.401	Detected	-1.334	0.015	GT	Sens	contig22	contig22	Ethylene	ATTGGA	contig22	Solyc02g	Solyc02g	Ethylene	GO:0003	GO:0003	contig22	Solyc02g	Ethylene	GO:0003	SL2.40ch	AT1G283	ERF12. A	ERF12 (E	chr1:995	446.051	516.829	136.442	205.717	212.743	193.314
GT	Sens	Sense	0.133	Detected	-0.133	Detected	0.000	-1.266	Detected	-1.400	Detected	-1.333	0.012	GT	Sens	contig221	contig221	Lipid tran	CTTAAG	contig221	Solyc02g	Solyc02g	Lipid tran	GO:0006	GO:0006	contig221	Solyc02g	Lipid tran	GO:0006	SL2.40ch	AT1G192	ARF19. IA	ARF19 (A	chr1:662	1714.47	1341.32	866.169	725.758	672.319	611.05
GT	Sens	Sense	0.240	Detected	-0.240	Detected	0.000	-2.781	Detected	-2.453	Detected	-2.617	0.012	GT	Sens	contig221	contig221	S-adenos	GTTGTA	contig221	Solyc01g	Solyc01g	S-adenos	GO:0008	GO:0008	contig221	Solyc01g	S-adenos	GO:0008	SL2.40ch	AT5G37990.1		S-adeno	chr5:151	166.498	112.332	24.876	22.1145	21.2181	26.5595
GT	Sens	Sense	0.119	Detected	-0.119	Detected	0.000	-1.373	Detected	-1.177	Detected	-1.275	0.014	GT	Sens	contig221	contig221	Pectinace	AACAAA	contig221	Solyc10g	Solyc10g	Pectinacetylesterase like prote			contig221	Solyc10g	Pectinacetylesteras		SL2.40ch	AT3G09405.1		FUNCTIO	chr3:289	204.208	162.993	67.6074	86.4131	75.1374	85.7807
GT	Sens	Sense	0.195	Detected	-0.195	Detected	0.000	-1.914	Detected	-0.971	Detected	-1.442	0.106	GT	Sens	contig221	contig221	Microtub	CGGGTT	contig221	Solyc03g	Solyc03g	Microtub	GO:0005	GO:0005	contig221	Solyc03g	Microtub	GO:0005	SL2.40ch	AT5G62580.1		binding	chr5:251	783.375	562.863	156.829	243.546	187.936	360.184
GT	Sens	Sense	0.616	Detected	-0.616	Detected	0.000	-1.321	Detected	-1.589	Detected	-1.455	0.147	GT	Sens	contig221	contig221	Myb-relat	GGAGGA	contig221	Solyc05g	Solyc05g	Myb-relat	GO:0003	GO:0003	contig221	Solyc05g	Myb-relat	GO:0003	SL2.40ch	AT2G311	ATMYB1	MYB14 (I	chr2:132	60.5544	24.2433	21.5804	15.7926	16.3525	13.5422
GT	Sens	Sense	0.380	Detected	-0.380	Detected	0.000	-2.096	Detected	-1.944	Detected	-2.020	0.035	GT	Sens	contig221	contig221	Unknown	GTGATT	contig221	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig221	Solyc08g	Unknown Protein (A		SL2.40ch	AT2G35290.1		unknow	chr2:148	5323.47	2957.06	1329.98	2568.09	989.622	1096.66
GT	Sens	Sense	0.048	Detected	-0.048	Detected	0.000	-1.420	Detected	-1.110	Detected	-1.265	0.016	GT	Sens	contig221	contig221	Chalcone	GTGTAT	contig221	Solyc01g	Solyc01g	Chalcone	GO:0008	GO:0008	contig221	Solyc01g	Chalcone	GO:0008	SL2.40ch	AT4G34850.1		chalcone	chr4:166	86.0312	75.765	49.8802	53.3473	32.1786	39.7689

GT	Sense	Sense	-0.080	Detected	0.080	Detected	0.000	-1.447	Detected	-1.149	Detected	-1.298	0.017	GT	Sens	contig254	contig254	Glycosyl	AAGGAT
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-1.423	Detected	-1.112	Detected	-1.268	0.017	GT	Sens	contig255	contig255	Os03g01	CAAGAA
GT	Sense	Sense	0.062	Detected	-0.062	Detected	0.000	-1.481	Detected	-1.466	Detected	-1.474	0.002	GT	Sens	contig255	contig255	Aquapori	GGGCCT
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-3.886	Comprom	-3.159	Detected	-3.523	0.011	GT	Sens	contig255	contig255	Transcri	AGAGCA
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-1.352	Detected	-1.480	Detected	-1.416	0.009	GT	Sens	contig255	contig255	Uncharac	GTACCA
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	-2.460	Detected	-1.678	Detected	-2.069	0.035	GT	Sens	contig255	contig255	Late emb	ATTGAT
GT	Sense	Sense	-0.055	Detected	0.055	Detected	0.000	-1.327	Detected	-1.068	Detected	-1.198	0.014	GT	Sens	contig255	contig255	Xylanase	ATGTGT
GT	Sense	Sense	0.240	Detected	-0.240	Detected	0.000	-1.547	Detected	-1.651	Detected	-1.599	0.023	GT	Sens	contig256	contig256	NAC dom	GGCTTT
GT	Sense	Sense	0.083	Detected	-0.083	Detected	0.000	-1.298	Detected	-0.859	Detected	-1.079	0.044	GT	Sens	contig256	contig256	Phospho	CCCACA
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.408	Detected	-1.024	Detected	-1.216	0.025	GT	Sens	contig256	contig256	Glutathio	ACAAAA
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	-1.668	Detected	-1.649	Detected	-1.658	0.002	GT	Sens	contig256	contig256	SRC2 hor	ATATCC
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-3.267	Comprom	-2.903	Comprom	-3.085	0.006	GT	Sens	contig256	contig256	Serine/th	GCCTAG
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	-0.922	Detected	-1.671	Detected	-1.296	0.094	GT	Sens	contig256	contig256	AP2-like	AACAAT
GT	Sense	Sense	0.214	Detected	-0.214	Detected	0.000	-1.657	Detected	-1.129	Detected	-1.393	0.055	GT	Sens	contig256	contig256	Mitotic ch	GCATCC
GT	Sense	Sense	0.074	Detected	-0.074	Detected	0.000	-1.348	Detected	-1.491	Detected	-1.419	0.005	GT	Sens	contig256	contig256	UDP-gluc	ATCCTT
GT	Sense	Sense	0.199	Detected	-0.199	Detected	0.000	-2.539	Detected	-1.852	Detected	-2.196	0.031	GT	Sens	contig257	contig257	ABC tran	CCGCGA
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-2.269	Detected	-1.896	Detected	-2.082	0.009	GT	Sens	contig257	contig257	Cellulose	CAGGAC
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-2.726	Detected	-2.043	Detected	-2.385	0.021	GT	Sens	contig257	contig257	Receptor	ACACTT
GT	Sense	Sense	-0.195	Detected	0.195	Detected	0.000	-1.105	Detected	-1.129	Detected	-1.117	0.029	GT	Sens	contig257	contig257	Ring H2 fi	CAATAT
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.809	Detected	-3.572	Comprom	-2.690	0.093	GT	Sens	contig258	contig258	GRAS fan	CGGATG
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.951	Detected	-1.600	Detected	-1.775	0.010	GT	Sens	contig258	contig258	LRR rece	CAGTTG
GT	Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-1.283	Detected	-1.019	Detected	-1.151	0.020	GT	Sens	contig258	contig258	GDSL est	AACGGA
GT	Sense	Sense	0.009	Detected	-0.009	Detected	0.000	-1.183	Detected	-1.168	Detected	-1.176	0.000	GT	Sens	contig259	contig259	Unknown	ATAAAA
GT	Sense	Sense	0.336	Detected	-0.336	Detected	0.000	-2.572	Detected	-2.597	Detected	-2.585	0.016	GT	Sens	contig259	contig259	Omega-3	CAGGGG
GT	Sense	Sense	0.032	Detected	-0.032	Detected	0.000	-1.336	Detected	-1.553	Detected	-1.444	0.006	GT	Sens	contig259	contig259	Kinesin h	CTTGTT
GT	Sense	Sense	0.075	Detected	-0.075	Detected	0.000	-1.656	Detected	-1.573	Detected	-1.614	0.003	GT	Sens	contig259	contig259	MtN21 no	AATAAC
GT	Sense	Sense	0.338	Detected	-0.338	Detected	0.000	-2.758	Detected	-3.703	Comprom	-3.230	0.031	GT	Sens	contig259	contig259	Dof zinc f	GAGGAG
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-2.287	Comprom	-1.954	Comprom	-2.121	0.007	GT	Sens	contig259	contig259	ATP-bind	GAACTA
GT	Sense	Sense	0.306	Detected	-0.306	Detected	0.000	-1.315	Detected	-1.627	Detected	-1.471	0.050	GT	Sens	contig260	contig260	F-box fan	TGAGAG
GT	Sense	Sense	0.578	Detected	-0.578	Detected	0.000	-1.344	Detected	-2.157	Comprom	-1.750	0.132	GT	Sens	contig260	contig260	Calmodul	AGACCT
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-0.942	Detected	-1.248	Detected	-1.095	0.030	GT	Sens	contig260	contig260	Glycerol-	AAGGGG
GT	Sense	Sense	0.353	Detected	-0.353	Detected	0.000	-3.159	Detected	-3.204	Detected	-3.181	0.012	GT	Sens	contig260	contig260	Calmodul	TCGGAT
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-0.910	Detected	-1.109	Detected	-1.009	0.031	GT	Sens	contig260	contig260	Atcambp	TGTTTT
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	-1.446	Detected	-1.199	Detected	-1.322	0.079	GT	Sens	contig260	contig260	UDP-gluc	TTTGCA
GT	Sense	Sense	0.261	Detected	-0.261	Detected	0.000	-0.973	Detected	-1.118	Detected	-1.045	0.061	GT	Sens	contig260	contig260	F-box pro	AACAGT
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-1.203	Detected	-1.297	Detected	-1.250	0.003	GT	Sens	contig260	contig260	Integrin-li	TTATCT
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-2.257	Detected	-1.880	Detected	-2.068	0.012	GT	Sens	contig260	contig260	Blue cop	TGTTAT
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.396	Detected	-1.079	Detected	-1.238	0.019	GT	Sens	contig260	contig260	cDNA clo	GTTGAT
GT	Sense	Sense	0.173	Detected	-0.173	Detected	0.000	-1.656	Detected	-0.911	Detected	-1.284	0.089	GT	Sens	contig261	contig261	Patatin-lik	GGCAAA
GT	Sense	Sense	0.194	Detected	-0.194	Detected	0.000	-1.287	Detected	-1.358	Detected	-1.322	0.022	GT	Sens	contig261	contig261	Membran	TGTGTG
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-2.438	Comprom	-1.098	Comprom	-1.768	0.119	GT	Sens	contig261	contig261	Unknown	TCGTAG
GT	Sense	Sense	0.566	Detected	-0.566	Detected	0.000	-3.810	Detected	-3.212	Detected	-3.511	0.032	GT	Sens	contig261	contig261	cDNA clo	CAGTTC
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-2.289	Detected	-2.470	Detected	-2.380	0.002	GT	Sens	contig261	contig261	Acyl-CoA	CCTCAG
GT	Sense	Sense	-0.404	Detected	0.404	Detected	0.000	-1.886	Detected	-0.958	Detected	-1.422	0.147	GT	Sens	contig262	contig262	Endogluc	GAGGTC
GT	Sense	Sense	0.000	Detected	0.000	Detected	0.000	-2.328	Detected	-1.463	Detected	-1.895	0.048	GT	Sens	contig262	contig262	Expansin	AATTGG
GT	Sense	Sense	0.243	Detected	-0.243	Detected	0.000	-1.061	Detected	-1.093	Detected	-1.077	0.048	GT	Sens	contig262	contig262	Ribosom	TACAGA
GT	Sense	Sense	-0.128	Detected	0.128	Detected	0.000	-1.040	Detected	-0.969	Detected	-1.004	0.017	GT	Sens	contig262	contig262	TPR dom	AAGCTG
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-1.478	Detected	-2.049	Detected	-1.764	0.032	GT	Sens	contig262	contig262	Unknown	TGCACA
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-3.876	Detected	-2.454	Detected	-3.165	0.047	GT	Sens	contig263	contig263	Pectate ly	AATTGC
GT	Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-1.324	Detected	-0.895	Detected	-1.109	0.043	GT	Sens	contig263	contig263	2-phosph	CGCTTC
GT	Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-1.297	Detected	-1.004	Detected	-1.150	0.016	GT	Sens	contig263	contig263	Low affin	GTGGTT
GT	Sense	Sense	0.240	Detected	-0.240	Detected	0.000	-2.958	Detected	-1.863	Detected	-2.410	0.056	GT	Sens	contig263	contig263	Non-spec	CTCAAC
GT	Sense	Sense	0.212	Detected	-0.212	Detected	0.000	-1.363	Detected	-1.178	Detected	-1.270	0.032	GT	Sens	contig263	contig263	Diacylgly	CATGCT
GT	Sense	Sense	0.267	Detected	-0.267	Detected	0.000	-4.258	Detected	-3.102	Detected	-3.680	0.029	GT	Sens	contig263	contig263	Unknown	GCTACA
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-1.485	Detected	-1.317	Detected	-1.401	0.007	GT	Sens	contig263	contig263	Transcrip	AGTTCC
GT	Sense	Sense	-0.103	Detected	0.103	Detected	0.000	-1.919	Detected	-1.667	Detected	-1.793	0.008	GT	Sens	contig263	contig263	Purple ac	ATAGAA
GT	Sense	Sense	-0.492	Detected	0.492	Detected	0.000	-2.858	Detected	-2.884	Detected	-2.871	0.028	GT	Sens	contig264	contig264	Genomic	TCTACT
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-1.354	Detected	-1.618	Detected	-1.486	0.010	GT	Sens	contig264	contig264	Acid phos	CATTTT
GT	Sense	Sense	0.292	Detected	-0.292	Detected	0.000	-3.304	Detected	-1.874	Detected	-2.589	0.079	GT	Sens	contig264	contig264	UDP-D-al	ATGAGC
GT	Sense	Sense	0.143	Detected	-0.143	Detected	0.000	-1.324	Detected	-1.074	Detected	-1.199	0.024	GT	Sens	contig264	contig264	Catalase	AACATT
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	-2.838	Detected	-1.784	Detected	-2.311	0.048	GT	Sens	contig264	contig264	Genomic	TTATTG
GT	Sense	Sense	0.395	Detected	-0.395	Detected	0.000	-1.352	Detected	-1.055	Detected	-1.203	0.104	GT	Sens	contig265	contig265	LRR rece	CTTGAG
GT	Sense	Sense	-0.084	Detected	0.084	Detected	0.000	-0.991	Detected	-1.188	Detected	-1.089	0.014	GT	Sens	contig265	contig265	Verticilliu	CAGCAG
GT	Sense	Sense	0.197	Detected	-0.197	Detected	0.000	-2.914	Detected	-1.647	Detected	-2.281	0.075	GT	Sens	contig265	contig265	Chloropla	TTGACG

GT	Sense	Sense	0.572	Detected	-0.572	Detected	0.000	-2.136	Comprom	-1.882	Comprom	-2.009	0.076
GT	Sense	Sense	-0.381	Detected	0.381	Detected	0.000	-2.095	Detected	-1.973	Detected	-2.034	0.034
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-1.014	Detected	-1.097	Detected	-1.055	0.019
GT	Sense	Sense	0.497	Detected	-0.497	Detected	0.000	-2.042	Detected	-1.062	Detected	-1.552	0.156
GT	Sense	Sense	0.946	Detected	-0.946	Detected	0.000	-4.307	Comprom	-3.261	Detected	-3.784	0.073
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-1.742	Detected	-1.374	Detected	-1.558	0.014
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.749	Detected	-1.289	Detected	-1.519	0.023
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-1.243	Detected	-1.333	Detected	-1.288	0.002
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	-2.760	Comprom	-1.588	Detected	-2.174	0.069
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-1.207	Detected	-1.038	Detected	-1.123	0.006
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	-3.218	Comprom	-2.659	Comprom	-2.939	0.009
GT	Sense	Sense	0.347	Detected	-0.347	Detected	0.000	-1.570	Detected	-1.440	Detected	-1.505	0.051
GT	Sense	Sense	0.065	Detected	-0.065	Detected	0.000	-1.332	Detected	-0.928	Detected	-1.130	0.034
GT	Sense	Sense	0.444	Detected	-0.444	Detected	0.000	-1.951	Detected	-1.106	Detected	-1.529	0.130
GT	Sense	Sense	2.264	Detected	-2.264	Detected	0.000	-3.019	Comprom	-3.110	Comprom	-3.065	0.309
GT	Sense	Sense	-0.150	Detected	0.150	Detected	0.000	-1.170	Comprom	-1.102	Comprom	-1.136	0.018
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	-1.123	Detected	-1.370	Detected	-1.247	0.014
GT	Sense	Sense	0.200	Detected	-0.200	Detected	0.000	-1.221	Detected	-1.093	Detected	-1.157	0.031
GT	Sense	Sense	0.369	Detected	-0.369	Detected	0.000	-1.471	Detected	-1.088	Detected	-1.280	0.092
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.628	Detected	-2.134	Detected	-1.881	0.018
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-4.577	Comprom	-3.965	Comprom	-4.271	0.005
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-1.071	Detected	-0.990	Detected	-1.031	0.028
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	-3.020	Comprom	-1.650	Comprom	-2.335	0.078
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-2.494	Detected	-1.401	Detected	-1.947	0.071
GT	Sense	Sense	0.062	Detected	-0.062	Detected	0.000	-1.294	Detected	-1.000	Detected	-1.147	0.019
GT	Sense	Sense	-0.268	Detected	0.268	Detected	0.000	-1.504	Detected	-1.629	Detected	-1.566	0.030
GT	Sense	Sense	0.191	Detected	-0.191	Detected	0.000	-1.627	Detected	-1.096	Detected	-1.362	0.053
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-2.427	Detected	-1.944	Detected	-2.185	0.012
GT	Sense	Sense	0.192	Detected	-0.192	Detected	0.000	-0.856	Detected	-2.500	Detected	-1.678	0.185
GT	Sense	Sense	0.346	Detected	-0.346	Detected	0.000	-3.470	Detected	-2.711	Detected	-3.091	0.027
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-1.659	Detected	-1.019	Detected	-1.339	0.053
GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-2.457	Detected	-2.271	Detected	-2.364	0.007
GT	Sense	Sense	0.091	Detected	-0.091	Detected	0.000	-1.391	Detected	-1.202	Detected	-1.297	0.010
GT	Sense	Sense	0.385	Detected	-0.385	Detected	0.000	-2.501	Detected	-3.599	Detected	-3.050	0.045
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	-1.422	Detected	-1.061	Detected	-1.241	0.021
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	-3.230	Detected	-2.172	Detected	-2.701	0.036
GT	Sense	Sense	0.214	Detected	-0.214	Detected	0.000	-1.720	Detected	-1.512	Detected	-1.616	0.021
GT	Sense	Sense	-0.128	Detected	0.128	Detected	0.000	-1.094	Detected	-0.924	Detected	-1.009	0.022
GT	Sense	Sense	-0.141	Detected	0.141	Detected	0.000	-1.099	Detected	-1.477	Detected	-1.288	0.032
GT	Sense	Sense	0.138	Detected	-0.138	Detected	0.000	-0.860	Detected	-1.168	Detected	-1.014	0.039
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	-1.348	Detected	-1.421	Detected	-1.385	0.002
GT	Sense	Sense	0.332	Detected	-0.332	Detected	0.000	-2.497	Detected	-1.704	Detected	-2.100	0.056
GT	Sense	Sense	0.062	Detected	-0.062	Detected	0.000	-1.572	Detected	-1.320	Detected	-1.446	0.009
GT	Sense	Sense	-0.120	Detected	0.120	Detected	0.000	-1.551	Detected	-1.345	Detected	-1.448	0.012
GT	Sense	Sense	0.153	Detected	-0.153	Detected	0.000	-2.465	Detected	-1.735	Detected	-2.100	0.034
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-2.536	Detected	-2.376	Detected	-2.456	0.001
GT	Sense	Sense	0.376	Detected	-0.376	Detected	0.000	-1.357	Detected	-1.299	Detected	-1.328	0.072
GT	Sense	Sense	0.129	Detected	-0.129	Detected	0.000	-0.960	Detected	-1.042	Detected	-1.001	0.018
GT	Sense	Sense	0.124	Detected	-0.124	Detected	0.000	-1.884	Detected	-1.832	Detected	-1.858	0.005
GT	Sense	Sense	0.320	Detected	-0.320	Detected	0.000	-2.034	Detected	-2.046	Detected	-2.040	0.024
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-2.191	Detected	-1.602	Detected	-1.896	0.025
GT	Sense	Sense	0.409	Detected	-0.409	Detected	0.000	-2.448	Comprom	-1.096	Detected	-1.772	0.154
GT	Sense	Sense	-0.050	Detected	0.050	Detected	0.000	-1.895	Detected	-1.257	Detected	-1.576	0.040
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	-1.835	Detected	-1.570	Detected	-1.702	0.012
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-0.968	Detected	-1.070	Detected	-1.019	0.007
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	-2.854	Detected	-1.251	Detected	-2.053	0.126
GT	Sense	Sense	-0.049	Detected	0.049	Detected	0.000	-1.209	Detected	-0.818	Detected	-1.014	0.037
GT	Sense	Sense	0.095	Detected	-0.095	Detected	0.000	-1.760	Detected	-1.075	Detected	-1.417	0.058
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	-1.684	Detected	-1.326	Detected	-1.505	0.014
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.319	Comprom	-2.472	Comprom	-1.896	0.082
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-2.918	Detected	-4.052	Comprom	-3.485	0.026
GT	Sense	Sense	0.222	Detected	-0.222	Detected	0.000	-1.433	Detected	-1.998	Detected	-1.716	0.041
GT	Sense	Sense	-0.378	Detected	0.378	Detected	0.000	-0.857	Detected	-1.955	Detected	-1.406	0.169
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-3.248	Detected	-2.646	Detected	-2.947	0.013
GT	Sense	Sense	0.343	Detected	-0.343	Detected	0.000	-1.387	Detected	-1.022	Detected	-1.205	0.090
GT	Sense	Sense	0.255	Detected	-0.255	Detected	0.000	-1.335	Detected	-1.315	Detected	-1.325	0.035
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-2.763	Detected	-0.971	Detected	-1.867	0.174
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	-1.024	Detected	-1.062	Detected	-1.043	0.026
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-1.177	Detected	-1.080	Detected	-1.129	0.022
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-1.363	Detected	-2.078	Detected	-1.720	0.042
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	-1.882	Detected	-1.449	Detected	-1.665	0.028
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	-1.504	Detected	-1.454	Detected	-1.479	0.005
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	-2.226	Detected	-1.179	Detected	-1.703	0.084
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-1.758	Detected	-0.963	Detected	-1.361	0.076
GT	Sense	Sense	-0.081	Detected	0.081	Detected	0.000	-1.072	Detected	-1.014	Detected	-1.043	0.007
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-1.001	Detected	-1.029	Detected	-1.015	0.016
GT	Sense	Sense	0.116	Detected	-0.115	Detected	0.000	-2.450	Detected	-1.548	Detected	-1.999	0.050
GT	Sense	Sense	0.216	Detected	-0.216	Detected	0.000	-2.329	Detected	-1.477	Detected	-1.903	0.058
GT	Sense	Sense	0.177	Detected	-0.177	Detected	0.000	-2.129	Detected	-1.923	Detected	-2.026	0.010
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.855	Detected	-1.767	Detected	-1.811	0.001
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.229	Comprom	-1.453	Comprom	-1.341	0.016
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	-1.038	Detected	-1.036	Detected	-1.037	0.000
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	-1.595	Detected	-1.277	Detected	-1.436	0.013
GT	Sense	Sense	0.095	Detected	-0.095	Detected	0.000	-1.354	Detected	-1.157	Detected	-1.255	0.012
GT	Sense	Sense	-1.218	Detected	1.218	Detected	0.000	-1.175	Detected	-2.076	Comprom	-1.626	0.337
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-1.368	Detected	-1.183	Detected	-1.275	0.008
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	-1.534	Detected	-1.314	Detected	-1.424	0.007
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-1.075	Detected	-2.090	Detected	-1.582	0.090
GT	Sense	Sense	0.653	Detected	-0.653	Detected	0.000	-2.106	Comprom	-1.323	Comprom	-1.715	0.153
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-2.110	Comprom	-1.703	Comprom	-1.906	0.011
GT	Sense	Sense	-0.079	Detected	0.079	Detected	0.000	-1.526	Detected	-1.254	Detected	-1.390	0.013
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-2.001	Detected	-1.604	Detected	-1.802	0.016
GT	Sense	Sense	0.313	Detected	-0.313	Detected	0.000	-2.019	Detected	-1.147	Detected	-1.583	0.098
GT	Sense	Sense	0.513	Detected	-0.513	Detected	0.000	-0.894	Detected	-1.794	Detected	-1.344	0.188
GT	Sense	Sense	-0.021	Detected	0.021	Detected	0.000	-0.849	Detected	-1.155	Detected	-1.002	0.023
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-2.349	Detected	-1.913	Detected	-2.131	0.012
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-1.194	Detected	-1.011	Detected	-1.102	0.007
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.187	Detected	-1.062	Detected	-1.125	0.005
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	-2.662	Comprom	-2.497	Comprom	-2.579	0.001
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-4.479	Comprom	-2.572	Detected	-3.526	0.066
GT	Sense	Sense	-0.203	Detected	0.203	Detected	0.000	-3.248	Comprom	-1.994	Comprom	-2.621	0.058
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-1.400	Detected	-1.161	Detected	-1.280	0.010
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-2.047	Comprom	-0.992	Comprom	-1.519	0.107
GT	Sense	Sense	0.336	Detected	-0.336	Detected	0.000	-1.107	Detected	-1.623	Detected	-1.365	0.084
GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-1.288	Comprom	-1.402	Comprom	-1.345	0.020
GT	Sense	Sense	0.699	Detected	-0.699	Detected	0.000	-2.046	Comprom	-2.045	Comprom	-2.045	0.100
GT	Sense	Sense	1.134	Detected	-1.134	Detected	0.000	-2.803	Detected	-2.616	Detected	-2.710	0.140
GT	Sense	Sense	0.260	Detected	-0.260	Detected	0.000	-1.147	Detected	-2.104	Comprom	-1.626	0.096
GT	Sense	Sense	-0.160	Detected	0.160	Detected	0.000	-1.182	Detected	-1.304	Detected	-1.243	0.019
GT	Sense	Sense	-0.082	Detected	0.082	Detected	0.000	-0.836	Detected	-2.459	Comprom	-1.648	0.181
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-1.023	Detected	-1.083	Detected	-1.053	0.011
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.204	Detected	-1.068	Detected	-1.136	0.008
GT	Sense	Sense	-0.362	Detected	0.362	Detected	0.000	-4.154	Comprom	-3.849	Comprom	-4.002	0.009
GT	Sense	Sense	-0.380	Detected	0.380	Detected	0.000	-3.498	Comprom	-3.267	Comprom	-3.383	0.014
GT	Sense	Sense	0.717	Detected	-0.717	Detected	0.000	-2.060	Comprom	-1.500	Comprom	-1.780	0.147
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	-1.810	Detected	-1.268	Detected	-1.539	0.030
GT	Sense	Sense	-0.121	Detected	0.121	Detected	0.000	-1.021	Detected	-1.849	Comprom	-1.435	0.080
GT	Sense	Sense	0.162	Detected	-0.162	Detected	0.000	-1.664	Detected	-1.304	Detected	-1.484	0.026
GT	Sense	Sense	-0.116	Detected	0.116	Detected	0.000	-0.980	Detected	-1.021	Detected	-1.001	0.014
GT	Sense	Sense	0.364	Detected	-0.364	Detected	0.000	-1.290	Comprom	-1.927	Comprom	-1.608	0.080
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	-1.008	Comprom	-2.894	Comprom	-1.951	0.178
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-2.565	Comprom	-2.414	Comprom	-2.489	0.001
GT	Sense	Sense	0.314	Detected	-0.314	Detected	0.000	-1.547	Detected	-1.447	Detected	-1.497	0.042
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-0.894	Detected	-1.223	Detected	-1.058	0.024
GT	Sense	Sense	-0.016	Detected	0.016	Detected	0.000	-1.015	Detected	-1.429	Detected	-1.222	0.028
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-1.114	Detected	-0.898	Detected	-1.006	0.021
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	-2.686	Detected	-1.971	Detected	-2.328	0.028
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.805	Detected	-1.682	Detected	-1.744	0.001
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.714	Detected	-1.186	Detected	-1.450	0.036
GT	Sense	Sense	0.595	Detected	-0.595	Detected	0.000	-0.841	Detected	-1.680	Comprom	-1.261	0.225
GT	Sense	Sense	0.480	Detected	-0.480	Detected	0.000	-2.571	Comprom	-2.040	Detected	-2.305	0.052
GT	Sense	Sense	0.211	Detected	-0.211	Detected	0.000	-3.297	Detected	-2.583	Detected	-2.940	0.019
GT	Sense	Sense	0.179	Detected	-0.179	Detected	0.000	-1.725	Detected	-1.297	Detected	-1.511	0.032
GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-1.566	Detected	-1.263	Detected	-1.415	0.022
GT	Sense	Sense	0.163	Detected	-0.163	Detected	0.000	-1.727	Detected	-1.018	Detected	-1.373	0.072
GT	Sense	Sense	0.181	Detected	-0.181	Detected	0.000	-2.911	Comprom	-0.864	Comprom	-1.887	0.211
GT	Sense	Sense	-0.026	Detected	0.026	Detected	0.000	-1.403	Detected	-1.228	Detected	-1.315	0.005
GT	Sense	Sense	0.306	Detected	-0.306	Detected	0.000	-2.031	Detected	-2.257	Detected	-2.144	0.022
GT	Sense	Sense	0.388	Detected	-0.388	Detected	0.000	-1.950	Detected	-2.041	Detected	-1.996	0.036
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-0.909	Detected	-1.219	Detected	-1.064	0.021
GT	Sense	Sense	0.194	Detected	-0.194	Detected	0.000	-1.229	Detected	-1.183	Detected	-1.206	0.025
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.255	Detected	-0.807	Detected	-1.031	0.045
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-1.144	Detected	-1.104	Detected	-1.124	0.008
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	-2.670	Comprom	-2.914	Comprom	-2.792	0.002
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-1.239	Detected	-1.318	Detected	-1.279	0.005
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-2.160	Detected	-1.460	Detected	-1.810	0.035
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-1.011	Detected	-1.192	Detected	-1.102	0.009
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-1.301	Detected	-1.045	Detected	-1.173	0.012
GT	Sense	Sense	0.967	Detected	-0.967	Detected	0.000	-1.848	Comprom	-1.116	Detected	-1.482	0.288
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-1.295	Detected	-1.016	Detected	-1.156	0.025
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	-1.537	Detected	-1.083	Detected	-1.310	0.043
GT	Sense	Sense	0.636	Detected	-0.636	Detected	0.000	-1.066	Detected	-1.363	Detected	-1.215	0.204
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	-1.582	Detected	-0.947	Detected	-1.264	0.059
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.519	Detected	-1.002	Detected	-1.261	0.040
GT	Sense	Sense	-0.091	Detected	0.091	Detected	0.000	-1.109	Detected	-1.717	Comprom	-1.413	0.047
GT	Sense	Sense	0.120	Detected	-0.120	Detected	0.000	-1.159	Detected	-0.982	Detected	-1.071	0.019
GT	Sense	Sense	0.218	Detected	-0.218	Detected	0.000	-1.395	Comprom	-0.956	Comprom	-1.176	0.063
GT	Sense	Sense	0.197	Detected	-0.197	Detected	0.000	-1.235	Detected	-1.019	Detected	-1.127	0.037
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-1.389	Detected	-1.100	Detected	-1.244	0.027
GT	Sense	Sense	0.124	Detected	-0.124	Detected	0.000	-1.117	Detected	-0.915	Detected	-1.016	0.024
GT	Sense	Sense	-0.430	Detected	0.430	Detected	0.000	-1.222	Comprom	-1.130	Comprom	-1.176	0.113
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-2.072	Detected	-1.491	Detected	-1.782	0.032
GT	Sense	Sense	-0.090	Detected	0.090	Detected	0.000	-1.430	Comprom	-1.012	Comprom	-1.221	0.033
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	-1.832	Detected	-1.626	Detected	-1.729	0.011
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-0.888	Detected	-1.359	Detected	-1.124	0.044
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.196	Detected	-1.250	Detected	-1.223	0.002
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	-0.995	Detected	-1.052	Detected	-1.023	0.002
GT	Sense	Sense	0.357	Detected	-0.357	Detected	0.000	-1.994	Detected	-0.993	Detected	-1.493	0.136
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-1.311	Detected	-0.895	Detected	-1.103	0.048
GT	Sense	Sense	0.162	Detected	-0.162	Detected	0.000	-1.598	Detected	-1.184	Detected	-1.391	0.034
GT	Sense	Sense	0.168	Detected	-0.168	Detected	0.000	-1.325	Detected	-1.345	Detected	-1.335	0.016
GT	Sense	Sense	0.136	Detected	-0.136	Detected	0.000	-1.455	Detected	-1.128	Detected	-1.292	0.026
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-1.589	Detected	-1.737	Detected	-1.663	0.004
GT	Sense	Sense	-0.693	Detected	0.693	Detected	0.000	-0.981	Detected	-1.167	Comprom	-1.074	0.264
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-0.986	Detected	-1.046	Detected	-1.016	0.016
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-1.275	Comprom	-1.193	Comprom	-1.234	0.014
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-2.078	Detected	-1.523	Detected	-1.800	0.023
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	-2.101	Detected	-1.323	Detected	-1.712	0.053
GT	Sense	Sense	0.210	Detected	-0.210	Detected	0.000	-2.298	Detected	-1.507	Detected	-1.902	0.051
GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-0.976	Detected	-1.065	Detected	-1.021	0.024
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-1.050	Detected	-1.080	Detected	-1.065	0.001
GT	Sense	Sense	0.399	Detected	-0.399	Detected	0.000	-3.427	Detected	-3.092	Detected	-3.260	0.017
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	-1.800	Detected	-0.905	Detected	-1.353	0.094
GT	Sense	Sense	0.365	Detected	-0.365	Detected	0.000	-1.687	Comprom	-1.491	Comprom	-1.589	0.052
GT	Sense	Sense	0.069	Detected	-0.069	Detected	0.000	-1.946	Detected	-1.628	Detected	-1.787	0.009
GT	Sense	Sense	0.251	Detected	-0.251	Detected	0.000	-0.994	Detected	-1.600	Detected	-1.297	0.081
GT	Sense	Sense	0.621	Detected	-0.621	Detected	0.000	-2.377	Detected	-1.770	Detected	-2.074	0.095
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	-1.750	Detected	-1.167	Detected	-1.459	0.041
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-1.813	Detected	-2.242	Detected	-2.027	0.018
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	-1.624	Detected	-1.399	Detected	-1.511	0.014
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-4.224	Detected	-2.768	Detected	-3.496	0.043
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	-4.378	Detected	-2.910	Detected	-3.644	0.041
GT	Sense	Sense	-0.051	Detected	0.051	Detected	0.000	-1.238	Detected	-0.971	Detected	-1.105	0.016
GT	Sense	Sense	0.174	Detected	-0.174	Detected	0.000	-1.890	Detected	-1.571	Detected	-1.730	0.018
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	-1.873	Detected	-1.570	Detected	-1.721	0.016
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-1.132	Detected	-1.615	Detected	-1.373	0.040
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-1.135	Detected	-2.303	Detected	-1.719	0.100
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-1.243	Detected	-1.345	Detected	-1.294	0.002
GT	Sense	Sense	0.222	Detected	-0.222	Detected	0.000	-1.959	Comprom	-1.403	Comprom	-1.681	0.042
GT	Sense	Sense	0.313	Detected	-0.313	Detected	0.000	-1.973	Detected	-1.490	Detected	-1.731	0.048
GT	Sense	Sense	0.294	Detected	-0.294	Detected	0.000	-1.786	Detected	-0.940	Detected	-1.363	0.118
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-2.402	Detected	-0.957	Detected	-1.679	0.146
GT	Sense	Sense	-1.541	Detected	1.541	Detected	0.000	-3.348	Comprom	-4.039	Comprom	-3.693	0.144
GT	Sense	Sense	-0.103	Detected	0.103	Detected	0.000	-2.028	Detected	-1.313	Detected	-1.671	0.046
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	-1.337	Detected	-1.171	Detected	-1.254	0.009
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.578	Detected	-1.337	Detected	-1.457	0.008
GT	Sense	Sense	0.428	Detected	-0.428	Detected	0.000	-3.683	Detected	-2.037	Detected	-2.860	0.091
GT	Sense	Sense	0.280	Detected	-0.280	Detected	0.000	-1.042	Detected	-1.116	Detected	-1.079	0.062
GT	Sense	Sense	-0.914	Detected	0.914	Detected	0.000	-2.571	Comprom	-2.797	Comprom	-2.684	0.100
GT	Sense	Sense	-1.529	Detected	1.529	Detected	0.000	-4.643	Comprom	-4.213	Comprom	-4.428	0.103
GT	Sense	Sense	-0.096	Detected	0.096	Detected	0.000	-1.003	Detected	-1.022	Detected	-1.012	0.009
GT	Sense	Sense	-0.219	Detected	0.219	Detected	0.000	-1.196	Detected	-1.013	Detected	-1.104	0.043
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-1.244	Detected	-1.256	Detected	-1.250	0.004
GT	Sense	Sense	-0.051	Detected	0.051	Detected	0.000	-1.553	Detected	-1.318	Detected	-1.435	0.008
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	-1.277	Detected	-0.907	Detected	-1.092	0.030
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-1.418	Detected	-0.832	Detected	-1.125	0.063
GT	Sense	Sense	0.240	Detected	-0.240	Detected	0.000	-1.127	Detected	-1.257	Detected	-1.192	0.041
GT	Sense	Sense	0.166	Detected	-0.166	Detected	0.000	-1.824	Detected	-1.178	Detected	-1.501	0.054
GT	Sense	Sense	0.320	Detected	-0.320	Detected	0.000	-1.191	Detected	-0.903	Detected	-1.047	0.096
GT	Sense	Sense	-0.031	Detected	0.031	Detected	0.000	-1.295	Detected	-1.031	Detected	-1.163	0.013
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-2.028	Detected	-1.471	Detected	-1.750	0.026
GT	Sense	Sense	0.111	Detected	-0.111	Detected	0.000	-1.965	Detected	-1.310	Detected	-1.637	0.042
GT	Sense	Sense	0.510	Detected	-0.510	Detected	0.000	-2.886	Detected	-2.615	Detected	-2.751	0.035
GT	Sense	Sense	0.368	Detected	-0.368	Detected	0.000	-1.534	Detected	-2.640	Comprom	-2.087	0.088
GT	Sense	Sense	0.412	Detected	-0.412	Detected	0.000	-2.310	Detected	-2.534	Detected	-2.422	0.030
GT	Sense	Sense	0.354	Detected	-0.354	Detected	0.000	-2.242	Comprom	-1.944	Comprom	-2.093	0.032
GT	Sense	Sense	-0.091	Detected	0.091	Detected	0.000	-2.010	Comprom	-1.087	Comprom	-1.549	0.081
GT	Sense	Sense	0.236	Detected	-0.236	Detected	0.000	-0.989	Detected	-1.989	Detected	-1.489	0.115
GT	Sense	Sense	0.268	Detected	-0.268	Detected	0.000	-1.671	Detected	-1.086	Detected	-1.379	0.074
GT	Sense	Sense	0.281	Detected	-0.281	Detected	0.000	-1.477	Detected	-0.848	Detected	-1.162	0.110
GT	Sense	Sense	-0.436	Detected	0.436	Detected	0.000	-2.130	Comprom	-1.264	Comprom	-1.697	0.110
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	-1.212	Detected	-1.016	Detected	-1.114	0.029
GT	Sense	Sense	-0.602	Detected	0.602	Detected	0.000	-0.977	Detected	-1.617	Detected	-1.297	0.197
GT	Sense	Sense	0.360	Detected	-0.360	Detected	0.000	-1.200	Detected	-1.297	Detected	-1.248	0.075
GT	Sense	Sense	0.346	Detected	-0.346	Detected	0.000	-1.302	Detected	-1.177	Detected	-1.240	0.072
GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-1.622	Detected	-1.218	Detected	-1.420	0.035
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-1.290	Detected	-1.258	Detected	-1.274	0.007
GT	Sense	Sense	-0.100	Detected	0.100	Detected	0.000	-1.206	Detected	-1.049	Detected	-1.128	0.013
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-1.288	Detected	-0.821	Detected	-1.054	0.059
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	-1.232	Detected	-1.431	Comprom	-1.332	0.015
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.843	Detected	-2.220	Detected	-2.031	0.009
GT	Sense	Sense	0.223	Detected	-0.223	Detected	0.000	-1.791	Detected	-2.094	Detected	-1.943	0.019
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	-1.923	Comprom	-1.298	Detected	-1.611	0.036
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-1.743	Detected	-1.351	Detected	-1.547	0.020

GT	Sense	Sense	-0.060	Detected	0.060	Detected	0.000	-0.960	Detected	-1.183	Detected	-1.072	0.014	GT	Sens	contig350	contig350	Unannota	GGACTGATTAGTGCTTTTTTGTTATTATACCCTGACTGATTGTGCTCAA	contig350	Solvc10g	Cellular n	GO:00082	SL2.40ch	AT5G197	RAP2.11	RAP2.11	chr5:668	57.7559	59.0413	22.9045	32.9265	32.0114	27.3411
GT	Sense	Sense	-0.023	Detected	0.023	Detected	0.000	-0.871	Detected	-1.285	Detected	-1.078	0.035	GT	Sens	contig350	contig350	Unannota	TTACTAGTGAAGTTAGGGTCTTATGTAGCAAGAGTCTTAATCAAATGAG	contig350	Solvc10g	Cellular n	GO:00082	SL2.40ch	AT5G197	RAP2.11	RAP2.11	chr5:668	61.1687	59.3882	25.7599	25.0286	35.152	26.3045
GT	Sense	Sense	-0.890	Detected	0.890	Detected	0.000	-1.939	Comprom	-2.110	Comprom	-2.025	0.152	GT	Sens	contig351	contig351	Unannota	GAATTGAATCTTATGCTATGTGAGAAATGTAATGTGTTCCTCTCGAATT	contig351	Solvc09g	Caffeoyl-(	GO:00424	SL2.40ch	AT5G49370.1				12.7363	41.1737	4.98844	7.37586	6.36668	5.64059
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.418	Detected	-1.037	Detected	-1.228	0.026	GT	Sens	contig351	contig351	Unannota	GCAAAAGATAATTATGATCCATACAATCCCCTTCCAATGTTTTTTCATGA	contig351	Solvc09g	Peptide tr	GO:00429	SL2.40ch	AT4G212	PSBO, PS	oxygen-e	chr4:113	251.137	257.59	83.1376	191.873	101.467	131.743
GT	Sense	Sense	-0.088	Detected	0.088	Detected	0.000	-1.323	Detected	-1.097	Detected	-1.210	0.014	GT	Sens	contig351	contig351	Unannota	TCAGTCTAGACCTTTGAGTTGCTAACTTGCATCATTTCTGATACTTCAA	contig351	Solvc09g	Peptide tr	GO:00429	SL2.40ch	AT4G212	PSBO, PS	oxygen-e	chr4:113	249.847	265.493	78.6947	203.954	109.781	128.006
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-1.074	Detected	-0.927	Detected	-1.001	0.011	GT	Sens	contig351	contig351	Unannota	CATCCCCATGTAATTCCACGAGTCTCTTCTGGAAAAGGTAGAGTGTATC	contig351	Solvc10g	Receptor-	GO:00064	SL2.40ch	AT5G514	EYE	EYE (EM	chr5:208	14210.8	12011.9	6773.14	6811.79	6616.37	7306.36
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	-1.206	Detected	-0.839	Detected	-1.023	0.040	GT	Sens	contig351	contig351	Unannota	CTAAGCTTTGCTTTCCTGATGTTGTATCCTGATTTTTGACATCTTGTCC	contig351	Solvc09g	Unknown Protein (A		SL2.40ch	AT2G01818.1		zinc ion I	chr2:353	100.138	81.8556	49.1244	68.5568	41.8358	53.8037
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.130	Detected	-0.971	Detected	-1.050	0.007	GT	Sens	contig351	contig351	Unannota	ATCGATTCTTGGGTTTTGAGCTTTGTGGGGGTGTTTATCTTGGTTCATC	contig351	Solvc08g	Unknown Protein (A		SL2.40ch	AT5G448	CHR4	CHR4 (CI	chr5:180	645.343	577.13	367.219	338.385	297.422	330.986
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	-2.266	Comprom	-2.199	Comprom	-2.232	0.001	GT	Sens	contig352	contig352	Unannota	CTTCTTGCAATTAGGATGGAAGAATTAGGAGGTCGGAGGTTATTGCAG	contig352	Solvc11g	GDSL est	GO:00066	SL2.40ch	AT5G04500.1		glycosylt	chr5:128	13.6773	14.3464	2.96494	5.70893	3.10644	3.24453
GT	Sense	Sense	0.498	Detected	-0.498	Detected	0.000	-1.940	Detected	-1.663	Detected	-1.802	0.073	GT	Sens	contig352	contig352	Unannota	GTACACCATTCGAGCTGAACAGAAGTCTAAACACACCGACAACAAAAAA	contig352	Solvc04g	Cellular retinaldehy		SL2.40ch	AT5G11160.1				258.583	121.957	108.793	95.1119	49.3491	59.6122
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-2.219	Detected	-1.953	Detected	-2.086	0.005	GT	Sens	contig353	contig353	Serine ca	ATATATA contig353 Solvc03g Solvc03g Serine ca GO:00041 GO:00041	contig353	Solvc03g	Serine ca	GO:00428	SL2.40ch	AT2G335	scpl46	scpl46 (s	chr2:141	3989.79	3513.8	790.366	654.785	857.857	1028.31
GT	Sense	Sense	0.238	Detected	-0.238	Detected	0.000	-1.110	Comprom	-1.269	Comprom	-1.190	0.042	GT	Sens	contig353	contig353	Unannota	CAAAAAAGAGTGATAGTCAACATTACAAGCAGAGCCATCTAATTACTATC	contig353	Solvc12g	Major alle	GO:00096	SL2.40ch	AT4G34881.1		unknown	chr4:166	19.8834	13.4476	3.37529	5.45188	8.07641	7.21446
GT	Sense	Sense	-0.157	Detected	0.157	Detected	0.000	-1.442	Comprom	-0.855	Comprom	-1.149	0.075	GT	Sens	contig353	contig353	Unannota	CTACAAAATCCAAGATGCGATTACCAAAAAGGAGCATCTCATCTAGTGC	contig353	Solvc10g	Helicase-l	GO:00080	SL2.40ch	AT3G13772.1		endomer	chr3:452	11.6999	13.6923	13.0605	2.82535	4.96894	7.43737
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	-1.469	Detected	-1.057	Detected	-1.263	0.029	GT	Sens	contig353	contig353	Unannota	CTTATGGATTATTCAGTGTGAATTCCATTTCACCTTTAAATTATCATGTT	contig353	Solvc08g	cytochror	GO:00198	SL2.40ch	AT3G57050.3				45.9486	38.6296	13.9497	14.2726	16.2318	21.5347
GT	Sense	Sense	0.031	Detected	-0.031	Detected	0.000	-1.371	Detected	-1.019	Detected	-1.195	0.022	GT	Sens	contig353	contig353	Unannota	CAACATGGAGTATGCTTGTTCATCTCTTATCTTAAATCAGTAATTGTGA	contig353	Solvc08g	cytochror	GO:00198	SL2.40ch	AT3G57050.3				138.484	124.775	45.3616	54.2195	54.2093	68.9819
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-1.284	Detected	-1.407	Detected	-1.345	0.003	GT	Sens	contig353	contig353	Unannota	ACAGGTTAGATTCCGTTAGCACCATTTCTTGAAATTGCTTATTCTTTAT	contig353	Solvc08g	BHLH trai	GO:00305	SL2.40ch	AT3G52700.1		unknown	chr3:195	69.4593	69.8962	26.4121	29.6506	30.5074	27.9412
GT	Sense	Sense	-0.117	Detected	0.117	Detected	0.000	-1.065	Detected	-1.350	Detected	-1.208	0.023	GT	Sens	contig353	contig353	Unannota	GCCCCCGAAGAGAAGAGATATCTAAAAAGTTAAAACCTTCATTGCTAC	contig353	Solvc08g	BHLH trai	GO:00305	SL2.40ch	AT3G52700.1		unknown	chr3:195	28.2884	31.2892	14.7944	13.2805	15.1668	12.4054
GT	Sense	Sense	0.640	Detected	-0.640	Detected	0.000	-1.884	Detected	-0.924	Detected	-1.404	0.222	GT	Sens	contig354	contig354	Unannota	TCTCAAGTCCAAACTTGTTGCTCAGGTGAACATTAAGTTTCACATTGGT	contig354	Solvc12g	ATP-bind	GO:00160	SL2.40ch	AT1G70949.1				451.587	174.91	101.556	128.93	81.2102	157.532
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-1.230	Comprom	-1.712	Comprom	-1.471	0.027	GT	Sens	contig354	contig354	Unannota	GGCTGATGCAATGATTTAGGTTGTTATTTTTGTGGAGATTGGAGGAGC	contig354	Solvc08g	Growth-re	GO:00056	SL2.40ch	AT1G53635.1				18.6519	16.2355	9.65759	4.95541	7.90878	5.6469
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-1.187	Detected	-0.837	Detected	-1.012	0.048	GT	Sens	contig354	contig354	Unannota	GTCTGGCAGTGAACGTAATTTGAGAATTTAAGATGGGTACACAATCCTA	contig354	Solvc12g	Plant synaptotagmi		SL2.40ch	ATCG001	RPS2	Chloropl	chrC:150	430.608	328.634	216.679	223.237	176.211	223.933
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-1.233	Detected	-0.881	Detected	-1.057	0.045	GT	Sens	contig355	contig355	Unannota	ATACTGTGTAGCTAGGATTCATATTCGGGGGTTTCGAAATCGAGACATA	contig355	Solvc03g	Unknown Protein (A		SL2.40ch	AT5G071	ERL2	ERL2 (EF	chr5:222	344.23	262.887	85.2784	132.043	136.457	173.692
GT	Sense	Sense	0.202	Detected	-0.202	Detected	0.000	-1.262	Detected	-0.860	Detected	-1.061	0.065	GT	Sens	contig355	contig355	Unannota	GGATGAAATAGTCTCGTCATTTCATTGTCTACGGTGAAACATAAAAGTT	contig355	Solvc03g	Unknown Protein (A		SL2.40ch	AT5G071	ERL2	ERL2 (EF	chr5:222	177.161	126.039	44.9234	57.8224	66.4377	87.5309
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	-1.821	Detected	-0.935	Detected	-1.378	0.095	GT	Sens	contig355	contig355	Unannota	TTAAATTTACATGTGCACTTAAGGGTGTCAAACGGGGGCCGATTGGGC	contig355	Solvc06g	Pentatricopeptide (F		SL2.40ch	AT4G16150.1		calmodu	chr4:914	45.6741	50.1843	17.6178	28.9076	14.4515	26.6188
GT	Sense	Sense	0.195	Detected	-0.195	Detected	0.000	-1.025	Detected	-0.977	Detected	-1.001	0.037	GT	Sens	contig355	contig355	Unannota	GGGTGTGTGGGTATTAGCAATTACAGTGATAAATTATTGAAATTGACAA	contig355	Solvc02g	Major facilitator sup		SL2.40ch	AT3G48050.2		DNA binc	chr3:177	191.069	137.164	92.5586	106.024	84.8102	87.4565
GT	Sense	Sense	-0.210	Detected	0.210	Detected	0.000	-1.145	Detected	-2.006	Detected	-1.576	0.081	GT	Sens	contig356	contig356	Unknown	TTTGGG contig356 Solvc08g Solvc08g Unknown Protein (AHRD V1)%	contig356	Solvc08g	Unknown Protein (A		SL2.40ch	AT5G16520.1		unknown	chr5:539	244.278	307.485	94.2697	84.7587	132.192	72.5198
GT	Sense	Sense	0.548	Detected	-0.548	Detected	0.000	-1.884	Comprom	-1.062	Comprom	-1.473	0.164	GT	Sens	contig357	contig357	Unannota	CTACAGAATTTGTCCAGTAGTTATAACCTGTGATCTGAAGAGGTTATTA	contig357	Solvc06g	Glycosylt	GO:00472	SL2.40ch	AT5G64980.1		unknown	chr5:259	32.8938	14.4834	5.66073	10.2203	6.30578	11.1139
GT	Sense	Sense	0.054	Detected	-0.054	Detected	0.000	-1.101	Detected	-1.225	Detected	-1.163	0.005	GT	Sens	contig357	contig357	Unannota	TTGCTTCTGGTAGGTTAACTTAGTCACATATACTAGCTTTTGCAGCTAT	contig357	Solvc06g	Glycosylt	GO:00472	SL2.40ch	AT5G64980.1		unknown	chr5:259	31.5335	27.5476	9.44486	13.6178	14.6489	13.4077
GT	Sense	Sense	0.108	Detected	-0.108	Detected	0.000	-1.454	Detected	-1.315	Detected	-1.384	0.009	GT	Sens	contig357	contig357	Unannota	GGACGACTACAGTATACATGTTTCCTTCAATATTTTTCTGCTTATTCTT	contig357	Solvc12g	Unknown	GO:00160	SL2.40ch	AT4G13110.1		BSD don	chr4:764	254.51	206.11	86.6533	151.432	89.1659	97.8666
GT	Sense	Sense	0.039	Detected	-0.039	Detected	0.000	-1.005	Detected	-1.180	Detected	-1.093	0.008	GT	Sens	contig358	contig358	Unannota	TACAAGAAGTACAAGGATCAAGGTTTGTCCAATTCTCCCGAACCAACTG	contig358	Solvc08g	Glutathio	GO:00551	SL2.40ch	AT1G63460.1		glutathio	chr1:235	42.2884	37.6878	16.957	15.6121	21.2057	18.7305
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.533	Detected	-1.016	Detected	-1.275	0.039	GT	Sens	contig358	contig358	Unannota	GGCGTTCGCCCTGACATATTTCTGCAAAGAGAACTTAAATAAAATGGAT	contig358	Solvc08g	Glutathio	GO:00551	SL2.40ch	AT1G63460.1		glutathio	chr1:235	40.0131	38.932	20.6986	17.9097	14.5434	20.7458
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-1.598	Detected	-1.288	Detected	-1.443	0.017	GT	Sens	contig358	contig358	Unannota	ATGGTGAGAACTTCAGCCAACTGGGTGGAACTAGGAAGTTGTTTTCTTC	contig358	Solvc05g	MYC2b tr	GO:00037	SL2.40ch	AT4G04570.2		protein k	chr4:229	123.524	99.3624	42.0091	62.3942	39.0363	48.2428
GT	Sense	Sense	-0.411	Detected	0.411	Detected	0.000	-0.863	Detected	-1.268	Comprom	-1.066	0.146	GT	Sens	contig358	contig358	Unannota	GGGACCAAAATCCAAAATTCACTAACTCTAACCCAGAATAGTTCCAACT	contig358	Solvc08g	Unknown Protein (A		SL2.40ch	AT1G21890.1		nodulin M	chr1:768	14.6326	24.347	5.33397	16.7371	11.0684	8.3312
GT	Sense	Sense	0.143	Detected	-0.143	Detected	0.000	-1.304	Detected	-0.886	Detected	-1.095	0.050	GT	Sens	contig358	contig358	Unannota	AACGAGTATGGCATTTTGTGAGGTAGTTTTGATTTCCACATTTAGTTTT	contig358	Solvc06g	Reticulon	GO:00057	SL2.40ch	AT1G598	CCB4	CCB4 (C	chr1:220	2945.95	2273.66	1134.53	1931	1117.95	1489.15
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.467	Detected	-1.037	Detected	-1.252	0.034	GT	Sens	contig358	contig358	Unannota	GCGACTTCCTTTGTTAGAGCCCTTTAGTTACTGGCTTTGCTTTATTACA	contig358	Solvc06g	Reticulon	GO:00057	SL2.40ch	AT1G598	CCB4	CCB4 (C	chr1:220	5085.66	4176.01	1674.48	3013.75	1777.71	2388
GT	Sense	Sense	0.230	Detected	-0.230	Detected	0.000	-1.154	Comprom	-0.888	Comprom	-1.021	0.062	GT	Sens	contig358	contig358	Unannota	ATCCTAAAATGCTTATAATTTCAAGATGAGTCGCTAGCACCGTCCCATG	contig358	Solvc09g	Unknown Protein (A		SL2.40ch	AT5G40340.1		PWWP d	chr5:161	17.2406	11.7884	9.45767	14.1713	6.832	8.19021
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.286	Comprom	-1.976	Comprom	-1.631	0.043	GT	Sens	contig359	contig359	Unannota	TTTGTAGTTGAGCTTACAGCAAGAACCAATAAAGAAGCCAAATCTCCTT	contig359	Solvc11g	Aspartic i	GO:00065	SL2.40ch	AT4G123	CYP706A	CYP706A	chr4:731	16.7984	14.8161	4.67709	3.8075	6.89827	4.26332
GT	Sense	Sense	0.217	Detected	-0.217	Detected	0.000	-1.501	Detected	-1.074	Detected	-1.288	0.052	GT	Sens	contig359	contig359	Unannota	GATAGTAGCTGCAAAATGTGCGGCGCTGCTTAAACTTGCTATTGATTTA	contig359	Solvc01g	Aspartic i	GO:00065	SL2.40ch	AT1G086	ZIGA4	ZIGA4 (A	chr1:276	112042	78068.9	40837.5	47495.1	35227.3	47230.3
GT	Sense	Sense	0.427	Detected	-0.427	Detected	0.000	-1.928	Detected	-1.244	Detected	-1.586	0.101	GT	Sens	contig359	contig359	Unannota	GGGTCTGACAATTTTGATGATTTCGTTCAATATCAGTTGAAGAATTGGA	contig359	Solvc01g	Aspartic i	GO:00065	SL2.40ch	AT1G086	ZIGA4	ZIGA4 (A	chr1:276	1583.11	823.606	486.109	561.894	319.994	512.433
GT	Sense	Sense	-0.455	Detected	0.455	Detected	0.000	-1.676	Comprom	-1.952	Comprom	-1.814	0.062	GT	Sens	contig359	contig359	Unannota	TGCATCAGCTGGTGTTTATATGTGCTAGGAGGCGGAAGAGGATTTAGA	contig359	Solvc04g	Phosphol	GO:00055	SL2.40ch	AT5G11600.1		unknown	chr5:373	12.8752	22.7492	10.5066	13.2426	5.71238	4.70407
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.876	Comprom	-1.219	Comprom	-1.547	0.042	GT	Sens	contig359	contig359	Unannota	AAATACATTGACTGGCAGGGACAACGACAGGTCTTTCGTGATGATTATC	contig359	Solvc03g	Uncharacterized co		SL2.40ch	AT5G57960.1		GTP-binc	chr5:234	19.4365	18.1863	10.3892	11.8631	5.46141	8.58872
GT	Sense	Sense	0.268	Detected	-0.268	Detected	0.000	-1.290	Comprom	-2.386	Comprom	-1.838	0.095	GT	Sens	contig360	contig360	Unannota	CATGTATGTGGTCGCTGAATATTTATCTTCAGTTCCTATTAATCTGTCA	contig360	Solvc01g	DNA poly	GO:00036	SL2.40ch	AT2G19240.1		RabGAP/	chr2:834	16.7557	10.8805	2.56317	3.84252	5.88895	2.74603
GT	Sense	Sense	0.122	Detected	-0.122	Detected	0.000	-1.319	Detected	-1.292	Detected	-1.306	0.009	GT	Sens	contig360	contig360	Unannota	CTAGTTAATCGGTGACATAACTGCTGAACTAAGGATGATGATGTTTGTT	contig360	Solvc05g	Phosphat	GO:00442	SL2.40ch	AT3G42870.1		unknown	chr3:149	138.127	109.695	36.0904	87.3432	52.5977	53.4603
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-1.595	Detected	-1.377	Detected	-1.486	0.011	GT	Sens	contig360	contig360	Unannota	AAGCTAGTGGTTTAGAAGTCTGGATGGAATAGCATACTCTTCTGACATT	contig360	Solvc05g	Phosphat	GO:00442	SL2.40ch	AT3G42870.1		unknown	chr3:149	155.621	125.764	41.6874	101.517	49.3671	57.2616
GT	Sense	Sense	0.208	Detected	-0.208	Detected	0.000	-1.224	Detected	-0.838	Detected	-1.031	0.068	GT	Sens	contig360	contig360	Unannota	GAATTGTCCTGATAGCCTCAACTAAAACCAAACATGTTCCCTTGTCCAA	contig360	Solvc04g	Choline k	GO:00041	SL2.40ch	AT2G328	BGLU33	BGLU33	chr2:139	46.4024	32.7367	16.88	17.8074	17.7981	23.1832
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-1.030	Detected	-1.408	Detected	-1.219	0.023	GT	Sens	contig360	contig360	Unannota	CCTGCTATAATGTTCTTGCTTTGACCGGGGAAAAGTATCATTACTTGTT	contig360	Solvc12g	Unknown Protein (A		SL2.40ch	AT5G43570.1		serine-ty	chr5:175	83.1732	79.125	23.0958	29.8223	42.3669	32.508
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-1.399	Detected	-1.547	Detected	-1.473	0.009	GT	Sens	contig360	contig360	Unannota	GATATAATTGGGTTAAAACTGTCTGTATGAGAAGTCAGTGTTACAGATT	contig360	Solvc07g	Fructose-	GO:00055	SL2.40ch	AT5G04050.2		FUNCTIO	chr5:109	84.9168	67.5553	23.6401	36.2824	30.6215	27.5607
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.366	Detected	-1.484	Detected	-1.425	0.006	GT	Sens	contig360	contig360	Unannota	TTTCTCAATTGTTGCAAGTGGAAGTGGTGATATATCCTGGTTGTTGACA	contig360	Solvc07g	Fructose-	GO:00055	SL2.40ch	AT5G04050.2		FUNCTIO	chr5:109	199.369	164.608	61.1645	80.4218	74.9335	68.8392
GT	Sense	Sense	0.363	Detected	-0.363	Detected	0.000	-2.053	Detected	-1.540	Detected	-1.796	0.056	GT	Sens	contig361	contig361	Malate sy	AGCTATC contig361 Solvc03g Solvc03g Malate sy GO:00060 GO:00060	contig361	Solvc03g	Malate sy	GO:00044	SL2.40ch	AT5G038	MLS	MLS (MA	chr5:103	50.7409	28.8797	8.40348	6.23112	9.83972	13.9946
GT	Sense	Sense	0.352	Detected	-0.352	Detected	0.000	-1.078	Detected	-1.699	Comprom	-1.389	0.098	GT	Sens	contig361	contig361	Unannota	GAGAATATATTTGGTAACTCCAGATAAACATGTCATATATAAACAATAGC	contig361	Solvc10g	Ubiquitin-	GO:00048	SL2.40ch	AT4G279	UBC9	UBC9 (UE	chr4:139	35.2747	20.3712	3.67149	14.3814	13.5394	8.7754
GT	Sense	Sense	0.220	Detected	-0.220	Detected	0.000	-1.683	Detected	-1.294	Detected	-1.489	0.037	GT	Sens	contig361	contig361	Unannota	GGCTTCAGTCCATCTTGTACTGATTCTTGGAGTGCATTATTGTTTATAT	contig361	Solvc10g	Ubiquitin-	GO:00048	SL2.40ch	AT4G279	UBC9	UBC9 (UE	chr4:139	281.656	195.381	51.9776	125.853	77.8958	101.688
GT	Sense	Sense	0.188	Detected	-0.188	Detected	0.000	-1.535	Detected	-1.049	Detected	-1.292	0.052	GT	Sens	contig361	contig361	Unannota	CCCACAAAGAGAGACAATAACAAGCTCAAACAACGAGAATCTTTATAGT	contig361	Solvc06g	Mitotic checkpoint s		SL2.40ch	AT5G47400.1		unknown	chr5:192	69.4717	50.3742	11.7129	19.2442	21.7746	30.4079
GT	Sense	Sense	0.736	Detected	-0.736	Detected	0.000	-1.754	Detected	-1.855	Detected	-1.805	0.134	GT	Sens	contig362	contig362	Unannota	TAACATTATACTGATAGTATGATAGTATAAACCATAACTCTTTATACTAT	contig362	Solvc12g	1-aminoc	GO:00164	SL2.40ch	AT1G12010.1		1-aminoc	chr1:405	86.4309	29.2975	5.25019	5.47042	15.9089	14.7861
GT	Sense	Sense	0.689	Detected	-0.689	Detected	0.000	-2.423	Detected	-2.045	Detected	-2.234	0.089	GT	Sens	contig362	contig362	Unannota	TTGAGTCAGAATAACATGACTTTTTGTTGGTTGAGCCCTAATGTGTTGC	contig362	Solvc12g	1-aminoc	GO:00164	SL2.40ch	AT1G12010.1		1-aminoc	chr1:405	502.806	181.987	32.0512	39.9702	60.1457	77.9361
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	-1.234	Detected	-1.096	Detected	-1.165	0.004	GT	Sens	contig362	contig362	Unannota	TAACTAGGTAACTTCACACATTCGAAGTACTCATGAACTTAGCTTTACG	contig362	Solvc05g	CONSTAN	GO:00055	SL2.40ch	AT3G076	COL9	COL9 (CO	chr3:244	1042.48	1031.79	396.474	534.506	470.315	515.864
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	-1.362	Detected	-1.158	Detected	-1.260	0.007	GT	Sens	contig362	contig362	Unannota	CCGGAGATTGTGAATTCCTCGGCTATTTATGTTAACATATCATGTATAT	contig362	Solvc05g	CONSTAN	GO:00055	SL2.40ch	AT3G076	COL9	COL9 (CO	chr3:244	1560.73	1448.66	569.766	768.62	623.949	716.441
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-1.070	Detected	-1.177	Detected	-1.123	0.007	GT	Sens	contig362	contig362	Unannota	CAGATGAAACATGGTTTGTTTGTCTGAAATAGATAACTGAAGCCAGTTG	contig362	Solvc01g	COBRA-like protein		SL2.40ch	AT3G537	ATCHX20	ATCHX20	chr3:199	674.733	570.065	229.24	517.384	315.017	291.659
GT	Sense	Sense	0.310	Detected	-0.310	Detected	0.000	-1.458	Detected	-1.334	Detected	-1.396	0.048	GT	Sens	contig362	contig362	Unannota	TGAAGGAATTGCATTTGACTCTTACCAGAATTCTACTTTTAAGTTTAGG	contig362	Solvc01g	COBRA-like protein		SL2.40ch	AT3G537	ATCHX20	ATCHX20	chr3:199	206.084	126.213	58.8889	95.2841	62.6174	68.0045
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	-1.251	Detected	-0.985	Detected	-1.118	0.014	GT	Sens	contig363	contig363	Unannota	TTGTTATAAGCATCCTTTTCTTCCTCCCACTCAAGAGCACAGGATTCCC	contig363	Solvc11g	Exostosin	GO:00160	SL2.40ch	AT4G38070.1		bHLH fan	chr4:178	38.2067	36.4801	19.5729	18.0469	16.7309	20.0522
GT	Sense	Sense	0.206	Detected	-0.206	Detected	0.000	-1.683	Detected	-1.528	Detected	-1.606	0.018	GT	Sens	contig363	contig363	Ethylene-	ATTAATC contig363 Solvc11g Solvc11g Ethylene- GO:00063 GO:00063	contig363	Solvc11g	Ethylene-	GO:00036	SL2.40ch	AT1G71450.1		AP2 dom	chr1:269	65.2003	46.1046	10.9515	14.414	18.2034	20.2108
GT	Sense	Sense	0.220	Detected	-0.220	Detected	0.000	-2.142	Detected	-1.873	Detected	-2.007	0.016	GT	Sens	contig364	contig364	Unannota	AGACACGACAACAATTTTAAAGAGTCCAAGCACAAAAAAAGTAGAGTGG	contig364	Solvc05g	Pectate ly	GO:00168	SL2.40ch	AT4G13210.1		lyase/ pe	chr4:767	88.8685	61.6103	15.0834	23.59	17.8762	21.4847
GT	Sense	Sense	0.247	Detected	-0.247	Detected	0.000	-2.147	Detected	-1.780	Detected	-1.964	0.024	GT	Sens	contig364	contig364	Unannota	GAAATAAAAATGTATGGTTAGTTACTTTATTAACCTATTTAAGTAGGGAC	contig364	Solvc05g	Pectate ly	GO:00168	SL2.40ch	AT4G13210.1		lyase/ pe	chr4:767	58.2258	38.9091	11.2548	14.0286	11.4619	14.7309
GT	Sense	Sense	-1.863	Detected	1.863	Detected	0.000	-1.822	Detected	-1.067	Detected	-1.444	0.527	GT	Sens	contig364	contig364	Unannota	CCTGAATATAGCATAAACAACAACAACATACATGGTCTAGTCCTACAAAC	contig364	Solvc05g	Ureide pe	GO:00052	SL2.40ch	AT2G43890.1		polygalac	chr2:181	12.3086	153.283	9.7057	17.4495	13.1029	22.0451
GT	Sense	Sense	0.276	Detected	-0.276	Detected	0.000	-1.398	Comprom	-1.497	Comprom	-1.447	0.036	GT	Sens	contig364	contig364	Unannota	GCAAGAGATTTTAACACAAGACGAGGCCGTTTCATCAGAATTTACTACA	contig364	Solvc10g	Serine/thi	GO:00191	SL2.40ch	AT4G17140.2		FUNCTIO	chr4:961	19.4814	12.5057	7.83527	8.25023	6.31687	5.87929
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	-1.906	Comprom	-1.483	Comprom	-1.694	0.020	GT	Sens	contig364	contig364	Unannota	TTTGGCGTAACTAGTAAAATTGTTGCCATGTGACTTGATGGTCATGGGT	contig364	Solvc01g	Expressed protein (		SL2.40ch	AT5G672	CYCD3:2	CYCD3:2	chr5:268	19.1569	21.1072	2.7515	11.3339	5.72102	7.65052
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-1.124	Detected	-1.132	Detected	-1.128	0.001	GT	Sens	contig365	contig365	Unannota	CTCTTATCTTGTTCGCCAGTACTCTTATATGTGTCTGGTATAGCAGATA	contig365	Solvc12g	Unknown Protein (A		SL2.40ch	AT5G50830.2		unknown	chr5:206	155.794	155.676	87.3136	139.832	76.1869	75.5525
GT	Sense	Sense	0.152	Detected	-0.152	Detected	0.000	-1.435	Detected	-1.705	Detected	-1.570	0.016	GT	Sens	contig365	contig365	Unannota	GGATGATTCAAGTTGTCGTCATTGTTGTGATCTTTCTACTTCTTGTCTA	contig365	Solvc05g	Dihydrofl	GO:00040	SL2.40ch	AT5G016	BRCA2B.	BRCA2B	chr5:235	60.2378	45.9043	11.8322	22.1721	20.7331	17.1511
GT	Sense	Sense	0.219	Detected	-0.219	Detected	0.000	-2.752	Detected	-1.798	Detected	-2.275	0.049	GT	Sens	contig365	contig365	Prephena	CTATTCA contig365 Solvc06g Solvc06g Prephena GO:00065 GO:00065	contig365	Solvc06g	Prephena	GO:00081	SL2.40ch	AT1G15710.1		prephena	chr1:540	4293.8	2980.68	849.562	1282.76	566.253	1094.15
GT	Sense	Sense	0.166	Detected	-0.166	Detected	0.000	-1.426	Detected	-1.151	Detected	-1.288	0.027	GT	Sens	contig366	contig366	Alpha-1 6	TCCTAAT contig366 Solvc01g Solvc01g Alpha-1 6 GO:00160 GO:00160	contig366	Solvc01g	Alpha-1 6	GO:00160	SL2.40ch	AT5G07720.1		galactosy	chr5:245	1882.08	1406.82	379.28	499.098	645.815	779.152
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-1.967	Detected	-1.016	Detected	-1.491	0.089	GT	Sens	contig367	contig367	Unannota	AGTCGAAATCGAATCTCAGGTGTTGGTTCGGATTCTGAATCGATCGTCC	contig367	Solvc10g009250.1.1				AT1G79150.1		binding	chr1:297	191.718	170.081	33.9914	82.9478	49.2621	94.9675
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	-2.169	Detected	-1.183	Detected	-1.676	0.078	GT	Sens	contig367	contig367	Unannota	TTTGAAAGTTGGGTATCAGGTTGCGCGTCAAGGTCATATTTCGATTTGA	contig367	Solvc10g009250.1.1				AT1G79150.1		binding	chr1:297	236.309	246.444	38.8959	105.408	57.2181	113.013
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	-1.197	Detected	-1.167	Detected	-1.182	0.011	GT	Sens	contig367	contig367	Unannota	GCACCAAATCTATGAAGATACATCGAAGGAACGATTCTTCAAACACGAA	contig367	Solvc02g	GDP-L-ga	GO:00055	SL2.40ch	AT5G64030.1		dehydrat	chr5:256	304.199	241.527	202.016	261.518	126.098	128.37
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	-1.303	Detected	-1.459	Detected	-1.381	0.004	GT	Sens	contig367	contig367	Unannota	GACCGTCAAGAGGAAAGATTCCACAAGCAAGAAACCTCATCAACATTAT	contig367	Solvc02g	GDP-L-ga	GO:00055	SL2.40ch	AT5G64030.1		dehydrat	chr5:256	796.8	711.088	527.619	706.124	325.408	291.072
GT	Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-1.318	Detected	-1.490	Detected	-1.404	0.004	GT	Sens	contig370	contig370	Peptide tr	AAAGCTC contig370 Solvc09g Solvc09g Peptide tr GO:00429 GO:00429	contig370	Solvc09g	Peptide tr	GO:00429	SL2.40ch	AT5G460	ATPTR3.	PTR3 (PE	chr5:186	1925.4	1845.03	946.21	697.303	806.156	713.214
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-1.364	Comprom	-1.198	Comprom	-1.281	0.009	GT	Sens	contig370	contig370	Unannota	CGGTAGTTACTTCAGATCTCTGACCTCATTTCACTATAGATGCACAAAC	contig370	Solvc10g	DUF647 domain-cor		SL2.40ch	AT3G52700.1		unknown	chr3:195	21.2515	22.7744	25.2325	29.3012	9.11206	10.1952
GT	Sense	Sense	0.208	Detected	-0.208	Detected	0.000	-1.163	Detected	-1.040	Detected	-1.102	0.037	GT	Sens	contig371	contig371	Unannota	GTCTCCTTCCCTTAGAGCCAATGGCCGATTTTTGGTATTAGAGGTGC	contig371	Solvc02g	Derlin-2 (	GO:00422	SL2.40ch	AT5G623	IRE	IRE (INC	chr5:250	891.665	628.704	340.031	424.896	356.559	387.141
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	-1.754	Detected	-1.691	Comprom	-1.722	0.003	GT	Sens	contig371	contig371	Unannota	ATGTTGACGTGCTGCTCAATGGAACGGTGTCAGTTGACACCACTTGAA	contig371	Solvc04g	Purple ac	GO:00047	SL2.40ch	AT4G33540.1				16.5153	13.594	4.78126	10.9413	4.73733	4.93436
GT	Sense	Sense	0.412	Detected	-0.412	Detected	0.000	-1.619	Detected	-1.363	Detected	-1.491	0.075	GT	Sens	contig371	contig371	Unannota	TATTGATCAGTCTACCCGATTTGAACTGGGGAAAAAGGATTTGCACAA	contig371	Solvc09g	CWF19-like 2 (AHRD		SL2.40ch	AT5G66620.1				54.9379	29.1824	11.9082	22.4925	13.9041	16.5525
GT	Sense	Sense	0.526	Detected	-0.526	Detected	0.000	-3.893	Comprom	-3.799	Comprom	-3.846	0.018	GT	Sens	contig371	contig371	Unannota	GGTATCATTGCATCTTTGAGACTTCACACTCGTATTGATGCAATAAAAA	contig371	Solvc09g031670.1.1				AT4G35270.1		RWP-RK	chr4:167	160.721	72.9019	13.7457	12.9053	7.7671	8.26733
GT	Sense	Sense	0.719	Detected	-0.719	Detected	0.000	-3.041	Comprom	-3.621	Comprom	-3.331	0.050	GT	Sens	contig371	contig371	Unannota	CTGACTGATAAGATAGTAGCAAGTGCTAAGAAAATGCTATCAAAAGTT	contig371	Solvc09g031670.1.1				AT4G35270.1		RWP-RK	chr4:167	107.042	37.1871	14.5296	3.44186	8.17345	5.4503
GT	Sense	Sense	0.371	Detected	-0.371	Detected	0.000	-1.803	Detected	-1.148	Detected	-1.475	0.096	GT	Sens	contig372	contig372	Unannota	TGAAAATGGGAAGTCTGAGTTGGTTTAGAAATTTGCTTTCAGCTGTTG	contig372	Solvc09g	GPN-loop	GO:00055	SL2.40ch	AT5G28190.1		unknown	chr5:101	74.7601	42.0821	17.7403	19.6765	17.1406	26.9139
GT	Sense	Sense	0.162	Detected	-0.162	Detected	0.000	-1.326	Detected	-0.898	Detected	-1.112	0.054	GT	Sens	contig372	contig372	Unannota	GTTGCAAGTTATGTGCTGCACGAGTTCTATCATACTATTATGTAATCTT	contig372	Solvc09g	GPN-loop	GO:00055	SL2.40ch	AT5G28190.1		unknown	chr5:101	82.7913	62.2182	30.796	35.8746	30.5245	40.9533
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	-1.015	Detected	-1.013	Detected	-1.014	0.033	GT	Sens	contig372	contig372	Unannota	TTGGAGGATTCATGTTTTAAACTACCGTTTGACTCTAGTCTTCCATATT	contig372	Solvc06g	GTP cycl	GO:00039	SL2.40ch	AT3G036	WOX11	WOX11 (	chr3:889	39.3751	48.0689	27.2998	31.5684	22.9605	22.9129
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-1.558	Detected	-2.397	Detected	-1.977	0.045	GT	Sens	contig372	contig372	Unannota	TGTGTGACAGTTTGAAGTACAACCACAACATACCATGTGTAACAATGTG	contig372	Solvc06g	Aquapori	GO:00152	SL2.40ch	AT2G36830.1				67.3075	54.3518	18.166	13.0485	21.9059	12.2112
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	-0.927	Detected	-1.254	Detected	-1.091	0.043	GT	Sens	contig373	contig373	Dynamin	AAGTATC contig373 Solvc10g Solvc10g Dynamin GO:00055 GO:00055	contig373	Solvc10g	Dynamin	GO:00039	SL2.40ch	AT1G148	ADL1C. A	ADL1C (	chr1:510	1426.6	1065.33	318.45	393.905	691.449	549.459
GT	Sense	Sense	0.358	Detected	-0.358	Detected	0.000	-2.064	Detected	-1.017	Detected	-1.541	0.136	GT	Sens	contig373	contig373	Unannota	GAAAAATAGTTAGATTTGCAATAGAGATGAGGGTAGTTAGGTAGCTGC	contig373	Solvc07g	Protein re	GO:00036	SL2.40ch	AT1G039	VPS2.3	VPS2.3 (	chr1:101	196.77	112.789	85.4882	109.721	37.9847	78.2701
GT	Sense	Sense	0.228	Detected	-0.228	Detected	0.000	-2.315	Detected	-1.962	Detected	-2.139	0.018	GT	Sens	contig373	contig373	Glycerol-	AGAGAAC contig373 Solvc04g Solvc04g Glycerol- GO:00512 GO:00512	contig373	Solvc04g	Glycerol-	GO:00043	SL2.40ch	AT2G415	GPDHC1	GPDHC1	chr2:173	5539.05	3800.27	1189.72	1340.15	983.177	1251.9
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-1.770	Comprom	-1.093	Comprom	-1.432	0.053	GT	Sens	contig374	contig374	Unannota	GCTAATTAAGCCATCTGTTTGTCCTTCCCATGCTCTTATGAGTGGTA	contig374	Solvc08g080810.1.1				AT4G04960.1		lectin pro	chr4:253	14.8218	12.819	9.07058	7.7037	4.31062	6.86858
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-1.423	Detected	-1.123	Detected	-1.273	0.022	GT	Sens	contig375	contig375	Unannota	ACTCCTCAAGAACGCAGTAGATAACTTAATCTACGATGTAGTTGCATGT	contig375	Solvc01g	Zinc finge	GO:00037	SL2.40ch	AT2G17570.1		undecap	chr2:764	268.292	213.382	83.2094	120.46	95.1402	116.815
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-1.643	Detected	-1.710	Detected	-1.676	0.002	GT	Sens	contig375	contig375	AP2-like	TTAATTC contig375 Solvc11g Solvc11g AP2-like GO:00030 GO:00030	contig375	Solvc11g	AP2-like	GO:00030	SL2.40ch	AT2G285	RAP2.7. T	RAP2.7 (	chr2:122	1703.48	1750.74	558.085	568.031	589.844	561.327
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	-0.988	Comprom	-1.395	Comprom	-1.192	0.028	GT	Sens	contig375	contig375	Solute ca	ATGATAT contig375 Solvc11g Solvc11g Solute ca GO:00160 GO:00160	contig375	Solvc11g	Solute ca	GO:00160	SL2.40ch	AT1G21870.1		glucose-	chr1:767	15.2655	14.1677	9.15129	7.53254	7.905	5.94081
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	-1.584	Detected	-1.440	Detected	-1.512	0.009	GT	Sens	contig375	contig375	NBS-LRR	GCTGCAC contig375 Solvc07g Solvc07g NBS-LRR class disease resista	contig375	Solvc07g	NBS-LRR class dise		SL2.40ch	AT3G09540.1		pectate l	chr3:292	3548.43	3956.29	760.431	980.828	1332.97	1467.77
GT	Sense	Sense	0.226	Detected	-0.226	Detected	0.000	-1.111	Detected	-1.131	Detected	-1.121	0.038	GT	Sens	contig375	contig375	Unannota	TTGTTGTCCCTGCTACCCGACAATTTTGGGCAATCGATCTCTCAAAGAT	contig375	Solvc03g	NADH deh	GO:00055	SL2.40ch	AT4G33390.1		unknown	chr4:160	80.6209	55.4689	31.6965	43.3067	33.0055	32.4613
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	-1.030	Detected	-1.320	Detected	-1.175	0.015	GT	Sens	contig375	contig375	Unannota	CTCACCATTCACGCTTATCTATTGCAATTCTCATAAATTTTGCAAGTTTC	contig375	Solvc08g	Inhibitor o	GO:00082	SL2.40ch	AT3G26150.1				100.286	96.6049	28.7219	34.3589	51.3891	41.9186
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-0.918	Detected	-1.282	Detected	-1.100	0.035	GT	Sens	contig375	contig375	Unannota	GAGGATATACCACTTCAAAATCACAAAGTTGAGGGTAAATCGAATCGTC	contig375	Solvc08g	Inhibitor o	GO:00082	SL2.40ch	AT3G26150.1				91.6992	74.4431	28.789	33.9212	46.6352	36.1176
GT	Sense	Sense	0.163	Detected	-0.163	Detected	0.000	-1.269	Detected	-0.823	Detected	-1.046	0.063	GT	Sens	contig376	contig376	Unannota	GATTGATATTGATCAAACTTCTGGACCATTTTGTTCTTGATCTTTTCAC	contig376	Solvc01g	G-box bin	GO:00435	SL2.40ch	AT2G462	GBF3	GBF3 (G	chr2:190	39.9515	29.9917	13.6619	19.9814	15.3173	20.8088
GT	Sense	Sense	0.140	Detected	-0.140	Detected	0.000	-1.514	Detected	-1.515	Detected	-1.514	0.008	GT	Sens	contig376	contig376	Unannota	GGGTCTGGGGTTAATGGTGTGTATGCTAATGTCATCAACAATAATAAC	contig376	Solvc09g	Uncharac	GO:00103	SL2.40ch	AT1G68875.1				1986.39	1539.83	672.088	1020.21	653.073	650.567
GT	Sense	Sense	0.721	Detected	-0.721	Detected	0.000	-2.049	Comprom	-2.233	Comprom	-2.141	0.099	GT	Sens	contig376	contig376	Unannota	GAAGAGTTTTTGGTGTATCAAAAGCATCTACTATATCCATCCCAGGTAA	contig376	Solvc02g	Nucleoso	GO:00423	SL2.40ch	AT5G42280.1		DC1 dom	chr5:169	36.1423	12.5095	8.42685	13.3725	5.4799	4.81015
GT	Sense	Sense	0.260	Detected	-0.260	Detected	0.000	-2.079	Detected	-1.469	Detected	-1.774	0.047	GT	Sens	contig377	contig377	Unannota	TGTCTTGGAATTTTAGCAACATCAACTCACTTCAATTAGGTTGGTTATT	contig377	Solvc07g054590.1.1				AT3G077	OBE1	OBE1 (O	chr3:248	1874.98	1230.37	373.616	693.131	383.402	583.367
GT	Sense	Sense	0.263	Detected	-0.263	Detected	0.000	-2.709	Detected	-1.935	Detected	-2.322	0.038	GT	Sens	contig377	contig377	Unannota	CCCACATTAGTTACCAAATGTACCTGTGGCTGTGAATCATAGTTAAAAT	contig377	Solvc07g054590.1.1				AT3G077	OBE1	OBE1 (O	chr3:248	2042.25	1334.89	317.774	644.004	269.19	459.111
GT	Sense	Sense	0.227	Detected	-0.227	Detected	0.000	-1.267	Detected	-1.008	Detected	-1.137	0.049	GT	Sens	contig377	contig377	Unannota	CGGTACCAAGGAGTTCATTGTCTACTGTACATACAAAAGAATCAATGTT	contig377	Solvc07g	MLO-like	GO:00160	SL2.40ch	AT1G21610.2		wound-re	chr1:757	44.4392	30.5294	17.4664	15.4594	16.3193	19.4791
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-1.397	Detected	-0.984	Detected	-1.191	0.029	GT	Sens	contig377	contig377	Porin/vol	AACAAGC contig377 Solvc03g Solvc03g Porin/vol GO:00055 GO:00055	contig377	Solvc03g	Porin/vol	GO:00055	SL2.40ch	AT5G150	VDAC3. A	VDAC3 (	chr5:488	4092.65	3705.72	1668.71	1703.29	1577.03	2093.01
GT	Sense	Sense	0.211	Detected	-0.211	Detected	0.000	-2.672	Detected	-1.952	Detected	-2.312	0.031	GT	Sens	contig377	contig377	Ethylene-	CTTTGAT contig377 Solvc11g Solvc11g Ethylene- GO:00063 GO:00063	contig377	Solvc11g	Ethylene-	GO:00036	SL2.40ch	AT1G21910.1		AP2 dom	chr1:769	304.9	214.046	69.8055	95.7598	42.7497	70.1934
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-1.341	Detected	-1.242	Detected	-1.291	0.009	GT	Sens	contig377	contig377	Unannota	TAACTATCCAGTTAAAGGCACATTCGTGGGATGCTGATGGAACGACT	contig377	Solvc06g	Serine/threonine-pr		SL2.40ch	AT2G28360.1		INVOLVE	chr2:121	3183.51	2571.87	928.868	1213.8	1204.82	1285.88
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-1.837	Detected	-1.005	Detected	-1.421	0.081	GT	Sens	contig378	contig378	Unannota	GGTGACGGGTCATATGTTAATTAGCATTATGGAAGCTTATTAACAATCC	contig378	Solvc10g	Endochiti	GO:00088	SL2.40ch	AT3G52700.1		unknown	chr3:195	19297	15589.2	9988.15	9894.4	5176.38	9190.15
GT	Sense	Sense	-0.031	Detected	0.031	Detected	0.000	-1.479	Detected	-0.919	Detected	-1.199	0.051	GT	Sens	contig378	contig378	Unannota	GCCACTAGCCCTAGGGGATTTTTCAGTTATAAAGTAGAAGTACATTAAA	contig378	Solvc06g	Unknown Protein (A		SL2.40ch	AT4G28420.2				34.8567	34.249	13.655	12.9323	13.2154	19.4216
GT	Sense	Sense	0.117	Detected	-0.117	Detected	0.000	-1.838	Detected	-1.407	Detected	-1.622	0.022	GT	Sens	contig378	contig378	Unannota	TTGAATGTGGAATTTGAGATAGGGCTCCTGTTTGACCTTTATTTACTAC	contig378	Solvc06g	Unknown Protein (A		SL2.40ch	AT4G28420.2				50.6912	40.5498	12.0977	15.0437	13.5242	18.1797
GT	Sense	Sense	0.085	Detected	-0.085	Detected	0.000	-1.642	Detected	-1.201	Detected	-1.422	0.027	GT	Sens	contig378	contig378	Adenylyl	GGTTCGC contig378 Solvc01g Solvc01g Adenylyl GO:00037 GO:00037	contig378	Solvc01g	Adenylyl	GO:00037	SL2.40ch	AT4G344	ATCAP1.	ATCAP1	chr4:164	234.846	196.455	70.5764	110.015	73.3837	99.3353
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	-1.280	Detected	-1.617	Detected	-1.448	0.014	GT	Sens	contig379	contig379	Unannota	CCACTGGGTATATGTTGTTGTAGTTGCTTTGTTTAATGATCTTTGTTTT	contig379	Solvc12g	Homeobo	GO:00056	SL2.40ch	AT5G30520.1				164.887	161.107	88.0546	61.0325	71.5956	56.4807
GT	Sense	Sense	0.022	Detected	-0.022	Detected	0.000	-1.152	Detected	-1.411	Detected	-1.282	0.010	GT	Sens	contig379	contig379	Unannota	AACTTGAAATATGCCGGCGAAAGTCAAAAGGGTGCATAATATTTTTATGT	contig379	Solvc12g	Homeobo	GO:00056	SL2.40ch	AT5G30520.1				134.054	122.388	68.7909	45.4043	61.4485	51.2123
GT	Sense	Sense	0.208	Detected	-0.208	Detected	0.000	-1.933	Detected	-0.914	Detected	-1.423	0.123	GT	Sens	contig379	contig379	Unannota	ATAGCCTTAAATGACAGTCCTGACTCTGCTACTAGCCAATAGCTAACGC	contig379	Solvc01g	Unknown Protein (A		SL2.40ch	AT3G25610.1		haloacid	chr3:930	1255.94	885.924	430.389	529.785	294.509	595.381
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	-1.477	Detected	-1.069	Detected	-1.273	0.035	GT	Sens	contig379	contig379	Unannota	GAAGTGTGAATGCTTCTATTTGCTGCTTGGAGGGTAAAACTTGTTTCTC	contig379	Solvc12g	Integral membrane		SL2.40ch	AT3G06880.1		nucleotid	chr3:217	2498.88	1957.75	774.471	979.804	847.53	1120.68
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-1.390	Comprom	-1.703	Comprom	-1.547	0.010	GT	Sens	contig379	contig379	Unannota	CTTCCACGTAAAGTACAACTCTGTTTGTATTGTTTATGCTTTCTGACTT	contig379	Solvc01g	Dolichyl-	GO:00055	SL2.40ch	AT5G666	DGL1	DGL1: d	chr5:266	12.9175	12.2915	4.94556	3.55844	5.12646	4.11371
GT	Sense	Sense	-0.025	Detected	0.025	Detected	0.000	-1.254	Comprom	-0.987	Comprom	-1.120	0.014	GT	Sens	contig379	contig379	Unannota	CGCGCCTTTAATTGTTGTTTGAAGTGCTAGTCTTACTTTCTTAATTTGG	contig379	Solvc02g	Wound responsive		SL2.40ch	AT1G145	MIOX1	MIOX1 (M	chr1:496	12.9876	12.6527	1.88097	2.3447	5.73181	6.87831
GT	Sense	Sense	-0.221	Detected	0.221	Detected	0.000	-1.173	Detected	-0.946	Comprom	-1.060	0.051	GT	Sens	contig379	contig379	Unannota	TAAGGAGGTTTATGTTCACACTCACGGCTTAAGGCCACCAGGCCCAAA	contig379	Solvc05g	Threonyl-	GO:00428	SL2.40ch	AT5G14770.1		pentatric	chr5:477	16.6137	21.2356	10.6905	4.80171	8.88107	10.3624
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-1.036	Detected	-1.031	Detected	-1.034	0.004	GT	Sens	contig380	contig380	Unannota	AGTCTGAGGGAAGTCCCATGTAATGAATTCTTGTTTCATGCATGTTCTC	contig380	Solvc05g	Phospho	GO:00036	SL2.40ch	AT2G43210.2				286.131	245.78	92.6147	97.6062	137.872	137.976
GT	Sense	Sense	0.074	Detected	-0.074	Detected	0.000	-1.116	Detected	-1.302	Detected	-1.209	0.010	GT	Sens	contig380	contig380	Unannota	ATCAAAATCACAATCAAATATTCATGGAAGAGTGCAACTATATATTCGCA	contig380	Solvc11g	Metal ion	GO:00300	SL2.40ch	AT2G29770.1				53.641	45.5318	24.574	27.5487	24.3076	21.3111
GT	Sense	Sense	0.304	Detected	-0.304	Detected	0.000	-1.410	Detected	-1.111	Detected	-1.260	0.065	GT	Sens	contig380	contig380	Unannota	ACGAACTCATCGTTGAAATTCTGAGAAAACTTCCTGCTAAGTCTCTAAT	contig380	Solvc11g	Metal ion	GO:00300	SL2.40ch	AT2G29770.1				95.9258	59.193	33.8641	41.4895	30.2409	37.0936
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.234	Detected	-0.903	Detected	-1.068	0.026	GT	Sens	contig380	contig380	Phosphat	ATCAAGA contig380 Solvc05g Solvc05g Phosphat GO:00038 GO:00038	contig380	Solvc05g	Phosphat	GO:00082	SL2.40ch	AT3G12620.2		protein p	chr3:400	590.923	606.222	259.112	428.249	271.415	340.309
GT	Sense	Sense	0.057	Detected	-0.057	Detected	0.000	-2.233	Comprom	-1.540	Comprom	-1.887	0.033	GT	Sens	contig381	contig381	Unannota	GTTTTATAGACTGCAGGAAAATTGATTCAGCAATTACTGGGACACACT	contig381	Solvc04g	Alpha alp	GO:00038	SL2.40ch	AT5G590	COPT1	COPT1 (	chr5:238	23.2769	20.2453	11.6756	5.68222	4.9233	7.93785
GT	Sense	Sense	0.202	Detected	-0.202	Detected	0.000	-1.859	Comprom	-0.913	Comprom	-1.386	0.115	GT	Sens	contig381	contig381	Unannota	CACTAATGGGGAGGTTGTTCTTTGAATTCTTGCAATAAAAGATAATGA	contig381	Solvc02g	Palmitoyl	GO:00164	SL2.40ch	AT5G41060.1				16.978	12.0793	12.6324	10.2649	4.21087	8.08835
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-1.143	Detected	-0.949	Detected	-1.046	0.016	GT	Sens	contig381	contig381	Unannota	CTCTTTCTCGAACCTTACATAAACGGGATGTTTTATGTACTGAACTGGA	contig381	Solvc07g	WRKY tra	GO:00454	SL2.40ch	AT5G43570.1		serine-ty	chr5:175	19999.5	16545.8	9958.7	10509.2	8781.41	10016.2
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-1.308	Detected	-1.018	Detected	-1.163	0.032	GT	Sens	contig381	contig381	Unannota	GGAGGAGATGGGTTGAAGGATATATGGTTTTATTTTTAGTTATTTGCAT	contig381	Solvc07g	WRKY tra	GO:00454	SL2.40ch	AT5G43570.1		serine-ty	chr5:175	18080.8	13669.3	8850.39	9176.46	6772.66	8251.33
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.440	Detected	-1.615	Detected	-1.527	0.003	GT	Sens	contig381	contig381	E3 ubiqui	ATTTTCA contig381 Solvc08g Solvc08g E3 ubiqui GO:00055 GO:00055	contig381	Solvc08g	E3 ubiqui	GO:00055	SL2.40ch	AT5G38070.1		zinc fing	chr5:151	2900.21	2673.26	1303.27	900.271	1094.14	966.756
GT	Sense	Sense	-0.023	Detected	0.023	Detected	0.000	-1.290	Detected	-0.962	Detected	-1.126	0.021	GT	Sens	contig382	contig382	Early nod	AAGGGTT contig382 Solvc02g Solvc02g Early noc GO:00090 GO:00090	contig382	Solvc02g	Early nod	GO:00090	SL2.40ch	AT1G48940.1		plastocy	chr1:181	3582.41	3479.48	1720.58	4170.38	1539.51	1927.45
GT	Sense	Sense	0.231	Detected	-0.231	Detected	0.000	-0.974	Comprom	-1.866	Comprom	-1.420	0.106	GT	Sens	contig382	contig382	Unannota	GGCGAGAAAAAAACCTGGGAGGTAAGTTTCGGCTACTGAATGGGTTTG	contig382	Solvc06g	Unknown Protein (A		SL2.40ch	AT3G14370.1				19.0937	13.0436	3.39016	4.79927	8.56734	4.60251
GT	Sense	Sense	0.107	Detected	-0.107	Detected	0.000	-1.039	Detected	-1.152	Detected	-1.096	0.012	GT	Sens	contig382	contig382	Unannota	TTTAGGATTCCATGGTTATGGGGAAAAGATTGATTTTTGCAAAGGCTGA	contig382	Solvc07g	Cell divisi	GO:00064	SL2.40ch	AT1G47670.1		amino ac	chr1:175	164.52	133.434	47.9049	45.755	76.89	70.8829
GT	Sense	Sense	0.002	Detected	-0.002	Detected	0.000	-1.175	Detected	-1.086	Detected	-1.131	0.002	GT	Sens	contig382	contig382	Unannota	TGTAGTTTTGCAACAGCAGGGGAAGGTTTTCGGTTGGGTTTTCGTTGA	contig382	Solvc07g	Cell divisi	GO:00064	SL2.40ch	AT1G47670.1		amino ac	chr1:175	384.262	360.664	125.567	123.1	175.778	186.475
GT	Sense	Sense	0.199	Detected	-0.199	Detected	0.000	-0.867	Detected	-1.172	Detected	-1.019	0.056	GT	Sens	contig383	contig383	Unannota	CCCATAGTACTTGTCTCCTTGTTTCTTGAAAATCCCACAAAAAATTGGG	contig383	Solvc10g	Unknown	GO:00167	SL2.40ch	AT3G022	BIG. DOC	BIG (BIG	chr3:431	64.2122	45.8389	13.6878	25.2461	31.72	25.6032
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	-1.727	Detected	-1.062	Detected	-1.395	0.053	GT	Sens	contig383	contig383	Unannota	GCTCCCTTTGGTTCACACATAATTCCGGCTCTGTTTAATCTCCTCACTG	contig383	Solvc12g	UDP-gluc	GO:00060	SL2.40ch	AT5G64700.1		nodulin M	chr5:258	55.2285	54.8356	14.7082	26.103	17.7278	28.0149
GT	Sense	Sense	-0.226	Detected	0.226	Detected	0.000	-1.535	Detected	-1.753	Comprom	-1.644	0.022	GT	Sens	contig383	contig383	Unannota	CCTGTCACTTTCTGCGAAAAGACTTTGCTAACAATGGAACAGACTAATT	contig383	Solvc12g	UDP-gluc	GO:00060	SL2.40ch	AT5G64700.1		nodulin M	chr5:258	27.7998	36.0149	5.18878	7.27992	11.6876	10.0196
GT	Sense	Sense	0.140	Detected	-0.140	Detected	0.000	-1.802	Detected	-1.883	Detected	-1.842	0.006	GT	Sens	contig383	contig383	Unknown	TTGTCTC contig383 Solvc07g Solvc07g Unknown Protein (AHRD V1)%	contig383	Solvc07g	Unknown Protein (A		SL2.40ch	AT2G30990.2		unknown	chr2:131	98.6148	76.4597	21.3714	31.1251	26.5563	25.0294
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-1.189	Detected	-1.418	Detected	-1.303	0.022	GT	Sens	contig383	contig383	Unannota	ACAAGAAGAAGGTTCTGTTAATTCGACGGTGAAGCGGAATTTGAGCTTC	contig383	Solvc03g	Ring H2 fi	GO:00048	SL2.40ch	AT5G27420.1		zinc fing	chr5:968	1410.28	1065.57	306.497	355.208	573.513	487.646
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.199	Detected	-1.474	Detected	-1.337	0.020	GT	Sens	contig383	contig383	Unannota	GAGAAACTTGAGTTTCAACGTGCCGATTCAACCACCGAGATCAATTTCC	contig383	Solvc03g	Ring H2 fi	GO:00048	SL2.40ch	AT5G27420.1		zinc fing	chr5:968	3759.29	2942.62	851.526	963.756	1544.54	1272.77
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-1.450	Detected	-1.180	Detected	-1.315	0.023	GT	Sens	contig383	contig383	Aquapori	CTTGTCA contig383 Solvc03g Solvc03g Aquapori GO:00160 GO:00160	contig383	Solvc03g	Aquapori	GO:00152	SL2.40ch	AT1G016	PIP1C. TI	PIP1C (P	chr1:225	16934.7	12932.9	5730.11	4446.02	5774.84	6943.38
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-1.247	Detected	-0.991	Detected	-1.119	0.013	GT	Sens	contig384	contig384	Unannota	ATTGAAAAGTGTTGAACAACACAAAGTTCCCTTGGTCTGATTTGTAGAA	contig384	Solvc07g	Arabinogalactan-pro		SL2.40ch	AT4G02871.1		unknown	chr4:127	1521.53	1437.39	999.743	1011.2	664.366	791.239
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-0.913	Detected	-1.425	Comprom	-1.169	0.059	GT	Sens	contig384	contig384	Unannota	CCTCTTTCGATTATCAATGGAAACGTTCAACTTGAGCTAAATCAGGTTT	contig384	Solvc07g	Jasmona	GO:00055	SL2.40ch	AT1G06640.2				27.1948	20.7887	4.97572	11.356	13.4675	9.41504
GT	Sense	Sense	0.155	Detected	-0.155	Detected	0.000	-1.160	Detected	-0.881	Detected	-1.020	0.039	GT	Sens	contig384	contig384	Unannota	CTTCCTCTTCTGATTAGAGCATCAACAATCAATTAAAACTACTATCACC	contig384	Solvc07g	Jasmona	GO:00055	SL2.40ch	AT1G06640.2				28.3257	21.4981	10.2425	12.9996	11.7757	14.2473
GT	Sense	Sense	0.235	Detected	-0.235	Detected	0.000	-0.890	Detected	-1.554	Detected	-1.222	0.095	GT	Sens	contig384	contig384	Unannota	GGACGAAATTGGGGTTGTATTGTGTTATTTAATGATGGGTATTGAGTAA	contig384	Solvc09g	Endogluc	GO:00045	SL2.40ch	AT3G61310.1		DNA-bind	chr3:226	71.6038	48.67	18.6352	15.414	33.9751	21.3727
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-1.087	Detected	-1.361	Detected	-1.224	0.021	GT	Sens	contig384	contig384	Unannota	TGGTTAGTGTTGCTGAATATAGATTACACAAAATGGAAGGGATGGAAC	contig384	Solvc04g	Glutathio	GO:00043	SL2.40ch	AT2G37770.2		aldo/keto	chr2:158	99.4321	79.898	25.4264	46.7882	44.7447	36.8946
GT	Sense	Sense	0.576	Detected	-0.576	Detected	0.000	-2.008	Detected	-2.504	Detected	-2.256	0.069	GT	Sens	contig384	contig384	C4-dicarl	ACTGCTT contig384 Solvc07g Solvc07g C4-dicarl GO:00160 GO:00160	contig384	Solvc07g	C4-dicarb	GO:00160	SL2.40ch	AT1G622	SLAH4	SLAH4 (S	chr1:230	84.5802	35.8151	1.90135	10.4764	14.5889	10.313
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	-1.638	Detected	-1.396	Detected	-1.517	0.019	GT	Sens	contig386	contig386	Unannota	CAGACCTTACACAATCTGCACTGTTTTCCTTTTTACTTGTCATGTTTCC	contig386	Solvc12g	Serine/thi	GO:00191	SL2.40ch	AT2G17060.1				74.5554	55.3313	10.84	25.6767	22.0028	25.9568
GT	Sense	Sense	0.256	Detected	-0.256	Detected	0.000	-4.186	Detected	-3.319	Detected	-3.753	0.018	GT	Sens	contig386	contig386	WRKY tra	TGGCTGT contig386 Solvc03g Solvc03g WRKY tra GO:0045449	contig386	Solvc03g	WRKY tra	GO:00454	SL2.40ch	AT1G188	WRKY61.	WRKY61	chr1:650	3165.47	2089.16	258.612	258.705	150.641	273.924
GT	Sense	Sense	-0.309	Detected	0.309	Detected	0.000	-1.469	Comprom	-1.043	Comprom	-1.256	0.079	GT	Sens	contig386	contig386	Unannota	CCCATTTTGAATCAGTACTTGGTAGAGAAGACCATTTAAACGAAAAGAA	contig386	Solvc07g	ATP-bind	GO:00160	SL2.40ch	AT4G20840.1		FAD-bind	chr4:111	14.4424	20.862	9.98779	7.04367	6.68457	8.95832
GT	Sense	Sense	1.136	Detected	-1.136	Detected	0.000	-1.872	Detected	-2.272	Comprom	-2.072	0.214	GT	Sens	contig387	contig387	Unannota	GACTTGATGATAGCAAGGATGCATGCAACAGCTGCATGATGCATTTGTA	contig387	Solvc03g	Unknown Protein (A		SL2.40ch	AT5G06750.3		protein p	chr5:208	81.0287	15.781	14.2023	14.7928	10.4211	7.87178
GT	Sense	Sense	0.236	Detected	-0.236	Detected	0.000	-1.619	Detected	-0.858	Detected	-1.239	0.109	GT	Sens	contig387	contig387	Unannota	GGATTTTCACACTGAAAGCAAGTGTGTTATTGATTTCTGATGTTTCATT	contig387	Solvc02g	Receptor	GO:00046	SL2.40ch	AT5G01420.1				5104.78	3464.42	1547.46	2250.52	1459.85	2466.13
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	-1.732	Detected	-0.986	Detected	-1.359	0.101	GT	Sens	contig387	contig387	Unannota	GATGGTCTGAACTGGTAAAATCTGTTTGTTTATCAACTTTGGTATTAGT	contig387	Solvc02g	Receptor	GO:00046	SL2.40ch	AT5G01420.1				8982.64	5714.15	2668.52	3883.45	2299.83	3846.8
GT	Sense	Sense	0.613	Detected	-0.613	Detected	0.000	-4.103	Comprom	-1.420	Comprom	-2.762	0.202	GT	Sens	contig387	contig387	Unannota	ATAGCGAATGTGTTTGTTCTCTATTGGCTCATCTGCCTATTTTCCTTTC	contig387	Solvc01g	Unknown Protein (A		SL2.40ch	AT5G563	ATACA8.	ACA8 (AU	chr5:228	58.2872	23.4502	2.29994	6.29174	2.29385	14.6868
GT	Sense	Sense	0.083	Detected	-0.083	Detected	0.000	-1.181	Detected	-0.900	Detected	-1.040	0.024	GT	Sens	contig387	contig387	Unannota	CAGCATATAGAACTGGCAGCTAGCAACCCCAAAAGGATTTTAAAGAGAA	contig387	Solvc11g	DNA (Cyto	GO:00081	SL2.40ch	AT5G01250.1		alpha 1.4	chr5:102	38.7107	32.4591	24.0506	35.7942	16.6733	20.1966
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-1.421	Detected	-1.021	Detected	-1.221	0.026	GT	Sens	contig387	contig387	Unannota	ACTAGTAAGATGGTTAACAGGACGACGAAGAGGAAAATTAGGATTCCG	contig387	Solvc10g	Unknown Protein (A		SL2.40ch	AT5G06330.1				537.382	486.182	278.337	286.18	203.504	267.798
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	-1.395	Detected	-1.035	Detected	-1.215	0.021	GT	Sens	contig387	contig387	Unannota	TTTCGTTTTTTGTCTTTGTGGTGAGTGCACTCCTTGACTGACATGGTG	contig387	Solvc10g	Unknown Protein (A		SL2.40ch	AT5G06330.1				1928.98	1852.46	1068.46	1064.12	766.621	980.814
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	-1.903	Comprom	-1.632	Comprom	-1.768	0.006	GT	Sens	contig388	contig388	Unannota	TGTGATCCTTCTTTTGTTCAATGTTAATGCCAGACGCTTTGTGCACCAA	contig388	Solvc03g	RING fing	GO:00082	SL2.40ch	AT5G10840.1		endomer	chr5:342	11.7093	11.5606	2.45458	11.3165	3.31647	3.99052
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-1.231	Comprom	-0.958	Comprom	-1.095	0.018	GT	Sens	contig388	contig388	Unannota	TTCTTGCTGAAGATAATGGCACCCCATTTTGTGGTTTAGCTTAAAGTT	contig388	Solvc10g	Beta-1 3-(	GO:00160	SL2.40ch	AT5G07570.1		glycine/p	chr5:239	12.9226	13.2901	5.69234	4.1844	5.95328	7.17249
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.027	Detected	-1.150	Detected	-1.088	0.004	GT	Sens	contig388	contig388	Unannota	AAGGGTTGAGACTCCGAAGAAAAGCAATGAAATGGTTAAGCCTAGTCTC	contig388	Solvc12g	Receptor	GO:00055	SL2.40ch	AT5G08520.1		myb fam	chr5:275	43.9584	40.1946	13.0209	20.2388	21.1934	20.1424
GT	Sense	Sense	0.000	Detected	0.000	Detected	0.000	-0.913	Detected	-1.331	Detected	-1.122	0.033	GT	Sens	contig388	contig388	Unannota	AGATATACTGGTGGCACCAGTGAGTTACAAAGTCAGAGCAGCGGTGAT	contig388	Solvc12g	Receptor	GO:00055	SL2.40ch	AT5G08520.1		myb fam	chr5:275	53.5494	50.3619	19.8789	15.0814	29.4006	21.9421
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-1.280	Detected	-1.304	Detected	-1.292	0.009	GT	Sens	contig389	contig389	Os01g09	GTACACT contig389 Solvc06g Solvc06g Os01g091 GO:00038 GO:00038	contig389	Solvc06g	Os01g091	GO:00038	SL2.40ch	AT3G07210.1		unknown	chr3:229	888.219	706.824	211.429	305.001	347.969	341.254
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.901	Detected	-1.442	Detected	-1.671	0.019	GT	Sens	contig389	contig389	Unannota	GGAAGATTCATCTGATACATCAGAAGAAGATATTCCTGATAACTGTTCT	contig389	Solvc09g	Baculovir	GO:00082	SL2.40ch	AT3G01345.1				51.8268	45.3013	13.247	19.2628	13.8357	18.9639
GT	Sense	Sense	0.162	Detected	-0.162	Detected	0.000	-1.527	Detected	-1.094	Detected	-1.310	0.040	GT	Sens	contig389	contig389	Unannota	TACTTGGTGTTGTTACTTGTTGAGTTAATTACTTCTCTAGAATCTTAAG	contig389	Solvc12g	Solute ca	GO:00160	SL2.40ch	AT4G161	ARA1. ISA	ARA1 (AF	chr4:912	613.551	461.507	195.347	239.277	196.959	265.018
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-1.099	Comprom	-1.287	Comprom	-1.193	0.016	GT	Sens	contig389	contig389	Unannota	TCAGGAAATTACTCGATTGACGCCTACTGCTGCAATTTCCAGACTCATT	contig389	Solvc09g	Unknown Protein (A		SL2.40ch	AT4G04500.1		protein k	chr4:223	14.7872	16.4163	3.3984	8.28098	7.75745	6.78632
GT	Sense	Sense	-0.320	Detected	0.320	Detected	0.000	-1.656	Detected	-0.897	Detected	-1.277	0.124	GT	Sens	contig389	contig389	Unannota	TGGAGGAGTATCTGGCACTTTCTTAAATTACATCATCACTTCGCCTTAC	contig389	Solvc06g	Os03g0169000 prot		SL2.40ch	AT3G21190.1		unknown	chr3:743	33.2923	48.7964	14.1666	21.0853	13.6394	23.0059
GT	Sense	Sense	0.294	Detected	-0.294	Detected	0.000	-3.483	Detected	-3.431	Detected	-3.457	0.007	GT	Sens	contig389	contig389	Unannota	ATCTATCTTATGACTAGTACTATTAAGCAGTGATGAATGTCTTATGTGT	contig389	Solvc06g	Aluminun	GO:00085	SL2.40ch	AT4G36680.1				11863.8	7425.18	2674.44	2349.65	894.943	925.488
GT	Sense	Sense	0.211	Detected	-0.211	Detected	0.000	-3.639	Detected	-3.650	Detected	-3.645	0.008	GT	Sens	contig389	contig389	Unannota	GATGAATGGACATATTGAGCTCTATTTACTCCCAAGTATATGTATCAA	contig389	Solvc06g	Aluminun	GO:00085	SL2.40ch	AT4G36680.1				15976.8	11216.4	3435.93	3261.47	1145.55	1133.62
GT	Sense	Sense	-0.138	Detected	0.138	Detected	0.000	-1.166	Detected	-1.006	Detected	-1.086	0.021	GT	Sens	contig390	contig390	Unannota	AACGTATGCAAAACATTAGAAAACGTGCTACTAAATTCCTACAGCACAT	contig390	Solvc06g	Nucellin-l	GO:00065	SL2.40ch	AT5G01730.1				10.7236	12.2123	9.73548	6.07695	5.44035	6.06027
GT	Sense	Sense	-0.431	Detected	0.431	Detected	0.000	-1.510	Detected	-1.252	Detected	-1.381	0.092	GT	Sens	contig390	contig390	Unannota	GACGATCAAAGTTAACCCGCAATGAGCTTACTCTCACTCGTAGCCCCT	contig390	Solvc06g	Nucellin-l	GO:00065	SL2.40ch	AT5G01730.1				78.8269	134.856	43.2009	65.2306	38.6102	46.0132
GT	Sense	Sense	0.260	Detected	-0.260	Detected	0.000	-2.629	Detected	-1.656	Detected	-2.142	0.060	GT	Sens	contig391	contig391	Unannota	CCCCAAAAAAGATAATGTGTCCTCCTCTACAAATATTCTTTCGGTCTTT	contig391	Solvc09g	Calmodul	GO:00055	SL2.40ch	AT1G01130.1		unknown	chr1:619	400.995	263.157	55.4198	84.4872	56.0088	109.589
GT	Sense	Sense	0.333	Detected	-0.333	Detected	0.000	-2.815	Detected	-1.651	Detected	-2.233	0.080	GT	Sens	contig391	contig391	Unannota	TTGAGCTCTTTGTTCGTCATTTGGAGTTCTAGTTATTTTTTCCCCCTTT	contig391	Solvc09g	Calmodul	GO:00055	SL2.40ch	AT1G01130.1		unknown	chr1:619	797.415	473.207	103.734	163.005	93.1083	208.027
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-1.392	Detected	-1.110	Detected	-1.251	0.013	GT	Sens	contig391	contig391	Unannota	GGTTAGAGTCTAATTAGTCTCAAAAGTTTCTGCCCTTTGGAAATAAAGG	contig391	Solvc03g	Regulator	GO:00050	SL2.40ch	AT4G167	ACX1. AT	ACX1 (AC	chr4:942	38.6206	38.2382	12.2416	16.0287	15.6163	18.9356
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	-1.284	Comprom	-0.911	Comprom	-1.097	0.029	GT	Sens	contig391	contig391	Unannota	ACATTCTGAACTCACTAGTGGTAGATCTTGGAAATGCCTCTTCCTAAAG	contig391	Solvc09g	Gibberelli	GO:00045	SL2.40ch	AT3G28770.1		unknown	chr3:107	16.9135	16.7132	3.18541	4.67986	7.36327	9.50654
GT	Sense	Sense	0.019	Detected	-0.019	Detected	0.000	-1.519	Detected	-1.088	Detected	-1.304	0.027	GT	Sens	contig392	contig392	Unannota	GCCTTTTAAGGTGTTTATCGACTTTGTTGATTGTTAGGTCACAATCTTA	contig392	Solvc03g	Unknown Protein (A		SL2.40ch	AT5G59660.1		leucine-r	chr5:240	4324.52	3964.89	1753.9	2347.24	1540.39	2071.2
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	-1.502	Detected	-1.021	Detected	-1.262	0.034	GT	Sens	contig392	contig392	Unannota	GTGATCAATTGATGTTGACTTCTTCACATTTCACCAAATTCCCAAGTTC	contig392	Solvc03g	Unknown Protein (A		SL2.40ch	AT5G59660.1		leucine-r	chr5:240	3462.05	3209.32	1515.52	1908.66	1255.16	1745.88
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-1.159	Comprom	-1.977	Comprom	-1.568	0.063	GT	Sens	contig393	contig393	Unannota	ATAGTCATTAAGGAGGATAGGGGTTGAAGAAAATCTTGAGGTCGGTGT	contig393	Solvc04g	Phosphat	GO:00044	SL2.40ch	AT4G23940.1		FtsH pro	chr4:124	13.5831	11.5972	8.90101	3.43459	5.99207	3.38945
GT	Sense	Sense	0.057	Detected	-0.057	Detected	0.000	-1.416	Detected	-1.386	Detected	-1.401	0.002	GT	Sens	contig393	contig393	Arginine	ATGGAAC contig393 Solvc01g Solvc01g Arginine GO:00082 GO:00082	contig393	Solvc01g	Arginine	GO:00087	SL2.40ch	AT4G347	ADC2. SP	ADC2 (AF	chr4:165	65108.9	56590.2	16132.1	23348.6	24263.3	24690.9
GT	Sense	Sense	-0.388	Detected	0.388	Detected	0.000	-1.712	Comprom	-2.205	Comprom	-1.959	0.051	GT	Sens	contig393	contig393	Unknown	ATATTTC contig393 Solvc10g Solvc10g Unknown Protein (AHRD V1)	contig393	Solvc10g	Unknown Protein (A		SL2.40ch	AT5G19050.1		unknown	chr5:636	12.3441	19.8978	5.30564	11.2636	5.10097	3.6136
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	-1.080	Detected	-1.579	Detected	-1.330	0.034	GT	Sens	contig394	contig394	Unannota	ATAATGCGCACACACACGTTGTGGGACCCTACACCTACTTGAAGCATCA	contig394	Solvc02g	Lipase (A	GO:00060	SL2.40ch	AT1G36920.1		unknown	chr1:139	133.533	121.503	41.3489	31.2697	64.2328	45.3263
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-2.730	Detected	-2.129	Detected	-2.430	0.017	GT	Sens	contig394	contig394	Unannota	TATTACCTATATAACTGTGTATCCAACTCAAGCTGTGCGTAAACTGTAA	contig394	Solvc01g	SOUL heme-binding		SL2.40ch	AT5G447	REV1. AT	REV1: DI	chr5:180	224.566	178.712	43.573	70.69	32.2	48.6844
GT	Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-2.437	Detected	-1.862	Detected	-2.149	0.019	GT	Sens	contig394	contig394	Unannota	GTGGATCTAAGATCAGAGTATATGAAGCTCAAATAGAACATCTGATT	contig394	Solvc01g	SOUL heme-binding		SL2.40ch	AT5G447	REV1. AT	REV1: DI	chr5:180	128.886	105.459	29.9719	46.9733	22.9651	34.0904
GT	Sense	Sense	0.470	Detected	-0.470	Detected	0.000	-2.515	Comprom	-1.624	Comprom	-2.070	0.086	GT	Sens	contig394	contig394	Unannota	TATAATGCGTTGAAGCTTCCAGCACATTAATCGACCAAACCAGCAATCT	contig394	Solvc11g	Unknown Protein (A		SL2.40ch	AT1G62180.1				28.3631	11.7033	5.07499	6.37199	3.11668	5.7638
GT	Sense	Sense	0.211	Detected	-0.211	Detected	0.000	-1.362	Detected	-0.936	Detected	-1.149	0.062	GT	Sens	contig394	contig394	Unannota	GTTCGTCGAAAATTATTCAGAATTGAGATTGAGGCATAGTTTTTATGGT	contig394	Solvc12g	Peptide-N4-(N-acety		SL2.40ch	AT5G24420.1				2850.65	2001.47	1432.68	1897.85	991.044	1327.12
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	-1.327	Detected	-1.570	Detected	-1.448	0.021	GT	Sens	contig394	contig394	Unannota	CCAAAAGGCGCGACCAAGACCTAGACAAGCACATAAGTTTGAGGACCT	contig394	Solvc08g	Cytochro	GO:00198	SL2.40ch	AT5G10140.3		FLC (FLC	chr5:317	498.557	367.848	160.372	157.442	182.039	153.363
GT	Sense	Sense	0.195	Detected	-0.195	Detected	0.000	-1.302	Detected	-1.510	Detected	-1.406	0.024	GT	Sens	contig394	contig394	Unannota	ACAAAGAGTTCCCATAGTACTTGAGATATAGTACACCACAAAGGGTATG	contig394	Solvc08g	Cytochro	GO:00198	SL2.40ch	AT5G10140.3		FLC (FLC	chr5:317	355.171	255.038	128.781	124.169	130.185	112.329
GT	Sense	Sense	0.504	Detected	-0.504	Detected	0.000	-1.293	Detected	-2.351	Detected	-1.822	0.130	GT	Sens	contig394	contig394	Unannota	CTGACTTCGTATTAGACTAAAATATGCCACAACAACTTATTGTGAACCT	contig394	Solvc07g	Cytochro	GO:00198	SL2.40ch	AT3G146	CYP72A1	CYP72A1	chr3:493	129.171	60.4479	25.0923	34.8803	38.4489	18.4117
GT	Sense	Sense	0.558	Detected	-0.558	Detected	0.000	-1.353	Detected	-2.470	Detected	-1.911	0.137	GT	Sens	contig394	contig394	Unannota	CAGTATTTGCAAGTGACGAAAAATTGGGATGCACATATGAAAGTTAGC	contig394	Solvc07g	Cytochro	GO:00198	SL2.40ch	AT3G146	CYP72A1	CYP72A1	chr3:493	125.987	54.6735	19.7002	33.2067	34.6548	15.9319
GT	Sense	Sense	0.477	Detected	-0.477	Detected	0.000	-1.060	Detected	-2.588	Comprom	-1.824	0.180	GT	Sens	contig394	contig394	Unannota	GGCAACATGGGAGAGATCATTAGCCCTCCATTCTAACAAGCACATGCA	contig394	Solvc12g	Coatomer	GO:00301	SL2.40ch	ATCG011	YCF1.2	hypothet	chrC:123	30.2607	14.6934	3.18853	9.6063	10.7815	3.72737
GT	Sense	Sense	0.316	Detected	-0.316	Detected	0.000	-1.659	Detected	-0.923	Detected	-1.291	0.117	GT	Sens	contig395	contig395	Unannota	CAACCCCATGGTGTAAAAAATGTATGACATGGATATGCCTAGCTCGAAT	contig395	Solvc03g	Auxin-res	GO:00055	SL2.40ch	AT2G166	ATTOC13	TOC132	chr2:721	187.643	113.883	72.3853	97.3666	49.3691	81.9732
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-1.163	Detected	-1.111	Detected	-1.137	0.009	GT	Sens	contig395	contig395	Unannota	GTATTCCTAGCAGTGAAGAGCCGAGATTTCCGTTCTTACTCGTAT	contig395	Solvc02g	Unknown Protein (A		SL2.40ch	AT1G15740.1		leucine-r	chr1:541	2071.69	1682.64	960.665	1116.78	889.12	919.252
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	-1.130	Detected	-1.095	Detected	-1.112	0.013	GT	Sens	contig396	contig396	CBS dom	ATATTCT contig396 Solvc02g Solvc02g CBS domain containing protei	contig396	Solvc02g	CBS domain contai		SL2.40ch	AT4G38870.1		F-box fan	chr4:181	6735.87	5324.87	2434.65	2574.95	2918.34	2981.86
GT	Sense	Sense	0.237	Detected	-0.237	Detected	0.000	-3.883	Comprom	-1.717	Comprom	-2.800	0.127	GT	Sens	contig396	contig396	Unannota	CCCTACTAATTTCCTTATAGCCCACATACCCCTACGAATAATATGATGT	contig396	Solvc06g	Rhomboi	GO:00042	SL2.40ch	AT1G32300.1		FAD-bind	chr1:116	33.6204	22.776	9.27826	16.4442	1.99989	8.94976
GT	Sense	Sense	0.140	Detected	-0.140	Detected	0.000	-1.492	Detected	-2.477	Comprom	-1.984	0.061	GT	Sens	contig396	contig396	Unannota	GAAAATAACGTCCTAACGTTCCATTTGACAGGCCACATTCCCAACTCAA	contig396	Solvc06g	Rhomboi	GO:00042	SL2.40ch	AT1G32300.1		FAD-bind	chr1:116	33.5739	26.0352	6.94573	23.0466	11.2123	5.6447
GT	Sense	Sense	0.224	Detected	-0.224	Detected	0.000	-1.103	Detected	-1.205	Detected	-1.154	0.037	GT	Sens	contig396	contig396	Unannota	CTTGTTGGTTTGCCAAGAAAATAAAAACAGAATCTTTGCCCATCTGGTA	contig396	Solvc10g	Response	GO:00063	SL2.40ch	AT3G28480.1		oxidored	chr3:106	1180.14	814.154	516.612	479.183	486.764	452.156
GT	Sense	Sense	0.325	Detected	-0.325	Detected	0.000	-1.282	Detected	-1.513	Detected	-1.398	0.056	GT	Sens	contig396	contig396	Unannota	CGGATGCACAGATTAAAGCATCTCTCAGTTAATCCCTTTTTTGTTTATC	contig396	Solvc10g	Response	GO:00063	SL2.40ch	AT3G28480.1		oxidored	chr3:106	117.774	70.5914	47.5349	44.6583	39.988	33.9586
GT	Sense	Sense	0.141	Detected	-0.141	Detected	0.000	-0.979	Detected	-1.659	Detected	-1.319	0.070	GT	Sens	contig396	contig396	Unannota	ATTGGGGAATTTGAGTCCGACCCAGATGACATGAGGATTGGGAGGAGT	contig396	Solvc09g	Unknown Protein (A		SL2.40ch	AT5G22310.1		unknown	chr5:738	26.7553	20.7184	10.1336	13.6706	12.7398	7.9242
GT	Sense	Sense	0.333	Detected	-0.333	Detected	0.000	-1.591	Detected	-1.296	Detected	-1.443	0.058	GT	Sens	contig396	contig396	Unknown	TACGTTA contig396 Solvc04g Solvc04g Unknown Protein (AHRD V1)	contig396	Solvc04g	Unknown Protein (A		SL2.40ch	AT3G266	SNM1	SNM1 (SI	chr3:980	8563.51	5079.75	1706.48	3451.72	2334.79	2856.26
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-1.159	Detected	-1.184	Detected	-1.172	0.004	GT	Sens	contig396	contig396	Unannota	TTGTTTATGTGTGTGTTGTTGTCCCTATACTCCATTTAATAAGAGTCTACG	contig396	Solvc06g	Unknown Protein (A		SL2.40ch	AT1G20130.1				763.015	645.09	266.543	302.612	334.947	328.34
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-0.835	Detected	-2.023	Comprom	-1.429	0.141	GT	Sens	contig397	contig397	Unannota	GGTTGGGTTTTTATGTTGCTAGTAGAACTTATCAGTCAAGTGAACTGAT	contig397	Solvc07g	MLO-like	GO:00160	SL2.40ch	AT3G04980.1		DNAJ he	chr3:137	27.8436	22.9269	12.1341	7.91939	15.1021	6.60937
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	-1.654	Comprom	-1.299	Comprom	-1.477	0.023	GT	Sens	contig397	contig397	Unannota	TAGTAGAGTTTGATTTGATTTGAAGTTCTGGTAGATTAGTTGGAAAGAC	contig397	Solvc07g	MLO-like	GO:00160	SL2.40ch	AT3G04980.1		DNAJ he	chr3:137	16.2527	12.6122	4.78698	1.92644	4.85098	6.18463
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	-1.380	Detected	-0.930	Detected	-1.155	0.052	GT	Sens	contig397	contig397	TIM-barre	TATGTAC contig397 Solvc02g Solvc02g TIM-barre GO:00055 GO:00055	contig397	Solvc02g	TIM-barre	GO:00055	SL2.40ch	AT5G66420.2		LOCATE	chr5:265	963.464	730.138	344.598	334.738	343.606	467.947
GT	Sense	Sense	-0.121	Detected	0.121	Detected	0.000	-1.882	Detected	-2.195	Detected	-2.038	0.009	GT	Sens	contig397	contig397	Unannota	AACAGCAACTTCCATCCAACATTTTGCTTCCCTTTTAATCGCCATTTCT	contig397	Solvc04g	S-adenos	GO:00087	SL2.40ch	AT5G39785.2		structura	chr5:159	198.642	221.073	30.9544	34.5909	60.6473	48.6511
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-2.238	Detected	-2.841	Detected	-2.539	0.016	GT	Sens	contig397	contig397	Unannota	CTACTCGTGAAAATTACACGAAATAGAGTGTTCAGTACTACTCTGCTCT	contig397	Solvc04g	S-adenos	GO:00087	SL2.40ch	AT5G39785.2		structura	chr5:159	102.916	81.3791	13.2472	12.4971	20.6893	13.579
GT	Sense	Sense	0.224	Detected	-0.224	Detected	0.000	-1.877	Detected	-1.399	Detected	-1.638	0.038	GT	Sens	contig398	contig398	Unannota	TGTATAAAGATGTAGGAGGTTATAGTAAAGAAGTAGATGACATATAGTT	contig398	Solvc05g	tRNA/rRNA	GO:00089	SL2.40ch	AT4G04760.1				363.17	250.576	110.67	163.163	87.5915	121.589
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-2.055	Detected	-1.421	Detected	-1.738	0.036	GT	Sens	contig398	contig398	Unannota	TAGTGTTAAGAGATGAAAATGGAGTCAGGCTAAGGCAGCTTTAGTGTTA	contig398	Solvc05g	tRNA/rRNA	GO:00089	SL2.40ch	AT4G04760.1				2990.63	2402.43	916.505	1230.86	688.01	1064.37
GT	Sense	Sense	0.271	Detected	-0.271	Detected	0.000	-1.402	Detected	-1.898	Detected	-1.650	0.046	GT	Sens	contig398	contig398	Cytokinin	CTCATTA contig398 Solvc04g Solvc04g Cytokinin GO:00191 GO:00191	contig398	Solvc04g	Cytokinin	GO:00191	SL2.40ch	AT1G754	CKX5. AT	CKX5 (CY	chr1:283	6547.86	4232.83	1412.38	1673.13	2124.19	1502
GT	Sense	Sense	0.228	Detected	-0.228	Detected	0.000	-1.593	Detected	-1.042	Detected	-1.318	0.066	GT	Sens	contig398	contig398	Unannota	GAATCTGTCTCATTCTCATTGTAATTAGCATCATTGGCCTTTTCATTTC	contig398	Solvc03g	Chromod	GO:00045	SL2.40ch	AT2G19530.1		unknown	chr2:846	3445.68	2363.86	1071.6	1404.93	1008.59	1473.61
GT	Sense	Sense	0.238	Detected	-0.238	Detected	0.000	-1.477	Detected	-0.998	Detected	-1.238	0.067	GT	Sens	contig398	contig398	Unannota	CAATGCCTCTTTTAACTTTAAGTAAGATGGAAGAGATATGCCATTGTTT	contig398	Solvc03g	Chromod	GO:00045	SL2.40ch	AT2G19530.1		unknown	chr2:846	1500.94	1016.07	509.757	625.738	473.027	657.39
GT	Sense	Sense	-0.290	Detected	0.290	Detected	0.000	-2.626	Comprom	-0.858	Detected	-1.742	0.202	GT	Sens	contig399	contig399	Unannota	TCAGTGTTTGTAAATATCCAAGGATGTGTGCATTAATAAGGCTTACACC	contig399	Solvc07g	Protein ar	GO:00055	SL2.40ch	AT5G28340.1				18.3164	25.7734	2.22945	11.7015	3.75291	12.7417
GT	Sense	Sense	0.311	Detected	-0.311	Detected	0.000	-6.221	Comprom	-5.365	Comprom	-5.793	0.008	GT	Sens	contig399	contig399	Unannota	CAAAAACACATTTGTTCTAGTGGGAATTGCTTGTGGCATTTAGATGGA	contig399	Solvc10g	Unknown	GO:00160	SL2.40ch	AT3G138	AtIDD11	AtIDD11	chr3:454	172.356	105.436	1.74059	2.98097	1.92689	3.47836
GT	Sense	Sense	0.322	Detected	-0.322	Detected	0.000	-4.787	Comprom	-5.035	Comprom	-4.911	0.005	GT	Sens	contig399	contig399	Unannota	GGCAATTAAAAAGGCTACATAATACAATTCAAAGAGGTAGGTTTCTCAT	contig399	Solvc10g	Unknown	GO:00160	SL2.40ch	AT3G138	AtIDD11	AtIDD11	chr3:454	93.0546	56.0465	2.01737	3.11597	2.78936	2.34169
GT	Sense	Sense	0.052	Detected	-0.052	Detected	0.000	-1.192	Detected	-0.943	Detected	-1.067	0.016	GT	Sens	contig4	contig4	Post-GPI	AACTTCT contig4 Solvc11g Solvc11g Post-GPI attachment to protein	contig4	Solvc11g	Post-GPI attachmen		SL2.40ch	AT1G16560.3		Per1-like	chr1:566	2270.3	1988.97	836.95	1078.29	991.981	1175.23
GT	Sense	Sense	-0.210	Detected	0.210	Detected	0.000	-1.474	Detected	-1.218	Detected	-1.346	0.032	GT	Sens	contig400	contig400	Ethylene-	AATTTTC contig400 Solvc03g Solvc03g Ethylene- GO:00165 GO:00165	contig400	Solvc03g	Ethylene-	GO:00165	SL2.40ch	AT5G519	CBF4. DR	CBF4 (C-	chr5:211	82.0402	103.332	41.5426	54.6126	35.3547	42.0695
GT	Sense	Sense	0.312	Detected	-0.312	Detected	0.000	-1.688	Detected	-0.899	Detected	-1.293	0.124	GT	Sens	contig400	contig400	Unannota	GTTTTCATTTGGGTAATAGACTGTTCTGGAAGATTTTCATTGAAGTTGAC	contig400	Solvc02g	MAProte	GO:00230	SL2.40ch	AT2G01740.1				56.5342	34.5377	13.7554	16.5923	14.6279	25.1945
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	-1.271	Detected	-1.119	Detected	-1.195	0.025	GT	Sens	contig400	contig400	Unannota	GGTTGTACTGAAGCTTTTTCTGTGGAGTCAAGGATGCAGCCTCAAGT	contig400	Solvc02g	MAProte	GO:00230	SL2.40ch	AT2G01740.1				103.091	76.0808	26.5362	33.7724	39.1319	43.3495
GT	Sense	Sense	0.267	Detected	-0.267	Detected	0.000	-1.807	Detected	-0.999	Detected	-1.403	0.101	GT	Sens	contig400	contig400	Unannota	GTGTATAGTCATCATGTGTTTCTTTTGCCATGTTTATACTGATTTTAG	contig400	Solvc09g	Acetyl est	GO:00055	SL2.40ch	AT3G089	ATERDJ3	ATERDJ3	chr3:273	50.3926	32.764	18.3916	15.0539	12.3858	21.6204
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-1.935	Detected	-1.147	Detected	-1.541	0.067	GT	Sens	contig400	contig400	Unannota	CATCAATCTACTTTTAGTGTCATGAGGAGATGTCTATTATAGGTCATAC	contig400	Solvc09g	Acetyl est	GO:00055	SL2.40ch	AT3G089	ATERDJ3	ATERDJ3	chr3:273	47.4076	35.1784	15.777	16.6666	11.5501	19.8786
GT	Sense	Sense	0.271	Detected	-0.271	Detected	0.000	-1.658	Detected	-1.569	Detected	-1.613	0.028	GT	Sens	contig400	contig400	Unannota	TGGGCTAGTTTTATCCAAAAGTGAACAGCCCAAAGCCTAAAAAATAAGA	contig400	Solvc03g	Xyloglucu	GO:00167	SL2.40ch	AT5G50540.1		unknown	chr5:205	461.657	298.392	102.892	260.96	125.421	133.008
GT	Sense	Sense	0.253	Detected	-0.253	Detected	0.000	-3.155	Detected	-2.991	Detected	-3.073	0.007	GT	Sens	contig400	contig400	Unannota	CATGTTCAATTTATCCACCTATTGTAAAGATATAGTTGACCCCATGGCT	contig400	Solvc01g	Transcrip	GO:00037	SL2.40ch	AT5G53010.1		calcium-	chr5:214	978.396	648.012	159.906	66.7348	95.3321	106.477
GT	Sense	Sense	0.379	Detected	-0.379	Detected	0.000	-3.254	Detected	-3.083	Detected	-3.169	0.015	GT	Sens	contig400	contig400	Unannota	GGTTGAGAAATTCAACGTATACCAAGTGGTTAGAGAAAAGGGCAATAC	contig400	Solvc01g	Transcrip	GO:00037	SL2.40ch	AT5G53010.1		calcium-	chr5:214	1172.63	652.658	196.551	74.7534	97.7649	109.77
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	-1.535	Comprom	-1.905	Comprom	-1.720	0.012	GT	Sens	contig401	contig401	Unannota	GAAGGACAAATCAAATTTCTAGCTCCGCTCTTAATAGTAGATTTGACA	contig401	Solvc07g	Genomic DNA chror		SL2.40ch	AT5G65090.1				13.5575	13.5263	3.16092	7.03676	4.98215	3.84415
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-2.303	Detected	-2.634	Detected	-2.468	0.007	GT	Sens	contig401	contig401	Unannota	TAAACCCTGGACACCAGAGTTCAAATTCCAGCAGAGCCATCTATTCCTC	contig401	Solvc11g	Glutamyl-	GO:00168	SL2.40ch	AT4G04650.1				221.895	178.505	47.6726	143.081	43.0206	34.0922
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	-2.271	Detected	-2.793	Detected	-2.532	0.015	GT	Sens	contig401	contig401	Unannota	AAGAGAAAAGTTGTAACTAGACTGCATCCAACAGTGGCCAAGTGGTCA	contig401	Solvc11g	Glutamyl-	GO:00168	SL2.40ch	AT4G04650.1				193.11	142.491	36.3608	98.5805	36.6413	25.4426
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	-1.206	Detected	-1.345	Detected	-1.275	0.008	GT	Sens	contig401	contig401	Unannota	CTTCTAAACTCAAAACTGGTTTGAAATGCCCCATTTTGAGCTGGTTCAG	contig401	Solvc10g	ATP synt	GO:00452	SL2.40ch	AT5G55770.1		DC1 dom	chr5:225	27.5614	29.26	11.6481	4.51347	13.1301	11.8885
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-1.628	Detected	-1.342	Detected	-1.485	0.013	GT	Sens	contig401	contig401	Unannota	CGCTTATCTAGATTTCACTAATTGTGAGCTTCTGTTATTTTGGTCATTT	contig401	Solvc10g	ATP synt	GO:00452	SL2.40ch	AT5G55770.1		DC1 dom	chr5:225	36.2687	38.8549	8.00752	13.144	12.9549	15.7418
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-2.145	Comprom	-1.716	Comprom	-1.931	0.013	GT	Sens	contig401	contig401	Unannota	TCTTGAAGGCCATATTTTGGATAGGAATTATATGGTCCGAGTAGAGCA	contig401	Solvc11g	Flowering	GO:00084	SL2.40ch	AT4G24974.1				19.8316	17.5235	3.40024	11.0606	4.49593	6.03121
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-2.752	Comprom	-1.573	Comprom	-2.163	0.069	GT	Sens	contig401	contig401	Unannota	GGCTTGAGGCTTAGCTATTGAGTTGATTAAATATAGTTCTTACTATTGT	contig401	Solvc01g	Actin (AH	GO:00052	SL2.40ch	AT5G21430.2				18.7921	15.121	3.88551	2.16056	2.66882	6.02193
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.273	Detected	-1.590	Detected	-1.431	0.013	GT	Sens	contig401	contig401	NAC dom	TGAACTC contig401 Solvc10g Solvc10g NAC dom GO:0045449	contig401	Solvc10g	NAC dom	GO:00454	SL2.40ch	AT1G528	ANAC019	ANAC019	chr1:196	870.669	872.329	575.509	381.546	384.68	307.705
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.397	Detected	-0.906	Detected	-1.151	0.044	GT	Sens	contig402	contig402	Unannota	TTGAGACTGAAGCATAGTTGTTGTTTTTGGTTCTCCTGGAATCACAGTC	contig402	Solvc12g	Unknown Protein (A		SL2.40ch	AT3G256	CHUP1	CHUP1 (C	chr3:935	108.213	95.6418	47.3859	69.127	41.2083	57.73
GT	Sense	Sense	0.074	Detected	-0.074	Detected	0.000	-1.182	Detected	-1.172	Detected	-1.177	0.004	GT	Sens	contig402	contig402	Unannota	GCATGGAAATCTAAACCTCTCCAGGTAGAACCAAGGTATAGCAGAAGTA	contig402	Solvc02g	DNA mism	GO:00055	SL2.40ch	AT1G70700.1				173.213	147.184	57.1765	102.315	75.0364	75.3296
GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-1.186	Detected	-1.056	Detected	-1.121	0.021	GT	Sens	contig402	contig402	Unannota	ATGCTTTGCTCGGGACCAGGTTTGAAGATGGGATTGAATTTTCTACTA	contig402	Solvc02g	DNA mism	GO:00055	SL2.40ch	AT1G70700.1				1418.56	1078.9	600.259	1038.07	579.892	632.545
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	-1.340	Detected	-0.936	Detected	-1.138	0.042	GT	Sens	contig402	contig402	Unannota	GGGGGTTCTAATTGGTATGCTCTTTCAAATGCCAATCAACTTTTAAT	contig402	Solvc07g	Tyrosine	GO:00055	SL2.40ch	AT5G16480.1		tyrosine	chr5:538	50.7688	57.1241	20.5467	26.6393	22.6838	29.9328
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	-1.642	Detected	-3.300	Comprom	-2.471	0.097	GT	Sens	contig402	contig402	Unannota	CTGATGTCTAGTCTAGTTGTCTCGCTATCCATGGTAAAGTATATTAAA	contig402	Solvc03g	SET and MYND dom		SL2.40ch	AT2G347	EMB1611	MEE22 (I	chr2:146	32.8963	28.8526	7.97282	2.89117	10.5244	3.32554
GT	Sense	Sense	0.355	Detected	-0.355	Detected	0.000	-0.918	Detected	-1.266	Comprom	-1.092	0.110	GT	Sens	contig402	contig402	Unannota	TTAATGTGCACTTTAGCTTCGTCATCAAGGAACAAAGGCATACTTATCC	contig402	Solvc03g	Ataxin-2 (AHRD V1 *		SL2.40ch	AT4G02170.1				29.0088	16.676	6.88812	7.213	12.4162	9.72011
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-3.230	Comprom	-2.571	Comprom	-2.901	0.013	GT	Sens	contig402	contig402	Unannota	CTAGTAAGTTCACTAAATCTGTGATGATCTGCATCATTAGCATTATGGC	contig402	Solvc10g	F-box pro	GO:00302	SL2.40ch	AT5G38435.1				22.7644	20.1055	2.24017	5.50234	2.43123	3.82819
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-1.326	Comprom	-1.718	Comprom	-1.522	0.018	GT	Sens	contig402	contig402	Unannota	TCAAAACGACAAATTCCTGAAAACCTTTTTCCTTGCTGGCCACAATTC	contig402	Solvc10g	F-box pro	GO:00302	SL2.40ch	AT5G38435.1				25.6367	21.8004	2.81893	8.51403	10.0522	7.6395
GT	Sense	Sense	0.180	Detected	-0.180	Detected	0.000	-1.643	Detected	-1.421	Detected	-1.532	0.019	GT	Sens	contig403	contig403	Unannota	GCCTTGTAAAAATTAGAGCATATATACGTCCTTCAATCTAACGGAAGAC	contig403	Solvc06g	Cinnamoy	GO:00337	SL2.40ch	AT4G12750.1		sequenc	chr4:749	103.18	75.6342	49.5922	65.8409	30.1594	35.0731
GT	Sense	Sense	0.251	Detected	-0.251	Detected	0.000	-1.415	Detected	-1.637	Detected	-1.526	0.031	GT	Sens	contig403	contig403	Unannota	GTGACACAATCGTCTTATCCGGCAATGTGATTTTTAATTAATGTCGAAT	contig403	Solvc06g	Cinnamoy	GO:00337	SL2.40ch	AT4G12750.1		sequenc	chr4:749	157.671	104.711	89.1183	106.21	51.387	43.9386
GT	Sense	Sense	-0.243	Detected	0.243	Detected	0.000	-2.081	Comprom	-1.626	Comprom	-1.853	0.031	GT	Sens	contig403	contig403	Unannota	TTCTGATCTCCTTGATTTTCCTTTCTTGCGATGAGAGTGTGTCGGGAA	contig403	Solvc06g	Zinc finge	GO:00037	SL2.40ch	AT5G55350.1		membrar	chr5:224	11.2137	14.7753	2.84329	14.3113	3.24443	4.43473
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	-1.428	Comprom	-1.021	Comprom	-1.225	0.034	GT	Sens	contig404	contig404	Unannota	GTATCTTAACTAGGATGACTTGATGGGTGTACCAGTATAGGTAAGGAT	contig404	Solvc03g	Receptor	GO:00046	SL2.40ch	AT5G52000.1				15.7675	17.3622	6.22175	5.42232	6.55782	8.66731
GT	Sense	Sense	-0.150	Detected	0.150	Detected	0.000	-1.131	Detected	-0.905	Comprom	-1.018	0.032	GT	Sens	contig404	contig404	Unannota	CATAGATGTTAGGATTCATGGACATTCAGATGAGTAGAGTTCATTTAGT	contig404	Solvc01g	Unknown Protein (A		SL2.40ch	AT1G273	AHK3	AHK3 (AI	chr1:948	13.0355	15.0924	5.87095	6.40247	6.83031	7.96455
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	-1.203	Comprom	-0.841	Comprom	-1.022	0.044	GT	Sens	contig404	contig404	Unannota	CTCTTCTTAAGCACAAACTTAAAAACAAACTAGGGTTCCATTGCATCCC	contig404	Solvc08g	Delta-ami	GO:00428	SL2.40ch	AT1G443	hemb2	hemb2:	chr1:168	12.0813	13.5979	13.37	3.6548	5.93684	7.60714
GT	Sense	Sense	0.353	Detected	-0.353	Detected	0.000	-1.335	Detected	-1.100	Detected	-1.218	0.082	GT	Sens	contig405	contig405	Unannota	CATTGTTGTGTTCCGCATTTGTTGCCTTTATTACCGCAAATATTATTTC	contig405	Solvc08g	Peroxisome biogen		SL2.40ch	AT5G09580.1				527.288	304.203	185.324	180.95	169.345	198.588
GT	Sense	Sense	0.198	Detected	-0.198	Detected	0.000	-2.133	Comprom	-1.061	Detected	-1.597	0.108	GT	Sens	contig406	contig406	Unannota	TTACACGTGTCCCACGCTACTCAAGTCCTGATATCTCACTTTCGCATAC	contig406	Solvc09g	PHD fino	GO:00036	SL2.40ch	AT1G73770.2				31.961	22.8609	32.8691	15.449	6.57389	13.7732
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-1.415	Detected	-1.075	Detected	-1.245	0.025	GT	Sens	contig406	contig406	Hydrolasi	AAGAAGT contig406 Solvc10g Solvc10g Hydrolasi GO:00167 GO:00167	contig406	Solvc10g	Hydrolasi	GO:00167	SL2.40ch	AT3G266	ATNUDT1	ATNUDX	chr3:980	2111.51	1717.76	961.197	1196.21	761.666	961.118
GT	Sense	Sense	0.155	Detected	-0.155	Detected	0.000	-1.127	Detected	-1.107	Detected	-1.117	0.019	GT	Sens	contig406	contig406	Unannota	ACTCAATGAAATAGTCGAGGTATGTGGCTTGAACAGCAGAGGTATGTG	contig406	Solvc03g	Membran	GO:00080	SL2.40ch	AT5G204	XIK. ATXI	XIK: mot	chr5:692	106.067	80.5058	36.1599	47.6175	45.106	45.6033
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	-1.671	Comprom	-1.878	Comprom	-1.775	0.003	GT	Sens	contig406	contig406	Unannota	GGACGTACTTTTGTACCTATTCAACCCAAGTATGAAAGGCAATATATTC	contig406	Solvc07g	LRR rece	GO:00046	SL2.40ch	AT4G23220.1		kinase	chr4:121	13.7768	12.7692	3.68011	7.94428	4.4409	3.8358
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	-1.822	Detected	-1.216	Detected	-1.519	0.046	GT	Sens	contig406	contig406	Glycerol-	TCATCGA contig406 Solvc02g Solvc02g Glycerol- GO:00093 GO:00093	contig406	Solvc02g	Glycerol-	GO:00043	SL2.40ch	AT5G40610.1		glycerol-	chr5:162	759.153	583.078	203.194	323.499	200.619	304.432
GT	Sense	Sense	0.129	Detected	-0.129	Detected	0.000	-1.245	Detected	-0.803	Detected	-1.024	0.057	GT	Sens	contig406	contig406	Unannota	GCCGTTTGAAGTTATTTTTGTTTCTGTGCTACTCATAAGAGTTGCTTGA	contig406	Solvc03g	Os11g0198100 prot		SL2.40ch	AT5G43730.1		disease r	chr5:175	98.0008	77.1129	21.8534	39.4732	39.1068	52.9759
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-1.251	Detected	-0.963	Detected	-1.107	0.039	GT	Sens	contig406	contig406	Unannota	ATCGAAAACAACCTCTCTACTACTATTTTCCTCAAGGCTTAGACTGCAC	contig406	Solvc03g	Os11g0198100 prot		SL2.40ch	AT5G43730.1		disease r	chr5:175	114.269	84.7087	19.8923	32.9351	44.0823	53.6446

GT	Sense	Sense	6.469	Detected	-6.469	Detected	0.000	-7.692	Comprom	-7.718	Comprom	-7.705	0.356	GT	Sens	contig407	contig407	Unannota	GTATGACATGTTACTCTATAAAAAGGACAATGCATGAAGTAGGCGTACT							contig407	Solyc11g	Pentatric	GO:0008	SL2.40ch	AT3G59830.1		ankyrin	chr3:221	118184	14.166	10.3047	2.94101	6.67155	6.5316
GT	Sense	Sense	0.129	Detected	-0.129	Detected	0.000	-2.576	Detected	-1.496	Detected	-2.036	0.067	GT	Sens	contig407	contig407	Unannota	TGGTTTATCCAACTTGAGGTTTGTCTCATTGGATCATTTCTCGATTTGT							contig407	Solyc08g	Pectinace	GO:0004	SL2.40ch	AT4G19410.1		pectinac	chr4:105	234.273	184.314	75.3143	88.3004	37.1694	78.3207
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-2.318	Comprom	-1.634	Comprom	-1.976	0.032	GT	Sens	contig408	contig408	Unannota	GCCAACCACAAGAAGGCTCGTTCAATGAATATTTTTTACAACAAGCACA							contig408	Solyc02g	Solute ca	GO:0015	SL2.40ch	AT4G02050.1		sugar tra	chr4:898	13.5887	15.0756	1.70607	14.3158	3.06157	4.9016
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	-2.372	Detected	-0.876	Detected	-1.624	0.170	GT	Sens	contig408	contig408	Glycosylt	CTCCAC(	contig408	Solyc01g	Solyc01g	Glycosyltransferase CAZy fam			contig408	Solyc01g	Glycosyltransferase		SL2.40ch	AT2G458	DTA2	DTA2 (D	chr2:188	396.142	285.087	115.714	153.497	69.2062	194.624
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-2.186	Detected	-1.764	Detected	-1.975	0.011	GT	Sens	contig409	contig409	Transme	ATTACA	contig409	Solyc02g	Solyc02g	Transme	GO:0016	GO:0016	contig409	Solyc02g	Transme	GO:0015	SL2.40ch	AT5G378	NIP4:1. N	NIP4:1 (N	chr5:150	2988.48	2843.44	1079.83	1062.08	683.173	912.433
GT	Sense	Sense	-0.217	Detected	0.217	Detected	0.000	-1.057	Comprom	-1.431	Comprom	-1.244	0.049	GT	Sens	contig409	contig409	Unannota	GATCACTAGTGAGTAATATCTTTAAATGCAACTAAGTCTATTCCTTTCT							contig409	Solyc01g	Aspartyl	GO:0006	SL2.40ch	ATCG001	RPOB	Chloropl	chrC:231	10.9165	13.8771	6.34143	4.81062	6.30732	4.85172
GT	Sense	Sense	0.871	Detected	-0.871	Detected	0.000	-1.228	Detected	-1.458	Comprom	-1.343	0.266	GT	Sens	contig409	contig409	Unannota	CAGACCTCAGTCTCCTACCTTAAATTTTTTAGTTTGACATACATGAGAT							contig409	Solyc08g	Exostosin	GO:0003	SL2.40ch	AT5G38850.1		disease	chr5:155	41.8585	11.7706	7.81902	8.32467	10.1021	8.58979
GT	Sense	Sense	0.264	Detected	-0.264	Detected	0.000	-1.539	Comprom	-0.851	Comprom	-1.195	0.110	GT	Sens	contig409	contig409	Unannota	CTGTGTTCTAAACATAAGATTTTAGCATGGCGGTCAATCAATGTGGGA							contig409	Solyc09g	NAD-depe	GO:0005	SL2.40ch	AT5G37200.1		zinc fing	chr5:147	19.8326	12.9391	6.01704	16.6651	5.88015	9.44495
GT	Sense	Sense	0.169	Detected	-0.169	Detected	0.000	-2.072	Detected	-0.906	Detected	-1.489	0.134	GT	Sens	contig409	contig409	Ferredox	TTTTCC	contig409	Solyc07g	Solyc07g	Ferredoxin-like (AHRD V1 ***- (			contig409	Solyc07g	Ferredoxin-like (AH		SL2.40ch	AT5G46250.3		RNA reco	chr5:187	1986.14	1477.98	513.873	619.555	434.616	972.089
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-1.744	Comprom	-1.747	Comprom	-1.746	0.001	GT	Sens	contig409	contig409	Unannota	CCTATCAGTGCATTATAGCTCCTTGTGACTGAATAAGTGCCACATTTTG							contig409	Solyc11g	BEL1-like	GO:0005	SL2.40ch	AT5G03510.1		zinc fing	chr5:880	15.3909	15.3131	6.80167	9.20203	4.88626	4.86309
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	-2.915	Comprom	-3.577	Comprom	-3.246	0.017	GT	Sens	contig410	contig410	Unannota	GGTGTTCTTGCGAATATCTACGAATTTCACCTCTACACTCGCAGTTCCA							contig410	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G54470.1		uridine 5	chr3:201	40.8358	25.9748	46.3697	74.1464	4.60419	2.90103
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-1.367	Detected	-0.800	Detected	-1.083	0.063	GT	Sens	contig410	contig410	Unannota	AGTCACTAGGGAGCGAAGTGGAAAAGAGCCACTGGTTGCGATTGGCTC							contig410	Solyc00g075440.1.1				AT1G624	LRX2	LRX2 (LE	chr1:231	25.6828	25.1967	11.818	13.2385	10.5185	15.5325
GT	Sense	Sense	0.308	Detected	-0.308	Detected	0.000	-0.977	Detected	-1.205	Detected	-1.091	0.080	GT	Sens	contig410	contig410	Unannota	GGTTTGGTAGATGAATCATTGTGCCTTGCACCTTTGGTGACATTAGTT							contig410	Solyc09g	Mutator-li	GO:0008	SL2.40ch	AT4G33870.1				187.92	115.395	90.9521	63.628	79.7563	67.8989
GT	Sense	Sense	0.535	Detected	-0.535	Detected	0.000	-4.200	Comprom	-3.214	Comprom	-3.707	0.036	GT	Sens	contig411	contig411	Unannota	GAGATTTTAGAATGTTTGTACAACTCTACCAGGAAAGTTGTTATGGGTT							contig411	Solyc04g	MADS-bo	GO:0046	SL2.40ch	AT5G185	FASS. TO	FASS (FA	chr5:617	47.4198	21.2577	1.72347	1.89715	1.84178	3.63774
GT	Sense	Sense	-0.044	Detected	0.044	Detected	0.000	-1.717	Comprom	-0.901	Comprom	-1.309	0.086	GT	Sens	contig411	contig411	Unannota	CAACGGAGTTGTTTGTTTATTCGTCCTAGTGTCTGACATACTTTTGTTT							contig411	Solyc07g	C2 domain-containi		SL2.40ch	AT3G53380.1		lectin pro	chr3:197	12.7923	12.7887	2.94774	2.93587	4.14994	7.28109
GT	Sense	Sense	0.399	Detected	-0.399	Detected	0.000	-1.680	Detected	-1.076	Detected	-1.378	0.111	GT	Sens	contig411	contig411	Unannota	CTGGTGGAATTATCCGTACGGAATACTGGTAAACTTCATAAAAATTTAC							contig411	Solyc04g	Poly poly	GO:0003	SL2.40ch	AT2G463	SPA1	SPA1 (SU	chr2:190	49.1376	26.5881	20.595	25.762	12.0269	18.2314
GT	Sense	Sense	0.295	Detected	-0.295	Detected	0.000	-2.273	Detected	-1.611	Detected	-1.942	0.048	GT	Sens	contig411	contig411	Unannota	GATCGTCTCCTTTAGTTTCTGTGGTGAAGCTTATCTGAATATATCTCTT							contig411	Solyc04g	Poly poly	GO:0003	SL2.40ch	AT2G463	SPA1	SPA1 (SU	chr2:190	86.6689	54.1871	12.5586	38.4448	15.1204	23.8482
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-1.785	Comprom	-1.713	Comprom	-1.749	0.001	GT	Sens	contig411	contig411	Unannota	CTGGATTCTACATCTAATCTACTGCAGGTTGTATTGAAAAATCTAACAA							contig411	Solyc01g	Pumilio-fa	GO:0005	SL2.40ch	AT2G37240.1		INVOLVE	chr2:156	21.0727	18.7164	4.93202	11.1808	6.14663	6.44122
GT	Sense	Sense	0.402	Detected	-0.402	Detected	0.000	-1.180	Detected	-0.822	Detected	-1.001	0.151	GT	Sens	contig412	contig412	Lipase-lik	GGCAGG	contig412	Solyc02g	Solyc02g	Lipase-lik	GO:0047	GO:0047	contig412	Solyc02g	Lipase-lik	GO:0047	SL2.40ch	AT2G31100.1		triacylgly	chr2:132	640.649	345.183	146.552	12.5229	221.375	282.902
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-1.173	Detected	-0.950	Detected	-1.061	0.022	GT	Sens	contig412	contig412	Unannota	TAATTAAAAGACCCAAATCTAACAGGTCCTGTTCCTATCACACAAAACC							contig412	Solyc09g059810.1.1				AT1G63140.2		O-methyl	chr1:234	54.2023	43.4781	14.3771	19.8718	22.9556	26.7228
GT	Sense	Sense	-0.085	Detected	0.085	Detected	0.000	-1.904	Detected	-1.130	Detected	-1.517	0.062	GT	Sens	contig412	contig412	Unannota	TAGCTCCAACCGTCAGTGTTGATTAGGACAGCTTTAGAGATCTTTGGA							contig412	Solyc04g	Organic a	GO:0008	SL2.40ch	AT4G37820.1		unknown	chr4:177	746.932	790.671	175.837	207.551	218.947	373.407
GT	Sense	Sense	-0.063	Detected	0.063	Detected	0.000	-1.875	Detected	-1.149	Detected	-1.512	0.055	GT	Sens	contig412	contig412	Unannota	GCTGATGGTGTTTTAGTTTAGCCTATCTCCTTCTGTATATAACTTTTGG							contig412	Solyc04g	Organic a	GO:0008	SL2.40ch	AT4G37820.1		unknown	chr4:177	907.666	932.277	202.641	250.752	267.35	440.967
GT	Sense	Sense	0.138	Detected	-0.138	Detected	0.000	-0.839	Detected	-1.365	Comprom	-1.102	0.066	GT	Sens	contig412	contig412	Unannota	TGTTTTCAGTAAGTTGGATGTGTGCCATGCAGTTCCAGATGATCATTA							contig412	Solyc06g	Unknown Protein (A		SL2.40ch	AT3G09040.1		pentatric	chr3:276	17.9082	13.9202	6.28734	3.18286	9.41442	6.51849
GT	Sense	Sense	0.185	Detected	-0.185	Detected	0.000	-2.844	Detected	-1.475	Detected	-2.159	0.093	GT	Sens	contig412	contig412	Unannota	AATAACAAGAATCTTGTGTTTTTGACCTTTTTTACCTAGGGATGAACGA							contig412	Solyc11g	Gibberelli	GO:0005	SL2.40ch	AT4G178	UBP20	UBP20 (U	chr4:993	116.319	84.6825	18.6745	22.5841	14.7453	37.9681
GT	Sense	Sense	0.464	Detected	-0.464	Detected	0.000	-0.890	Detected	-1.908	Comprom	-1.399	0.179	GT	Sens	contig413	contig413	Unannota	TCTTTCTGTCTACTCGAAGACTTCACGTAAAATGGAACGTTCCACTCCA							contig413	Solyc11g	Os01g0841200 prot		SL2.40ch	AT1G544	AIN1. EIN	XRN4 (EX	chr1:203	35.1071	17.366	3.98642	8.404	14.2055	6.99608
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	-1.164	Detected	-0.954	Detected	-1.059	0.039	GT	Sens	contig413	contig413	Unannota	ACAACTCCAATATATTTTCCAGATCTAACAAAAAGCCAACACTCCAGTA							contig413	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G33480.1		unknown	chr4:161	60.5852	44.0165	24.3342	34.358	24.5787	28.3414
GT	Sense	Sense	1.348	Detected	-1.348	Detected	0.000	-1.241	Detected	-1.310	Detected	-1.276	0.444	GT	Sens	contig413	contig413	Unannota	AATCTAGGGACTCTTGTGAGTTTAGCAAAGTTGCCTAAAAGAGAGAAGA							contig413	Solyc09g	LRR rece	GO:0005	SL2.40ch	AT5G458	SCRL27	SCRL27	chr5:186	78.5331	11.3993	7.09398	12.783	13.4981	12.8269
GT	Sense	Sense	0.168	Detected	-0.168	Detected	0.000	-1.718	Detected	-1.901	Detected	-1.809	0.011	GT	Sens	contig413	contig413	Unannota	TATGTGATACATGTATGTTTAAACGATCCATTTGGCTCAGCCTTGATAC							contig413	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G10230.1				70.3438	52.4361	12.3436	38.013	19.6845	17.2923
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	-1.850	Detected	-2.013	Detected	-1.931	0.012	GT	Sens	contig413	contig413	Unannota	AGACATTGCTAGTATATTCGATTCTGTGTTCCATTATTCTAGCTTGTCT							contig413	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G10230.1				59.8553	43.0783	15.0517	33.6569	15.0205	13.38
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-2.592	Comprom	-2.440	Comprom	-2.516	0.001	GT	Sens	contig414	contig414	Unannota	TTAGATCACTTCAGCCCAAATAATTTCATTTATCTCAGCTCATCTTGAC							contig414	Solyc09g	3-ketoacy	GO:0003	SL2.40ch	AT1G67800.4				32.846	28.9181	5.07008	10.2525	5.45213	6.03894
GT	Sense	Sense	0.141	Detected	-0.141	Detected	0.000	-1.560	Detected	-1.426	Detected	-1.493	0.011	GT	Sens	contig414	contig414	Unannota	TAGTTTGGTGCCAGGAATAAGTGACAGAATCGCGGAGCAAAAGTTCCT							contig414	Solyc09g	3-ketoacy	GO:0003	SL2.40ch	AT1G67800.4				84.7029	65.5296	21.8305	17.6763	26.9527	29.4866
GT	Sense	Sense	-0.117	Detected	0.117	Detected	0.000	-1.266	Comprom	-1.880	Comprom	-1.573	0.041	GT	Sens	contig414	contig414	Unannota	ATAAGTCTTCTTTTCTACACCCTACTCAATCTTATGTACTCTTGTGACG							contig414	Solyc02g	DNA misn	GO:0005	SL2.40ch	AT5G10650.2				21.0436	23.2794	11.6677	16.4857	9.81442	6.39265
GT	Sense	Sense	-0.135	Detected	0.135	Detected	0.000	-1.090	Comprom	-1.059	Comprom	-1.074	0.016	GT	Sens	contig415	contig415	Unannota	TACAGCTTCACACTGGCATCAGGCCGGTCATGTGCAGGATAGGTGGTA							contig415	Solyc01g	Lipoprotein (AHRD V		SL2.40ch	AT5G20680.3		unknown	chr5:699	15.4462	17.5225	21.0983	19.1316	8.24229	8.39716
GT	Sense	Sense	-0.602	Detected	0.602	Detected	0.000	-1.229	Detected	-1.252	Detected	-1.241	0.176	GT	Sens	contig415	contig415	Unannota	ATAAGGATAACGGGAGCTACAAGGGTTCCTGTGGTTGGAGTCAAAGTG							contig415	Solyc09g	Unknown Protein (A		SL2.40ch	AT3G52700.1		unknown	chr3:195	119.981	260.203	86.9338	160.044	80.3965	78.8477
GT	Sense	Sense	0.387	Detected	-0.387	Detected	0.000	-2.098	Comprom	-1.131	Detected	-1.615	0.121	GT	Sens	contig415	contig415	Unannota	TGAAATCAAACCTTGGGGAATAGAGTCGTCTTTAGTATGGAGTGGTTTA							contig415	Solyc10g	Importin	GO:0005	SL2.40ch	AT4G02180.1		DC1 dom	chr4:959	41.1743	22.6643	7.30471	18.9083	7.60827	14.8255
GT	Sense	Sense	-0.101	Detected	0.101	Detected	0.000	-1.839	Comprom	-2.484	Comprom	-2.161	0.024	GT	Sens	contig416	contig416	Kunitz try	GACAGA	contig416	Solyc03g	Solyc03g	Kunitz try	GO:0004	GO:0004	contig416	Solyc03g	Kunitz try	GO:0004	SL2.40ch	AT1G73325.1		trypsin a	chr1:275	20.1409	21.7959	24.4583	10.4298	6.24655	3.98119
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-1.256	Detected	-0.878	Detected	-1.067	0.030	GT	Sens	contig416	contig416	Asparagi	TCACAT(	contig416	Solyc09g	Solyc09g	Asparagine synthetase B (AHF			contig416	Solyc09g	Asparagine synthet		SL2.40ch	AT3G22850.1		unknown	chr3:808	24193.8	23479.2	11308.1	13579.4	10638.2	13789.2
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.322	Detected	-0.888	Detected	-1.105	0.038	GT	Sens	contig416	contig416	Unannota	ATGGATATCTGTTTTGTTAGGACTGAGCACAGGAGGGTTGCGGAACTG							contig416	Solyc05g	Kelch repeat-contai		SL2.40ch	AT5G608	ATMYB3	MYB34 (I	chr5:244	261.795	233.207	112.005	121.981	105.424	141.946
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-0.870	Detected	-1.385	Detected	-1.128	0.057	GT	Sens	contig416	contig416	Unannota	CGTACAAATTTTTAATAAAGGTAGGTAGCTCCGTCCTGATGAAGTGTGT							contig416	Solyc02g	Gibberellin regulate		SL2.40ch	AT5G43570.1		serine-ty	chr5:175	309.186	248.207	75.9312	90.1844	161.584	112.802
GT	Sense	Sense	0.460	Detected	-0.460	Detected	0.000	-3.227	Detected	-1.206	Detected	-2.216	0.184	GT	Sens	contig416	contig416	Unannota	TTATTACTTGTATAATCGCTAATTCATTTGATTTTTTTTCTTTATATATT							contig416	Solyc11g	Peroxidas	GO:0055	SL2.40ch	AT3G52700.1		unknown	chr3:195	2222.41	1105.57	333.012	708.671	178.523	722.415
GT	Sense	Sense	0.504	Detected	-0.504	Detected	0.000	-3.554	Detected	-1.592	Detected	-2.573	0.145	GT	Sens	contig416	contig416	Unannota	AAGAATGAAATAAATCTTCCTTGTGAAAGAAAATGTTTGGCAATGTAAC							contig416	Solyc11g	Peroxidas	GO:0055	SL2.40ch	AT3G52700.1		unknown	chr3:195	2803.46	1311.01	296.527	690.731	174.039	676.044
GT	Sense	Sense	0.219	Detected	-0.219	Detected	0.000	-1.905	Detected	-1.287	Detected	-1.596	0.052	GT	Sens	contig416	contig416	Unannota	CGTACATCGATATCCTACCTTCCCAATATCCAACTTGTGAAATTACACT							contig416	Solyc08g	Monooxy	GO:0008	SL2.40ch	AT3G50910.1		unknown	chr3:189	108.084	75.0274	33.0515	44.4661	25.6477	39.227
GT	Sense	Sense	0.234	Detected	-0.234	Detected	0.000	-1.478	Detected	-1.067	Detected	-1.273	0.055	GT	Sens	contig416	contig416	Unannota	CTACTTTCTAGTGGTGTTATACAAACCATGGTTTAAACGGTTGAGATTA							contig416	Solyc08g	Monooxy	GO:0008	SL2.40ch	AT3G50910.1		unknown	chr3:189	65.3577	44.4311	17.0919	26.5452	20.6296	27.346
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	-1.543	Detected	-1.083	Detected	-1.313	0.035	GT	Sens	contig417	contig417	Unannota	TCGGCGAATGAGTTTAGAAATGAAGAAAATTAGGGTTCAGATGTGTGG							contig417	Solyc05g	Unknown Protein (A		SL2.40ch	AT4G049	ATALN	ATALN (	chr4:252	157.498	129.083	112.679	155.966	52.1916	71.5719
GT	Sense	Sense	-0.331	Detected	0.331	Detected	0.000	-1.539	Detected	-1.421	Detected	-1.480	0.048	GT	Sens	contig417	contig417	Unannota	GTGCAGTATCGTTTTTTGGGTAAGTGGGGACTGATTCAGTTTGTTTTA							contig417	Solyc12g049460.1.1				AT5G583	CIPK10. F	SIP1 (SO	chr5:235	80.6236	119.956	34.4912	38.2684	36.0813	39.0608
GT	Sense	Sense	-0.196	Detected	0.196	Detected	0.000	-2.137	Comprom	-1.401	Comprom	-1.769	0.051	GT	Sens	contig417	contig417	Unannota	CGTGGTTTCATCATCACTTGTTAGTTTCAAGGGCCAGTTGGGCCAAAA							contig417	Solyc12g062470.1.1				AT5G43570.1		serine-ty	chr5:175	11.5725	14.2824	5.17959	9.23333	3.11607	5.17567
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-1.257	Detected	-0.871	Detected	-1.064	0.033	GT	Sens	contig417	contig417	Unannota	GTCCTTCGCTTCATTTGACAAATGCTCTTCTAAATAGAATACATGTTTC							contig417	Solyc02g090550.1.1				AT5G209	TSL	TSL (TO	chr5:709	50.7478	50.2928	15.3874	20.5506	22.5402	29.3717
GT	Sense	Sense	0.242	Detected	-0.242	Detected	0.000	-1.426	Detected	-1.161	Detected	-1.293	0.043	GT	Sens	contig417	contig417	Unannota	GTGTAAGAATAACACATATCATATGCAAAGATTGCAAGTACGGGTATCC							contig417	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G376	SHR. SGF	SHR (SH	chr4:176	271.484	182.616	102.6	161.814	88.3932	105.863
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-1.924	Detected	-1.381	Detected	-1.652	0.028	GT	Sens	contig417	contig417	Unannota	CATCACAAAGTCCATGTTTTCCTCTAATCCAAGTAAAACACTGGAAAAT							contig417	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G376	SHR. SGF	SHR (SH	chr4:176	162.151	137.806	60.4021	97.8459	42.0163	61.0297
GT	Sense	Sense	-0.776	Detected	0.776	Detected	0.000	-2.263	Comprom	-2.064	Comprom	-2.163	0.110	GT	Sens	contig418	contig418	Unknown	AAGCAG	contig418	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig418	Solyc08g	Unknown Protein (A		SL2.40ch	AT3G12000.1				11.3763	31.3682	2.70904	2.73586	4.19672	4.80404
GT	Sense	Sense	0.381	Detected	-0.381	Detected	0.000	-1.334	Detected	-1.303	Detected	-1.319	0.074	GT	Sens	contig418	contig418	Transpos	GAATACT	contig418	Solyc12g	Solyc12g	Transpos	GO:0006	GO:0006	contig418	Solyc03g	SLL2-S9-protein-like		SL2.40ch	AT5G27650.1		PWWP d	chr5:978	1233.71	684.8	423.111	448.339	388.852	395.975
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	-1.421	Detected	-1.423	Detected	-1.422	0.006	GT	Sens	contig418	contig418	Unannota	CCAACATTTTCCCCCTTTTTGATGATGATAAACAATGTTTTATCACACG							contig418	Solyc10g	EDS5 (AH	GO:0016	SL2.40ch	AT5G26710.1		glutamat	chr5:930	362.532	399.493	126.289	147.489	151.583	150.946
GT	Sense	Sense	-0.138	Detected	0.138	Detected	0.000	-1.138	Detected	-1.072	Detected	-1.105	0.016	GT	Sens	contig418	contig418	Unannota	TCAAGACTTTGTTTCTATCATCAAAACTACAAACATCATGTTCTCTCATT							contig418	Solyc10g	EDS5 (AH	GO:0016	SL2.40ch	AT5G26710.1		glutamat	chr5:930	305.81	348.311	135.974	133.333	158.108	165.029
GT	Sense	Sense	-0.044	Detected	0.044	Detected	0.000	-2.582	Detected	-1.031	Detected	-1.807	0.145	GT	Sens	contig418	contig418	Unannota	AGAGTCCCTTCAACTATAAGAACTCTTTTTACTGTCCAACTTTGTCACT							contig418	Solyc12g	Unknown Protein (A		SL2.40ch	AT2G43445.1				86.3198	86.3114	63.3721	85.4144	15.3739	44.8989
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	-2.424	Comprom	-2.114	Comprom	-2.269	0.005	GT	Sens	contig418	contig418	Unannota	TCACCACAATTTATATATACTAAAAGCCGTCTTTCTAGCAATGAATATG							contig418	Solyc12g	Unknown Protein (A		SL2.40ch	AT2G43445.1				24.114	21.8485	18.1635	22.8729	4.56121	5.63918
GT	Sense	Sense	0.237	Detected	-0.237	Detected	0.000	-1.311	Detected	-0.933	Detected	-1.122	0.066	GT	Sens	contig418	contig418	Unannota	GGATCTCACAGGCCATAATGTTGAATGTGCTGTAGGATATATCAAATGT							contig418	Solyc05g	UDP-gala	GO:0005	SL2.40ch	AT1G143	ATUTR3.	UTR3 (UD	chr1:491	284.428	192.765	72.8705	135.894	100.632	130.361
GT	Sense	Sense	0.169	Detected	-0.169	Detected	0.000	-1.295	Detected	-1.026	Detected	-1.161	0.033	GT	Sens	contig418	contig418	Unannota	CTTGTGGATGAAAAATGCAGTTTTTCACTTGTATTCATCTGCATGGGAT							contig418	Solyc05g	UDP-gala	GO:0005	SL2.40ch	AT1G143	ATUTR3.	UTR3 (UD	chr1:491	152.926	113.865	45.9363	65.1031	57.3395	68.88
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	-1.685	Comprom	-1.630	Comprom	-1.658	0.006	GT	Sens	contig419	contig419	Unannota	CTTTCCAACAATTCCACCAGATTGATCGCATGTATTGTTGTTAATTGTT							contig419	Solyc01g	Ureide pe	GO:0005	SL2.40ch	AT5G21222.1		protein k	chr5:720	19.0424	15.1157	1.86688	3.65541	5.62486	5.82867
GT	Sense	Sense	-0.301	Detected	0.301	Detected	0.000	-1.144	Detected	-1.596	Comprom	-1.370	0.068	GT	Sens	contig420	contig420	Unannota	TACTTACTGGATTTGTTCAACCGGTTTTGGGTACATTTCCTTATATCAC							contig420	Solyc06g	Histone-l	GO:0005	SL2.40ch	AT3G50130.1		unknown	chr3:185	19.4613	27.779	9.54799	19.3304	11.2196	8.17722
GT	Sense	Sense	0.440	Detected	-0.440	Detected	0.000	-1.002	Detected	-1.334	Detected	-1.168	0.131	GT	Sens	contig420	contig420	Unannota	CCGCCAATTCTCTCACAGGTCACTTCTTCTCTTTTTGCTTATGTTTAAT							contig420	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G624	CDF1	CDF1 (C)	chr5:250	38.4348	19.6587	13.7212	10.795	14.6343	11.5936
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	-1.361	Detected	-1.040	Detected	-1.201	0.018	GT	Sens	contig420	contig420	Unannota	AATAAACACAGTTTAAAATCCCTTCAACACCTGTTAGTTCCCCTCTTCA							contig420	Solyc03g	V-type pr	GO:0033	SL2.40ch	AT2G07170.1		binding	chr2:297	292.62	262.571	135.798	215.843	115.106	143.283
GT	Sense	Sense	-0.020	Detected	0.020	Detected	0.000	-1.435	Detected	-1.000	Detected	-1.218	0.031	GT	Sens	contig420	contig420	Unannota	ATCCAAGTGATTCACTCTATCGAGATCCAAGTGATCAATTTCTTGCTGA							contig420	Solyc03g	V-type pr	GO:0033	SL2.40ch	AT2G07170.1		binding	chr2:297	487.908	472.038	217.905	338.751	189.246	255.044
GT	Sense	Sense	0.318	Detected	-0.318	Detected	0.000	-2.464	Detected	-3.024	Comprom	-2.744	0.023	GT	Sens	contig420	contig420	Unannota	TTGATATTGCCATACTGCTGCTATAACTGGAAACGTGATTTCAGGCAAA							contig420	Solyc10g	Cytochro	GO:0008	SL2.40ch	AT2G16535.1				70.0835	42.4439	5.2716	14.0823	10.5408	7.13097
GT	Sense	Sense	0.344	Detected	-0.344	Detected	0.000	-3.544	Comprom	-3.394	Comprom	-3.469	0.010	GT	Sens	contig420	contig420	Unannota	CACTGGACTTGTTCTCTAATTTCAAGATCGATCTTCATGTGTATCTGTA							contig420	Solyc10g	Cytochro	GO:0008	SL2.40ch	AT2G16535.1				46.0031	26.8729	4.35591	10.0566	3.21361	3.55594
GT	Sense	Sense	0.182	Detected	-0.182	Detected	0.000	-1.812	Detected	-1.882	Detected	-1.847	0.010	GT	Sens	contig421	contig421	Unannota	AGAACACAGTTTATCCTACTTAAGTCTTGTTTGGCAGCCTTGCATTCTG							contig421	Solyc05g	Pyrrolido	GO:0008	SL2.40ch	AT1G79650.1				79.8481	58.3646	17.69	17.7327	20.732	19.695
GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-3.832	Comprom	-2.185	Comprom	-3.008	0.070	GT	Sens	contig421	contig421	Unannota	GCGTGTCTCTAAAATTTCGGGTATAGGTTAAAGGGACTACTTAAATTGA							contig421	Solyc07g	Protein ki	GO:0005	SL2.40ch	AT3G27680.1				28.9425	22.0128	1.70459	5.55054	1.88968	5.90301
GT	Sense	Sense	-0.046	Detected	0.046	Detected	0.000	-3.280	Detected	-2.023	Detected	-2.651	0.052	GT	Sens	contig421	contig421	Unannota	GCATATTAATTGAATCCGAGTCCTTTTCCTCTTATTAATTAAACCTGGC							contig421	Solyc07g	Protein ki	GO:0005	SL2.40ch	AT3G27680.1				145.719	146.165	55.1912	54.5732	16.0243	38.1758
GT	Sense	Sense	-0.101	Detected	0.101	Detected	0.000	-1.634	Detected	-1.077	Detected	-1.356	0.045	GT	Sens	contig421	contig421	Unannota	ATAACCCCAAAGAACCAGATCCCTTTAGACGATACGACGAGCTACATAG							contig421	Solyc04g	Nonsense	GO:0042	SL2.40ch	AT2G23370.1		unknown	chr2:995	444.504	481.374	141.462	238.944	158.919	233.106
GT	Sense	Sense	-0.136	Detected	0.136	Detected	0.000	-1.367	Detected	-0.939	Detected	-1.153	0.045	GT	Sens	contig421	contig421	Unannota	TTGTATCACAATCGTTGCAACAAGACTGGAGGAGAGTTTTTGGTATG							contig421	Solyc04g	Nonsense	GO:0042	SL2.40ch	AT2G23370.1		unknown	chr2:995	534.842	608.007	181.345	345.922	235.719	316.15
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-1.249	Detected	-1.003	Detected	-1.126	0.012	GT	Sens	contig422	contig422	Unannota	GTATCTATGGATATATTTGGGTTAGCTGGTGCTTCCTTGATGGGTTAT							contig422	Solyc09g	Ulp1 protease family		SL2.40ch	AT5G16110.1		unknown	chr5:526	29.9517	29.364	13.0993	14.0749	13.3045	15.7276
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-0.916	Detected	-1.405	Comprom	-1.161	0.043	GT	Sens	contig422	contig422	Unannota	GGGATAGATTATGTCCGTGGTTCTAAATTTATTCTGTAATGGTGCTTGC							contig422	Solyc09g	Ulp1 protease family		SL2.40ch	AT5G16110.1		unknown	chr5:526	20.7657	18.2855	15.4359	10.7928	11.013	7.82091
GT	Sense	Sense	0.494	Detected	-0.494	Detected	0.000	-2.473	Comprom	-1.308	Detected	-1.890	0.132	GT	Sens	contig422	contig422	Unannota	GTTAGACAATAGCATGGAACAATAGATTTAGTTGTTGGATGGGTTTAGA							contig422	Solyc08g	Neurochondrin fami		SL2.40ch	AT5G04050.2		FUNCTIO	chr5:109	44.1128	20.9257	18.5125	12.1591	5.83467	13.0499
GT	Sense	Sense	0.346	Detected	-0.346	Detected	0.000	-2.455	Detected	-1.778	Detected	-2.117	0.049	GT	Sens	contig422	contig422	Unannota	CTCGATTAGCGACAGATCATCTATGGACAAACACATATGTTATGTGGCA							contig422	Solyc08g	Neurochondrin fami		SL2.40ch	AT5G04050.2		FUNCTIO	chr5:109	128.945	75.1233	39.122	33.0629	19.1349	30.5137
GT	Sense	Sense	0.352	Detected	-0.352	Detected	0.000	-1.417	Detected	-0.840	Detected	-1.129	0.131	GT	Sens	contig422	contig422	Unannota	ATGTGATGAATATATCGAGAAGTTTAAGTGGCGGGTTGTTGTTGAACT							contig422	Solyc08g	Inositol-te	GO:0005	SL2.40ch	AT5G274	MVK. MK	MK (MEV	chr5:969	538.052	310.928	208.8	198.922	163.336	242.917
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	-1.145	Detected	-0.913	Detected	-1.029	0.034	GT	Sens	contig422	contig422	Unannota	CCTTCCTTTTGTTTCATACTAGTGTCGAGAAGAAGTAACTACTCTATCA							contig422	Solyc12g	Integral m	GO:0008	SL2.40ch	AT5G42420.1		transpor	chr5:169	56.2573	42.6312	19.7389	30.8229	23.6206	27.6499
GT	Sense	Sense	0.039	Detected	-0.039	Detected	0.000	-1.604	Detected	-1.441	Detected	-1.523	0.004	GT	Sens	contig423	contig423	Unannota	GTTTTAGGATAGTATTTTTTGCGTACATACCGAGCACAAGAAGATTAGT							contig423	Solyc01g	Cysteine	GO:0008	SL2.40ch	AT1G12150.1		FUNCTIO	chr1:412	51.9357	46.2833	15.6852	15.755	17.1948	19.2037
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	-1.687	Detected	-1.171	Detected	-1.429	0.035	GT	Sens	contig423	contig423	Unannota	CCTTCCTTTATACCGAACACACCCTTAATGTCCTCTCATATGTTTCTAA							contig423	Solyc01g	Cysteine	GO:0008	SL2.40ch	AT1G12150.1		FUNCTIO	chr1:412	94.1402	77.4116	21.2478	30.9041	28.2788	40.3137
GT	Sense	Sense	-0.034	Detected	0.034	Detected	0.000	-1.619	Detected	-0.832	Detected	-1.225	0.090	GT	Sens	contig423	contig423	Unannota	AAATCCAAACGATACAGTGGGTAGGAACCAGAATCCTAATTTTACAGAT							contig423	Solyc10g	Adenosin	GO:0006	SL2.40ch	AT3G52700.1		unknown	chr3:195	34.8974	34.3991	10.8914	12.3992	12.0324	20.6873
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	-1.000	Detected	-1.066	Detected	-1.033	0.026	GT	Sens	contig423	contig423	Unannota	TATAAATACTACTGATAAGTTTTAGCTGTATATATACATCAATATCACCA							contig423	Solyc04g	Calcium-d	GO:0006	SL2.40ch	AT5G64020.1		unknown	chr5:256	955.272	714.976	437.865	478.755	440.524	419.827
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-1.238	Detected	-1.322	Detected	-1.280	0.005	GT	Sens	contig423	contig423	Unannota	AAACTGAGGAGAAAGAAAAGCCCTTTATTGGAGAAGGGGGTTCCCTCT							contig423	Solyc04g	Calcium-d	GO:0006	SL2.40ch	AT5G64020.1		unknown	chr5:256	5127.56	4292.09	1835.78	2404	2120.34	1994.5
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-0.882	Detected	-1.607	Comprom	-1.244	0.082	GT	Sens	contig424	contig424	Unannota	GCCTTCTTGCTCATTGTTCTCACTGCCACTTCATGGAGAAATAACTTAA							contig424	Solyc09g	Unknown	GO:0009	SL2.40ch	AT3G545	ATHRGP1	ATHRGP	chr3:202	19.5787	15.6194	3.24158	3.76172	10.1187	6.10449
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-2.327	Detected	-1.118	Detected	-1.723	0.104	GT	Sens	contig424	contig424	Unannota	ATCTGCTATTCACACTACCAAATGAAACAAACAAAAACTCTGTAAGAGG							contig424	Solyc08g	Phospho	GO:0006	SL2.40ch	AT1G43020.2		unknown	chr1:161	376.209	346.818	98.2143	123.497	76.7643	176.913
GT	Sense	Sense	-0.856	Detected	0.856	Detected	0.000	-1.492	Detected	-0.921	Detected	-1.207	0.313	GT	Sens	contig424	contig424	Expansin	AGTAGC	contig424	Solyc01g	Solyc01g	Expansin	GO:0005	GO:0005	contig424	Solyc01g	Expansin	GO:0005	SL2.40ch	AT5G10190.1		transpor	chr5:319	29.5321	91.0459	17.8567	4.43246	19.6558	29.1107
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-1.078	Detected	-1.039	Detected	-1.059	0.013	GT	Sens	contig424	contig424	Unannota	CATGTGGTGGATACCAAACACAAACAGGGCATTGTACTCTGAATCTACT							contig424	Solyc12g	60S ribosomal prote		SL2.40ch	AT4G11810.1		SPX (SY	chr4:710	92.06	73.5077	45.8376	63.2592	41.5509	42.5504
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	-1.973	Detected	-1.240	Detected	-1.607	0.048	GT	Sens	contig424	contig424	Unannota	TTTCTTGAAGGGAGAAGTTGGTTGGTCAATGTGGTGGGAAGTTGGTTC							contig424	Solyc12g	60S ribosomal prote		SL2.40ch	AT4G11810.1		SPX (SY	chr4:710	650.574	591.074	349.685	366.772	168.442	279.095
GT	Sense	Sense	0.510	Detected	-0.510	Detected	0.000	-1.738	Comprom	-1.008	Detected	-1.373	0.160	GT	Sens	contig424	contig424	Cyclin-de	GCGGAA	contig424	Solyc01g	Solyc01g	Cyclin-de	GO:0005	GO:0005	contig424	Solyc01g	Cyclin-de	GO:0005	SL2.40ch	AT1G496	KRP7. ICI	ICK5: cy	chr1:183	31.2683	14.5093	4.64723	4.98276	6.80763	11.2595
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.390	Detected	-1.157	Detected	-1.273	0.010	GT	Sens	contig426	contig426	Unannota	GTTGAGGAGCTGGTTCTCCCTTTCACAATGGGGAAATCTTTTATATATT							contig426	Solyc01g080980.1.1				AT1G11060.1		unknown	chr1:368	162.31	141.863	71.9287	117.719	61.7517	72.3534
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.497	Detected	-1.424	Detected	-1.460	0.002	GT	Sens	contig426	contig426	Unannota	TAAACATCAAGCTCAAACATGTGTCATTTGGTATGTTTGATCTGAGAAA							contig426	Solyc01g080980.1.1				AT1G11060.1		unknown	chr1:368	46.3506	40.9162	12.3097	24.6832	16.4584	17.251
GT	Sense	Sense	0.208	Detected	-0.208	Detected	0.000	-2.281	Detected	-1.823	Detected	-2.052	0.022	GT	Sens	contig426	contig426	AT2G203	CTTCCTCCAAGGTTCAATGAAGATATGCTTAAGGAATGTAGAACTCTTA							contig426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	59.2397	41.755	4.77765	15.9378	10.9153	14.9433
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-1.471	Detected	-1.393	Detected	-1.432	0.008	GT	Sens	contig426	contig426	Putative	AGGAAATGCGTCAAGGTATGTGAAATTGACGAAAGATCAAGCGCCTCG							contig426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	444.838	354.134	95.1714	117.896	152.719	160.713
GT	Sense	Sense	-0.513	Detected	0.513	Detected	0.000	-2.688	Comprom	-1.932	Comprom	-2.310	0.068	GT	Sens	contig427	contig427	Calmodul	GTTTTGAAGAAAATGGCTGGGAATTGCATTTGGTTTTTGGATTGTAAAC							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	22.8257	43.7576	14.2511	14.5178	5.22961	8.80334
GT	Sense	Sense	0.602	Detected	-0.602	Detected	0.000	-2.070	Detected	-2.172	Detected	-2.121	0.072	GT	Sens	contig427	contig427	Transcrip	TCAGTACCACCACAGCTTCCACTGCGTGGAAATGATGCGGACCGGCTT							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	101.135	41.3294	13.0544	11.5974	16.4197	15.2554
GT	Sense	Sense	0.494	Detected	-0.494	Detected	0.000	-2.097	Detected	-0.986	Detected	-1.542	0.174	GT	Sens	contig427	contig427	Auxin-res	CTAGATTATGGCGTTACTGGGACTATGTCACAATATATTCCAACTCTTA							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1122.15	532.327	238.548	282.393	192.624	414.902
GT	Sense	Sense	0.007	Detected	-0.007	Detected	0.000	-1.713	Comprom	-1.328	Comprom	-1.521	0.016	GT	Sens	contig427	contig427	E3 ubiqui	ACAGAATTCTAATTCATTTTTGAGGTTCTGGAAATGGACGATGAGCTCA							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	15.2692	14.2269	2.41848	6.73433	4.79466	6.23976
GT	Sense	Sense	0.060	Detected	-0.060	Detected	0.000	-1.380	Detected	-1.317	Detected	-1.349	0.002	GT	Sens	contig427	contig427	Eukaryot	ACAAAGTGGTTGAGGAGAGTAGAGGTCCATCTGCATTTATTGCAACTCC							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	707.689	612.993	185.369	163.438	269.855	281.022
GT	Sense	Sense	-0.138	Detected	0.138	Detected	0.000	-2.229	Detected	-1.573	Detected	-1.901	0.033	GT	Sens	contig428	contig428	BZIP tran	TATTCT(	contig428	Solyc04g	Solyc04g	BZIP transcription factor (AHR			contig428	Solyc04g	BZIP transcription fa		SL2.40ch	AT2G01810.1		PHD fing	chr2:347	51.8215	59.0747	12.6813	22.2421	12.5815	19.7727
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.147	Detected	-1.356	Detected	-1.252	0.010	GT	Sens	contig428	contig428	AT5G454	ACTAATTTTTCCTTCTCAAGCCCCATTGGTTTGCCCATTCCAGTACGTG							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	287.61	299.213	88.5811	159.28	141.241	121.842
GT	Sense	Sense	0.177	Detected	-0.177	Detected	0.000	-1.474	Detected	-1.225	Detected	-1.349	0.025	GT	Sens	contig428	contig428	AT3G518	AAAGATTCACCAGCTACCATCGCATTGATTTCAAGGAGATGCACAAGAC							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	257.141	189.283	49.0276	62.6941	84.7189	100.319

GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-1.151	Detected	-1.056	Detected	-1.103	0.028	GT	Sens	contig625	contig625	Myb famil	AAGCTT	contig625	Solyc08g	Solyc08g	Myb fami	GO:0003	GO:0003	contig625	Solyc08g	Myb famil	GO:0003	SL2.40ch	AT5G45580.1		transcrip	chr5:184	572.111	417.842	209.536	307.793	234.731	250.1
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	-1.885	Detected	-1.796	Detected	-1.840	0.013	GT	Sens	contig626	contig626	BTB/POZ	TTACTA	contig626	Solyc04g	Solyc04g	BTB/POZ	GO:0005	GO:0005	contig626	Solyc04g	BTB/POZ	GO:0005	SL2.40ch	AT2G30600.4		BTB/POZ	chr2:130	1730.19	1226.01	253.519	387.643	420.415	446.021
GT	Sense	Sense	0.455	Detected	-0.455	Detected	0.000	-1.588	Detected	-1.542	Detected	-1.565	0.075	GT	Sens	contig627	contig627	Expansin	CACCAC	contig627	Solyc08g	Solyc08g	Expansin-like protein (AHRD V			contig627	Solyc08g	Expansin-like protei		SL2.40ch	AT5G59480.2		haloacid	chr5:239	313.948	157.185	100.663	222.119	78.7947	81.1267
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.450	Detected	-0.816	Detected	-1.133	0.081	GT	Sens	contig627	contig627	ER glycer	GGCTAA	contig627	Solyc07g	Solyc07g	ER glycer	GO:0008	GO:0008	contig627	Solyc07g	ER glycer	GO:0003	SL2.40ch	AT1G016	ATGPAT4	GPAT4 (	chr1:221	57657.2	45131.4	21568.5	30789.3	19908.2	30809.2
GT	Sense	Sense	0.415	Detected	-0.415	Detected	0.000	-3.877	Detected	-3.003	Detected	-3.440	0.029	GT	Sens	contig631	contig631	Pectate ly	CAGACC	contig631	Solyc09g	Solyc09g	Pectate ly	GO:0016	GO:0016	contig631	Solyc09g	Pectate ly	GO:0016	SL2.40ch	AT5G48900.1		pectate l	chr5:198	354.178	187.401	12.8594	15.7953	18.7013	34.1676
GT	Sense	Sense	0.169	Detected	-0.169	Detected	0.000	-1.762	Detected	-1.090	Detected	-1.426	0.063	GT	Sens	contig631	contig631	Major fac	AATTTT	contig631	Solyc08g	Solyc08g	Major facilitator superfamily d			contig631	Solyc08g	Major facilitator sup		SL2.40ch	AT4G27720.1		LOCATE	chr4:138	1108.61	824.693	331.781	465.609	300.568	477.677
GT	Sense	Sense	-0.007	Detected	0.007	Detected	0.000	-2.556	Detected	-1.644	Detected	-2.100	0.044	GT	Sens	contig632	contig632	Pyrimidin	AGGCAT	contig632	Solyc06g	Solyc06g	Pyrimidin	GO:0008	GO:0008	contig632	Solyc06g	Pyrimidin	GO:0008	SL2.40ch	AT5G59480.2		haloacid	chr5:239	1358.37	1290.71	420.792	465.656	240.057	450.46
GT	Sense	Sense	-0.093	Detected	0.093	Detected	0.000	-2.037	Detected	-1.849	Detected	-1.943	0.005	GT	Sens	contig636	contig636	Stig1 (Fra	TCGAGG	contig636	Solyc02g	Solyc02g	Stig1 (Fragment) (AHRD V1 *-*-			contig636	Solyc02g	Stig1 (Fragment) (AH		SL2.40ch	AT1G11925.1		Encodes	chr1:402	324.998	347.89	74.3522	104.397	87.3664	99.241
GT	Sense	Sense	-0.203	Detected	0.203	Detected	0.000	-0.966	Comprom	-1.297	Comprom	-1.131	0.050	GT	Sens	contig636	contig636	Cytochro	GGGACA	contig636	Solyc10g	Solyc10g	Cytochro	GO:0019	GO:0019	contig636	Solyc10g	Cytochro	GO:0019	SL2.40ch	AT3G256	CHUP1	CHUP1 (C	chr3:935	11.8104	14.7252	4.86554	10.0779	7.20012	5.70575
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.366	Detected	-1.147	Detected	-1.256	0.013	GT	Sens	contig640	contig640	Neutral in	TGCTAT	contig640	Solyc06g	Solyc06g	Neutral in	GO:0005	GO:0005	contig640	Solyc06g	Neutral in	GO:0005	SL2.40ch	AT1G355	CINV1	CINV1 (cy	chr1:131	3728.23	3078.58	875.231	1265.64	1402.01	1626.95
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	-1.375	Detected	-0.839	Detected	-1.107	0.054	GT	Sens	contig641	contig641	Unknown	AATATT	contig641	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig641	Solyc04g	Unknown Protein (A		SL2.40ch	AT2G300	ZIP6. ATZ	ZIP6: cat	chr2:128	2141.45	1984.31	558.473	568.807	847.3	1225.12
GT	Sense	Sense	-0.050	Detected	0.050	Detected	0.000	-1.302	Detected	-0.889	Detected	-1.095	0.036	GT	Sens	contig641	contig641	Yellow st	TTTGTG	contig641	Solyc02g	Solyc02g	Yellow st	GO:0015	GO:0015	contig641	Solyc02g	Yellow st	GO:0015	SL2.40ch	AT1G483	YSL8	YSL8 (YE	chr1:178	2646.43	2670.64	1234.08	1445.87	1149.94	1526.35
GT	Sense	Sense	0.129	Detected	-0.129	Detected	0.000	-2.812	Comprom	-3.232	Comprom	-3.022	0.007	GT	Sens	contig645	contig645	Plant-spe	TGCAGA	contig645	Solyc06g	Solyc06g	Plant-specific domain TIGR016			contig645	Solyc06g	Plant-specific doma		SL2.40ch	AT3G25240.1		unknown	chr3:919	61.0048	47.9796	4.55818	13.5551	8.21367	6.124
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.201	Detected	-1.118	Detected	-1.159	0.005	GT	Sens	contig645	contig645	Bifunctio	AGAGTT	contig645	Solyc09g	Solyc09g	Bifunctio	GO:0044	GO:0044	contig645	Solyc09g	Bifunctio	GO:0048	SL2.40ch	AT3G628	UXS2. AT	AUD1: UI	chr3:232	27077.8	23054.8	7181.08	9080.03	11593.3	12242.9
GT	Sense	Sense	-0.100	Detected	0.100	Detected	0.000	-1.710	Detected	-1.015	Detected	-1.362	0.064	GT	Sens	contig646	contig646	Beta-hex	TTGGCG	contig646	Solyc11g	Solyc11g	Beta-hex	GO:0005	GO:0005	contig646	Solyc11g	Beta-hex	GO:0016	SL2.40ch	AT1G655	HEXO3. A	HEXO3 (I	chr1:243	151.291	163.55	73.4556	57.2881	51.282	82.7574
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	-1.214	Detected	-0.960	Detected	-1.087	0.017	GT	Sens	contig646	contig646	Glucosylt	AGAGAT	contig646	Solyc02g	Solyc02g	Glucosylt	GO:0080	GO:0080	contig646	Solyc02g	Glucosylt	GO:0080	SL2.40ch	AT1G072	UGT71C4	UGT71C4	chr1:222	1682.59	1448.16	934.242	756.562	717.645	853.238
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	-2.053	Detected	-2.614	Detected	-2.334	0.014	GT	Sens	contig650	contig650	Chaperon	TGAGGA	contig650	Solyc09g	Solyc09g	Chaperon	GO:0004	GO:0004	contig650	Solyc09g	Chaperon	GO:0004	SL2.40ch	AT5G031	ATP58IPK	ATP58IP	chr5:750	6062.48	5616.28	1906.87	2784.7	1499.63	1013.08
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-0.862	Detected	-2.328	Detected	-1.595	0.164	GT	Sens	contig652	contig652	Acetyl co	GTATGT	contig652	Solyc07g	Solyc07g	Acetyl co	GO:0010	GO:0010	contig652	Solyc07g	Acetyl co	GO:0010	SL2.40ch	AT3G034	CHAT	CHAT (ac	chr3:828	7273.7	5908.16	3867.01	1408.77	3846.08	1388.33
GT	Sense	Sense	0.160	Detected	-0.160	Detected	0.000	-4.565	Comprom	-4.691	Comprom	-4.628	0.001	GT	Sens	contig655	contig655	Xylanase	GGAGAA	contig655	Solyc02g	Solyc02g	Xylanase	GO:0006	GO:0006	contig655	Solyc02g	Xylanase	GO:0006	SL2.40ch	AT5G60250.1		zinc fing	chr5:242	117.51	88.6098	15.9915	21.5457	4.59752	4.20104
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-2.508	Detected	-1.949	Detected	-2.228	0.016	GT	Sens	contig655	contig655	Leaf sene	AACTTA	contig655	Solyc02g	Solyc02g	Leaf senescence protein-like (			contig655	Solyc02g	Leaf senescence pr		SL2.40ch	AT3G28150.1		unknown	chr3:104	459.506	405.113	136.199	73.3496	80.9038	118.845
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	-0.963	Detected	-1.286	Detected	-1.124	0.023	GT	Sens	contig659	contig659	NHL repe	AGTTAT	contig659	Solyc03g	Solyc03g	NHL repeat-containing protein			contig659	Solyc03g	NHL repeat-containi		SL2.40ch	AT5G14890.1		NHL repe	chr5:481	2447.73	2111.68	842.564	1150.9	1243.63	991.42
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	-1.240	Detected	-1.012	Detected	-1.126	0.024	GT	Sens	contig660	contig660	Heteroge	GGACTT	contig660	Solyc12g	Solyc12g	Heteroge	GO:0000	GO:0000	contig660	Solyc12g	Heteroge	GO:0003	SL2.40ch	AT3G07810.2		heteroge	chr3:249	2179.16	1701.33	777.596	1090.66	869.569	1014.98
GT	Sense	Sense	0.636	Detected	-0.636	Detected	0.000	-1.315	Detected	-0.839	Detected	-1.077	0.253	GT	Sens	contig661	contig661	Acetyl es	GGGAAG	contig661	Solyc02g	Solyc02g	Acetyl es	GO:0016	GO:0016	contig661	Solyc02g	Acetyl es	GO:0016	SL2.40ch	AT3G256	CHUP1	CHUP1 (C	chr3:935	1453.67	566.744	988.67	489.971	388.931	539.387
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	-1.159	Detected	-1.040	Detected	-1.099	0.018	GT	Sens	contig662	contig662	Eukaryot	TAGAGA	contig662	Solyc02g	Solyc02g	Eukaryot	GO:0005	GO:0005	contig662	Solyc02g	Eukaryot	GO:0006	SL2.40ch	AT1G36730.1		eukaryot	chr1:138	304.77	237.132	93.653	107.701	128.39	139.024
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-1.572	Comprom	-2.570	Comprom	-2.071	0.055	GT	Sens	contig662	contig662	Unknown	TTGCTT	contig662	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig662	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G16220.1		octicosa	chr5:529	21.0058	17.3005	3.19055	8.46193	6.83875	3.41245
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-1.102	Comprom	-1.849	Comprom	-1.476	0.060	GT	Sens	contig664	contig664	Unknown	TCCATC	contig664	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig664	Solyc05g	Unknown Protein (A		SL2.40ch	AT3G54740.2		unknown	chr3:202	14.7801	12.6197	3.41412	3.1552	6.78346	4.03132
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-1.882	Detected	-1.020	Detected	-1.451	0.079	GT	Sens	contig665	contig665	Zinc-bind	TCTTGT	contig665	Solyc04g	Solyc04g	Zinc-bind	GO:0008	GO:0008	contig665	Solyc04g	Zinc-bind	GO:0008	SL2.40ch	AT2G01818.1		zinc ion b	chr2:353	1178.62	1177.94	480.522	446.917	340.881	617.858
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.391	Detected	-2.602	Detected	-1.996	0.081	GT	Sens	contig669	contig669	Os06g020	TAAAAG	contig669	Solyc01g	Solyc01g	Os06g0207500 protein (Fragm			contig669	Solyc01g	Os06g0207500 prot		SL2.40ch	AT5G64470.1		unknown	chr5:257	106.499	93.0582	29.1027	32.7282	40.4679	17.4395
GT	Sense	Sense	0.074	Detected	-0.074	Detected	0.000	-1.414	Detected	-1.031	Detected	-1.222	0.027	GT	Sens	contig672	contig672	Short-cha	AATGTG	contig672	Solyc01g	Solyc01g	Short-cha	GO:0008	GO:0008	contig672	Solyc01g	Short-cha	GO:0008	SL2.40ch	AT1G54870.1		binding /	chr1:204	28.3395	24.0704	7.25108	19.3239	10.4512	13.5915
GT	Sense	Sense	0.181	Detected	-0.181	Detected	0.000	-1.730	Detected	-1.324	Detected	-1.527	0.030	GT	Sens	contig672	contig672	Aspartic	ATTACT	contig672	Solyc01g	Solyc01g	Aspartic	GO:0006	GO:0006	contig672	Solyc01g	Aspartic	GO:0006	SL2.40ch	AT1G01300.1		aspartyl	chr1:117	66737.2	48870.8	15897.5	20360.3	18362.1	24252.7
GT	Sense	Sense	-0.002	Detected	0.002	Detected	0.000	-1.606	Detected	-1.609	Detected	-1.607	0.000	GT	Sens	contig680	contig680	Transcrip	ATGCAA	contig680	Solyc05g	Solyc05g	Transcrip	GO:0005	GO:0005	contig680	Solyc05g	Transcrip	GO:0003	SL2.40ch	AT4G16430.1		basic hel	chr4:926	3131.58	2956.72	740.338	811.203	1066.22	1060.49
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	-1.080	Detected	-0.933	Detected	-1.006	0.075	GT	Sens	contig681	contig681	ATP synt	AGGTAC	contig681	Solyc10g	Solyc10g	ATP synt	GO:0016	GO:0016	contig681	Solyc10g	ATP synt	GO:0016	SL2.40ch	ATCG001	ATPA	Encodes	chrC:993	2962.97	1884.75	1165.63	1154.73	1192.3	1316.18
GT	Sense	Sense	-0.191	Detected	0.191	Detected	0.000	-1.233	Detected	-0.802	Detected	-1.017	0.071	GT	Sens	contig681	contig681	Protein ki	GTTGCG	contig681	Solyc03g	Solyc03g	Protein ki	GO:0006	GO:0006	contig681	Solyc03g	Protein ki	GO:0006	SL2.40ch	AT5G58950.1		protein k	chr5:238	526.057	644.601	333.799	244.854	264.274	355.086
GT	Sense	Sense	0.726	Detected	-0.726	Detected	0.000	-1.862	Detected	-2.516	Detected	-2.189	0.111	GT	Sens	contig682	contig682	3-methyl-	GGAGAA	contig682	Solyc06g	Solyc06g	3-methyl-	GO:0008	GO:0008	contig682	Solyc06g	3-methyl-	GO:0003	SL2.40ch	AT5G09300.2		2-oxoiso	chr5:288	706.281	242.909	116.143	111.143	121.533	76.9997
GT	Sense	Sense	-0.210	Detected	0.210	Detected	0.000	-1.120	Detected	-1.511	Detected	-1.315	0.044	GT	Sens	contig684	contig684	Tobacco	CAGAAT	contig684	Solyc07g	Solyc07g	Tobacco rattle virus-induced r			contig684	Solyc07g	Tobacco rattle virus		SL2.40ch	AT1G735	PIN1. ATF	PIN1 (PIN	chr1:276	49.5855	62.4137	20.1892	26.9812	27.3004	20.7593
GT	Sense	Sense	0.215	Detected	-0.215	Detected	0.000	-1.725	Detected	-1.334	Detected	-1.529	0.034	GT	Sens	contig686	contig686	Chaperon	GAGTCT	contig686	Solyc05g	Solyc05g	Chaperon	GO:0031	GO:0031	contig686	Solyc05g	Chaperon	GO:0031	SL2.40ch	AT1G71000.1		heat sho	chr1:267	640.036	447.186	274.087	383.821	172.585	225.618
GT	Sense	Sense	-0.298	Detected	0.298	Detected	0.000	-1.139	Detected	-1.647	Detected	-1.393	0.071	GT	Sens	contig687	contig687	LL-diami	TTCCTG	contig687	Solyc11g	Solyc11g	LL-diami	GO:0030	GO:0030	contig687	Solyc11g	LL-diami	GO:0010	SL2.40ch	AT2G138	ALD1	ALD1 (AC	chr2:576	345.945	491.941	69.4613	91.236	199.744	140.036
GT	Sense	Sense	0.508	Detected	-0.508	Detected	0.000	-1.546	Comprom	-3.049	Comprom	-2.297	0.127	GT	Sens	contig687	contig687	Os05g027	TTTATG	contig687	Solyc02g	Solyc02g	Os05g0272200 protein (Fragm			contig687	Solyc02g	Os05g0272200 prot		SL2.40ch	AT1G17030.1		unknown	chr1:582	30.9724	14.413	5.57764	9.43476	7.71763	2.71404
GT	Sense	Sense	-0.187	Detected	0.187	Detected	0.000	-1.145	Detected	-0.999	Detected	-1.072	0.033	GT	Sens	contig687	contig687	Tyrosine	AGAAAA	contig687	Solyc07g	Solyc07g	Tyrosine	GO:0005	GO:0005	contig687	Solyc07g	Tyrosine	GO:0005	SL2.40ch	AT4G03960.1		tyrosine	chr4:188	3739.07	4556.28	1551.79	1447.27	1990.65	2196.05
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-1.509	Detected	-1.228	Detected	-1.368	0.011	GT	Sens	contig688	contig688	CONSTAN	CTATTG	contig688	Solyc12g	Solyc12g	CONSTAN	GO:0003	GO:0003	contig688	Solyc12g	CONSTAN	GO:0005	SL2.40ch	AT5G48250.1		zinc fing	chr5:195	396.107	358.17	155.907	176.165	141.175	170.961
GT	Sense	Sense	0.327	Detected	-0.327	Detected	0.000	-2.118	Detected	-1.398	Detected	-1.758	0.069	GT	Sens	contig689	contig689	Speckle-t	TCCTTT	contig689	Solyc02g	Solyc02g	Speckle-t	GO:0005	GO:0005	contig689	Solyc02g	Speckle-t	GO:0030	SL2.40ch	AT5G674	BT4	BT4 (BTE	chr5:269	3679.13	2198.93	575.41	1088.09	698.585	1147.27
GT	Sense	Sense	0.199	Detected	-0.199	Detected	0.000	-1.684	Detected	-1.426	Detected	-1.555	0.023	GT	Sens	contig692	contig692	Lipase-lik	CCTACT	contig692	Solyc08g	Solyc08g	Lipase-lik	GO:0047	GO:0047	contig692	Solyc08g	Lipase-lik	GO:0047	SL2.40ch	AT1G06250.1		lipase cla	chr1:191	156.44	111.648	64.2111	88.2187	43.8642	52.2831
GT	Sense	Sense	-0.128	Detected	0.128	Detected	0.000	-1.403	Detected	-1.291	Detected	-1.347	0.011	GT	Sens	contig692	contig692	Receptor	AAGGAC	contig692	Solyc06g	Solyc06g	Receptor	GO:0005	GO:0005	contig692	Solyc06g	Receptor	GO:0005	SL2.40ch	AT1G24650.1		leucine-r	chr1:873	383.213	430.304	142.682	210.774	163.796	176.496
GT	Sense	Sense	0.178	Detected	-0.178	Detected	0.000	-1.417	Detected	-1.466	Detected	-1.441	0.015	GT	Sens	contig696	contig696	Ran GTPa	AATGCT	contig696	Solyc06g	Solyc06g	Ran GTPa	GO:0008	GO:0008	contig696	Solyc06g	Ran GTPa	GO:0008	SL2.40ch	AT5G585	RANBP1	RANBP1	chr5:236	4428.92	3257.88	1740.78	2142.17	1517.37	1462.03
GT	Sense	Sense	0.152	Detected	-0.152	Detected	0.000	-1.289	Detected	-1.078	Detected	-1.183	0.024	GT	Sens	contig696	contig696	Glycosyl	AGTATT	contig696	Solyc07g	Solyc07g	Glycosyl	GO:0016	GO:0016	contig696	Solyc07g	Glycosyl	GO:0016	SL2.40ch	AT1G12990.1		glycosyl	chr1:443	288.313	219.835	86.2868	94.661	109.874	126.801
GT	Sense	Sense	0.311	Detected	-0.311	Detected	0.000	-2.232	Detected	-1.579	Detected	-1.906	0.052	GT	Sens	contig697	contig697	UPA23 (A	AACTAT	contig697	Solyc11g	Solyc11g	UPA23 (AHRD V1 ***- C8YZB5			contig697	Solyc11g	UPA23 (AHRD V1 ***		SL2.40ch	AT5G55830.1		lectin pro	chr5:225	6655.43	4071.4	1109.6	2746.32	1181.63	1852.14
GT	Sense	Sense	-0.060	Detected	0.060	Detected	0.000	-1.239	Detected	-1.496	Detected	-1.367	0.011	GT	Sens	contig698	contig698	Multidrug	ATTTAC	contig698	Solyc06g	Solyc06g	Multidrug	GO:0016	GO:0016	contig698	Solyc06g	Multidrug	GO:0005	SL2.40ch	AT4G25640.1		MATE eff	chr4:130	2203.05	2254.06	694.038	1157.9	1006.91	839.947
GT	Sense	Sense	0.174	Detected	-0.174	Detected	0.000	-1.282	Detected	-1.416	Detected	-1.349	0.019	GT	Sens	contig699	contig699	Calmodul	CTCGGC	contig699	Solyc10g	Solyc10g	Calmodul	GO:0005	GO:0005	contig699	Solyc10g	Calmodul	GO:0005	SL2.40ch	AT2G41410.1		calmodu	chr2:172	14565.3	10760.3	4383.61	5351.62	5489.73	4989.54
GT	Sense	Sense	-0.070	Detected	0.070	Detected	0.000	-0.884	Detected	-2.954	Comprom	-1.919	0.206	GT	Sens	contig699	contig699	Unknown	ACATCT	contig699	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig699	Solyc06g	Unknown Protein (A		SL2.40ch	AT1G35340.1		ATP-dep	chr1:129	25.9942	26.9529	10.102	7.69072	15.2945	3.63068
GT	Sense	Sense	0.632	Detected	-0.632	Detected	0.000	-2.646	Detected	-2.417	Detected	-2.531	0.059	GT	Sens	contig700	contig700	1-aminoc	CAGCTC	contig700	Solyc12g	Solyc12g	1-aminoc	GO:0016	GO:0016	contig700	Solyc12g	1-aminoc	GO:0016	SL2.40ch	AT1G623	ACO2. AT	ACO2 (AC	chr1:230	35935.9	14078.4	3622.67	3411.86	3831.35	4478.83
GT	Sense	Sense	0.212	Detected	-0.212	Detected	0.000	-2.082	Detected	-1.062	Detected	-1.572	0.105	GT	Sens	contig702	contig702	Oxidation	TTTCCA	contig702	Solyc09g	Solyc09g	Oxidation resistance 1-like pro			contig702	Solyc09g	Oxidation resistanc		SL2.40ch	AT2G05590.2		FUNCTIO	chr2:206	1170.72	820.726	248.765	392.956	246.9	499.204
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	-1.800	Detected	-0.978	Detected	-1.389	0.078	GT	Sens	contig703	contig703	Unknown	CCCTGT	contig703	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)%:			contig703	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G44940.1		unknown	chr3:164	7094.21	6531.17	3104.45	3716.52	2084.75	3673.17
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	-1.192	Detected	-0.911	Detected	-1.051	0.021	GT	Sens	contig703	contig703	GDSL est	ATAGGA	contig703	Solyc01g	Solyc01g	GDSL est	GO:0006	GO:0006	contig703	Solyc01g	GDSL est	GO:0004	SL2.40ch	AT4G21880.1		FUNCTIO	chr4:116	8066.88	6948.81	4037.82	5535.42	3495.75	4231.92
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	-2.381	Detected	-1.464	Detected	-1.923	0.057	GT	Sens	contig704	contig704	Glycosyl	TCCAAA	contig704	Solyc06g	Solyc06g	Glycosyl transferase family 8 (			contig704	Solyc06g	Glycosyl transferas		SL2.40ch	AT1G64980.1		unknown	chr1:241	4848.28	3728.84	1022.75	1690.03	870.151	1638.83
GT	Sense	Sense	0.266	Detected	-0.266	Detected	0.000	-1.280	Detected	-1.264	Detected	-1.272	0.041	GT	Sens	contig704	contig704	Os03g027	TTGTTG	contig704	Solyc10g	Solyc10g	Os03g0270500 protein (Fragm			contig704	Solyc10g	Avr9/Cf-9 rapidly eli		SL2.40ch	AT5G24220.1		lipase cla	chr5:822	342.589	222.895	71.8126	147.102	121.321	122.371
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.641	Detected	-1.433	Detected	-1.537	0.005	GT	Sens	contig705	contig705	Expansin	AAATCA	contig705	Solyc01g	Solyc01g	Expansin	GO:0005	GO:0005	contig705	Solyc01g	Expansin	GO:0005	SL2.40ch	AT3G459	ATEXLA1	ATEXLA1	chr3:168	33671.5	32754.3	16005.5	21207.1	11352.4	13074.7
GT	Sense	Sense	0.065	Detected	-0.065	Detected	0.000	-2.759	Comprom	-3.033	Comprom	-2.896	0.003	GT	Sens	contig705	contig705	Ethylene	AACTCT	contig705	Solyc01g	Solyc01g	Ethylene	GO:0006	GO:0006	contig705	Solyc01g	Ethylene	GO:0003	SL2.40ch	AT2G448	ATERF13	ERF13 (E	chr2:184	20.0283	17.2118	3.55492	2.1621	2.92464	2.41182
GT	Sense	Sense	0.733	Detected	-0.733	Detected	0.000	-2.308	Detected	-2.815	Detected	-2.561	0.081	GT	Sens	contig709	contig709	Cytochro	ATTGGC	contig709	Solyc04g	Solyc04g	Cytochro	GO:0019	GO:0019	contig709	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT4G373	CYP81D5	CYP81D5	chr4:175	166.487	56.7173	4.66358	10.8763	20.9255	14.6819
GT	Sense	Sense	-0.063	Detected	0.063	Detected	0.000	-2.176	Comprom	-2.963	Comprom	-2.569	0.023	GT	Sens	contig711	contig711	SAUR fam	AACAGG	contig711	Solyc03g	Solyc03g	SAUR fam	GO:0005	GO:0005	contig711	Solyc03g	SAUR fam	GO:0005	SL2.40ch	AT4G00880.1		auxin-res	chr4:366	15.9917	16.422	2.91005	3.44869	3.8246	2.20944
GT	Sense	Sense	0.009	Detected	-0.009	Detected	0.000	-1.497	Detected	-1.257	Detected	-1.377	0.008	GT	Sens	contig714	contig714	3-oxoacy	TGTTTC	contig714	Solyc08g	Solyc08g	3-oxoacy	GO:0005	GO:0005	contig714	Solyc08g	3-oxoacy	GO:0005	SL2.40ch	AT5G462	KAS I	KAS I (3-I	chr5:187	671.802	624.375	224.823	221.417	244.65	288.082
GT	Sense	Sense	-0.034	Detected	0.034	Detected	0.000	-0.967	Detected	-1.151	Detected	-1.059	0.008	GT	Sens	contig716	contig716	POT fami	AAGGAA	contig716	Solyc06g	Solyc06g	POT family domain containing			contig716	Solyc06g	POT family domain		SL2.40ch	AT3G31402.1		FUNCTIO	chr3:127	3499.99	3451.22	1432.69	1720.22	1895.67	1664.09
GT	Sense	Sense	-0.076	Detected	0.076	Detected	0.000	-1.134	Detected	-0.955	Detected	-1.044	0.012	GT	Sens	contig718	contig718	Pseudo r	TGACAA	contig718	Solyc06g	Solyc06g	Pseudo r	GO:0010	GO:0010	contig718	Solyc06g	Pseudo r	GO:0030	SL2.40ch	AT5G613	TOC1. AP	TOC1 (TI	chr5:246	925.833	967.979	332.014	351.456	459.993	519.265
GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-2.477	Detected	-2.030	Detected	-2.254	0.014	GT	Sens	contig721	contig721	Phospho	TCTGAA	contig721	Solyc04g	Solyc04g	Phospho	GO:0042	GO:0042	contig721	Solyc04g	Phospho	GO:0004	SL2.40ch	AT4G378	PCK1. PE	PCK1 (PI	chr4:178	14886.1	11312.5	2981.74	4267.59	2486.13	3377.54
GT	Sense	Sense	0.296	Detected	-0.296	Detected	0.000	-1.518	Detected	-1.669	Detected	-1.593	0.035	GT	Sens	contig722	contig722	Cathepsi	ACAAGT	contig722	Solyc02g	Solyc02g	Cathepsi	GO:0004	GO:0004	contig722	Solyc02g	Cathepsi	GO:0004	SL2.40ch	AT3G49340.1		cysteine	chr3:182	1120.75	699.827	613.17	591.531	329.787	296.099
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	-1.325	Comprom	-1.695	Comprom	-1.510	0.031	GT	Sens	contig723	contig723	Unknown	TAGAGG	contig723	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig723	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G20160.1		LOCATE	chr4:108	14.7446	10.4759	2.66946	3.15026	5.29006	4.08237
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-2.559	Detected	-1.346	Detected	-1.952	0.086	GT	Sens	contig724	contig724	WRKY tra	CTACAA	contig724	Solyc08g	Solyc08g	WRKY tra	GO:0003	GO:0003	contig724	Solyc08g	WRKY tra	GO:0003	SL2.40ch	AT4G238	WRKY53.	WRKY53	chr4:123	2797.71	2327.05	655.305	1105.71	461.882	1067.15
GT	Sense	Sense	0.526	Detected	-0.526	Detected	0.000	-0.971	Detected	-1.607	Detected	-1.289	0.171	GT	Sens	contig724	contig724	Non-spec	AGCATA	contig724	Solyc06g	Solyc06g	Non-spec	GO:0006	GO:0006	contig724	Solyc06g	Non-spec	GO:0006	SL2.40ch	AT5G49610.1		F-box far	chr5:201	143.319	65.0656	46.2708	43.5215	52.5414	33.7157
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	-1.397	Detected	-0.880	Detected	-1.139	0.049	GT	Sens	contig724	contig724	Receptor-	TTTAGG	contig724	Solyc10g	Solyc10g	Receptor-	GO:0006	GO:0006	contig724	Solyc10g	Receptor-	GO:0006	SL2.40ch	AT5G59010.1		protein k	chr5:238	1310.72	1173.02	509.011	748.756	502.054	716.365
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	-1.576	Detected	-1.164	Detected	-1.370	0.022	GT	Sens	contig726	contig726	Acyltrans	TGATCA	contig726	Solyc02g	Solyc02g	Acyltrans	GO:0016	GO:0016	contig726	Solyc02g	Acyltrans	GO:0016	SL2.40ch	AT1G03390.1		transfera	chr1:841	392.864	356.097	231.737	301.05	133.784	177.519
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.134	Detected	-1.396	Detected	-1.265	0.012	GT	Sens	contig727	contig727	Beige/BE	CTTCAC	contig727	Solyc09g	Solyc09g	Beige/BE	GO:0005	GO:0005	contig727	Solyc09g	Beige/BE	GO:0005	SL2.40ch	AT1G03060.1		WD-40 re	chr1:712	824.279	728.871	290.98	399.196	376.723	313.192
GT	Sense	Sense	0.060	Detected	-0.060	Detected	0.000	-1.297	Detected	-1.427	Detected	-1.362	0.004	GT	Sens	contig729	contig729	Calmodul	TCCAAA	contig729	Solyc03g	Solyc03g	Calmodul	GO:0005	GO:0005	contig729	Solyc03g	Calmodul	GO:0005	SL2.40ch	AT1G73805.1		calmodu	chr1:277	814.588	705.007	177.152	244.318	328.797	299.652
GT	Sense	Sense	0.039	Detected	-0.039	Detected	0.000	-1.028	Detected	-1.047	Detected	-1.037	0.001	GT	Sens	contig734	contig734	Os10g04	ATGAAC	contig734	Solyc12g	Solyc12g	Os10g0422600 protein (Fragm			contig734	Solyc12g	Os10g0422600 prot		SL2.40ch	AT5G20700.1		senesce	chr5:700	1376.51	1227.78	550.85	985.315	680.06	668.829
GT	Sense	Sense	0.075	Detected	-0.075	Detected	0.000	-1.107	Detected	-1.036	Detected	-1.072	0.006	GT	Sens	contig738	contig738	Receptor	AGGTTA	contig738	Solyc09g	Solyc09g	Receptor	GO:0004	GO:0004	contig738	Solyc09g	Pto-like. S	GO:0004	SL2.40ch	AT3G515	FER	FER (FEF	chr3:191	14669.5	12438.7	5333.8	7458.62	6686.56	7003.23
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	-3.415	Detected	-2.608	Detected	-3.012	0.020	GT	Sens	contig740	contig740	HMG type	GCAGAT	contig740	Solyc06g	Solyc06g	HMG type	GO:0003	GO:0003	contig740	Solyc06g	HMG type	GO:0003	SL2.40ch	AT5G54550.1		unknown	chr5:221	1001.73	769.43	80.0053	27.7611	87.7708	153.091
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	-1.932	Detected	-1.633	Detected	-1.783	0.032	GT	Sens	contig743	contig743	Zinc finge	ACGATG	contig743	Solyc05g	Solyc05g	Zinc finge	GO:0003	GO:0003	contig743	Solyc05g	Zinc finge	GO:0003	SL2.40ch	AT5G03510.1		zinc fing	chr5:880	747.08	469.593	197.02	185.794	165.474	203.005
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	-1.493	Detected	-0.869	Detected	-1.181	0.074	GT	Sens	contig743	contig743	GDP-man	TATATC	contig743	Solyc03g	Solyc03g	GDP-mannose transporter (AH			contig743	Solyc03g	GDP-mannose trans		SL2.40ch	AT1G76340.1		integral r	chr1:286	159.505	124.096	37.4467	50.8434	53.3042	81.8871
GT	Sense	Sense	0.198	Detected	-0.198	Detected	0.000	-1.738	Detected	-1.402	Detected	-1.570	0.026	GT	Sens	contig744	contig744	Zinc-bind	AGAGGA	contig744	Solyc10g	Solyc10g	Zinc-binding family protein (AH			contig744	Solyc10g	Zinc-binding family		SL2.40ch	AT2G27930.1		binding	chr2:118	358.658	256.525	67.6202	130.351	96.9907	122.075
GT	Sense	Sense	0.399	Detected	-0.399	Detected	0.000	-1.507	Detected	-1.454	Detected	-1.481	0.066	GT	Sens	contig750	contig750	U-box do	GGCAAG	contig750	Solyc11g	Solyc11g	U-box do	GO:0005	GO:0005	contig750	Solyc11g	U-box do	GO:0005	SL2.40ch	AT3G524	PUB22	PUB22 (F	chr3:194	43.5242	23.559	6.53055	11.2454	12.0121	12.4278
GT	Sense	Sense	0.229	Detected	-0.229	Detected	0.000	-4.357	Detected	-3.456	Detected	-3.906	0.016	GT	Sens	contig751	contig751	Inositol 2	CATGAT	contig751	Solyc08g	Solyc08g	Inositol 2	GO:0008	GO:0008	contig751	Solyc08g	Inositol 2-	GO:0008	SL2.40ch	AT4G17370.1		oxidored	chr4:970	1738.57	1190.61	136.079	141.448	74.876	139.426
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	-1.495	Detected	-1.279	Detected	-1.387	0.009	GT	Sens	contig752	contig752	Bifunctio	ACAGTG	contig752	Solyc10g	Solyc10g	Bifunctio	GO:0044	GO:0044	contig752	Solyc10g	Bifunctio	GO:0044	SL2.40ch	AT3G535	UXS1. AT	UXS1 (UI	chr3:198	933.047	783.452	277.621	310.36	323.526	374.661
GT	Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-2.574	Detected	-1.816	Detected	-2.195	0.029	GT	Sens	contig753	contig753	Polyprote	TTGGTG	contig753	Solyc05g	Solyc05g	Polyprote	GO:0008	GO:0008	contig753	Solyc05g	Polyprote	GO:0008	SL2.40ch	AT5G40700.3		unknown	chr5:162	84.8381	81.318	21.7078	15.2108	14.8765	25.0812
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-1.235	Detected	-1.260	Detected	-1.248	0.004	GT	Sens	contig756	contig756	Zinc finge	ACACGA	contig756	Solyc02g	Solyc02g	Zinc finger CCCH domain-cont			contig756	Solyc02g	Zinc finger CCCH do		SL2.40ch	AT3G51120.1		DNA bind	chr3:189	2562.11	2162.61	576.278	896.773	1066.32	1045.02
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-3.119	Comprom	-3.484	Comprom	-3.301	0.003	GT	Sens	contig756	contig756	Expansin	GTTGAA	contig756	Solyc12g	Solyc12g	Expansin	GO:0005	GO:0005	contig756	Solyc12g	Expansin	GO:0005	SL2.40ch	AT1G267	ATEXPA1	ATEXPA1	chr1:925	39.5848	35.5703	4.1135	4.32563	4.60714	3.56639
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-1.269	Detected	-1.085	Detected	-1.177	0.015	GT	Sens	contig759	contig759	Heteroge	TAGTGG	contig759	Solyc12g	Solyc12g	Heteroge	GO:0003	GO:0003	contig759	Solyc12g	Heteroge	GO:0003	SL2.40ch	AT3G07810.2		heteroge	chr3:249	2625.05	2111.63	904.035	1221.52	1041.67	1179.61
GT	Sense	Sense	0.254	Detected	-0.254	Detected	0.000	-1.132	Detected	-1.172	Detected	-1.152	0.045	GT	Sens	contig767	contig767	Fasciclin-	AAGTTT	contig767	Solyc12g	Solyc12g	Fasciclin-like arabinogalactan			contig767	Solyc12g	Fasciclin-like arabin		SL2.40ch	AT5G65170.1		VQ motif-	chr5:260	346.732	229.559	78.7146	121.468	137.283	133.141
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	-1.781	Detected	-1.982	Detected	-1.882	0.005	GT	Sens	contig767	contig767	Unknown	TTGCTT	contig767	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig767	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G185	PUCHI	PUCHI: D	chr5:616	89.7795	94.1123	22.2599	65.4625	28.5145	24.7395
GT	Sense	Sense	0.120	Detected	-0.120	Detected	0.000	-2.889	Detected	-2.027	Detected	-2.458	0.032	GT	Sens	contig770	contig770	Unknown	TTGATT	contig770	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig770	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G65207.1		unknown	chr5:260	76865.1	61234.4	12640	22773.5	9876.41	17894.2
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-2.348	Detected	-2.255	Detected	-2.302	0.000	GT	Sens	contig771	contig771	Hydrolas	TCAATG	contig771	Solyc02g	Solyc02g	Hydrolas	GO:0016	GO:0016	contig771	Solyc02g	Hydrolas	GO:0016	SL2.40ch	AT2G47560.1		zinc fing	chr2:195	1568.39	1465.24	414.481	381.462	317.456	337.711
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.950	Detected	-1.333	Detected	-1.641	0.035	GT	Sens	contig771	contig771	MLO-like	TCAATT	contig771	Solyc00g	Solyc00g	MLO-like	GO:0016	GO:0016	contig771	Solyc00g	MLO-like	GO:0016	SL2.40ch	AT2G174	MLO8. AT	MLO8 (M	chr2:759	936.57	797.417	246.884	232.738	238.54	364.721
GT	Sense	Sense	-0.038	Detected	0.038	Detected	0.000	-1.337	Detected	-1.197	Detected	-1.267	0.004	GT	Sens	contig772	contig772	TMV resp	AGGACT	contig772	Solyc04g	Solyc04g	TMV response-related protein			contig772	Solyc04g	TMV response-relat		SL2.40ch	AT1G56550.1		UDP-xylo	chr1:211	3426.23	3398.32	1291.61	1994.64	1440.67	1582.22
GT	Sense	Sense	0.444	Detected	-0.444	Detected	0.000	-2.715	Detected	-3.076	Detected	-2.896	0.026	GT	Sens	contig772	contig772	AAA-ATP	CTCGAA	contig772	Solyc12g	Solyc12g	AAA-ATP	GO:0017	GO:0017	contig772	Solyc12g	AAA-ATP	GO:0005	SL2.40ch	AT5G57480.1		AAA-type	chr5:232	265.279	134.959	22.6644	28.2278	30.7253	23.8576
GT	Sense	Sense	0.002	Detected	-0.002	Detected	0.000	-1.285	Detected	-1.022	Detected	-1.154	0.013	GT	Sens	contig773	contig773	BZIP tran	GCTTAG	contig773	Solyc01g	Solyc01g	BZIP tran	GO:0006	GO:0006	contig773	Solyc01g	BZIP tran	GO:0003	SL2.40ch	AT2G21230.1		bZIP fam	chr2:909	16985.3	15932.7	5744.95	8634.08	7196.76	8614.18
GT	Sense	Sense	-0.237	Detected	0.237	Detected	0.000	-1.151	Detected	-1.231	Detected	-1.191	0.038	GT	Sens	contig774	contig774	CONSTAN	AGTTTC	contig774	Solyc07g	Solyc07g	CONSTAN	GO:0003	GO:0003	contig774	Solyc07g	CONSTAN	GO:0005	SL2.40ch	AT5G48250.1		zinc fing	chr5:195	1100.16	1438.14	529.484	607.421	603.902	569.734
GT	Sense	Sense	-0.659	Detected	0.659	Detected	0.000	-1.981	Comprom	-2.374	Comprom	-2.177	0.087	GT	Sens	contig776	contig776	Zinc ion b	ACTTAC	contig776	Solyc01g	Solyc01g	Zinc ion binding protein (AHRD			contig776	Solyc01g	Zinc ion binding pro		SL2.40ch	AT5G36670.1		PHD fing	chr5:144	12.6236	29.6141	10.2892	2.09151	5.22434	3.96563
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-1.070	Detected	-1.067	Detected	-1.069	0.021	GT	Sens	contig777	contig777	MYB tran	GCTCTA	contig777	Solyc05g	Solyc05g	MYB tran	GO:0003	GO:0003	contig777	Solyc05g	MYB tran	GO:0003	SL2.40ch	AT1G480	MYB112.	MYB112	chr1:177	13323.5	10074	4209.83	5607.8	5883.97	5879.81
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	-1.992	Detected	-1.967	Detected	-1.980	0.005	GT	Sens	contig777	contig777	Glutamat	AGAAAA	contig777	Solyc03g	Solyc03g	Glutamat	GO:0005	GO:0005	contig777	Solyc03g	Glutamat	GO:0005	SL2.40ch	AT5G534	GLT1	GLT1: gl	chr5:217	3476.15	2716.29	626.221	965.93	823.685	835.588
GT	Sense	Sense	0.200	Detected	-0.200	Detected	0.000	-3.336	Detected	-2.754	Detected	-3.045	0.013	GT	Sens	contig781	contig781	Pectinest	CTCTGA	contig781	Solyc11g	Solyc11g	Pectinest	GO:0030	GO:0030	contig781	Solyc11g	Pectinest	GO:0030	SL2.40ch	AT5G62360.1		invertase	chr5:250	22912.7	16333.3	4698.84	3407.46	2043.3	3049.23
GT	Sense	Sense	0.514	Detected	-0.514	Detected	0.000	-2.326	Comprom	-1.389	Comprom	-1.857	0.116	GT	Sens	contig782	contig782	Glutathio	TTGTGG	contig782	Solyc07g	Solyc07g	Glutathio	GO:0004	GO:0004	contig782	Solyc07g	Glutathio	GO:0004	SL2.40ch	AT1G17180.1				33.7909	15.5839	6.78155	10.8429	4.88161	9.31803
GT	Sense	Sense	0.361	Detected	-0.361	Detected	0.000	-2.821	Comprom	-1.688	Comprom	-2.255	0.078	GT	Sens	contig786	contig786	Peroxida	AATACA	contig786	Solyc05g	Solyc05g	Peroxida	GO:0005	GO:0005	contig786	Solyc05g	Peroxida	GO:0004	SL2.40ch	AT2G41480.1		electron	chr2:172	38.9909	22.2528	11.0481	7.32121	4.44447	9.71809
GT	Sense	Sense	0.189	Detected	-0.189	Detected	0.000	-3.451	Detected	-1.344	Detected	-2.397	0.155	GT	Sens	contig796	contig796	Peroxida	TAGTGG	contig796	Solyc11g	Solyc11g	Peroxida	GO:0055	GO:0055	contig796	Solyc11g	Peroxida	GO:0055	SL2.40ch	AT2G41480.1		electron	chr2:172	2976.25	2153.9	384.372	889.987	246.904	1060.73
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-1.011	Detected	-1.235	Detected	-1.123	0.028	GT	Sens	contig797	contig797	Oleosin (	TCAAAC	contig797	Solyc12g	Solyc12g	Oleosin (	GO:0016	GO:0016	contig797	Solyc12g	Oleosin (A	GO:0016	SL2.40ch	AT2G228	AtGRF1	AtGRF1 (	chr2:972	67.3439	50.9001	12.7117	23.5962	30.9746	26.4484
GT	Sense	Sense	0.225	Detected	-0.225	Detected	0.000	-3.833	Detected	-3.824	Detected	-3.829	0.003	GT	Sens	contig799	contig799	RING fing	GTATGT	contig799	Solyc01g	Solyc01g	RING fing	GO:0008	GO:0008	contig799	Solyc01g	RING fing	GO:0008	SL2.40ch	AT5G57540.1		xylogluca	chr5:233	775.458	534.175	88.897	72.734	48.1688	48.3023
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-1.210	Detected	-0.851	Detected	-1.030	0.030	GT	Sens	contig801	contig801	Non-spec	GGTTTA	contig801	Solyc11g	Solyc11g	Non-specific lipid-transfer prot			contig801	Solyc11g	Non-specific lipid-tra		SL2.40ch	AT4G17210.1		myosin h	chr4:965	108784	98374.4	50145.9	67695.8	47687.2	60989.8
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	-0.975	Detected	-1.055	Detected	-1.015	0.002	GT	Sens	contig803	contig803	Cytochro	ATTGGC	contig803	Solyc04g	Solyc04g	Cytochro	GO:0019	GO:0019	contig803	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT3G287	CYP81D1	CYP81D1	chr3:107	4846.68	4670.93	2283.7	2380.6	2581.58	2434.71
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	-3.403	Detected	-1.982	Detected	-2.692	0.065	GT	Sens	contig804	contig804	Expansin	CAATCA	contig804	Solyc04g	Solyc04g	Expansin	GO:0009	GO:0009	contig804	Solyc04g	Expansin	GO:0005	SL2.40ch	AT1G201	ATEXPA1	ATEXPA1	chr1:699	9022.93	7108.2	1992.01	2496.07	807.259	2155.89
GT	Sense	Sense	0.231	Detected	-0.231	Detected	0.000	-2.044	Detected	-1.359	Detected	-1.701	0.054	GT	Sens	contig804	contig804	Progeste	TATGTT	contig804	Solyc01g	Solyc01g	Progeste	GO:0008	GO:0008	contig804	Solyc01g	Progeste	GO:0008	SL2.40ch	AT5G44010.1		unknown	chr5:177	4949.19	3379.68	1093.3	1598.01	1057.86	1695.19
GT	Sense	Sense	0.355	Detected	-0.355	Detected	0.000	-1.619	Detected	-1.769	Detected	-1.694	0.043	GT	Sens	contig805	contig805	Calmodul	CGATGG	contig805	Solyc03g	Solyc03g	Calmodul	GO:0005	GO:0005	contig805	Solyc03g	Calmodul	GO:0005	SL2.40ch	AT5G58000.1		LOCATE	chr5:234	52.5308	30.2243	11.4825	18.1411	13.8302	12.4327
GT	Sense	Sense	0.421	Detected	-0.421	Detected	0.000	-2.066	Detected	-1.660	Detected	-1.863	0.057	GT	Sens	contig806	contig806	Unknown	TAAGAG	contig806	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig806	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G644	AtFAAH	AtFAAH (	chr5:257	247.596	130.006	37.831	49.0415	45.6819	60.3463
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-2.084	Detected	-2.192	Detected	-2.138	0.001	GT	Sens	contig807	contig807	Xylogluca	AAGTTA	contig807	Solyc05g	Solyc05g	Xylogluca	GO:0005	GO:0005	contig807	Solyc05g	Xylogluca	GO:0016	SL2.40ch	AT2G018	EXGT-A3	EXGT-A3	chr2:385	1774.4	1604.91	596.701	772.344	424.34	392.712
GT	Sense	Sense	0.112	Detected	-0.112	Detected	0.000	-2.286	Comprom	-2.681	Comprom	-2.483	0.008	GT	Sens	contig807	contig807	Rhomboi	ACTATT	contig807	Solyc06g	Solyc06g	Rhomboi	GO:0004	GO:0004	contig807	Solyc06g	Rhomboi	GO:0004	SL2.40ch	AT1G52580.1				24.4783	19.7144	6.60568	15.1974	4.8047	3.6425
GT	Sense	Sense	0.109	Detected	-0.109	Detected	0.000	-1.202	Detected	-0.895	Detected	-1.049	0.031	GT	Sens	contig807	contig807	Glycosylt	TGTGTT	contig807	Solyc03g	Solyc03g	Glycosylt	GO:0016	GO:0016	contig807	Solyc03g	Glycosylt	GO:0016	SL2.40ch	AT1G185	GAUT11	GAUT11	chr1:639	2038.52	1649.26	818.284	980.89	849.913	1048.21
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.292	Detected	-1.091	Detected	-1.191	0.007	GT	Sens	contig808	contig808	Unknown	TTTTGA	contig808	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig808	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G21580.1		cobalt io	chr3:760	2320.94	2139.22	1168.59	826.337	970.711	1112.36
GT	Sense	Sense	-0.023	Detected	0.023	Detected	0.000	-2.480	Detected	-2.267	Detected	-2.373	0.002	GT	Sens	contig809	contig809	Laccase	TTCAAA	contig809	Solyc05g	Solyc05g	Laccase	GO:0048	GO:0048	contig809	Solyc05g	Laccase	GO:0004	SL2.40ch	AT2G403	LAC5	LAC5 (la	chr2:168	75.4334	73.2872	12.1809	11.2019	14.2161	16.4215
GT	Sense	Sense	0.074	Detected	-0.074	Detected	0.000	-1.781	Detected	-1.487	Detected	-1.634	0.010	GT	Sens	contig809	contig809	Unknown	TTTTGA	contig809	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig809	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G34930.1		disease	chr2:147	4264.91	3622.69	1365.7	1275.46	1219.34	1490.95
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	-0.924	Detected	-1.079	Detected	-1.001	0.016	GT	Sens	contig810	contig810	CTV.22 (	TCCTTC	contig810	Solyc04g	Solyc04g	CTV.22 (AHRD V1 *-*- O8H6O7			contig810	Solyc04g	CTV.22 (AHRD V1 *-		SL2.40ch	AT3G561	EIF3C. AT	EIF3C (E	chr3:208	138.887	150.901	40.7102	54.6912	81.3888	72.8627
GT	Sense	Sense	0.007	Detected	-0.007	Detected	0.000	-1.819	Detected	-1.371	Detected	-1.595	0.019	GT	Sens	contig810	contig810	Transcrip	GTCGAG	contig810	Solyc12g	Solyc12g	Transcrip	GO:0005	GO:0005	contig810	Solyc12g	Transcrip	GO:0005	SL2.40ch	AT2G24260.1		basic hel	chr2:103	76.1987	70.9944	14.3564	20.8649	22.2344	30.2253
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	-1.347	Detected	-1.441	Detected	-1.394	0.003	GT	Sens	contig811	contig811	Dehydrin	TTTCTA	contig811	Solyc04g	Solyc04g	Dehydrin	GO:0009	GO:0009	contig811	Solyc04g	Dehydrin	GO:0009	SL2.40ch	AT1G204	LTI29. LT	ERD10 (E	chr1:708	16776.1	14392.5	5627.97	7326.47	6514.21	6083.55
GT	Sense	Sense	-0.093	Detected	0.093	Detected	0.000	-1.226	Detected	-0.998	Detected	-1.112	0.017	GT	Sens	contig816	contig816	WD-repea	GTAATT	contig816	Solyc03g	Solyc03g	WD-repeat protein (AHRD V1 **			contig816	Solyc03g	WD-repeat protein (		SL2.40ch	AT5G07590.1		WD-40 re	chr5:240	226.936	242.84	83.2561	116.548	107.016	124.944
GT	Sense	Sense	0.232	Detected	-0.232	Detected	0.000	-1.549	Detected	-1.394	Detected	-1.471	0.026	GT	Sens	contig818	contig818	Exostosi	GTAAGG	contig818	Solyc10g	Solyc10g	Exostosi	GO:0016	GO:0016	contig818	Solyc10g	Exostosi	GO:0016	SL2.40ch	AT3G45400.1		exostosi	chr3:166	358.199	244.428	103.558	174.807	107.868	119.693
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-1.140	Detected	-1.289	Detected	-1.215	0.004	GT	Sens	contig818	contig818	Kinase fa	TTGTGA	contig818	Solyc05g	Solyc05g	Kinase family protein (AHRD V			contig818	Solyc05g	Kinase family protei		SL2.40ch	AT1G18390.2		ATP bind	chr1:632	237.149	218.713	112.87	107.379	110.203	99.0776
GT	Sense	Sense	0.363	Detected	-0.363	Detected	0.000	-1.655	Detected	-1.417	Detected	-1.536	0.057	GT	Sens	contig818	contig818	Glutamin	ATGGGG	contig818	Solyc02g	Solyc02g	Glutamin	GO:0006	GO:0006	contig818	Solyc02g	Glutamin	GO:0006	SL2.40ch	AT5G38200.1		hydrolas	chr5:152	2001.87	1138.99	214.673	499.769	511.438	601.038
GT	Sense	Sense	0.147	Detected	-0.147	Detected	0.000	-2.207	Comprom	-1.989	Comprom	-2.098	0.008	GT	Sens	contig820	contig820	ABC tran	AACAAA	contig820	Solyc00g	Solyc00g	ABC transporter-like protein (A			contig820	Solyc00g	ABC transporter-like		SL2.40ch	AT1G51460.1		ABC tran	chr1:190	14.5908	11.1967	1.79127	2.27951	2.95127	3.42421
GT	Sense	Sense	0.321	Detected	-0.321	Detected	0.000	-2.109	Detected	-0.993	Detected	-1.551	0.138	GT	Sens	contig821	contig821	AT4g034	GAGTGC	contig821	Solyc01g	Solyc01g	AT4g03420/F9H3_4 (AHRD V1			contig821	Solyc01g	AT4g03420/F9H3_4		SL2.40ch	AT5G42120.1		lectin pro	chr5:168	82.1062	49.4784	15.4007	12.2336	15.7605	34.0523
GT	Sense	Sense	0.225	Detected	-0.225	Detected	0.000	-2.105	Detected	-1.543	Detected	-1.824	0.037	GT	Sens	contig821	contig821	NAD depe	GTAAAA	contig821	Solyc12g	Solyc12g	NAD depe	GO:0008	GO:0008	contig821	Solyc12g	NAD depe	GO:0044	SL2.40ch	AT4G304	GAE1	GAE1 (UI	chr4:148	5524.68	3806.3	1073.56	1861.76	1137.1	1672.71
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.091	Detected	-1.406	Detected	-1.249	0.017	GT	Sens	contig821	contig821	Methyltra	TCGGAG	contig821	Solyc07g	Solyc07g	Methyltra	GO:0008	GO:0008	contig821	Solyc07g	Methyltra	GO:0008	SL2.40ch	AT3G15530.2		methyltra	chr3:525	51060.4	44636.1	25884.3	20176.8	23896.1	19155.7
GT	Sense	Sense	0.254	Detected	-0.254	Detected	0.000	-3.174	Detected	-1.539	Detected	-2.356	0.111	GT	Sens	contig824	contig824	Armadillo	GCATTA	contig824	Solyc03g	Solyc03g	Armadillo	GO:0005	GO:0005	contig824	Solyc03g	Armadillo	GO:0005	SL2.40ch	AT4G349	ARO1	ARO1 (AI	chr4:166	118.556	78.4432	11.6285	21.6059	11.3922	35.2901
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-1.001	Detected	-1.142	Detected	-1.072	0.005	GT	Sens	contig825	contig825	Unknown	ATTTAG	contig825	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig825	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G19980.1		integral r	chr5:674	8962.55	8168.12	3568.5	4893.29	4558.84	4120.93
GT	Sense	Sense	0.191	Detected	-0.191	Detected	0.000	-2.771	Detected	-2.438	Detected	-2.604	0.009	GT	Sens	contig827	contig827	Patatin-lik	TTGGTA	contig827	Solyc02g	Solyc02g	Patatin-lik	GO:0004	GO:0004	contig827	Solyc02g	Patatin-lik	GO:0004	SL2.40ch	AT1G61390.2		S-locus r	chr1:226	1363.35	984.061	167.491	251.317	180.979	227.308
GT	Sense	Sense	0.198	Detected	-0.198	Detected	0.000	-2.011	Detected	-1.431	Detected	-1.721	0.039	GT	Sens	contig827	contig827	Seed mat	TCAAGA	contig827	Solyc03g	Solyc03g	Seed maturation protein PM41			contig827	Solyc03g	Seed maturation pro		SL2.40ch	AT3G11920.1		glutared	chr3:377	1599.86	1143.58	397.29	593.559	357.745	533.377
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-2.255	Detected	-1.695	Detected	-1.975	0.021	GT	Sens	contig827	contig827	Pto-like s	GACACC	contig827	Solyc07g	Solyc07g	Pto-like s	GO:0005	GO:0005	contig827	Solyc07g	Pto-like. S	GO:0005	SL2.40ch	AT1G30570.1		protein k	chr1:108	2840.57	2360.94	686.005	885.356	578.598	850.415
GT	Sense	Sense	0.294	Detected	-0.294	Detected	0.000	-2.690	Detected	-3.237	Detected	-2.964	0.018	GT	Sens	contig834	contig834	Os01g061	CTTAGA	contig834	Solyc06g	Solyc06g	Os01g0611000 protein (Fragm			contig834	Solyc06g	Os01g0611000 prot		SL2.40ch	AT5G25460.1		unknown	chr5:886	37296.9	23350.7	2282.95	3384.17	4877.76	3326.9
GT	Sense	Sense	0.050	Detected	-0.050	Detected	0.000	-1.308	Detected	-1.084	Detected	-1.196	0.010	GT	Sens	contig837	contig837	LRR rece	AAGAGT	contig837	Solyc03g	Solyc03g	LRR rece	GO:0004	GO:0004	contig837	Solyc03g	Receptor	GO:0004	SL2.40ch	AT4G186	MRH1	MRH1 (m	chr4:102	3857.21	3385.69	1647.44	2287.92	1556.38	1812.6
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	-1.300	Detected	-1.257	Detected	-1.279	0.002	GT	Sens	contig84	contig84	Alpha-L-a	TTCAAC	contig84	Solyc01g	Solyc01g	Alpha-L-a	GO:0005	GO:0005	contig84	Solyc01g	Alpha-L-a	GO:0009	SL2.40ch	AT5G645	XYL4. AT	XYL4: hy	chr5:258	10101.4	8771.68	7278.75	5709.56	4075.62	4188.06
GT	Sense	Sense	-0.049	Detected	0.049	Detected	0.000	-1.176	Detected	-1.801	Detected	-1.488	0.042	GT	Sens	contig841	contig841	Receptor-	CAATGA	contig841	Solyc05g	Solyc05g	Receptor-	GO:0006	GO:0006	contig841	Solyc05g	Receptor-	GO:0006	SL2.40ch	AT1G17910.1		wall-asso	chr1:615	38.1492	38.4242	40.484	18.7859	18.0726	11.6808
GT	Sense	Sense	0.394	Detected	-0.394	Detected	0.000	-1.572	Detected	-1.545	Detected	-1.558	0.058	GT	Sens	contig842	contig842	CBL-inter	CGTTGA	contig842	Solyc06g	Solyc06g	CBL-inter	GO:0004	GO:0004	contig842	Solyc06g	CBL-inter	GO:0004	SL2.40ch	AT5G458	CIPK19. S	CIPK19 (	chr5:185	2603.88	1419.63	578.042	910.847	689.637	700.516
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-2.305	Detected	-1.900	Detected	-2.102	0.014	GT	Sens	contig844	contig844	Trehalos	TACAGA	contig844	Solyc03g	Solyc03g	Trehalos	GO:0004	GO:0004	contig844	Solyc03g	Trehalos	GO:0004	SL2.40ch	AT5G514	ATTPPA	ATTPPA:	chr5:209	1822.51	1390.27	206.141	549.882	343.574	453.616
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	-1.792	Detected	-1.613	Detected	-1.703	0.009	GT	Sens	contig845	contig845	Unknown	AAAGGA	contig845	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig845	Solyc03g	Unknown Protein (A		SL2.40ch	AT4G27580.1		unknown	chr4:137	366.52	286.039	42.639	36.8972	99.6983	112.533
GT	Sense	Sense	0.258	Detected	-0.258	Detected	0.000	-2.371	Detected	-1.560	Detected	-1.965	0.055	GT	Sens	contig845	contig845	Unknown	TAACTT	contig845	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig845	Solyc10g	Unknown Protein (A		SL2.40ch	AT3G23450.1		unknown	chr3:841	62.9586	41.4248	16.4896	19.4794	10.527	18.4206
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	-1.457	Detected	-1.554	Detected	-1.505	0.008	GT	Sens	contig846	contig846	Lipase (A	GCTTGT	contig846	Solyc12g	Solyc12g	Lipase (A	GO:0006	GO:0006	contig846	Solyc12g	Lipase (A	GO:0006	SL2.40ch	AT3G14360.1		lipase cla	chr3:479	178.529	141.148	40.0198	44.7917	61.6716	57.4891
GT	Sense	Sense	0.477	Detected	-0.477	Detected	0.000	-4.781	Comprom	-4.693	Comprom	-4.737	0.010	GT	Sens	contig847	contig847	Pentatric	AATACT	contig847	Solyc07g	Solyc07g	Pentatricopeptide (PPR) repea			contig847	Solyc07g	Pentatricopeptide (F		SL2.40ch	AT5G43690.1		sulfotran	chr5:175	226.313	109.921	22.6361	39.7491	6.11886	6.48487
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-2.037	Detected	-1.256	Detected	-1.647	0.055	GT	Sens	contig850	contig850	Serine/thr	GCAGGA	contig850	Solyc11g	Solyc11g	Serine/thr	GO:0006	GO:0006	contig850	Solyc11g	Serine/thr	GO:0006	SL2.40ch	AT3G442	ATNEK6.	NEK6 ("N	chr3:159	79.6469	65.5657	24.2866	21.8473	18.7814	32.1606
GT	Sense	Sense	0.209	Detected	-0.209	Detected	0.000	-1.851	Detected	-1.538	Detected	-1.694	0.023	GT	Sens	contig851	contig851	Serine/thr	GAGGCA	contig851	Solyc07g	Solyc07g	Serine/thr	GO:0003	GO:0003	contig851	Solyc07g	Serine/thr	GO:0004	SL2.40ch	AT2G20630.1		protein p	chr2:889	12840.3	9044.99	2894.21	4332.04	3186.18	3945.13
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.740	Detected	-1.224	Detected	-1.482	0.036	GT	Sens	contig852	contig852	Receptor	AGGCCG	contig852	Solyc08g	Solyc08g	Receptor	GO:0004	GO:0004	contig852	Solyc08g	Receptor	GO:0004	SL2.40ch	AT1G24650.1		leucine-r	chr1:873	240.005	187.897	55.3349	112.885	67.8017	96.68
GT	Sense	Sense	0.249	Detected	-0.249	Detected	0.000	-2.852	Comprom	-1.551	Detected	-2.201	0.087	GT	Sens	contig854	contig854	Cytochro	TATGTT	contig854	Solyc02g	Solyc02g	Cytochro	GO:0019	GO:0019	contig854	Solyc02g	Cytochro	GO:0019	SL2.40ch	AT3G485	CYP94B3	CYP94B3	chr3:179	76.8425	51.2162	10.8182	28.4457	9.26746	22.7687
GT	Sense	Sense	-0.092	Detected	0.092	Detected	0.000	-1.162	Detected	-1.056	Detected	-1.109	0.009	GT	Sens	contig856	contig856	Elicitor-re	AGCAGC	contig856	Solyc10g	Solyc10g	Elicitor-responsive protein 3 (			contig856	Solyc10g	Elicitor-responsive		SL2.40ch	AT1G34160.1		pentatric	chr1:124	3060.39	3270.97	1091.4	1717.21	1507.98	1618.08
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.923	Detected	-1.870	Detected	-1.897	0.001	GT	Sens	contig857	contig857	Auxin res	AGTCTA	contig857	Solyc03g	Solyc03g	Auxin res	GO:0005	GO:0005	contig857	Solyc03g	Auxin res	GO:0005	SL2.40ch	AT3G10810.1		zinc fing	chr3:338	5665.52	5004.47	1186.4	2849.45	1497.34	1548.38
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.149	Detected	-1.087	Detected	-1.118	0.007	GT	Sens	contig858	contig858	Solute ca	GTTGGT	contig858	Solyc09g	Solyc09g	Solute ca	GO:0005	GO:0005	contig858	Solyc09g	Solute ca	GO:0005	SL2.40ch	AT3G07080.1		membrar	chr3:224	5495.09	4583.99	2308.86	2946.25	2412.68	2511.13
GT	Sense	Sense	0.076	Detected	-0.076	Detected	0.000	-1.960	Detected	-1.340	Detected	-1.650	0.035	GT	Sens	contig858	contig858	DNA-bind	TCAAGT	contig858	Solyc02g	Solyc02g	DNA-bind	GO:0003	GO:0003	contig858	Solyc02g	DNA-bind	GO:0003	SL2.40ch	AT3G272	GTE8	GTE8: DI	chr3:100	2563.41	2169.9	652.838	1356.09	646.489	990.564
GT	Sense	Sense	-0.071	Detected	0.071	Detected	0.000	-1.071	Detected	-1.060	Detected	-1.065	0.004	GT	Sens	contig860	contig860	DnaJ hon	AAATCC	contig860	Solyc03g	Solyc03g	DnaJ hon	GO:0031	GO:0031	contig860	Solyc03g	DnaJ hon	GO:0031	SL2.40ch	AT3G61340.1		F-box far	chr3:227	1539.67	1598.82	583.278	772.421	796.571	800.353
GT	Sense	Sense	0.263	Detected	-0.263	Detected	0.000	-2.139	Detected	-2.232	Detected	-2.186	0.015	GT	Sens	contig864	contig864	Circadian	ATGGGC	contig864	Solyc09g	Solyc09g	Circadian clock coupling facto			contig864	Solyc09g	Circadian clock cou		SL2.40ch	AT3G630	EDL3	EDL3 (EI	chr3:233	106.55	69.6649	23.824	34.1102	20.857	19.4917
GT	Sense	Sense	0.358	Detected	-0.358	Detected	0.000	-2.568	Detected	-1.409	Detected	-1.988	0.100	GT	Sens	contig866	contig866	UDP-gluc	TGACCA	contig866	Solyc12g	Solyc12g	UDP-gluc	GO:0008	GO:0008	contig866	Solyc12g	UDP-gluc	GO:0008	SL2.40ch	AT1G01390.1		UDP-gluc	chr1:148	400.415	229.224	50.5726	66.2001	54.4993	121.284
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	-1.569	Detected	-1.616	Detected	-1.593	0.000	GT	Sens	contig869	contig869	Receptor-	TCCACA	contig869	Solyc12g	Solyc12g	Receptor	GO:0006	GO:0006	contig869	Solyc12g	Receptor	GO:0005	SL2.40ch	AT3G23750.1		leucine-r	chr3:855	1302.66	1243.84	313.377	369.026	457.441	441.536
GT	Sense	Sense	0.400	Detected	-0.400	Detected	0.000	-3.768	Detected	-3.319	Detected	-3.543	0.016	GT	Sens	contig869	contig869	Trehalos	ATTCTT	contig869	Solyc08g	Solyc08g	Trehalos	GO:0005	GO:0005	contig869	Solyc08g	Trehalos	GO:0008	SL2.40ch	AT4G12430.1		trehalose	chr4:736	6985.91	3777.35	456.276	894.906	402.13	547.275
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.187	Detected	-0.863	Detected	-1.025	0.026	GT	Sens	contig87	contig87	Unknown	CAAGGA	contig87	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig87	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G202	PI	PI (PISTI	chr5:682	2115.98	1864.3	1146.74	1065.76	930.239	1160.67
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.214	Detected	-1.002	Detected	-1.108	0.009	GT	Sens	contig871	contig871	Dehydrat	TTCTCT	contig871	Solyc04g	Solyc04g	Dehydrat	GO:0016	GO:0016	contig871	Solyc04g	Dehydrat	GO:0016	SL2.40ch	AT1G13860.3		dehydrat	chr1:474	569.336	520.514	172.464	310.377	250.24	288.963
GT	Sense	Sense	0.155	Detected	-0.155	Detected	0.000	-1.051	Detected	-0.969	Detected	-1.010	0.024	GT	Sens	contig873	contig873	Jasmona	GATAGA	contig873	Solyc12g	Solyc12g	Jasmona	GO:0005	GO:0005	contig873	Solyc12g	Jasmona	GO:0005	SL2.40ch	AT5G35390.1		leucine-r	chr5:135	24536.9	18633.9	6140.25	6390.27	11005.5	11616.7
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-1.596	Detected	-1.673	Detected	-1.634	0.001	GT	Sens	contig874	contig874	Aquapori	TGGTGT	contig874	Solyc10g	Solyc10g	Aquapori	GO:0016	GO:0016	contig874	Solyc10g	Aquapori	GO:0015	SL2.40ch	AT4G351	PIP3. PIP	PIP3 (PL	chr4:167	23362.8	21114.4	5169.05	6357.12	7835.42	7406.88
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.047	Detected	-0.962	Detected	-1.004	0.007	GT	Sens	contig876	contig876	Heteroge	TTTTAC	contig876	Solyc11g	Solyc11g	Heteroge	GO:0003	GO:0003	contig876	Solyc11g	Heteroge	GO:0003	SL2.40ch	AT1G33470.2		RNA reco	chr1:121	331.341	344.41	121.87	181.851	174.403	184.345
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	-1.110	Detected	-0.939	Detected	-1.025	0.026	GT	Sens	contig877	contig877	Protein tr	TGGTGG	contig877	Solyc02g	Solyc02g	Protein tr	GO:0005	GO:0005	contig877	Solyc02g	Protein tr	GO:0005	SL2.40ch	AT3G07100.1		protein tr	chr3:224	4420.84	3403.49	1521.79	1860.14	1916.05	2151.17
GT	Sense	Sense	0.109	Detected	-0.109	Detected	0.000	-2.308	Detected	-1.705	Detected	-2.006	0.025	GT	Sens	contig878	contig878	Serine/thr	TCTCCA	contig878	Solyc01g	Solyc01g	Serine/thr	GO:0005	GO:0005	contig878	Solyc01g	Serine/thr	GO:0005	SL2.40ch	AT3G442	ATNEK6.	NEK6 ("N	chr3:159	14932.8	12076	2690.5	4447.29	2892.32	4380.61
GT	Sense	Sense	-0.224	Detected	0.224	Detected	0.000	-1.659	Detected	-2.098	Detected	-1.879	0.027	GT	Sens	contig881	contig881	Beta-fruc	GTTTAC	contig881	Solyc03g	Solyc03g	Beta-fruc	GO:0005	GO:0005	contig881	Solyc03g	Beta-fruc	GO:0004	SL2.40ch	AT5G119	AtcwINV6	AtcwINV6	chr5:383	615.063	789.922	348.918	378.773	235.312	173.056
GT	Sense	Sense	0.153	Detected	-0.153	Detected	0.000	-1.778	Detected	-1.099	Detected	-1.438	0.061	GT	Sens	contig881	contig881	Unknown	CTGTAG	contig881	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig881	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G28310.1		unknown	chr4:140	217.45	165.568	114.436	69.596	59.0108	94.2053
GT	Sense	Sense	-0.038	Detected	0.038	Detected	0.000	-1.108	Detected	-1.084	Detected	-1.096	0.001	GT	Sens	contig884	contig884	Adiponec	TTAATC	contig884	Solyc07g	Solyc07g	Adiponec	GO:0046	GO:0046	contig884	Solyc07g	Adiponec	GO:0046	SL2.40ch	AT5G202	HHP1	HHP1 (HE	chr5:684	3263.37	3236.54	1870.63	1830.21	1608.36	1629.56
GT	Sense	Sense	0.261	Detected	-0.261	Detected	0.000	-2.278	Detected	-2.037	Detected	-2.158	0.017	GT	Sens	contig884	contig884	Tir-nbs-lr	GGAAGA	contig884	Solyc06g	Solyc06g	Tir-nbs-lrr resistance protein (			contig884	Solyc06g	Lrr, resis	GO:0019	SL2.40ch	AT1G656	SMP1	SMP1 (S	chr1:244	227.091	148.759	58.8354	78.3932	40.4175	47.6095
GT	Sense	Sense	0.148	Detected	-0.148	Detected	0.000	-2.002	Detected	-1.544	Detected	-1.773	0.023	GT	Sens	contig888	contig888	Kinase-S	CTTGCA	contig888	Solyc06g	Solyc06g	Kinase-S	GO:0035	GO:0035	contig888	Solyc06g	Kinase-S	GO:0035	SL2.40ch	AT2G28320.1		pleckstri	chr2:120	478.664	366.664	210.481	212.861	111.532	152.793
GT	Sense	Sense	0.326	Detected	-0.326	Detected	0.000	-1.776	Detected	-2.622	Detected	-2.199	0.054	GT	Sens	contig888	contig888	Predicted	ACTTTG	contig888	Solyc02g	Solyc02g	Predicted by genscan and ger			contig888	Solyc02g	Predicted by gensca		SL2.40ch	AT5G54910.1		DEAD/DE	chr5:222	387.639	232.243	125.769	125.568	93.4293	51.8221
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.880	Detected	-1.853	Detected	-1.866	0.000	GT	Sens	contig889	contig889	Transcrip	TTGCAG	contig889	Solyc06g	Solyc06g	Transcrip	GO:0003	GO:0003	contig889	Solyc06g	Transcrip	GO:0003	SL2.40ch	AT5G59570.1		myb fami	chr5:240	515.311	460.773	186.53	269.931	141.174	143.417
GT	Sense	Sense	0.251	Detected	-0.251	Detected	0.000	-1.661	Detected	-1.130	Detected	-1.396	0.062	GT	Sens	contig892	contig892	Harpin-in	GAAAAG	contig892	Solyc12g	Solyc12g	Harpin-induced 1 (AHRD V1 **-			contig892	Solyc12g	Harpin-induced 1 (A		SL2.40ch	AT5G045	DME	DME (DE	chr5:130	686.012	456.028	180.11	209.649	188.549	271.676
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	-3.178	Detected	-2.124	Detected	-2.651	0.037	GT	Sens	contig893	contig893	Ethylene-	CATGAG	contig893	Solyc06g	Solyc06g	Ethylene-	GO:0003	GO:0003	contig893	Solyc06g	Ethylene-	GO:0003	SL2.40ch	AT5G25190.1		ethylene-	chr5:870	1004.69	924.613	170.302	249.59	113.554	235.066
GT	Sense	Sense	0.316	Detected	-0.316	Detected	0.000	-2.576	Comprom	-1.885	Comprom	-2.231	0.041	GT	Sens	contig893	contig893	Protein p	ATACCA	contig893	Solyc10g	Solyc10g	Protein p	GO:0003	GO:0003	contig893	Solyc10g	Protein p	GO:0003	SL2.40ch	AT3G094	PLL3	PLL3: ca	chr3:289	47.9876	29.146	6.08355	6.00926	6.68892	10.7621
GT	Sense	Sense	0.228	Detected	-0.228	Detected	0.000	-1.074	Detected	-1.038	Detected	-1.056	0.044	GT	Sens	contig894	contig894	Cation/H(	AACTTA	contig894	Solyc08g	Solyc08g	Cation/H(	GO:0015	GO:0015	contig894	Solyc08g	Cation/H(	GO:0015	SL2.40ch	AT5G416	ATCHX18	ATCHX18	chr5:166	1782.88	1222.12	726.823	720.584	747.913	764.425
GT	Sense	Sense	0.305	Detected	-0.305	Detected	0.000	-1.833	Detected	-1.594	Detected	-1.713	0.035	GT	Sens	contig897	contig897	Unknown	ATATTT	contig897	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig897	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G18350.1		ATP bind	chr5:607	1521.73	937.765	399.813	595.981	357.547	420.795
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-1.094	Detected	-1.436	Detected	-1.265	0.019	GT	Sens	contig898	contig898	Unknown	AGGAGA	contig898	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig898	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G14075.1		lipase cla	chr3:466	199.317	201.696	59.8194	62.8704	100.157	78.7778
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	-1.699	Detected	-1.214	Detected	-1.457	0.027	GT	Sens	contig902	contig902	WD-repea	GGTTCC	contig902	Solyc04g	Solyc04g	WD-repea	GO:0046	GO:0046	contig902	Solyc04g	WD-repea	GO:0046	SL2.40ch	AT5G08390.1		FUNCTIO	chr5:270	74.6014	66.8454	12.8669	26.9671	23.1952	32.3616
GT	Sense	Sense	0.144	Detected	-0.144	Detected	0.000	-1.518	Detected	-1.134	Detected	-1.326	0.031	GT	Sens	contig906	contig906	U-box do	CACAAG	contig906	Solyc04g	Solyc04g	U-box do	GO:0000	GO:0000	contig906	Solyc04g	U-box do	GO:0005	SL2.40ch	AT3G524	PUB22	PUB22 (F	chr3:194	6333.04	4883.7	1510.87	2968.69	2071.03	2693.92
GT	Sense	Sense	0.264	Detected	-0.264	Detected	0.000	-1.176	Detected	-0.846	Detected	-1.011	0.083	GT	Sens	contig907	contig907	Unknown	AGTGTT	contig907	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig907	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G24130.1		unknown	chr5:816	58.7319	38.3112	22.6814	23.1396	22.3948	28.0509
GT	Sense	Sense	-0.159	Detected	0.159	Detected	0.000	-1.243	Detected	-1.328	Detected	-1.285	0.016	GT	Sens	contig912	contig912	3-phenyl	AGTATA	contig912	Solyc12g	Solyc12g	3-phenyl	GO:0008	GO:0008	contig912	Solyc12g	Short cha	GO:0010	SL2.40ch	AT3G26770.1		short-cha	chr3:984	12335.5	14471.3	6431.04	7357.96	6019.24	5659.88
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	-1.345	Detected	-1.339	Detected	-1.342	0.000	GT	Sens	contig912	contig912	SNAP25 h	GAAAAA	contig912	Solyc06g	Solyc06g	SNAP25 h	GO:0005	GO:0005	contig912	Solyc06g	SNAP25 h	GO:0005	SL2.40ch	AT5G612	SNAP33.	SNAP33	chr5:246	5930.84	5481.49	1908.29	2424.2	2393.63	2396.68
GT	Sense	Sense	0.310	Detected	-0.310	Detected	0.000	-2.317	Detected	-2.133	Detected	-2.225	0.020	GT	Sens	contig912	contig912	Heat stre	CAAGGA	contig912	Solyc09g	Solyc09g	Heat stre	GO:0005	GO:0005	contig912	Solyc09g	Heat stre	GO:0005	SL2.40ch	AT3G029	ATHSFA1	ATHSFA1	chr3:673	84.7161	51.8911	14.8462	20.0373	14.192	16.0713
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.166	Detected	-0.922	Detected	-1.044	0.014	GT	Sens	contig913	contig913	BHLH tra	ATCATA	contig913	Solyc08g	Solyc08g	BHLH tra	GO:0005	GO:0005	contig913	Solyc08g	BHLH tra	GO:0030	SL2.40ch	AT4G05170.1		DNA bind	chr4:266	8434.19	7657.78	4205.78	3359.43	3819.04	4510.84
GT	Sense	Sense	0.511	Detected	-0.511	Detected	0.000	-2.053	Detected	-2.106	Detected	-2.080	0.056	GT	Sens	contig914	contig914	Disease r	GTGTTT	contig914	Solyc10g	Solyc10g	Disease resistance response (			contig914	Solyc10g	Disease resistance		SL2.40ch	AT5G542	MRE11. A	MRE11 (r	chr5:220	5148.4	2385.33	1340.55	1160.34	900.659	865.28
GT	Sense	Sense	0.112	Detected	-0.112	Detected	0.000	-1.368	Detected	-1.253	Detected	-1.310	0.009	GT	Sens	contig916	contig916	Organic a	GACGAG	contig916	Solyc10g	Solyc10g	Organic a	GO:0008	GO:0008	contig916	Solyc10g	Organic a	GO:0008	SL2.40ch	AT3G14410.1		transpor	chr3:481	1247.15	1005.36	444.33	534.346	462.657	499.492
GT	Sense	Sense	0.117	Detected	-0.117	Detected	0.000	-1.344	Detected	-0.987	Detected	-1.166	0.032	GT	Sens	contig916	contig916	Conserve	TTTATG	contig916	Solyc03g	Solyc03g	Conserve	GO:0005	GO:0005	contig916	Solyc03g	Conserve	GO:0005	SL2.40ch	AT5G16300.3		FUNCTIO	chr5:533	1686.08	1349.84	480.935	705.202	633.746	809.089
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-1.180	Detected	-0.837	Detected	-1.009	0.032	GT	Sens	contig918	contig918	14-3-3 pro	GAACTG	contig918	Solyc11g	Solyc11g	14-3-3 pro	GO:0019	GO:0019	contig918	Solyc11g	14-3-3 pro	GO:0019	SL2.40ch	AT1G783	GRF2. 14-	GRF2 (GI	chr1:294	20607.7	17591.5	10920.9	9579.88	8963.08	11329
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-1.542	Detected	-2.400	Detected	-1.971	0.046	GT	Sens	contig919	contig919	BZIP tran	AGTGAA	contig919	Solyc04g	Solyc04g	BZIP tran	GO:0003	GO:0003	contig919	Solyc04g	BZIP tran	GO:0003	SL2.40ch	AT5G652	TGA1	TGA1: DI	chr5:260	70.3079	58.1635	24.179	17.7847	23.4123	12.8798
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-3.083	Detected	-2.281	Detected	-2.682	0.022	GT	Sens	contig920	contig920	Peroxida	GGCTCG	contig920	Solyc03g	Solyc03g	Peroxida	GO:0005	GO:0005	contig920	Solyc03g	Peroxida	GO:0005	SL2.40ch	AT5G58400.1		peroxida	chr5:236	88592.2	77176	17396.8	10055.4	10405.8	18085.8
GT	Sense	Sense	-0.034	Detected	0.034	Detected	0.000	-1.157	Detected	-0.965	Detected	-1.061	0.009	GT	Sens	contig921	contig921	WD-repea	TACAAT	contig921	Solyc12g	Solyc12g	WD-repeat protein-like (AHRD			contig921	Solyc12g	WD-repeat protein-li		SL2.40ch	AT1G78070.1		FUNCTIO	chr1:293	3539.95	3493.71	1210.42	2311.29	1681.8	1915.3
GT	Sense	Sense	0.249	Detected	-0.249	Detected	0.000	-2.125	Detected	-1.492	Detected	-1.809	0.046	GT	Sens	contig923	contig923	Ornithine	TGTGGG	contig923	Solyc03g	Solyc03g	Ornithine	GO:0003	GO:0003	contig923	Solyc03g	Ornithine	GO:0004	SL2.40ch	AT2G271	SE	SE (SERI	chr2:115	1311.56	873.337	162.875	334.349	261.562	404.475
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-1.760	Detected	-1.743	Detected	-1.752	0.003	GT	Sens	contig929	contig929	Cell numl	TTCTTA	contig929	Solyc03g	Solyc03g	Cell number regulator 13 (AHR			contig929	Solyc03g	Cell number regulat		SL2.40ch	AT5G638	BGAL10	BGAL10	chr5:255	519.156	431.693	178.024	116.408	149.014	150.389
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	-1.144	Detected	-1.294	Detected	-1.219	0.007	GT	Sens	contig930	contig930	F-box pro	AGATTT	contig930	Solyc12g	Solyc12g	F-box protein PP2-B1 (AHRD V			contig930	Solyc12g	F-box protein PP2-E		SL2.40ch	AT5G63120.2		ethylene	chr5:253	103.348	88.5878	87.3217	40.0237	46.177	41.4803
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	-1.963	Detected	-1.469	Detected	-1.716	0.025	GT	Sens	contig932	contig932	Novel pla	ACTGAT	contig932	Solyc08g	Solyc08g	Novel pla	GO:0008	GO:0008	contig932	Solyc08g	Novel pla	GO:0008	SL2.40ch	AT2G351	NPSN11.	NPSN11	chr2:148	5054.65	4010.64	912.883	1965.55	1231.72	1728.67
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.021	Detected	-1.037	Detected	-1.029	0.002	GT	Sens	contig933	contig933	Os03g016	TGAGAT	contig933	Solyc01g	Solyc01g	Os03g0169000 protein (Fragm			contig933	Solyc01g	Os03g0169000 prot		SL2.40ch	AT2G44500.1		unknown	chr2:183	762.582	673.258	163.841	246.441	376.572	371.246
GT	Sense	Sense	-0.053	Detected	0.053	Detected	0.000	-1.500	Detected	-1.097	Detected	-1.298	0.025	GT	Sens	contig933	contig933	Os02g07	ACTTGA	contig933	Solyc04g	Solyc04g	Os02g07	GO:0005	GO:0005	contig933	Solyc04g	Os02g07	GO:0005	SL2.40ch	AT1G49890.1		unknown	chr1:184	1169.83	1184.76	405.301	679.027	443.917	585.071
GT	Sense	Sense	0.149	Detected	-0.149	Detected	0.000	-1.826	Detected	-1.393	Detected	-1.609	0.026	GT	Sens	contig935	contig935	Lysine ke	TTATGA	contig935	Solyc02g	Solyc02g	Lysine ketoglutarate reductas			contig935	Solyc02g	Lysine ketoglutarate		SL2.40ch	AT1G11170.1		unknown	chr1:374	30316.1	23209	9814.04	12823.5	7980.36	10738.8
GT	Sense	Sense	0.311	Detected	-0.311	Detected	0.000	-2.558	Detected	-1.428	Detected	-1.993	0.091	GT	Sens	contig937	contig937	Xylanase	CATTGT	contig937	Solyc01g	Solyc01g	Xylanase	GO:0006	GO:0006	contig937	Solyc01g	Xylanase	GO:0006	SL2.40ch	AT4G119	ATNUDT1	ATNUDX	chr4:718	16707.8	10211.6	3549.91	4370.68	2364.74	5161.13
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	-2.038	Detected	-1.218	Detected	-1.628	0.058	GT	Sens	contig937	contig937	Calmodul	TGTGAT	contig937	Solyc01g	Solyc01g	Calmodul	GO:0005	GO:0005	contig937	Solyc01g	Calmodul	GO:0005	SL2.40ch	AT3G568	CAM3. ac	CAM3 (C	chr3:210	1018.59	914.134	413.69	485.291	250.589	440.948
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-2.141	Detected	-1.964	Detected	-2.052	0.008	GT	Sens	contig939	contig939	cDNA clo	GGTGAA	contig939	Solyc04g	Solyc04g	cDNA clone J033025P19 full in			contig939	Solyc04g	cDNA clone J03302		SL2.40ch	AT1G35780.1		unknown	chr1:132	630.917	472.812	72.8161	133.623	132.045	148.885
GT	Sense	Sense	0.009	Detected	-0.009	Detected	0.000	-2.516	Detected	-2.052	Detected	-2.284	0.010	GT	Sens	contig940	contig940	Copia-typ	CACTTG	contig940	Solyc04g	Solyc04g	Copia-type polyprotein (AHRD			contig940	Solyc04g	Copia-type polyprot		SL2.40ch	AT5G24790.1		unknown	chr5:851	8063.41	7488.61	1396.37	1526.33	1448.5	1992.64
GT	Sense	Sense	-0.026	Detected	0.026	Detected	0.000	-2.101	Detected	-1.781	Detected	-1.941	0.007	GT	Sens	contig943	contig943	Potassiu	AAACAT	contig943	Solyc05g	Solyc05g	Potassiu	GO:0005	GO:0005	contig943	Solyc05g	Potassiu	GO:0005	SL2.40ch	AT3G028	SKOR	SKOR: c	chr3:619	718.188	700.382	153.756	202.58	176.268	219.402
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.112	Detected	-1.113	Detected	-1.113	0.002	GT	Sens	contig944	contig944	LOB dom	AGAGCT	contig944	Solyc01g	Solyc01g	LOB domain protein 30 (AHRD			contig944	Solyc01g	LOB domain proteir		SL2.40ch	AT2G454	LBD18	LBD18 (L	chr2:187	217.984	218.335	105.382	158.167	107.625	107.203
GT	Sense	Sense	-0.051	Detected	0.051	Detected	0.000	-1.477	Comprom	-1.623	Comprom	-1.550	0.003	GT	Sens	contig945	contig945	Pectinest	CGTTTG	contig945	Solyc11g	Solyc11g	Pectinest	GO:0046	GO:0046	contig945	Solyc11g	Pectinest	GO:0046	SL2.40ch	AT5G646	C/VIF2. A	C/VIF2 (C	chr5:258	22.1368	22.3684	14.9525	11.2972	8.52217	7.68158
GT	Sense	Sense	-0.053	Detected	0.053	Detected	0.000	-1.809	Detected	-1.977	Detected	-1.893	0.003	GT	Sens	contig945	contig945	Unknown	GAAGTG	contig945	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig945	Solyc05g	Unknown Protein (A		SL2.40ch	AT1G71110.1		unknown	chr1:268	14088.6	14259.5	4282.01	5124.06	4313.07	3827.86
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-2.184	Detected	-1.545	Detected	-1.865	0.029	GT	Sens	contig930	contig930	RNA-bind	CATGCT	contig930	Solyc04g	Solyc04g	RNA-bind	GO:0003	GO:0003	contig930	Solyc04g	RNA-bind	GO:0003	SL2.40ch	AT1G78260.2		RNA reco	chr1:294	1355.22	1205.52	413.499	657.523	299.871	465.625
GT	Sense	Sense	0.219	Detected	-0.219	Detected	0.000	-1.622	Detected	-1.692	Detected	-1.657	0.018	GT	Sens	contig948	contig948	Nodulin-li	GAATAT	contig948	Solyc06g	Solyc06g	Nodulin-li	GO:0016	GO:0016	contig948	Solyc06g	Nodulin-li	GO:0016	SL2.40ch	AT5G252	KNAT3	KNAT3 (I	chr5:873	224.853	156.08	49.7705	105.183	64.9031	61.6527
GT	Sense	Sense	0.317	Detected	-0.317	Detected	0.000	-0.819	Detected	-1.435	Detected	-1.127	0.125	GT	Sens	contig948	contig948	Unknown	CATTAC	contig948	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig948	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G12350.1		Ran GTP	chr5:399	1751.73	1062.63	539.223	671.605	824.771	536.509
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	-0.810	Detected	-1.412	Detected	-1.111	0.068	GT	Sens	contig950	contig950	Cellulose	AACTTG	contig950	Solyc07g	Solyc07g	Cellulose	GO:0016	GO:0016	contig950	Solyc07g	Cellulose	GO:0016	SL2.40ch	AT1G558	ATCSLE1	ATCSLE1	chr1:208	370.734	321.859	178.562	180.444	210.065	138.053
GT	Sense	Sense	0.378	Detected	-0.378	Detected	0.000	-3.020	Detected	-2.099	Detected	-2.560	0.050	GT	Sens	contig955	contig955	BZIP tran	GAGTTA	contig955	Solyc07g	Solyc07g	BZIP tran	GO:0005	GO:0005	contig955	Solyc07g	BZIP tran	GO:0016	SL2.40ch	AT3G581	ATBZIP61	BZIP61: I	chr3:215	257.786	143.586	37.9699	56.5484	25.289	47.7314
GT	Sense	Sense	-0.098	Detected	0.098	Detected	0.000	-1.988	Comprom	-1.113	Detected	-1.551	0.074	GT	Sens	contig955	contig955	Glutamat	GGAGAG	contig955	Solyc04g	Solyc04g	Glutamat	GO:0005	GO:0005	contig955	Solyc04g	Glutamat	GO:0005	SL2.40ch	AT3G133	BRL3	BRL3 (BF	chr3:434	22.046	23.7633	16.7777	15.2632	6.15112	11.2493
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	-1.061	Detected	-1.006	Detected	-1.034	0.024	GT	Sens	contig959	contig959	LisH dom	GTTGTG	contig959	Solyc02g	Solyc02g	LisH dom	GO:0005	GO:0005	contig959	Solyc02g	LisH dom	GO:0005	SL2.40ch	AT5G16210.1		HEAT rep	chr5:529	214.62	161.62	65.6477	82.1513	95.1716	98.5805
GT	Sense	Sense	-0.067	Detected	0.067	Detected	0.000	-1.343	Detected	-1.220	Detected	-1.281	0.005	GT	Sens	contig960	contig960	Tubby-lik	AAGGTC	contig960	Solyc02g	Solyc02g	Tubby-lik	GO:0051	GO:0051	contig960	Solyc02g	Tubby-lik	GO:0051	SL2.40ch	AT1G472	AtTLP6	AtTLP6 (	chr1:173	679.467	701.604	226.185	537.876	290.32	315.191
GT	Sense	Sense	0.236	Detected	-0.236	Detected	0.000	-1.175	Detected	-1.262	Detected	-1.218	0.037	GT	Sens	contig960	contig960	Unknown	AAGAAA	contig960	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig960	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G50000.1		protein k	chr5:203	519.172	352.112	258.173	217.344	201.936	189.6
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-1.917	Detected	-1.710	Detected	-1.813	0.007	GT	Sens	contig961	contig961	Zinc finge	TTGCAC	contig961	Solyc11g	Solyc11g	Zinc finge	GO:0005	GO:0005	contig961	Solyc11g	Zinc finge	GO:0005	SL2.40ch	AT5G26770.3		unknown	chr5:940	291.831	234.739	74.2615	107.279	73.9019	85.0815
GT	Sense	Sense	0.412	Detected	-0.412	Detected	0.000	-2.097	Detected	-2.299	Detected	-2.198	0.035	GT	Sens	contig961	contig961	Expresse	AATGTC	contig961	Solyc10g	Solyc10g	Expressed protein (Fragment)			contig961	Solyc10g	Expressed protein (		SL2.40ch	AT2G172	EXL5	EXL5 (EX	chr2:749	796.788	423.546	137.422	138.653	144.833	125.525
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	-1.827	Detected	-1.365	Detected	-1.596	0.021	GT	Sens	contig963	contig963	Pectate ly	ACAGTC	contig963	Solyc03g	Solyc03g	Pectate ly	GO:0016	GO:0016	contig963	Solyc03g	Pectate ly	GO:0016	SL2.40ch	AT4G13210.1		lyase/ pe	chr4:767	173.239	151.965	43.498	60.3834	48.7644	66.9586
GT	Sense	Sense	0.319	Detected	-0.319	Detected	0.000	-1.390	Detected	-1.439	Detected	-1.414	0.048	GT	Sens	contig964	contig964	Aminotra	GTACTA	contig964	Solyc10g	Solyc10g	Aminotra	GO:0030	GO:0030	contig964	Solyc10g	Aminotra	GO:0030	SL2.40ch	AT3G08860.1		alanine--	chr3:269	41434.9	25043	11343.1	9331.27	13106.9	12632.7
GT	Sense	Sense	-0.315	Detected	0.315	Detected	0.000	-2.901	Detected	-1.331	Detected	-2.116	0.129	GT	Sens	contig965	contig965	UDP-N-ac	CTGGTT	contig965	Solyc03g	Solyc03g	UDP-N-ac	GO:0005	GO:0005	contig965	Solyc03g	UDP-N-ac	GO:0008	SL2.40ch	AT5G18000.1		transcrip	chr5:596	93.2216	135.766	17.0781	55.469	16.0609	47.5381
GT	Sense	Sense	-0.085	Detected	0.085	Detected	0.000	-1.466	Detected	-1.098	Detected	-1.282	0.024	GT	Sens	contig969	contig969	Dihydrofl	CATTGA	contig969	Solyc05g	Solyc05g	Dihydrofl	GO:0008	GO:0008	contig969	Solyc05g	Dihydrofl	GO:0008	SL2.40ch	AT1G61980.1				126.588	134.049	74.5681	63.2392	50.2711	64.7128
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	-2.234	Detected	-1.089	Detected	-1.662	0.101	GT	Sens	contig970	contig970	MYB tran	CTTCGA	contig970	Solyc11g	Solyc11g	MYB tran	GO:0003	GO:0003	contig970	Solyc11g	MYB tran	GO:0003	SL2.40ch	AT5G166	MYB43. A	MYB43 (I	chr5:543	211.296	196.072	78.6173	83.2571	46.1297	101.745
GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	-1.374	Detected	-1.259	Detected	-1.317	0.008	GT	Sens	contig974	contig974	Desiccati	CTCCAG	contig974	Solyc09g	Solyc09g	Desiccation-related protein PC			contig974	Solyc09g	Desiccation-related		SL2.40ch	AT3G58050.1		unknown	chr3:214	8709.59	9483.23	4814.21	7516.29	3739.31	4036.38
GT	Sense	Sense	0.293	Detected	-0.293	Detected	0.000	-1.768	Detected	-1.368	Detected	-1.568	0.048	GT	Sens	contig974	contig974	Short inte	GGCGGT	contig974	Solyc03g	Solyc03g	Short internode related seque			contig974	Solyc03g	Short internode rela		SL2.40ch	AT5G085	ILP1	ILP1 (inc	chr5:276	13080.6	8197.94	2805.95	4384.06	3242.88	4264.36
GT	Sense	Sense	0.049	Detected	-0.049	Detected	0.000	-2.237	Detected	-1.642	Detected	-1.940	0.023	GT	Sens	contig976	contig976	Protein s	GGCAAA	contig976	Solyc12g	Solyc12g	Protein s	GO:0006	GO:0006	contig976	Solyc12g	Protein s	GO:0006	SL2.40ch	AT5G668	MAPKKK	MAPKKK	chr5:266	601.76	529.287	200.524	181.964	127.657	192.22
GT	Sense	Sense	0.221	Detected	-0.221	Detected	0.000	-1.155	Detected	-1.360	Comprom	-1.257	0.036	GT	Sens	contig982	contig982	Resistanc	TATCTT	contig982	Solyc05g	Solyc05g	Resistanc	GO:0007	GO:0007	contig982	Solyc05g	Cc-nbs-lr	GO:0006	SL2.40ch	AT1G703	UPL2	UPL2 (UE	chr1:264	23.4184	16.2139	8.19686	5.10505	9.33331	8.07159
GT	Sense	Sense	-0.201	Detected	0.201	Detected	0.000	-1.684	Detected	-0.941	Detected	-1.312	0.090	GT	Sens	contig983	contig983	Peptide tr	GTGCTA	contig983	Solyc07g	Solyc07g	Peptide tr	GO:0016	GO:0016	contig983	Solyc07g	Peptide tr	GO:0042	SL2.40ch	AT3G541	ATPTR1.	PTR1 (PE	chr3:200	9259.12	11504.7	2786.71	3490.79	3426.38	5716.44
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.076	Detected	-0.987	Detected	-1.032	0.002	GT	Sens	contig984	contig984	ATP-depe	CCATCG	contig984	Solyc10g	Solyc10g	ATP-depe	GO:0005	GO:0005	contig984	Solyc10g	ATP-depe	GO:0004	SL2.40ch	AT4G00660.1		DEAD/DE	chr4:274	1985.15	1931.54	749.319	855.934	990.302	1050.41
GT	Sense	Sense	0.384	Detected	-0.384	Detected	0.000	-1.769	Detected	-1.298	Detected	-1.534	0.077	GT	Sens	contig986	contig986	Unknown	TAGTAG	contig986	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig986	Solyc06g	Unknown Protein (A		SL2.40ch	AT1G48400.1		F-box far	chr1:178	66.4712	36.7317	17.5548	19.4621	15.4575	21.3653
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.801	Detected	-1.214	Detected	-1.508	0.040	GT	Sens	contig986	contig986	Receptor-	GCAGCT	contig986	Solyc11g	Solyc11g	Receptor	GO:0006	GO:0006	contig986	Solyc11g	Pto-like. S	GO:0004	SL2.40ch	AT2G41970.1		protein k	chr2:175	269.927	221.834	110.235	160.707	74.8598	112.112
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	-1.273	Detected	-1.145	Detected	-1.209	0.015	GT	Sens	contig988	contig988	NBS-codi	GGCTTC	contig988	Solyc12g	Solyc12g	NBS-codi	GO:0006	GO:0006	contig988	Solyc12g	Cc-nbs-lr	GO:0005	SL2.40ch	AT1G109	LOV1	LOV1: AT	chr1:364	257.831	201.351	127.704	119.011	100.52	109.527
GT	Sense	Sense	0.730	Detected	-0.730	Detected	0.000	-1.260	Detected	-1.741	Detected	-1.500	0.190	GT	Sens	contig994	contig994	Cytochro	ACTGCC	contig994	Solyc02g	Solyc02g	Cytochro	GO:0019	GO:0019	contig994	Solyc02g	cytochro	GO:0008	SL2.40ch	AT5G384	CYP735A	CYP735A	chr5:153	62.2874	21.2931	10.7023	5.26981	16.2181	11.5869
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	-1.363	Detected	-1.044	Detected	-1.203	0.017	GT	Sens	contig995	contig995	Sec1-4 sy	ATAAGC	contig995	Solyc01g	Solyc01g	Sec1-4 sy	GO:0005	GO:0005	contig995	Solyc01g	Sec1-4 sy	GO:0008	SL2.40ch	AT4G121	SEC1B. A	SEC1B:	chr4:725	55.1714	52.7643	23.2582	19.4643	22.3747	27.8299
GT	Sense	Sense	-0.145	Detected	0.145	Detected	0.000	-1.824	Detected	-2.550	Detected	-2.187	0.030	GT	Sens	contig998	contig998	Protein Y	AGACGA	contig998	Solyc01g	Solyc01g	Protein YdiU (AHRD V1 ***- B5N			contig998	Solyc01g	Protein YdiU (AHRD		SL2.40ch	AT5G13030.1		unknown	chr5:413	858.225	986.775	254.414	284.706	277.152	167.091
GT	Sense	Sense	0.409	Detected	-0.409	Detected	0.000	-2.755	Detected	-2.533	Detected	-2.644	0.025	GT	Sens	LeGH3-3	LeGH3-3	Solanum	AGACGAGGACGTTCAGCAGAATTAGGTTTGTACGTTATGGCTCAGTTAACCTGTGAAAAT																15571.8	8307.98	1946.72	4323.05	1797.39	2088.98
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	-1.699	Detected	-1.022	Detected	-1.361	0.057	GT	Sens	U13055	U13055	LEU1305	CAGCCCATTCTAATTGATATAAACATGTGTAAAGAGAGAATGTAGTGGTGTGCAAAGGCC																1425.99	1330.03	583.207	419.642	452.232	720.925
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-0.850	Detected	-1.799	Detected	-1.324	0.108	GT	Sens	contig102	contig102	UDP-gluc	AGCCAA	contig102	Solyc10g	Solyc10g	UDP-gluc	GO:0008	GO:0008	contig102	Solyc10g	UDP-gluc	GO:0008	SL2.40ch	AT5G12890.1		UDP-gluc	chr5:406	140.806	127.464	43.6654	60.1651	79.2789	40.9394
GT	Sense	Sense	0.149	Detected	-0.149	Detected	0.000	-1.008	Detected	-1.615	Detected	-1.312	0.060	GT	Sens	contig102	contig102	UDP-gluc	TTTTTG	contig102	Solyc10g	Solyc10g	UDP-gluc	GO:0008	GO:0008	contig102	Solyc10g	UDP-gluc	GO:0008	SL2.40ch	AT5G12890.1		UDP-gluc	chr5:406	141.352	108.154	64.893	54.8038	65.5519	42.9189
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-1.187	Detected	-1.095	Detected	-1.141	0.004	GT	Sens	contig103	contig103	Multidrug	GGTAGC	contig103	Solyc03g	Solyc03g	Multidrug	GO:0015	GO:0015	contig103	Solyc03g	Multidrug	GO:0015	SL2.40ch	AT4G23030.1		MATE eff	chr4:120	877.29	764.823	378.819	551.517	383.553	407.706
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-1.432	Detected	-1.228	Detected	-1.330	0.009	GT	Sens	contig103	contig103	Multidrug	CGCTGT	contig103	Solyc03g	Solyc03g	Multidrug	GO:0015	GO:0015	contig103	Solyc03g	Multidrug	GO:0015	SL2.40ch	AT4G23030.1		MATE eff	chr4:120	1120.44	944.684	460.344	657.964	406.693	467.108
GT	Sense	Sense	0.419	Detected	-0.419	Detected	0.000	-2.931	Detected	-3.069	Detected	-3.000	0.019	GT	Sens	contig104	contig104	Disease r	GAAAGG	contig104	Solyc01g	Solyc01g	Disease resistance response			contig104	Solyc01g	Disease resistance		SL2.40ch	AT1G58170.1		disease r	chr1:215	394.499	207.635	68.0711	41.8965	40.0177	36.2493
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-1.870	Detected	-1.632	Detected	-1.751	0.009	GT	Sens	contig105	contig105	Fatty acid	TGTGTA	contig105	Solyc10g	Solyc10g	Fatty acid	GO:0009	GO:0009	contig105	Solyc10g	Fatty acid	GO:0009	SL2.40ch	AT5G437	KCS20	KCS20 (3	chr5:175	69774.9	55759.8	17291.5	22385.2	18193.6	21394.8
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.734	Detected	-1.575	Detected	-1.654	0.006	GT	Sens	contig105	contig105	Fatty acid	ATATGA	contig105	Solyc10g	Solyc10g	Fatty acid	GO:0009	GO:0009	contig105	Solyc10g	Fatty acid	GO:0009	SL2.40ch	AT5G437	KCS20	KCS20 (3	chr5:175	57192.1	46993.4	15760.8	20156.1	16624.7	18494.5
GT	Sense	Sense	0.153	Detected	-0.153	Detected	0.000	-2.496	Detected	-1.990	Detected	-2.243	0.017	GT	Sens	contig106	contig106	Transcrip	ATTCAC	contig106	Solyc06g	Solyc06g	Transcrip	GO:0003	GO:0003	contig106	Solyc06g	Transcrip	GO:0003	SL2.40ch	AT3G07340.1		basic hel	chr3:234	4187.91	3187.25	617.909	1119.65	690.65	977.805
GT	Sense	Sense	0.280	Detected	-0.280	Detected	0.000	-2.516	Detected	-2.022	Detected	-2.269	0.026	GT	Sens	contig106	contig106	Transcrip	CTGAGC	contig106	Solyc06g	Solyc06g	Transcrip	GO:0003	GO:0003	contig106	Solyc06g	Transcrip	GO:0003	SL2.40ch	AT3G07340.1		basic hel	chr3:234	378.638	241.537	69.6832	118.344	56.3982	79.1575
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	-2.421	Detected	-0.950	Detected	-1.686	0.154	GT	Sens	AF077339	AF077339	Lycopers	TTAAAGTAGTAGTGGATGGAGTCACATAATTTATTAACTAAAGTAAGTGTTGTAGCAGAA																12489.8	9601.16	1331.89	1651.85	2179.8	6026.73
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	-1.186	Detected	-1.282	Detected	-1.234	0.011	GT	Sens	contig100	contig100	Major fac	GTTATC	contig100	Solyc05g	Solyc05g	Major fac	GO:0055	GO:0055	contig100	Solyc05g	Major fac	GO:0005	SL2.40ch	AT1G43020.4		unknown	chr1:161	724.76	807.271	324.372	381.251	358.51	334.411
GT	Sense	Sense	0.246	Detected	-0.246	Detected	0.000	-1.142	Detected	-1.430	Detected	-1.286	0.046	GT	Sens	contig102	contig102	Cytochro	GAAGAA	contig102	Solyc09g	Solyc09g	Cytochro	GO:0020	GO:0020	contig102	Solyc07g	Cytochro	GO:0019	SL2.40ch	AT3G54790.2		armadillo	chr3:202	182.778	122.219	58.9022	42.7459	72.2249	58.9652

GT	Sense	Sense	0.130	Detected	-0.130	Detected	0.000	-1.232	Detected	-0.897	Detected	-1.065	0.037	GT	Sens	contig105	contig105	Adenosyl	TTAATGA	contig105	Solyc09g	Solyc09g	Adenosyl	GO:0004	GO:0004	contig105	Solyc09g	Adenosyl	GO:0004	SL2.40ch	AT4G139	HOG1. EM	MEE58 (I	chr4:805	8016.59	6298.25	2358.64	2417.52	3225.95	4056.32
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.330	Detected	-1.060	Detected	-1.195	0.016	GT	Sens	contig106	contig106	N-acetyltr	AAGTCT	contig106	Solyc08g	Solyc08g	N-acetyltr	GO:00081	GO:00081	contig106	Solyc08g	N-acetyltr	GO:00081	SL2.40ch	AT4G37920.1		unknown	chr4:178	12899.8	13409.4	5524.32	5788.84	5579.07	6707.63
GT	Sense	Sense	0.250	Detected	-0.250	Detected	0.000	-3.909	Comprom	-3.902	Comprom	-3.905	0.004	GT	Sens	contig109	contig109	Acyltrans	GGACACA	contig109	Solyc11g	Solyc11g	Acyltrans	GO:00167	GO:00167	contig109	Solyc11g	Acyltrans	GO:00167	SL2.40ch	AT5G241	SOP1	SOP1: sc	chr5:817	99.9373	66.4582	16.2616	19.1308	5.78549	5.79686
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	-3.929	Detected	-2.901	Detected	-3.415	0.022	GT	Sens	contig109	contig109	HIN1-like	ATCCTAC	contig109	Solyc10g	Solyc10g	HIN1-like protein (Fragment) (A			contig109	Solyc10g	HIN1-like protein (Fr		SL2.40ch	AT5G63900.1		PHD fing	chr5:255	1640.01	1663.89	228.763	350.425	115.689	235.163
GT	Sense	Sense	-0.502	Detected	0.502	Detected	0.000	-0.954	Detected	-2.001	Comprom	-1.478	0.179	GT	Sens	contig109	contig109	UDP-gluc	TTTGAAC	contig109	Solyc10g	Solyc10g	UDP-gluc	GO:00081	GO:00081	contig109	Solyc10g	UDP-gluc	GO:00081	SL2.40ch	AT2G36970.1		UDP-gluc	chr2:155	23.4798	44.3276	20.8631	17.3158	17.7616	8.56656
GT	Sense	Sense	-0.005	Detected	0.005	Detected	0.000	-1.653	Detected	-1.145	Detected	-1.399	0.031	GT	Sens	contig110	contig110	Ycf2 (AHF	TTTCCTC	contig110	Solyc02g	Solyc02g	Ycf2 (AHF	GO:00095	GO:00095	contig110	Solyc09g	RING fing	GO:00065	SL2.40ch	AT3G218	ATXR2. S	ATXR2 (H	chr3:768	2442.68	2315.95	1075.3	822.965	806.331	1143.41
GT	Sense	Sense	-0.149	Detected	0.149	Detected	0.000	-2.129	Detected	-1.471	Detected	-1.800	0.038	GT	Sens	contig110	contig110	Chitinase	TTTTTTC	contig110	Solyc10g	Solyc10g	Chitinase	GO:0008	GO:0008	contig110	Solyc10g	Chitinase	GO:00059	SL2.40ch	AT5G08300.1		succinyl-	chr5:266	2024	2342.13	1205.77	1003.73	530.97	835.219
GT	Sense	Sense	0.348	Detected	-0.348	Detected	0.000	-2.439	Detected	-2.565	Detected	-2.502	0.019	GT	Sens	contig110	contig110	Auxin-res	ATTAACC	contig110	Solyc01g	Solyc01g	Auxin-responsive GH3 produc			contig110	Solyc01g	Auxin-responsive G		SL2.40ch	AT2G149	GH3.1	GH3.1	chr2:645	869.011	504.964	77.9446	169.987	130.293	118.981
GT	Sense	Sense	0.138	Detected	-0.138	Detected	0.000	-1.556	Detected	-1.084	Detected	-1.320	0.040	GT	Sens	contig111	contig111	Plant syn	CCAGTT	contig111	Solyc12g	Solyc12g	Plant synaptotagmin (AHRD V1			contig111	Solyc12g	Synaptotagmin-7 (A		SL2.40ch	AT1G055	SYTE. AT	NTMC2T	chr1:162	378.133	293.964	100.03	125.62	120.937	167.241
GT	Sense	Sense	0.411	Detected	-0.411	Detected	0.000	-1.361	Detected	-0.988	Detected	-1.175	0.121	GT	Sens	contig112	contig112	Cc-nbs-lr	GAGAAG	contig112	Solyc11g	Solyc11g	Cc-nbs-lrr resistance protein (			contig112	Solyc05g014620.1.1				AT1G086	ZIGA4	ZIGA4 (A	chr1:276	22881.9	12174.2	7345.05	8106.73	6927.47	8946.83
GT	Sense	Sense	-0.080	Detected	0.080	Detected	0.000	-1.420	Detected	-1.274	Detected	-1.347	0.006	GT	Sens	contig112	contig112	ATP-bind	TTGGAG	contig112	Solyc03g	Solyc03g	ATP-bind	GO:00168	GO:00168	contig112	Solyc03g	ATP-bind	GO:00426	SL2.40ch	AT3G477	ATATH6.	ATATH6:	chr3:176	1971.49	2071.56	704.097	986.065	805.207	888.188
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-2.152	Detected	-1.637	Detected	-1.894	0.018	GT	Sens	contig112	contig112	Unknown	ACTGGT	contig112	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig112	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G27870.1		haloacid	chr3:103	88.2875	80.508	48.4368	34.9382	20.2353	28.8189
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.317	Detected	-1.021	Detected	-1.169	0.017	GT	Sens	contig113	contig113	Squalene	ACACTG	contig113	Solyc10g	Solyc10g	Squalene	GO:0016	GO:0016	contig113	Solyc01g	Squalene	GO:00055	SL2.40ch	AT4G346	SOS1. ER	SOS1 (S	chr4:165	1199.31	1058.87	405.906	406.456	482.398	590.237
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-1.153	Detected	-1.040	Detected	-1.096	0.010	GT	Sens	contig114	contig114	Receptor	ATTCACT	contig114	Solyc10g	Solyc10g	Receptor	GO:00064	GO:00064	contig114	Solyc10g	Receptor	GO:00064	SL2.40ch	AT1G075	APK1A. A	APK1A: I	chr1:233	4607.81	4940.99	1984.26	2106.26	2288.9	2467.82
GT	Sense	Sense	0.017	Detected	-0.017	Detected	0.000	-1.215	Detected	-1.618	Detected	-1.416	0.020	GT	Sens	contig116	contig116	cDNA clo	ATATTTA	contig116	Solyc11g	Solyc11g	cDNA clo	GO:0016	GO:0016	contig116	Solyc05g	NPH3 domain conta		SL2.40ch	AT5G638	PP7. ATP	PP7 (SEF	chr5:255	1119.75	1028.68	281.946	429.577	492.973	371.791
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	-1.650	Detected	-1.492	Detected	-1.571	0.003	GT	Sens	contig116	contig116	Phi-1 pro	TCTTGCA	contig116	Solyc04g	Solyc04g	Phi-1 protein (Fragment) (AHRI			contig116	Solyc04g	Phi-1 protein (Fragn		SL2.40ch	AT4G089	EXO	EXO (EX	chr4:574	2128.59	1994.39	504.567	855.075	700.289	778.74
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-1.212	Detected	-1.005	Detected	-1.108	0.010	GT	Sens	contig118	contig118	Unknown	CAAGAAC	contig118	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig118	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G62350.1				801.589	794.18	340.868	481.268	367.343	422.71
GT	Sense	Sense	0.364	Detected	-0.364	Detected	0.000	-1.256	Detected	-1.102	Detected	-1.179	0.087	GT	Sens	contig118	contig118	U-box do	TTTGAGT	contig118	Solyc01g	Solyc01g	U-box do	GO:00054	GO:00054	contig118	Solyc01g	U-box do	GO:00054	SL2.40ch	AT4G02430.2		pre-mRN	chr4:106	932.842	530.236	179.352	154.927	314	348.293
GT	Sense	Sense	0.210	Detected	-0.210	Detected	0.000	-1.807	Detected	-1.000	Detected	-1.403	0.091	GT	Sens	contig119	contig119	Galactoki	GAAGGCT	contig119	Solyc09g	Solyc09g	Galactoki	GO:00057	GO:00057	contig119	Solyc09g	Galactoki	GO:00057	SL2.40ch	AT3G10700.1		GHMP ki	chr3:334	1436.14	1010.01	300.33	427.199	367.075	640.215
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	-1.732	Detected	-1.640	Detected	-1.686	0.003	GT	Sens	contig121	contig121	Unknown	AGTTGCT	contig121	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig121	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G424	ARC6	ARC6 (AC	chr5:169	325.626	271.82	67.3772	109.442	95.5105	101.525
GT	Sense	Sense	0.008	Detected	-0.008	Detected	0.000	-2.226	Detected	-1.377	Detected	-1.801	0.051	GT	Sens	contig121	contig121	Decarbox	CGAGAA	contig121	Solyc08g	Solyc08g	Decarbox	GO:00301	GO:00301	contig121	Solyc08g	Decarbox	GO:00301	SL2.40ch	AT1G437	emb1075	emb1075	chr1:164	514.25	478.363	87.2725	163.699	113.078	203.086
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	-1.023	Detected	-0.982	Detected	-1.003	0.001	GT	Sens	contig121	contig121	V-type AT	ATCACAC	contig121	Solyc01g	Solyc01g	V-type AT	GO:00164	GO:00164	contig121	Solyc01g	V-type AT	GO:00469	SL2.40ch	AT1G76030.1		vacuolar	chr1:285	4316.48	3928.37	1745.61	1651.01	2161.29	2215.89
GT	Sense	Sense	0.213	Detected	-0.213	Detected	0.000	-2.035	Detected	-1.489	Detected	-1.762	0.037	GT	Sens	contig125	contig125	Pectinace	GTATGTT	contig125	Solyc08g	Solyc08g	Pectinace	GO:0004	GO:0004	contig125	Solyc08g	Pectinace	GO:0004	SL2.40ch	AT4G19410.1		pectinac	chr4:105	658.389	461.095	152.673	129.935	143.333	208.646
GT	Sense	Sense	0.419	Detected	-0.419	Detected	0.000	-1.807	Detected	-1.221	Detected	-1.514	0.098	GT	Sens	contig126	contig126	Patatin-lik	CCTCAGT	contig126	Solyc04g	Solyc04g	Patatin-lik	GO:00162	GO:00162	contig126	Solyc04g	Patatin-lik	GO:00457	SL2.40ch	AT4G370	PLP4. PL	PLP4 (PA	chr4:174	829.249	436.216	69.0488	115.033	183.285	274.281
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-2.107	Detected	-1.392	Detected	-1.750	0.043	GT	Sens	contig127	contig127	Polygalac	AATGCCA	contig127	Solyc02g	Solyc02g	Polygalac	GO:00059	GO:00059	contig127	Solyc02g	Polygalac	GO:00059	SL2.40ch	AT2G43870.1		polygala	chr2:181	168971	134977	42325.1	74930.4	37372.2	61176.6
GT	Sense	Sense	0.755	Detected	-0.755	Detected	0.000	-2.479	Detected	-1.546	Detected	-2.012	0.151	GT	Sens	contig127	contig127	Acyl-CoA	ATATCTC	contig127	Solyc07g	Solyc07g	Acyl-CoA	GO:00188	GO:00188	contig127	Solyc07g	Acyl-CoA	GO:00188	SL2.40ch	AT2G17650.1		AMP-dep	chr2:767	362.155	119.71	26.7084	49.0698	39.8303	75.8069
GT	Sense	Sense	0.444	Detected	-0.444	Detected	0.000	-1.462	Detected	-1.863	Detected	-1.662	0.076	GT	Sens	contig128	contig128	Lipase (A	GCAATTT	contig128	Solyc02g	Solyc02g	Lipase (A	GO:00066	GO:00066	contig128	Solyc02g	Lipase (A	GO:00066	SL2.40ch	AT5G67050.1		lipase cla	chr5:267	751.302	381.885	143.735	107.729	207.367	156.599
GT	Sense	Sense	0.210	Detected	-0.210	Detected	0.000	-1.600	Detected	-1.647	Detected	-1.624	0.017	GT	Sens	contig128	contig128	Long-cha	GCAAGA	contig128	Solyc09g	Solyc09g	Long-cha	GO:00081	GO:00081	contig128	Solyc09g	Long-cha	GO:00044	SL2.40ch	AT3G059	LACS6. A	LACS6 (I	chr3:178	91.9073	64.6189	45.576	45.4792	27.1107	26.1569
GT	Sense	Sense	0.147	Detected	-0.147	Detected	0.000	-0.941	Detected	-1.853	Detected	-1.397	0.100	GT	Sens	contig129	contig129	UDP-gluc	GGAAAG	contig129	Solyc12g	Solyc12g	UDP-gluc	GO:00081	GO:00081	contig129	Solyc12g	UDP-gluc	GO:00081	SL2.40ch	AT1G223	AtUGT85	AtUGT85	chr1:789	81.9261	62.8354	17.1846	18.9812	39.8632	21.1134
GT	Sense	Sense	0.374	Detected	-0.374	Detected	0.000	-2.339	Comprom	-0.946	Detected	-1.643	0.173	GT	Sens	contig131	contig131	Gag-Pol r	CTCCGA	contig131	Solyc01g	Solyc01g	Gag-Pol r	GO:00082	GO:00082	contig131	Solyc02g	Transpos	GO:00036	SL2.40ch	AT1G57610.3		unknown	chr1:213	40.2014	22.5204	11.9269	17.8036	6.34081	16.6012
GT	Sense	Sense	0.263	Detected	-0.263	Detected	0.000	-1.312	Detected	-1.217	Detected	-1.264	0.042	GT	Sens	contig132	contig132	LRR rece	TGAATG	contig132	Solyc04g	Solyc04g	LRR rece	GO:00046	GO:00046	contig132	Solyc04g014200.1.1				AT4G208	FAH2. AT	FAH2 (FA	chr4:111	102.253	66.7868	34.1851	27.2927	35.4982	37.8084
GT	Sense	Sense	0.644	Detected	-0.644	Detected	0.000	-4.408	Detected	-3.960	Detected	-4.184	0.026	GT	Sens	contig132	contig132	Acyltrans	GTGTGT	contig132	Solyc11g	Solyc11g	Acyltrans	GO:00167	GO:00167	contig132	Solyc11g	Acyltrans	GO:00167	SL2.40ch	AT5G59400.2		unknown	chr5:239	451.637	173.948	66.0745	190.369	14.0815	19.1495
GT	Sense	Sense	-0.320	Detected	0.320	Detected	0.000	-0.992	Detected	-1.056	Detected	-1.024	0.086	GT	Sens	contig135	contig135	Copper io	TGGGGC	contig135	Solyc10g	Solyc10g	Copper ion binding protein (AI			contig135	Solyc10g	Copper ion binding		SL2.40ch	AT5G07650.1		formin ho	chr5:241	260.418	381.963	100.647	95.2032	169.118	161.234
GT	Sense	Sense	0.316	Detected	-0.316	Detected	0.000	-0.978	Detected	-1.429	Detected	-1.203	0.090	GT	Sens	contig137	contig137	Glutathio	TGGAAG	contig137	Solyc03g	Solyc03g	Glutathio	GO:00043	GO:00043	contig137	Solyc09g	UDP-gluc	GO:00081	SL2.40ch	#N/A	#N/A	#N/A	#N/A	49.2413	29.8856	15.7026	13.213	20.767	15.1489
GT	Sense	Sense	0.076	Detected	-0.076	Detected	0.000	-1.998	Detected	-1.638	Detected	-1.818	0.011	GT	Sens	contig141	contig141	Peroxidas	TTGACTC	contig141	Solyc02g	Solyc02g	Peroxidas	GO:00055	GO:00055	contig141	Solyc02g	Peroxidas	GO:00046	SL2.40ch	AT5G19890.1		peroxida	chr5:672	1386.36	1173.59	306.987	370.668	340.595	435.866
GT	Sense	Sense	-0.079	Detected	0.079	Detected	0.000	-2.233	Detected	-1.725	Detected	-1.979	0.018	GT	Sens	contig142	contig142	Laccase	CAACTAT	contig142	Solyc04g	Solyc04g	Laccase	GO:00551	GO:00551	contig142	Solyc04g	Laccase 1	GO:00055	SL2.40ch	AT4G39830.1		L-ascorb	chr4:184	2886.42	3028.61	416.235	914.65	670.532	950.863
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-1.978	Detected	-1.984	Detected	-1.981	0.002	GT	Sens	contig143	contig143	Zinc fing	TGGTGA	contig143	Solyc05g	Solyc05g	Zinc fing	GO:00037	GO:00037	contig143	Solyc05g	Zinc fing	GO:00037	SL2.40ch	AT5G03510.1		zinc fing	chr5:880	454.15	375.44	74.2863	89.3182	111.74	110.96
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-2.749	Detected	-3.106	Detected	-2.928	0.004	GT	Sens	contig143	contig143	Receptor	ATCAGTT	contig143	Solyc03g	Solyc03g	Receptor	GO:00055	IGO:0004	contig143	Solyc03g	Receptor	GO:00046	SL2.40ch	AT5G24080.1		protein k	chr5:813	4795.62	4427.67	994.042	1043.5	730.848	568.88
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-1.633	Detected	-1.375	Detected	-1.504	0.011	GT	Sens	contig147	contig147	Glycosylt	GTATATC	contig147	Solyc02g	Solyc02g	Glycosylt	GO:00472	GO:00472	contig147	Solyc02g	Glycosylt	GO:00472	SL2.40ch	AT5G154	GAUT14	GAUT14	chr5:502	1353.43	1126.97	263.867	470.083	424.726	506.361
GT	Sense	Sense	1.481	Detected	-1.481	Detected	0.000	-1.137	Detected	-3.962	Comprom	-2.549	0.339	GT	Sens	contig148	contig148	Receptor	ATCTTCA	contig148	Solyc12g	Solyc12g	Receptor	GO:00064	GO:00064	contig148	Solyc12g	RLK. Rec	GO:00046	SL2.40ch	AT4G27290.1		ATP bind	chr4:136	139.289	16.812	21.2838	10.7026	23.4623	3.30199
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-2.073	Detected	-1.179	Detected	-1.626	0.068	GT	Sens	contig148	contig148	Decarbox	GTGCAAC	contig148	Solyc08g	Solyc08g	Decarbox	GO:00197	GO:00197	contig148	Solyc08g	Decarbox	GO:00301	SL2.40ch	AT1G437	emb1075	emb1075	chr1:164	616.334	595.207	130.716	237.414	153.466	284.438
GT	Sense	Sense	-0.395	Detected	0.395	Detected	0.000	-1.643	Detected	-1.864	Detected	-1.754	0.051	GT	Sens	contig148	contig148	Proteinas	TGGATT	contig148	Solyc03g	Solyc03g	Proteinas	GO:00048	GO:00048	contig148	Solyc03g	Proteinas	GO:00048	SL2.40ch	AT4G15830.1		binding	chr4:899	1181.3	1921.12	684.628	1118.75	514.276	440.055
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	-1.325	Detected	-0.855	Detected	-1.090	0.055	GT	Sens	contig148	contig148	Coatomer	TTTGGAT	contig148	Solyc12g	Solyc12g	Coatomer	GO:00055	GO:00055	contig148	Solyc12g	Coatomer	GO:00055	SL2.40ch	AT3G09800.2		protein b	chr3:300	338.002	266.649	116.974	154.889	127.788	176.473
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-1.290	Detected	-0.965	Detected	-1.128	0.021	GT	Sens	contig150	contig150	Unknown	CCGGTG	contig150	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig150	Solyc10g	Unknown Protein (A		SL2.40ch	AT2G200	HBT. CDC	HBT (HO	chr2:863	1799.79	1627.88	946.438	956.162	746.216	932.354
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	-1.828	Detected	-2.620	Detected	-2.224	0.037	GT	Sens	contig154	contig154	Unknown	GTAGTC	contig154	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)%			contig154	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G19680.1		unknown	chr3:684	575.775	413.094	74.5269	96.5718	146.44	84.3241
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	-1.353	Detected	-0.898	Detected	-1.125	0.039	GT	Sens	contig154	contig154	Cytochro	TGTTGG	contig154	Solyc06g	Solyc06g	Cytochro	GO:0020	GO:0020	contig154	Solyc06g	Cytochro	GO:00451	SL2.40ch	AT5G488	ATB5-B. I	CB5-D (C	chr5:197	11575.6	10746.8	4290.29	5360.54	4657.63	6365.12
GT	Sense	Sense	0.222	Detected	-0.222	Detected	0.000	-3.147	Detected	-3.309	Detected	-3.228	0.005	GT	Sens	contig157	contig157	Dirigent-l	ATGGAAC	contig157	Solyc01g	Solyc01g	Dirigent-like protein 1 (AHRD V			contig157	Solyc01g	Disease resistance		SL2.40ch	AT1G58170.1		disease r	chr1:215	7137.47	4936.79	1235.13	889.039	714.768	636.612
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-1.388	Detected	-0.977	Detected	-1.183	0.034	GT	Sens	contig158	contig158	Adenosyl	TAATGAC	contig158	Solyc09g	Solyc09g	Adenosyl	GO:0004	GO:0004	contig158	Solyc09g	Adenosyl	GO:0004	SL2.40ch	AT4G139	HOG1. EM	MEE58 (I	chr4:805	8484.26	7066.06	2528.39	2600.38	3153.94	4181.62
GT	Sense	Sense	0.109	Detected	-0.109	Detected	0.000	-1.180	Detected	-0.909	Detected	-1.044	0.027	GT	Sens	contig158	contig158	Adenosyl	TTAATGA	contig158	Solyc12g	Solyc12g	Adenosyl	GO:00067	GO:00067	contig158	Solyc12g	Adenosyl	GO:00067	SL2.40ch	AT4G139	HOG1. EM	MEE58 (I	chr4:805	4552.02	3684.64	1374.22	1426.53	1927.18	2319.57
GT	Sense	Sense	0.076	Detected	-0.076	Detected	0.000	-0.961	Detected	-1.444	Comprom	-1.202	0.041	GT	Sens	contig158	contig158	Zeatin O-	TCTCCAT	contig158	Solyc07g	Solyc07g	Zeatin O-glucosyltransferase (			contig158	Solyc07g	UDP-gluc	GO:00080	SL2.40ch	AT3G496	UBP26. S	UBP26 (U	chr3:183	25.1233	21.2822	10.47	12.3329	12.6636	9.03853
GT	Sense	Sense	0.160	Detected	-0.160	Detected	0.000	-1.159	Detected	-1.059	Detected	-1.109	0.022	GT	Sens	contig160	contig160	Tudor / n	ATAAATG	contig160	Solyc03g	Solyc03g	Tudor / n	GO:00037	GO:00037	contig160	Solyc03g	Tudor / n	GO:00037	SL2.40ch	AT5G07350.2		tudor do	chr5:231	9577.34	7222.41	2984.68	3484.54	3971.73	4243.23
GT	Sense	Sense	-0.057	Detected	0.057	Detected	0.000	-0.985	Detected	-2.093	Detected	-1.539	0.110	GT	Sens	contig160	contig160	Glutathio	TTTACAC	contig160	Solyc01g	Solyc01g	Glutathione S-transferase (AHI			contig160	Solyc01g	Glutathione S-trans		SL2.40ch	AT2G294	ATGSTU	ATGSTU	chr2:126	164.204	167.296	80.4146	54.0148	89.2767	41.3083
GT	Sense	Sense	-0.159	Detected	0.159	Detected	0.000	-2.077	Detected	-1.372	Detected	-1.725	0.047	GT	Sens	contig161	contig161	Histone H	AAGTTCT	contig161	Solyc05g	Solyc05g	Histone H	GO:00056	GO:00056	contig161	Solyc05g	Histone H	GO:00056	SL2.40ch	AT2G287	HIS4	HIS4: DN	chr2:123	420.91	493.746	252.718	115.49	115.181	187.294
GT	Sense	Sense	0.239	Detected	-0.239	Detected	0.000	-2.900	Detected	-2.160	Detected	-2.530	0.029	GT	Sens	contig161	contig161	Unknown	CCTGTG	contig161	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig161	Solyc02g067600.1.1				AT5G25590.1		INVOLVE	chr5:890	503.691	340.05	102.828	206.262	59.1101	98.4507
GT	Sense	Sense	-0.405	Detected	0.405	Detected	0.000	-1.099	Detected	-0.988	Detected	-1.044	0.125	GT	Sens	contig165	contig165	Unknown	GCATAAC	contig165	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig165	Solyc11g	Agenet d	GO:00036	SL2.40ch	AT3G10595.1				357.343	589.332	198.019	229.711	228.477	245.911
GT	Sense	Sense	-0.159	Detected	0.159	Detected	0.000	-1.222	Detected	-1.167	Detected	-1.194	0.018	GT	Sens	contig166	contig166	Histidine	TAGCACC	contig166	Solyc08g	Solyc08g	Histidine decarboxylase (AHRI			contig166	Solyc08g	Histidine decarboxy		SL2.40ch	AT5G130	ATGSL12	ATGSL12	chr5:411	180.903	212.204	76.5623	109.123	89.5977	92.7735
GT	Sense	Sense	0.311	Detected	-0.311	Detected	0.000	-2.846	Detected	-2.148	Detected	-2.497	0.033	GT	Sens	contig167	contig167	FAD-bind	TGGGGT	contig167	Solyc02g	Solyc02g	FAD-bind	GO:00506	GO:00506	contig167	Solyc02g	FAD-bind	GO:00506	SL2.40ch	AT5G44390.1		FAD-bind	chr5:178	37273.7	22798	5400.47	7789.1	4323.32	6994.71
GT	Sense	Sense	0.241	Detected	-0.241	Detected	0.000	-0.964	Detected	-1.977	Comprom	-1.470	0.120	GT	Sens	contig167	contig167	CK25 (AH	AACCGG	contig167	Solyc07g	Solyc07g	CK25 (AHRD V1 ***- Q1W1G0_T			contig167	Solyc07g	CK25 (AHRD V1 ***-		SL2.40ch	AT4G222	IM. IM1	IM (IMMU	chr4:117	22.6834	15.272	4.59155	6.89221	10.1769	5.02593
GT	Sense	Sense	0.344	Detected	-0.344	Detected	0.000	-0.903	Detected	-1.276	Comprom	-1.089	0.108	GT	Sens	contig173	contig173	Copper io	TTTTCTT	contig173	Solyc01g	Solyc01g	Copper ion binding protein (AI			contig173	Solyc01g	Copper ion binding		SL2.40ch	AT3G07840.1		polygala	chr3:250	22.6622	13.2392	1.69633	1.91995	9.878	7.60523
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-1.393	Detected	-1.617	Detected	-1.505	0.006	GT	Sens	contig174	contig174	Aquapori	GTTGGT	contig174	Solyc09g	Solyc09g	Aquapori	GO:0016	GO:0016	contig174	Solyc09g	Aquapori	GO:00152	SL2.40ch	AT4G004	TMP-C. P	PIP1;4 (P	chr4:186	14303	14071.3	5666.54	3280.26	5758.51	4918.85
GT	Sense	Sense	0.157	Detected	-0.157	Detected	0.000	-1.944	Detected	-1.809	Detected	-1.876	0.008	GT	Sens	contig174	contig174	SEC14 cy	ATTATCA	contig174	Solyc01g	Solyc01g	SEC14 cy	GO:00052	GO:00052	contig174	Solyc01g	SEC14 cy	GO:00052	SL2.40ch	AT1G14820.1		SEC14 cy	chr1:510	645.385	488.676	154.006	169.331	155.678	170.424
GT	Sense	Sense	0.122	Detected	-0.122	Detected	0.000	-1.793	Detected	-1.738	Detected	-1.766	0.005	GT	Sens	contig174	contig174	Phospho	ACGTGTT	contig174	Solyc10g	Solyc10g	Phospho	GO:00055	GO:00055	contig174	Solyc10g	Phospho	GO:00055	SL2.40ch	AT3G149	ATPPC3	ATPPC3	chr3:502	8467.08	6728.87	1464.7	2131	2322.26	2405.03
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	-1.469	Detected	-0.887	Detected	-1.178	0.067	GT	Sens	contig176	contig176	Kinase fa	AAAGAAC	contig176	Solyc01g	Solyc01g	Kinase family protein (AHRD V			contig176	Solyc01g	Receptor	GO:00064	SL2.40ch	AT4G02010.1		protein k	chr4:881	90.2646	103.031	27.2062	24.6799	37.1518	55.4408
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-1.056	Detected	-1.115	Detected	-1.086	0.005	GT	Sens	contig176	contig176	Beta-1 3-	ACAAGG	contig176	Solyc07g	Solyc07g	Beta-1 3-	GO:0016	GO:0016	contig176	Solyc07g	Beta-1 3-	GO:0016	SL2.40ch	AT2G32430.1		galactos	chr2:137	746.701	637.933	200.056	208.78	353.929	338.835
GT	Sense	Sense	-0.137	Detected	0.137	Detected	0.000	-1.126	Detected	-1.207	Detected	-1.166	0.015	GT	Sens	contig176	contig176	Cycloarte	CCGGAC	contig176	Solyc12g	Solyc12g	Cycloarte	GO:00168	GO:00168	contig176	Solyc12g	Cycloarte	GO:00168	SL2.40ch	AT1G78950.1		beta-amy	chr1:296	664.554	755.705	186.433	188.061	346.365	326.436
GT	Sense	Sense	0.275	Detected	-0.275	Detected	0.000	-4.373	Comprom	-2.461	Detected	-3.417	0.075	GT	Sens	contig177	contig177	Unknown	GGTTTT	contig177	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig177	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G11760.1		unknown	chr3:371	70.7703	45.4729	4.34958	15.5231	2.91932	10.9561
GT	Sense	Sense	0.290	Detected	-0.290	Detected	0.000	-1.904	Detected	-1.598	Detected	-1.751	0.033	GT	Sens	contig178	contig178	Equilibrat	TATGTC	contig178	Solyc02g	Solyc02g	Equilibrat	GO:00053	GO:00053	contig178	Solyc02g079330.2.1				AT4G05140.1		equilibra	chr4:265	306.362	192.95	62.1317	72.1214	69.2666	85.3834
GT	Sense	Sense	0.723	Detected	-0.723	Detected	0.000	-2.412	Detected	-1.983	Detected	-2.197	0.100	GT	Sens	contig178	contig178	CM0216.3	CCTTTC	contig178	Solyc02g	Solyc02g	CM0216.330.nc protein (AHRD			contig178	Solyc02g	CM0216.330.nc prot		SL2.40ch	AT3G15080.1		exonucle	chr3:507	94.3552	32.6043	9.60416	10.9768	11.1163	14.9206
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-3.298	Detected	-2.649	Detected	-2.974	0.013	GT	Sens	contig179	contig179	Ornithine	CATTTAC	contig179	Solyc03g	Solyc03g	Ornithine	GO:00038	GO:00038	contig179	Solyc03g	Ornithine	GO:00045	SL2.40ch	AT5G42130.1		mitochon	chr5:168	2802.16	2280.59	383.861	460.769	274.009	428.549
GT	Sense	Sense	0.122	Detected	-0.122	Detected	0.000	-2.433	Comprom	-3.344	Comprom	-2.888	0.026	GT	Sens	contig180	contig180	Protein pl	CGCGAG	contig180	Solyc08g	Solyc08g	Protein pl	GO:00038	GO:00038	contig180	Solyc08g	Protein pl	GO:00038	SL2.40ch	AT5G26010.1		catalytic/	chr5:908	23.0889	18.3373	8.78104	1.97824	4.0644	2.15501
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	-4.323	Comprom	-2.219	Comprom	-3.271	0.090	GT	Sens	contig181	contig181	Agenet d	TATCAGT	contig181	Solyc06g	Solyc06g	Agenet domain-containing pro			contig181	Solyc06g	Agenet domain-cont		SL2.40ch	AT5G49960.1		binding /	chr5:203	36.6911	38.2552	6.06268	4.78321	1.99626	8.55751
GT	Sense	Sense	0.099	Detected	-0.099	Detected	0.000	-1.654	Detected	-1.450	Detected	-1.552	0.008	GT	Sens	contig181	contig181	Xylogluc	TCTTCTT	contig181	Solyc03g	Solyc03g	Xylogluc	GO:00059	GO:00059	contig181	Solyc03g	Xylogluc	GO:00167	SL2.40ch	AT4G258	XTR6. XT	XTR6 (XY	chr4:131	9830.25	8059.18	2710.56	5507.83	3016.71	3464.05
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	-1.025	Detected	-1.092	Detected	-1.059	0.002	GT	Sens	contig182	contig182	Kinase-S	CCAGTAT	contig182	Solyc08g	Solyc08g	Kinase-S	GO:00082	GO:00082	contig182	Solyc12g	Kinase-START 1 (Fr		SL2.40ch	AT4G190	EDR2	EDR2: lip	chr4:104	228.522	207.238	58.6779	83.2908	114.051	108.526
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.263	Detected	-0.814	Detected	-1.039	0.044	GT	Sens	contig183	contig183	Calcium-	GGCAAG	contig183	Solyc04g	Solyc04g	Calcium-	GO:00046	GO:00046	contig183	Solyc04g	Calcium-	GO:00046	SL2.40ch	AT5G048	CPK1. AT	CPK1 (C	chr5:141	26531.7	24448.4	9663.31	16334.5	11318.6	15398
GT	Sense	Sense	0.065	Detected	-0.065	Detected	0.000	-1.152	Detected	-1.138	Detected	-1.145	0.003	GT	Sens	contig183	contig183	Fumarate	TCAAGG	contig183	Solyc06g	Solyc06g	Fumarate	GO:00038	GO:00038	contig183	Solyc06g	Fumarate	GO:00038	SL2.40ch	AT2G475	FUM1	FUM1 (FU	chr2:194	749.18	643.864	209.928	262.618	333.396	335.522
GT	Sense	Sense	0.266	Detected	-0.266	Detected	0.000	-3.797	Detected	-2.385	Detected	-3.091	0.055	GT	Sens	contig184	contig184	DC1 dom	ACTGCAT	contig184	Solyc01g	Solyc01g	DC1 domain containing protei			contig184	Solyc01g	CHP-rich zinc finger		SL2.40ch	AT2G16250.1		leucine-r	chr2:703	204.23	132.838	51.9778	65.6966	12.6393	33.5205
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-1.829	Detected	-1.615	Detected	-1.722	0.005	GT	Sens	contig184	contig184	Phi-1 pro	GAAGCT	contig184	Solyc04g	Solyc04g	Phi-1 protein (Fragment) (AHRI			contig184	Solyc04g	Phi-1 protein (Fragn		SL2.40ch	AT4G089	EXO	EXO (EX	chr4:574	53285.6	46377.9	12231.3	24512.1	14922.2	17260
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	-3.828	Detected	-2.783	Detected	-3.305	0.026	GT	Sens	contig185	contig185	Polygalac	AAAGAG	contig185	Solyc12g	Solyc12g	Polygalac	GO:00059	GO:00059	contig185	Solyc12g	Polygalac	GO:00059	SL2.40ch	AT5G14650.1		polygala	chr5:472	65044.9	50989.8	12370.6	23655.8	4325.57	8896.8
GT	Sense	Sense	0.210	Detected	-0.210	Detected	0.000	-1.554	Detected	-1.137	Detected	-1.345	0.045	GT	Sens	contig186	contig186	Unknown	TGATCG	contig186	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig186	Solyc04g045490.1.1				AT4G014	GAMMA-T	TIP1;3 (T	chr4:625	168.628	118.668	48.3973	66.1274	51.365	68.4026
GT	Sense	Sense	-0.085	Detected	0.085	Detected	0.000	-1.517	Detected	-1.494	Detected	-1.505	0.003	GT	Sens	contig187	contig187	Unknown	AGCCTG	contig187	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig187	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G27700.2		RNA reco	chr3:102	267.706	283.224	77.8651	102.924	102.629	103.971
GT	Sense	Sense	0.190	Detected	-0.190	Detected	0.000	-3.737	Detected	-1.850	Detected	-2.794	0.101	GT	Sens	contig189	contig189	Mutant re	CTCCAA	contig189	Solyc08g	Solyc08g	Mutant required to maintain re			contig189	Solyc08g077640.1.1				AT4G38200.1		guanine	chr4:179	649.877	470.191	82.2662	174.382	44.2061	163.033
GT	Sense	Sense	0.155	Detected	-0.155	Detected	0.000	-2.426	Detected	-2.085	Detected	-2.256	0.010	GT	Sens	contig190	contig190	CNGC5-lik	TTCTGT	contig190	Solyc06g	Solyc06g	CNGC5-like protein (Fragment			contig190	Solyc11g	Cyclic nu	GO:0016	SL2.40ch	AT5G531	CNGC1. A	CNGC1 ((	chr5:215	850.325	645.057	153.179	138.111	146.916	185.594
GT	Sense	Sense	0.326	Detected	-0.326	Detected	0.000	-2.842	Detected	-2.766	Detected	-2.804	0.013	GT	Sens	contig190	contig190	Unknown	CATGGG	contig190	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig190	Solyc01g	Disease resistance		SL2.40ch	AT3G13650.1				13437.9	8048.44	2800.83	1853.79	1546.71	1625.5
GT	Sense	Sense	-0.007	Detected	0.007	Detected	0.000	-1.913	Detected	-2.054	Detected	-1.984	0.001	GT	Sens	contig192	contig192	Os06g02	GTGCTT	contig192	Solyc04g	Solyc04g	Os06g0220000 protein (Fragm			contig192	Solyc04g	Os06g0220000 prot		SL2.40ch	AT4G089	EXO	EXO (EX	chr4:574	1534.48	1458.72	283.31	568.733	423.582	383.003
GT	Sense	Sense	-0.169	Detected	0.169	Detected	0.000	-0.809	Detected	-1.567	Detected	-1.188	0.103	GT	Sens	contig192	contig192	Cytochro	TTTCAA	contig192	Solyc03g	Solyc03g	Cytochro	GO:0020	GO:0020	contig192	Solyc03g	Cytochro	GO:00045	SL2.40ch	AT3G483	CYP71A2	CYP71A2	chr3:178	308.61	366.869	145.47	87.8045	204.778	120.733
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.543	Detected	-1.015	Detected	-1.279	0.040	GT	Sens	contig192	contig192	3-phosph	AATCTC	contig192	Solyc01g	Solyc01g	3-phosph	GO:00038	GO:00038	contig192	Solyc01g	3-phosph	GO:00038	SL2.40ch	AT2G45300.1		3-phosph	chr2:186	1563.08	1429.31	382.38	397.465	547.107	786.52
GT	Sense	Sense	0.362	Detected	-0.362	Detected	0.000	-1.553	Detected	-1.420	Detected	-1.486	0.056	GT	Sens	contig193	contig193	U-box do	AAATGGT	contig193	Solyc01g	Solyc01g	U-box do	GO:00054	GO:00054	contig193	Solyc01g	U-box do	GO:00048	SL2.40ch	AT1G105	PUB18. A	PUB18 (F	chr1:348	944.864	538.431	127.288	127.959	259.204	283.459
GT	Sense	Sense	0.315	Detected	-0.315	Detected	0.000	-0.955	Detected	-1.937	Detected	-1.446	0.132	GT	Sens	contig193	contig193	Alcohol d	GGTAAT	contig193	Solyc12g	Solyc12g	Alcohol d	GO:00081	GO:00081	contig193	Solyc12g	Alcohol d	GO:00081	SL2.40ch	AT5G16980.1		NADP-de	chr5:557	6363.37	3869.33	1820.25	792.073	2730.08	1377.43
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	-2.232	Detected	-1.949	Detected	-2.091	0.006	GT	Sens	contig193	contig193	Purple ac	ATGTGG	contig193	Solyc01g	Solyc01g	Purple ac	GO:00468	GO:00468	contig193	Solyc01g	Purple ac	GO:00047	SL2.40ch	AT2G164	PAP10. A	PAP10 (F	chr2:712	2612.53	2737.57	1032.57	407.227	606.852	736.519
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	-2.440	Detected	-2.696	Detected	-2.568	0.005	GT	Sens	contig194	contig194	UDP-gluc	AAACATC	contig194	Solyc12g	Solyc12g	UDP-gluc	GO:00081	GO:00081	contig194	Solyc12g	UDP-gluc	GO:00081	SL2.40ch	AT1G223	AtUGT85	AtUGT85	chr1:789	908.468	712.212	96.313	127.456	158.121	132.007
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	-1.156	Detected	-1.731	Comprom	-1.443	0.070	GT	Sens	contig194	contig194	Cytochro	TCAGTG	contig194	Solyc10g	Solyc10g	Cytochro	GO:0020	GO:0020	contig194	Solyc10g084590.2.1				AT4G153	CYP705A	CYP705A	chr4:875	29.9423	19.0645	5.84719	7.62336	11.437	7.65478
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	-2.415	Detected	-1.748	Detected	-2.082	0.027	GT	Sens	contig196	contig196	Polygalac	TGTGAC	contig196	Solyc02g	Solyc02g	Polygalac	GO:00059	GO:00059	contig196	Solyc02g	Polygalac	GO:00059	SL2.40ch	AT3G59850.1		polygala	chr3:221	131799	108466	24392.7	46330.9	23904.9	37841.3
GT	Sense	Sense	0.336	Detected	-0.336	Detected	0.000	-1.345	Detected	-0.869	Detected	-1.107	0.115	GT	Sens	contig196	contig196	Unknown	AGGTAC	contig196	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig196	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G07630.1		lipid tran	chr5:241	61.7533	36.4816	23.3854	48.8014	19.9201	27.6213
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-1.774	Detected	-1.654	Detected	-1.714	0.003	GT	Sens	contig197	contig197	Phi-1 pro	TTACAA	contig197	Solyc04g	Solyc04g	Phi-1 protein (Fragment) (AHRI			contig197	Solyc04g	Phi-1 protein (Fragn		SL2.40ch	AT4G089	EXO	EXO (EX	chr4:574	57204.9	49150.5	12496.1	24665.9	16533.8	17917.6
GT	Sense	Sense	0.639	Detected	-0.639	Detected	0.000	-2.071	Comprom	-1.719	Detected	-1.895	0.104	GT	Sens	contig201	contig201	Glutaredo	GAGAAG	contig201	Solyc05g	Solyc05g	Glutaredo	GO:00454	GO:00454	contig201	Solyc05g	Glutaredo	GO:00087	SL2.40ch	AT1G47350.1		F-box far	chr1:173	58.4434	22.6876	19.3976	5.94361	9.24301	11.7601
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-0.934	Detected	-1.249	Detected	-1.091	0.027	GT	Sens	contig206	contig206	Leucine-r	GATGAC	contig206	Solyc12g	Solyc12g	Leucine-r	GO:00055	GO:00055	contig206	Solyc12g009690.1.1				AT1G25320.1		leucine-r	chr1:887	275.804	295.759	85.0677	91.2706	159.399	127.785
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	-3.288	Detected	-3.151	Detected	-3.220	0.001	GT	Sens	contig206	contig206	Peroxidas	GAAACC	contig206	Solyc05g	Solyc05g	Peroxidas	GO:00055	GO:00055	contig206	Solyc05g	Peroxidas	GO:00046	SL2.40ch	AT3G21770.1		peroxida	chr3:767	892.324	729.202	175.749	156.073	88.0565	96.5475
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.952	Detected	-1.799	Detected	-1.876	0.002	GT	Sens	contig207	contig207	Dof zinc f	TTACTAT	contig207	Solyc00g	Solyc00g	Dof zinc f	GO:0045449		contig207	Solyc04g	Dof zinc f	GO:00454	SL2.40ch	AT3G212	ADOF2	ADOF2: I	chr3:747	824.364	733.288	120.61	127.279	214.233	237.579
GT	Sense	Sense	-0.361	Detected	0.361	Detected	0.000	-0.923	Detected	-1.184	Detected	-1.054	0.111	GT	Sens	contig208	contig208	Desiccati	TACAAA	contig208	Solyc01g	Solyc01g	Desiccation-related protein PC			contig208	Solyc01g	Desiccation-related		SL2.40ch	AT1G47980.1		unknown	chr1:176	520.64	807.983	646.645	486.959	364.764	303.475
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-1.097	Detected	-1.561	Detected	-1.329	0.030	GT	Sens	contig210	contig210	Endochiti	TTCTTTC	contig210	Solyc10g	Solyc10g	Endochiti	GO:00059	GO:00059	contig210	Solyc10g	Endochiti	GO:00088	SL2.40ch	AT3G125	ATHCHIB	ATHCHIB	chr3:396	49.7706	43.8195	11.2168	13.4721	23.2783	16.8311
GT	Sense	Sense	0.049	Detected	-0.049	Detected	0.000	-1.648	Detected	-1.571	Detected	-1.610	0.001	GT	Sens	contig210	contig210	Os06g02	CACAGA	contig210	Solyc00g	Solyc00g	Os06g0220000 protein (Fragm			contig210	Solyc00g206460.1.1				AT4G089	EXO	EXO (EX	chr4:574	58438.6	51379.7	14577.8	25893.2	18640.3	19605.8
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	-2.180	Detected	-2.272	Detected	-2.226	0.001	GT	Sens	contig210	contig210	S-like ribo	AGCAGAT	contig210	Solyc04g	Solyc04g	S-like ribo	GO:00338	GO:00338	contig210	Solyc05g	Ribonucle	GO:00045	SL2.40ch	AT2G029	RNS1. AT	RNS1 (RI	chr2:873	30399.7	30332.8	13665	9974.54	7143.75	6684.19
GT	Sense	Sense	0.292	Detected	-0.292	Detected	0.000	-1.774	Comprom	-1.228	Comprom	-1.501	0.064	GT	Sens	contig211	contig211	Folate/bio	ATTCCTT	contig211	Solyc06g	Solyc06g	Folate/biopterin transporter fa			contig211	Solyc06g	Folate/bio	GO:00152	SL2.40ch	AT1G24460.1		unknown	chr1:866	28.7461	18.0536	10.4529	20.3664	7.10185	10.3405
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-1.821	Detected	-2.415	Detected	-2.118	0.021	GT	Sens	contig212	contig212	Receptor	CATTGCT	contig212	Solyc06g	Solyc06g	Receptor	GO:00055	IGO:0004	contig212	Solyc06g	Receptor	GO:00046	SL2.40ch	AT5G24080.1		protein k	chr5:813	537.293	446.458	116.65	124.806	147.867	97.6519
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-1.274	Detected	-1.194	Detected	-1.234	0.002	GT	Sens	contig213	contig213	Unknown	TACTCAA	contig213	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig213	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G10390.2		nucleop	chr1:340	2416.17	2184.77	626.483	1185.72	1013.49	1067.77
GT	Sense	Sense	0.421	Detected	-0.421	Detected	0.000	-1.707	Detected	-1.106	Detected	-1.406	0.113	GT	Sens	contig214	contig214	Cytochro	CAAATGT	contig214	Solyc09g	Solyc09g	Cytochro	GO:00198	GO:00198	contig214	Solyc09g	Cytochro	GO:00198	SL2.40ch	AT3G262	CYP71B2	CYP71B2	chr3:959	25860.4	13576.5	4848.81	8144.29	6120.41	9255.4
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.955	Detected	-1.170	Detected	-1.563	0.059	GT	Sens	contig215	contig215	Unknown	CCATCCT	contig215	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)%			contig215	Solyc08g	Homology to unkno		SL2.40ch	AT2G25800.1		INVOLVE	chr2:110	49.555	43.3056	10.2006	14.7473	12.7437	21.8848
GT	Sense	Sense	-0.002	Detected	0.002	Detected	0.000	-1.282	Detected	-0.962	Detected	-1.122	0.020	GT	Sens	contig215	contig215	Tubulin a	ATGAATT	contig215	Solyc08g	Solyc08g	Tubulin a	GO:00432	GO:00432	contig215	Solyc08g	Tubulin a	GO:00469	SL2.40ch	AT4G149	TUA6	TUA6: st	chr4:854	41191.3	38864.6	14840.6	16322.6	17543.6	21839.5
GT	Sense	Sense	0.497	Detected	-0.497	Detected	0.000	-2.890	Comprom	-1.197	Comprom	-2.044	0.173	GT	Sens	contig215	contig215	D-galactu	TTCCTAC	contig215	Solyc09g	Solyc09g	D-galacturonic acid-1-P kinase			contig215	Solyc07g	Galactoki	GO:00163	SL2.40ch	AT1G146	ATNHX8.	ATNHX8:	chr1:503	29.7246	14.0514	2.13884	5.649	2.9401	9.47618
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	-1.830	Detected	-1.484	Detected	-1.657	0.020	GT	Sens	contig215	contig215	UDP-gluc	TATTCTC	contig215	Solyc02g	Solyc02g	UDP-gluc	GO:00039	GO:00039	contig215	Solyc02g	UDP-gluc	GO:00039	SL2.40ch	AT5G15490.1		UDP-gluc	chr5:502	16327.6	12224.3	2649.56	3892.67	4238.76	5371.11
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-1.738	Detected	-1.541	Detected	-1.639	0.006	GT	Sens	contig215	contig215	Xylogluc	TCTTCTT	contig215	Solyc03g	Solyc03g	Xylogluc	GO:00167	GO:00167	contig215	Solyc03g	Xylogluc	GO:00167	SL2.40ch	AT4G258	XTR6. XT	XTR6 (XY	chr4:131	18515.1	15513.9	5143.63	10802.5	5417.22	6193.38
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-1.795	Detected	-1.570	Detected	-1.683	0.007	GT	Sens	contig218	contig218	Xylogluc	TCTTCTT	contig218	Solyc03g	Solyc03g	Xylogluc	GO:00059	GO:00059	contig218	Solyc03g	Xylogluc	GO:00167	SL2.40ch	AT4G258	XTR6. XT	XTR6 (XY	chr4:131	17521.3	14566.9	5071.36	10158.4	4907.94	5719.11
GT	Sense	Sense	0.328	Detected	-0.328	Detected	0.000	-3.014	Detected	-2.613	Detected	-2.814	0.018	GT	Sens	contig218	contig218	Short cha	TCATCTC	contig218	Solyc06g	Solyc06g	Short cha	GO:00055	GO:00055	contig218	Solyc06g	Short cha	GO:00055	SL2.40ch	AT2G29310.1		tropinon	chr2:125	2740.4	1635.48	306.457	286.785	279.379	368.004
GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-2.023	Detected	-1.414	Detected	-1.718	0.037	GT	Sens	contig222	contig222	Leucine-r	GGCAAT	contig222	Solyc01g	Solyc01g	Leucine-r	GO:00055	GO:00055	contig222	Solyc01g	LRR rece	GO:00163	SL2.40ch	AT4G08850.2		kinase	chr4:563	66.891	50.8589	8.8088	21.4701	15.3023	23.2739
GT	Sense	Sense	0.424	Detected	-0.424	Detected	0.000	-2.629	Detected	-1.980	Detected	-2.304	0.050	GT	Sens	contig222	contig222	FAD-bind	GTCTAC	contig222	Solyc02g	Solyc02g	FAD-bind	GO:00506	GO:00506	contig222	Solyc02g070160.1.1				AT5G44400.1		FAD-bind	chr5:178	6977.1	3644.99	761.874	1533.95	869.431	1359.19
GT	Sense	Sense	0.018	Detected	-0.018	Detected	0.000	-1.285	Detected	-1.379	Detected	-1.332	0.001	GT	Sens	contig224	contig224	Vesicle-fu	TGTCAAC	contig224	Solyc01g	Solyc01g	Vesicle-fu	GO:00055	GO:00055	contig224	Solyc01g	Vesicle-fu	GO:00055	SL2.40ch	AT4G049	NSF	NSF (N-et	chr4:248	207.406	190.343	89.1556	105.465	86.9788	81.2037
GT	Sense	Sense	-0.063	Detected	0.063	Detected	0.000	-1.574	Detected	-1.192	Detected	-1.383	0.021	GT	Sens	contig224	contig224	Beta-gluc	TACATTC	contig224	Solyc02g	Solyc02g	Beta-gluc	GO:00059	GO:00059	contig224	Solyc02g	Beta-gluc	GO:00477	SL2.40ch	AT1G618	BGLU46	BGLU46	chr1:228	2443.44	2509.18	794.354	890.982	886.602	1152.31
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.161	Detected	-1.040	Detected	-1.100	0.005	GT	Sens	contig226	contig226	Lipid A ex	TATCAAT	contig226	Solyc06g	Solyc06g	Lipid A ex	GO:00103	GO:00103	contig226	Solyc06g	Lipid A ex	GO:00103	SL2.40ch	AT2G470	MDR4. PC	ABCB4 (/	chr2:193	6867.95	6068.57	2417.21	2904.27	3079.45	3339.14
GT	Sense	Sense	0.238	Detected	-0.238	Detected	0.000	-1.366	Detected	-1.294	Detected	-1.330	0.031	GT	Sens	contig226	contig226	U-box do	GGTTTC	contig226	Solyc01g	Solyc01g	U-box do	GO:00054	GO:00054	contig226	Solyc01g	U-box do	GO:00048	SL2.40ch	AT3G524	PUB22	PUB22 (F	chr3:194	3433.71	2322.33	829.598	971.856	1168.26	1224.31
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-1.301	Detected	-1.230	Detected	-1.266	0.007	GT	Sens	contig228	contig228	Lysine ke	TGCTCA	contig228	Solyc05g	Solyc05g	Lysine ketoglutarate reductas			contig228	Solyc05g	Lysine ketoglutarat		SL2.40ch	AT1G13000.2		unknown	chr1:443	20495.1	16686	6835.32	12455	8005.38	8379.29
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	-2.440	Detected	-2.325	Detected	-2.383	0.003	GT	Sens	contig229	contig229	Serine/thr	AAATAAC	contig229	Solyc01g	Solyc01g	Serine/thr	GO:00191	GO:00191	contig229	Solyc01g	RLK. Rec	GO:00191	SL2.40ch	AT1G70520.1		protein k	chr1:265	80.3316	63.7648	12.5296	30.1634	14.0622	15.185
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-1.066	Detected	-1.044	Detected	-1.055	0.006	GT	Sens	contig231	contig231	Low affin	TGCAATT	contig231	Solyc12g	Solyc12g	Low affin	GO:00080	GO:00080	contig231	Solyc12g	Solute ca	GO:00160	SL2.40ch	AT3G541	ATPTR1.	PTR1 (PE	chr3:200	4581.9	4834.72	2164.25	2225.32	2397.09	2427.4
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-2.058	Detected	-0.842	Detected	-1.450	0.141	GT	Sens	contig231	contig231	Mutator-l	AGTTAG	contig231	Solyc01g	Solyc01g	Mutator-like transposase (AHF			contig231	Solyc01g	Mutator-like transpo		SL2.40ch	AT5G03406.1		ATP bind	chr5:839	59.1864	50.8274	20.0106	56.0949	14.0458	32.5374
GT	Sense	Sense	-0.110	Detected	0.110	Detected	0.000	-1.160	Detected	-0.949	Detected	-1.055	0.020	GT	Sens	contig234	contig234	N-acetyltr	ACCCCT	contig234	Solyc08g	Solyc08g	N-acetyltr	GO:00081	GO:00081	contig234	Solyc08g	N-acetyltr	GO:00081	SL2.40ch	AT5G01240.1		amino ac	chr5:982	14116.8	15468.4	7149.78	7097.07	7051.01	8137.59
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-1.233	Detected	-1.054	Detected	-1.143	0.016	GT	Sens	contig235	contig235	Transmem	CAATTGC	contig235	Solyc04g	Solyc04g	Transmem	GO:00048	GO:00048	contig235	Solyc04g	Transmem	GO:00055	SL2.40ch	AT5G37310.1		LOCATE	chr5:147	2006.33	1610	532.482	660.29	815.5	920.387
GT	Sense	Sense	0.157	Detected	-0.157	Detected	0.000	-1.293	Detected	-1.392	Detected	-1.342	0.015	GT	Sens	contig238	contig238	Eukaryot	TGTGTG	contig238	Solyc01g	Solyc01g	Eukaryot	GO:00058	GO:00058	contig238	Solyc01g102570.2.1				AT3G561	EIF3C. AT	EIF3C (E	chr3:208	141.389	107.01	48.0542	42.6694	53.5467	49.83
GT	Sense	Sense	0.050	Detected	-0.050	Detected	0.000	-1.579	Detected	-0.909	Detected	-1.244	0.067	GT	Sens	contig239	contig239	Cycloarte	TTCTTTA	contig239	Solyc04g	Solyc04g	Cycloartenol synthase (AHRD			contig239	Solyc04g	Lanoster	GO:00002	SL2.40ch	AT1G64180.1		intracellu	chr1:238	597.635	524.972	157.406	129.525	199.957	317.229
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-1.653	Detected	-1.243	Detected	-1.448	0.021	GT	Sens	contig239	contig239	Legumin	TTTTTTC	contig239	Solyc01g	Solyc01g	Legumin	GO:00082	GO:00082	contig239	Solyc01g	Legumin	GO:00082	SL2.40ch	AT3G176	YSL5. PD	YSL5 (YE	chr3:603	5080.88	5135.2	2466.7	2724.03	1732.24	2294.05
GT	Sense	Sense	0.283	Detected	-0.283	Detected	0.000	-1.437	Detected	-1.522	Detected	-1.479	0.036	GT	Sens	contig239	contig239	Transpor	TTTACAT	contig239	Solyc10g	Solyc10g	Transporter CorA family (AHRI			contig239	Solyc08g	Zinc transport prote		SL2.40ch	AT5G62630.1				226.229	143.718	42.1727	62.4062	71.026	66.747
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.259	Detected	-1.168	Detected	-1.213	0.003	GT	Sens	contig239	contig239	Receptor	ATCCTGA	contig239	Solyc09g	Solyc09g	Receptor	GO:00055	GO:00055	contig239	Solyc09g	Receptor	GO:00055	SL2.40ch	AT3G23750.1		leucine-r	chr3:855	1484.22	1308.09	443.9	554.609	620.886	659.464
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	-2.431	Detected	-2.747	Detected	-2.589	0.005	GT	Sens	contig241	contig241	Peroxidas	AAGAATC	contig241	Solyc05g	Solyc05g	Peroxidas	GO:00055	GO:00055	contig241	Solyc05g046020.2.1				AT3G21770.1		peroxida	chr3:767	628.291	524.827	135.44	116.083	113.557	90.924
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	-1.344	Detected	-1.283	Detected	-1.314	0.006	GT	Sens	contig242	contig242	Leaf sene	ATGGAAC	contig242	Solyc02g	Solyc02g	Leaf senescence protein-like (			contig242	Solyc02g	Leaf senescence pr		SL2.40ch	AT5G15900.1		unknown	chr5:518	4562.99	3738.01	1518.94	1632.61	1734.6	1803.88
GT	Sense	Sense	-0.023	Detected	0.023	Detected	0.000	-1.060	Detected	-1.154	Detected	-1.107	0.002	GT	Sens	contig245	contig245	Cytochro	AGGTGT	contig245	Solyc01g	Solyc01g	Cytochro	GO:0020	GO:0020	contig245	Solyc04g	Cytochro	GO:00198	SL2.40ch	AT5G249	CYP71A1	CYP71A1	chr5:859	4263.85	4142.56	1764.09	1837.57	2148.98	2007.43
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-1.668	Detected	-1.421	Detected	-1.544	0.012	GT	Sens	contig245	contig245	3-oxoacy	ATGATGA	contig245	Solyc02g	Solyc02g	3-oxoacy	GO:00055	GO:00055	contig245	Solyc02g	3-oxoacy	GO:00055	SL2.40ch	AT5G462	KAS I	KAS I (3-I	chr5:187	978.529	785.152	450.719	445.924	294.226	348.081
GT	Sense	Sense	-0.060	Detected	0.060	Detected	0.000	-1.801	Detected	-1.520	Detected	-1.660	0.008	GT	Sens	contig248	contig248	ATP-bind	TTCACAC	contig248	Solyc03g	Solyc03g	ATP-bind	GO:00168	GO:00168	contig248	Solyc03g	ATP-bind	GO:00426	SL2.40ch	AT3G477	ATATH6.	ATATH6:	chr3:176	6602.78	6756.11	1999.02	2971.18	2044.07	2476.89
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	-2.537	Detected	-1.520	Detected	-2.028	0.058	GT	Sens	contig248	contig248	Gibberelli	TCAATGT	contig248	Solyc11g	Solyc11g	Gibberelli	GO:00055	GO:00055	contig248	Solyc11g	Gibberelli	GO:00055	SL2.40ch	AT3G028	GASA5	GASA5 ((	chr3:638	23505.5	21503.7	7465.92	6472.12	4130.64	8335.87
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	-1.553	Detected	-0.845	Detected	-1.199	0.087	GT	Sens	contig250	contig250	Caffeoyl-	TAGCAGA	contig250	Solyc10g	Solyc10g	Caffeoyl-	GO:00424	GO:00424	contig250	Solyc10g	Caffeoyl-	GO:00162	SL2.40ch	AT4G34050.1		caffeoyl-	chr4:163	30543.8	23834.8	18507.4	18798	9802.53	15968.3
GT	Sense	Sense	-0.221	Detected	0.221	Detected	0.000	-1.815	Detected	-0.945	Detected	-1.380	0.105	GT	Sens	contig251	contig251	Cyclin A-l	CAAAGTA	contig251	Solyc12g	Solyc12g	Cyclin A-l	GO:00056	GO:00056	contig251	Solyc12g	Cyclin A-l	GO:00056	SL2.40ch	AT1G472	CYCA3;2	cyclin fai	chr1:173	97.9239	125.09	45.3193	23.6839	33.5505	61.1268
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-1.530	Detected	-2.141	Detected	-1.836	0.030	GT	Sens	contig251	contig251	Cyclopro	ATTTCAC	contig251	Solyc09g	Solyc09g	Cyclopro	GO:00055	GO:00055	contig251	Solyc09g	Cyclopro	GO:00055	SL2.40ch	AT3G23510.1		cyclopro	chr3:842	3540.28	2874.23	815.483	581.964	1177.68	768.736
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-1.505	Detected	-0.953	Detected	-1.229	0.049	GT	Sens	contig251	contig251	Unknown	CGACCCT	contig251	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig251	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G47490.1		unknown	chr5:192	122.664	106.324	41.6746	117.022	42.8976	62.7055
GT	Sense	Sense	-0.125	Detected	0.125	Detected	0.000	-1.045	Detected	-1.157	Detected	-1.101	0.015	GT	Sens	contig252	contig252	Cytochro	TGCCAT	contig252	Solyc07g	Solyc07g	Cytochro	GO:0020	GO:0020	contig252	Solyc07g	Cytochro	GO:00198	SL2.40ch	AT3G146	CYP72A7	CYP72A7	chr3:491	38.3858	42.9824	17.5495	8.59567	20.9929	19.3717
GT	Sense	Sense	0.180	Detected	-0.180	Detected	0.000	-1.189	Detected	-0.933	Detected	-1.061	0.041	GT	Sens	contig253	contig253	MADS-bo	CGGAGG	contig253	Solyc12g	Solyc12g	MADS-bo	GO:00056	GO:00056	contig253	Solyc04g	MADS-bo	GO:00056	SL2.40ch	AT3G572	AGL16	AGL16 (A	chr3:211	359.392	263.44	129.99	130.3	143.967	171.356
GT	Sense	Sense	0.568	Detected	-0.568	Detected	0.000	-2.150	Detected	-1.781	Detected	-1.966	0.081	GT	Sens	contig254	contig254	Phloem le	AATCACT	contig254	Solyc02g	Solyc02g	Phloem lectin (AHRD V1 --*- O8			contig254	Solyc02g	Phloem le	GO:00302	SL2.40ch	AT1G11270.3				1101.89	471.479	266.127	401.721	173.124	222.913
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-1.397	Detected	-1.227	Detected	-1.312	0.016	GT	Sens	contig255	contig255	Cysteine	AAGTAGC	contig255	Solyc01g	Solyc01g	Cysteine	GO:00081	GO:00081	contig255	Solyc01g	Cysteine	GO:00081	SL2.40ch	AT3G224	OASA2	OASA2 ((	chr3:796	6499.62	5020.7	2119.95	2551.38	2313.83	2595.22
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	-1.593	Detected	-1.524	Detected	-1.559	0.012	GT	Sens	contig255	contig255	Coatomer	ACAAGA	contig255	Solyc01g	Solyc01g	Coatomer	GO:00301	GO:00301	contig255	Solyc01g058380.1.1				AT4G34450.1		coatome	chr4:164	555.438	412.22	86.1783	112.703	169.101	176.852
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-1.467	Detected	-0.912	Detected	-1.189	0.050	GT	Sens	contig255	contig255	Decarbox	AGAAAAC	contig255	Solyc08g	Solyc08g	Decarbox	GO:00197	GO:00197	contig255	Solyc08g	Decarbox	GO:00301	SL2.40ch	AT1G437	emb1075	emb1075	chr1:164	359.971	342.545	99.3537	168.001	135.485	198.452
GT	Sense	Sense	0.174	Detected	-0.174	Detected	0.000	-2.147	Detected	-1.325	Detected	-1.736	0.060	GT	Sens	contig260	contig260	Cytochro	GTTCTTA	contig260	Solyc03g	Solyc03g	Cytochro	GO:00198	GO:00198	contig260	Solyc03g	Cytochro	GO:00198	SL2.40ch	AT5G634	CYP94B1	CYP94B1	chr5:254	112.487	83.1342	22.7184	10.0442	23.2754	41.0266
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.269	Detected	-1.006	Detected	-1.138	0.013	GT	Sens	contig260	contig260	Mitochon	ATTATGT	contig260	Solyc05g	Solyc05g	Mitochon	GO:00468	GO:00468	contig260	Solyc12g	Mitochon	GO:00065	SL2.40ch	AT4G16730.1				237.814	222.448	62.0548	63.9374	101.765	121.762
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.878	Detected	-1.948	Detected	-1.913	0.000	GT	Sens	contig260	contig260	Peptide tr	ATTGGC	contig260	Solyc09g	Solyc09g	Peptide tr	GO:00429	GO:00429	contig260	Solyc05g	Peptide tr	GO:00429	SL2.40ch	AT5G46040.1		proton-d	chr5:186	270.453	249.139	135.139	89.4494	75.324	71.5046
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	-2.430	Detected	-3.643	Detected	-3.037	0.038	GT	Sens	contig261	contig261	FAD-bind	ACATTGT	contig261	Solyc06g	Solyc06g	FAD-bind	GO:00506	GO:00506	contig261	Solyc06g	FAD-bind	GO:00506	SL2.40ch	AT4G20840.1		FAD-bind	chr4:111	150.144	144.231	10.4031	15.9976	29.1122	12.5235
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-1.243	Detected	-1.125	Detected	-1.184	0.012	GT	Sens	contig261	contig261	Peptide tr	AGTTTTC	contig261	Solyc11g	Solyc11g	Peptide tr	GO:00160	GO:00160	contig261	Solyc10g	Fasciclin-like arabin		SL2.40ch	AT5G490	OVA2	OVA2 (ov	chr5:198	5147.71	4114.14	2217.27	2327.8	2073.08	2243.35
GT	Sense	Sense	-0.060	Detected	0.060	Detected	0.000	-1.120	Detected	-0.941	Detected	-1.031	0.011	GT	Sens	contig264	contig264	UDP-gluc	GAAGGA	contig264	Solyc03g	Solyc03g	UDP-gluc	GO:00009	GO:00009	contig264	Solyc03g	UDP-gluc	GO:00039	SL2.40ch	AT5G39320.1		UDP-gluc	chr5:157	366.827	375.261	82.1316	125.996	181.988	205.43
GT	Sense	Sense	0.032	Detected	-0.032	Detected	0.000	-1.450	Detected	-1.082	Detected	-1.266	0.021	GT	Sens	contig265	contig265	Histidine	GTTGCT	contig265	Solyc05g	Solyc05g	Histidine	GO:00151	GO:00151	contig265	Solyc02g	Histidine	GO:00151	SL2.40ch	AT1G244	LHT2. AA	LHT2 (LY	chr1:865	12319.3	11086.3	2797.42	4293.68	4561.98	5867.94
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	-1.219	Detected	-1.757	Detected	-1.488	0.039	GT	Sens	contig266	contig266	Unknown	ATGGAA	contig266	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)%			contig266	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G14819.1		unknown	chr4:850	124.099	96.301	84.0142	56.0207	50.094	34.3854
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-1.021	Detected	-1.218	Detected	-1.120	0.008	GT	Sens	contig267	contig267	Unknown	TGGAGA	contig267	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig267	Solyc08g	Genomic DNA chror		SL2.40ch	AT5G42050.1		FUNCTIO	chr5:168	4782.69	4621.85	2189.14	2050.56	2470.33	2148.94
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-1.661	Detected	-0.869	Detected	-1.265	0.088	GT	Sens	contig267	contig267	Omega-6	GTTGTAT	contig267	Solyc04g	Solyc04g	Omega-6	GO:00423	GO:00423	contig267	Solyc04g	Omega-6	GO:00423	SL2.40ch	AT3G121	FAD2	FAD2 (FA	chr3:386	222.722	232.666	54.126	278.788	76.7774	132.485
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	-2.056	Detected	-1.359	Detected	-1.707	0.042	GT	Sens	contig268	contig268	Xylogluc	GCAGAT	contig268	Solyc12g	Solyc12g	Xylogluc	GO:00059	GO:00059	contig268	Solyc12g	Xylogluc	GO:00059	SL2.40ch	AT3G23730.1		xylogluc	chr3:855	37714.8	31004.1	8568	18755.9	8769.83	14174.9
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.007	Detected	-1.197	Detected	-1.102	0.009	GT	Sens	contig268	contig268	Hydroxyc	TTCAGC	contig268	Solyc03g	Solyc03g	Hydroxycinnamoyl-CoA shikin			contig268	Solyc03g	Hydroxycinnamoyl-		SL2.40ch	AT5G65460.1		kinesin n	chr5:261	4381.46	3898.89	1846.45	1575.53	2193.57	1916.75
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	-1.632	Detected	-1.231	Detected	-1.431	0.019	GT	Sens	contig268	contig268	Adaptin N	AAAGTG	contig268	Solyc00g	Solyc00g	Adaptin N terminal region fami			contig268	Solyc11g	AP-2 com	GO:00301	SL2.40ch	AT1G595	CW7	CW7	chr1:218	86.5871	82.6995	10.8613	19.6008	29.1182	38.3328
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.572	Detected	-0.974	Detected	-1.273	0.052	GT	Sens	contig268	contig268	Chitinase	AGCAAAT	contig268	Solyc07g	Solyc07g	Chitinase	GO:0008	GO:0008	contig268	Solyc07g	Chitinase	GO:0008	SL2.40ch	AT4G01290.2		unknown	chr4:538	190117	169077	111391	116681	64295.1	97016.7
GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-1.075	Detected	-1.433	Detected	-1.254	0.039	GT	Sens	contig269	contig269	Unknown	ATTGGA	contig269	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig269	Solyc10g	Kinase fa	GO:00081	SL2.40ch	AT3G58150.1		FUNCTIO	chr3:215	265.462	193.887	80.9336	81.4112	114.798	89.3085
GT	Sense	Sense	0.236	Detected	-0.236	Detected	0.000	-2.865	Detected	-2.292	Detected	-2.578	0.020	GT	Sens	contig272	contig272	Unknown	CTGTGA	contig272	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig272	Solyc02g	Unknown Protein (A		SL2.40ch	AT1G18170.1		immunor	chr1:625	1177.44	798.914	202.218	439.998	141.997	210.517
GT	Sense	Sense	-0.243	Detected	0.243	Detected	0.000	-1.724	Detected	-1.975	Detected	-1.850	0.021	GT	Sens	contig272	contig272	Peptide tr	CTTTCA	contig272	Solyc06g	Solyc06g	Peptide tr	GO:0008	GO:0008	contig272	Solyc06g075450.1.1				AT1G60060.1		unknown	chr1:221	211.44	278.489	102.015	33.4067	78.3385	65.6154
GT	Sense	Sense	0.955	Detected	-0.955	Detected	0.000	-3.106	Detected	-1.688	Detected	-2.397	0.181	GT	Sens	contig272	contig272	Acyl-CoA	ATCTTGA	contig272	Solyc07g	Solyc07g	Acyl-CoA	GO:00081	GO:00081	contig272	Solyc07g	Acyl-CoA	GO:00156	SL2.40ch	AT2G17650.1		AMP-dep	chr2:767	677.896	169.675	21.5303	50.4342	42.012	111.904
GT	Sense	Sense	-0.167	Detected	0.167	Detected	0.000	-1.359	Detected	-0.882	Detected	-1.120	0.061	GT	Sens	contig273	contig273	Histone H	TCCGTG	contig273	Solyc11g	Solyc11g	Histone H	GO:00056	GO:00056	contig273	Solyc11g	Histone H	GO:00435	SL2.40ch	AT5G59690.1		histone h	chr5:240	3409.56	4041.47	2243.48	1951.78	1542.84	2142.1
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	-2.947	Detected	-1.705	Detected	-2.326	0.067	GT	Sens	contig274	contig274	Vicilin-lik	AAACAA	contig274	Solyc09g	Solyc09g	Vicilin-lik	GO:00457	GO:00457	contig274	Solyc09g	Vicilin-lik	GO:00457	SL2.40ch	AT5G60730.1		anion-tra	chr5:244	1274.97	996.622	416.519	590.826	155.913	367.651
GT	Sense	Sense	0.417	Detected	-0.417	Detected	0.000	-2.381	Detected	-1.501	Detected	-1.941	0.085	GT	Sens	contig277	contig277	FAD-bind	CGCGGT	contig277	Solyc02g	Solyc02g	FAD-bind	GO:00506	GO:00506	contig277	Solyc02g	FAD-bind	GO:00506	SL2.40ch	AT4G20860.1		FAD-bind	chr4:111	33088.8	17473.6	6117.62	12840.4	4921.26	9031.61
GT	Sense	Sense	-0.071	Detected	0.071	Detected	0.000	-1.497	Detected	-1.141	Detected	-1.319	0.020	GT	Sens	contig278	contig278	Serpin 3	TTCTCCA	contig278	Solyc04g	Solyc04g	Serpin 3	GO:00048	GO:00048	contig278	Solyc04g	Serpin 3 (	GO:00048	SL2.40ch	AT5G452	RRS1. AT	RRS1 (RE	chr5:183	36.1943	37.5754	4.68695	25.0572	13.9302	17.7806
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-1.519	Detected	-1.043	Detected	-1.281	0.033	GT	Sens	contig278	contig278	UDP-gluc	CATGCAC	contig278	Solyc01g	Solyc01g	UDP-gluc	GO:00102	GO:00102	contig278	Solyc05g	UDP-gluc	GO:00102	SL2.40ch	AT1G01390.1		UDP-gluc	chr1:148	86334.4	79647.6	25472.8	31956	30851.3	42787.2
GT	Sense	Sense	0.331	Detected	-0.331	Detected	0.000	-4.242	Detected	-4.173	Detected	-4.208	0.006	GT	Sens	contig278	contig278	MYB tran	TTGGAAT	contig278	Solyc12g	Solyc12g	MYB tran	GO:0045449		contig278	Solyc02g	MYB tran	GO:00037	SL2.40ch	AT2G359	BLH1	BLH1 (BE	chr2:150	370.323	220.086	23.9583	21.7246	16.0881	16.8248
GT	Sense	Sense	-0.016	Detected	0.016	Detected	0.000	-1.183	Detected	-1.083	Detected	-1.133	0.002	GT	Sens	contig279	contig279	ATP bind	GATGCC	contig279	Solyc05g	Solyc05g	ATP bind	GO:00055	GO:00055	contig279	Solyc05g053930.2.1				AT1G075	APK1A. A	APK1A: I	chr1:233	5473.82	5264.01	2101.08	2291.64	2521.11	2694.23
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.186	Detected	-1.130	Detected	-1.158	0.001	GT	Sens	contig281	contig281	Cytochro	ATTCTTA	contig281	Solyc03g	Solyc03g	Cytochro	GO:0016	GO:0016	contig281	Solyc00g	Cytochro	GO:0016	SL2.40ch	ATMG007	COX3	Encodes	chrM:21	41257.9	38874.9	17318.5	17940.2	18774.9	19455.8
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-1.137	Detected	-1.499	Detected	-1.318	0.033	GT	Sens	contig281	contig281	Unknown	GACGTG	contig281	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig281	Solyc00g047700.2.1				AT4G16830.3		nuclear F	chr4:947	7607.06	5701.17	1850.26	1511.65	3192.98	2476.7
GT	Sense	Sense	0.409	Detected	-0.409	Detected	0.000	-1.337	Detected	-2.450	Detected	-1.893	0.111	GT	Sens	contig284	contig284	Cytochro	ATTAAGA	contig284	Solyc07g	Solyc07g	Cytochro	GO:00198	GO:00198	contig284	Solyc07g055440.1.1				AT3G146	CYP72A9	CYP72A9	chr3:491	507.131	270.721	47.8563	88.6057	156.434	72.0971
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	-1.228	Detected	-1.417	Detected	-1.323	0.015	GT	Sens	contig284	contig284	Endogluc	CCAGGT	contig284	Solyc08g	Solyc08g	Endogluc	GO:00059	GO:00059	contig284	Solyc08g	Endogluc	GO:00059	SL2.40ch	AT4G235	AtGH9B1	AtGH9B1	chr4:122	14843.4	11591.6	5100.36	7605.07	5972.08	5221.86
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	-1.010	Detected	-1.265	Detected	-1.138	0.016	GT	Sens	contig284	contig284	Unknown	GGGAAA	contig284	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)%			contig284	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G17640.1		unknown	chr5:581	6237.58	6502.83	2760.39	2349.07	3371.6	2817.79
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.955	Detected	-1.665	Detected	-1.810	0.007	GT	Sens	contig289	contig289	Ribonucl	TACATC	contig289	Solyc05g	Solyc05g	Ribonucl	GO:00454	GO:00454	contig289	Solyc09g	Ribonucleoside hyd		SL2.40ch	AT5G372	RVE2. CIF	RVE2 (RE	chr5:147	44066.4	39227.4	9869.99	16195.5	11432.5	13941
GT	Sense	Sense	0.475	Detected	-0.475	Detected	0.000	-0.904	Detected	-2.044	Detected	-1.474	0.185	GT	Sens	contig290	contig290	Unknown	TGTTTG	contig290	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig290	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G236	PAKRP1L	KINESIN-	chr3:851	61.458	29.9545	3.13575	7.63528	24.4487	11.0639
GT	Sense	Sense	0.234	Detected	-0.234	Detected	0.000	-1.074	Comprom	-0.934	Comprom	-1.004	0.054	GT	Sens	contig291	contig291	Genomic	CAGAGG	contig291	Solyc11g	Solyc11g	Genomic DNA chromosome 5			contig291	Solyc05g	Genomic DNA chror		SL2.40ch	AT3G556	ATROPGI	ROPGEF	chr3:206	20.5024	13.9521	8.42902	2.42999	8.56805	9.41141
GT	Sense	Sense	-0.082	Detected	0.082	Detected	0.000	-1.687	Detected	-0.906	Detected	-1.296	0.083	GT	Sens	contig291	contig291	Histone H	TGATAAC	contig291	Solyc06g	Solyc06g	Histone H	GO:00056	GO:00056	contig291	Solyc06g	Histone H	GO:00435	SL2.40ch	AT2G287	HIS4	HIS4: DN	chr2:123	286.878	302.545	190.608	97.7413	97.5887	167.169
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-1.755	Detected	-1.756	Detected	-1.755	0.006	GT	Sens	contig292	contig292	FAD-bind	AATCTCC	contig292	Solyc02g	Solyc02g	FAD-bind	GO:00506	GO:00506	contig292	Solyc02g	FAD-bind	GO:00506	SL2.40ch	AT5G44410.1		FAD-bind	chr5:178	71.3369	55.9514	7.41085	29.8491	19.9657	19.8895
GT	Sense	Sense	0.209	Detected	-0.209	Detected	0.000	-1.220	Detected	-0.961	Detected	-1.090	0.047	GT	Sens	contig293	contig293	U-box do	GGTTAG	contig293	Solyc01g	Solyc01g	U-box do	GO:00001	GO:00001	contig293	Solyc01g	U-box do	GO:00048	SL2.40ch	AT3G465	PUB13. A	PUB13 (F	chr3:171	2183.48	1538.61	596.523	652.772	839.207	1001.03
GT	Sense	Sense	-0.209	Detected	0.209	Detected	0.000	-1.017	Detected	-0.987	Comprom	-1.002	0.041	GT	Sens	contig293	contig293	Glutamat	ATCCAT	contig293	Solyc06g	Solyc06g	Glutamat	GO:00052	GO:00052	contig293	Solyc06g	Glutamat	GO:00052	SL2.40ch	AT3G18773.1				17.6863	22.2202	9.54096	15.3026	10.4492	10.634
GT	Sense	Sense	0.122	Detected	-0.122	Detected	0.000	-1.523	Detected	-0.873	Detected	-1.198	0.075	GT	Sens	contig294	contig294	Adenosin	GGATGC	contig294	Solyc10g	Solyc10g	Adenosin	GO:00061	GO:00061	contig294	Solyc10g	Adenosin	GO:00061	SL2.40ch	AT5G033	ADK2	ADK2 (AI	chr5:796	33498.1	26632.6	12098.1	11457.1	11080	17338.4
GT	Sense	Sense	0.062	Detected	-0.062	Detected	0.000	-1.520	Detected	-1.026	Detected	-1.273	0.038	GT	Sens	contig295	contig295	Chitinase	TAAGTGT	contig295	Solyc10g	Solyc10g	Chitinase	GO:0008	GO:0008	contig295	Solyc10g017970.1.1				AT5G463	KCO2. AT	KCO2 (C	chr5:188	126895	109641	63055.2	66923.3	43861.2	61566.9
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.282	Detected	-1.066	Detected	-1.174	0.008	GT	Sens	contig296	contig296	Tubulin a	ATTCTTC	contig296	Solyc04g	Solyc04g	Tubulin a	GO:00469	GO:00469	contig296	Solyc04g	Tubulin a	GO:00469	SL2.40ch	AT4G149	TUA6	TUA6: st	chr4:854	17399.2	16404.3	5016.68	6196.59	7407.23	8576.59
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-1.786	Detected	-1.446	Detected	-1.616	0.013	GT	Sens	contig296	contig296	Delta-6 de	TGCTACA	contig296	Solyc10g	Solyc10g	Delta-6 de	GO:00047	GO:00047	contig296	Solyc10g	Delta-6 de	GO:00047	SL2.40ch	AT3G61580.1		delta-8 s	chr3:227	5130.21	4407.4	1625.62	1618.49	1470	1855.91
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.249	Detected	-1.358	Detected	-1.304	0.002	GT	Sens	contig299	contig299	Serine/thr	TGTCGC	contig299	Solyc12g	Solyc12g	Serine/threonine protein kinas			contig299	Solyc12g	Kinase fa	GO:00064	SL2.40ch	AT4G31170.3		protein k	chr4:151	401.145	375.295	122.209	125.284	174.029	160.976
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-1.149	Detected	-1.138	Detected	-1.143	0.001	GT	Sens	contig299	contig299	Unknown	TGGGAA	contig299	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)%			contig299	Solyc02g	Multidrug	GO:00155	SL2.40ch	AT5G43160.1		unknown	chr5:173	72.5111	70.9775	41.5406	33.9856	34.5014	34.6547
GT	Sense	Sense	0.435	Detected	-0.435	Detected	0.000	-1.403	Detected	-1.407	Detected	-1.405	0.084	GT	Sens	contig299	contig299	Calmodul	CTCCTA	contig299	Solyc11g	Solyc11g	Calmodul	GO:00055	GO:00055	contig299	Solyc11g071750.1.1				AT5G423	CML39. C	CML37 ((	chr5:169	409.802	210.885	121.476	156.177	118.508	117.89
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.592	Detected	-1.196	Detected	-1.394	0.024	GT	Sens	contig300	contig300	GDSL est	GCTTCT	contig300	Solyc09g	Solyc09g	GDSL est	GO:00066	GO:00066	contig300	Solyc09g008690.1.1				AT5G22810.1		GDSL-m	chr5:762	5568.62	4597.14	1528.26	1570.71	1789.37	2348.62
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	-1.685	Detected	-1.408	Detected	-1.546	0.015	GT	Sens	contig300	contig300	COBRA-li	GAAGAAT	contig300	Solyc03g	Solyc03g	COBRA-like protein 4 (AHRD V			contig300	Solyc03g	COBRA-like protein		SL2.40ch	AT3G022	COBL1	COBL1 ((	chr3:409	511.593	402.944	97.6807	117.076	150.589	181.904
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-1.538	Detected	-0.968	Detected	-1.253	0.050	GT	Sens	contig301	contig301	Equilibrat	TTAAGA	contig301	Solyc02g	Solyc02g	Equilibrat	GO:00053	GO:00053	contig301	Solyc02g079330.2.1				AT4G051	ATENT6.	equilibra	chr4:262	2546.52	2209.34	779.983	963.181	871.283	1289.41
GT	Sense	Sense	0.229	Detected	-0.229	Detected	0.000	-2.132	Detected	-1.519	Detected	-1.826	0.041	GT	Sens	contig301	contig301	Pectinace	CCAGCA	contig301	Solyc08g	Solyc08g	Pectinace	GO:0004	GO:0004	contig301	Solyc08g	Pectinace	GO:0004	SL2.40ch	AT4G19420.1		pectinac	chr4:105	116.88	80.1157	29.2045	19.1283	23.5386	35.896
GT	Sense	Sense	0.544	Detected	-0.544	Detected	0.000	-1.263	Comprom	-2.373	Comprom	-1.818	0.144	GT	Sens	contig301	contig301	Alcohol d	AAACATT	contig301	Solyc12g	Solyc12g	Alcohol d	GO:00081	GO:00081	contig301	Solyc12g	Alcohol d	GO:00081	SL2.40ch	AT5G16990.1		NADP-de	chr5:558	27.9546	12.3724	7.57959	1.89843	8.26089	3.81643
GT	Sense	Sense	0.350	Detected	-0.350	Detected	0.000	-1.035	Detected	-1.083	Detected	-1.059	0.094	GT	Sens	contig302	contig302	Cellulose	AGCAAT	contig302	Solyc12g	Solyc12g	Cellulose synthase-like C1-1 g			contig302	Solyc04g	Cellulose	GO:00167	SL2.40ch	AT4G079	ATCSLC1	ATCSLC	chr4:480	58.037	33.6237	21.5925	23.925	22.9969	22.1717
GT	Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-1.703	Detected	-1.137	Detected	-1.420	0.042	GT	Sens	contig302	contig302	Transmem	GCACTT	contig302	Solyc05g	Solyc05g	Transmem	GO:00048	GO:00048	contig302	Solyc05g	Transmem	GO:00055	SL2.40ch	AT5G37310.1		LOCATE	chr5:147	968.018	792.034	221.022	259.439	286.787	423.409
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	-1.865	Detected	-1.876	Detected	-1.871	0.000	GT	Sens	contig303	contig303	Os06g02	CTCACT	contig303	Solyc04g	Solyc04g	Os06g0220000 protein (Fragm			contig303	Solyc04g	Os06g0220000 prot		SL2.40ch	AT4G089	EXO	EXO (EX	chr4:574	1269.74	1138.64	255.389	467.59	351.934	348.295
GT	Sense	Sense	0.441	Detected	-0.441	Detected	0.000	-0.933	Detected	-2.186	Detected	-1.560	0.179	GT	Sens	contig306	contig306	Cytochro	ATATTAC	contig306	Solyc07g	Solyc07g	Cytochro	GO:00198	GO:00198	contig306	Solyc07g	Cytochro	GO:00198	SL2.40ch	AT3G52690.1		FUNCTIO	chr3:195	585.794	299.218	86.0055	140.161	233.793	97.8284
GT	Sense	Sense	1.405	Detected	-1.405	Detected	0.000	-0.894	Detected	-1.123	Detected	-1.009	0.549	GT	Sens	contig307	contig307	Unknown	ACGACA	contig307	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig307	Solyc03g116210.1.1				AT5G229	F8H	F8H (FRA	chr5:767	192.443	25.8275	39.9795	66.4438	40.4555	34.4106
GT	Sense	Sense	0.116	Detected	-0.116	Detected	0.000	-2.616	Detected	-1.818	Detected	-2.217	0.033	GT	Sens	contig307	contig307	Polygalac	TGACAGT	contig307	Solyc02g	Solyc02g	Polygalac	GO:00059	GO:00059	contig307	Solyc02g	Polygalac	GO:00059	SL2.40ch	AT2G43870.1		polygala	chr2:181	137792	110434	22926.4	41468	21458.7	37187.2
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.236	Detected	-1.089	Detected	-1.163	0.005	GT	Sens	contig308	contig308	Unknown	TCTCAT	contig308	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig308	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G79380.1				386.721	344.036	107.813	152.058	165.12	182.303
GT	Sense	Sense	0.147	Detected	-0.147	Detected	0.000	-1.779	Detected	-1.179	Detected	-1.479	0.047	GT	Sens	contig309	contig309	Serine/thr	ACTTCTA	contig309	Solyc02g	Solyc02g	Serine/thr	GO:00191	GO:00191	contig309	Solyc02g	Serine/thr	GO:00191	SL2.40ch	AT1G61610.1		S-locus l	chr1:227	260.4	199.849	65.7343	93.668	70.8858	107.094
GT	Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-1.413	Detected	-0.893	Detected	-1.153	0.054	GT	Sens	contig309	contig309	Bifunctio	GAAACT	contig309	Solyc11g	Solyc11g	Bifunctio	GO:00442	GO:00442	contig309	Solyc11g	Bifunctio	GO:00442	SL2.40ch	AT1G082	AXS2	AXS2 (UE	chr1:257	2701.83	2208.67	768.282	984.908	978.091	1398.92
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-2.104	Detected	-1.508	Detected	-1.806	0.031	GT	Sens	contig311	contig311	RNA-bind	ACTGGA	contig311	Solyc00g	Solyc00g	RNA-bind	GO:00037	GO:00037	contig311	Solyc11g	Poly(RC)	GO:00037	SL2.40ch	AT5G044	BTR1. BT	BTR1L (E	chr5:125	557.87	436.535	140.302	189.023	122.421	184.483
GT	Sense	Sense	-0.483	Detected	0.483	Detected	0.000	-2.494	Detected	-0.893	Detected	-1.693	0.212	GT	Sens	contig322	contig322	Peroxidas	GATGGA	contig322	Solyc05g	Solyc05g	Peroxidas	GO:00055	GO:00055	contig322	Solyc05g	Peroxidas	GO:00046	SL2.40ch	AT3G21770.1		peroxida	chr3:767	190.937	350.975	147.185	105.67	49.014	148.201
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-1.796	Detected	-1.275	Detected	-1.535	0.028	GT	Sens	contig323	contig323	Legumin-	TCTCCCT	contig323	Solyc01g	Solyc01g	Legumin-	GO:00082	GO:00082	contig323	Solyc01g	Legumin-	GO:00082	SL2.40ch	AT3G54600.1		DJ-1 fam	chr3:202	4462.41	4244.22	2286.85	2607.32	1336.37	1912.59
GT	Sense	Sense	0.643	Detected	-0.643	Detected	0.000	-1.790	Detected	-1.733	Detected	-1.761	0.112	GT	Sens	contig329	contig329	cDNA clo	ACATCAC	contig329	Solyc02g	Solyc02g	cDNA clone J023049H21 full in			contig329	Solyc02g	BZIP tran	GO:00055	SL2.40ch	AT4G12700.1		unknown	chr4:748	357.505	137.991	49.2163	114.329	68.4962	71.0527
GT	Sense	Sense	-0.175	Detected	0.175	Detected	0.000	-1.305	Detected	-2.200	Detected	-1.753	0.068	GT	Sens	contig333	contig333	Transcrip	GGAAGA	contig333	Solyc02g	Solyc02g	Transcription factor CYCLOID			contig333	Solyc02g	Transcription factor		SL2.40ch	AT1G54740.1		FUNCTIO	chr1:204	2844.8	3412.53	1189.13	487.892	1345.04	720.721
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-2.150	Detected	-1.992	Detected	-2.071	0.002	GT	Sens	contig340	contig340	Ulp1 prot	TTCAGAT	contig340	Solyc11g	Solyc11g	Ulp1 protease family C-termina			contig340	Solyc01g	Endo-1 4-	GO:00088	SL2.40ch	AT2G42870.1				688.477	691.631	224.043	253.005	165.836	184.429
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-2.098	Detected	-1.719	Detected	-1.909	0.011	GT	Sens	contig355	contig355	BURP do	ACGACT	contig355	Solyc05g	Solyc05g	BURP do	GO:00046	GO:00046	contig355	Solyc05g	BURP do	GO:00046	SL2.40ch	AT1G237	JP630	JP630: p	chr1:840	21300.4	18410.7	6449.63	5671.64	4931.01	6395.96
GT	Sense	Sense	0.074	Detected	-0.074	Detected	0.000	-2.649	Detected	-2.158	Detected	-2.403	0.011	GT	Sens	contig355	contig355	Endogluc	TTACAAC	contig355	Solyc08g	Solyc08g	Endogluc	GO:00059	GO:00059	contig355	Solyc08g	Endogluc	GO:00302	SL2.40ch	AT1G643	AtGH9C2	AtGH9C2	chr1:239	461.172	391.813	50.5995	63.971	72.2891	101.269
GT	Sense	Sense	0.237	Detected	-0.237	Detected	0.000	-2.251	Detected	-1.725	Detected	-1.988	0.030	GT	Sens	contig368	contig368	Xylogluc	AACGCT	contig368	Solyc07g	Solyc07g	Xylogluc	GO:00480	GO:00480	contig368	Solyc07g	Xylogluc	GO:00167	SL2.40ch	AT3G23730.1		xylogluc	chr3:855	21346.4	14462.7	4014.6	8090.1	3936.14	5651.84
GT	Sense	Sense	-0.224	Detected	0.224	Detected	0.000	-2.629	Detected	-3.181	Detected	-2.905	0.015	GT	Sens	contig377	contig377	Polyphen	TGAAGG	contig377	Solyc08g	Solyc08g	Polyphen	GO:00081	GO:00081	contig377	Solyc08g	Polyphen	GO:00081	SL2.40ch	AT3G52700.1		unknown	chr3:195	143.642	184.349	3.6787	3.10237	28.0508	19.0726
GT	Sense	Sense	0.018	Detected	-0.018	Detected	0.000	-1.235	Detected	-0.928	Detected	-1.081	0.020	GT	Sens	contig380	contig380	Dihydroli	TAGGGA	contig380	Solyc07g	Solyc07g	Dihydroli	GO:00081	GO:00081	contig380	Solyc07g	Dihydroli	GO:00041	SL2.40ch	AT4G26910.1		2-oxoaci	chr4:135	4385.12	4023.56	1277.58	1695.7	1903.19	2347.74
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	-1.940	Detected	-1.766	Detected	-1.853	0.012	GT	Sens	contig384	contig384	Catalytic/	TATTCAC	contig384	Solyc05g	Solyc05g	Catalytic/	GO:00038	GO:00038	contig384	Solyc07g	Serine/thr	GO:00047	SL2.40ch	AT1G47260.1				3103.81	2255	571.329	831.229	735.464	827.229
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-2.347	Comprom	-1.596	Detected	-1.972	0.035	GT	Sens	contig389	contig389	Receptor	TTTCGTA	contig389	Solyc06g	Solyc06g	Receptor	GO:00046	GO:00046	contig389	Solyc06g	Receptor	GO:00428	SL2.40ch	AT5G071	ERL2	ERL2 (EF	chr5:222	38.7062	39.1601	9.29297	12.2621	8.15756	13.69
GT	Sense	Sense	0.083	Detected	-0.083	Detected	0.000	-1.296	Detected	-0.879	Detected	-1.087	0.040	GT	Sens	contig390	contig390	Uridine ki	ATGTTGT	contig390	Solyc07g	Solyc07g	Uridine ki	GO:00167	GO:00167	contig390	Solyc07g	Uridine ki	GO:00048	SL2.40ch	AT4G26510.2		ATP bind	chr4:133	1405.79	1179.27	364.994	482.711	559.222	744.358
GT	Sense	Sense	0.253	Detected	-0.253	Detected	0.000	-1.509	Detected	-1.417	Detected	-1.463	0.030	GT	Sens	contig391	contig391	Unknown	ATGCTTT	contig391	Solyc01g	Solyc01g	Unknown	GO:00062	GO:00062	contig391	Solyc01g	Unknown	GO:00062	SL2.40ch	AT5G40750.1		FUNCTIO	chr5:163	51.446	34.0906	15.7939	26.9125	15.689	16.6705
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-1.453	Detected	-1.006	Detected	-1.230	0.036	GT	Sens	contig395	contig395	Unknown	ATGAGG	contig395	Solyc01g	Solyc01g	Unknown	GO:00094	GO:00094	contig395	Solyc01g	Unknown	GO:00094	SL2.40ch	AT5G153	ATMYB1	ATMYB1	chr5:497	472.865	396.09	236.377	311.551	168.59	229.05
GT	Sense	Sense	0.247	Detected	-0.247	Detected	0.000	-2.802	Detected	-2.732	Detected	-2.767	0.008	GT	Sens	contig402	contig402	Long-cha	ATAGCAC	contig402	Solyc09g	Solyc09g	Long-cha	GO:00081	GO:00081	contig402	Solyc09g	Long-cha	GO:00044	SL2.40ch	AT3G059	LACS6. A	LACS6 (I	chr3:178	179.22	119.716	78.8843	82.5654	22.3902	23.4466
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	-1.250	Detected	-2.284	Detected	-1.767	0.079	GT	Sens	contig405	contig405	Glycine-r	TATGCAT	contig405	Solyc07g	Solyc07g	Glycine-r	GO:00036	GO:00036	contig405	Solyc07g065510.2.1				AT5G55670.1		RNA reco	chr5:225	76.7768	84.3416	34.0589	33.0947	36.0828	17.5657
GT	Sense	Sense	-0.055	Detected	0.055	Detected	0.000	-1.685	Comprom	-0.835	Detected	-1.260	0.099	GT	Sens	contig407	contig407	Cold accl	ATTACTA	contig407	Solyc05g	Solyc05g	Cold acclimation protein WCO			contig407	Solyc05g	Cold acclimation pr		SL2.40ch	AT1G77780.1				34.5652	35.0981	15.944	12.0653	11.5551	20.7584
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.290	Detected	-1.170	Detected	-1.230	0.003	GT	Sens	contig417	contig417	Lipid A ex	TCTTATC	contig417	Solyc06g	Solyc06g	Lipid A ex	GO:00171	GO:00171	contig417	Solyc06g	Lipid A ex	GO:00103	SL2.40ch	AT2G470	MDR4. PC	ABCB4 (/	chr2:193	2920.12	2594.67	971.124	1115.19	1200.69	1300.49
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-1.721	Detected	-1.531	Detected	-1.626	0.007	GT	Sens	contig421	contig421	Dehydrat	TTCTTTC	contig421	Solyc01g	Solyc01g	Dehydration-responsive prote			contig421	Solyc01g	Dehydration-respor		SL2.40ch	AT2G03480.2		dehydrat	chr2:105	463.973	377.7	106.997	178.324	135.423	154.019
GT	Sense	Sense	0.340	Detected	-0.340	Detected	0.000	-0.960	Detected	-1.057	Detected	-1.009	0.099	GT	Sens	contig427	contig427	Pre-mRNA	AATGATC	contig427	Solyc03g	Solyc03g	Pre-mRNA	GO:00037	GO:00037	contig427	Solyc03g	Pre-mRNA	GO:00055	SL2.40ch	AT1G80930.1		MIF4G do	chr1:304	84.5749	49.6387	23.7844	32.0558	35.5152	33.1048
GT	Sense	Sense	0.253	Detected	-0.253	Detected	0.000	-1.371	Detected	-1.094	Detected	-1.232	0.051	GT	Sens	contig428	contig428	AAF0152	GGTTTGAAGTGAATAACCAAATTCTTAATGCATTGTTTACTCTCATGTG							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	214.172	141.902	44.8176	74.347	71.8908	86.8364
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	-1.071	Detected	-1.108	Detected	-1.090	0.000	GT	Sens	contig429	contig429	AT5G050	CTCTTGACGAGGAAGGAGTTTGCAGGACAGCATTTGAGCTTATCTTTG							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	241.226	223.209	80.3652	97.7176	117.773	114.449
GT	Sense	Sense	0.431	Detected	-0.431	Detected	0.000	-1.201	Detected	-1.076	Detected	-1.139	0.120	GT	Sens	contig429	contig429	Probable	GAGAGGTTGAGTTACTTTGGTATAGCCACAAGTTTGATCATTTACCTAA							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	219.906	113.832	58.739	47.2952	73.3641	79.7691
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-1.456	Detected	-1.337	Detected	-1.397	0.007	GT	Sens	contig429	contig429	Cross hy	TTGGTACTTTGAACATGCTGGGATTGGCTAAAAGAGTCGGTGCGAGGT							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	8511.96	6931.31	1669.12	2028.39	2985.92	3231.9
GT	Sense	Sense	-0.090	Detected	0.090	Detected	0.000	-1.520	Detected	-1.117	Detected	-1.319	0.027	GT	Sens	contig430	contig430	Nicotia ta	TTGATTCCCAAAATCCGGCTACCATGTCACAACCAGCTGCTAAAGATCA							contig430	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	47.8737	51.0142	14.3696	15.7881	18.3707	24.2263
GT	Sense	Sense	-0.378	Detected	0.378	Detected	0.000	-2.995	Detected	-0.902	Detected	-1.948	0.222	GT	Sens	contig434	contig434	Nicotia ta	ACTAGTACTCGTACTTGCCTTCACTCTAACTTTTGCATGGCCTTTATAC							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1285.39	2041.96	2039.47	2549.14	216.692	922.005
GT	Sense	Sense	0.143	Detected	-0.143	Detected	0.000	-1.147	Detected	-0.872	Detected	-1.010	0.037	GT	Sens	contig438	contig438	Unknown	AAGTTG	contig438	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig438	Solyc00g	Unknown Protein (A		SL2.40ch	ATCG010	NDHD	Represen	chrC:115	957.821	738.729	502.122	444.12	405.148	488.508
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-1.690	Detected	-2.027	Detected	-1.859	0.010	GT	Sens	contig443	contig443	Calcium-	ATTATGT	contig443	Solyc04g	Solyc04g	Calcium-	GO:00064	GO:00064	contig443	Solyc04g	Calcium-	GO:00064	SL2.40ch	AT3G045	PPCK2. P	PPCK2: I	chr3:122	1675.49	1412.75	496.148	595.585	508.38	401.246
GT	Sense	Sense	-0.156	Detected	0.156	Detected	0.000	-1.712	Detected	-0.805	Detected	-1.258	0.120	GT	Sens	contig445	contig445	Endochiti	TTTCTTA	contig445	Solyc10g	Solyc10g	Endochiti	GO:00088	GO:00088	contig445	Solyc10g	Endochiti	GO:00088	SL2.40ch	AT3G125	ATHCHIB	ATHCHIB	chr3:396	1216.97	1421.05	659.763	518.857	428.186	800.146
GT	Sense	Sense	0.292	Detected	-0.292	Detected	0.000	-1.278	Detected	-1.677	Detected	-1.478	0.053	GT	Sens	contig463	contig463	Vacuolar	GATAAC	contig463	Solyc08g	Solyc08g	Vacuolar	GO:00041	GO:00041	contig463	Solyc08g	Vacuolar	GO:00041	SL2.40ch	AT5G41320.1		unknown	chr5:165	54.119	33.9826	9.81116	20.9006	18.8571	14.2585
GT	Sense	Sense	0.052	Detected	-0.052	Detected	0.000	-1.332	Detected	-1.076	Detected	-1.204	0.013	GT	Sens	contig468	contig468	ATP-citra	AGAGCC	contig468	Solyc04g	Solyc04g	ATP-citra	GO:00055	GO:00055	contig468	Solyc05g	ATP-citra	GO:00038	SL2.40ch	AT1G608	ACLA-2	ACLA-2:	chr1:223	22212.5	19446.1	6657.5	9096.2	8804.21	10484.4
GT	Sense	Sense	0.199	Detected	-0.199	Detected	0.000	-1.119	Detected	-0.957	Detected	-1.038	0.040	GT	Sens	contig477	contig477	Os03g01	TCAAAC	contig477	Solyc03g	Solyc03g	Os03g0169000 protein (Fragm			contig477	Solyc03g	Os03g0169000 prot		SL2.40ch	AT5G15740.1		unknown	chr5:513	1281.81	914.805	351.69	459.891	531.744	592.951
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	-1.311	Detected	-0.932	Detected	-1.122	0.028	GT	Sens	contig480	contig480	Unknown	AATAATC	contig480	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)%			contig480	Solyc12g	H-ATPase	GO:00160	SL2.40ch	AT2G13720.1				4630.47	4281.35	2157.78	1778.13	1913.54	2481.1
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-2.305	Detected	-2.830	Detected	-2.568	0.012	GT	Sens	contig484	contig484	UDP-gluc	AATAGG	contig484	Solyc12g	Solyc12g	UDP-gluc	GO:00081	GO:00081	contig484	Solyc12g	UDP-gluc	GO:00081	SL2.40ch	AT1G223	AtUGT85	AtUGT85	chr1:789	363.027	289.581	41.9791	55.8984	69.9775	48.4641
GT	Sense	Sense	0.197	Detected	-0.197	Detected	0.000	-1.261	Detected	-0.822	Detected	-1.041	0.072	GT	Sens	contig488	contig488	1-aminoc	AAGATAT	contig488	Solyc02g	Solyc02g	1-aminoc	GO:00166	GO:00166	contig488	Solyc02g071480.2.1				AT4G25310.1		oxidored	chr4:129	259.838	186.072	66.1371	92.2737	97.8318	132.25
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	-1.214	Detected	-0.941	Detected	-1.077	0.016	GT	Sens	contig503	contig503	Unknown	GTAGATC	contig503	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig503	Solyc08g	Unknown Protein (A		SL2.40ch	AT3G559	CCR3. AT	CCR3 (AI	chr3:207	249.086	243.187	88.0804	97.4901	113.159	136.28
GT	Sense	Sense	0.405	Detected	-0.405	Detected	0.000	-1.182	Detected	-1.715	Detected	-1.449	0.096	GT	Sens	contig518	contig518	Xylogluc	GTGGAA	contig518	Solyc12g	Solyc12g	Xylogluc	GO:00059	GO:00059	contig518	Solyc12g	Xylogluc	GO:00059	SL2.40ch	AT3G23730.1		xylogluc	chr3:855	553.659	297.283	145.315	131.49	190.672	131.345
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-1.159	Detected	-1.235	Detected	-1.197	0.002	GT	Sens	contig538	contig538	Inorganic	CATGAAC	contig538	Solyc06g	Solyc06g	Inorganic	GO:00053	GO:00053	contig538	Solyc09g	Inorganic	GO:00053	SL2.40ch	AT2G32830.1				1932.75	1923.12	702.264	1054.24	920.802	870.814

GT	Sense	Sense	0.211	Detected	-0.211	Detected	0.000	-0.839	Detected	-1.304	Detected	-1.072	0.076	GT	Sens	contig552	contig552	Pseudo-r	GCAGCT	contig552	Solyc03g	Solyc03g	Pseudo-r	GO:00065	GO:00065	contig552	Solyc03g	Pseudo-r	GO:00065	SL2.40ch	AT5G028	PRR7, AP	PRR7 (PS	chr5:638	206.789	145.241	58.0192	63.3428	103.278	74.6347
GT	Sense	Sense	-0.334	Detected	0.334	Detected	0.000	-1.627	Detected	-1.086	Detected	-1.356	0.087	GT	Sens	contig570	contig570	Epoxide h	GTATTG	contig570	Solyc01g	Solyc01g	Epoxide h	GO:00038	GO:00038	contig570	Solyc01g	Epoxide h	GO:00043	SL2.40ch	AT4G15960.1		catalytic/	chr4:904	9341.08	13962.4	6676.26	10229.9	3943.9	5720.11
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.280	Detected	-1.092	Detected	-1.186	0.010	GT	Sens	contig591	contig591	AP-2 com	CAAACT	contig591	Solyc11g	Solyc11g	AP-2 com	GO:00301	GO:00301	contig591	Solyc11g	AP-2 com	GO:00301	SL2.40ch	AT5G227	alpha-AD	alpha-AD	chr5:757	1054.43	897.516	248.597	334.808	427.223	485.104
GT	Sense	Sense	0.254	Detected	-0.254	Detected	0.000	-2.672	Detected	-1.136	Detected	-1.904	0.143	GT	Sens	contig592	contig592	UDP-gluc	ACAAGA	contig592	Solyc04g	Solyc04g	UDP-gluc	GO:00081	GO:00081	contig592	Solyc04g	UDP-gluc	GO:00150	SL2.40ch	AT3G531	UGT73C7	UGT73C7	chr3:197	235.585	155.9	31.0156	49.9844	32.0593	92.7328
GT	Sense	Sense	0.599	Detected	-0.599	Detected	0.000	-3.894	Detected	-4.041	Detected	-3.967	0.022	GT	Sens	contig600	contig600	Acyltrans	CCAAGT	contig600	Solyc11g	Solyc11g	Acyltrans	GO:00167	GO:00167	contig600	Solyc11g	Acyltrans	GO:00167	SL2.40ch	AT4G37950.1		lyase	chr4:178	1634.61	670.145	293.818	829.989	75.0738	67.6202
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-3.092	Detected	-1.383	Detected	-2.238	0.121	GT	Sens	contig606	contig606	Receptor	TTGTCA	contig606	Solyc09g	Solyc09g	Receptor	GO:00055	GO:00055	contig606	Solyc09g	Receptor	GO:00055	SL2.40ch	AT2G39360.1		protein k	chr2:164	173.644	148.253	43.9537	32.3027	20.0631	65.4022
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	-2.468	Detected	-1.456	Detected	-1.962	0.062	GT	Sens	contig612	contig612	Cysteine	AAGTAC	contig612	Solyc11g	Solyc11g	Cysteine	GO:00081	GO:00081	contig612	Solyc11g	Cysteine	GO:00081	SL2.40ch	AT4G30260.1		integral r	chr4:148	258.021	217.078	53.5008	75.3693	45.6111	91.7332
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	-1.379	Detected	-1.127	Detected	-1.253	0.012	GT	Sens	contig623	contig623	Glycosylt	TACACT	contig623	Solyc09g	Solyc09g	Glycosylt	GO:00167	GO:00167	contig623	Solyc06g	Glycosylt	GO:00472	SL2.40ch	AT3G251	GAUT8, Q	QUA1 (QU	chr3:915	8079.94	6965.03	2803.26	3571.92	3076.23	3651.32
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-1.429	Detected	-1.291	Detected	-1.360	0.004	GT	Sens	contig625	contig625	Auxin-ind	GGCATT	contig625	Solyc01g	Solyc01g	Auxin-ind	GO:00055	GO:00055	contig625	Solyc01g	Auxin-ind	GO:00055	SL2.40ch	AT4G34760.1		auxin-res	chr4:165	530.004	461.615	151.996	328.891	195.87	214.953
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-1.165	Detected	-0.871	Detected	-1.018	0.021	GT	Sens	contig640	contig640	UDP-gluc	AGATGT	contig640	Solyc02g	Solyc02g	UDP-gluc	GO:00060	GO:00060	contig640	Solyc02g	UDP-gluc	GO:00480	SL2.40ch	AT5G444	DUR	DUR (DEI	chr5:179	5123.41	5026.15	2205.22	2707.64	2413.23	2949.46
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-1.221	Detected	-1.092	Detected	-1.156	0.004	GT	Sens	contig644	contig644	Unknown	GTAGAT	contig644	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig644	Solyc00g	Unknown Protein (A		SL2.40ch	AT3G559	CCR3, AT	CCR3 (AR	chr3:207	259.188	234.162	77.9808	98.4186	112.678	122.914
GT	Sense	Sense	0.170	Detected	-0.170	Detected	0.000	-1.085	Detected	-0.949	Detected	-1.017	0.031	GT	Sens	contig666	contig666	CBL-inter	GTCTTG	contig666	Solyc06g	Solyc06g	CBL-inter	GO:00046	GO:00046	contig666	Solyc06g050290.1.1				AT5G583	CIPK10, F	SIP1 (SO	chr5:235	5064.67	3764.51	1302.82	2431.02	2195.35	2405.55
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	-3.427	Comprom	-1.877	Detected	-2.652	0.080	GT	Sens	contig671	contig671	Cytochro	GTTCAA	contig671	Solyc10g	Solyc10g	Cytochro	GO:00200	GO:00200	contig671	Solyc10g	Cytochro	GO:00464	SL2.40ch	AT2G408	CYP98A3	CYP98A3	chr2:170	87.2294	62.5529	14.2201	12.7902	7.32582	21.3841
GT	Sense	Sense	0.381	Detected	-0.381	Detected	0.000	-3.149	Detected	-2.572	Detected	-2.861	0.027	GT	Sens	contig683	contig683	Pyridine	GTGAAA	contig683	Solyc11g	Solyc11g	Pyridine	GO:00551	GO:00551	contig683	Solyc11g	Nitric oxide reducta		SL2.40ch	AT3G102	LYC	LYC (LYC	chr3:316	348.06	193.192	36.3001	69.6139	31.1827	46.3492
GT	Sense	Sense	-0.002	Detected	0.002	Detected	0.000	-1.837	Detected	-1.468	Detected	-1.653	0.012	GT	Sens	contig690	contig690	Fatty acid	AAAGCA	contig690	Solyc10g	Solyc10g	Fatty acid	GO:00047	GO:00047	contig690	Solyc10g	Fatty acid	GO:00047	SL2.40ch	AT3G61580.1		delta-8 sp	chr3:227	10452	9861.19	3446.19	3668.14	3029.32	3900.74
GT	Sense	Sense	0.206	Detected	-0.206	Detected	0.000	-1.302	Detected	-1.329	Detected	-1.316	0.024	GT	Sens	contig698	contig698	ABC tran	TGCTAG	contig698	Solyc06g	Solyc06g	ABC tran	GO:00171	GO:00171	contig698	Solyc03g	ABC tran	GO:00085	SL2.40ch	AT1G178	WBC11, A	WBC11 (W	chr1:614	185.033	130.892	55.8269	35.7373	67.293	65.8728
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	-1.071	Detected	-1.138	Detected	-1.105	0.001	GT	Sens	contig714	contig714	GTPase a	AATGAA	contig714	Solyc06g	Solyc06g	GTPase a	GO:00056	GO:00056	contig714	Solyc06g	GTPase a	GO:00056	SL2.40ch	AT3G49350.1		RAB GTP	chr3:182	720.374	682.031	202.102	268.772	355.863	338.549
GT	Sense	Sense	0.711	Detected	-0.711	Detected	0.000	-0.864	Detected	-1.502	Detected	-1.183	0.268	GT	Sens	contig725	contig725	Salicylic	TCCTTG	contig725	Solyc09g	Solyc09g	Salicylic	GO:00081	GO:00081	contig725	Solyc09g	Salicylic	GO:00087	SL2.40ch	AT4G36470.1		S-adenos	chr4:172	165.567	58.1529	69.3762	3.2412	57.4706	36.8342
GT	Sense	Sense	0.159	Detected	-0.159	Detected	0.000	-2.531	Detected	-1.758	Detected	-2.144	0.036	GT	Sens	contig729	contig729	Beta-fruc	GAGAAT	contig729	Solyc09g	Solyc09g	Beta-fruc	GO:00059	GO:00059	contig729	Solyc10g	Beta-fruc	GO:00059	SL2.40ch	AT3G52700.1		unknown	chr3:195	62562.5	47232.7	12406.3	18487.2	10028.4	17092.4
GT	Sense	Sense	0.136	Detected	-0.136	Detected	0.000	-3.635	Detected	-2.992	Detected	-3.313	0.011	GT	Sens	contig732	contig732	Globulin-	AATCAA	contig732	Solyc09g	Solyc09g	Globulin-	GO:00457	GO:00457	contig732	Solyc09g	Vicilin-like	GO:00457	SL2.40ch	AT2G43560.1		immunop	chr2:180	174.683	136.165	23.8679	48.1812	13.2405	20.6153
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-3.146	Detected	-2.447	Detected	-2.797	0.016	GT	Sens	contig749	contig749	Abscisic	ACCGTT	contig749	Solyc04g	Solyc04g	Abscisic	GO:00069	GO:00069	contig749	Solyc04g	Abscisic	GO:00069	SL2.40ch	AT1G76940.1		RNA reco	chr1:289	321.173	282.9	43.5141	43.544	36.3009	58.7916
GT	Sense	Sense	-0.135	Detected	0.135	Detected	0.000	-2.777	Detected	-1.970	Detected	-2.374	0.031	GT	Sens	contig756	contig756	Peroxida	TTTTCA	contig756	Solyc02g	Solyc02g	Peroxida	GO:00055	GO:00055	contig756	Solyc02g	Peroxida	GO:00046	SL2.40ch	AT1G14540.1		anionic p	chr1:497	30472.3	34550.8	7303.67	5629.95	5048.85	8803.31
GT	Sense	Sense	0.635	Detected	-0.635	Detected	0.000	-4.162	Comprom	-2.086	Comprom	-3.124	0.124	GT	Sens	contig761	contig761	Cytochro	GAATGC	contig761	Solyc02g	Solyc02g	Cytochro	GO:00198	GO:00198	contig761	Solyc02g	Cytochro	GO:00083	SL2.40ch	AT5G384	CYP735A	CYP735A	chr5:153	50.5369	19.7139	6.01537	7.63431	1.87981	7.90172
GT	Sense	Sense	-0.310	Detected	0.310	Detected	0.000	-1.514	Detected	-1.600	Detected	-1.557	0.038	GT	Sens	contig769	contig769	Proteinas	TACTCA	contig769	Solyc03g	Solyc03g	Proteinas	GO:00048	GO:00048	contig769	Solyc03g	Proteinas	GO:00048	SL2.40ch	AT4G15830.1		binding	chr4:899	7399.16	10696.1	4832.43	7458.89	3321.66	3119.72
GT	Sense	Sense	0.667	Detected	-0.667	Detected	0.000	-0.914	Detected	-2.509	Detected	-1.712	0.241	GT	Sens	contig776	contig776	Unknown	TATGAT	contig776	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig776	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G14020.1		INVOLVE	chr5:452	610.72	227.945	43.6162	26.0922	211.131	69.6704
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-1.403	Detected	-1.092	Detected	-1.247	0.023	GT	Sens	contig797	contig797	Ras-like	CAGCCA	contig797	Solyc02g	Solyc02g	Ras-like	GO:00039	GO:00039	contig797	Solyc02g	Ras-like	GO:00039	SL2.40ch	AT1G200	ARAC4, R	ROP2 (RH	chr1:696	6430.65	5162.32	1765.55	2742.21	2324.08	2874.46
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-3.017	Detected	-2.335	Detected	-2.676	0.017	GT	Sens	contig810	contig810	Abscisic	CACCGT	contig810	Solyc04g	Solyc04g	Abscisic	GO:00069	GO:00069	contig810	Solyc04g071590.1.1				AT3G44590.1		60S acidi	chr3:161	323.356	273.004	32.8925	56.4069	39.1472	62.5922
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	-3.049	Detected	-1.591	Detected	-2.320	0.087	GT	Sens	contig816	contig816	Auxin-ind	TCTTCA	contig816	Solyc07g	Solyc07g	Auxin-induced protein-like (AH			contig816	Solyc07g	Auxin-induced prote		SL2.40ch	AT3G07730.1		unknown	chr3:246	109.761	94.1702	24.2466	45.9353	13.0952	35.8714
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	-1.680	Detected	-1.336	Detected	-1.508	0.025	GT	Sens	contig837	contig837	Ras-relat	ATTCCG	contig837	Solyc07g	Solyc07g	Ras-relat	GO:00055	GO:00055	contig837	Solyc07g	Ras-relat	GO:00150	SL2.40ch	AT3G150	AtRABA1	AtRABA1	chr3:506	463.068	343.542	102.831	120.669	132.735	167.997
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-3.528	Detected	-3.976	Detected	-3.752	0.004	GT	Sens	contig843	contig843	Glutathio	GGCGTA	contig843	Solyc01g	Solyc01g	Glutathione-S-transferase (AH			contig843	Solyc01g	Glutathione-S-transf		SL2.40ch	AT3G492	emb1796	emb1796	chr3:182	8061.34	8794.29	1176.48	809.895	778.404	569.078
GT	Sense	Sense	0.692	Detected	-0.692	Detected	0.000	-0.857	Detected	-2.063	Detected	-1.460	0.252	GT	Sens	contig854	contig854	Unknown	GATCAA	contig854	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig854	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G236	PAKRP1L	KINESIN-	chr3:851	256.914	92.6733	20.8997	19.6888	90.824	39.2536
GT	Sense	Sense	-0.160	Detected	0.160	Detected	0.000	-0.951	Detected	-1.683	Detected	-1.317	0.081	GT	Sens	contig856	contig856	Cytochro	TCAAAA	contig856	Solyc03g	Solyc03g	Cytochro	GO:00200	GO:00200	contig856	Solyc03g	Cytochro	GO:00045	SL2.40ch	AT3G483	CYP71A2	CYP71A2	chr3:178	679.757	798.194	265.454	183.481	406.437	243.833
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.364	Detected	-1.561	Detected	-1.462	0.005	GT	Sens	contig86	contig86	Calcium-	TTTACG	contig86	Solyc04g	Solyc04g	Calcium-	GO:00064	GO:00064	contig86	Solyc04g	Calcium-	GO:00046	SL2.40ch	AT1G086	PPCK1	PPCK1 (P	chr1:275	1872.02	1699.27	657.508	718.556	739.132	642.616
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.344	Detected	-0.871	Detected	-1.107	0.044	GT	Sens	contig870	contig870	Alpha-1 4	AAACTT	contig870	Solyc05g	Solyc05g	Alpha-1 4	GO:00167	GO:00167	contig870	Solyc05g	Alpha-1 4	GO:00167	SL2.40ch	AT3G022	RGP1, AT	RGP1 (RE	chr3:415	9109.1	8039.21	2896.27	4176.27	3595.28	4974.79
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	-1.344	Detected	-0.945	Detected	-1.144	0.030	GT	Sens	contig879	contig879	Pyrophos	AAAGAA	contig879	Solyc07g	Solyc07g	Pyrophos	GO:00160	GO:00160	contig879	Solyc07g	Pyrophos	GO:00096	SL2.40ch	AT1G156	AVP1, AT	AVP1: AT	chr1:539	3636.7	3262.19	1156.73	1263.76	1447.15	1902.05
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	-0.979	Detected	-1.187	Detected	-1.083	0.024	GT	Sens	contig879	contig879	Protein ki	CCATTG	contig879	Solyc07g	Solyc07g	Protein kinase family protein (.			contig879	Solyc01g	Receptor-	GO:00064	SL2.40ch	AT1G09440.1		protein k	chr1:304	938.671	732.983	226.175	229.817	448.703	387.335
GT	Sense	Sense	0.228	Detected	-0.228	Detected	0.000	-1.724	Comprom	-1.467	Comprom	-1.596	0.026	GT	Sens	contig909	contig909	Inosine-u	GCATAC	contig909	Solyc01g	Solyc01g	Inosine-u	GO:00167	GO:00167	contig909	Solyc01g	Inosine-u	GO:00167	SL2.40ch	AT5G18890.1		inosine-u	chr5:630	17.3706	11.9176	2.12974	16.7163	4.6435	5.53241
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-1.938	Detected	-1.038	Detected	-1.488	0.081	GT	Sens	contig911	contig911	Pectate ly	ATTTTG	contig911	Solyc06g	Solyc06g	Pectate ly	GO:00168	GO:00168	contig911	Solyc06g071840.1.1				AT4G24780.1		pectate ly	chr4:127	3975.09	3854.04	1289.82	1240.72	1089.58	2026.16
GT	Sense	Sense	0.200	Detected	-0.200	Detected	0.000	-2.011	Detected	-1.287	Detected	-1.649	0.057	GT	Sens	contig931	contig931	Auxin-ind	ATACCT	contig931	Solyc01g	Solyc01g	Auxin-ind	GO:00055	GO:00055	contig931	Solyc01g	Auxin-ind	GO:00055	SL2.40ch	AT4G38840.1		auxin-res	chr4:181	6374.94	4547.93	1272.42	2582.89	1424.8	2345.66
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-1.351	Detected	-1.611	Detected	-1.481	0.008	GT	Sens	contig938	contig938	Laccase	GTTATT	contig938	Solyc05g	Solyc05g	Laccase	GO:00480	GO:00480	contig938	Solyc07g	Laccase	GO:00055	SL2.40ch	AT5G589	LAC16	LAC16 (la	chr5:237	1120.02	1047.22	621.951	495.869	452.631	377.038
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-2.908	Comprom	-2.910	Comprom	-2.909	0.000	GT	Sens	contig964	contig964	NifS-like	TAGAGA	contig964	Solyc11g	Solyc11g	NifS-like	GO:00081	GO:00081	contig964	Solyc11g005830.1.1				AT3G48670.2		XH/XS do	chr3:180	38.4059	37.7695	5.5804	9.30441	5.41116	5.38815
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	-1.121	Detected	-1.021	Detected	-1.071	0.020	GT	Sens	contig978	contig978	KH domai	ATTAGA	contig978	Solyc10g	Solyc10g	KH domai	GO:00037	GO:00037	contig978	Solyc10g	KH domai	GO:00037	SL2.40ch	AT3G08620.1		KH doma	chr3:261	3022.76	2321.91	1199.32	1015.18	1299.02	1388.15
GT	Sense	Sense	0.177	Detected	-0.177	Detected	0.000	-1.478	Detected	-1.429	Detected	-1.453	0.015	GT	Sens	contig979	contig979	Potassiur	CTCTCT	contig979	Solyc10g	Solyc10g	Potassiur	GO:00160	GO:00160	contig979	Solyc06g	Potassiur	GO:00096	SL2.40ch	AT1G703	KUP6	KUP6: po	chr1:264	86.1045	63.3532	30.4747	24.1633	28.2787	29.1607
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-1.259	Detected	-1.046	Detected	-1.152	0.018	GT	Sens	contig979	contig979	Cytochro	ACTATA	contig979	Solyc05g	Solyc05g	Cytochro	GO:00160	GO:00160	contig979	Solyc05g	Cytochro	GO:00160	SL2.40ch	ATMG001	COX2	cytochro	chrM:405	1811.3	1456.64	736.182	668.851	723.776	836.458
GT	Sense	Sense	-0.739	Detected	0.739	Detected	0.000	-1.324	Detected	-0.892	Detected	-1.108	0.287	GT	Sens	contig995	contig995	Pectinest	ATTATA	contig995	Solyc07g	Solyc07g	Pectinest	GO:00305	GO:00305	contig995	Solyc07g	Pectinest	GO:00056	SL2.40ch	AT5G64640.1		pectinest	chr5:258	27.1557	71.1974	13.8221	19.0628	18.7267	25.2002
GT	Sense	Sense	-0.061	Detected	0.061	Detected	0.000	-1.572	Detected	-1.188	Detected	-1.380	0.021	GT	Sens	NM_0012	NM_0012	Solanum	CAGAACAGCCCATTATTATTCCAGCAGCCCAACAAAACAATTTGTTCACCAATAATAACA																2120.41	2170.06	1291.25	1107.29	769.399	1001.32
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-1.279	Detected	-1.566	Detected	-1.423	0.015	GT	Sens	U13054	U13054	Cel1: Cro	GCCCAAACTTTACTAGCTAAGGAATACCTTAATGGAAAGAGCAATTTGGAAAAATTCAAG																16960.8	13795.4	5517.97	7993.57	6721.07	5491.68
GT	Sense	Sense	0.168	Detected	-0.168	Detected	0.000	-2.614	Detected	-1.849	Detected	-2.232	0.033	GT	Sens	U23053	U23053	LEU2305	CAAGAGTTAGGAGTCCAAAATGTGACAGTTAAGACTGTGACTTTCAGTGGAACAACAAAT																140820	105036	21734.1	40192.3	21180.3	35900.5
GT	Sense	Sense	0.108	Detected	-0.108	Detected	0.000	-2.135	Detected	-1.407	Detected	-1.771	0.043	GT	Sens	U23053	U23053	TAPG1: C	GCCAGAGGAAGAGTTTCTGGTTTACAAAAACCTACCAATTGCCTATTAAAAAGTTAGATA																166114	134545	44248.4	75243.7	36285.6	59928.1
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-2.804	Detected	-1.893	Detected	-2.349	0.038	GT	Sens	U70480	U70480	LEU7048	GCTGGAAACAACAAGAGTTGGGAGTCCAAAATGTGACAGTTAAGACTGTGACTTTTAGTG																150729	118004	23161.7	42916.5	20359.5	38170.2
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-2.283	Detected	-1.292	Detected	-1.788	0.069	GT	Sens	U70481	U70481	LEU7048	CTGGAGGAAGAGCTTCTGGTTTTGAAGAACTTAGTAAATGCTTATAAATTATACAACAAA																142211	128708	96985.6	113955	29637.8	58733.5
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	-3.100	Detected	-2.111	Detected	-2.605	0.035	GT	Sens	U70481	U70481	TAPG4: C	AAGAGCAAGGAGTACAAAATGTGACAGTTAAGATGGTTAGCTTCACAAGTACTGAGAATG																132592	116321	57908.7	75525.2	15449.5	30574.9
GT	Sense	Sense	-0.363	Detected	0.363	Detected	0.000	-1.944	Detected	-1.094	Detected	-1.519	0.113	GT	Sens	Y11268	Y11268	L.esculen	ATGAACGTACTGATTATAGTCATTCGGAGCCAGCTACTTACATTAATGCTGCTATTGTTG																1723.61	2680.96	818	515.736	595.677	1070.88

GO ID	GO ACCESSION	GO Term	p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
6888	GO:0009611|GO:00022	response to wounding	0.00	14	1.4752371	66	0.1906027
9600	GO:0016491	oxidoreductase activity	0.00	81	8.5353	1724	4.9787736
3472	GO:0004866	endopeptidase inhibitor	0.00	13	1.369863	95	0.27435237
28101	GO:0061135	endopeptidase regulato	0.00	13	1.369863	95	0.27435237
8159	GO:0010951	negative regulation of e	0.00	13	1.369863	95	0.27435237
26712	GO:0052548	regulation of endopepti	0.00	13	1.369863	95	0.27435237
7690	GO:0010466	negative regulation of p	0.00	13	1.369863	110	0.31767118
12946	GO:0030414	peptidase inhibitor activ	0.00	13	1.369863	110	0.31767118
25636	GO:0051346	negative regulation of h	0.00	13	1.369863	110	0.31767118
28100	GO:0061134	peptidase regulator acti	0.00	13	1.369863	112	0.32344702
26711	GO:0052547	regulation of peptidase	0.00	13	1.369863	112	0.32344702
3473	GO:0004867	serine-type endopeptida	0.00	9	0.9483667	66	0.1906027
3464	GO:0004857	enzyme inhibitor activity	0.00	14	1.4752371	157	0.4534034
22409	GO:0046906	tetrapyrrole binding	0.00	33	3.4773445	596	1.7212002
19255	GO:0042938	dipeptide transport	0.00	11	1.1591148	105	0.3032316
19253	GO:0042936	dipeptide transporter ac	0.00	11	1.1591148	105	0.3032316
26959	GO:0055114	oxidation-reduction pro	0.00	98	10.326659	2490	7.1909204
4641	GO:0006508	proteolysis	0.00	46	4.8472075	965	2.7868426
9396	GO:0016168	chlorophyll binding	0.00	7	0.73761857	46	0.13284431
2896	GO:0004090	carbonyl reductase (NA	0.00	4	0.4214963	13	0.037542958
19393	GO:0043086	negative regulation of c	0.00	14	1.4752371	188	0.54292893
20342	GO:0044092	negative regulation of n	0.00	14	1.4752371	188	0.54292893
9813	GO:0016759	cellulose synthase activ	0.00	7	0.73761857	57	0.16461143
9768	GO:0016706	oxidoreductase activity,	0.00	13	1.369863	175	0.505386
8607	GO:0015197|GO:00156	peptide transporter acti	0.00	11	1.1591148	139	0.40142086
8608	GO:0015198	oligopeptide transporter	0.00	11	1.1591148	139	0.40142086
4944	GO:0006857	oligopeptide transport	0.00	11	1.1591148	141	0.4071967
9099	GO:0015833	peptide transport	0.00	11	1.1591148	141	0.4071967
9784	GO:0016723	oxidoreductase activity,	0.00	4	0.4214963	20	0.0577584
225	GO:0000293	ferric-chelate reductase	0.00	4	0.4214963	20	0.0577584
9266	GO:0016020	membrane	0.00	131	13.804005	3741	10.803708
28364	GO:0065007	biological regulation	0.00	150	15.806111	4376	12.637537
15570	GO:0033170	protein-DNA loading AT	0.00	2	0.21074815	3	0.00866376
2635	GO:0003689	DNA clamp loader activ	0.00	2	0.21074815	3	0.00866376
8489	GO:0015066	alpha-amylase inhibitor	0.00	4	0.4214963	22	0.06353424
3307	GO:0004675	transmembrane recepto	0.00	20	2.1074815	367	1.0598665
25626	GO:0051336	regulation of hydrolase	0.00	13	1.369863	196	0.5660323
9808	GO:0016754	sinapoylglucose-malate	0.00	4	0.4214963	23	0.06642216
9807	GO:0016753	O-sinapoyltransferase a	0.00	4	0.4214963	23	0.06642216
9806	GO:0016752	sinapoyltransferase act	0.00	4	0.4214963	23	0.06642216
5702	GO:0008146	sulfotransferase activity	0.00	6	0.63224447	54	0.15594767
6826	GO:0009538	photosystem I reaction	0.00	3	0.31612223	12	0.03465504
25094	GO:0050789|GO:00507	regulation of biological	0.00	146	15.384615	4315	12.461374
5729	GO:0008191	metalloendopeptidase i	0.00	2	0.21074815	4	0.011551679
23942	GO:0048551	metalloenzyme inhibitor	0.00	2	0.21074815	4	0.011551679
7792	GO:0010576	metalloenzyme regulato	0.00	2	0.21074815	4	0.011551679
9718	GO:0016636	oxidoreductase activity,	0.00	2	0.21074815	4	0.011551679
11931	GO:0020037	heme binding	0.01	26	2.739726	550	1.5883559
6809	GO:0009521|GO:00300	photosystem	0.01	4	0.4214963	28	0.080861755
6940	GO:0009672	auxin:hydrogen sympor	0.01	4	0.4214963	28	0.080861755
18502	GO:0042132	fructose 1,6-bisphospha	0.01	2	0.21074815	5	0.0144396
6810	GO:0009522	photosystem I	0.01	3	0.31612223	15	0.043318797
2868	GO:0004062	aryl sulfotransferase ac	0.01	3	0.31612223	15	0.043318797
3872	GO:0005506	iron ion binding	0.01	26	2.739726	563	1.6258988
31431	GO:0080054	low affinity nitrate trans	0.01	5	0.52687037	45	0.1299564
22049	GO:0046527	glucosyltransferase acti	0.01	15	1.5806112	270	0.77973837
3065	GO:0004382	guanosine-diphosphata	0.01	2	0.21074815	6	0.01732752
21331	GO:0045735	nutrient reservoir activit	0.01	7	0.73761857	89	0.25702485
11776	GO:0019825	oxygen binding	0.01	19	2.0021074	389	1.1234008
9783	GO:0016722	oxidoreductase activity,	0.01	5	0.52687037	50	0.14439599
20630	GO:0044436	thylakoid part	0.01	7	0.73761857	90	0.2599128
5792	GO:0008271	secondary active sulfate	0.01	3	0.31612223	18	0.051982556
8736	GO:0015381	high affinity sulfate trans	0.01	3	0.31612223	18	0.051982556
25098	GO:0050794|GO:00512	regulation of cellular pro	0.01	132	13.909378	3987	11.514136
9933	GO:0016903	oxidoreductase activity,	0.01	8	0.8429926	113	0.32633495
6863	GO:0009579	thylakoid	0.01	7	0.73761857	94	0.27146447
9832	GO:0016782	transferase activity, tran	0.02	6	0.63224447	74	0.21370606
6201	GO:0008794	arsenate reductase (glu	0.02	3	0.31612223	20	0.0577584
13086	GO:0030611	arsenate reductase acti	0.02	3	0.31612223	20	0.0577584
13088	GO:0030613	oxidoreductase activity,	0.02	3	0.31612223	20	0.0577584
13089	GO:0030614	oxidoreductase activity,	0.02	3	0.31612223	20	0.0577584
10057	GO:0017110	nucleoside-diphosphata	0.02	2	0.21074815	8	0.023103358
11202	GO:0019199	transmembrane recepto	0.02	22	2.3182297	504	1.4555116
8967	GO:0015698	inorganic anion transpo	0.02	10	1.0537407	176	0.5082739
9769	GO:0016707	gibberellin 3-beta-dioxy	0.02	2	0.21074815	9	0.025991278
24627	GO:0050308	sugar-phosphatase acti	0.02	2	0.21074815	9	0.025991278
8526	GO:0015112	nitrate transmembrane	0.03	5	0.52687037	61	0.1761631
8975	GO:0015706|GO:00068	nitrate transport	0.03	5	0.52687037	61	0.1761631
8517	GO:0015103	inorganic anion transme	0.03	9	0.9483667	154	0.44473964
16738	GO:0034357	photosynthetic membra	0.03	6	0.63224447	83	0.23969735
28365	GO:0065008	regulation of biological	0.03	15	1.5806112	316	0.9125827
8651	GO:0015248	sterol transporter activit	0.03	2	0.21074815	10	0.0288792
9178	GO:0015918	sterol transport	0.03	2	0.21074815	10	0.0288792
10072	GO:0017127	cholesterol transporter	0.03	2	0.21074815	10	0.0288792
12859	GO:0030301	cholesterol transport	0.03	2	0.21074815	10	0.0288792
26022	GO:0051740	ethylene binding	0.03	2	0.21074815	10	0.0288792
30687	GO:0072328	alkene binding	0.03	2	0.21074815	10	0.0288792
21145	GO:0045543	gibberellin 2-beta-dioxy	0.03	3	0.31612223	25	0.072197996
21058	GO:0045454|GO:00305	cell redox homeostasis	0.03	11	1.1591148	211	0.6093511
5704	GO:0008150|GO:00000	biological_process	0.03	636	67.017914	22215	64.155136
8673	GO:0015291|GO:00152	secondary active transm	0.03	18	1.8967334	407	1.1753833
8530	GO:0015116	sulfate transmembrane	0.03	3	0.31612223	26	0.075085916
9765	GO:0016702	oxidoreductase activity,	0.03	5	0.52687037	66	0.1906027
12574	GO:0022892	substrate-specific trans	0.03	52	5.479452	1463	4.2250266
4329	GO:0006096|GO:00196	glycolysis	0.04	4	0.4214963	46	0.13284431
5981	GO:0008509	anion transmembrane t	0.04	12	1.2644889	245	0.70754033
9767	GO:0016705	oxidoreductase activity,	0.04	15	1.5806112	329	0.95012563

22415	GO:0046914	transition metal ion bind	**0.04**	86	9.062171	2599	7.5057034
5793	GO:0008272|GO:0006	sulfate transport	**0.04**	3	0.31612223	28	0.080861755
4917	GO:0006820|GO:0006	anion transport	**0.04**	12	1.2644889	247	0.7133162
3386	GO:0004773	steryl-sulfatase activity	**0.04**	2	0.21074815	12	0.03465504
3397	GO:0004784|GO:0004	superoxide dismutase a	**0.04**	2	0.21074815	12	0.03465504
5965	GO:0008484	sulfuric ester hydrolase	**0.04**	2	0.21074815	12	0.03465504
9704	GO:0016621	cinnamoyl-CoA reducta	**0.04**	2	0.21074815	12	0.03465504
9782	GO:0016721	oxidoreductase activity,	**0.04**	2	0.21074815	12	0.03465504
3490	GO:0004888|GO:0004	transmembrane recepto	**0.04**	23	2.4236038	571	1.6490022
7074	GO:0009815	1-aminocyclopropane-1	**0.04**	4	0.4214963	49	0.14150807
2986	GO:0004252	serine-type endopeptida	**0.05**	8	0.8429926	144	0.41586044
9764	GO:0016701	oxidoreductase activity,	**0.05**	5	0.52687037	72	0.20793022
7166	GO:0009914	hormone transport	**0.05**	4	0.4214963	50	0.14439599
27891	GO:0060918	auxin transport	**0.05**	4	0.4214963	50	0.14439599
31536	GO:0080161	auxin transmembrane t	**0.05**	4	0.4214963	50	0.14439599
2870	GO:0004064	arylesterase activity	**0.05**	3	0.31612223	30	0.086637594
3013	GO:0004328|GO:0034	formamidase activity	**0.05**	1	0.105374075	2	0.00577584
3152	GO:0004493	methylmalonyl-CoA epi	**0.05**	1	0.105374075	2	0.00577584
3604	GO:0005031|GO:0005	tumor necrosis factor re	**0.05**	1	0.105374075	2	0.00577584
3606	GO:0005035	death receptor activity	**0.05**	1	0.105374075	2	0.00577584
5907	GO:0008413	8-oxo-7,8-dihydroguan	**0.05**	1	0.105374075	2	0.00577584
6790	GO:0009496	plastoquinol-plastocyan	**0.05**	1	0.105374075	2	0.00577584
6828	GO:0009540	zeaxanthin epoxidase [	**0.05**	1	0.105374075	2	0.00577584
8612	GO:0015204|GO:0015	urea transmembrane tr	**0.05**	1	0.105374075	2	0.00577584
9106	GO:0015840	urea transport	**0.05**	1	0.105374075	2	0.00577584
11186	GO:0019177	dihydroneopterin tripho	**0.05**	1	0.105374075	2	0.00577584
11223	GO:0019221	cytokine-mediated sign	**0.05**	1	0.105374075	2	0.00577584
11870	GO:0019955|GO:0019	cytokine binding	**0.05**	1	0.105374075	2	0.00577584
14849	GO:0032441	pheophorbide a oxyger	**0.05**	1	0.105374075	2	0.00577584
15608	GO:0033209	tumor necrosis factor-m	**0.05**	1	0.105374075	2	0.00577584
16481	GO:0034097	response to cytokine st	**0.05**	1	0.105374075	2	0.00577584
16991	GO:0034612	response to tumor necr	**0.05**	1	0.105374075	2	0.00577584
18651	GO:0042300	beta-amyrin synthase a	**0.05**	1	0.105374075	2	0.00577584
19204	GO:0042887	amide transmembrane	**0.05**	1	0.105374075	2	0.00577584
19424	GO:0043120	tumor necrosis factor bi	**0.05**	1	0.105374075	2	0.00577584
21947	GO:0046422	violaxanthin de-epoxida	**0.05**	1	0.105374075	2	0.00577584
22490	GO:0046995	oxidoreductase activity,	**0.05**	1	0.105374075	2	0.00577584
24561	GO:0050242	pyruvate, phosphate dik	**0.05**	1	0.105374075	2	0.00577584
24767	GO:0050454	coenzyme F420 hydrog	**0.05**	1	0.105374075	2	0.00577584
24925	GO:0050619	phytochromobilin:ferred	**0.05**	1	0.105374075	2	0.00577584
24931	GO:0050625|GO:0018	2-hydroxy-1,4-benzoqu	**0.05**	1	0.105374075	2	0.00577584
26025	GO:0051743	red chlorophyll catabolit	**0.05**	1	0.105374075	2	0.00577584
29709	GO:0071345	cellular response to cyt	**0.05**	1	0.105374075	2	0.00577584
29720	GO:0071356	cellular response to tum	**0.05**	1	0.105374075	2	0.00577584
30280	GO:0071918	urea transmembrane tr	**0.05**	1	0.105374075	2	0.00577584
2748	GO:0003913	DNA photolyase activity	**0.05**	1	0.105374075	2	0.00577584
11224	GO:0019222	regulation of metabolic	**0.05**	100	10.537408	3115	8.995871
7413	GO:0010181	FMN binding	**0.05**	2	0.21074815	14	0.040430877
25510	GO:0051213	dioxygenase activity	0.06	5	0.52687037	75	0.21659398
9750	GO:0016679	oxidoreductase activity,	0.06	4	0.4214963	53	0.15305975
11695	GO:0019725	cellular homeostasis	0.06	11	1.1591148	234	0.67577326
25195	GO:0050896|GO:0051	response to stimulus	0.06	63	6.638567	1881	5.432177
4530	GO:0006355|GO:0032	regulation of transcripti	0.06	84	8.851422	2591	7.4826
12650	GO:0030060	L-malate dehydrogenas	0.06	2	0.21074815	15	0.043318797
25544	GO:0051252	regulation of RNA meta	0.06	84	8.851422	2593	7.488376
18925	GO:0042592	homeostatic process	0.06	11	1.1591148	238	0.68732494
7692	GO:0010468	regulation of gene expr	0.07	85	8.956797	2635	7.6096687
12516	GO:0022804	active transmembrane	0.07	29	3.0558484	787	2.2727928
7141	GO:0009889	regulation of biosynthet	0.07	84	8.851422	2605	7.523031
7772	GO:0010556	regulation of macromol	0.07	84	8.851422	2605	7.523031
13756	GO:0031326	regulation of cellular bi	0.07	84	8.851422	2605	7.523031
32213	GO:2000112	regulation of cellular ma	0.07	84	8.851422	2605	7.523031
3742	GO:0005242	inward rectifier potassiu	0.07	2	0.21074815	16	0.046206716
3829	GO:0005381|GO:0005	iron ion transmembrane	0.07	2	0.21074815	16	0.046206716
7178	GO:0009927	histidine phosphotransf	0.07	2	0.21074815	16	0.046206716
17134	GO:0034755	iron ion transmembrane	0.07	2	0.21074815	16	0.046206716
11206	GO:0019203	carbohydrate phosphat	0.07	3	0.31612223	35	0.10107719
22375	GO:0046872	metal ion binding	0.07	95	10.010537	2985	8.6204405
5766	GO:0008236	serine-type peptidase a	0.07	10	1.0537407	214	0.6180149
8028	GO:0010817	regulation of hormone l	0.07	4	0.4214963	58	0.16749935
8494	GO:0015075	ion transmembrane tra	0.07	30	3.1612225	827	2.3883097
9393	GO:0016165	lipoxygenase activity	0.08	3	0.31612223	36	0.10396511
19470	GO:0043167	ion binding	0.08	95	10.010537	2997	8.655096
19472	GO:0043169	cation binding	0.08	95	10.010537	2997	8.655096
4910	GO:0006811	ion transport	0.08	34	3.5827186	959	2.769515
27228	GO:0060255	regulation of macromol	0.08	85	8.956797	2660	7.6818666
5018	GO:0006950	response to stress	0.08	23	2.4236038	611	1.764519
3405	GO:0004794	L-threonine ammonia-l	0.08	1	0.105374075	3	0.00866376
16603	GO:0034220	ion transmembrane tra	0.08	30	3.1612225	833	2.4056373
4327	GO:0006091	generation of precurso	0.08	5	0.52687037	84	0.24258527
10103	GO:0017171	serine hydrolase activit	0.08	10	1.0537407	220	0.63534236
2981	GO:0004190	aspartic-type endopepti	0.09	2	0.21074815	18	0.051982556
6450	GO:0009081	branched chain family a	0.09	2	0.21074815	18	0.051982556
10899	GO:0018858	benzoate-CoA ligase a	0.09	2	0.21074815	18	0.051982556
22917	GO:0047429	nucleoside-triphosphat	0.09	2	0.21074815	18	0.051982556
28368	GO:0070001	aspartic-type peptidase	0.09	2	0.21074815	18	0.051982556
9267	GO:0016021	integral to membrane	0.09	38	4.004215	1103	3.1853757
9812	GO:0016758	transferase activity, tra	0.10	19	2.0021074	501	1.4468478
3475	GO:0004871|GO:0005	signal transducer activi	0.10	28	2.9504743	787	2.2727928
27063	GO:0060089	molecular transducer a	0.10	28	2.9504743	787	2.2727928
4921	GO:0006826|GO:0015	iron ion transport	0.10	2	0.21074815	20	0.0577584
9706	GO:0016623	oxidoreductase activity,	0.10	2	0.21074815	20	0.0577584
9707	GO:0016624	oxidoreductase activity,	0.10	2	0.21074815	20	0.0577584
24482	GO:0050162	oxalate oxidase activity	0.10	2	0.21074815	20	0.0577584
2900	GO:0004096|GO:0016	catalase activity	0.11	1	0.105374075	4	0.011551679
2953	GO:0004151	dihydroorotase activity	0.11	1	0.105374075	4	0.011551679
3033	GO:0004349	glutamate 5-kinase acti	0.11	1	0.105374075	4	0.011551679
3057	GO:0004373	glycogen (starch) synth	0.11	1	0.105374075	4	0.011551679
3101	GO:0004435	phosphatidylinositol ph	0.11	1	0.105374075	4	0.011551679
4039	GO:0005751|GO:0005	mitochondrial respirato	0.11	1	0.105374075	4	0.011551679
5942	GO:0008456	alpha-N-acetylgalactos	0.11	1	0.105374075	4	0.011551679

6350	GO:0008965	phosphoenolpyruvate-p	0.11	1	0.105374075	4	0.011551679
7170	GO:0009918	sterol delta7 reductase	0.11	1	0.105374075	4	0.011551679
7406	GO:0010174	nucleoside transmembr	0.11	1	0.105374075	4	0.011551679
7534	GO:0010309	acireductone dioxygena	0.11	1	0.105374075	4	0.011551679
8459	GO:0015018	galactosylgalactosylxylo	0.11	1	0.105374075	4	0.011551679
8594	GO:0015184	L-cystine transmembrar	0.11	1	0.105374075	4	0.011551679
8885	GO:0015603	iron chelate transmemb	0.11	1	0.105374075	4	0.011551679
8902	GO:0015623|GO:0015	iron-chelate-transportin	0.11	1	0.105374075	4	0.011551679
8957	GO:0015688	iron chelate transport	0.11	1	0.105374075	4	0.011551679
9080	GO:0015811	L-cystine transport	0.11	1	0.105374075	4	0.011551679
9351	GO:0016119	carotene metabolic pro	0.11	1	0.105374075	4	0.011551679
9352	GO:0016120	carotene biosynthetic p	0.11	1	0.105374075	4	0.011551679
9760	GO:0016695	oxidoreductase activity,	0.11	1	0.105374075	4	0.011551679
9790	GO:0016730	oxidoreductase activity,	0.11	1	0.105374075	4	0.011551679
9810	GO:0016756|GO:0042	glutathione gamma-glut	0.11	1	0.105374075	4	0.011551679
9819	GO:0016767	geranylgeranyl-diphosp	0.11	1	0.105374075	4	0.011551679
10039	GO:0017084	delta1-pyrroline-5-carb	0.11	1	0.105374075	4	0.011551679
11549	GO:0019566	arabinose metabolic pr	0.11	1	0.105374075	4	0.011551679
16639	GO:0034256	chlorophyll(ide) b reduc	0.11	1	0.105374075	4	0.011551679
18575	GO:0042214	terpene metabolic proc	0.11	1	0.105374075	4	0.011551679
20901	GO:0045277|GO:0045	respiratory chain compl	0.11	1	0.105374075	4	0.011551679
21791	GO:0046246	terpene biosynthetic pr	0.11	1	0.105374075	4	0.011551679
21902	GO:0046373	L-arabinose metabolic	0.11	1	0.105374075	4	0.011551679
22408	GO:0046905	phytoene synthase acti	0.11	1	0.105374075	4	0.011551679
23084	GO:0047598	7-dehydrocholesterol re	0.11	1	0.105374075	4	0.011551679
24646	GO:0050327	testosterone 17-beta-de	0.11	1	0.105374075	4	0.011551679
31507	GO:0080132	fatty acid alpha-hydroxy	0.11	1	0.105374075	4	0.011551679
75	GO:0000099	sulfur amino acid trans	0.11	1	0.105374075	4	0.011551679
77	GO:0000101	sulfur amino acid transp	0.11	1	0.105374075	4	0.011551679
11221	GO:0019219	regulation of nucleobas	0.11	84	8.851422	2675	7.7251854
25468	GO:0051171	regulation of nitrogen c	0.11	84	8.851422	2675	7.7251854
8461	GO:0015020|GO:0003	glucuronosyltransferase	0.11	3	0.31612223	42	0.121292636
9698	GO:0016615	malate dehydrogenase	0.11	2	0.21074815	21	0.060646318
3476	GO:0004872|GO:0019	receptor activity	0.12	24	2.5289779	672	1.9406822
9699	GO:0016616	oxidoreductase activity,	0.12	11	1.1591148	266	0.7681867
9753	GO:0016682	oxidoreductase activity,	0.12	3	0.31612223	44	0.12706847
9722	GO:0016641	oxidoreductase activity,	0.12	4	0.4214963	69	0.19926646
8679	GO:0015297	antiporter activity	0.13	7	0.73761857	152	0.4389638
8682	GO:0015300	solute:solute antiporter	0.13	7	0.73761857	152	0.4389638
12573	GO:0022891	substrate-specific trans	0.13	41	4.3203373	1241	3.5839086
4678	GO:0006549	isoleucine metabolic pr	0.13	1	0.105374075	5	0.0144396
6465	GO:0009097	isoleucine biosynthetic	0.13	1	0.105374075	5	0.0144396
21949	GO:0046424	ferulate 5-hydroxylase a	0.13	1	0.105374075	5	0.0144396
31465	GO:0080090	regulation of primary m	0.13	84	8.851422	2710	7.826263
7527	GO:0010302	2-oxoglutarate-depende	0.13	2	0.21074815	23	0.06642216
3744	GO:0005244	voltage-gated ion chan	0.14	4	0.4214963	72	0.20793022
12528	GO:0022832	voltage-gated channel a	0.14	4	0.4214963	72	0.20793022
15280	GO:0032879	regulation of localizatio	0.14	4	0.4214963	72	0.20793022
17141	GO:0034762	regulation of transmem	0.14	4	0.4214963	72	0.20793022
17144	GO:0034765	regulation of ion transm	0.14	4	0.4214963	72	0.20793022
19568	GO:0043269	regulation of ion transp	0.14	4	0.4214963	72	0.20793022
25348	GO:0051049	regulation of transport	0.14	4	0.4214963	72	0.20793022
8493	GO:0015074	DNA integration	0.14	3	0.31612223	47	0.13573223
4247	GO:0006007	glucose catabolic proce	0.14	4	0.4214963	73	0.21081814
9703	GO:0016620	oxidoreductase activity,	0.14	4	0.4214963	73	0.21081814
11313	GO:0019320	hexose catabolic proce	0.14	4	0.4214963	73	0.21081814
20525	GO:0044275	cellular carbohydrate c	0.14	4	0.4214963	73	0.21081814
21726	GO:0046164	alcohol catabolic proce	0.14	4	0.4214963	73	0.21081814
21894	GO:0046365	monosaccharide catab	0.14	4	0.4214963	73	0.21081814
2976	GO:0004176|GO:0004	ATP-dependent peptida	0.14	3	0.31612223	48	0.13862015
12794	GO:0030234	enzyme regulator activi	0.14	15	1.5806112	403	1.1638317
13656	GO:0031224	intrinsic to membrane	0.15	39	4.109589	1193	3.4452884
13753	GO:0031323	regulation of cellular m	0.15	85	8.956797	2770	7.999538
973	GO:0001653	peptide receptor activity	0.15	2	0.21074815	25	0.072197996
12608	GO:0030001	metal ion transport	0.15	14	1.4752371	374	1.080082
8810	GO:0015491	cation:cation antiporter	0.15	4	0.4214963	75	0.21659398
3183	GO:0004525	ribonuclease III activity	0.15	1	0.105374075	6	0.01732752
3413	GO:0004802	transketolase activity	0.15	1	0.105374075	6	0.01732752
3845	GO:0005452	inorganic anion exchan	0.15	1	0.105374075	6	0.01732752
5810	GO:0008290	F-actin capping protein	0.15	1	0.105374075	6	0.01732752
7250	GO:0010012	steroid 22-alpha hydrox	0.15	1	0.105374075	6	0.01732752
9825	GO:0016774	phosphotransferase ac	0.15	1	0.105374075	6	0.01732752
9831	GO:0016781	phosphotransferase ac	0.15	1	0.105374075	6	0.01732752
12826	GO:0030267	glyoxylate reductase (N	0.15	1	0.105374075	6	0.01732752
13832	GO:0031409	pigment binding	0.15	1	0.105374075	6	0.01732752
13982	GO:0031559	oxidosqualene cyclase	0.15	1	0.105374075	6	0.01732752
14264	GO:0031849	olfactory receptor bindi	0.15	1	0.105374075	6	0.01732752
19203	GO:0042886	amide transport	0.15	1	0.105374075	6	0.01732752
23230	GO:0047746	chlorophyllase activity	0.15	1	0.105374075	6	0.01732752
30707	GO:0072348	sulfur compound transp	0.15	1	0.105374075	6	0.01732752
2713	GO:0003863	3-methyl-2-oxobutanoa	0.15	1	0.105374075	6	0.01732752
2846	GO:0004038	allantoinase activity	0.15	1	0.105374075	6	0.01732752
9709	GO:0016627	oxidoreductase activity,	0.16	5	0.52687037	104	0.30034366
9744	GO:0016671	oxidoreductase activity,	0.16	2	0.21074815	26	0.075085916
126	GO:0000160	two-component signal t	0.16	2	0.21074815	26	0.075085916
8919	GO:0015645	fatty acid ligase activity	0.17	2	0.21074815	27	0.077973835
2975	GO:0004175|GO:0016	endopeptidase activity	0.17	12	1.2644889	320	0.9241344
4909	GO:0006810|GO:0015	transport	0.18	71	7.4815598	2315	6.6855345
25529	GO:0051234	establishment of localiz	0.18	71	7.4815598	2315	6.6855345
5732	GO:0008194	UDP-glycosyltransferas	0.18	12	1.2644889	322	0.9299102
3021	GO:0004337	geranyltranstransferase	0.18	1	0.105374075	7	0.020215439
3255	GO:0004615|GO:0008	phosphomannomutase	0.18	1	0.105374075	7	0.020215439
3357	GO:0004738	pyruvate dehydrogenas	0.18	1	0.105374075	7	0.020215439
3358	GO:0004739	pyruvate dehydrogenas	0.18	1	0.105374075	7	0.020215439
6801	GO:0009512	cytochrome b6f comple	0.18	1	0.105374075	7	0.020215439
16115	GO:0033729	anthocyanidin reductas	0.18	1	0.105374075	7	0.020215439
2833	GO:0004024	alcohol dehydrogenase	0.18	2	0.21074815	28	0.080861755
25476	GO:0051179	localization	0.18	71	7.4815598	2319	6.697086
6668	GO:0009314	response to radiation	0.18	4	0.4214963	81	0.23392151
6751	GO:0009416	response to light stimul	0.18	4	0.4214963	81	0.23392151
9697	GO:0016614	oxidoreductase activity,	0.18	11	1.1591148	293	0.84616053
3787	GO:0005319	lipid transporter activity	0.19	4	0.4214963	83	0.23969735
8680	GO:0015298	solute:cation antiporter	0.19	5	0.52687037	112	0.32344702

9730	GO:0016651	oxidoreductase activity,	0.19	5	0.52687037	112	0.32344702
9883	GO:0016846	carbon-sulfur lyase acti	0.20	3	0.31612223	56	0.16172351
8683	GO:0015301|GO:00153	anion:anion antiporter a	0.20	2	0.21074815	30	0.086637594
3306	GO:0004674|GO:00046	protein serine/threonine	0.20	34	3.5827186	1062	3.0669708
3048	GO:0004364	glutathione transferase	0.20	4	0.4214963	84	0.24258527
3254	GO:0004614	phosphoglucomutase a	0.20	1	0.105374075	8	0.023103358
3402	GO:0004791	thioredoxin-disulfide red	0.20	1	0.105374075	8	0.023103358
4035	GO:0005746	mitochondrial respirator	0.20	1	0.105374075	8	0.023103358
5953	GO:0008471	laccase activity	0.20	1	0.105374075	8	0.023103358
6613	GO:0009250	glucan biosynthetic pro	0.20	1	0.105374075	8	0.023103358
18639	GO:0042284	sphingolipid delta-4 des	0.20	1	0.105374075	8	0.023103358
22076	GO:0046556	alpha-N-arabinofuranos	0.20	1	0.105374075	8	0.023103358
28833	GO:0070469	respiratory chain	0.20	1	0.105374075	8	0.023103358
30696	GO:0072337	modified amino acid tra	0.20	1	0.105374075	8	0.023103358
30708	GO:0072349	modified amino acid tra	0.20	1	0.105374075	8	0.023103358
5195	GO:0007165|GO:00230	signal transduction	0.20	31	3.2665963	961	2.775291
12602	GO:0023052|GO:00230	signaling	0.20	31	3.2665963	961	2.775291
4911	GO:0006812|GO:00068	cation transport	0.21	22	2.3182297	662	1.9118029
9811	GO:0016757|GO:00169	transferase activity, tran	0.21	24	2.5289779	729	2.1052935
19952	GO:0043687	post-translational protei	0.21	4	0.4214963	86	0.24836111
4913	GO:0006814|GO:00068	sodium ion transport	0.21	3	0.31612223	58	0.16749935
8499	GO:0015081|GO:00228	sodium ion transmembr	0.21	3	0.31612223	58	0.16749935
18086	GO:0035725	sodium ion transmembr	0.21	3	0.31612223	58	0.16749935
29800	GO:0071436	sodium ion export	0.21	3	0.31612223	58	0.16749935
4954	GO:0006869	lipid transport	0.21	8	0.8429926	208	0.6006873
8085	GO:0010876	lipid localization	0.21	8	0.8429926	208	0.6006873
4246	GO:0006006	glucose metabolic proc	0.22	4	0.4214963	87	0.25124902
4481	GO:0006284	base-excision repair	0.22	2	0.21074815	32	0.09241343
21041	GO:0045431	flavonol synthase activi	0.22	2	0.21074815	32	0.09241343
25836	GO:0051552	flavone metabolic proce	0.22	2	0.21074815	32	0.09241343
25837	GO:0051553	flavone biosynthetic pro	0.22	2	0.21074815	32	0.09241343
25838	GO:0051554	flavonol metabolic proc	0.22	2	0.21074815	32	0.09241343
25839	GO:0051555	flavonol biosynthetic pro	0.22	2	0.21074815	32	0.09241343
2831	GO:0004022	alcohol dehydrogenase	0.22	3	0.31612223	59	0.17038727
4322	GO:0006084	acetyl-CoA metabolic p	0.22	1	0.105374075	9	0.025991278
4332	GO:0006099	tricarboxylic acid cycle	0.22	1	0.105374075	9	0.025991278
6429	GO:0009060	aerobic respiration	0.22	1	0.105374075	9	0.025991278
6476	GO:0009109	coenzyme catabolic pro	0.22	1	0.105374075	9	0.025991278
6670	GO:0009317	acetyl-CoA carboxylase	0.22	1	0.105374075	9	0.025991278
7225	GO:0009978	allene oxide synthase a	0.22	1	0.105374075	9	0.025991278
19254	GO:0042937	tripeptide transporter ac	0.22	1	0.105374075	9	0.025991278
19342	GO:0043027	caspase inhibitor activit	0.22	1	0.105374075	9	0.025991278
19343	GO:0043028	caspase regulator activ	0.22	1	0.105374075	9	0.025991278
19458	GO:0043154|GO:00017	negative regulation of c	0.22	1	0.105374075	9	0.025991278
19579	GO:0043281|GO:00430	regulation of caspase a	0.22	1	0.105374075	9	0.025991278
21885	GO:0046356	acetyl-CoA catabolic pr	0.22	1	0.105374075	9	0.025991278
25484	GO:0051187	cofactor catabolic proce	0.22	1	0.105374075	9	0.025991278
2837	GO:0004028	3-chloroallyl aldehyde d	0.22	1	0.105374075	9	0.025991278
24966	GO:0050660	flavin adenine dinucleot	0.22	5	0.52687037	118	0.34077454
5840	GO:0008324	cation transmembrane	0.23	18	1.8967334	538	1.5537009
9719	GO:0016638	oxidoreductase activity,	0.23	4	0.4214963	89	0.25702485
3723	GO:0005215|GO:00054	transporter activity	0.23	56	5.9009485	1844	5.325324
22376	GO:0046873	metal ion transmembra	0.23	8	0.8429926	213	0.6151269
3749	GO:0005249	voltage-gated potassiu	0.24	2	0.21074815	34	0.09818927
5827	GO:0008308|GO:00228	voltage-gated anion cha	0.24	2	0.21074815	34	0.09818927
20321	GO:0044070	regulation of anion trans	0.24	2	0.21074815	34	0.09818927
9294	GO:0016052|GO:00060	carbohydrate catabolic	0.24	4	0.4214963	91	0.2628007
3040	GO:0004356	glutamate-ammonia liga	0.24	1	0.105374075	10	0.0288792
3203	GO:0004557	alpha-galactosidase act	0.24	1	0.105374075	10	0.0288792
3264	GO:0004629|GO:00422	phospholipase C activit	0.24	1	0.105374075	10	0.0288792
3842	GO:0005432	calcium:sodium antiport	0.24	1	0.105374075	10	0.0288792
5678	GO:0008113|GO:00337	peptide-methionine-(S)-	0.24	1	0.105374075	10	0.0288792
9424	GO:0016211	ammonia ligase activity	0.24	1	0.105374075	10	0.0288792
9741	GO:0016668|GO:00166	oxidoreductase activity,	0.24	1	0.105374075	10	0.0288792
9826	GO:0016775	phosphotransferase act	0.24	1	0.105374075	10	0.0288792
9912	GO:0016880	acid-ammonia (or amid	0.24	1	0.105374075	10	0.0288792
11205	GO:0019202	amino acid kinase activ	0.24	1	0.105374075	10	0.0288792
12918	GO:0030374	ligand-dependent nucle	0.24	1	0.105374075	10	0.0288792
31707	GO:0090116	C-5 methylation of cyto	0.24	1	0.105374075	10	0.0288792
983	GO:0001664	G-protein-coupled rece	0.24	1	0.105374075	10	0.0288792
2736	GO:0003886|GO:00083	DNA (cytosine-5-)-meth	0.24	1	0.105374075	10	0.0288792
4215	GO:0005975	carbohydrate metabolic	0.25	31	3.2665963	990	2.8590407
17016	GO:0034637	cellular carbohydrate bi	0.25	3	0.31612223	63	0.18193895
21146	GO:0045544	gibberellin 20-oxidase a	0.25	2	0.21074815	35	0.10107719
17617	GO:0035251	UDP-glucosyltransferas	0.25	8	0.8429926	218	0.62956655
26931	GO:0055085	transmembrane transpo	0.25	47	4.952582	1548	4.4705
9293	GO:0016051|GO:00060	carbohydrate biosynthe	0.26	3	0.31612223	64	0.18482687
4236	GO:0005996	monosaccharide metab	0.26	5	0.52687037	125	0.36099
4232	GO:0005992	trehalose biosynthetic p	0.26	2	0.21074815	36	0.10396511
8739	GO:0015385|GO:00155	sodium:hydrogen antipo	0.26	2	0.21074815	36	0.10396511
9185	GO:0015925	galactosidase activity	0.26	2	0.21074815	36	0.10396511
3380	GO:0004766	spermidine synthase ac	0.26	1	0.105374075	11	0.03176712
3416	GO:0004806	triglyceride lipase activi	0.26	1	0.105374075	11	0.03176712
11152	GO:0019139|GO:00464	cytokinin dehydrogenas	0.26	1	0.105374075	11	0.03176712
13809	GO:0031386	protein tag	0.26	1	0.105374075	11	0.03176712
19256	GO:0042939	tripeptide transport	0.26	1	0.105374075	11	0.03176712
9710	GO:0016628	oxidoreductase activity,	0.26	3	0.31612223	65	0.18771479
3761	GO:0005275|GO:00052	amine transmembrane	0.26	5	0.52687037	126	0.3638779
25998	GO:0051716	cellular response to stir	0.26	35	3.6880927	1138	3.2864528
3318	GO:0004693|GO:00165	cyclin-dependent protei	0.27	2	0.21074815	37	0.10685303
3758	GO:0005267	potassium channel activ	0.27	2	0.21074815	37	0.10685303
24968	GO:0050662	coenzyme binding	0.27	7	0.73761857	191	0.5515927
5791	GO:0008270	zinc ion binding	0.28	56	5.9009485	1880	5.4292893
4231	GO:0005991	trehalose metabolic pro	0.28	2	0.21074815	38	0.10974095
8501	GO:0015085	calcium ion transmemb	0.28	2	0.21074815	38	0.10974095
12538	GO:0022843	voltage-gated cation ch	0.28	2	0.21074815	38	0.10974095
6383	GO:0009008	DNA-methyltransferase	0.28	1	0.105374075	12	0.03465504
6451	GO:0009082	branched chain family a	0.28	1	0.105374075	12	0.03465504
7526	GO:0010301|GO:00337	xanthoxin dehydrogena	0.28	1	0.105374075	12	0.03465504
8748	GO:0015398	high affinity secondary a	0.28	1	0.105374075	12	0.03465504
9235	GO:0015976|GO:00159	carbon utilization	0.28	1	0.105374075	12	0.03465504
14848	GO:0032440	2-alkenal reductase act	0.28	1	0.105374075	12	0.03465504
16148	GO:0033764	steroid dehydrogenase	0.28	1	0.105374075	12	0.03465504

20943	GO:0045333	cellular respiration	0.28	1	0.105374075	12	0.03465504
4990	GO:0006915|GO:00086	apoptosis	0.29	8	0.8429926	227	0.6555578
6796	GO:0009507	chloroplast	0.29	8	0.8429926	229	0.6613336
21710	GO:0046148	pigment biosynthetic pr	0.29	3	0.31612223	69	0.19926646
31420	GO:0080043	quercetin 3-O-glucosylt	0.29	3	0.31612223	69	0.19926646
9422	GO:0016209	antioxidant activity	0.30	6	0.63224447	165	0.47650677
7072	GO:0009813	flavonoid biosynthetic p	0.30	2	0.21074815	40	0.1155168
11311	GO:0019318	hexose metabolic proce	0.30	4	0.4214963	101	0.2916799
6811	GO:0009523	photosystem II	0.30	1	0.105374075	13	0.037542958
8149	GO:0010941	regulation of cell death	0.30	1	0.105374075	13	0.037542958
19043	GO:0042719	mitochondrial intermem	0.30	1	0.105374075	13	0.037542958
19298	GO:0042981	regulation of apoptosis	0.30	1	0.105374075	13	0.037542958
19381	GO:0043067|GO:00430	regulation of programm	0.30	1	0.105374075	13	0.037542958
5874	GO:0008374	O-acyltransferase activi	0.31	4	0.4214963	102	0.29456782
28378	GO:0070011	peptidase activity, actin	0.31	17	1.7913593	537	1.550813
4408	GO:0006200	ATP catabolic process	0.31	20	2.1074815	641	1.8511566
9918	GO:0016887|GO:00040	ATPase activity	0.31	20	2.1074815	641	1.8511566
21600	GO:0046034	ATP metabolic process	0.31	20	2.1074815	641	1.8511566
9103	GO:0015837	amine transport	0.31	5	0.52687037	135	0.38986918
12547	GO:0022857|GO:00053	transmembrane transpo	0.31	44	4.6364594	1483	4.282785
9740	GO:0016667	oxidoreductase activity,	0.32	3	0.31612223	72	0.20793022
30069	GO:0071705	nitrogen compound tran	0.32	7	0.73761857	202	0.5833598
20532	GO:0044282	small molecule cataboli	0.32	26	2.739726	854	2.4662836
3753	GO:0005253	anion channel activity	0.32	2	0.21074815	42	0.121292636
6666	GO:0009312	oligosaccharide biosynt	0.32	2	0.21074815	42	0.121292636
9370	GO:0016138	glycoside biosynthetic p	0.32	2	0.21074815	42	0.121292636
13884	GO:0031461	cullin-RING ubiquitin lig	0.32	2	0.21074815	42	0.121292636
21880	GO:0046351	disaccharide biosynthet	0.32	2	0.21074815	42	0.121292636
7844	GO:0010629	negative regulation of g	0.32	1	0.105374075	14	0.040430877
9399	GO:0016174	NAD(P)H oxidase activ	0.32	1	0.105374075	14	0.040430877
9433	GO:0016229	steroid dehydrogenase	0.32	1	0.105374075	14	0.040430877
9854	GO:0016812	hydrolase activity, actin	0.32	1	0.105374075	14	0.040430877
9879	GO:0016841	ammonia-lyase activity	0.32	1	0.105374075	14	0.040430877
15178	GO:0032776	DNA methylation on cyt	0.32	1	0.105374075	14	0.040430877
21460	GO:0045892|GO:00164	negative regulation of tr	0.32	1	0.105374075	14	0.040430877
21502	GO:0045934	negative regulation of n	0.32	1	0.105374075	14	0.040430877
24970	GO:0050664	oxidoreductase activity,	0.32	1	0.105374075	14	0.040430877
25469	GO:0051172	negative regulation of n	0.32	1	0.105374075	14	0.040430877
25545	GO:0051253	negative regulation of R	0.32	1	0.105374075	14	0.040430877
6899	GO:0009628	response to abiotic stim	0.32	6	0.63224447	170	0.49094638
18786	GO:0042440	pigment metabolic proc	0.32	3	0.31612223	73	0.21081814
5756	GO:0008219	cell death	0.33	8	0.8429926	239	0.69021285
8209	GO:0012501|GO:00162	programmed cell death	0.33	8	0.8429926	239	0.69021285
9462	GO:0016265	death	0.33	8	0.8429926	239	0.69021285
8675	GO:0015293	symporter activity	0.34	6	0.63224447	173	0.49961013
25095	GO:0050790	regulation of catalytic ac	0.34	15	1.5806112	480	1.3862015
4914	GO:0006816	calcium ion transport	0.34	2	0.21074815	44	0.12706847
7071	GO:0009812	flavonoid metabolic pro	0.34	2	0.21074815	44	0.12706847
28952	GO:0070588	calcium ion transmemb	0.34	2	0.21074815	44	0.12706847
7520	GO:0010294	abscisic acid glucosyltra	0.34	1	0.105374075	15	0.043318797
9340	GO:0016108	tetraterpenoid metaboli	0.34	1	0.105374075	15	0.043318797
9341	GO:0016109	tetraterpenoid biosynthe	0.34	1	0.105374075	15	0.043318797
9348	GO:0016116	carotenoid metabolic pr	0.34	1	0.105374075	15	0.043318797
9349	GO:0016117	carotenoid biosynthetic	0.34	1	0.105374075	15	0.043318797
10079	GO:0017134	fibroblast growth factor	0.34	1	0.105374075	15	0.043318797
16081	GO:0033692	cellular polysaccharide	0.34	1	0.105374075	15	0.043318797
8676	GO:0015294	solute:cation symporter	0.34	5	0.52687037	141	0.4071967
5663	GO:0008094|GO:00040	DNA-dependent ATPas	0.35	3	0.31612223	76	0.2194819
28366	GO:0065009	regulation of molecular	0.35	15	1.5806112	484	1.3977532
8666	GO:0015276	ligand-gated ion channe	0.35	2	0.21074815	45	0.1299564
12530	GO:0022834	ligand-gated channel ac	0.35	2	0.21074815	45	0.1299564
4304	GO:0006066	alcohol metabolic proce	0.36	5	0.52687037	143	0.41297254
9795	GO:0016740	transferase activity	0.36	107	11.275026	3764	10.870131
5995	GO:0008524	glucose 6-phosphate:ph	0.36	1	0.105374075	16	0.046206716
7142	GO:0009890	negative regulation of b	0.36	1	0.105374075	16	0.046206716
7774	GO:0010558	negative regulation of m	0.36	1	0.105374075	16	0.046206716
7820	GO:0010605	negative regulation of m	0.36	1	0.105374075	16	0.046206716
8694	GO:0015315	organophosphate:inorg	0.36	1	0.105374075	16	0.046206716
9189	GO:0015929	hexosaminidase activity	0.36	1	0.105374075	16	0.046206716
9390	GO:0016161	beta-amylase activity	0.36	1	0.105374075	16	0.046206716
9727	GO:0016647	oxidoreductase activity,	0.36	1	0.105374075	16	0.046206716
9878	GO:0016840	carbon-nitrogen lyase a	0.36	1	0.105374075	16	0.046206716
13757	GO:0031327	negative regulation of c	0.36	1	0.105374075	16	0.046206716
18757	GO:0042409	caffeoyl-CoA O-methylt	0.36	1	0.105374075	16	0.046206716
22110	GO:0046592	polyamine oxidase activ	0.36	1	0.105374075	16	0.046206716
22412	GO:0046910	pectinesterase inhibitor	0.36	1	0.105374075	16	0.046206716
32214	GO:2000113	negative regulation of c	0.36	1	0.105374075	16	0.046206716
206	GO:0000271	polysaccharide biosynth	0.36	1	0.105374075	16	0.046206716
219	GO:0000287	magnesium ion binding	0.36	1	0.105374075	16	0.046206716
8943	GO:0015672	monovalent inorganic c	0.36	12	1.2644889	383	1.1060733
9909	GO:0016877	ligase activity, forming c	0.36	3	0.31612223	78	0.22525774
6425	GO:0009056	catabolic process	0.36	31	3.2665963	1051	3.0352037
6824	GO:0009536	plastid	0.37	8	0.8429926	247	0.7133162
20512	GO:0044262|GO:00060	cellular carbohydrate m	0.37	8	0.8429926	248	0.7162041
4044	GO:0005758|GO:00319	mitochondrial intermem	0.38	1	0.105374075	17	0.049094636
9923	GO:0016892	endoribonuclease activ	0.38	1	0.105374075	17	0.049094636
9925	GO:0016894	endonuclease activity, a	0.38	1	0.105374075	17	0.049094636
14383	GO:0031970	organelle envelope lum	0.38	1	0.105374075	17	0.049094636
16281	GO:0033897	ribonuclease T2 activity	0.38	1	0.105374075	17	0.049094636
20619	GO:0044425	membrane part	0.38	44	4.6364594	1523	4.398302
22478	GO:0046982	protein heterodimerizati	0.38	4	0.4214963	114	0.32922286
5763	GO:0008233	peptidase activity	0.38	17	1.7913593	565	1.6316746
3756	GO:0005261|GO:00152	cation channel activity	0.39	2	0.21074815	49	0.14150807
3844	GO:0005451	monovalent cation:hydr	0.39	2	0.21074815	49	0.14150807
9725	GO:0016645	oxidoreductase activity,	0.39	2	0.21074815	49	0.14150807
31421	GO:0080044	quercetin 7-O-glucosylt	0.39	2	0.21074815	49	0.14150807
3832	GO:0005388	calcium-transporting AT	0.39	1	0.105374075	18	0.051982556
4134	GO:0005874	microtubule	0.39	1	0.105374075	18	0.051982556
6416	GO:0009044	xylan 1,4-beta-xylosidas	0.39	1	0.105374075	18	0.051982556
12887	GO:0030332	cyclin binding	0.39	1	0.105374075	18	0.051982556
9818	GO:0016765|GO:00167	transferase activity, tran	0.40	6	0.63224447	185	0.53426516
4912	GO:0006813|GO:00154	potassium ion transport	0.41	3	0.31612223	84	0.24258527
30168	GO:0071804	cellular potassium ion tr	0.41	3	0.31612223	84	0.24258527

30169	GO:0071805	potassium ion transmer	0.41	3	0.31612223	84	0.24258527
8584	GO:0015171|GO:0015	amino acid transmembr	0.41	4	0.4214963	118	0.34077454
2521	GO:0003333	amino acid transmembr	0.41	4	0.4214963	118	0.34077454
7173	GO:0009922	fatty acid elongase acti	0.41	2	0.21074815	51	0.14728391
9733	GO:0016655	oxidoreductase activity,	0.41	2	0.21074815	51	0.14728391
9975	GO:0016998	cell wall macromolecule	0.41	2	0.21074815	51	0.14728391
9809	GO:0016755	transferase activity, trar	0.41	1	0.105374075	19	0.054870475
9891	GO:0016855	racemase and epimera	0.41	1	0.105374075	19	0.054870475
2895	GO:0004089	carbonate dehydratase	0.41	1	0.105374075	19	0.054870475
5097	GO:0007049	cell cycle	0.42	2	0.21074815	52	0.15017183
6965	GO:0009699	phenylpropanoid biosyr	0.42	2	0.21074815	52	0.15017183
20287	GO:0044036	cell wall macromolecule	0.42	2	0.21074815	52	0.15017183
3124	GO:0004462	lactoylglutathione lyase	0.43	1	0.105374075	20	0.0577584
3747	GO:0005247	voltage-gated chloride c	0.43	1	0.105374075	20	0.0577584
3754	GO:0005254	chloride channel activity	0.43	1	0.105374075	20	0.0577584
3798	GO:0005337	nucleoside transmembr	0.43	1	0.105374075	20	0.0577584
5991	GO:0008519	ammonium transmemb	0.43	1	0.105374075	20	0.0577584
8726	GO:0015368	calcium:cation antiporte	0.43	1	0.105374075	20	0.0577584
8965	GO:0015696	ammonium transport	0.43	1	0.105374075	20	0.0577584
9122	GO:0015858	nucleoside transport	0.43	1	0.105374075	20	0.0577584
9799	GO:0016744|GO:0016	transferase activity, trar	0.43	1	0.105374075	20	0.0577584
30844	GO:0072488	ammonium transmemb	0.43	1	0.105374075	20	0.0577584
2675	GO:0003825	alpha,alpha-trehalose-p	0.43	1	0.105374075	20	0.0577584
12532	GO:0022836	gated channel activity	0.43	4	0.4214963	122	0.3523262
119	GO:0000151	ubiquitin ligase complex	0.43	3	0.31612223	88	0.25413695
4951	GO:0006865|GO:0006	amino acid transport	0.44	4	0.4214963	123	0.35521415
2897	GO:0004091|GO:0004	carboxylesterase activit	0.44	6	0.63224447	194	0.5602564
3129	GO:0004467	long-chain fatty acid-Co	0.44	1	0.105374075	21	0.060646318
3474	GO:0004869|GO:0004	cysteine-type endopept	0.44	1	0.105374075	21	0.060646318
9902	GO:0016868|GO:0016	intramolecular transfera	0.44	1	0.105374075	21	0.060646318
12999	GO:0030506	ankyrin binding	0.44	1	0.105374075	21	0.060646318
23518	GO:0048040	UDP-glucuronate decar	0.44	1	0.105374075	21	0.060646318
716	GO:0001071	nucleic acid binding trar	0.45	40	4.214963	1417	4.0921826
2643	GO:0003700|GO:0000	sequence-specific DNA	0.45	40	4.214963	1417	4.0921826
9533	GO:0016405	CoA-ligase activity	0.45	2	0.21074815	55	0.15883559
4224	GO:0005984	disaccharide metabolic	0.46	2	0.21074815	56	0.16172351
9369	GO:0016137	glycoside metabolic pro	0.46	2	0.21074815	56	0.16172351
10032	GO:0017075	syntaxin-1 binding	0.46	1	0.105374075	22	0.06353424
12660	GO:0030077	plasma membrane light	0.46	1	0.105374075	22	0.06353424
13038	GO:0030551	cyclic nucleotide binding	0.46	1	0.105374075	22	0.06353424
19040	GO:0042716	plasma membrane-deri	0.46	1	0.105374075	22	0.06353424
19325	GO:0043008	ATP-dependent protein	0.46	1	0.105374075	22	0.06353424
24858	GO:0050551	myrcene synthase activ	0.46	1	0.105374075	22	0.06353424
4405	GO:0006195	purine nucleotide catab	0.46	22	2.3182297	773	2.232362
6508	GO:0009143	nucleoside triphosphate	0.46	22	2.3182297	773	2.232362
6509	GO:0009144	purine nucleoside tripho	0.46	22	2.3182297	773	2.232362
6511	GO:0009146	purine nucleoside tripho	0.46	22	2.3182297	773	2.232362
6519	GO:0009154	purine ribonucleotide ca	0.46	22	2.3182297	773	2.232362
6530	GO:0009166	nucleotide catabolic pro	0.46	22	2.3182297	773	2.232362
6567	GO:0009203	ribonucleoside triphosp	0.46	22	2.3182297	773	2.232362
6569	GO:0009205	purine ribonucleoside tr	0.46	22	2.3182297	773	2.232362
6571	GO:0009207	purine ribonucleoside tr	0.46	22	2.3182297	773	2.232362
6624	GO:0009261	ribonucleotide catabolic	0.46	22	2.3182297	773	2.232362
17034	GO:0034655	nucleobase, nucleoside	0.46	22	2.3182297	773	2.232362
17035	GO:0034656	nucleobase, nucleoside	0.46	22	2.3182297	773	2.232362
22209	GO:0046700	heterocycle catabolic pr	0.46	22	2.3182297	773	2.232362
30879	GO:0072523	purine-containing comp	0.46	22	2.3182297	773	2.232362
5715	GO:0008171	O-methyltransferase ac	0.47	2	0.21074815	57	0.16461143
9910	GO:0016878	acid-thiol ligase activity	0.47	2	0.21074815	57	0.16461143
20520	GO:0044270	cellular nitrogen compo	0.47	22	2.3182297	777	2.2439137
4918	GO:0006821	chloride transport	0.47	1	0.105374075	23	0.06642216
22753	GO:0047262|GO:0050	polygalacturonate 4-alp	0.47	1	0.105374075	23	0.06642216
2633	GO:0003684	damaged DNA binding	0.47	1	0.105374075	23	0.06642216
6665	GO:0009311	oligosaccharide metabo	0.47	2	0.21074815	58	0.16749935
9801	GO:0016747	transferase activity, trar	0.48	13	1.369863	456	1.3168914
30066	GO:0071702	organic substance trans	0.48	15	1.5806112	529	1.5277096
9900	GO:0016866	intramolecular transfera	0.48	2	0.21074815	59	0.17038727
18981	GO:0042651	thylakoid membrane	0.48	2	0.21074815	59	0.17038727
11712	GO:0019748	secondary metabolic pr	0.48	3	0.31612223	95	0.27435237
18633	GO:0042277	peptide binding	0.48	3	0.31612223	95	0.27435237
4311	GO:0006073	cellular glucan metaboli	0.49	1	0.105374075	24	0.06931008
7144	GO:0009892	negative regulation of m	0.49	1	0.105374075	24	0.06931008
13754	GO:0031324	negative regulation of c	0.49	1	0.105374075	24	0.06931008
20293	GO:0044042	glucan metabolic proce	0.49	1	0.105374075	24	0.06931008
20498	GO:0044248	cellular catabolic proces	0.49	25	2.634352	894	2.5818002
3304	GO:0004672|GO:0050	protein kinase activity	0.49	37	3.898841	1333	3.8495972
2980	GO:0004185	serine-type carboxypep	0.49	2	0.21074815	60	0.17327519
6964	GO:0009698	phenylpropanoid metab	0.49	2	0.21074815	60	0.17327519
28375	GO:0070008	serine-type exopeptidas	0.49	2	0.21074815	60	0.17327519
9800	GO:0016746	transferase activity, trar	0.50	14	1.4752371	498	1.438184
6563	GO:0009199	ribonucleoside triphosp	0.50	22	2.3182297	790	2.2814567
9482	GO:0016291|GO:0008	acyl-CoA thioesterase a	0.50	1	0.105374075	25	0.072197996
31493	GO:0080118	brassinosteroid sulfotra	0.50	1	0.105374075	25	0.072197996
6515	GO:0009150	purine ribonucleotide m	0.50	22	2.3182297	791	2.2843447
5712	GO:0008168|GO:0004	methyltransferase activ	0.50	7	0.73761857	244	0.7046524
8681	GO:0015299	solute:hydrogen antipor	0.51	3	0.31612223	98	0.28301615
25379	GO:0051082	unfolded protein binding	0.51	3	0.31612223	98	0.28301615
2978	GO:0004180	carboxypeptidase activi	0.51	2	0.21074815	62	0.17905103
3801	GO:0005342	organic acid transmemb	0.51	4	0.4214963	136	0.3927571
22444	GO:0046943	carboxylic acid transme	0.51	4	0.4214963	136	0.3927571
6506	GO:0009141	nucleoside triphosphate	0.51	22	2.3182297	796	2.2987843
3210	GO:0004565	beta-galactosidase acti	0.51	1	0.105374075	26	0.075085916
3415	GO:0004805	trehalose-phosphatase	0.51	1	0.105374075	26	0.075085916
4030	GO:0005741	mitochondrial outer mer	0.51	1	0.105374075	26	0.075085916
8516	GO:0015101	organic cation transmer	0.51	1	0.105374075	26	0.075085916
8964	GO:0015695	organic cation transport	0.51	1	0.105374075	26	0.075085916
9421	GO:0016208	AMP binding	0.51	1	0.105374075	26	0.075085916
9884	GO:0016847|GO:0034	1-aminocyclopropane-1	0.51	1	0.105374075	26	0.075085916
10911	GO:0018871	1-aminocyclopropane-1	0.51	1	0.105374075	26	0.075085916
17147	GO:0034768	(E)-beta-ocimene synth	0.51	1	0.105374075	26	0.075085916
18579	GO:0042218	1-aminocyclopropane-1	0.51	1	0.105374075	26	0.075085916
30689	GO:0072330	monocarboxylic acid bio	0.51	1	0.105374075	26	0.075085916
14667	GO:0032259	methylation	0.52	8	0.8429926	285	0.8230572

22416	GO:0046915	transition metal ion tran	0.53	2	0.21074815	64	0.18482687
25820	GO:0051536	iron-sulfur cluster bindin	0.53	2	0.21074815	64	0.18482687
25824	GO:0051540	metal cluster binding	0.53	2	0.21074815	64	0.18482687
9346	GO:0016114	terpenoid biosynthetic p	0.53	1	0.105374075	27	0.077973835
9389	GO:0016160	amylase activity	0.53	1	0.105374075	27	0.077973835
4849	GO:0006730|GO:00197	one-carbon metabolic p	0.53	9	0.9483667	325	0.93857396
10058	GO:0017111	nucleoside-triphosphata	0.53	24	2.5289779	878	2.5355935
25314	GO:0051015	actin filament binding	0.54	2	0.21074815	65	0.18771479
3724	GO:0005216	ion channel activity	0.54	4	0.4214963	140	0.40430877
9579	GO:0016462	pyrophosphatase activi	0.54	26	2.739726	954	2.7550755
3284	GO:0004650	polygalacturonase activ	0.54	1	0.105374075	28	0.080861755
3812	GO:0005355|GO:00155	glucose transmembran	0.54	1	0.105374075	28	0.080861755
6079	GO:0008654	phospholipid biosynthet	0.54	1	0.105374075	28	0.080861755
9027	GO:0015758	glucose transport	0.54	1	0.105374075	28	0.080861755
9238	GO:0015980	energy derivation by ox	0.54	1	0.105374075	28	0.080861755
23911	GO:0048519|GO:00431	negative regulation of b	0.54	1	0.105374075	28	0.080861755
23915	GO:0048523|GO:00512	negative regulation of c	0.54	1	0.105374075	28	0.080861755
139	GO:0000175	3'-5'-exoribonuclease a	0.54	1	0.105374075	28	0.080861755
23515	GO:0048037	cofactor binding	0.54	9	0.9483667	327	0.94434977
3180	GO:0004521	endoribonuclease activ	0.54	2	0.21074815	66	0.1906027
9890	GO:0016854	racemase and epimera	0.54	2	0.21074815	66	0.1906027
9859	GO:0016818	hydrolase activity, actin	0.54	26	2.739726	956	2.7608514
4373	GO:0006163	purine nucleotide metab	0.55	22	2.3182297	810	2.339215
4916	GO:0006818	hydrogen transport	0.55	8	0.8429926	292	0.84327257
9246	GO:0015992	proton transport	0.55	8	0.8429926	292	0.84327257
6166	GO:0008757	S-adenosylmethionine-	0.55	5	0.52687037	180	0.5198256
9858	GO:0016817	hydrolase activity, actin	0.55	26	2.739726	959	2.769515
2668	GO:0003779	actin binding	0.55	3	0.31612223	105	0.3032316
6622	GO:0009259|GO:00091	ribonucleotide metaboli	0.55	22	2.3182297	812	2.344991
4755	GO:0006629	lipid metabolic process	0.55	16	1.6859852	590	1.7038727
4841	GO:0006721	terpenoid metabolic pro	0.55	1	0.105374075	29	0.083749674
11834	GO:0019905	syntaxin binding	0.55	1	0.105374075	29	0.083749674
3195	GO:0004540	ribonuclease activity	0.56	3	0.31612223	106	0.3061195
2999	GO:0004312	fatty acid synthase activ	0.56	2	0.21074815	68	0.19637854
32	GO:0000041	transition metal ion tran	0.56	2	0.21074815	68	0.19637854
12572	GO:0022890|GO:00150	inorganic cation transm	0.56	9	0.9483667	332	0.9587894
3009	GO:0004322	ferroxidase activity	0.57	1	0.105374075	30	0.086637594
3310	GO:0004679	AMP-activated protein k	0.57	1	0.105374075	30	0.086637594
3886	GO:0005527	macrolide binding	0.57	1	0.105374075	30	0.086637594
3887	GO:0005528	FK506 binding	0.57	1	0.105374075	30	0.086637594
4498	GO:0006305	DNA alkylation	0.57	1	0.105374075	30	0.086637594
4499	GO:0006306	DNA methylation	0.57	1	0.105374075	30	0.086637594
6216	GO:0008810	cellulase activity	0.57	1	0.105374075	30	0.086637594
9785	GO:0016724	oxidoreductase activity,	0.57	1	0.105374075	30	0.086637594
12533	GO:0022838	substrate-specific chan	0.57	6	0.63224447	221	0.63823026
3620	GO:0005057	receptor signaling prote	0.57	2	0.21074815	69	0.19926646
11522	GO:0019538|GO:00064	protein metabolic proce	0.57	112	11.801897	4134	11.938661
3873	GO:0005507	copper ion binding	0.57	4	0.4214963	146	0.42163628
9486	GO:0016298	lipase activity	0.57	5	0.52687037	185	0.53426516
9191	GO:0015931	nucleobase, nucleoside	0.58	2	0.21074815	70	0.20215438
9192	GO:0015932	nucleobase, nucleoside	0.58	2	0.21074815	70	0.20215438
9796	GO:0016741	transferase activity, tran	0.58	7	0.73761857	261	0.7537471
19590	GO:0043295	glutathione binding	0.58	1	0.105374075	31	0.08952551
20514	GO:0044264	cellular polysaccharide	0.58	1	0.105374075	31	0.08952551
4478	GO:0006281	DNA repair	0.59	4	0.4214963	149	0.43030006
5037	GO:0006974|GO:00349	response to DNA dama	0.59	4	0.4214963	149	0.43030006
30877	GO:0072521	purine-containing comp	0.59	22	2.3182297	827	2.3883097
8660	GO:0015267|GO:00152	channel activity	0.59	6	0.63224447	226	0.6526699
12515	GO:0022803	passive transmembran	0.59	6	0.63224447	226	0.6526699
3190	GO:0004532	exoribonuclease activity	0.59	1	0.105374075	32	0.09241343
3717	GO:0005199	structural constituent of	0.59	1	0.105374075	32	0.09241343
4614	GO:0006470	protein dephosphorylati	0.59	1	0.105374075	32	0.09241343
6942	GO:0009674	potassium:sodium symp	0.59	1	0.105374075	32	0.09241343
9537	GO:0016409	palmitoyltransferase ac	0.59	1	0.105374075	32	0.09241343
9927	GO:0016896	exoribonuclease activity	0.59	1	0.105374075	32	0.09241343
12522	GO:0022820	potassium ion symporte	0.59	1	0.105374075	32	0.09241343
12833	GO:0030275	LRR domain binding	0.59	1	0.105374075	32	0.09241343
14381	GO:0031968	organelle outer membra	0.59	1	0.105374075	32	0.09241343
4459	GO:0006259|GO:00551	DNA metabolic process	0.60	13	1.369863	493	1.4237444
4526	GO:0006351|GO:00063	transcription, DNA-depe	0.60	42	4.425711	1575	4.548474
15176	GO:0032774	RNA biosynthetic proce	0.60	42	4.425711	1575	4.548474
4493	GO:0006298|GO:00063	mismatch repair	0.60	1	0.105374075	33	0.09530135
2632	GO:0003682	chromatin binding	0.60	1	0.105374075	33	0.09530135
3955	GO:0005634	nucleus	0.61	38	4.004215	1433	4.138389
4497	GO:0006304	DNA modification	0.61	1	0.105374075	34	0.09818927
5270	GO:0007264	small GTPase mediated	0.61	1	0.105374075	34	0.09818927
5700	GO:0008144	drug binding	0.61	1	0.105374075	34	0.09818927
6004	GO:0008536	Ran GTPase binding	0.61	1	0.105374075	34	0.09818927
6072	GO:0008645	hexose transport	0.61	1	0.105374075	34	0.09818927
8562	GO:0015149	hexose transmembrane	0.61	1	0.105374075	34	0.09818927
17794	GO:0035428	hexose transmembrane	0.61	1	0.105374075	34	0.09818927
18382	GO:0040029	regulation of gene expr	0.61	1	0.105374075	34	0.09818927
6424	GO:0009055|GO:00090	electron carrier activity	0.61	4	0.4214963	154	0.44473964
2674	GO:0003824	catalytic activity	0.61	291	30.663857	10750	31.045137
9488	GO:0016301	kinase activity	0.62	46	4.8472075	1740	5.0249805
4538	GO:0006364|GO:00063	rRNA processing	0.62	1	0.105374075	35	0.10107719
9310	GO:0016072	rRNA metabolic proces	0.62	1	0.105374075	35	0.10107719
9480	GO:0016289	CoA hydrolase activity	0.62	1	0.105374075	35	0.10107719
9922	GO:0016891	endoribonuclease activ	0.62	1	0.105374075	35	0.10107719
9114	GO:0015849	organic acid transport	0.62	4	0.4214963	156	0.45051548
22443	GO:0046942	carboxylic acid transpor	0.62	4	0.4214963	156	0.45051548
5604	GO:0008017	microtubule binding	0.63	2	0.21074815	77	0.22236982
3877	GO:0005516	calmodulin binding	0.63	6	0.63224447	236	0.6815491
3888	GO:0005529	sugar binding	0.63	4	0.4214963	158	0.45629135
3804	GO:0005345	purine base transmemb	0.63	1	0.105374075	36	0.10396511
4949	GO:0006863|GO:00158	purine base transport	0.63	1	0.105374075	36	0.10396511
5902	GO:0008408	3'-5' exonuclease activi	0.63	1	0.105374075	36	0.10396511
11314	GO:0019321	pentose metabolic proc	0.63	1	0.105374075	36	0.10396511
20649	GO:0044455	mitochondrial membran	0.63	1	0.105374075	36	0.10396511
30865	GO:0072509	divalent inorganic catio	0.63	2	0.21074815	78	0.22525774
5705	GO:0008152	metabolic process	0.64	473	49.841938	17432	50.34222
19831	GO:0043565	sequence-specific DNA	0.64	4	0.4214963	159	0.45917925
8934	GO:0015662	ATPase activity, couple	0.64	1	0.105374075	37	0.10685303

3874	GO:0005509	calcium ion binding	0.65	7	0.73761857	279	0.8057296
9875	GO:0016836	hydro-lyase activity	0.65	2	0.21074815	80	0.2310336
9637	GO:0016538|GO:00037	cyclin-dependent protei	0.65	1	0.105374075	38	0.10974095
117	GO:0000149	SNARE binding	0.65	1	0.105374075	38	0.10974095
3827	GO:0005372	water transmembrane t	0.65	2	0.21074815	81	0.23392151
4927	GO:0006833	water transport	0.65	2	0.21074815	81	0.23392151
8652	GO:0015250	water channel activity	0.65	2	0.21074815	81	0.23392151
18429	GO:0042044	fluid transport	0.65	2	0.21074815	81	0.23392151
3260	GO:0004620	phospholipase activity	0.66	3	0.31612223	123	0.35521415
29202	GO:0070838	divalent metal ion trans	0.66	2	0.21074815	82	0.23680943
19473	GO:0043170|GO:00432	macromolecule metabo	0.66	175	18.440464	6553	18.92454
20488	GO:0044238	primary metabolic proce	0.66	246	25.922024	9167	26.47356
4476	GO:0006278	RNA-dependent DNA re	0.67	4	0.4214963	166	0.4793947
5891	GO:0008395|GO:00083	steroid hydroxylase acti	0.67	1	0.105374075	40	0.1155168
8613	GO:0015205|GO:00153	nucleobase transmemb	0.67	1	0.105374075	40	0.1155168
9116	GO:0015851	nucleobase transport	0.67	1	0.105374075	40	0.1155168
9843	GO:0016796	exonuclease activity, ac	0.67	1	0.105374075	40	0.1155168
11804	GO:0019867	outer membrane	0.67	1	0.105374075	40	0.1155168
4643	GO:0006511	ubiquitin-dependent pro	0.67	2	0.21074815	84	0.24258527
11864	GO:0019941	modification-dependent	0.67	2	0.21074815	84	0.24258527
19898	GO:0043632	modification-dependent	0.67	2	0.21074815	84	0.24258527
20507	GO:0044257	cellular protein catabolic	0.67	2	0.21074815	84	0.24258527
25887	GO:0051603	proteolysis involved in c	0.67	2	0.21074815	84	0.24258527
30867	GO:0072511	divalent inorganic cation	0.67	2	0.21074815	84	0.24258527
26932	GO:0055086	nucleobase, nucleoside	0.68	24	2.5289779	944	2.7261963
20627	GO:0044433	cytoplasmic vesicle par	0.68	1	0.105374075	41	0.118404716
5661	GO:0008092	cytoskeletal protein bind	0.68	6	0.63224447	249	0.719092
5768	GO:0008238	exopeptidase activity	0.69	2	0.21074815	86	0.24836111
12734	GO:0030163	protein catabolic proces	0.69	2	0.21074815	86	0.24836111
20515	GO:0044265|GO:00349	cellular macromolecule	0.69	2	0.21074815	86	0.24836111
12805	GO:0030246	carbohydrate binding	0.69	6	0.63224447	251	0.7248679
3718	GO:0005200	structural constituent of	0.69	1	0.105374075	42	0.121292636
5033	GO:0006970	response to osmotic str	0.69	1	0.105374075	42	0.121292636
12659	GO:0030076	light-harvesting comple	0.69	1	0.105374075	42	0.121292636
18956	GO:0042626	ATPase activity, couple	0.69	5	0.52687037	211	0.6093511
4867	GO:0006753	nucleoside phosphate r	0.69	23	2.4236038	914	2.6395588
6484	GO:0009117	nucleotide metabolic pr	0.69	23	2.4236038	914	2.6395588
9861	GO:0016820	hydrolase activity, actin	0.69	5	0.52687037	212	0.612239
3156	GO:0004497	monooxygenase activity	0.70	4	0.4214963	172	0.49672222
5694	GO:0008137	NADH dehydrogenase	0.70	1	0.105374075	43	0.124180555
8589	GO:0015179	L-amino acid transmem	0.70	1	0.105374075	43	0.124180555
9076	GO:0015807	L-amino acid transport	0.70	1	0.105374075	43	0.124180555
13833	GO:0031410	cytoplasmic vesicle	0.70	1	0.105374075	43	0.124180555
14393	GO:0031982	vesicle	0.70	1	0.105374075	43	0.124180555
20624	GO:0044430	cytoskeletal part	0.70	2	0.21074815	88	0.25413695
8495	GO:0015077	monovalent inorganic c	0.70	5	0.52687037	214	0.6180149
4605	GO:0006457|GO:00070	protein folding	0.70	4	0.4214963	173	0.49961013
15949	GO:0033554	cellular response to stre	0.70	4	0.4214963	173	0.49961013
9824	GO:0016773	phosphotransferase act	0.70	38	4.004215	1493	4.311664
2982	GO:0004197	cysteine-type endopept	0.71	2	0.21074815	90	0.2599128
18953	GO:0042623	ATPase activity, couple	0.71	13	1.369863	537	1.550813
8787	GO:0015450	P-P-bond-hydrolysis-dri	0.71	1	0.105374075	45	0.1299564
9924	GO:0016893	endonuclease activity, a	0.71	1	0.105374075	45	0.1299564
11780	GO:0019829	cation-transporting ATP	0.71	1	0.105374075	45	0.1299564
24456	GO:0050136	NADH dehydrogenase	0.71	1	0.105374075	45	0.1299564
26845	GO:0052689	carboxylic ester hydrola	0.72	13	1.369863	538	1.5537009
3242	GO:0004601|GO:00166	peroxidase activity	0.72	3	0.31612223	135	0.38986918
9754	GO:0016684	oxidoreductase activity,	0.72	3	0.31612223	135	0.38986918
8749	GO:0015399	primary active transmer	0.72	6	0.63224447	260	0.75085914
8753	GO:0015405	P-P-bond-hydrolysis-dri	0.72	6	0.63224447	260	0.75085914
4558	GO:0006396|GO:00063	RNA processing	0.72	5	0.52687037	219	0.63245445
12498	GO:0022613	ribonucleoprotein comp	0.72	1	0.105374075	46	0.13284431
18614	GO:0042254|GO:00070	ribosome biogenesis	0.72	1	0.105374075	46	0.13284431
31895	GO:0090304	nucleic acid metabolic p	0.72	60	6.322445	2340	6.7577324
5714	GO:0008170	N-methyltransferase ac	0.73	1	0.105374075	47	0.13573223
8497	GO:0015079|GO:00228	potassium ion transmer	0.73	1	0.105374075	47	0.13573223
9308	GO:0016070	RNA metabolic process	0.73	47	4.952582	1855	5.3570914
9823	GO:0016772	transferase activity, tran	0.73	49	5.1633296	1932	5.579461
14591	GO:0032183	SUMO binding	0.74	1	0.105374075	48	0.13862015
4460	GO:0006260|GO:00551	DNA replication	0.74	5	0.52687037	224	0.64689404
6483	GO:0009116	nucleoside metabolic pr	0.74	1	0.105374075	49	0.14150807
6750	GO:0009415	response to water	0.74	1	0.105374075	49	0.14150807
8909	GO:0015630	microtubule cytoskeleto	0.74	1	0.105374075	49	0.14150807
11784	GO:0019838	growth factor binding	0.74	1	0.105374075	49	0.14150807
3185	GO:0004527|GO:00088	exonuclease activity	0.75	1	0.105374075	50	0.14439599
4216	GO:0005976	polysaccharide metabo	0.75	1	0.105374075	50	0.14439599
9993	GO:0017016	Ras GTPase binding	0.75	1	0.105374075	50	0.14439599
29674	GO:0071310	cellular response to org	0.75	1	0.105374075	50	0.14439599
30886	GO:0072530	purine-containing comp	0.75	1	0.105374075	50	0.14439599
3293	GO:0004659	prenyltransferase activi	0.76	1	0.105374075	51	0.14728391
8908	GO:0015629	actin cytoskeleton	0.76	1	0.105374075	51	0.14728391
30207	GO:0071843	cellular component biog	0.76	1	0.105374075	51	0.14728391
2628	GO:0003677	DNA binding	0.76	30	3.1612225	1224	3.534814
15436	GO:0033036	macromolecule localiza	0.76	9	0.9483667	397	1.1465042
4915	GO:0006817	phosphate transport	0.76	1	0.105374075	52	0.15017183
8528	GO:0015114	phosphate transmembr	0.76	1	0.105374075	52	0.15017183
17801	GO:0035435	phosphate transmembr	0.76	1	0.105374075	52	0.15017183
2809	GO:0003993	acid phosphatase activi	0.76	1	0.105374075	52	0.15017183
2778	GO:0003954	NADH dehydrogenase	0.77	1	0.105374075	53	0.15305975
19758	GO:0043492	ATPase activity, couple	0.77	5	0.52687037	235	0.67866117
17918	GO:0035556|GO:00072	intracellular signal trans	0.78	1	0.105374075	54	0.15594767
29251	GO:0070887	cellular response to che	0.78	1	0.105374075	54	0.15594767
11828	GO:0019899	enzyme binding	0.78	5	0.52687037	237	0.684437
4029	GO:0005740	mitochondrial envelope	0.79	3	0.31612223	151	0.4360759
13697	GO:0031267	small GTPase binding	0.79	1	0.105374075	56	0.16172351
6426	GO:0009057|GO:00432	macromolecule catabol	0.79	2	0.21074815	106	0.3061195
7557	GO:0010333	terpene synthase activi	0.80	1	0.105374075	57	0.16461143
8910	GO:0015631	tubulin binding	0.80	2	0.21074815	107	0.30900744
4357	GO:0006139|GO:00551	nucleobase, nucleoside	0.80	83	8.746049	3285	9.486816
3323	GO:0004702	receptor signaling prote	0.80	1	0.105374075	58	0.16749935
5819	GO:0008299|GO:00092	isoprenoid biosynthetic	0.80	1	0.105374075	58	0.16749935
8558	GO:0015145	monosaccharide transm	0.80	1	0.105374075	58	0.16749935
9018	GO:0015749	monosaccharide transp	0.80	1	0.105374075	58	0.16749935

11820	GO:0019887	protein kinase regulator	0.80	1	0.105374075	58	0.16749935
3946	GO:0005623	cell	0.80	215	22.655426	8227	23.758917
20657	GO:0044464	cell part	0.80	215	22.655426	8227	23.758917
5909	GO:0008415	acyltransferase activity	0.80	7	0.73761857	330	0.95301354
11833	GO:0019904	protein domain specific	0.80	2	0.21074815	109	0.31478328
30700	GO:0072341	modified amino acid bin	0.81	1	0.105374075	59	0.17038727
4840	GO:0006720|GO:0016	isoprenoid metabolic pr	0.81	1	0.105374075	60	0.17327519
5652	GO:0008081|GO:0004	phosphoric diester hydr	0.81	1	0.105374075	60	0.17327519
14811	GO:0032403	protein complex binding	0.81	1	0.105374075	60	0.17327519
25319	GO:0051020	GTPase binding	0.81	1	0.105374075	60	0.17327519
29918	GO:0071554	cell wall organization or	0.82	2	0.21074815	112	0.32344702
4768	GO:0006644	phospholipid metabolic	0.82	1	0.105374075	61	0.1761631
2818	GO:0004003	ATP-dependent DNA h	0.82	1	0.105374075	61	0.1761631
8496	GO:0015078	hydrogen ion transmem	0.82	3	0.31612223	160	0.4620672
6018	GO:0008559|GO:0005	xenobiotic-transporting	0.82	1	0.105374075	62	0.17905103
11210	GO:0019207	kinase regulator activity	0.82	1	0.105374075	62	0.17905103
19225	GO:0042908	xenobiotic transport	0.82	1	0.105374075	62	0.17905103
19227	GO:0042910	xenobiotic transporter a	0.82	1	0.105374075	62	0.17905103
14379	GO:0031966	mitochondrial membran	0.82	2	0.21074815	114	0.32922286
3103	GO:0004437	inositol or phosphatidyli	0.83	1	0.105374075	64	0.18482687
20623	GO:0044429	mitochondrial part	0.83	3	0.31612223	165	0.47650677
9838	GO:0016790	thiolester hydrolase act	0.84	1	0.105374075	65	0.18771479
11616	GO:0019637	organophosphate meta	0.84	1	0.105374075	65	0.18771479
19526	GO:0043227	membrane-bounded or	0.84	52	5.479452	2142	6.185924
19530	GO:0043231	intracellular membrane-	0.84	52	5.479452	2142	6.185924
25416	GO:0051119	sugar transmembrane t	0.84	2	0.21074815	118	0.34077454
5809	GO:0008289	lipid binding	0.84	5	0.52687037	258	0.74508333
2629	GO:0003678|GO:0003	DNA helicase activity	0.84	1	0.105374075	67	0.19349062
17024	GO:0034645|GO:0034	cellular macromolecule	0.85	48	5.0579557	1999	5.7729516
18955	GO:0042625	ATPase activity, couple	0.85	1	0.105374075	68	0.19637854
6884	GO:0009607	response to biotic stimu	0.85	2	0.21074815	122	0.3523262
6428	GO:0009059|GO:0043	macromolecule biosynt	0.85	48	5.0579557	2003	5.7845035
5726	GO:0008187	poly-pyrimidine tract bin	0.86	1	0.105374075	70	0.20215438
5788	GO:0008266	poly(U) RNA binding	0.86	1	0.105374075	70	0.20215438
5838	GO:0008320	protein transmembrane	0.86	1	0.105374075	70	0.20215438
9853	GO:0016811	hydrolase activity, actin	0.86	1	0.105374075	70	0.20215438
12568	GO:0022884	macromolecule transme	0.86	1	0.105374075	70	0.20215438
23522	GO:0048046	apoplast	0.86	1	0.105374075	70	0.20215438
2649	GO:0003713	transcription coactivato	0.86	1	0.105374075	70	0.20215438
4067	GO:0005783	endoplasmic reticulum	0.86	3	0.31612223	174	0.50249803
3200	GO:0004553|GO:0016	hydrolase activity, hydro	0.86	6	0.63224447	312	0.90103096
7691	GO:0010467	gene expression	0.86	47	4.952582	1974	5.7007537
9845	GO:0016798	hydrolase activity, actin	0.86	8	0.8429926	401	1.1580559
9771	GO:0016709	oxidoreductase activity,	0.86	1	0.105374075	71	0.2050423
9869	GO:0016829	lyase activity	0.86	10	1.0537407	488	1.4093049
4121	GO:0005856	cytoskeleton	0.86	2	0.21074815	126	0.3638779
20531	GO:0044281	small molecule metabo	0.87	42	4.425711	1788	5.1636004
3311	GO:0004683|GO:0004	calmodulin-dependent	0.87	1	0.105374075	74	0.21370606
4394	GO:0006184	GTP catabolic process	0.88	2	0.21074815	132	0.3812054
21605	GO:0046039	GTP metabolic process	0.88	2	0.21074815	132	0.3812054
2758	GO:0003924	GTPase activity	0.88	2	0.21074815	132	0.3812054
6529	GO:0009165	nucleotide biosynthetic	0.88	1	0.105374075	77	0.22236982
9877	GO:0016838	carbon-oxygen lyase ac	0.88	1	0.105374075	77	0.22236982
9852	GO:0016810	hydrolase activity, actin	0.89	2	0.21074815	134	0.38698125
5196	GO:0007166	cell surface receptor lin	0.89	1	0.105374075	78	0.22525774
3903	GO:0005575|GO:0008	cellular_component	0.89	218	22.971548	8515	24.590637
22007	GO:0046483	heterocycle metabolic p	0.89	24	2.5289779	1094	3.1593843
9682	GO:0016597	amino acid binding	0.89	1	0.105374075	80	0.2310336
19479	GO:0043176	amine binding	0.89	1	0.105374075	80	0.2310336
15189	GO:0032787	monocarboxylic acid me	0.89	1	0.105374075	81	0.23392151
18674	GO:0042325	regulation of phosphory	0.89	1	0.105374075	81	0.23392151
4942	GO:0006855	drug transmembrane tr	0.90	2	0.21074815	139	0.40142086
8642	GO:0015238|GO:0015	drug transmembrane tr	0.90	2	0.21074815	139	0.40142086
9154	GO:0015893	drug transport	0.90	2	0.21074815	139	0.40142086
18832	GO:0042493|GO:0017	response to drug	0.90	2	0.21074815	139	0.40142086
2658	GO:0003729	mRNA binding	0.90	1	0.105374075	82	0.23680943
3895	GO:0005543	phospholipid binding	0.90	2	0.21074815	140	0.40430877
6046	GO:0008610	lipid biosynthetic proces	0.90	2	0.21074815	141	0.4071967
22479	GO:0046983	protein dimerization act	0.90	10	1.0537407	517	1.4930545
8557	GO:0015144	carbohydrate transmem	0.91	2	0.21074815	143	0.41297254
16602	GO:0034219	carbohydrate transmem	0.91	2	0.21074815	143	0.41297254
11222	GO:0019220	regulation of phosphate	0.91	1	0.105374075	85	0.24547319
25471	GO:0051174	regulation of phosphoru	0.91	1	0.105374075	85	0.24547319
4032	GO:0005743	mitochondrial inner me	0.91	1	0.105374075	88	0.25413695
6071	GO:0008643|GO:0006	carbohydrate transport	0.91	2	0.21074815	147	0.42452422
14380	GO:0031967	organelle envelope	0.92	3	0.31612223	201	0.5804719
9874	GO:0016835	carbon-oxygen lyase ac	0.92	3	0.31612223	202	0.5833598
11426	GO:0019438	aromatic compound bio	0.92	2	0.21074815	149	0.43030006
14590	GO:0032182	small conjugating prote	0.92	1	0.105374075	90	0.2599128
3644	GO:0005102	receptor binding	0.92	1	0.105374075	91	0.2628007
14387	GO:0031975	envelope	0.92	3	0.31612223	205	0.59202355
16785	GO:0034404	nucleobase, nucleoside	0.92	1	0.105374075	92	0.26568863
17033	GO:0034654	nucleobase, nucleoside	0.92	1	0.105374075	92	0.26568863
20336	GO:0044085	cellular component bio	0.92	1	0.105374075	93	0.26857653
3808	GO:0005351|GO:0005	sugar:hydrogen sympo	0.93	1	0.105374075	94	0.27146447
3835	GO:0005402	cation:sugar symporter	0.93	1	0.105374075	94	0.27146447
11803	GO:0019866	organelle inner membra	0.93	1	0.105374075	94	0.27146447
3178	GO:0004519	endonuclease activity	0.93	6	0.63224447	356	1.0280994
4906	GO:0006807	nitrogen compound me	0.93	89	9.378293	3725	10.757502
4612	GO:0006468	protein phosphorylation	0.93	50	5.268704	2205	6.367863
19126	GO:0042803	protein homodimerizati	0.93	4	0.4214963	265	0.7652988
8677	GO:0015295	solute:hydrogen sympo	0.93	1	0.105374075	98	0.28301615
13829	GO:0031406	carboxylic acid binding	0.93	1	0.105374075	98	0.28301615
16851	GO:0034470	ncRNA processing	0.94	1	0.105374075	99	0.28590405
17039	GO:0034660	ncRNA metabolic proce	0.94	1	0.105374075	99	0.28590405
13041	GO:0030554	adenyl nucleotide bindi	0.94	10	1.0537407	550	1.5883559
14965	GO:0032559	adenyl ribonucleotide b	0.94	10	1.0537407	550	1.5883559
9870	GO:0016830	carbon-carbon lyase ac	0.94	2	0.21074815	161	0.4649551
7271	GO:0010033	response to organic su	0.94	1	0.105374075	100	0.28879198
16430	GO:0034046	poly(G) RNA binding	0.94	1	0.105374075	100	0.28879198
17020	GO:0034641	cellular nitrogen compo	0.94	87	9.167544	3678	10.621769
5764	GO:0008234|GO:0004	cysteine-type peptidase	0.94	2	0.21074815	163	0.47073093
4028	GO:0005739	mitochondrion	0.94	3	0.31612223	219	0.63245445

19125	GO:0042802	identical protein binding	0.95	13	1.369863	697	2.01288
4649	GO:0006520|GO:0006	cellular amino acid meta	0.95	4	0.4214963	277	0.7999538
9494	GO:0016311	dephosphorylation	0.95	7	0.73761857	425	1.227366
6077	GO:0008652	cellular amino acid bios	0.95	2	0.21074815	169	0.48805845
3177	GO:0004518	nuclease activity	0.95	7	0.73761857	427	1.2331418
3884	GO:0005524	ATP binding	0.95	9	0.9483667	524	1.51327
9839	GO:0016791|GO:0016	phosphatase activity	0.95	6	0.63224447	383	1.1060733
13531	GO:0031072	heat shock protein bind	0.95	3	0.31612223	230	0.6642216
9493	GO:0016310	phosphorylation	0.96	56	5.9009485	2504	7.2313514
29081	GO:0070717	poly-purine tract binding	0.96	1	0.105374075	112	0.32344702
4850	GO:0006732|GO:0006	coenzyme metabolic pr	0.96	1	0.105374075	113	0.32633495
19686	GO:0043414	macromolecule methyla	0.96	1	0.105374075	113	0.32633495
3904	GO:0005576	extracellular region	0.96	2	0.21074815	178	0.5140497
13082	GO:0030599	pectinesterase activity	0.96	2	0.21074815	178	0.5140497
9837	GO:0016788	hydrolase activity, actin	0.96	32	3.3719704	1534	4.430069
6020	GO:0008565|GO:0015	protein transporter activ	0.96	1	0.105374075	115	0.3321108
9871	GO:0016831	carboxy-lyase activity	0.96	1	0.105374075	115	0.3321108
6663	GO:0009309	amine biosynthetic proc	0.96	2	0.21074815	181	0.5227135
18912	GO:0042578	phosphoric ester hydrol	0.96	7	0.73761857	444	1.2822365
20505	GO:0044255	cellular lipid metabolic p	0.96	2	0.21074815	184	0.53137726
4844	GO:0006725	cellular aromatic compo	0.96	2	0.21074815	185	0.53426516
3885	GO:0005525	GTP binding	0.97	3	0.31612223	245	0.70754033
11032	GO:0019001	guanyl nucleotide bindi	0.97	3	0.31612223	245	0.70754033
14967	GO:0032561	guanyl ribonucleotide b	0.97	3	0.31612223	245	0.70754033
2657	GO:0003727|GO:0003	single-stranded RNA bi	0.97	2	0.21074815	188	0.54292893
20356	GO:0044106	cellular amine metaboli	0.97	4	0.4214963	303	0.8750397
9889	GO:0016853	isomerase activity	0.97	4	0.4214963	306	0.8837035
12741	GO:0030170	pyridoxal phosphate bi	0.97	1	0.105374075	126	0.3638779
28643	GO:0070279	vitamin B6 binding	0.97	1	0.105374075	126	0.3638779
634	GO:0000988	protein binding transcri	0.97	1	0.105374075	126	0.3638779
635	GO:0000989	transcription factor bind	0.97	1	0.105374075	126	0.3638779
2648	GO:0003712	transcription cofactor a	0.97	1	0.105374075	126	0.3638779
6662	GO:0009308	amine metabolic proces	0.97	4	0.4214963	314	0.9068068
19533	GO:0043234	protein complex	0.97	15	1.5806112	848	2.448956
20499	GO:0044249	cellular biosynthetic pro	0.98	57	6.0063224	2635	7.6096687
9836	GO:0016787	hydrolase activity	0.98	84	8.851422	3723	10.751725
3449	GO:0004842|GO:0004	ubiquitin-protein ligase	0.98	4	0.4214963	326	0.94146186
18582	GO:0042221	response to chemical s	0.98	4	0.4214963	328	0.94723773
9295	GO:0016053	organic acid biosyntheti	0.98	2	0.21074815	211	0.6093511
21922	GO:0046394	carboxylic acid biosynth	0.98	2	0.21074815	211	0.6093511
9654	GO:0016567	protein ubiquitination	0.98	4	0.4214963	332	0.9587894
14854	GO:0032446	protein modification by	0.98	4	0.4214963	332	0.9587894
29011	GO:0070647	protein modification by	0.98	4	0.4214963	332	0.9587894
3716	GO:0005198	structural molecule acti	0.98	5	0.52687037	393	1.1349525
11747	GO:0019787|GO:0008	small conjugating prote	0.98	4	0.4214963	339	0.9790048
4897	GO:0006793	phosphorus metabolic	0.98	63	6.638567	2925	8.4471655
4900	GO:0006796	phosphate metabolic pr	0.98	63	6.638567	2925	8.4471655
5019	GO:0006952|GO:0002	defense response	0.98	2	0.21074815	221	0.63823026
14959	GO:0032553	ribonucleotide binding	0.99	13	1.369863	795	2.2958963
14961	GO:0032555	purine ribonucleotide bi	0.99	13	1.369863	795	2.2958963
10033	GO:0017076	purine nucleotide bindi	0.99	13	1.369863	797	2.3016722
13547	GO:0031090	organelle membrane	0.99	2	0.21074815	224	0.64689404
14386	GO:0031974	membrane-enclosed lu	0.99	1	0.105374075	154	0.44473964
4609	GO:0006464	protein modification pro	0.99	59	6.2170706	2781	8.031305
6427	GO:0009058	biosynthetic process	0.99	59	6.2170706	2796	8.074624
18000	GO:0035639	purine ribonucleoside tr	0.99	12	1.2644889	769	2.2208104
25483	GO:0051186	cofactor metabolic proc	0.99	1	0.105374075	164	0.47361887
4320	GO:0006082	organic acid metabolic	0.99	4	0.4214963	369	1.0656425
11716	GO:0019752	carboxylic acid metabol	0.99	4	0.4214963	369	1.0656425
19707	GO:0043436	oxoacid metabolic proc	0.99	4	0.4214963	369	1.0656425
2660	GO:0003735|GO:0003	structural constituent of	0.99	2	0.21074815	246	0.7104283
131	GO:0000166	nucleotide binding	0.99	21	2.2128556	1213	3.5030468
18541	GO:0042180	cellular ketone metabol	0.99	4	0.4214963	375	1.0829699
11787	GO:0019842	vitamin binding	0.99	1	0.105374075	177	0.5111618
9906	GO:0016874	ligase activity	0.99	8	0.8429926	597	1.7240882
19684	GO:0043412	macromolecule modific	0.99	60	6.322445	2900	8.374968
20510	GO:0044260|GO:0034	cellular macromolecule	0.99	126	13.277134	5577	16.105928
5610	GO:0008026	ATP-dependent helicas	0.99	1	0.105374075	183	0.52848935
28401	GO:0070035	purine NTP-dependent	0.99	1	0.105374075	183	0.52848935
8466	GO:0015031|GO:0015	protein transport	0.99	1	0.105374075	185	0.53426516
20820	GO:0045184	establishment of protei	0.99	1	0.105374075	185	0.53426516
9913	GO:0016881	acid-amino acid ligase	0.99	4	0.4214963	391	1.1291766
3068	GO:0004386	helicase activity	0.99	1	0.105374075	189	0.54581684
5669	GO:0008104	protein localization	0.99	1	0.105374075	189	0.54581684
9911	GO:0016879	ligase activity, forming	1.00	5	0.52687037	456	1.3168914
3340	GO:0004721	phosphoprotein phosph	1.00	1	0.105374075	199	0.57469606
20533	GO:0044283	small molecule biosynth	1.00	3	0.31612223	347	1.0021082
2626	GO:0003674|GO:0005	molecular_function	1.00	630	66.385666	24394	70.447914
30204	GO:0071840	cellular component org	1.00	3	0.31612223	362	1.045427
19525	GO:0043226	organelle	1.00	60	6.322445	3013	8.701303
19528	GO:0043229	intracellular organelle	1.00	60	6.322445	3013	8.701303
20517	GO:0044267	cellular protein metabol	1.00	65	6.849315	3225	9.313541
20521	GO:0044271	cellular nitrogen compo	1.00	3	0.31612223	367	1.0598665
7229	GO:0009987|GO:0008	cellular process	1.00	250	26.34352	10601	30.614838
20487	GO:0044237	cellular metabolic proce	1.00	185	19.494204	8185	23.637625
30205	GO:0071841	cellular component org	1.00	1	0.105374075	285	0.8230572
20618	GO:0044424	intracellular part	1.00	75	7.9030557	3853	11.127155
3876	GO:0005515|GO:0045	protein binding	1.00	147	15.489989	6933	20.021948
20640	GO:0044446	intracellular organelle p	1.00	6	0.63224447	710	2.0504231
20616	GO:0044422	organelle part	1.00	6	0.63224447	712	2.0561988
3945	GO:0005622	intracellular	1.00	92	9.694415	4751	13.720507
2627	GO:0003676	nucleic acid binding	1.00	39	4.109589	2453	7.0840673
4109	GO:0005840|GO:0033	ribosome	1.00	5	0.52687037	682	1.9695613
20638	GO:0044444	cytoplasmic part	1.00	21	2.2128556	1644	4.7477403
13018	GO:0030529	ribonucleoprotein comp	1.00	5	0.52687037	741	2.1399486
15392	GO:0032991	macromolecular compl	1.00	20	2.1074815	1616	4.666878
19527	GO:0043228	non-membrane-bound	1.00	7	0.73761857	923	2.66555
19531	GO:0043232	intracellular non-memb	1.00	7	0.73761857	923	2.66555
4027	GO:0005737	cytoplasm	1.00	25	2.634352	2001	5.7787275
3863	GO:0005488	binding	1.00	308	32.455215	13903	40.15075
2653	GO:0003723	RNA binding	1.00	3	0.31612223	797	2.3016722

GO ID	GO ACCESSION	GO Term	p-value	Count in Selection	% Count in Selectio	Count in Total	% Count in Total
5704	GO:0008150|GO:000	biological_process	0.00	922	71.806854	22215	64.155136
2674	GO:0003824	catalytic activity	0.00	474	36.91589	10750	31.045137
4612	GO:0006468	protein phosphorylat	0.00	123	9.579439	2205	6.367863
9493	GO:0016310	phosphorylation	0.00	136	10.5919	2504	7.2313514
4897	GO:0006793	phosphorus metabol	0.00	154	11.99377	2925	8.4471655
4900	GO:0006796	phosphate metaboli	0.00	154	11.99377	2925	8.4471655
9795	GO:0016740	transferase activity	0.00	189	14.719626	3764	10.870131
5705	GO:0008152	metabolic process	0.00	721	56.15265	17432	50.34222
9488	GO:0016301	kinase activity	0.00	99	7.7102804	1740	5.0249805
9824	GO:0016773	phosphotransferase	0.00	86	6.697819	1493	4.311664
3304	GO:0004672|GO:00	protein kinase activit	0.00	78	6.074766	1333	3.8495972
4215	GO:0005975	carbohydrate metab	0.00	61	4.7507787	990	2.8590407
3874	GO:0005509	calcium ion binding	0.00	24	1.8691589	279	0.8057296
3306	GO:0004674|GO:000	protein serine/threon	0.00	63	4.906542	1062	3.0669708
3490	GO:0004888|GO:000	transmembrane rece	0.00	39	3.037383	571	1.6490022
9823	GO:0016772	transferase activity,	0.00	102	7.9439254	1932	5.579461
24968	GO:0050662	coenzyme binding	0.00	18	1.4018692	191	0.5515927
3904	GO:0005576	extracellular region	0.00	17	1.3239875	178	0.5140497
3476	GO:0004872|GO:00	receptor activity	0.00	43	3.3489096	672	1.9406822
24966	GO:0050660	flavin adenine dinucl	0.00	13	1.0124611	118	0.34077454
9845	GO:0016798	hydrolase activity, a	0.00	29	2.258567	401	1.1580559
9486	GO:0016298	lipase activity	0.00	17	1.3239875	185	0.53426516
11202	GO:0019199	transmembrane rece	0.00	34	2.647975	504	1.4555116
4609	GO:0006464	protein modification	0.00	135	10.514019	2781	8.031305
9813	GO:0016759	cellulose synthase a	0.00	8	0.62305295	57	0.16461143
3167	GO:0004508	steroid 17-alpha-mo	0.00	2	0.15576324	2	0.00577584
9847	GO:0016801	hydrolase activity, a	0.00	4	0.31152648	14	0.040430877
25098	GO:0050794|GO:00	regulation of cellular	0.00	182	14.174455	3987	11.514136
3475	GO:0004871|GO:000	signal transducer act	0.00	46	3.5825546	787	2.2727928
27063	GO:0060089	molecular transduce	0.00	46	3.5825546	787	2.2727928
3260	GO:0004620	phospholipase activi	0.00	12	0.93457943	123	0.35521415
5981	GO:0008509	anion transmembran	0.00	19	1.4797508	245	0.70754033
8980	GO:0015711	organic anion transp	0.00	6	0.46728972	37	0.10685303
4917	GO:0006820|GO:000	anion transport	0.00	19	1.4797508	247	0.7133162
25094	GO:0050789|GO:00	regulation of biologi	0.00	194	15.109035	4315	12.461374
8159	GO:0010951	negative regulation	0.00	10	0.7788162	95	0.27435237
3472	GO:0004866	endopeptidase inhibi	0.00	10	0.7788162	95	0.27435237
26712	GO:0052548	regulation of endope	0.00	10	0.7788162	95	0.27435237
28101	GO:0061135	endopeptidase regul	0.00	10	0.7788162	95	0.27435237
9816	GO:0016762	xyloglucan:xylogluco	0.00	5	0.3894081	27	0.077973835
3473	GO:0004867	serine-type endopep	0.00	8	0.62305295	66	0.1906027
5891	GO:0008395|GO:000	steroid hydroxylase	0.00	6	0.46728972	40	0.1155168
3723	GO:0005215|GO:000	transporter activity	0.00	91	7.0872273	1844	5.325324
19684	GO:0043412	macromolecule mod	0.00	135	10.514019	2900	8.374968
5986	GO:0008514	organic anion transm	0.00	5	0.3894081	29	0.083749674
9848	GO:0016802	trialkylsulfonium hyd	0.00	2	0.15576324	3	0.00866376
2822	GO:0004013	adenosylhomocystei	0.00	2	0.15576324	3	0.00866376
28364	GO:0065007	biological regulation	0.00	194	15.109035	4376	12.637537
3242	GO:0004601|GO:00	peroxidase activity	0.00	12	0.93457943	135	0.38986918
9754	GO:0016684	oxidoreductase activ	0.00	12	0.93457943	135	0.38986918
12602	GO:0023052|GO:00	signaling	0.00	52	4.0498443	961	2.775291
5195	GO:0007165|GO:00	signal transduction	0.00	52	4.0498443	961	2.775291
23116	GO:0047631	ADP-ribose diphosp	0.01	3	0.23364486	10	0.0288792
2797	GO:0003979	UDP-glucose 6-deh	0.01	3	0.23364486	10	0.0288792
3307	GO:0004675	transmembrane rece	0.01	24	1.8691589	367	1.0598665
23515	GO:0048037	cofactor binding	0.01	22	1.7133956	327	0.94434977
26931	GO:0055085	transmembrane tran	0.01	77	5.996885	1548	4.4705
21331	GO:0045735	nutrient reservoir act	0.01	9	0.7009346	89	0.25702485
3464	GO:0004857	enzyme inhibitor acti	0.01	13	1.0124611	157	0.4534034
13082	GO:0030599	pectinesterase activi	0.01	14	1.0903426	178	0.5140497
3877	GO:0005516	calmodulin binding	0.01	17	1.3239875	236	0.6815491
7690	GO:0010466	negative regulation	0.01	10	0.7788162	110	0.31767118
12946	GO:0030414	peptidase inhibitor a	0.01	10	0.7788162	110	0.31767118
25636	GO:0051346	negative regulation	0.01	10	0.7788162	110	0.31767118
6293	GO:0008898	homocysteine S-met	0.01	2	0.15576324	4	0.011551679
16227	GO:0033843	xyloglucan 6-xylosyl	0.01	2	0.15576324	4	0.011551679
6018	GO:0008559|GO:000	xenobiotic-transporti	0.01	7	0.5451713	62	0.17905103
19225	GO:0042908	xenobiotic transport	0.01	7	0.5451713	62	0.17905103
19227	GO:0042910	xenobiotic transporte	0.01	7	0.5451713	62	0.17905103
12547	GO:0022857|GO:000	transmembrane tran	0.01	73	5.685358	1483	4.282785
26711	GO:0052547	regulation of peptida	0.01	10	0.7788162	112	0.32344702
28100	GO:0061134	peptidase regulator	0.01	10	0.7788162	112	0.32344702
12806	GO:0030247	polysaccharide bindi	0.01	5	0.3894081	35	0.10107719
1169	GO:0001871	pattern binding	0.01	5	0.3894081	35	0.10107719
5636	GO:0008061	chitin binding	0.01	4	0.31152648	23	0.06642216
26845	GO:0052689	carboxylic ester hyd	0.01	31	2.4143302	538	1.5537009
9814	GO:0016760	cellulose synthase (	0.01	3	0.23364486	13	0.037542958
3213	GO:0004568	chitinase activity	0.01	4	0.31152648	24	0.06931008
6248	GO:0008843	endochitinase activit	0.01	4	0.31152648	24	0.06931008
25578	GO:0051287|GO:00	NAD binding	0.01	4	0.31152648	24	0.06931008
3229	GO:0004586	ornithine decarboxyl	0.01	2	0.15576324	5	0.0144396
9812	GO:0016758	transferase activity,	0.01	29	2.258567	501	1.4468478
2999	GO:0004312	fatty acid synthase	0.01	7	0.5451713	68	0.19637854
11157	GO:0019144	ADP-sugar diphosph	0.01	3	0.23364486	14	0.040430877

4909	GO:0006810|GO:001	transport	**0.01**	106	8.255452	2315	6.6855345
25529	GO:0051234	establishment of loca	**0.01**	106	8.255452	2315	6.6855345
4942	GO:0006855	drug transmembrane	**0.01**	11	0.8566978	139	0.40142086
8642	GO:0015238|GO:001	drug transmembrane	**0.01**	11	0.8566978	139	0.40142086
9154	GO:0015893	drug transport	**0.01**	11	0.8566978	139	0.40142086
18832	GO:0042493|GO:001	response to drug	**0.01**	11	0.8566978	139	0.40142086
25626	GO:0051336	regulation of hydrola	**0.01**	14	1.0903426	196	0.5660323
9811	GO:0016757|GO:001	transferase activity, t	**0.01**	39	3.037383	729	2.1052935
25476	GO:0051179	localization	**0.02**	106	8.255452	2319	6.697086
119	GO:0000151	ubiquitin ligase comp	**0.02**	8	0.62305295	88	0.25413695
3209	GO:0004564	beta-fructofuranosida	**0.02**	3	0.23364486	15	0.043318797
3305	GO:0004673|GO:000	protein histidine kina	**0.02**	2	0.15576324	6	0.01732752
4118	GO:0005852	eukaryotic translation	**0.02**	2	0.15576324	6	0.01732752
11899	GO:0019992	diacylglycerol binding	**0.02**	2	0.15576324	6	0.01732752
18640	GO:0042285	xylosyltransferase ac	**0.02**	2	0.15576324	6	0.01732752
3382	GO:0004768|GO:001	stearoyl-CoA 9-desa	**0.02**	3	0.23364486	16	0.046206716
9427	GO:0016215	CoA desaturase activ	**0.02**	3	0.23364486	16	0.046206716
9422	GO:0016209	antioxidant activity	**0.02**	12	0.93457943	165	0.47650677
18738	GO:0042389	omega-3 fatty acid d	**0.02**	3	0.23364486	17	0.049094636
19393	GO:0043086	negative regulation o	**0.02**	13	1.0124611	188	0.54292893
20342	GO:0044092	negative regulation o	**0.02**	13	1.0124611	188	0.54292893
6216	GO:0008810	cellulase activity	**0.02**	4	0.31152648	30	0.086637594
3200	GO:0004553|GO:001	hydrolase activity, hy	**0.02**	19	1.4797508	312	0.90103096
12805	GO:0030246	carbohydrate binding	**0.03**	16	1.2461059	251	0.7248679
6416	GO:0009044	xylan 1,4-beta-xylosi	**0.03**	3	0.23364486	18	0.051982556
9871	GO:0016831	carboxy-lyase activit	**0.03**	9	0.7009346	115	0.3321108
25998	GO:0051716	cellular response to s	**0.03**	55	4.283489	1138	3.2864528
6424	GO:0009055|GO:000	electron carrier activ	**0.03**	11	0.8566978	154	0.44473964
3265	GO:0004630	phospholipase D act	**0.03**	4	0.31152648	32	0.09241343
3785	GO:0005315|GO:000	inorganic phosphate	**0.03**	4	0.31152648	32	0.09241343
19758	GO:0043492	ATPase activity, cou	**0.03**	15	1.1682243	235	0.67866117
3827	GO:0005372	water transmembran	**0.03**	7	0.5451713	81	0.23392151
4927	GO:0006833	water transport	**0.03**	7	0.5451713	81	0.23392151
8652	GO:0015250	water channel activit	**0.03**	7	0.5451713	81	0.23392151
18429	GO:0042044	fluid transport	**0.03**	7	0.5451713	81	0.23392151
9800	GO:0016746	transferase activity, t	**0.03**	27	2.1028037	498	1.438184
3051	GO:0004367	glycerol-3-phosphate	**0.03**	2	0.15576324	8	0.023103358
5698	GO:0008142	oxysterol binding	**0.03**	2	0.15576324	8	0.023103358
6684	GO:0009331	glycerol-3-phosphate	**0.03**	2	0.15576324	8	0.023103358
15335	GO:0032934|GO:000	sterol binding	**0.03**	2	0.15576324	8	0.023103358
18639	GO:0042284	sphingolipid delta-4	**0.03**	2	0.15576324	8	0.023103358
4755	GO:0006629	lipid metabolic proce	**0.03**	31	2.4143302	590	1.7038727
6750	GO:0009415	response to water	**0.03**	5	0.3894081	49	0.14150807
11221	GO:0019219	regulation of nucleob	**0.03**	117	9.112149	2675	7.7251854
25468	GO:0051171	regulation of nitrogen	**0.03**	117	9.112149	2675	7.7251854
12533	GO:0022838	substrate-specific ch	**0.04**	14	1.0903426	221	0.63823026
21046	GO:0045437	uridine nucleosidase	**0.04**	1	0.07788162	1	0.00288792
24582	GO:0050263	ribosylpyrimidine nuc	**0.04**	1	0.07788162	1	0.00288792
31465	GO:0080090	regulation of primary	**0.04**	118	9.190031	2710	7.826263
9836	GO:0016787	hydrolase activity	**0.04**	158	12.305296	3723	10.751725
23199	GO:0047714	galactolipase activity	**0.04**	4	0.31152648	35	0.10107719
7213	GO:0009966|GO:001	regulation of signal t	**0.04**	5	0.3894081	51	0.14728391
12601	GO:0023051	regulation of signalin	**0.04**	5	0.3894081	51	0.14728391
4530	GO:0006355|GO:001	regulation of transcri	**0.04**	113	8.800623	2591	7.4826
25544	GO:0051252	regulation of RNA me	**0.04**	113	8.800623	2593	7.488376
23518	GO:0048040	UDP-glucuronate de	**0.04**	3	0.23364486	21	0.060646318
13753	GO:0031323	regulation of cellular	**0.04**	120	9.345795	2770	7.999538
3734	GO:0005227	calcium activated ca	**0.04**	2	0.15576324	9	0.025991278
8661	GO:0015269	calcium-activated po	**0.04**	2	0.15576324	9	0.025991278
12534	GO:0022839	ion gated channel ac	**0.04**	2	0.15576324	9	0.025991278
19254	GO:0042937	tripeptide transporter	**0.04**	2	0.15576324	9	0.025991278
20517	GO:0044267	cellular protein meta	**0.04**	138	10.7476635	3225	9.313541
4915	GO:0006817	phosphate transport	**0.04**	5	0.3894081	52	0.15017183
8528	GO:0015114	phosphate transmem	**0.04**	5	0.3894081	52	0.15017183
17801	GO:0035435	phosphate transmem	**0.04**	5	0.3894081	52	0.15017183
8660	GO:0015267|GO:001	channel activity	**0.04**	14	1.0903426	226	0.6526699
12515	GO:0022803	passive transmembra	**0.04**	14	1.0903426	226	0.6526699
23522	GO:0048046	apoplast	**0.05**	6	0.46728972	70	0.20215438
7141	GO:0009889	regulation of biosynt	**0.05**	113	8.800623	2605	7.523031
7772	GO:0010556	regulation of macron	**0.05**	113	8.800623	2605	7.523031
13756	GO:0031326	regulation of cellular	**0.05**	113	8.800623	2605	7.523031
32213	GO:2000112	regulation of cellular	**0.05**	113	8.800623	2605	7.523031
2626	GO:0003674|GO:000	molecular_function	**0.05**	932	72.58567	24394	70.447914
8489	GO:0015066	alpha-amylase inhibi	**0.05**	3	0.23364486	22	0.06353424
11224	GO:0019222	regulation of metabo	**0.05**	133	10.358255	3115	8.995871
5716	GO:0008172	S-methyltransferase	**0.05**	2	0.15576324	10	0.0288792
6632	GO:0009269	response to desiccat	**0.05**	2	0.15576324	10	0.0288792
9826	GO:0016775	phosphotransferase	**0.05**	2	0.15576324	10	0.0288792
18956	GO:0042626	ATPase activity, cou	**0.05**	13	1.0124611	211	0.6093511
12644	GO:0030054	cell junction	**0.05**	3	0.23364486	23	0.06642216
22414	GO:0046912	transferase activity, t	**0.05**	3	0.23364486	23	0.06642216
9861	GO:0016820	hydrolase activity, ac	**0.05**	13	1.0124611	212	0.612239
8494	GO:0015075	ion transmembrane t	**0.05**	40	3.115265	827	2.3883097
9801	GO:0016747	transferase activity, t	0.06	24	1.8691589	456	1.3168914
9779	GO:0016717	oxidoreductase activ	0.06	3	0.23364486	24	0.06931008
27228	GO:0060255	regulation of macron	0.06	114	8.878505	2660	7.6818666

2897	GO:0004091|GO:000	carboxylesterase act	0.06	12	0.93457943	194	0.5602564
7692	GO:0010468	regulation of gene ex	0.06	113	8.800623	2635	7.6096687
12574	GO:0022892	substrate-specific tra	0.06	66	5.140187	1463	4.2250266
16603	GO:0034220	ion transmembrane t	0.06	40	3.115265	833	2.4056373
23973	GO:0048583	regulation of respons	0.06	5	0.3894081	57	0.16461143
2989	GO:0004301	epoxide hydrolase ac	0.06	2	0.15576324	11	0.03176712
4250	GO:0006012	galactose metabolic	0.06	2	0.15576324	11	0.03176712
9849	GO:0016803	ether hydrolase activ	0.06	2	0.15576324	11	0.03176712
19256	GO:0042939	tripeptide transport	0.06	2	0.15576324	11	0.03176712
8517	GO:0015103	inorganic anion trans	0.06	10	0.7788162	154	0.44473964
8749	GO:0015399	primary active transn	0.06	15	1.1682243	260	0.75085914
8753	GO:0015405	P-P-bond-hydrolysis-	0.06	15	1.1682243	260	0.75085914
22478	GO:0046982	protein heterodimeriz	0.06	8	0.62305295	114	0.32922286
8558	GO:0015145	monosaccharide tran	0.06	5	0.3894081	58	0.16749935
9018	GO:0015749	monosaccharide tran	0.06	5	0.3894081	58	0.16749935
8967	GO:0015698	inorganic anion trans	0.06	11	0.8566978	176	0.5082739
2831	GO:0004022	alcohol dehydrogena	0.07	5	0.3894081	59	0.17038727
9909	GO:0016877	ligase activity, formin	0.07	6	0.46728972	78	0.22525774
7000	GO:0009734	auxin mediated signa	0.07	3	0.23364486	26	0.075085916
7540	GO:0010315	auxin efflux	0.07	3	0.23364486	26	0.075085916
7553	GO:0010329	auxin efflux transmen	0.07	3	0.23364486	26	0.075085916
29729	GO:0071365	cellular response to a	0.07	3	0.23364486	26	0.075085916
3864	GO:0005496	steroid binding	0.07	2	0.15576324	12	0.03465504
6946	GO:0009678	hydrogen-translocati	0.07	2	0.15576324	12	0.03465504
7526	GO:0010301|GO:003	xanthoxin dehydroge	0.07	2	0.15576324	12	0.03465504
9699	GO:0016616	oxidoreductase activ	0.07	15	1.1682243	266	0.7681867
2804	GO:0003988	acetyl-CoA C-acyltra	0.07	1	0.07788162	2	0.00577584
2951	GO:0004149	dihydrolipoyllysine-re	0.07	1	0.07788162	2	0.00577584
2990	GO:0004303	estradiol 17-beta-del	0.07	1	0.07788162	2	0.00577584
3148	GO:0004489|GO:000	methylenetetrahydro	0.07	1	0.07788162	2	0.00577584
4699	GO:0006570	tyrosine metabolic pr	0.07	1	0.07788162	2	0.00577584
4700	GO:0006571	tyrosine biosynthetic	0.07	1	0.07788162	2	0.00577584
5941	GO:0008455	alpha-1,6-mannosylg	0.07	1	0.07788162	2	0.00577584
6593	GO:0009229	thiamine diphosphate	0.07	1	0.07788162	2	0.00577584
9190	GO:0015930	glutamate synthase a	0.07	1	0.07788162	2	0.00577584
9282	GO:0016040	glutamate synthase (	0.07	1	0.07788162	2	0.00577584
9419	GO:0016206	catechol O-methyltra	0.07	1	0.07788162	2	0.00577584
9686	GO:0016602	CCAAT-binding facto	0.07	1	0.07788162	2	0.00577584
9802	GO:0016748	succinyltransferase a	0.07	1	0.07788162	2	0.00577584
9805	GO:0016751	S-succinyltransferase	0.07	1	0.07788162	2	0.00577584
15586	GO:0033187	inositol hexakisphos	0.07	1	0.07788162	2	0.00577584
18706	GO:0042357	thiamine diphosphate	0.07	1	0.07788162	2	0.00577584
20817	GO:0045181	glutamate synthase a	0.07	1	0.07788162	2	0.00577584
22759	GO:0047268	galactinol-raffinose g	0.07	1	0.07788162	2	0.00577584
168	GO:0000221	vacuolar proton-trans	0.07	1	0.07788162	2	0.00577584
535	GO:0000826	inositol pyrophospha	0.07	1	0.07788162	2	0.00577584
537	GO:0000828	inositol hexakisphos	0.07	1	0.07788162	2	0.00577584
2699	GO:0003849	3-deoxy-7-phosphoh	0.07	1	0.07788162	2	0.00577584
9837	GO:0016788	hydrolase activity, ac	0.07	68	5.29595	1534	4.430069
8526	GO:0015112	nitrate transmembrar	0.08	5	0.3894081	61	0.1761631
8975	GO:0015706|GO:000	nitrate transport	0.08	5	0.3894081	61	0.1761631
12573	GO:0022891	substrate-specific tra	0.08	56	4.3613706	1241	3.5839086
8919	GO:0015645	fatty acid ligase activ	0.08	3	0.23364486	27	0.077973835
9541	GO:0016413	O-acetyltransferase a	0.08	3	0.23364486	27	0.077973835
22049	GO:0046527	glucosyltransferase a	0.08	15	1.1682243	270	0.77973837
3002	GO:0004315	3-oxoacyl-[acyl-carri	0.08	2	0.15576324	13	0.037542958
7551	GO:0010327	acetyl CoA:(Z)-3-hex	0.08	2	0.15576324	13	0.037542958
8863	GO:0015562	efflux transmembran	0.08	3	0.23364486	28	0.080861755
14726	GO:0032318	regulation of Ras GT	0.08	4	0.31152648	45	0.1299564
22096	GO:0046578	regulation of Ras pro	0.08	4	0.31152648	45	0.1299564
25355	GO:0051056	regulation of small G	0.08	4	0.31152648	45	0.1299564
11931	GO:0020037	heme binding	0.09	27	2.1028037	550	1.5883559
12692	GO:0030117	membrane coat	0.09	6	0.46728972	84	0.24258527
23870	GO:0048475	coated membrane	0.09	6	0.46728972	84	0.24258527
3641	GO:0005099	Ras GTPase activato	0.09	2	0.15576324	14	0.040430877
9720	GO:0016639	oxidoreductase activ	0.09	2	0.15576324	14	0.040430877
14728	GO:0032320	positive regulation of	0.09	2	0.15576324	14	0.040430877
19253	GO:0042936	dipeptide transporter	0.10	7	0.5451713	105	0.3032316
19255	GO:0042938	dipeptide transport	0.10	7	0.5451713	105	0.3032316
3009	GO:0004322	ferroxidase activity	0.10	3	0.23364486	30	0.086637594
8683	GO:0015301|GO:001	anion:anion antiporte	0.10	3	0.23364486	30	0.086637594
9785	GO:0016724	oxidoreductase activ	0.10	3	0.23364486	30	0.086637594
5809	GO:0008289	lipid binding	0.10	14	1.0903426	258	0.74508333
3341	GO:0004722|GO:000	protein serine/threon	0.10	10	0.7788162	171	0.4938343
18912	GO:0042578	phosphoric ester hyd	0.10	22	1.7133956	444	1.2822365
25516	GO:0051219	phosphoprotein bindi	0.10	2	0.15576324	15	0.043318797
18582	GO:0042221	response to chemica	0.11	17	1.3239875	328	0.94723773
3872	GO:0005506	iron ion binding	0.11	27	2.1028037	563	1.6258988
19590	GO:0043295	glutathione binding	0.11	3	0.23364486	31	0.08952551
9600	GO:0016491	oxidoreductase activ	0.11	74	5.76324	1724	4.9787736
3134	GO:0004474	malate synthase acti	0.11	1	0.07788162	3	0.00866376
3252	GO:0004612	phosphoenolpyruvate	0.11	1	0.07788162	3	0.00866376
4319	GO:0006081	cellular aldehyde me	0.11	1	0.07788162	3	0.00866376
4330	GO:0006097	glyoxylate cycle	0.11	1	0.07788162	3	0.00866376
4376	GO:0006166	purine ribonucleoside	0.11	1	0.07788162	3	0.00866376
9478	GO:0016286	small conductance c	0.11	1	0.07788162	3	0.00866376
13651	GO:0031219	levanase activity	0.11	1	0.07788162	3	0.00866376
19408	GO:0043101	purine-containing co	0.11	1	0.07788162	3	0.00866376
19477	GO:0043174	nucleoside salvage	0.11	1	0.07788162	3	0.00866376
21936	GO:0046409	p-coumarate 3-hydro	0.11	1	0.07788162	3	0.00866376
22011	GO:0046487	glyoxylate metabolic	0.11	1	0.07788162	3	0.00866376

11522	GO:0019538|GO:000	protein metabolic pro	0.11	168	13.084112	4134	11.938661
9267	GO:0016021	integral to membrane	0.11	49	3.8161993	1103	3.1853757
5096	GO:0007047	cellular cell wall orga	0.11	4	0.31152648	50	0.14439599
6932	GO:0009664	plant-type cell wall o	0.11	4	0.31152648	50	0.14439599
20857	GO:0045229	external encapsulatir	0.11	4	0.31152648	50	0.14439599
30033	GO:0071669	plant-type cell wall o	0.11	4	0.31152648	50	0.14439599
20488	GO:0044238	primary metabolic pr	0.12	359	27.959501	9167	26.47356
12516	GO:0022804	active transmembran	0.12	36	2.8037384	787	2.2727928
4910	GO:0006811	ion transport	0.12	43	3.3489096	959	2.769515
3072	GO:0004396	hexokinase activity	0.12	2	0.15576324	16	0.046206716
3334	GO:0004713|GO:000	protein tyrosine kinas	0.12	2	0.15576324	16	0.046206716
15688	GO:0033293	monocarboxylic acid	0.12	2	0.15576324	16	0.046206716
22412	GO:0046910	pectinesterase inhibi	0.12	2	0.15576324	16	0.046206716
2982	GO:0004197	cysteine-type endope	0.12	6	0.46728972	90	0.2599128
7173	GO:0009922	fatty acid elongase a	0.12	4	0.31152648	51	0.14728391
3340	GO:0004721	phosphoprotein phos	0.12	11	0.8566978	199	0.57469606
2809	GO:0003993	acid phosphatase ac	0.13	4	0.31152648	52	0.15017183
9923	GO:0016892	endoribonuclease ac	0.13	2	0.15576324	17	0.049094636
9925	GO:0016894	endonuclease activit	0.13	2	0.15576324	17	0.049094636
16281	GO:0033897	ribonuclease T2 activ	0.13	2	0.15576324	17	0.049094636
6072	GO:0008645	hexose transport	0.13	3	0.23364486	34	0.09818927
8562	GO:0015149	hexose transmembra	0.13	3	0.23364486	34	0.09818927
17794	GO:0035428	hexose transmembra	0.13	3	0.23364486	34	0.09818927
9697	GO:0016614	oxidoreductase activ	0.13	15	1.1682243	293	0.84616053
29246	GO:0070882	cellular cell wall orga	0.13	4	0.31152648	53	0.15305975
6355	GO:0008970	phospholipase A1 ac	0.14	3	0.23364486	35	0.10107719
5702	GO:0008146	sulfotransferase activ	0.14	4	0.31152648	54	0.15594767
2872	GO:0004066	asparagine synthase	0.14	1	0.07788162	4	0.011551679
2900	GO:0004096|GO:001	catalase activity	0.14	1	0.07788162	4	0.011551679
2967	GO:0004165|GO:000	dodecenoyl-CoA delt	0.14	1	0.07788162	4	0.011551679
3093	GO:0004421	hydroxymethylglutary	0.14	1	0.07788162	4	0.011551679
3119	GO:0004457	lactate dehydrogena	0.14	1	0.07788162	4	0.011551679
3121	GO:0004459	L-lactate dehydroger	0.14	1	0.07788162	4	0.011551679
3291	GO:0004657	proline dehydrogena	0.14	1	0.07788162	4	0.011551679
3399	GO:0004788	thiamine diphosphok	0.14	1	0.07788162	4	0.011551679
3406	GO:0004795	threonine synthase a	0.14	1	0.07788162	4	0.011551679
3456	GO:0004849	uridine kinase activit	0.14	1	0.07788162	4	0.011551679
3639	GO:0005097	Rab GTPase activat	0.14	1	0.07788162	4	0.011551679
3661	GO:0005125	cytokine activity	0.14	1	0.07788162	4	0.011551679
3674	GO:0005138	interleukin-6 recepto	0.14	1	0.07788162	4	0.011551679
4328	GO:0006094	gluconeogenesis	0.14	1	0.07788162	4	0.011551679
4428	GO:0006222	UMP biosynthetic pro	0.14	1	0.07788162	4	0.011551679
5934	GO:0008446	GDP-mannose 4,6-d	0.14	1	0.07788162	4	0.011551679
6199	GO:0008792	arginine decarboxyla	0.14	1	0.07788162	4	0.011551679
6494	GO:0009129	pyrimidine nucleosid	0.14	1	0.07788162	4	0.011551679
6495	GO:0009130	pyrimidine nucleosid	0.14	1	0.07788162	4	0.011551679
6537	GO:0009173	pyrimidine ribonucle	0.14	1	0.07788162	4	0.011551679
6538	GO:0009174	pyrimidine ribonucle	0.14	1	0.07788162	4	0.011551679
7083	GO:0009824	AMP dimethylallyltra	0.14	1	0.07788162	4	0.011551679
7511	GO:0010285|GO:004	L,L-diaminopimelate	0.14	1	0.07788162	4	0.011551679
8637	GO:0015231	5-formyltetrahydrofol	0.14	1	0.07788162	4	0.011551679
8877	GO:0015578|GO:001	mannose transmemb	0.14	1	0.07788162	4	0.011551679
9030	GO:0015761	mannose transport	0.14	1	0.07788162	4	0.011551679
9147	GO:0015885	5-formyltetrahydrofol	0.14	1	0.07788162	4	0.011551679
9485	GO:0016297|GO:001	acyl-[acyl-carrier-pro	0.14	1	0.07788162	4	0.011551679
11312	GO:0019319	hexose biosynthetic	0.14	1	0.07788162	4	0.011551679
14721	GO:0032313	regulation of Rab GT	0.14	1	0.07788162	4	0.011551679
14891	GO:0032483	regulation of Rab pro	0.14	1	0.07788162	4	0.011551679
15252	GO:0032851	positive regulation of	0.14	1	0.07788162	4	0.011551679
21615	GO:0046049	UMP metabolic proc	0.14	1	0.07788162	4	0.011551679
22893	GO:0047405	pyrimidine-5'-nucleot	0.14	1	0.07788162	4	0.011551679
24433	GO:0050113	inositol oxygenase a	0.14	1	0.07788162	4	0.011551679
24692	GO:0050373	UDP-arabinose 4-ep	0.14	1	0.07788162	4	0.011551679
2753	GO:0003919	FMN adenylyltransfe	0.14	1	0.07788162	4	0.011551679
2799	GO:0003983	UTP:glucose-1-phos	0.14	1	0.07788162	4	0.011551679
5776	GO:0008252	nucleotidase activity	0.14	2	0.15576324	18	0.051982556
8213	GO:0012507|GO:003	ER to Golgi transpor	0.14	2	0.15576324	18	0.051982556
10899	GO:0018858	benzoate-CoA ligase	0.14	2	0.15576324	18	0.051982556
12702	GO:0030127	COPII vesicle coat	0.14	2	0.15576324	18	0.051982556
12708	GO:0030133	transport vesicle	0.14	2	0.15576324	18	0.051982556
12709	GO:0030134|GO:003	ER to Golgi transpor	0.14	2	0.15576324	18	0.051982556
13129	GO:0030658	transport vesicle me	0.14	2	0.15576324	18	0.051982556
9869	GO:0016829	lyase activity	0.14	23	1.7912773	488	1.4093049
9870	GO:0016830	carbon-carbon lyase	0.15	9	0.7009346	161	0.4649551
8607	GO:0015197|GO:001	peptide transporter a	0.15	8	0.62305295	139	0.40142086
8608	GO:0015198	oligopeptide transpo	0.15	8	0.62305295	139	0.40142086
4232	GO:0005992	trehalose biosyntheti	0.15	3	0.23364486	36	0.10396511
25416	GO:0051119	sugar transmembran	0.15	7	0.5451713	118	0.34077454
4944	GO:0006857	oligopeptide transpo	0.15	8	0.62305295	141	0.4071967
9099	GO:0015833	peptide transport	0.15	8	0.62305295	141	0.4071967
3290	GO:0004656	procollagen-proline 4	0.16	2	0.15576324	19	0.054870475
8212	GO:0012506	vesicle membrane	0.16	2	0.15576324	19	0.054870475
11752	GO:0019798	procollagen-proline d	0.16	2	0.15576324	19	0.054870475
12695	GO:0030120	vesicle coat	0.16	2	0.15576324	19	0.054870475
12710	GO:0030135|GO:000	coated vesicle	0.16	2	0.15576324	19	0.054870475
13130	GO:0030659	cytoplasmic vesicle r	0.16	2	0.15576324	19	0.054870475
13133	GO:0030662	coated vesicle memb	0.16	2	0.15576324	19	0.054870475
13966	GO:0031543	peptidyl-proline diox	0.16	2	0.15576324	19	0.054870475
13968	GO:0031545	peptidyl-proline 4-dic	0.16	2	0.15576324	19	0.054870475
13829	GO:0031406	carboxylic acid bindi	0.16	6	0.46728972	98	0.28301615
3758	GO:0005267	potassium channel a	0.16	3	0.23364486	37	0.10685303

8557	GO:0015144	carbohydrate transm	0.16	8	0.62305295	143	0.41297254
16602	GO:0034219	carbohydrate transm	0.16	8	0.62305295	143	0.41297254
9767	GO:0016705	oxidoreductase activ	0.17	16	1.2461059	329	0.95012563
4231	GO:0005991	trehalose metabolic	0.17	3	0.23364486	38	0.10974095
8501	GO:0015085	calcium ion transmer	0.17	3	0.23364486	38	0.10974095
22409	GO:0046906	tetrapyrrole binding	0.17	27	2.1028037	596	1.7212002
29919	GO:0071555	cell wall organization	0.17	4	0.31152648	58	0.16749935
12532	GO:0022836	gated channel activit	0.17	7	0.5451713	122	0.3523262
3328	GO:0004707|GO:000	MAP kinase activity	0.17	2	0.15576324	20	0.0577584
3798	GO:0005337	nucleoside transmem	0.17	2	0.15576324	20	0.0577584
8726	GO:0015368	calcium:cation antipo	0.17	2	0.15576324	20	0.0577584
9122	GO:0015858	nucleoside transport	0.17	2	0.15576324	20	0.0577584
25477	GO:0051180	vitamin transport	0.17	2	0.15576324	20	0.0577584
25480	GO:0051183	vitamin transporter a	0.17	2	0.15576324	20	0.0577584
3035	GO:0004351	glutamate decarboxy	0.17	1	0.07788162	5	0.0144396
3314	GO:0004689|GO:000	phosphorylase kinas	0.17	1	0.07788162	5	0.0144396
5989	GO:0008517	folic acid transporter	0.17	1	0.07788162	5	0.0144396
9146	GO:0015884	folic acid transport	0.17	1	0.07788162	5	0.0144396
22765	GO:0047274	galactinol-sucrose ga	0.17	1	0.07788162	5	0.0144396
31506	GO:0080131	hydroxyjasmonate su	0.17	1	0.07788162	5	0.0144396
6071	GO:0008643|GO:000	carbohydrate transpo	0.18	8	0.62305295	147	0.42452422
8673	GO:0015291|GO:001	secondary active tra	0.18	19	1.4797508	407	1.1753833
3129	GO:0004467	long-chain fatty acid-	0.18	2	0.15576324	21	0.060646318
9268	GO:0016023	cytoplasmic membra	0.18	2	0.15576324	21	0.060646318
14399	GO:0031988	membrane-bounded	0.18	2	0.15576324	21	0.060646318
9839	GO:0016791|GO:001	phosphatase activity	0.18	18	1.4018692	383	1.1060733
5652	GO:0008081|GO:000	phosphoric diester h	0.18	4	0.31152648	60	0.17327519
7021	GO:0009755	hormone-mediated s	0.18	3	0.23364486	40	0.1155168
15271	GO:0032870	cellular response to	0.18	3	0.23364486	40	0.1155168
3156	GO:0004497	monooxygenase acti	0.19	9	0.7009346	172	0.49672222
24858	GO:0050551	myrcene synthase ac	0.20	2	0.15576324	22	0.06353424
25195	GO:0050896|GO:005	response to stimulus	0.20	77	5.996885	1881	5.432177
17457	GO:0035091	phosphatidylinositol	0.20	4	0.31152648	62	0.17905103
20619	GO:0044425	membrane part	0.20	63	4.906542	1523	4.398302
4912	GO:0006813|GO:001	potassium ion transp	0.20	5	0.3894081	84	0.24258527
30168	GO:0071804	cellular potassium io	0.20	5	0.3894081	84	0.24258527
30169	GO:0071805	potassium ion transn	0.20	5	0.3894081	84	0.24258527
2906	GO:0004103	choline kinase activit	0.20	1	0.07788162	6	0.01732752
3131	GO:0004470	malic enzyme activity	0.20	1	0.07788162	6	0.01732752
3133	GO:0004473	malate dehydrogena	0.20	1	0.07788162	6	0.01732752
3208	GO:0004563	beta-N-acetylhexosa	0.20	1	0.07788162	6	0.01732752
3269	GO:0004634	phosphopyruvate hy	0.20	1	0.07788162	6	0.01732752
3342	GO:0004723|GO:000	calcium-dependent p	0.20	1	0.07788162	6	0.01732752
3413	GO:0004802	transketolase activity	0.20	1	0.07788162	6	0.01732752
3467	GO:0004860	protein kinase inhibit	0.20	1	0.07788162	6	0.01732752
3642	GO:0005100	Rho GTPase activate	0.20	1	0.07788162	6	0.01732752
3845	GO:0005452	inorganic anion exch	0.20	1	0.07788162	6	0.01732752
4059	GO:0005774	vacuolar membrane	0.20	1	0.07788162	6	0.01732752
4264	GO:0006026	aminoglycan catabol	0.20	1	0.07788162	6	0.01732752
4268	GO:0006030	chitin metabolic proc	0.20	1	0.07788162	6	0.01732752
4270	GO:0006032	chitin catabolic proce	0.20	1	0.07788162	6	0.01732752
4657	GO:0006528	asparagine metaboli	0.20	1	0.07788162	6	0.01732752
4658	GO:0006529	asparagine biosynth	0.20	1	0.07788162	6	0.01732752
4953	GO:0006868|GO:001	glutamine transport	0.20	1	0.07788162	6	0.01732752
5713	GO:0008169	C-methyltransferase	0.20	1	0.07788162	6	0.01732752
6000	GO:0008531	riboflavin kinase acti	0.20	1	0.07788162	6	0.01732752
6344	GO:0008959	phosphate acetyltran	0.20	1	0.07788162	6	0.01732752
7651	GO:0010427	abscisic acid binding	0.20	1	0.07788162	6	0.01732752
8505	GO:0015089	high affinity copper i	0.20	1	0.07788162	6	0.01732752
8596	GO:0015186	L-glutamine transme	0.20	1	0.07788162	6	0.01732752
9435	GO:0016231	beta-N-acetylglucosa	0.20	1	0.07788162	6	0.01732752
9584	GO:0016471	vacuolar proton-trans	0.20	1	0.07788162	6	0.01732752
14727	GO:0032319	regulation of Rho GT	0.20	1	0.07788162	6	0.01732752
14729	GO:0032321	positive regulation of	0.20	1	0.07788162	6	0.01732752
17394	GO:0035023	regulation of Rho pro	0.20	1	0.07788162	6	0.01732752
19761	GO:0043495	protein anchor	0.20	1	0.07788162	6	0.01732752
20631	GO:0044437	vacuolar part	0.20	1	0.07788162	6	0.01732752
21727	GO:0046165	alcohol biosynthetic	0.20	1	0.07788162	6	0.01732752
21893	GO:0046364	monosaccharide bios	0.20	1	0.07788162	6	0.01732752
26030	GO:0051748	UTP-monosaccharid	0.20	1	0.07788162	6	0.01732752
5	GO:0000007	low-affinity zinc ion t	0.20	1	0.07788162	6	0.01732752
135	GO:0000170	sphingosine hydroxy	0.20	1	0.07788162	6	0.01732752
2688	GO:0003838	sterol 24-C-methyltra	0.20	1	0.07788162	6	0.01732752
2713	GO:0003863	3-methyl-2-oxobutan	0.20	1	0.07788162	6	0.01732752
3718	GO:0005200	structural constituent	0.20	3	0.23364486	42	0.121292636
6666	GO:0009312	oligosaccharide bios	0.20	3	0.23364486	42	0.121292636
8461	GO:0015020|GO:000	glucuronosyltransfera	0.20	3	0.23364486	42	0.121292636
9370	GO:0016138	glycoside biosynthet	0.20	3	0.23364486	42	0.121292636
21880	GO:0046351	disaccharide biosynt	0.20	3	0.23364486	42	0.121292636
13656	GO:0031224	intrinsic to membran	0.20	50	3.894081	1193	3.4452884
8679	GO:0015297	antiporter activity	0.20	8	0.62305295	152	0.4389638
8682	GO:0015300	solute:solute antipor	0.20	8	0.62305295	152	0.4389638
17016	GO:0034637	cellular carbohydrate	0.21	4	0.31152648	63	0.18193895
3662	GO:0005126	cytokine receptor bin	0.21	2	0.15576324	23	0.06642216
22753	GO:0047262|GO:005	polygalacturonate 4-	0.21	2	0.15576324	23	0.06642216
9293	GO:0016051|GO:000	carbohydrate biosyn	0.21	4	0.31152648	64	0.18482687
4914	GO:0006816	calcium ion transport	0.22	3	0.23364486	44	0.12706847
28952	GO:0070588	calcium ion transmer	0.22	3	0.23364486	44	0.12706847
29859	GO:0071495	cellular response to	0.22	3	0.23364486	44	0.12706847
2821	GO:0004012|GO:000	phospholipid-translo	0.22	2	0.15576324	24	0.06931008
8559	GO:0015146	pentose transmembr	0.22	2	0.15576324	24	0.06931008

8561	GO:0015148	D-xylose transmemb	0.22	2	0.15576324	24	0.06931008
8829	GO:0015519	D-xylose:hydrogen s	0.22	2	0.15576324	24	0.06931008
9019	GO:0015750	pentose transport	0.22	2	0.15576324	24	0.06931008
9022	GO:0015753	D-xylose transport	0.22	2	0.15576324	24	0.06931008
2945	GO:0004143	diacylglycerol kinase	0.23	1	0.07788162	7	0.020215439
4260	GO:0006022	aminoglycan metabo	0.23	1	0.07788162	7	0.020215439
6527	GO:0009163	nucleoside biosynthe	0.23	1	0.07788162	7	0.020215439
18796	GO:0042451	purine nucleoside bi	0.23	1	0.07788162	7	0.020215439
18800	GO:0042455	ribonucleoside biosy	0.23	1	0.07788162	7	0.020215439
19401	GO:0043094	cellular metabolic co	0.23	1	0.07788162	7	0.020215439
21695	GO:0046129	purine ribonucleoside	0.23	1	0.07788162	7	0.020215439
8666	GO:0015276	ligand-gated ion cha	0.23	3	0.23364486	45	0.1299564
12530	GO:0022834	ligand-gated channel	0.23	3	0.23364486	45	0.1299564
31431	GO:0080054	low affinity nitrate tra	0.23	3	0.23364486	45	0.1299564
3888	GO:0005529	sugar binding	0.23	8	0.62305295	158	0.45629135
5070	GO:0007017	microtubule-based p	0.24	6	0.46728972	112	0.32344702
5071	GO:0007018	microtubule-based m	0.24	6	0.46728972	112	0.32344702
9846	GO:0016799	hydrolase activity, hy	0.24	2	0.15576324	25	0.072197996
31493	GO:0080118	brassinosteroid sulfo	0.24	2	0.15576324	25	0.072197996
973	GO:0001653	peptide receptor acti	0.24	2	0.15576324	25	0.072197996
6999	GO:0009733	response to auxin sti	0.24	3	0.23364486	46	0.13284431
20652	GO:0044459	plasma membrane p	0.24	3	0.23364486	46	0.13284431
5909	GO:0008415	acyltransferase activ	0.25	15	1.1682243	330	0.95301354
3415	GO:0004805	trehalose-phosphata	0.25	2	0.15576324	26	0.075085916
17147	GO:0034768	(E)-beta-ocimene sy	0.25	2	0.15576324	26	0.075085916
4773	GO:0006650|GO:000	glycerophospholipid	0.25	3	0.23364486	47	0.13573223
22010	GO:0046486	glycerolipid metaboli	0.25	3	0.23364486	47	0.13573223
31420	GO:0080043	quercetin 3-O-glucos	0.25	4	0.31152648	69	0.19926646
3098	GO:0004427	inorganic diphosphat	0.26	1	0.07788162	8	0.023103358
4778	GO:0006656	phosphatidylcholine	0.26	1	0.07788162	8	0.023103358
4779	GO:0006657	CDP-choline pathwa	0.26	1	0.07788162	8	0.023103358
5753	GO:0008216	spermidine metaboli	0.26	1	0.07788162	8	0.023103358
5815	GO:0008295	spermidine biosynthe	0.26	1	0.07788162	8	0.023103358
6262	GO:0008865	fructokinase activity	0.26	1	0.07788162	8	0.023103358
7779	GO:0010563	negative regulation	0.26	1	0.07788162	8	0.023103358
8725	GO:0015367	oxoglutarate:malate	0.26	1	0.07788162	8	0.023103358
9011	GO:0015742	alpha-ketoglutarate t	0.26	1	0.07788162	8	0.023103358
11209	GO:0019206	nucleoside kinase ac	0.26	1	0.07788162	8	0.023103358
11213	GO:0019210	kinase inhibitor activ	0.26	1	0.07788162	8	0.023103358
12736	GO:0030165	PDZ domain binding	0.26	1	0.07788162	8	0.023103358
13262	GO:0030795|GO:004	jasmonate O-methylt	0.26	1	0.07788162	8	0.023103358
18675	GO:0042326	negative regulation	0.26	1	0.07788162	8	0.023103358
18785	GO:0042439	ethanolamine-contai	0.26	1	0.07788162	8	0.023103358
21504	GO:0045936	negative regulation	0.26	1	0.07788162	8	0.023103358
21995	GO:0046470	phosphatidylcholine	0.26	1	0.07788162	8	0.023103358
22076	GO:0046556	alpha-N-arabinofura	0.26	1	0.07788162	8	0.023103358
22702	GO:0047209	coniferyl-alcohol glu	0.26	1	0.07788162	8	0.023103358
23264	GO:0047782	coniferin beta-glucos	0.26	1	0.07788162	8	0.023103358
28933	GO:0070569	uridylyltransferase a	0.26	1	0.07788162	8	0.023103358
4	GO:0000006	high affinity zinc upta	0.26	1	0.07788162	8	0.023103358
11	GO:0000015	phosphopyruvate hy	0.26	1	0.07788162	8	0.023103358
47	GO:0000062	fatty-acyl-CoA bindin	0.26	1	0.07788162	8	0.023103358
2728	GO:0003878|GO:004	ATP citrate synthase	0.26	1	0.07788162	8	0.023103358
15524	GO:0033124	regulation of GTP ca	0.26	4	0.31152648	70	0.20215438
19394	GO:0043087	regulation of GTPase	0.26	4	0.31152648	70	0.20215438
4188	GO:0005938	cell cortex	0.26	3	0.23364486	48	0.13862015
20642	GO:0044448	cell cortex part	0.26	3	0.23364486	48	0.13862015
113	GO:0000145	exocyst	0.26	3	0.23364486	48	0.13862015
3724	GO:0005216	ion channel activity	0.26	7	0.5451713	140	0.40430877
3895	GO:0005543	phospholipid binding	0.26	7	0.5451713	140	0.40430877
3725	GO:0005217	intracellular ligand-g	0.26	2	0.15576324	27	0.077973835
3808	GO:0005351|GO:000	sugar:hydrogen sym	0.27	5	0.3894081	94	0.27146447
3835	GO:0005402	cation:sugar symport	0.27	5	0.3894081	94	0.27146447
3756	GO:0005261|GO:001	cation channel activi	0.27	3	0.23364486	49	0.14150807
9725	GO:0016645	oxidoreductase activ	0.27	3	0.23364486	49	0.14150807
18633	GO:0042277	peptide binding	0.28	5	0.3894081	95	0.27435237
3744	GO:0005244	voltage-gated ion ch	0.28	4	0.31152648	72	0.20793022
12528	GO:0022832	voltage-gated chann	0.28	4	0.31152648	72	0.20793022
15280	GO:0032879	regulation of localiza	0.28	4	0.31152648	72	0.20793022
17141	GO:0034762	regulation of transme	0.28	4	0.31152648	72	0.20793022
17144	GO:0034765	regulation of ion tran	0.28	4	0.31152648	72	0.20793022
19568	GO:0043269	regulation of ion tran	0.28	4	0.31152648	72	0.20793022
25348	GO:0051049	regulation of transpo	0.28	4	0.31152648	72	0.20793022
3332	GO:0004711	ribosomal protein S6	0.28	2	0.15576324	28	0.080861755
3812	GO:0005355|GO:001	glucose transmembr	0.28	2	0.15576324	28	0.080861755
9027	GO:0015758	glucose transport	0.28	2	0.15576324	28	0.080861755
716	GO:0001071	nucleic acid binding	0.28	57	4.4392524	1417	4.0921826
2643	GO:0003700|GO:000	sequence-specific D	0.28	57	4.4392524	1417	4.0921826
4304	GO:0006066	alcohol metabolic pr	0.28	7	0.5451713	143	0.41297254
7166	GO:0009914	hormone transport	0.28	3	0.23364486	50	0.14439599
9783	GO:0016722	oxidoreductase activ	0.28	3	0.23364486	50	0.14439599
27891	GO:0060918	auxin transport	0.28	3	0.23364486	50	0.14439599
29674	GO:0071310	cellular response to	0.28	3	0.23364486	50	0.14439599
31536	GO:0080161	auxin transmembran	0.28	3	0.23364486	50	0.14439599
2801	GO:0003985	acetyl-CoA C-acetylt	0.29	1	0.07788162	9	0.025991278
3251	GO:0004611	phosphoenolpyruvat	0.29	1	0.07788162	9	0.025991278
3625	GO:0005080	protein kinase C bin	0.29	1	0.07788162	9	0.025991278
3694	GO:0005160	transforming growth	0.29	1	0.07788162	9	0.025991278
4322	GO:0006084	acetyl-CoA metaboli	0.29	1	0.07788162	9	0.025991278
4332	GO:0006099	tricarboxylic acid cy	0.29	1	0.07788162	9	0.025991278
6429	GO:0009060	aerobic respiration	0.29	1	0.07788162	9	0.025991278

6476	GO:0009109	coenzyme catabolic	0.29	1	0.07788162	9	0.025991278
7506	GO:0010279	indole-3-acetic acid a	0.29	1	0.07788162	9	0.025991278
9571	GO:0016453	C-acetyltransferase a	0.29	1	0.07788162	9	0.025991278
11785	GO:0019840	isoprenoid binding	0.29	1	0.07788162	9	0.025991278
13224	GO:0030755	quercetin 3-O-methy	0.29	1	0.07788162	9	0.025991278
15579	GO:0033180	proton-transporting V	0.29	1	0.07788162	9	0.025991278
19342	GO:0043027	caspase inhibitor act	0.29	1	0.07788162	9	0.025991278
19343	GO:0043028	caspase regulator ac	0.29	1	0.07788162	9	0.025991278
19458	GO:0043154|GO:000	negative regulation o	0.29	1	0.07788162	9	0.025991278
19579	GO:0043281|GO:004	regulation of caspase	0.29	1	0.07788162	9	0.025991278
21885	GO:0046356	acetyl-CoA catabolic	0.29	1	0.07788162	9	0.025991278
25484	GO:0051187	cofactor catabolic pr	0.29	1	0.07788162	9	0.025991278
17617	GO:0035251	UDP-glucosyltransfe	0.29	10	0.7788162	218	0.62956655
4427	GO:0006221	pyrimidine nucleotide	0.29	2	0.15576324	29	0.083749674
3311	GO:0004683|GO:000	calmodulin-depende	0.29	4	0.31152648	74	0.21370606
9832	GO:0016782	transferase activity, t	0.29	4	0.31152648	74	0.21370606
8677	GO:0015295	solute:hydrogen sym	0.30	5	0.3894081	98	0.28301615
8810	GO:0015491	cation:cation antiport	0.30	4	0.31152648	75	0.21659398
2666	GO:0003774	motor activity	0.31	2	0.15576324	30	0.086637594
5732	GO:0008194	UDP-glycosyltransfe	0.31	14	1.0903426	322	0.9299102
3024	GO:0004340	glucokinase activity	0.31	1	0.07788162	10	0.0288792
3056	GO:0004372	glycine hydroxymeth	0.31	1	0.07788162	10	0.0288792
3813	GO:0005356|GO:000	hydrogen:glucose sy	0.31	1	0.07788162	10	0.0288792
3815	GO:0005358	high-affinity hydroge	0.31	1	0.07788162	10	0.0288792
3842	GO:0005432	calcium:sodium antip	0.31	1	0.07788162	10	0.0288792
3849	GO:0005459	UDP-galactose trans	0.31	1	0.07788162	10	0.0288792
3871	GO:0005504	fatty acid binding	0.31	1	0.07788162	10	0.0288792
4309	GO:0006071	glycerol metabolic pr	0.31	1	0.07788162	10	0.0288792
4724	GO:0006596	polyamine biosynthe	0.31	1	0.07788162	10	0.0288792
5678	GO:0008113|GO:003	peptide-methionine-(	0.31	1	0.07788162	10	0.0288792
6464	GO:0009095	aromatic amino acid	0.31	1	0.07788162	10	0.0288792
6947	GO:0009679	hexose:hydrogen syr	0.31	1	0.07788162	10	0.0288792
8727	GO:0015369	calcium:hydrogen an	0.31	1	0.07788162	10	0.0288792
9054	GO:0015785	UDP-galactose trans	0.31	1	0.07788162	10	0.0288792
9828	GO:0016778	diphosphotransferase	0.31	1	0.07788162	10	0.0288792
11391	GO:0019400	alditol metabolic pro	0.31	1	0.07788162	10	0.0288792
11715	GO:0019751	polyol metabolic pro	0.31	1	0.07788162	10	0.0288792
13472	GO:0031013	troponin I binding	0.31	1	0.07788162	10	0.0288792
17563	GO:0035197	siRNA binding	0.31	1	0.07788162	10	0.0288792
25453	GO:0051156|GO:000	glucose 6-phosphate	0.31	1	0.07788162	10	0.0288792
26069	GO:0051787	misfolded protein bin	0.31	1	0.07788162	10	0.0288792
26975	GO:0060001	minus-end directed r	0.31	1	0.07788162	10	0.0288792
29215	GO:0070851	growth factor recepto	0.31	1	0.07788162	10	0.0288792
30693	GO:0072334	UDP-galactose trans	0.31	1	0.07788162	10	0.0288792
31441	GO:0080065	4-alpha-methyl-delta	0.31	1	0.07788162	10	0.0288792
114	GO:0000146	microfilament motor	0.31	1	0.07788162	10	0.0288792
196	GO:0000254	C-4 methylsterol oxid	0.31	1	0.07788162	10	0.0288792
9494	GO:0016311	dephosphorylation	0.32	18	1.4018692	425	1.227366
26959	GO:0055114	oxidation-reduction p	0.32	97	7.5545173	2490	7.1909204
9877	GO:0016838	carbon-oxygen lyase	0.32	4	0.31152648	77	0.22236982
14422	GO:0032012	regulation of ARF pro	0.32	2	0.15576324	31	0.08952551
14720	GO:0032312	regulation of ARF GT	0.32	2	0.15576324	31	0.08952551
30884	GO:0072528	pyrimidine-containing	0.32	2	0.15576324	31	0.08952551
30066	GO:0071702	organic substance tra	0.32	22	1.7133956	529	1.5277096
29251	GO:0070887	cellular response to c	0.32	3	0.23364486	54	0.15594767
5874	GO:0008374	O-acyltransferase ac	0.33	5	0.3894081	102	0.29456782
12794	GO:0030234	enzyme regulator act	0.33	17	1.3239875	403	1.1638317
30865	GO:0072509	divalent inorganic ca	0.33	4	0.31152648	78	0.22525774
25095	GO:0050790	regulation of catalytic	0.33	20	1.5576324	480	1.3862015
3717	GO:0005199	structural constituent	0.33	2	0.15576324	32	0.09241343
9533	GO:0016405	CoA-ligase activity	0.33	3	0.23364486	55	0.15883559
5733	GO:0008195|GO:000	phosphatidate phosp	0.34	1	0.07788162	11	0.03176712
11152	GO:0019139|GO:004	cytokinin dehydroger	0.34	1	0.07788162	11	0.03176712
16183	GO:0033799	myricetin 3'-O-methy	0.34	1	0.07788162	11	0.03176712
24696	GO:0050378	UDP-glucuronate 4-e	0.34	1	0.07788162	11	0.03176712
2669	GO:0003785	actin monomer bindi	0.34	1	0.07788162	11	0.03176712
28366	GO:0065009	regulation of molecul	0.34	20	1.5576324	484	1.3977532
4224	GO:0005984	disaccharide metabo	0.34	3	0.23364486	56	0.16172351
9369	GO:0016137	glycoside metabolic	0.34	3	0.23364486	56	0.16172351
4358	GO:0006140	regulation of nucleoti	0.35	4	0.31152648	80	0.2310336
7146	GO:0009894	regulation of catabol	0.35	4	0.31152648	80	0.2310336
9682	GO:0016597	amino acid binding	0.35	4	0.31152648	80	0.2310336
13278	GO:0030811	regulation of nucleoti	0.35	4	0.31152648	80	0.2310336
13759	GO:0031329	regulation of cellular	0.35	4	0.31152648	80	0.2310336
15521	GO:0033121	regulation of purine r	0.35	4	0.31152648	80	0.2310336
19479	GO:0043176	amine binding	0.35	4	0.31152648	80	0.2310336
4705	GO:0006576	cellular biogenic ami	0.35	2	0.15576324	33	0.09530135
9576	GO:0016459	myosin complex	0.35	2	0.15576324	33	0.09530135
8943	GO:0015672	monovalent inorganic	0.35	16	1.2461059	383	1.1060733
6166	GO:0008757	S-adenosylmethionin	0.35	8	0.62305295	180	0.5198256
7557	GO:0010333	terpene synthase act	0.35	3	0.23364486	57	0.16461143
9910	GO:0016878	acid-thiol ligase activ	0.35	3	0.23364486	57	0.16461143
9266	GO:0016020	membrane	0.36	143	11.137072	3741	10.803708
3749	GO:0005249	voltage-gated potass	0.36	2	0.15576324	34	0.09818927
5827	GO:0008308|GO:002	voltage-gated anion	0.36	2	0.15576324	34	0.09818927
6486	GO:0009119	ribonucleoside metal	0.36	2	0.15576324	34	0.09818927
11203	GO:0019200	carbohydrate kinase	0.36	2	0.15576324	34	0.09818927
20321	GO:0044070	regulation of anion tr	0.36	2	0.15576324	34	0.09818927
22341	GO:0046835	carbohydrate phosph	0.36	2	0.15576324	34	0.09818927
29202	GO:0070838	divalent metal ion tra	0.36	4	0.31152648	82	0.23680943
3037	GO:0004353	glutamate dehydroge	0.36	1	0.07788162	12	0.03465504

3386	GO:0004773	steryl-sulfatase activ	0.36	1	0.07788162	12	0.03465504
4506	GO:0006313|GO:000	transposition, DNA-n	0.36	1	0.07788162	12	0.03465504
4786	GO:0006664	glycolipid metabolic	0.36	1	0.07788162	12	0.03465504
5965	GO:0008484	sulfuric ester hydrola	0.36	1	0.07788162	12	0.03465504
6024	GO:0008574	plus-end-directed mi	0.36	1	0.07788162	12	0.03465504
6610	GO:0009247	glycolipid biosyntheti	0.36	1	0.07788162	12	0.03465504
14604	GO:0032196	transposition	0.36	1	0.07788162	12	0.03465504
14674	GO:0032266	phosphatidylinositol-	0.36	1	0.07788162	12	0.03465504
16148	GO:0033764	steroid dehydrogena	0.36	1	0.07788162	12	0.03465504
19047	GO:0042723	thiamine-containing	0.36	1	0.07788162	12	0.03465504
19048	GO:0042724	thiamine-containing	0.36	1	0.07788162	12	0.03465504
20943	GO:0045333	cellular respiration	0.36	1	0.07788162	12	0.03465504
21992	GO:0046467	membrane lipid bios	0.36	1	0.07788162	12	0.03465504
25436	GO:0051139	metal ion:hydrogen a	0.36	1	0.07788162	12	0.03465504
31380	GO:0080002	UDP-glucose:4-amin	0.36	1	0.07788162	12	0.03465504
29	GO:0000036	acyl carrier activity	0.36	1	0.07788162	12	0.03465504
3323	GO:0004702	receptor signaling pr	0.36	3	0.23364486	58	0.16749935
6665	GO:0009311	oligosaccharide meta	0.36	3	0.23364486	58	0.16749935
8028	GO:0010817	regulation of hormon	0.36	3	0.23364486	58	0.16749935
4954	GO:0006869	lipid transport	0.37	9	0.7009346	208	0.6006873
8085	GO:0010876	lipid localization	0.37	9	0.7009346	208	0.6006873
4426	GO:0006220	pyrimidine nucleotide	0.37	2	0.15576324	35	0.10107719
11206	GO:0019203	carbohydrate phosph	0.37	2	0.15576324	35	0.10107719
22012	GO:0046488|GO:003	phosphatidylinositol	0.37	2	0.15576324	35	0.10107719
30700	GO:0072341	modified amino acid	0.37	3	0.23364486	59	0.17038727
3048	GO:0004364	glutathione transfera	0.38	4	0.31152648	84	0.24258527
30867	GO:0072511	divalent inorganic ca	0.38	4	0.31152648	84	0.24258527
9393	GO:0016165	lipoxygenase activity	0.39	2	0.15576324	36	0.10396511
12626	GO:0030029	actin filament-based	0.39	2	0.15576324	36	0.10396511
12633	GO:0030036	actin cytoskeleton or	0.39	2	0.15576324	36	0.10396511
6436	GO:0009067	aspartate family ami	0.39	1	0.07788162	13	0.037542958
8149	GO:0010941	regulation of cell dea	0.39	1	0.07788162	13	0.037542958
8578	GO:0015165	pyrimidine nucleotide	0.39	1	0.07788162	13	0.037542958
9050	GO:0015781	pyrimidine nucleotide	0.39	1	0.07788162	13	0.037542958
18634	GO:0042278	purine nucleoside me	0.39	1	0.07788162	13	0.037542958
19298	GO:0042981	regulation of apoptos	0.39	1	0.07788162	13	0.037542958
19381	GO:0043067|GO:004	regulation of progran	0.39	1	0.07788162	13	0.037542958
20923	GO:0045309	protein phosphorylat	0.39	1	0.07788162	13	0.037542958
21694	GO:0046128	purine ribonucleoside	0.39	1	0.07788162	13	0.037542958
25118	GO:0050815	phosphoserine bindi	0.39	1	0.07788162	13	0.037542958
4768	GO:0006644	phospholipid metabo	0.40	3	0.23364486	61	0.1761631
8680	GO:0015298	solute:cation antiport	0.40	5	0.3894081	112	0.32344702
29918	GO:0071554	cell wall organization	0.40	5	0.3894081	112	0.32344702
4670	GO:0006541	glutamine metabolic	0.41	1	0.07788162	14	0.040430877
4723	GO:0006595	polyamine metabolic	0.41	1	0.07788162	14	0.040430877
5875	GO:0008375	acetylglucosaminyltr	0.41	1	0.07788162	14	0.040430877
8553	GO:0015140	malate transmembra	0.41	1	0.07788162	14	0.040430877
8859	GO:0015556	C4-dicarboxylate tra	0.41	1	0.07788162	14	0.040430877
9009	GO:0015740	C4-dicarboxylate tra	0.41	1	0.07788162	14	0.040430877
9012	GO:0015743	malate transport	0.41	1	0.07788162	14	0.040430877
9399	GO:0016174	NAD(P)H oxidase ac	0.41	1	0.07788162	14	0.040430877
9433	GO:0016229	steroid dehydrogena	0.41	1	0.07788162	14	0.040430877
9711	GO:0016629	12-oxophytodienoate	0.41	1	0.07788162	14	0.040430877
20671	GO:0045017	glycerolipid biosynth	0.41	1	0.07788162	14	0.040430877
20791	GO:0045153	electron transporter,	0.41	1	0.07788162	14	0.040430877
21998	GO:0046474	glycerophospholipid	0.41	1	0.07788162	14	0.040430877
24970	GO:0050664	oxidoreductase activ	0.41	1	0.07788162	14	0.040430877
25040	GO:0050734	hydroxycinnamoyltra	0.41	1	0.07788162	14	0.040430877
29787	GO:0071423	malate transmembra	0.41	1	0.07788162	14	0.040430877
270	GO:0000339	RNA cap binding	0.41	1	0.07788162	14	0.040430877
20624	GO:0044430	cytoskeletal part	0.41	4	0.31152648	88	0.25413695
19533	GO:0043234	protein complex	0.41	33	2.5700934	848	2.448956
5066	GO:0007010	cytoskeleton organiz	0.41	2	0.15576324	38	0.10974095
6749	GO:0009414	response to water de	0.41	2	0.15576324	38	0.10974095
8588	GO:0015175	neutral amino acid tr	0.41	2	0.15576324	38	0.10974095
9073	GO:0015804	neutral amino acid tr	0.41	2	0.15576324	38	0.10974095
12538	GO:0022843	voltage-gated cation	0.41	2	0.15576324	38	0.10974095
9535	GO:0016407	acetyltransferase act	0.42	5	0.3894081	115	0.3321108
8676	GO:0015294	solute:cation sympor	0.42	6	0.46728972	141	0.4071967
30883	GO:0072527	pyrimidine-containing	0.43	2	0.15576324	39	0.11262887
2868	GO:0004062	aryl sulfotransferase	0.43	1	0.07788162	15	0.043318797
7520	GO:0010294	abscisic acid glucosy	0.43	1	0.07788162	15	0.043318797
8635	GO:0015229	L-ascorbic acid trans	0.43	1	0.07788162	15	0.043318797
8740	GO:0015386	potassium:hydrogen	0.43	1	0.07788162	15	0.043318797
9144	GO:0015882	L-ascorbic acid trans	0.43	1	0.07788162	15	0.043318797
9536	GO:0016408	C-acyltransferase ac	0.43	1	0.07788162	15	0.043318797
12523	GO:0022821	potassium ion antipo	0.43	1	0.07788162	15	0.043318797
11616	GO:0019637	organophosphate me	0.44	3	0.23364486	65	0.18771479
20512	GO:0044262|GO:000	cellular carbohydrate	0.44	10	0.7788162	248	0.7162041
11829	GO:0019900	kinase binding	0.44	3	0.23364486	66	0.1906027
3638	GO:0005096	GTPase activator ac	0.45	2	0.15576324	41	0.118404716
19813	GO:0043547	positive regulation of	0.45	2	0.15576324	41	0.118404716
20627	GO:0044433	cytoplasmic vesicle	0.45	2	0.15576324	41	0.118404716
3742	GO:0005242	inward rectifier potas	0.45	1	0.07788162	16	0.046206716
3782	GO:0005310|GO:000	dicarboxylic acid tra	0.45	1	0.07788162	16	0.046206716
4767	GO:0006643	membrane lipid meta	0.45	1	0.07788162	16	0.046206716
4928	GO:0006835|GO:000	dicarboxylic acid tra	0.45	1	0.07788162	16	0.046206716
5691	GO:0008131|GO:000	primary amine oxida	0.45	1	0.07788162	16	0.046206716
5995	GO:0008524	glucose 6-phosphate	0.45	1	0.07788162	16	0.046206716
7521	GO:0010295	(+)-abscisic acid 8'-h	0.45	1	0.07788162	16	0.046206716
8694	GO:0015315	organophosphate:in	0.45	1	0.07788162	16	0.046206716

9189	GO:0015929	hexosaminidase acti	0.45	1	0.07788162	16	0.046206716
9797	GO:0016742	hydroxymethyl-, form	0.45	1	0.07788162	16	0.046206716
9898	GO:0016863	intramolecular oxido	0.45	1	0.07788162	16	0.046206716
18757	GO:0042409	caffeoyl-CoA O-meth	0.45	1	0.07788162	16	0.046206716
18899	GO:0042562	hormone binding	0.45	1	0.07788162	16	0.046206716
31396	GO:0080019	fatty-acyl-CoA reduc	0.45	1	0.07788162	16	0.046206716
2667	GO:0003777	microtubule motor ac	0.45	1	0.07788162	16	0.046206716
22479	GO:0046983	protein dimerization	0.46	20	1.5576324	517	1.4930545
3873	GO:0005507	copper ion binding	0.46	6	0.46728972	146	0.42163628
8675	GO:0015293	symporter activity	0.46	7	0.5451713	173	0.49961013
7229	GO:0009987|GO:000	cellular process	0.46	395	30.76324	10601	30.614838
3753	GO:0005253	anion channel activit	0.46	2	0.15576324	42	0.121292636
5607	GO:0008022	protein C-terminus b	0.46	2	0.15576324	42	0.121292636
3620	GO:0005057	receptor signaling pr	0.47	3	0.23364486	69	0.19926646
4135	GO:0005875	microtubule associat	0.47	1	0.07788162	17	0.049094636
8585	GO:0015172	acidic amino acid tra	0.47	1	0.07788162	17	0.049094636
9069	GO:0015800	acidic amino acid tra	0.47	1	0.07788162	17	0.049094636
30887	GO:0072531	pyrimidine-containin	0.47	1	0.07788162	17	0.049094636
3900	GO:0005548|GO:000	phospholipid transpo	0.48	2	0.15576324	43	0.124180555
9174	GO:0015914	phospholipid transpo	0.48	2	0.15576324	43	0.124180555
13833	GO:0031410	cytoplasmic vesicle	0.48	2	0.15576324	43	0.124180555
14393	GO:0031982	vesicle	0.48	2	0.15576324	43	0.124180555
9579	GO:0016462	pyrophosphatase act	0.48	36	2.8037384	954	2.7550755
9191	GO:0015931	nucleobase, nucleos	0.48	3	0.23364486	70	0.20215438
9192	GO:0015932	nucleobase, nucleos	0.48	3	0.23364486	70	0.20215438
9859	GO:0016818	hydrolase activity, ac	0.49	36	2.8037384	956	2.7608514
9753	GO:0016682	oxidoreductase activ	0.49	2	0.15576324	44	0.12706847
2642	GO:0003697|GO:000	single-stranded DNA	0.49	2	0.15576324	44	0.12706847
3832	GO:0005388	calcium-transporting	0.49	1	0.07788162	18	0.051982556
4134	GO:0005874	microtubule	0.49	1	0.07788162	18	0.051982556
4252	GO:0006014	D-ribose metabolic p	0.49	1	0.07788162	18	0.051982556
8662	GO:0015271	outward rectifier pota	0.49	1	0.07788162	18	0.051982556
9726	GO:0016646	oxidoreductase activ	0.49	1	0.07788162	18	0.051982556
12887	GO:0030332	cyclin binding	0.49	1	0.07788162	18	0.051982556
207	GO:0000272	polysaccharide catab	0.49	1	0.07788162	18	0.051982556
2737	GO:0003887|GO:000	DNA-directed DNA p	0.49	1	0.07788162	18	0.051982556
9858	GO:0016817	hydrolase activity, ac	0.49	36	2.8037384	959	2.769515
8681	GO:0015299	solute:hydrogen anti	0.49	4	0.31152648	98	0.28301615
4236	GO:0005996	monosaccharide me	0.50	5	0.3894081	125	0.36099
9893	GO:0016857	racemase and epime	0.50	2	0.15576324	45	0.1299564
11780	GO:0019829	cation-transporting A	0.50	2	0.15576324	45	0.1299564
9764	GO:0016701	oxidoreductase activ	0.50	3	0.23364486	72	0.20793022
3799	GO:0005338|GO:000	nucleotide-sugar tran	0.51	1	0.07788162	19	0.054870475
5230	GO:0007205	activation of protein	0.51	1	0.07788162	19	0.054870475
6435	GO:0009066	aspartate family ami	0.51	1	0.07788162	19	0.054870475
9049	GO:0015780	nucleotide-sugar tran	0.51	1	0.07788162	19	0.054870475
9490	GO:0016307	phosphatidylinositol	0.51	1	0.07788162	19	0.054870475
9491	GO:0016308|GO:000	1-phosphatidylinosito	0.51	1	0.07788162	19	0.054870475
14556	GO:0032147	activation of protein	0.51	1	0.07788162	19	0.054870475
18750	GO:0042401	cellular biogenic ami	0.51	1	0.07788162	19	0.054870475
2636	GO:0003690	double-stranded DN	0.51	2	0.15576324	46	0.13284431
11311	GO:0019318	hexose metabolic pr	0.52	4	0.31152648	101	0.2916799
9817	GO:0016763	transferase activity, t	0.52	3	0.23364486	74	0.21370606
4916	GO:0006818	hydrogen transport	0.52	11	0.8566978	292	0.84327257
9246	GO:0015992	proton transport	0.52	11	0.8566978	292	0.84327257
12608	GO:0030001	metal ion transport	0.52	14	1.0903426	374	1.080082
6442	GO:0009073|GO:001	aromatic amino acid	0.52	2	0.15576324	47	0.13573223
8497	GO:0015079|GO:002	potassium ion transm	0.52	2	0.15576324	47	0.13573223
21943	GO:0046417	chorismate metaboli	0.52	2	0.15576324	47	0.13573223
25510	GO:0051213	dioxygenase activity	0.53	3	0.23364486	75	0.21659398
3747	GO:0005247	voltage-gated chlori	0.53	1	0.07788162	20	0.0577584
3754	GO:0005254	chloride channel acti	0.53	1	0.07788162	20	0.0577584
6201	GO:0008794	arsenate reductase (	0.53	1	0.07788162	20	0.0577584
9707	GO:0016624	oxidoreductase activ	0.53	1	0.07788162	20	0.0577584
9799	GO:0016744|GO:001	transferase activity, t	0.53	1	0.07788162	20	0.0577584
13086	GO:0030611	arsenate reductase a	0.53	1	0.07788162	20	0.0577584
13088	GO:0030613	oxidoreductase activ	0.53	1	0.07788162	20	0.0577584
13089	GO:0030614	oxidoreductase activ	0.53	1	0.07788162	20	0.0577584
15575	GO:0033176	proton-transporting V	0.53	1	0.07788162	20	0.0577584
16445	GO:0034061	DNA polymerase act	0.53	1	0.07788162	20	0.0577584
22376	GO:0046873	metal ion transmemb	0.54	8	0.62305295	213	0.6151269
3844	GO:0005451	monovalent cation:hy	0.55	2	0.15576324	49	0.14150807
6483	GO:0009116	nucleoside metaboli	0.55	2	0.15576324	49	0.14150807
8909	GO:0015630	microtubule cytoskel	0.55	2	0.15576324	49	0.14150807
31421	GO:0080044	quercetin 7-O-glucos	0.55	2	0.15576324	49	0.14150807
3364	GO:0004745	retinol dehydrogenas	0.55	1	0.07788162	21	0.060646318
3474	GO:0004869|GO:000	cysteine-type endope	0.55	1	0.07788162	21	0.060646318
4420	GO:0006213	pyrimidine nucleosid	0.55	1	0.07788162	21	0.060646318
5878	GO:0008378	galactosyltransferas	0.55	1	0.07788162	21	0.060646318
6582	GO:0009218	pyrimidine ribonucle	0.55	1	0.07788162	21	0.060646318
6584	GO:0009220	pyrimidine ribonucle	0.55	1	0.07788162	21	0.060646318
9698	GO:0016615	malate dehydrogena	0.55	1	0.07788162	21	0.060646318
21697	GO:0046131	pyrimidine ribonucle	0.55	1	0.07788162	21	0.060646318
2668	GO:0003779	actin binding	0.55	4	0.31152648	105	0.3032316
3449	GO:0004842|GO:000	ubiquitin-protein ligas	0.55	12	0.93457943	326	0.94146186
19914	GO:0043648	dicarboxylic acid me	0.56	2	0.15576324	50	0.14439599
3828	GO:0005375|GO:000	copper ion transmem	0.56	1	0.07788162	22	0.06353424
3831	GO:0005385	zinc ion transmembr	0.56	1	0.07788162	22	0.06353424
4920	GO:0006825	copper ion transport	0.56	1	0.07788162	22	0.06353424
4924	GO:0006829	zinc ion transport	0.56	1	0.07788162	22	0.06353424
6521	GO:0009156	ribonucleoside mono	0.56	1	0.07788162	22	0.06353424

6525	GO:0009161	ribonucleoside mono	0.56	1	0.07788162	22	0.06353424
9545	GO:0016417	S-acyltransferase ac	0.56	1	0.07788162	22	0.06353424
17800	GO:0035434	copper ion transmem	0.56	1	0.07788162	22	0.06353424
21152	GO:0045551	cinnamyl-alcohol deh	0.56	1	0.07788162	22	0.06353424
29941	GO:0071577	zinc ion transmembra	0.56	1	0.07788162	22	0.06353424
2691	GO:0003841|GO:000	1-acylglycerol-3-phos	0.56	1	0.07788162	22	0.06353424
5764	GO:0008234|GO:000	cysteine-type peptida	0.56	6	0.46728972	163	0.47073093
3099	GO:0004428	inositol or phosphatid	0.57	2	0.15576324	51	0.14728391
8908	GO:0015629	actin cytoskeleton	0.57	2	0.15576324	51	0.14728391
9654	GO:0016567	protein ubiquitination	0.58	12	0.93457943	332	0.9587894
14854	GO:0032446	protein modification	0.58	12	0.93457943	332	0.9587894
29011	GO:0070647	protein modification	0.58	12	0.93457943	332	0.9587894
11833	GO:0019904	protein domain speci	0.58	4	0.31152648	109	0.31478328
4918	GO:0006821	chloride transport	0.58	1	0.07788162	23	0.06642216
9420	GO:0016207	4-coumarate-CoA lig	0.58	1	0.07788162	23	0.06642216
9806	GO:0016752	sinapoyltransferase a	0.58	1	0.07788162	23	0.06642216
9807	GO:0016753	O-sinapoyltransferas	0.58	1	0.07788162	23	0.06642216
9808	GO:0016754	sinapoylglucose-mal	0.58	1	0.07788162	23	0.06642216
16063	GO:0033674	positive regulation of	0.58	1	0.07788162	23	0.06642216
19815	GO:0043549	regulation of kinase a	0.58	1	0.07788162	23	0.06642216
21437	GO:0045859	regulation of protein	0.58	1	0.07788162	23	0.06642216
21438	GO:0045860	positive regulation of	0.58	1	0.07788162	23	0.06642216
25628	GO:0051338	regulation of transfer	0.58	1	0.07788162	23	0.06642216
25637	GO:0051347	positive regulation of	0.58	1	0.07788162	23	0.06642216
2633	GO:0003684	damaged DNA bindi	0.58	1	0.07788162	23	0.06642216
15189	GO:0032787	monocarboxylic acid	0.58	3	0.23364486	81	0.23392151
18674	GO:0042325	regulation of phosph	0.58	3	0.23364486	81	0.23392151
11776	GO:0019825	oxygen binding	0.58	14	1.0903426	389	1.1234008
9750	GO:0016679	oxidoreductase activ	0.59	2	0.15576324	53	0.15305975
25635	GO:0051345	positive regulation of	0.59	2	0.15576324	53	0.15305975
2661	GO:0003743|GO:000	translation initiation f	0.59	2	0.15576324	53	0.15305975
6991	GO:0009725	response to hormone	0.59	3	0.23364486	82	0.23680943
4526	GO:0006351|GO:000	transcription, DNA-de	0.60	57	4.4392524	1575	4.548474
15176	GO:0032774	RNA biosynthetic pro	0.60	57	4.4392524	1575	4.548474
3262	GO:0004622|GO:004	lysophospholipase a	0.60	1	0.07788162	24	0.06931008
4692	GO:0006563	L-serine metabolic p	0.60	1	0.07788162	24	0.06931008
7144	GO:0009892	negative regulation o	0.60	1	0.07788162	24	0.06931008
12694	GO:0030119	AP-type membrane c	0.60	1	0.07788162	24	0.06931008
12706	GO:0030131	clathrin adaptor com	0.60	1	0.07788162	24	0.06931008
13754	GO:0031324	negative regulation o	0.60	1	0.07788162	24	0.06931008
15390	GO:0032989	cellular component m	0.60	1	0.07788162	24	0.06931008
551	GO:0000902|GO:000	cell morphogenesis	0.60	1	0.07788162	24	0.06931008
11747	GO:0019787|GO:000	small conjugating pro	0.61	12	0.93457943	339	0.9790048
4503	GO:0006310	DNA recombination	0.61	1	0.07788162	25	0.072197996
9482	GO:0016291|GO:000	acyl-CoA thioesteras	0.61	1	0.07788162	25	0.072197996
13822	GO:0031399	regulation of protein	0.61	1	0.07788162	25	0.072197996
21145	GO:0045543	gibberellin 2-beta-dio	0.61	1	0.07788162	25	0.072197996
22357	GO:0046854|GO:004	phosphatidylinositol	0.61	1	0.07788162	25	0.072197996
22459	GO:0046961	proton-transporting A	0.61	1	0.07788162	25	0.072197996
31393	GO:0080016	(-)-E-beta-caryophyll	0.61	1	0.07788162	25	0.072197996
31394	GO:0080017	alpha-humulene synt	0.61	1	0.07788162	25	0.072197996
125	GO:0000159	protein phosphatase	0.61	1	0.07788162	25	0.072197996
1225	GO:0001932	regulation of protein	0.61	1	0.07788162	25	0.072197996
11222	GO:0019220	regulation of phospha	0.61	3	0.23364486	85	0.24547319
25471	GO:0051174	regulation of phosph	0.61	3	0.23364486	85	0.24547319
5840	GO:0008324	cation transmembran	0.62	19	1.4797508	538	1.5537009
6985	GO:0009719	response to endogen	0.62	3	0.23364486	86	0.24836111
3896	GO:0005544	calcium-dependent p	0.63	1	0.07788162	26	0.075085916
4030	GO:0005741	mitochondrial outer m	0.63	1	0.07788162	26	0.075085916
5978	GO:0008506	sucrose:hydrogen sy	0.63	1	0.07788162	26	0.075085916
5987	GO:0008515|GO:001	sucrose transmembr	0.63	1	0.07788162	26	0.075085916
8567	GO:0015154	disaccharide transme	0.63	1	0.07788162	26	0.075085916
9035	GO:0015766	disaccharide transpo	0.63	1	0.07788162	26	0.075085916
9039	GO:0015770	sucrose transport	0.63	1	0.07788162	26	0.075085916
9421	GO:0016208	AMP binding	0.63	1	0.07788162	26	0.075085916
9539	GO:0016411	acylglycerol O-acyltr	0.63	1	0.07788162	26	0.075085916
9744	GO:0016671	oxidoreductase activ	0.63	1	0.07788162	26	0.075085916
9884	GO:0016847|GO:003	1-aminocyclopropane	0.63	1	0.07788162	26	0.075085916
9897	GO:0016862	intramolecular oxidor	0.63	1	0.07788162	26	0.075085916
9899	GO:0016864	intramolecular oxidor	0.63	1	0.07788162	26	0.075085916
10911	GO:0018871	1-aminocyclopropane	0.63	1	0.07788162	26	0.075085916
18579	GO:0042218	1-aminocyclopropane	0.63	1	0.07788162	26	0.075085916
30689	GO:0072330	monocarboxylic acid	0.63	1	0.07788162	26	0.075085916
2665	GO:0003756	protein disulfide isom	0.63	1	0.07788162	26	0.075085916
5715	GO:0008171	O-methyltransferase	0.63	2	0.15576324	57	0.16461143
6441	GO:0009072	aromatic amino acid	0.63	2	0.15576324	57	0.16461143
9768	GO:0016706	oxidoreductase activ	0.63	6	0.46728972	175	0.505386
9796	GO:0016741	transferase activity, t	0.63	9	0.7009346	261	0.7537471
4913	GO:0006814|GO:000	sodium ion transport	0.64	2	0.15576324	58	0.16749935
8499	GO:0015081|GO:002	sodium ion transmem	0.64	2	0.15576324	58	0.16749935
11820	GO:0019887	protein kinase regula	0.64	2	0.15576324	58	0.16749935
18086	GO:0035725	sodium ion transmem	0.64	2	0.15576324	58	0.16749935
29800	GO:0071436	sodium ion export	0.64	2	0.15576324	58	0.16749935
3329	GO:0004708	MAP kinase kinase a	0.64	1	0.07788162	27	0.077973835
3631	GO:0005089	Rho guanyl-nucleotid	0.64	1	0.07788162	27	0.077973835
6433	GO:0009064	glutamine family ami	0.64	1	0.07788162	27	0.077973835
22340	GO:0046834	lipid phosphorylation	0.64	1	0.07788162	27	0.077973835
25481	GO:0051184	cofactor transporter a	0.64	1	0.07788162	27	0.077973835
1029	GO:0001727	lipid kinase activity	0.64	1	0.07788162	27	0.077973835
9719	GO:0016638	oxidoreductase activ	0.65	3	0.23364486	89	0.25702485
19126	GO:0042803	protein homodimeriz	0.65	9	0.7009346	265	0.7652988

2833	GO:0004024	alcohol dehydrogena	0.65	1	0.07788162	28	0.080861755
3284	GO:0004650	polygalacturonase ac	0.65	1	0.07788162	28	0.080861755
6079	GO:0008654	phospholipid biosynt	0.65	1	0.07788162	28	0.080861755
6438	GO:0009069	serine family amino a	0.65	1	0.07788162	28	0.080861755
6940	GO:0009672	auxin:hydrogen symp	0.65	1	0.07788162	28	0.080861755
9238	GO:0015980	energy derivation by	0.65	1	0.07788162	28	0.080861755
9827	GO:0016776	phosphotransferase	0.65	1	0.07788162	28	0.080861755
13144	GO:0030674	protein binding, bridg	0.65	1	0.07788162	28	0.080861755
23911	GO:0048519|GO:004	negative regulation c	0.65	1	0.07788162	28	0.080861755
23915	GO:0048523|GO:005	negative regulation c	0.65	1	0.07788162	28	0.080861755
27064	GO:0060090	binding, bridging	0.65	1	0.07788162	28	0.080861755
20487	GO:0044237	cellular metabolic pro	0.65	298	23.208723	8185	23.637625
20510	GO:0044260|GO:003	cellular macromolecu	0.66	202	15.732087	5577	16.105928
2980	GO:0004185	serine-type carboxyp	0.66	2	0.15576324	60	0.17327519
28375	GO:0070008	serine-type exopepti	0.66	2	0.15576324	60	0.17327519
3644	GO:0005102	receptor binding	0.66	3	0.23364486	91	0.2628007
4849	GO:0006730|GO:001	one-carbon metaboli	0.66	11	0.8566978	325	0.93857396
7558	GO:0010334	sesquiterpene syntha	0.67	1	0.07788162	29	0.083749674
9409	GO:0016192|GO:000	vesicle-mediated tra	0.67	1	0.07788162	29	0.083749674
16785	GO:0034404	nucleobase, nucleos	0.67	3	0.23364486	92	0.26568863
17033	GO:0034654	nucleobase, nucleos	0.67	3	0.23364486	92	0.26568863
2978	GO:0004180	carboxypeptidase ac	0.67	2	0.15576324	62	0.17905103
5213	GO:0007186	G-protein coupled re	0.67	2	0.15576324	62	0.17905103
11210	GO:0019207	kinase regulator acti	0.67	2	0.15576324	62	0.17905103
3310	GO:0004679	AMP-activated prote	0.68	1	0.07788162	30	0.086637594
3518	GO:0004930|GO:000	G-protein coupled re	0.68	1	0.07788162	30	0.086637594
3975	GO:0005667	transcription factor c	0.68	1	0.07788162	30	0.086637594
5916	GO:0008422|GO:001	beta-glucosidase act	0.68	1	0.07788162	30	0.086637594
6488	GO:0009123	nucleoside monopho	0.68	1	0.07788162	30	0.086637594
6489	GO:0009124	nucleoside monopho	0.68	1	0.07788162	30	0.086637594
24247	GO:0048869	cellular development	0.68	1	0.07788162	30	0.086637594
2774	GO:0003950	NAD+ ADP-ribosyltra	0.68	1	0.07788162	30	0.086637594
8495	GO:0015077	monovalent inorgani	0.68	7	0.5451713	214	0.6180149
9818	GO:0016765|GO:001	transferase activity, t	0.69	6	0.46728972	185	0.53426516
5712	GO:0008168|GO:000	methyltransferase ac	0.69	8	0.62305295	244	0.7046524
7222	GO:0009975	cyclase activity	0.69	1	0.07788162	31	0.08952551
25478	GO:0051181	cofactor transport	0.69	1	0.07788162	31	0.08952551
9114	GO:0015849	organic acid transpo	0.69	5	0.3894081	156	0.45051548
22443	GO:0046942	carboxylic acid trans	0.69	5	0.3894081	156	0.45051548
4121	GO:0005856	cytoskeleton	0.69	4	0.31152648	126	0.3638779
12741	GO:0030170	pyridoxal phosphate	0.69	4	0.31152648	126	0.3638779
28643	GO:0070279	vitamin B6 binding	0.69	4	0.31152648	126	0.3638779
22416	GO:0046915	transition metal ion t	0.69	2	0.15576324	64	0.18482687
9913	GO:0016881	acid-amino acid ligas	0.69	13	1.0124611	391	1.1291766
9583	GO:0016469	proton-transporting t	0.70	4	0.31152648	127	0.36676583
3861	GO:0005484|GO:000	SNAP receptor activi	0.70	2	0.15576324	65	0.18771479
9838	GO:0016790	thiolester hydrolase	0.70	2	0.15576324	65	0.18771479
25314	GO:0051015	actin filament binding	0.70	2	0.15576324	65	0.18771479
4757	GO:0006633|GO:000	fatty acid biosyntheti	0.70	1	0.07788162	32	0.09241343
6942	GO:0009674	potassium:sodium sy	0.70	1	0.07788162	32	0.09241343
9041	GO:0015772	oligosaccharide trans	0.70	1	0.07788162	32	0.09241343
12522	GO:0022820	potassium ion sympo	0.70	1	0.07788162	32	0.09241343
12833	GO:0030275	LRR domain binding	0.70	1	0.07788162	32	0.09241343
14381	GO:0031968	organelle outer mem	0.70	1	0.07788162	32	0.09241343
21041	GO:0045431	flavonol synthase ac	0.70	1	0.07788162	32	0.09241343
25836	GO:0051552	flavone metabolic pr	0.70	1	0.07788162	32	0.09241343
25837	GO:0051553	flavone biosynthetic	0.70	1	0.07788162	32	0.09241343
25838	GO:0051554	flavonol metabolic pr	0.70	1	0.07788162	32	0.09241343
25839	GO:0051555	flavonol biosynthetic	0.70	1	0.07788162	32	0.09241343
10058	GO:0017111	nucleoside-triphosph	0.70	30	2.3364487	878	2.5355935
3180	GO:0004521	endoribonuclease ac	0.71	2	0.15576324	66	0.1906027
9765	GO:0016702	oxidoreductase activ	0.71	2	0.15576324	66	0.1906027
9890	GO:0016854	racemase and epime	0.71	2	0.15576324	66	0.1906027
9906	GO:0016874	ligase activity	0.71	20	1.5576324	597	1.7240882
10103	GO:0017171	serine hydrolase acti	0.71	7	0.5451713	220	0.63534236
8496	GO:0015078	hydrogen ion transm	0.71	5	0.3894081	160	0.4620672
4493	GO:0006298|GO:000	mismatch repair	0.71	1	0.07788162	33	0.09530135
30878	GO:0072522	purine-containing co	0.71	1	0.07788162	33	0.09530135
2632	GO:0003682	chromatin binding	0.71	1	0.07788162	33	0.09530135
4320	GO:0006082	organic acid metabo	0.72	12	0.93457943	369	1.0656425
11716	GO:0019752	carboxylic acid meta	0.72	12	0.93457943	369	1.0656425
19707	GO:0043436	oxoacid metabolic pr	0.72	12	0.93457943	369	1.0656425
7271	GO:0010033	response to organic	0.72	3	0.23364486	100	0.28879198
18955	GO:0042625	ATPase activity, cou	0.72	2	0.15576324	68	0.19637854
32	GO:0000041	transition metal ion t	0.72	2	0.15576324	68	0.19637854
6004	GO:0008536	Ran GTPase binding	0.72	1	0.07788162	34	0.09818927
11208	GO:0019205	nucleobase, nucleos	0.72	1	0.07788162	34	0.09818927
11831	GO:0019902	phosphatase binding	0.72	1	0.07788162	34	0.09818927
11832	GO:0019903	protein phosphatase	0.72	1	0.07788162	34	0.09818927
4394	GO:0006184	GTP catabolic proce	0.73	4	0.31152648	132	0.3812054
21605	GO:0046039	GTP metabolic proce	0.73	4	0.31152648	132	0.3812054
2758	GO:0003924	GTPase activity	0.73	4	0.31152648	132	0.3812054
19473	GO:0043170|GO:004	macromolecule meta	0.73	235	18.302181	6553	18.92454
4911	GO:0006812|GO:000	cation transport	0.73	22	1.7133956	662	1.9118029
9480	GO:0016289	CoA hydrolase activi	0.73	1	0.07788162	35	0.10107719
12817	GO:0030258	lipid modification	0.73	1	0.07788162	35	0.10107719
18541	GO:0042180	cellular ketone meta	0.74	12	0.93457943	375	1.0829699
3804	GO:0005345	purine base transme	0.74	1	0.07788162	36	0.10396511
4949	GO:0006863|GO:001	purine base transpo	0.74	1	0.07788162	36	0.10396511
8739	GO:0015385|GO:001	sodium:hydrogen an	0.74	1	0.07788162	36	0.10396511
11314	GO:0019321	pentose metabolic p	0.74	1	0.07788162	36	0.10396511

9771	GO:0016709	oxidoreductase activ	0.75	2	0.15576324	71	0.2050423
19392	GO:0043085	positive regulation of	0.75	3	0.23364486	104	0.30034366
20343	GO:0044093	positive regulation of	0.75	3	0.23364486	104	0.30034366
4408	GO:0006200	ATP catabolic proces	0.75	21	1.635514	641	1.8511566
9918	GO:0016887|GO:000	ATPase activity	0.75	21	1.635514	641	1.8511566
21600	GO:0046034	ATP metabolic proce	0.75	21	1.635514	641	1.8511566
2975	GO:0004175|GO:001	endopeptidase activi	0.75	10	0.7788162	320	0.9241344
8934	GO:0015662	ATPase activity, cou	0.75	1	0.07788162	37	0.10685303
9915	GO:0016884|GO:001	carbon-nitrogen ligas	0.75	1	0.07788162	37	0.10685303
6899	GO:0009628	response to abiotic s	0.76	5	0.3894081	170	0.49094638
9637	GO:0016538|GO:000	cyclin-dependent pro	0.76	1	0.07788162	38	0.10974095
12834	GO:0030276	clathrin binding	0.76	1	0.07788162	38	0.10974095
9874	GO:0016835	carbon-oxygen lyase	0.76	6	0.46728972	202	0.5833598
22375	GO:0046872	metal ion binding	0.76	104	8.099689	2985	8.6204405
6623	GO:0009260	ribonucleotide biosyr	0.77	1	0.07788162	39	0.11262887
6046	GO:0008610	lipid biosynthetic pro	0.77	4	0.31152648	141	0.4071967
4573	GO:0006413|GO:000	translational initiatior	0.78	2	0.15576324	76	0.2194819
19470	GO:0043167	ion binding	0.78	104	8.099689	2997	8.655096
19472	GO:0043169	cation binding	0.78	104	8.099689	2997	8.655096
11828	GO:0019899	enzyme binding	0.78	7	0.5451713	237	0.684437
4058	GO:0005773	vacuole	0.78	1	0.07788162	40	0.1155168
7072	GO:0009813	flavonoid biosyntheti	0.78	1	0.07788162	40	0.1155168
8613	GO:0015205|GO:001	nucleobase transmer	0.78	1	0.07788162	40	0.1155168
9116	GO:0015851	nucleobase transpor	0.78	1	0.07788162	40	0.1155168
11804	GO:0019867	outer membrane	0.78	1	0.07788162	40	0.1155168
18953	GO:0042623	ATPase activity, cou	0.78	17	1.3239875	537	1.550813
5604	GO:0008017	microtubule binding	0.78	2	0.15576324	77	0.22236982
6529	GO:0009165	nucleotide biosynthe	0.78	2	0.15576324	77	0.22236982
3626	GO:0005083	small GTPase regula	0.78	3	0.23364486	111	0.3205591
2986	GO:0004252	serine-type endopep	0.79	4	0.31152648	144	0.41586044
4405	GO:0006195	purine nucleotide cat	0.79	25	1.9470406	773	2.232362
6508	GO:0009143	nucleoside triphosph	0.79	25	1.9470406	773	2.232362
6509	GO:0009144	purine nucleoside tri	0.79	25	1.9470406	773	2.232362
6511	GO:0009146	purine nucleoside tri	0.79	25	1.9470406	773	2.232362
6519	GO:0009154	purine ribonucleotide	0.79	25	1.9470406	773	2.232362
6530	GO:0009166	nucleotide catabolic	0.79	25	1.9470406	773	2.232362
6567	GO:0009203	ribonucleoside tripho	0.79	25	1.9470406	773	2.232362
6569	GO:0009205	purine ribonucleoside	0.79	25	1.9470406	773	2.232362
6571	GO:0009207	purine ribonucleoside	0.79	25	1.9470406	773	2.232362
6624	GO:0009261	ribonucleotide catab	0.79	25	1.9470406	773	2.232362
17034	GO:0034655	nucleobase, nucleos	0.79	25	1.9470406	773	2.232362
17035	GO:0034656	nucleobase, nucleos	0.79	25	1.9470406	773	2.232362
22209	GO:0046700	heterocycle catabolic	0.79	25	1.9470406	773	2.232362
30879	GO:0072523	purine-containing cor	0.79	25	1.9470406	773	2.232362
12572	GO:0022890|GO:001	inorganic cation trans	0.79	10	0.7788162	332	0.9587894
5196	GO:0007166	cell surface receptor	0.79	2	0.15576324	78	0.22525774
19832	GO:0043566	structure-specific DN	0.79	2	0.15576324	78	0.22525774
20520	GO:0044270	cellular nitrogen com	0.79	25	1.9470406	777	2.2439137
4756	GO:0006631	fatty acid metabolic	0.80	1	0.07788162	42	0.121292636
4874	GO:0006767	water-soluble vitami	0.80	1	0.07788162	42	0.121292636
13884	GO:0031461	cullin-RING ubiquitin	0.80	1	0.07788162	42	0.121292636
18713	GO:0042364	water-soluble vitami	0.80	1	0.07788162	42	0.121292636
9911	GO:0016879	ligase activity, formi	0.80	14	1.0903426	456	1.3168914
9875	GO:0016836	hydro-lyase activity	0.80	2	0.15576324	80	0.2310336
5694	GO:0008137	NADH dehydrogenas	0.80	1	0.07788162	43	0.124180555
8589	GO:0015179	L-amino acid transm	0.80	1	0.07788162	43	0.124180555
9076	GO:0015807	L-amino acid transpo	0.80	1	0.07788162	43	0.124180555
14676	GO:0032268	regulation of cellular	0.80	1	0.07788162	43	0.124180555
25538	GO:0051246	regulation of protein	0.80	1	0.07788162	43	0.124180555
6663	GO:0009309	amine biosynthetic p	0.81	5	0.3894081	181	0.5227135
6622	GO:0009259|GO:000	ribonucleotide metab	0.81	26	2.0249221	812	2.344991
11426	GO:0019438	aromatic compound	0.81	4	0.31152648	149	0.43030006
5766	GO:0008236	serine-type peptidas	0.81	6	0.46728972	214	0.6180149
4873	GO:0006766	vitamin metabolic pr	0.81	1	0.07788162	44	0.12706847
6477	GO:0009110	vitamin biosynthetic	0.81	1	0.07788162	44	0.12706847
7071	GO:0009812	flavonoid metabolic	0.81	1	0.07788162	44	0.12706847
9186	GO:0015926	glucosidase activity	0.81	1	0.07788162	44	0.12706847
20522	GO:0044272	sulfur compound bio	0.81	1	0.07788162	44	0.12706847
20505	GO:0044255	cellular lipid metabol	0.82	5	0.3894081	184	0.53137726
2628	GO:0003677	DNA binding	0.82	40	3.115265	1224	3.534814
3630	GO:0005088	Ras guanyl-nucleotid	0.82	1	0.07788162	45	0.1299564
12693	GO:0030118|GO:001	clathrin coat	0.82	1	0.07788162	45	0.1299564
24456	GO:0050136	NADH dehydrogenas	0.82	1	0.07788162	45	0.1299564
3787	GO:0005319	lipid transporter activ	0.82	2	0.15576324	83	0.23969735
6563	GO:0009199	ribonucleoside tripho	0.82	25	1.9470406	790	2.2814567
5661	GO:0008092	cytoskeletal protein b	0.82	7	0.5451713	249	0.719092
6515	GO:0009150	purine ribonucleotide	0.82	25	1.9470406	791	2.2843447
6662	GO:0009308	amine metabolic pro	0.83	9	0.7009346	314	0.9068068
4144	GO:0005886|GO:000	plasma membrane	0.83	3	0.23364486	120	0.34655038
5624	GO:0008047	enzyme activator act	0.83	2	0.15576324	85	0.24547319
6506	GO:0009141	nucleoside triphosph	0.83	25	1.9470406	796	2.2987843
5807	GO:0008287	protein serine/threon	0.83	1	0.07788162	47	0.13573223
20533	GO:0044283	small molecule biosy	0.83	10	0.7788162	347	1.0021082
30877	GO:0072521	purine-containing cor	0.83	26	2.0249221	827	2.3883097
14667	GO:0032259	methylation	0.83	8	0.62305295	285	0.8230572
5768	GO:0008238	exopeptidase activity	0.83	2	0.15576324	86	0.24836111
28930	GO:0070566	adenylyltransferase a	0.84	1	0.07788162	48	0.13862015
4246	GO:0006006	glucose metabolic pr	0.84	2	0.15576324	87	0.25124902
4951	GO:0006865|GO:000	amino acid transport	0.84	3	0.23364486	123	0.35521415
20531	GO:0044281	small molecule meta	0.84	59	4.5950155	1788	5.1636004
11830	GO:0019901	protein kinase bindin	0.84	1	0.07788162	49	0.14150807

19831	GO:0043565	sequence-specific D	0.84	4	0.31152648	159	0.45917925
30306	GO:0071944	cell periphery	0.85	7	0.5451713	259	0.74797124
4216	GO:0005976	polysaccharide meta	0.85	1	0.07788162	50	0.14439599
6921	GO:0009653	anatomical structure	0.85	1	0.07788162	50	0.14439599
9993	GO:0017016	Ras GTPase binding	0.85	1	0.07788162	50	0.14439599
30886	GO:0072530	purine-containing co	0.85	1	0.07788162	50	0.14439599
3876	GO:0005515|GO:004	protein binding	0.85	243	18.925234	6933	20.021948
4373	GO:0006163	purine nucleotide me	0.85	25	1.9470406	810	2.339215
9285	GO:0016043	cellular component o	0.85	7	0.5451713	261	0.7537471
9733	GO:0016655	oxidoreductase activ	0.85	1	0.07788162	51	0.14728391
9975	GO:0016998	cell wall macromolec	0.85	1	0.07788162	51	0.14728391
22410	GO:0046907	intracellular transpor	0.85	1	0.07788162	51	0.14728391
25925	GO:0051641	cellular localization	0.85	1	0.07788162	51	0.14728391
25933	GO:0051649	establishment of loca	0.85	1	0.07788162	51	0.14728391
13531	GO:0031072	heat shock protein bi	0.86	6	0.46728972	230	0.6642216
5693	GO:0008135	translation factor acti	0.86	2	0.15576324	92	0.26568863
5097	GO:0007049	cell cycle	0.86	1	0.07788162	52	0.15017183
6965	GO:0009699	phenylpropanoid bios	0.86	1	0.07788162	52	0.15017183
20287	GO:0044036	cell wall macromolec	0.86	1	0.07788162	52	0.15017183
2778	GO:0003954	NADH dehydrogenas	0.87	1	0.07788162	53	0.15305975
17918	GO:0035556|GO:000	intracellular signal tra	0.87	1	0.07788162	54	0.15594767
30069	GO:0071705	nitrogen compound t	0.87	5	0.3894081	202	0.5833598
15436	GO:0033036	macromolecule local	0.87	11	0.8566978	397	1.1465042
4894	GO:0006790	sulfur compound met	0.88	1	0.07788162	55	0.15883559
6077	GO:0008652	cellular amino acid b	0.88	4	0.31152648	169	0.48805845
20356	GO:0044106	cellular amine metab	0.88	8	0.62305295	303	0.8750397
9883	GO:0016846	carbon-sulfur lyase a	0.88	1	0.07788162	56	0.16172351
13697	GO:0031267	small GTPase bindin	0.88	1	0.07788162	56	0.16172351
15576	GO:0033177	proton-transporting t	0.88	1	0.07788162	56	0.16172351
15577	GO:0033178	proton-transporting t	0.88	1	0.07788162	56	0.16172351
9308	GO:0016070	RNA metabolic proce	0.88	60	4.6728973	1855	5.3570914
9103	GO:0015837	amine transport	0.88	3	0.23364486	135	0.38986918
25379	GO:0051082	unfolded protein bind	0.88	2	0.15576324	98	0.28301615
3801	GO:0005342	organic acid transme	0.88	3	0.23364486	136	0.3927571
22444	GO:0046943	carboxylic acid trans	0.88	3	0.23364486	136	0.3927571
5964	GO:0008483	transaminase activity	0.88	1	0.07788162	57	0.16461143
9821	GO:0016769	transferase activity, t	0.88	1	0.07788162	57	0.16461143
3333	GO:0004712	protein serine/threon	0.89	1	0.07788162	59	0.17038727
9900	GO:0016866	intramolecular transf	0.89	1	0.07788162	59	0.17038727
9295	GO:0016053	organic acid biosynth	0.90	5	0.3894081	211	0.6093511
21058	GO:0045454|GO:003	cell redox homeostas	0.90	5	0.3894081	211	0.6093511
21922	GO:0046394	carboxylic acid biosy	0.90	5	0.3894081	211	0.6093511
6964	GO:0009698	phenylpropanoid me	0.90	1	0.07788162	60	0.17327519
25319	GO:0051020	GTPase binding	0.90	1	0.07788162	60	0.17327519
11787	GO:0019842	vitamin binding	0.90	4	0.31152648	177	0.5111618
4641	GO:0006508	proteolysis	0.90	29	2.258567	965	2.7868426
13164	GO:0030695	GTPase regulator ac	0.90	3	0.23364486	142	0.4100846
28365	GO:0065008	regulation of biologic	0.90	8	0.62305295	316	0.9125827
20639	GO:0044445	cytosolic part	0.90	1	0.07788162	62	0.17905103
3195	GO:0004540	ribonuclease activity	0.91	2	0.15576324	106	0.3061195
26932	GO:0055086	nucleobase, nucleos	0.91	28	2.1806853	944	2.7261963
4867	GO:0006753	nucleoside phosphat	0.91	27	2.1028037	914	2.6395588
6484	GO:0009117	nucleotide metabolic	0.91	27	2.1028037	914	2.6395588
20532	GO:0044282	small molecule catab	0.91	25	1.9470406	854	2.4662836
8910	GO:0015631	tubulin binding	0.91	2	0.15576324	107	0.30900744
9710	GO:0016628	oxidoreductase activ	0.91	1	0.07788162	65	0.18771479
4844	GO:0006725	cellular aromatic com	0.92	4	0.31152648	185	0.53426516
9829	GO:0016779	nucleotidyltransferas	0.92	3	0.23364486	148	0.42741212
4478	GO:0006281	DNA repair	0.92	3	0.23364486	149	0.43030006
5037	GO:0006974|GO:003	response to DNA da	0.92	3	0.23364486	149	0.43030006
4561	GO:0006399	tRNA metabolic proc	0.92	1	0.07788162	66	0.1906027
5615	GO:0008033	tRNA processing	0.92	1	0.07788162	66	0.1906027
20498	GO:0044248	cellular catabolic pro	0.92	26	2.0249221	894	2.5818002
9730	GO:0016651	oxidoreductase activ	0.92	2	0.15576324	112	0.32344702
27562	GO:0060589	nucleoside-triphosph	0.92	3	0.23364486	152	0.4389638
4850	GO:0006732|GO:000	coenzyme metabolic	0.93	2	0.15576324	113	0.32633495
9933	GO:0016903	oxidoreductase activ	0.93	2	0.15576324	113	0.32633495
9722	GO:0016641	oxidoreductase activ	0.93	1	0.07788162	69	0.19926646
21710	GO:0046148	pigment biosynthetic	0.93	1	0.07788162	69	0.19926646
5726	GO:0008187	poly-pyrimidine tract	0.93	1	0.07788162	70	0.20215438
5788	GO:0008266	poly(U) RNA binding	0.93	1	0.07788162	70	0.20215438
2649	GO:0003713	transcription coactiva	0.93	1	0.07788162	70	0.20215438
20521	GO:0044271	cellular nitrogen com	0.93	9	0.7009346	367	1.0598665
6020	GO:0008565|GO:001	protein transporter a	0.93	2	0.15576324	115	0.3321108
6475	GO:0009108	coenzyme biosynthe	0.93	1	0.07788162	72	0.20793022
9740	GO:0016667	oxidoreductase activ	0.93	1	0.07788162	72	0.20793022
8584	GO:0015171|GO:001	amino acid transmen	0.94	2	0.15576324	118	0.34077454
2521	GO:0003333	amino acid transmen	0.94	2	0.15576324	118	0.34077454
9703	GO:0016620	oxidoreductase activ	0.94	1	0.07788162	73	0.21081814
18786	GO:0042440	pigment metabolic p	0.94	1	0.07788162	73	0.21081814
19125	GO:0042802	identical protein bind	0.94	19	1.4797508	697	2.01288
11695	GO:0019725	cellular homeostasis	0.94	5	0.3894081	234	0.67577326
10244	GO:0018130	heterocycle biosynth	0.94	4	0.31152648	199	0.57469606
3627	GO:0005085|GO:000	guanyl-nucleotide ex	0.94	1	0.07788162	75	0.21659398
3965	GO:0005654	nucleoplasm	0.94	1	0.07788162	75	0.21659398
20645	GO:0044451	nucleoplasm part	0.94	1	0.07788162	75	0.21659398
18925	GO:0042592	homeostatic process	0.94	5	0.3894081	238	0.68732494
7691	GO:0010467	gene expression	0.94	61	4.7507787	1974	5.7007537
4649	GO:0006520|GO:000	cellular amino acid m	0.95	6	0.46728972	277	0.7999538
2819	GO:0004004	ATP-dependent RNA	0.95	1	0.07788162	78	0.22525774
4100	GO:0005829	cytosol	0.95	1	0.07788162	78	0.22525774

5725	GO:0008186|GO:000	RNA-dependent ATP	0.95	1	0.07788162	78	0.22525774
3761	GO:0005275|GO:000	amine transmembran	0.95	2	0.15576324	126	0.3638779
634	GO:0000988	protein binding trans	0.95	2	0.15576324	126	0.3638779
635	GO:0000989	transcription factor b	0.95	2	0.15576324	126	0.3638779
2648	GO:0003712	transcription cofactor	0.95	2	0.15576324	126	0.3638779
2654	GO:0003724	RNA helicase activity	0.95	1	0.07788162	80	0.2310336
22007	GO:0046483	heterocycle metaboli	0.95	31	2.4143302	1094	3.1593843
2658	GO:0003729	mRNA binding	0.96	1	0.07788162	82	0.23680943
30205	GO:0071841	cellular component o	0.96	6	0.46728972	285	0.8230572
15949	GO:0033554	cellular response to	0.96	3	0.23364486	173	0.49961013
4327	GO:0006091	generation of precurs	0.96	1	0.07788162	84	0.24258527
4067	GO:0005783	endoplasmic reticulu	0.96	3	0.23364486	174	0.50249803
30204	GO:0071840	cellular component o	0.96	8	0.62305295	362	1.045427
24235	GO:0048856	anatomical structure	0.97	1	0.07788162	90	0.2599128
6428	GO:0009059|GO:004	macromolecule biosy	0.97	60	4.6728973	2003	5.7845035
9294	GO:0016052|GO:000	carbohydrate catabo	0.97	1	0.07788162	91	0.2628007
13547	GO:0031090	organelle membrane	0.97	4	0.31152648	224	0.64689404
13041	GO:0030554	adenyl nucleotide bin	0.97	13	1.0124611	550	1.5883559
14965	GO:0032559	adenyl ribonucleotide	0.97	13	1.0124611	550	1.5883559
11712	GO:0019748	secondary metabolic	0.97	1	0.07788162	95	0.27435237
9895	GO:0016860	intramolecular oxidor	0.97	2	0.15576324	146	0.42163628
17024	GO:0034645|GO:003	cellular macromolecu	0.97	59	4.5950155	1999	5.7729516
3884	GO:0005524	ATP binding	0.97	12	0.93457943	524	1.51327
6425	GO:0009056	catabolic process	0.98	28	2.1806853	1051	3.0352037
16851	GO:0034470	ncRNA processing	0.98	1	0.07788162	99	0.28590405
17039	GO:0034660	ncRNA metabolic pro	0.98	1	0.07788162	99	0.28590405
16430	GO:0034046	poly(G) RNA binding	0.98	1	0.07788162	100	0.28879198
5763	GO:0008233	peptidase activity	0.98	13	1.0124611	565	1.6316746
28378	GO:0070011	peptidase activity, ac	0.98	12	0.93457943	537	1.550813
9709	GO:0016627	oxidoreductase activ	0.98	1	0.07788162	104	0.30034366
3885	GO:0005525	GTP binding	0.98	4	0.31152648	245	0.70754033
11032	GO:0019001	guanyl nucleotide bin	0.98	4	0.31152648	245	0.70754033
14967	GO:0032561	guanyl ribonucleotide	0.98	4	0.31152648	245	0.70754033
6426	GO:0009057|GO:004	macromolecule catab	0.98	1	0.07788162	106	0.3061195
3942	GO:0005618	cell wall	0.98	1	0.07788162	107	0.30900744
12868	GO:0030312	external encapsulatin	0.99	1	0.07788162	111	0.3205591
5055	GO:0006996	organelle organizatio	0.99	2	0.15576324	164	0.47361887
25483	GO:0051186	cofactor metabolic pr	0.99	2	0.15576324	164	0.47361887
29081	GO:0070717	poly-purine tract bind	0.99	1	0.07788162	112	0.32344702
14379	GO:0031966	mitochondrial membr	0.99	1	0.07788162	114	0.32922286
9889	GO:0016853	isomerase activity	0.99	5	0.3894081	306	0.8837035
5019	GO:0006952|GO:000	defense response	0.99	3	0.23364486	221	0.63823026
14910	GO:0032502	developmental proce	0.99	1	0.07788162	121	0.3494383
6884	GO:0009607	response to biotic sti	0.99	1	0.07788162	122	0.3523262
14392	GO:0031981	nuclear lumen	0.99	1	0.07788162	123	0.35521415
25485	GO:0051188	cofactor biosynthetic	0.99	1	0.07788162	123	0.35521415
131	GO:0000166	nucleotide binding	0.99	31	2.4143302	1213	3.5030468
4572	GO:0006412|GO:000	translation	0.99	2	0.15576324	180	0.5198256
8466	GO:0015031|GO:001	protein transport	0.99	2	0.15576324	185	0.53426516
20820	GO:0045184	establishment of prot	0.99	2	0.15576324	185	0.53426516
3863	GO:0005488	binding	0.99	474	36.91589	13903	40.15075
20499	GO:0044249	cellular biosynthetic	0.99	76	5.919003	2635	7.6096687
2657	GO:0003727|GO:000	single-stranded RNA	0.99	2	0.15576324	188	0.54292893
5669	GO:0008104	protein localization	0.99	2	0.15576324	189	0.54581684
30206	GO:0071842	cellular component o	0.99	2	0.15576324	193	0.5573685
19532	GO:0043233	organelle lumen	0.99	1	0.07788162	137	0.39564502
28380	GO:0070013	intracellular organelle	0.99	1	0.07788162	137	0.39564502
22415	GO:0046914	transition metal ion b	0.99	74	5.76324	2599	7.5057034
6427	GO:0009058	biosynthetic process	1.00	80	6.23053	2796	8.074624
5018	GO:0006950	response to stress	1.00	12	0.93457943	611	1.764519
14959	GO:0032553	ribonucleotide bindin	1.00	17	1.3239875	795	2.2958963
14961	GO:0032555	purine ribonucleotide	1.00	17	1.3239875	795	2.2958963
3955	GO:0005634	nucleus	1.00	36	2.8037384	1433	4.138389
10033	GO:0017076	purine nucleotide bin	1.00	17	1.3239875	797	2.3016722
18000	GO:0035639	purine ribonucleoside	1.00	16	1.2461059	769	2.2208104
4029	GO:0005740	mitochondrial envelo	1.00	1	0.07788162	151	0.4360759
3716	GO:0005198	structural molecule a	1.00	6	0.46728972	393	1.1349525
31895	GO:0090304	nucleic acid metabol	1.00	64	4.9844236	2340	6.7577324
14386	GO:0031974	membrane-enclosed	1.00	1	0.07788162	154	0.44473964
4558	GO:0006396|GO:000	RNA processing	1.00	2	0.15576324	219	0.63245445
20623	GO:0044429	mitochondrial part	1.00	1	0.07788162	165	0.47650677
4990	GO:0006915|GO:000	apoptosis	1.00	2	0.15576324	227	0.6555578
4357	GO:0006139|GO:005	nucleobase, nucleos	1.00	93	7.2429905	3285	9.486816
4605	GO:0006457|GO:000	protein folding	1.00	1	0.07788162	173	0.49961013
5756	GO:0008219	cell death	1.00	2	0.15576324	239	0.69021285
8209	GO:0012501|GO:001	programmed cell dea	1.00	2	0.15576324	239	0.69021285
9462	GO:0016265	death	1.00	2	0.15576324	239	0.69021285
20622	GO:0044428	nuclear part	1.00	1	0.07788162	178	0.5140497
8211	GO:0012505	endomembrane syste	1.00	2	0.15576324	242	0.6988766
5610	GO:0008026	ATP-dependent helic	1.00	1	0.07788162	183	0.52848935
28401	GO:0070035	purine NTP-depende	1.00	1	0.07788162	183	0.52848935
3068	GO:0004386	helicase activity	1.00	1	0.07788162	189	0.54581684
3178	GO:0004519	endonuclease activit	1.00	4	0.31152648	356	1.0280994
14380	GO:0031967	organelle envelope	1.00	1	0.07788162	201	0.5804719
14387	GO:0031975	envelope	1.00	1	0.07788162	205	0.59202355
17020	GO:0034641	cellular nitrogen com	1.00	102	7.9439254	3678	10.621769
2653	GO:0003723	RNA binding	1.00	14	1.0903426	797	2.3016722
4906	GO:0006807	nitrogen compound r	1.00	103	8.021807	3725	10.757502
2627	GO:0003676	nucleic acid binding	1.00	62	4.8286605	2453	7.0840673
4028	GO:0005739	mitochondrion	1.00	1	0.07788162	219	0.63245445
6796	GO:0009507	chloroplast	1.00	1	0.07788162	229	0.6613336

5791	GO:0008270	zinc ion binding	1.00	43	3.3489096	1880	5.4292893
6824	GO:0009536	plastid	1.00	1	0.07788162	247	0.7133162
3177	GO:0004518	nuclease activity	1.00	4	0.31152648	427	1.2331418
3903	GO:0005575|GO:000	cellular_component	1.00	260	20.249222	8515	24.590637
15392	GO:0032991	macromolecular com	1.00	34	2.647975	1616	4.666878
20640	GO:0044446	intracellular organell	1.00	9	0.7009346	710	2.0504231
20616	GO:0044422	organelle part	1.00	9	0.7009346	712	2.0561988
4459	GO:0006259|GO:005	DNA metabolic proce	1.00	4	0.31152648	493	1.4237444
3946	GO:0005623	cell	1.00	242	18.847351	8227	23.758917
20657	GO:0044464	cell part	1.00	242	18.847351	8227	23.758917
19526	GO:0043227	membrane-bounded	1.00	44	3.4267912	2142	6.185924
19530	GO:0043231	intracellular membra	1.00	44	3.4267912	2142	6.185924
3945	GO:0005622	intracellular	1.00	106	8.255452	4751	13.720507
4027	GO:0005737	cytoplasm	1.00	29	2.258567	2001	5.7787275
4109	GO:0005840|GO:003	ribosome	1.00	1	0.07788162	682	1.9695613
13018	GO:0030529	ribonucleoprotein co	1.00	1	0.07788162	741	2.1399486
19525	GO:0043226	organelle	1.00	49	3.8161993	3013	8.701303
19527	GO:0043228	non-membrane-boun	1.00	5	0.3894081	923	2.66555
19528	GO:0043229	intracellular organell	1.00	49	3.8161993	3013	8.701303
19531	GO:0043232	intracellular non-me	1.00	5	0.3894081	923	2.66555
20618	GO:0044424	intracellular part	1.00	78	6.074766	3853	11.127155
20638	GO:0044444	cytoplasmic part	1.00	21	1.635514	1644	4.7477403