Table S3. Maize HapMap ver1 SNPs detected from genome-wide association study for 12 metabolites in the nested association mapping population and predicted genes contai

MapMan annotation (16) (http://mapman.gabipd.org/web/guest;jsessionid=6F668C7FEAD5974C806D217A3560EDF2.ajp13_mapman_gabipd_org) was used to assign genes
Mala, malate; Fuma, fumarate; Glut, glutamate; Chla, chlorophyll a; Chlb, chlorophyll b; Nitr, nitrate; Sucr, sucrose; Gluc, glucose; Fruc, fructose; Star, starch; AA, total aminc

Significant SNP Information										
SNP No.	**Trait**	**Chr**	**Physical Position (AGPv1)**	**Imputed cM on NAM Map**	**Resample Model Inclusion Probability**	**Average SNP effect**	**Distance to Gene**	**Bincode**	**Gene ID**	**Category**
1	AA	1	13935133	28.26096353	26	-0.085551628				
2	AA	1	16780363	33.28759975	31	-0.081912456				
3	AA	1	33393305	52.652275	11	0.097059759				
4	AA	1	165885858	91.92724657	9	0.091736639				
5	AA	1	177389147	95.59351325	20	-0.098789746				
6	AA	1	182391497	97.70267302	18	-0.094955313	Inside	27.3.25'	grmzm2g110135_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
7	AA	1	192608853	106.1391166	12	-0.107384883	Inside	'10.1.6'	grmzm2g161233_t01	'cell wall.precursor synthesis.GAE'
8	AA	1	205585447	117.8354213	6	-0.061343453	Inside	'10.6.3'	grmzm2g154124_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
9	AA	1	205728648	117.9733694	10	-0.053004958				
10	AA	1	207120770	119.3144261	15	-0.061520606				
11	AA	1	207135155	119.3282834	8	-0.073649634				
12	AA	1	208348395	120.4695879	10	-0.053930899				
13	AA	1	210147485	121.9613779	9	-0.073635914				
14	AA	1	211910691	123.4234132	9	-0.087541648				
15	AA	1	218527234	128.2400336	6	-0.056062356				
16	AA	2	3369867	8.460233144	8	0.081076721				
17	AA	2	4452933	12.54822136	11	0.119133386	Inside	'30.2.17'	grmzm2g076212_t01	'signalling.receptor kinases.DUF 26'
18	AA	2	5461777	16.38371574	10	0.080146925				
19	AA	2	6695031	20.19476759	27	0.044923744				
20	AA	2	10533238	30.11324699	5	0.050106955				

21	AA	2	11104224	31.84202766	21	0.071319845	Inside	'29.4'	grmzm2g102088_t01	'protein.postranslational modification'
22	AA	2	13443804	37.94791551	22	0.054661567				
23	AA	2	20521754	51.29525101	5	0.086430763				
24	AA	2	24175937	56.21986729	6	0.144114822				
25	AA	2	37317423	65.59856319	51	0.074663447				
26	AA	2	186765375	97.99753568	60	0.070644387				
27	AA	2	186894631	98.25116993	31	0.074688245	Inside	'27.3.35'	grmzm2g125934_t01	'RNA.regulation of transcription.bZIP transcription factor family'
28	AA	2	209329786	120.0730566	6	0.043269516				
29	AA	2	215989909	128.8383944	6	0.040326516				
30	AA	2	217758767	131.4548964	10	0.05228333				
31	AA	3	106253820	58.5935399	18	0.080180593				
32	AA	3	136272706	62.99233029	6	0.116539144				
33	AA	3	146217490	65.77990892	10	0.108646925				
34	AA	3	170786664	81.70076623	6	0.085704188				
35	AA	3	173982599	84.12121149	71	0.098605713				
36	AA	3	176799382	87.90057838	11	0.102983913	Inside	'27.3.26'	grmzm2g125522_t01	'RNA.regulation of transcription.MYB-related transcription factor family'
37	AA	3	211702191	122.6221889	6	-0.041297758				
38	AA	3	212222090	123.2709088	6	-0.046587836				
39	AA	3	212226136	123.2759574	5	-0.06529147				
40	AA	3	212726714	123.9011201	5	-0.044492619				
41	AA	3	214950753	128.5482503	22	-0.045348234	Inside	'11.3'	grmzm2g065203_t01	'lipid metabolism.Phospholipid synthesis'
42	AA	4	171000056	79.4221761	40	-0.050350535				
43	AA	4	171777409	80.83845057	9	-0.04494486				
44	AA	4	171777978	80.83927823	30	-0.046656729				
45	AA	4	172891786	82.70364317	8	-0.057980397	Inside	'27.3.3'	grmzm2g111415_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'

46	AA	4	238824264	119.1769941	5	-0.040095238				
47	AA	4	245327128	141.6682023	5	-0.092328356	Inside	'30.2.11'	grmzm2g322348_t01	'signalling.receptor kinases.leucine rich repeat XI'
48	AA	5	1122	-0.317541556	5	0.044960637				
49	AA	5	1049462	0.606846713	32	0.05132495				
50	AA	5	1621759	2.147079874	12	0.055070047				
51	AA	5	2598377	6.596313039	23	0.043582718	Inside	'16.8.3'	grmzm2g110881_t03	'secondary metabolism.flavonoids.dihydroflavonols'
52	AA	5	2608498	6.662437668	8	0.045011664	Inside	'16.8.3'	grmzm2g410865_t01	'secondary metabolism.flavonoids.dihydroflavonols'
53	AA	5	25375392	54.32828941	25	0.052640963	Inside	'34.19.2'	grmzm2g305446_t01	'transport.Major Intrinsic Proteins.TIP'
54	AA	5	27056845	54.96362449	17	0.05259327				
55	AA	5	27066959	54.96744605	6	0.0486529	Inside	'30.2.17'	grmzm2g102862_t01	'signalling.receptor kinases.DUF 26'
56	AA	5	27983433	55.3137347	6	0.164199593				
57	AA	5	28303009	55.43448613	8	0.241124487				
58	AA	5	29915257	56.04367218	6	0.057108904	Inside	'27.3.7'	grmzm2g123550_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
59	AA	5	30338901	56.28511551	23	0.221984742				
60	AA	5	30990738	56.84135946	15	0.062976606				
61	AA	5	31224995	57.04126226	6	0.071656737				
62	AA	5	61094522	63.52954633	39	0.213909802	Inside	'29.5.11.4.2'	grmzm2g069923_t02	'protein.degradation.ubiquitin.E3.RING'

63	AA	5	89493802	69.57132155	5	-0.046703904				
64	AA	5	185678096	95.1872289	9	-0.087360449				
65	AA	5	191362737	100.706813	70	0.073417146				
66	AA	5	200532850	108.3793509	5	-0.123414326				
67	AA	5	202772744	110.6933233	16	-0.07001925				
68	AA	5	204749015	116.8860416	7	0.083646321				
69	AA	5	206467622	122.460663	14	-0.121162674				
70	AA	5	207521465	125.022936	8	-0.056063751				
71	AA	5	207525531	125.0317036	16	-0.085116692	Inside	'26.7'	grmzm2g059958_t01	'misc.oxidases - copper, flavone etc.'
72	AA	5	209222556	128.3660113	6	-0.173721735				
73	AA	5	211196887	135.9702305	23	-0.069770475				
74	AA	5	211196920	135.9703687	64	-0.080191679				
75	AA	6	3992126	-6.319411877	5	-0.093170865				
76	AA	6	25737849	7.832137091	22	-0.098932689				
77	AA	6	31537911	8.165545093	17	-0.116422372				
78	AA	6	79774320	11.21454839	11	-0.073829076				
79	AA	6	97578306	23.60510141	10	-0.064507888	Inside	'11.9.2.1'	grmzm2g322892_t01	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
80	AA	6	97988317	23.94996475	41	-0.052440749				
81	AA	6	98199018	24.12718696	9	-0.053340471	Inside	'29.5'	grmzm2g073312_t01	'protein.degradation'
82	AA	6	98204433	24.13174155	5	-0.05362577	Inside	'29.5'	grmzm2g073312_t01	'protein.degradation'
83	AA	6	98282571	24.19746402	8	-0.0579035	Inside	'27.3.38'	grmzm2g180654_t04	'RNA.regulation of transcription.AT-rich interaction domain containing transcription factor family'
84	AA	6	99986756	25.63086689	5	-0.061329207				
85	AA	6	110900537	37.5884191	5	-0.050221184				
86	AA	6	163949428	95.77601009	10	0.05979466				
87	AA	6	164286396	96.9462491	7	0.091622048				

88	AA	6	165260207	101.8645066	9	0.099911569	Inside	'11.1.10'	grmzm2g160417_t01	'lipid metabolism.FA synthesis and FA elongation.beta ketoacyl CoA synthase'
89	AA	7	27056327	46.72949889	30	0.069854871				
90	AA	7	28113557	46.92394381	6	0.042729427				
91	AA	7	28365776	46.97033173	8	0.044151146				
92	AA	7	37151920	48.23780461	7	0.043532305				
93	AA	7	69012950	49.23292513	5	0.055519521				
94	AA	7	83079854	49.85510044	8	0.04954641				
95	AA	7	84174593	49.90284891	8	0.04989524				
96	AA	7	139404320	77.80580845	69	0.087922424				
97	AA	7	143287112	81.20148454	20	0.054812272	Inside	'13.1.6.5'	grmzm2g416484_t01	'amino acid metabolism.synthesis.aromatic aa.tryptophan'
98	AA	7	150564610	88.45717741	32	0.06982965	Inside	'10.2.1'	grmzm2g103972_t01	'cell wall.cellulose synthesis.cellulose synthase'
99	AA	7	167987389	129.6248256	6	-0.118145535				
100	AA	7	169227583	134.2608759	5	-0.06723496	Inside	'16.2.1.4'	grmzm2g307437_t01	'secondary metabolism.phenylpropanoids.lignin biosynthesis.HCT'
101	AA	8	103390158	58.85914851	73	0.067148754				
102	AA	8	117265267	63.49683053	11	0.076581176	Inside	'34.12'	grmzm2g366851_t01	'transport.metal'
103	AA	8	161883485	91.64355886	10	-0.044006499	Inside	'27.3.11'	ac183950.2_fgt002	'RNA.regulation of transcription.C2H2 zinc finger family'
104	AA	8	161918620	91.67206646	11	-0.049289191				
105	AA	8	161918881	91.67227822	36	-0.053035985				
106	AA	8	161918960	91.67234232	7	-0.052130376				
107	AA	8	163479600	95.34210376	11	-0.050996234				
108	AA	8	170533744	122.5329248	12	-0.071952615				
109	AA	8	170538447	122.5649034	10	-0.073601987				

110	AA	8	170538683	122.5665081	58	-0.067975625				
111	AA	9	5956414	5.403679997	8	-0.064234269				
112	AA	9	6999573	8.221311595	5	-0.059674728				
113	AA	9	7239482	8.869319404	9	-0.047569805				
114	AA	9	7239499	8.869365322	5	-0.043097808				
115	AA	9	9143611	13.42656327	6	-0.065774986	Inside	'33.99'	grmzm2g088053_t01	'development.unspecified'
116	AA	9	9143948	13.42709594	23	-0.0560366				
117	AA	9	20663923	36.69381857	30	-0.056366108				
118	AA	9	20665105	36.69570972	16	-0.062945098				
119	AA	9	20668477	36.70110477	32	-0.060619679				
120	AA	9	23215839	39.99840064	20	-0.058749345				
121	AA	9	86468357	46.72572703	12	-0.079201882				
122	AA	9	116766687	57.30110688	5	0.11081529				
123	AA	9	116766688	57.30110724	6	0.112627991				
124	AA	9	133018761	68.62115268	53	-0.087203152				
125	AA	9	135396489	72.43328428	16	-0.066126002				
126	AA	9	140748270	85.13070924	14	0.115475213	Inside	'20.1'	grmzm2g393507_t01	'stress.biotic'
127	AA	10	18523635	33.86783022	6	-0.110952691				
128	AA	10	99357506	43.32459092	9	-0.055016754				
129	AA	10	102164870	43.55066643	36	-0.048664179				
130	AA	10	102628153	43.57658233	13	-0.054721851				
131	AA	10	111326819	44.71918576	13	-0.049289342				
132	AA	10	140890733	72.76364342	23	0.113234282	Inside	'10.7'	grmzm2g091303_t01	'cell wall.modification'
133	AA	10	143035801	79.92097141	6	0.075903997				
134	AA	10	146203306	89.79952703	10	0.075504717				
135	AA	10	146234149	89.92263189	71	0.074311201				

136	AA	10	148094143	99.83248299	14	0.059544285				
137	AA	10	148490503	102.0543415	7	0.053929166	Inside	'29.4'	grmzm2g104658_t07	'protein.postranslational modification'
138	AA	10	148496397	102.0873812	22	0.050154105				
139	Chla	1	64135223	73.46224774	7	-1.078365591				
140	Chla	1	68902676	76.2644894	18	-1.11398638				
141	Chla	1	70951065	77.30587192	7	-1.009978169				
142	Chla	1	71560037	77.6154678	8	-1.079988686				
143	Chla	1	114166513	89.09571398	6	-1.00096502	Inside	'20.1'	grmzm2g107851_t01	'stress.biotic'
144	Chla	1	126428605	89.3753375	5	-1.429246348				
145	Chla	1	139906399	89.5123698	6	-1.832781348				
146	Chla	1	179696720	96.44277983	6	2.546725312				
147	Chla	1	280711700	175.6831083	16	-1.675800132				
148	Chla	1	283540151	178.0419378	6	-1.065382143				
149	Chla	1	283829657	178.2988059	23	-1.082471106				
150	Chla	1	283830436	178.2994971	6	-1.062943975				
151	Chla	1	284054336	178.4981554	14	-1.146037697	Inside	'31.1'	grmzm2g058734_t01	'cell.organisation'
152	Chla	2	1944162	3.262633877	5	0.896831894				
153	Chla	2	2021345	3.611041843	12	0.871536011				
154	Chla	2	2211569	4.4697226	48	0.962856414	Inside	'30.2.11'	grmzm2g452142_t01	'signalling.receptor kinases.leucine rich repeat XI'
155	Chla	2	3128671	6.982329207	6	0.876581025	Inside	'27.3.20'	grmzm2g035370_t01	'RNA.regulation of transcription.G2-like transcription factor family, GARP'

156	Chla	2	23800488	55.83244658	6	1.46067929	Inside	'34.16'	grmzm2g177812_t02	'transport.ABC transporters and multidrug resistance systems'
157	Chla	2	23881650	55.91619654	8	1.16323104				
158	Chla	2	24284899	56.33230369	13	1.367200877				
159	Chla	2	24312309	56.3605877	7	1.310766647	Inside	'33.99'	grmzm2g434557_t01	'development.unspecified'
160	Chla	2	25437487	57.05362901	6	1.199994036				
161	Chla	2	25437559	57.05368243	5	1.144917046				
162	Chla	2	26691735	57.98437622	14	1.092321355	Inside	'20.1'	grmzm2g474575_t01	'stress.biotic'
163	Chla	2	26773008	58.04468695	6	0.928679226				
164	Chla	2	44156463	69.46377693	6	-2.024801273				
165	Chla	2	175505228	86.58930765	7	1.255193753				
166	Chla	3	13632616	40.54644966	5	0.97166907				
167	Chla	3	17328400	45.32523697	9	1.191986808	Inside	'30.5'	grmzm2g166064_t01	'signalling.G-proteins'
168	Chla	3	20129322	48.94693416	8	1.760642777				
169	Chla	3	27862522	53.36115573	10	1.423867597				
170	Chla	3	142821459	64.10032051	8	2.211347578				
171	Chla	3	176382057	87.28804733	7	2.673712072				
172	Chla	3	212248700	123.3041123	17	-1.457436983	Inside	'26.28'	grmzm2g047129_t02	'misc.GDSL-motif lipase'
173	Chla	3	213848077	126.6554907	48	-1.687766558	Inside	'1.5.1'	grmzm2g348512_t03	'PS.carbon concentrating mechanism.C4'
174	Chla	3	213848298	126.6560335	10	-1.668877969	Inside	'1.5.1'	grmzm2g348512_t03	'PS.carbon concentrating mechanism.C4'

175	Chla	3	213894582	126.7697196	24	-1.531651849	Inside	'1.5.1'	grmzm2g121878_t04	'PS.carbon concentrating mechanism.C4'
176	Chla	3	214166666	127.4380314	10	-1.452335655	Inside	'16.8.3'	grmzm2g029547_t01	'secondary metabolism.flavonoids.dihydroflavonols'
177	Chla	3	214171011	127.4487039	27	-1.512209361	Inside	'16.8.3'	grmzm2g029547_t01	'secondary metabolism.flavonoids.dihydroflavonols'
178	Chla	3	215371494	129.1375553	18	-1.61194824				
179	Chla	3	215732765	129.6435644	14	-1.22775052				
180	Chla	4	25857163	48.23906117	17	1.151000831				
181	Chla	4	33663511	51.99288995	5	1.206422642	Inside	'34.16'	grmzm2g441722_t01	'transport.ABC transporters and multidrug resistance systems'
182	Chla	4	35498708	52.93310614	10	1.229496466				
183	Chla	4	36054065	53.09837236	5	1.000540179	Inside	'33.99'	grmzm2g407913_t01	'development.unspecified'
184	Chla	4	172424061	81.94381184	13	-3.771641365				
185	Chla	4	177225726	88.56915079	8	-1.412797811				
186	Chla	4	177329556	88.69420796	10	-2.097767711				
187	Chla	4	177855845	90.07794504	8	-2.176405818				
188	Chla	5	166987510	78.8793885	5	-2.122907288				
189	Chla	5	189389642	98.99515772	8	-1.297088271				
190	Chla	5	205646722	119.7979212	13	-1.057085938	Inside	'17.2.2'	grmzm2g074267_t01	'hormone metabolism.auxin.signal transduction'
191	Chla	5	205662084	119.8477507	30	-1.106120646				

192	Chla	5	205842860	120.4341313	9	-1.314471195	Inside	'34.19.2'	grmzm2g028325_t01	'transport.Major Intrinsic Proteins.TIP'
193	Chla	5	208092874	126.5365424	8	-1.242235214	Inside	'27.3.6'	grmzm2g045883_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
194	Chla	5	208411778	126.7985254	6	-1.034251892				
195	Chla	5	212548689	141.0955085	7	-1.625212605				
196	Chla	6	125640414	46.48436302	14	-2.050901443				
197	Chla	6	125640415	46.48436337	17	-2.07079645				
198	Chla	6	159559960	82.11064054	5	-0.859575964	Inside	'20.2.99'	grmzm2g043035_t01	'stress.abiotic.unspecified'
199	Chla	7	33122197	47.86676722	19	1.636985743				
200	Chla	7	35108196	48.14677419	7	2.022809364				
201	Chla	7	35397449	48.15875943	7	1.157786171				
202	Chla	7	42768959	48.86677354	5	0.867518993				
203	Chla	7	125979602	66.69618807	7	2.632081769				
204	Chla	7	157918090	102.0917472	6	1.307677429				
205	Chla	8	8405589	21.20394308	18	1.770676205				
206	Chla	9	21661674	38.29017663	5	-1.285619712				
207	Chla	9	21670412	38.30415705	15	-1.744014465				
208	Chla	9	23215197	39.99779948	11	-1.046360749	Inside	'2.1.2.2'	grmzm2g024993_t01	'major CHO metabolism.synthesis.starch.starch synthase'
209	Chla	9	26434264	43.26084016	59	-1.065132951				
210	Chla	10	143379980	80.93578714	10	1.736257572				
211	Chla	10	145845320	88.37068362	8	1.167874183				
212	Chla	10	148232936	100.610509	8	1.106911557				
213	Chla	10	148450393	101.8294985	36	1.201764063				
214	Chla	10	148497003	102.0907782	6	1.10547339	Inside	'29.4'	grmzm2g104658_t09	'protein.postranslational modification'
215	Chla	10	148499295	102.1036264	9	1.10891694				
216	Chlb	1	97031439	87.3597852	18	0.627113181				
217	Chlb	1	101441507	87.90304019	5	0.237222688				
218	Chlb	1	103855930	88.27009228	13	0.528617492				
219	Chlb	1	138458661	89.49765026	6	0.636936144				
220	Chlb	1	141762525	89.53124152	15	0.677150275				
221	Chlb	1	146716486	89.58160975	18	37.87537959				

222	Chlb	1	150498647	89.94777187	5	0.650291443				
223	Chlb	1	163239765	91.63742221	8	0.375622346				
224	Chlb	1	181947110	97.49187685	6	-0.41770935				
225	Chlb	1	187131514	101.742233	14	-0.546446647				
226	Chlb	1	202975799	116.1587985	10	-0.587258205				
227	Chlb	1	205257253	117.519266	7	-0.562896571				
228	Chlb	1	225624776	133.6401321	12	-0.665556716				
229	Chlb	1	228532522	135.6859584	17	-0.333710526	Inside	'31.1'	grmzm2g113202_t01	'cell.organisation'
230	Chlb	1	285864445	180.8598811	14	-1.175768963				
231	Chlb	1	291825337	191.0554431	5	1.628826253				
232	Chlb	1	294322791	196.7251432	76	0.398027959				
233	Chlb	1	294652893	197.2197826	22	-15.83957184	Inside	'27.3.9'	grmzm2g114775_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
234	Chlb	1	296022922	199.7554621	13	5.61697755				
235	Chlb	1	299894464	204.0221873	84	3.122396653				
236	Chlb	2	5923229	18.30060959	6	-0.432741117				
237	Chlb	2	6166067	18.83309554	9	-0.313343721				
238	Chlb	2	69741938	75.18951102	10	0.13773773				
239	Chlb	2	148856409	80.60314611	22	8.071915262				
240	Chlb	2	149429597	80.70039502	22	-9.971712092	Inside	'27.4'	grmzm2g444808_t01	'RNA.RNA binding'
241	Chlb	2	161877261	82.49985253	8	-4.135727968				
242	Chlb	2	172704855	85.0182288	5	0.153284287				
243	Chlb	2	185915577	96.74331495	10	0.145544258				
244	Chlb	2	186273082	97.1970181	7	0.137513277				
245	Chlb	2	186375668	97.32720814	5	0.150539465				
246	Chlb	2	191111571	102.3694697	8	0.135633799				
247	Chlb	2	192123634	103.2729858	11	0.120175148	Inside	'26.10'	grmzm2g034471_t01	'misc.cytochrome P450'
248	Chlb	3	139536229	63.68477456	6	0.147217046				
249	Chlb	3	144468014	65.40015782	12	0.134612198				
250	Chlb	3	147011536	66.05909566	44	0.123495734				
251	Chlb	3	148514014	66.58736723	21	0.148804648				
252	Chlb	3	212765471	123.9963177	8	-0.336927049				

253	Chlb	3	216243829	131.9068925	14	-0.259823327				
254	Chlb	4	10192700	27.53975118	5	-0.334206161	Inside	'30.2.11'	grmzm2g068398_t01	'signalling.receptor kinases.leucine rich repeat XI'
255	Chlb	4	10198136	27.55916751	33	-0.283755098				
256	Chlb	4	10624506	29.08207781	6	-0.499306784				
257	Chlb	4	154415397	65.4507691	5	-0.310092928				
258	Chlb	4	157107343	68.51092069	5	-0.175013014				
259	Chlb	4	159175723	70.53286161	16	-0.172099323	Inside	'27.3.80'	grmzm2g069365_t01	'RNA.regulation of transcription.zf-HD'
260	Chlb	4	241996729	128.0064472	6	3.240118253				
261	Chlb	4	242374367	129.5365429	7	-2.331473365				
262	Chlb	4	245553732	143.0029237	5	0.469486536				
263	Chlb	5	2383652	5.193426861	6	-0.572992605				
264	Chlb	5	6303981	23.51266789	6	0.790335738				
265	Chlb	5	20023828	50.73599959	10	0.15378392				
266	Chlb	5	26723660	54.83773092	24	0.136021297				
267	Chlb	5	35357979	58.09472562	36	0.135646841				
268	Chlb	5	45813768	59.90312559	5	0.138663161				
269	Chlb	6	162877409	92.80071368	5	0.254136304				
270	Chlb	7	1921276	4.495740497	6	0.440671843				
271	Chlb	7	2047654	4.972450239	9	0.308546552				
272	Chlb	7	5043354	21.45653923	59	-0.623660171	Inside	'26.28'	grmzm2g060866_t01	'misc.GDSL-motif lipase'
273	Chlb	7	5299542	22.83360349	5	-0.725829344	Inside	'34.2'	grmzm2g142063_t01	'transport.sugars'
274	Chlb	7	6484300	28.48085938	7	-0.385308166				
275	Chlb	7	9145904	33.10358602	7	-0.455155264				
276	Chlb	7	142898891	81.10232141	46	-0.930589021				
277	Chlb	7	151513769	89.4065889	57	2.205527693				
278	Chlb	7	152461246	91.18872855	6	0.1813481				
279	Chlb	7	157011468	100.2121602	5	-1.389177806				

280	Chlb	7	157185116	100.5721631	5	-1.554880555				
281	Chlb	7	157532548	101.2924508	11	-1.522378582				
282	Chlb	7	164316372	116.7981854	5	-0.786680562				
283	Chlb	7	167232557	126.3442442	8	0.152254886				
284	Chlb	7	167233412	126.3479602	14	0.1415427				
285	Chlb	8	926070	1.886736364	14	0.271650989	Inside	'27.3.6'	grmzm2g387528_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
286	Chlb	8	1359223	2.966202574	8	0.123826391				
287	Chlb	8	99959295	57.50014689	6	-0.51065178				
288	Chlb	8	147589704	77.10076187	7	-0.197854431				
289	Chlb	8	147830284	77.29378758	5	-0.28678081	Inside	'29.2.1.2.2.518'	grmzm2g126928_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L18A'
290	Chlb	8	147830665	77.29409327	7	-0.289989168	Inside	'29.2.1.2.2.518'	grmzm2g126928_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L18A'
291	Chlb	8	152152815	80.797802	13	-0.348119811				
292	Chlb	9	8793952	12.87388515	8	-0.136620476				
293	Chlb	9	9141388	13.42304955	6	-0.254049865				
294	Chlb	9	23231768	40.03154801	10	-0.113528991				
295	Chlb	9	25023438	42.41159442	6	-0.114018927				
296	Chlb	9	27036374	43.61692207	7	-0.146623845				
297	Chlb	9	64396713	45.73393561	5	-0.145382509				
298	Chlb	9	74140456	45.9421654	15	-2166.549455				
299	Chlb	9	85978653	46.6412055	5	-0.164686897	Inside	'19.21'	grmzm2g101004_t01	'tetrapyrrole synthesis.heme oxygenase'
300	Chlb	9	147213879	101.7957515	8	-0.318295344				
301	Chlb	10	107950213	44.02050592	22	-0.311582186	Inside	'11.1.4'	grmzm2g099696_t01	'lipid metabolism.FA synthesis and FA elongation.ACP oxoacyl reductase'
302	Chlb	10	118129854	47.02366267	15	-0.228236332				
303	Chlb	10	119651031	47.40080838	7	-0.115286868				

304	Chlb	10	129585091	52.11332474	32	0.256285226				
305	Chlb	10	132147651	55.92474833	6	0.240383766				
306	Chlb	10	148943495	104.5936596	7	-0.338495455				
307	Chlb	10	149647673	108.5410404	6	-0.456258788				
308	Fruc	1	16386798	32.84963222	6	-0.013777599				
309	Fruc	1	16770481	33.28017346	30	-0.015750944				
310	Fruc	1	16775647	33.28405569	10	-0.018370011	Inside	'11.1.10'	grmzm2g445602_t01	'lipid metabolism.FA synthesis and FA elongation.beta ketoacyl CoA synthase'
311	Fruc	1	17461111	33.79917927	6	-0.014967229	Inside	'27.3.3'	ac206951.3_fgt017	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
312	Fruc	1	35272897	54.48195467	5	-0.029642508				
313	Fruc	1	44348772	60.58908186	7	0.029290518				
314	Fruc	1	45121654	61.22096078	8	0.015684896	Inside	'16.8.1'	ac212219.3_fgt005	'secondary metabolism.flavonoids.anthocyanins'
315	Fruc	1	45567426	61.52614689	14	0.019975229				
316	Fruc	1	46712396	62.60179969	5	0.013786727	Inside	'31.1'	grmzm2g104534_t01	'cell.organisation'
317	Fruc	1	57438776	70.59917107	14	0.013567425	Inside	'33.99'	grmzm2g073755_t02	'development.unspecified'
318	Fruc	1	95550141	86.84633266	14	0.034688611				
319	Fruc	2	3327524	8.176087352	9	-0.011446215				
320	Fruc	2	3529245	9.556599097	7	-0.011598842	Inside	'25.7'	grmzm2g062420_t01	'C1-metabolism.GTP cyclohydrolase I'
321	Fruc	2	3534327	9.591591385	10	-0.012952906	Inside	'25.7'	grmzm2g062420_t01	'C1-metabolism.GTP cyclohydrolase I'
322	Fruc	2	3794582	10.51648703	20	-0.013392911				

323	Fruc	2	4042572	11.15390606	18	-0.012020005				
324	Fruc	2	4663012	13.34691454	5	-0.011982641	Inside	'29.4.1.57'	grmzm2g086577_t03	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
325	Fruc	2	34001062	63.56397414	5	-0.011897479	Inside	'20.1'	grmzm2g051943_t01	'stress.biotic'
326	Fruc	2	177151781	87.86279241	10	0.034341476				
327	Fruc	2	177266143	87.95845923	6	0.046944656	Inside	'1.1.6'	grmzm2g176129_t01	'PS.lightreaction.NADH DH'
328	Fruc	2	181271307	91.1333845	7	0.046476341	Inside	'5.1'	grmzm2g130440_t01	'fermentation.LDH'
329	Fruc	3	3386685	11.10786166	29	-0.021944149	Inside	'26.28'	grmzm2g400929_t01	'misc.GDSL-motif lipase'
330	Fruc	3	3903533	13.78234035	18	-0.016091322				
331	Fruc	3	4856540	18.3470876	47	-0.014548164				
332	Fruc	3	49918968	56.54435347	26	-0.016411713				
333	Fruc	3	171723196	82.25684086	47	0.040642762				
334	Fruc	3	172148591	82.5754152	7	0.064075885				
335	Fruc	3	173110658	83.38629476	18	0.042818427				
336	Fruc	3	173219900	83.47836954	11	0.066010087				
337	Fruc	3	195593529	103.3189453	7	0.02012706	Inside	'26.17'	grmzm2g010306_t01	'misc.dynamin'
338	Fruc	3	196183579	103.6950757	5	0.011501099				
339	Fruc	3	219127882	135.874024	20	-0.018693012				
340	Fruc	3	221010928	139.3762734	18	-0.017339804				
341	Fruc	4	596627	2.14232426	45	0.025189271				
342	Fruc	4	101026208	57.83942086	5	-0.028462957				

343	Fruc	4	109554972	58.01578487	6	-0.014600631				
344	Fruc	4	118225032	58.20188033	8	-0.015380681				
345	Fruc	4	121592260	58.27415502	6	-0.012488902				
346	Fruc	4	121913511	58.2810504	6	-0.014513129				
347	Fruc	4	122028538	58.28351935	8	-0.012822806				
348	Fruc	4	125159697	58.42149244	5	-0.016269091				
349	Fruc	4	139805548	59.87084184	6	-0.013396769				
350	Fruc	4	144536877	60.82876771	5	-0.01193395				
351	Fruc	4	170738228	78.91944426	9	-0.027117788				
352	Fruc	4	172300218	81.59892215	15	-0.0185491				
353	Fruc	4	240477479	123.4579602	5	-0.05014372	Inside	'23.1.99'	grmzm2g062716_t01	'nucleotide metabolism.synthesis.unspecified'
354	Fruc	5	1571929	2.012971503	16	-0.012617453				
355	Fruc	5	2279196	4.510973125	8	-0.011842701	Inside	'10.7'	grmzm2g445169_t02	'cell wall.modification'
356	Fruc	5	2358292	5.027739617	38	-0.013396885	Inside	'34.99'	grmzm2g003108_t01	'transport.misc'
357	Fruc	5	2367917	5.090623676	8	-0.012236849	Inside	'31.1'	grmzm2g002825_t01	'cell.organisation'
358	Fruc	5	163819573	76.76334725	49	0.022715483				
359	Fruc	5	166171297	78.20073394	5	0.023811543				
360	Fruc	5	204526436	116.1640652	41	0.018975985				
361	Fruc	5	206993797	123.8406652	29	0.022620899	Inside	'29.5.4'	grmzm2g335978_t01	'protein.degradation.aspartate protease'
362	Fruc	5	210780527	134.226701	7	0.0157951				
363	Fruc	5	214945363	152.2635928	8	0.024738523				
364	Fruc	6	83413352	12.31842953	47	-0.016984936				

365	Fruc	6	93728026	20.25312295	19	-0.018294395	Inside	'27.3.24'	grmzm2g161666_t01	'RNA.regulation of transcription.MADS box transcription factor family'
366	Fruc	6	117587976	42.56198959	5	-0.03397919	Inside	'11.1.10'	grmzm2g168304_t01	'lipid metabolism.FA synthesis and FA elongation.beta ketoacyl CoA synthase'
367	Fruc	6	119772986	44.24786955	23	-0.033796984				
368	Fruc	6	124203584	45.80014821	9	-0.025280441				
369	Fruc	6	128598095	47.52042761	5	-0.033664993				
370	Fruc	6	165119716	101.3985908	6	0.036582506	Inside	'27.3.32'	grmzm2g366795_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
371	Fruc	6	166794282	106.9690738	8	-0.011678556				
372	Fruc	6	166794417	106.9695432	5	-0.01610415				
373	Fruc	7	6022883	26.56544125	7	-0.013079036				
374	Fruc	7	9213492	33.2209742	16	-0.018141284	Inside	'27.3.17'	grmzm2g153754_t01	'RNA.regulation of transcription.CPP(Zn),CPP1-related transcription factor family'
375	Fruc	7	20233795	44.69829015	10	-0.017981407				
376	Fruc	7	21622999	45.56317348	15	-0.018042126	Inside	'34.12'	ac205008.4_fgt002	'transport.metal'
377	Fruc	7	32630669	47.75472755	8	-0.017704491				
378	Fruc	7	84574592	49.92029539	9	-0.01885016				
379	Fruc	7	86294238	49.99529999	25	-0.016277961				
380	Fruc	7	86760483	50.01070124	5	-0.018393153				
381	Fruc	7	95364029	50.42762301	14	-0.019020479				
382	Fruc	7	109178008	55.19093714	5	-0.016770261				
383	Fruc	7	156688517	99.54262593	5	0.025852571				
384	Fruc	9	2701441	-3.388186607	10	-0.03407797	Inside	'27.3.20'	grmzm2g026833_t02	'RNA.regulation of transcription.G2-like transcription factor family, GARP'

385	Fruc	9	5619750	4.494331447	5	-0.026190353	Inside	'3.2.2'	grmzm2g080354_t01	'minor CHO metabolism.trehalose.TPP'
386	Fruc	9	9558874	14.08293641	31	-0.038288541				
387	Fruc	9	10186494	15.44407336	7	-0.018017282				
388	Fruc	9	21993322	38.82079896	27	-0.037006124	Inside	'29.5.5'	grmzm2g148106_t02	'protein.degradation.serine protease'
389	Fruc	9	142204786	87.72532368	30	-0.022131324				
390	Fruc	9	143828279	91.48003191	5	-0.020830478				
391	Fruc	9	145268207	95.10905936	8	-0.014832567				
392	Fruc	10	5058530	14.79019912	28	-0.045641719	Inside	'27.3.35'	grmzm2g366264_t01	'RNA.regulation of transcription.bZIP transcription factor family'
393	Fruc	10	5258877	16.0525304	31	-0.045423584	Inside	'28.1'	grmzm2g113228_t01	'DNA.synthesis/chromatin structure'
394	Fruc	10	5571203	17.95328644	17	-0.045237542				
395	Fruc	10	11480453	29.34116571	8	-0.038039626				
396	Fruc	10	134630447	59.4071156	7	-0.017295414				
397	Fuma	1	195285519	108.2877857	22	0.010497833				
398	Fuma	1	195634638	108.6089505	6	0.010552372				
399	Fuma	1	196048817	109.0223788	6	0.007421199				
400	Fuma	1	205544235	117.795721	14	-0.006686224				
401	Fuma	1	205766088	118.0094361	13	-0.004995746				
402	Fuma	1	206425614	118.6447696	17	-0.005436419				
403	Fuma	1	207121477	119.3151072	6	-0.00753724				
404	Fuma	1	208533778	120.6233059	7	-0.007359341				
405	Fuma	1	208593470	120.672802	13	-0.004806602				
406	Fuma	1	272244444	164.542002	10	0.003610726				
407	Fuma	1	272244581	164.5421084	19	0.003781599				
408	Fuma	1	289899574	186.9723092	6	0.002963805				
409	Fuma	2	5934701	18.32576495	5	0.014046764				
410	Fuma	2	26788878	58.0564637	8	-0.007537765				
411	Fuma	2	40887517	67.93546257	5	-0.004119967				
412	Fuma	2	101178551	76.43228188	6	-0.003508264				
413	Fuma	2	126037868	77.45026254	6	-0.002840198				
414	Fuma	2	126357762	77.49091538	7	-0.003825335				

415	Fuma	2	128572754	77.77240149	5	0.006664527				
416	Fuma	2	140085774	79.23550166	9	-0.003129574				
417	Fuma	2	209368892	120.1686122	5	-0.003179256				
418	Fuma	2	210076932	121.1450848	6	-0.005447489				
419	Fuma	3	27871359	53.36404037	8	-0.003866516	Inside	'29.5.11.4.2'	ac183315.4_fgt006	'protein.degradation.ubiquitin.E3.RING'
420	Fuma	3	223869464	146.0056611	18	0.010366321				
421	Fuma	3	223869468	146.0056712	5	0.01094552				
422	Fuma	4	3544388	12.18913098	8	-0.013932612				
423	Fuma	4	4653906	15.97068346	12	-0.008852558				
424	Fuma	4	4655407	15.97579929	7	-0.008673224				
425	Fuma	4	168642940	76.90973825	5	-0.005552603				
426	Fuma	4	177728199	89.41877612	10	-0.003560153				
427	Fuma	4	177733636	89.446853	10	-0.002949415				
428	Fuma	4	179860377	92.79034271	8	-0.003276803				
429	Fuma	4	180517470	93.4957277	5	-0.002716131				
430	Fuma	4	182201693	95.89453425	8	-0.004834603				
431	Fuma	4	182528229	96.35961321	8	-0.003345301				
432	Fuma	4	182976299	96.99779073	7	-0.002979929				
433	Fuma	4	230346458	113.6832878	23	0.006178358				
434	Fuma	4	234235715	115.012717	20	0.005063297				
435	Fuma	4	244607562	137.8307023	33	-0.006210745	Inside	'20.2.1'	grmzm2g324956_t01	'stress.abiotic.heat'
436	Fuma	5	6670422	24.85176321	8	0.008168665				
437	Fuma	5	6828578	25.41836288	5	0.002267897				
438	Fuma	5	7550141	28.65678582	8	0.004885718				
439	Fuma	5	9280217	30.80111555	6	0.003874816				
440	Fuma	5	10073594	32.64114173	7	0.003647227				
441	Fuma	5	10073765	32.64153832	28	0.003494537				
442	Fuma	5	10085671	32.66915111	5	0.00489814				
443	Fuma	6	165445511	102.4790375	8	-0.005808279				
444	Fuma	7	57117438	49.15463724	6	-0.006367934				
445	Fuma	7	129970942	70.62091409	6	-0.005265067				
446	Fuma	7	159657824	105.8008762	37	0.003170054				
447	Fuma	7	162478003	113.1505321	5	0.004030903				
448	Fuma	7	162478193	113.1514273	13	0.004228173				
449	Fuma	7	162482540	113.1719093	13	0.003306758				

450	Fuma	8	156139987	82.72693349	6	-0.00298176	Inside	'26.16'	grmzm2g059299_t01	'misc.myrosinases-lectin-jacalin'
451	Fuma	8	160438189	89.3463314	64	0.003362949				
452	Fuma	8	160597062	89.61860448	5	0.004068163				
453	Fuma	8	160929154	90.26562868	10	0.003237693				
454	Fuma	10	89924492	41.55012521	6	0.006236087				
455	Fuma	10	148039817	99.52795003	15	0.003588536				
456	Fuma	10	148043393	99.54799587	25	0.004260238				
457	Gluc	1	19427291	35.91876596	7	-0.027454867				
458	Gluc	1	19427753	35.91919409	22	-0.037111842				
459	Gluc	1	19745377	36.21353287	15	-0.032734262	Inside	'27.3.39'	grmzm2g447551_t01	'RNA.regulation of transcription.AtSR Transcription Factor family'
460	Gluc	1	19745402	36.21355604	13	-0.045012011	Inside	'27.3.39'	grmzm2g447551_t01	'RNA.regulation of transcription.AtSR Transcription Factor family'
461	Gluc	1	45048717	61.17102638	9	0.038550257				
462	Gluc	1	48047150	63.48200445	8	0.034229401				
463	Gluc	1	51070607	65.47738632	7	0.029008336				
464	Gluc	1	56261977	69.68972945	5	0.023260105	Inside	'33.1'	grmzm2g054916_t01	'development.storage proteins'
465	Gluc	1	155941648	90.6953495	7	0.038011307				
466	Gluc	1	219996077	128.8274919	14	0.047101374				
467	Gluc	1	222371522	129.7775422	6	0.060501845				
468	Gluc	1	239603760	141.3379825	11	-0.05994586				
469	Gluc	2	3583432	9.929705575	9	-0.023800048				
470	Gluc	2	3583516	9.930283959	21	-0.023735882				
471	Gluc	2	3980052	10.9932083	9	-0.020514387				
472	Gluc	2	4089979	11.27575825	6	-0.027570085				
473	Gluc	2	4154747	11.44223414	8	-0.02251602				
474	Gluc	2	5500383	16.53049076	8	-0.031577515				
475	Gluc	2	21516360	52.5167576	7	-0.044827778				
476	Gluc	2	21991139	53.30019341	33	-0.044813254				
477	Gluc	2	21995485	53.30230537	23	-0.037693821				
478	Gluc	2	21996541	53.30281854	21	-0.033790264				
479	Gluc	2	61159379	74.01441319	8	-0.032013585				
480	Gluc	2	160568992	82.32572371	9	-0.041399233				

481	Gluc	2	175895506	86.83396756	12	0.048831829	Inside	'10.6.1'	grmzm2g703265_t01	'cell wall.degradation.cellulases and beta -1,4-glucanases'
482	Gluc	2	186768867	98.0043879	8	-0.035176619				
483	Gluc	2	188188473	99.75988308	11	-0.03166046				
484	Gluc	3	1878568	3.303968086	7	-0.028976818				
485	Gluc	3	1878573	3.303993959	5	-0.031384063				
486	Gluc	3	1878755	3.304935735	5	-0.021125504				
487	Gluc	3	4677417	17.51176627	6	-0.021815356				
488	Gluc	3	10108659	34.7208259	23	-0.027274921				
489	Gluc	3	10750452	36.00654788	19	-0.029665146	Inside	'34.18'	grmzm2g051753_t01	'transport.unspecified anions'
490	Gluc	3	13310374	40.12977866	10	-0.029446598				
491	Gluc	3	13634107	40.54837757	8	-0.028513384				
492	Gluc	3	16806728	44.65069551	9	-0.029377307				
493	Gluc	3	19194362	47.73799582	8	-0.033080281				
494	Gluc	3	49808116	56.5306869	16	-0.031996718				
495	Gluc	3	67958527	58.10223721	5	-0.033220713				
496	Gluc	3	84984528	58.15869307	19	-0.053941727				
497	Gluc	3	126612628	60.92265927	13	-0.036596401				
498	Gluc	3	135511148	62.83074525	10	-0.032809231				
499	Gluc	3	213286642	125.2764546	22	0.027989477	Inside	'27.3.22'	grmzm2g126239_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
500	Gluc	3	223962036	146.2391988	22	0.049820979	Inside	'21.1'	grmzm2g093436_t01	'redox.thioredoxin'
501	Gluc	4	82547651	56.71433525	9	-0.032568459				
502	Gluc	4	93788979	57.69805012	9	-0.054449121				
503	Gluc	4	94875017	57.72053661	9	-0.046879342				
504	Gluc	4	103678485	57.89068149	10	-0.02674891				
505	Gluc	4	110571777	58.03760973	7	-0.026815621				
506	Gluc	4	142457660	60.337891	31	-0.04524174				

507	Gluc	4	243115508	132.4118713	10	-0.035189308	Inside	'27.3.22'	grmzm2g166041_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
508	Gluc	4	243119871	132.428798	9	-0.053005896				
509	Gluc	5	1571929	2.012971503	64	-0.030891034				
510	Gluc	5	2357601	5.023225032	15	-0.03524917	Inside	'34.99'	grmzm2g003108_t01	'transport.misc'
511	Gluc	5	2358292	5.027739617	11	-0.034233745	Inside	'34.99'	grmzm2g003108_t01	'transport.misc'
512	Gluc	5	7584397	28.79525161	9	0.05608891				
513	Gluc	5	7815403	29.72899837	23	0.066760523				
514	Gluc	5	10372835	33.33515135	6	0.037017755	Inside	'29.4.1.57'	grmzm2g158359_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
515	Gluc	5	10642005	33.95941932	32	0.047231589				
516	Gluc	5	11555355	36.07769085	9	0.04595894				
517	Gluc	5	15080589	45.43333631	7	-0.041567563	Inside	'27.3.37'	grmzm2g079185_t01	'RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family'
518	Gluc	5	15334088	45.78544974	26	-0.0335316				
519	Gluc	5	23315145	53.64866829	8	-0.048304577				
520	Gluc	5	36811132	58.27317542	5	-0.030458025				
521	Gluc	5	36811154	58.27317812	24	-0.030783704				
522	Gluc	5	37443804	58.32813065	7	-0.027227488				
523	Gluc	5	38114919	58.37370611	5	-0.032853631	Inside	'17.4.2'	grmzm2g158252_t01	'hormone metabolism.cytokinin.signal transduction'
524	Gluc	5	88070567	69.41851202	9	-0.048661521				
525	Gluc	5	114204945	70.51015923	15	-0.037585673				
526	Gluc	5	149251475	73.13980408	9	-0.039233421				
527	Gluc	5	163819573	76.76334725	6	0.03892669				

528	Gluc	5	165729383	77.90457087	6	-0.068401599				
529	Gluc	5	167871133	79.69575659	8	-0.063461483	Inside	'28.1'	grmzm2g045188_t01	'DNA.synthesis/chromatin structure'
530	Gluc	5	168259864	79.99109637	14	-0.054728927				
531	Gluc	5	168260887	79.99218626	6	-0.044931698				
532	Gluc	5	192568110	101.6096752	10	0.062349209				
533	Gluc	5	200083354	107.7054585	5	-0.035928509				
534	Gluc	5	200531277	108.3769927	13	0.049459237	Inside	'27.3.8'	grmzm2g140694_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
535	Gluc	5	201231896	109.0981131	11	-0.04069251	Inside	'20.2.1'	grmzm2g481605_t01	'stress.abiotic.heat'
536	Gluc	5	209935600	130.9474516	5	0.054968328				
537	Gluc	5	212261524	139.7573696	29	0.03161962	Inside	'3.2.3'	grmzm2g122231_t01	'minor CHO metabolism.trehalose.potential TPS/TPP'
538	Gluc	5	213298320	144.5886587	7	0.03745947				
539	Gluc	6	1331502	-9.338084147	17	0.048982117	Inside	'29.5.11.4.2'	grmzm2g423956_t01	'protein.degradation.ubiquitin.E3.RING'
540	Gluc	6	1335665	-9.333360919	20	0.044914068				
541	Gluc	6	9189279	-0.422862181	10	0.0457043				
542	Gluc	6	49947554	8.548807235	13	0.050794602				
543	Gluc	6	122728773	45.27892524	28	-0.090243045				
544	Gluc	6	123562319	45.55520364	14	-0.085892259				
545	Gluc	6	157445216	76.89711855	5	-0.059505241				
546	Gluc	6	157953572	77.68801846	6	-0.050730304				
547	Gluc	7	3665692	13.3545418	11	-0.043550162				
548	Gluc	7	20233795	44.69829015	5	-0.032821318				
549	Gluc	7	27327128	46.7793044	15	-0.031600786	Inside	'34.13'	grmzm2g156794_t01	'transport.peptides and oligopeptides'
550	Gluc	7	32868948	47.79855164	40	-0.03385516				
551	Gluc	7	84574592	49.92029539	16	-0.03318546				
552	Gluc	7	151684587	89.72788592	23	0.050943726				
553	Gluc	7	151704874	89.76604438	13	0.063838907				
554	Gluc	7	159106172	104.5548504	6	-0.033343837				
555	Gluc	7	166657242	123.8438631	13	0.046507086				

556	Gluc	7	167223656	126.3055595	5	0.04371809				
557	Gluc	7	168146720	130.3172954	14	0.038042497	Inside	'27.3.20'	ac155434.2_fgt005	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
558	Gluc	7	168146779	130.3175518	16	0.050979889	Inside	'27.3.20'	ac155434.2_fgt005	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
559	Gluc	7	168259468	130.8073104	11	0.027577674				
560	Gluc	7	168322280	131.0802981	6	0.034001816				
561	Gluc	7	169418608	134.40687	6	0.032947988				
562	Gluc	7	169612994	134.5554328	6	-0.060679509				
563	Gluc	7	170074937	134.9084806	8	0.04615997				
564	Gluc	8	10208359	26.24898642	5	-0.026684796				
565	Gluc	8	10978629	28.40458338	9	-0.025432862				
566	Gluc	8	13271527	33.98105	6	-0.027208471				
567	Gluc	8	15541604	37.97326272	22	-0.033735477				
568	Gluc	8	17101531	39.8048484	7	-0.028932686	Inside	'30.2.11'	grmzm2g463493_t01	'signalling.receptor kinases.leucine rich repeat XI'
569	Gluc	8	17783857	40.90236227	24	-0.035698197	Inside	'33.99'	grmzm2g088356_t01	'development.unspecified'
570	Gluc	8	141607731	72.49035639	5	0.035922564				
571	Gluc	8	160611990	89.64768912	7	0.033050154				
572	Gluc	8	161247986	90.88681804	17	0.025027089				
573	Gluc	8	161456583	91.29323346	6	0.027119377				
574	Gluc	8	162617259	92.65142696	6	0.024273535	Inside	'11.9.2.1'	ac233916.1_fgt002	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
575	Gluc	8	173914014	136.3104872	19	0.020511215				
576	Gluc	9	2701441	-3.388186607	6	-0.065619148	Inside	'27.3.20'	grmzm2g026833_t02	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
577	Gluc	9	6998866	8.219401947	9	-0.027000187				
578	Gluc	9	7182819	8.716269429	28	-0.045797986				
579	Gluc	9	10186494	15.44407336	6	-0.034472041				

580	Gluc	9	26517167	43.30986818	6	0.044089609				
581	Gluc	9	26517266	43.30992673	33	0.044430659				
582	Gluc	9	60088439	45.65313865	30	0.055300858				
583	Gluc	9	144805016	93.75044572	11	0.03694982	Inside	'26.21'	grmzm2g004466_t01	'misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein'
584	Gluc	10	5427445	17.07840286	48	-0.069028108				
585	Gluc	10	37230981	36.08777546	15	0.057220632				
586	Gluc	10	52110744	36.32411544	18	0.071276311				
587	Gluc	10	76226092	38.27843109	8	0.042662267				
588	Gluc	10	76332289	38.30539729	11	0.043798998				
589	Gluc	10	85540940	40.43084945	33	0.066852209				
590	Gluc	10	138301683	66.29092836	9	-0.037590118				
591	Gluc	10	144247405	82.22431479	8	-0.040531525				
592	Gluc	10	148193563	100.3897975	8	-0.046829239				
593	Glut	1	52690146	67.43745454	13	-0.00764858				
594	Glut	1	182943941	98.00929506	43	0.004651268				
595	Glut	1	182944297	98.00949265	10	0.004698343				
596	Glut	1	183661710	98.46017249	25	0.005469687				
597	Glut	1	219467828	128.6162207	53	-0.006511624				
598	Glut	1	220903481	129.1904047	5	-0.011601406				
599	Glut	1	221341695	129.3656668	12	-0.009264172	Inside	'27.4'	grmzm2g411041_t01	'RNA.RNA binding'
600	Glut	1	277632495	170.2619536	14	0.010539017				
601	Glut	2	4153357	11.43866137	14	0.008070873				
602	Glut	2	4153720	11.4395944	56	0.009484778				
603	Glut	2	4299868	11.96628803	12	0.003568927				
604	Glut	2	12590485	36.29106182	5	-0.008475169				
605	Glut	2	133606697	78.41212615	8	-0.005723744				
606	Glut	2	185662626	96.4222994	8	0.005714311	Inside	'27.3.8'	grmzm2g009406_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
607	Glut	2	186287170	97.21489693	11	0.00486937				
608	Glut	2	186556918	97.58848824	7	0.00560792				
609	Glut	2	186556997	97.58864326	38	0.004943913				
610	Glut	2	186558389	97.59137473	6	0.004850272				
611	Glut	2	186558494	97.59158077	8	0.005489912				
612	Glut	2	209437807	120.3370062	6	-0.006286015				
613	Glut	2	210076624	121.1447377	5	-0.007333198				

614	Glut	2	233601849	155.7785003	5	-0.004272848				
615	Glut	3	201451737	108.647491	5	-0.009148834				
616	Glut	3	209190519	119.5728622	8	-0.008009729	Inside	'21.2'	grmzm2g024448_t01	'redox.ascorbate and glutathione'
617	Glut	3	210306116	120.8801933	6	-0.016920822				
618	Glut	3	210710907	121.3852837	8	-0.017895411				
619	Glut	3	210877159	121.5927298	12	-0.004934249				
620	Glut	3	210988072	121.7311249	6	-0.016726602				
621	Glut	3	211148597	121.9314249	16	-0.005852378				
622	Glut	3	212234516	123.2864138	7	-0.005205315				
623	Glut	3	212718903	123.8908226	5	-0.004685377				
624	Glut	3	213151216	124.9438117	7	-0.004725778				
625	Glut	3	213151324	124.944077	8	-0.004513687				
626	Glut	3	213890769	126.7603538	6	-0.010464009	Inside	'1.5.1'	grmzm2g121878_t05	'PS.carbon concentrating mechanism.C4'
627	Glut	3	215225785	128.93347	9	-0.005251452				
628	Glut	3	225244456	148.4971299	11	0.010839249	Inside	'27.3.60'	grmzm2g071322_t01	'RNA.regulation of transcription.NIN-like bZIP-related family'
629	Glut	3	228108627	153.4517969	9	-0.007734346	Inside	'31.2'	grmzm2g109618_t01	'cell.division'
630	Glut	4	113973202	58.11061842	7	0.012195634				
631	Glut	4	114035361	58.11195261	27	0.009580393				
632	Glut	4	114684938	58.12589523	19	0.012290204				
633	Glut	4	114784127	58.12802424	11	0.008190782				
634	Glut	4	177057914	88.36703104	8	-0.004129286				
635	Glut	4	177728199	89.41877612	7	-0.004671784				
636	Glut	4	180521118	93.50092348	6	-0.003964857				
637	Glut	4	180521269	93.50113855	12	-0.003984467				
638	Glut	5	2188871	3.920842986	34	0.004382943	Inside	'3.5'	grmzm2g085320_t01	'minor CHO metabolism.others'

639	Glut	5	2188935	3.921261124	7	0.004596176	Inside	'3.5'	grmzm2g085320_t01	'minor CHO metabolism.others'
640	Glut	5	22628584	52.93088442	10	0.004845342				
641	Glut	5	24406989	53.96237944	33	0.005600127	Inside	'27.3.25'	grmzm2g392823_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
642	Glut	5	26831469	54.87846643	28	0.004300894				
643	Glut	5	26968073	54.93008209	8	0.004561445				
644	Glut	5	204624078	116.4807852	18	-0.008453086				
645	Glut	5	207099285	124.0780936	14	-0.005034335				
646	Glut	5	207830710	126.0436057	6	-0.005515777				
647	Glut	5	208181590	126.6094235	22	-0.00481065				
648	Glut	5	211971359	138.4052511	12	-0.004321074				
649	Glut	6	5873783	-4.184534568	5	-0.004487679				
650	Glut	6	12079085	2.855833808	5	-0.006531182	Inside	'29.3.5'	grmzm2g166537_t01	'protein.targeting.peroxisomes'
651	Glut	6	17417589	5.992091218	17	-0.007355935				
652	Glut	7	46996523	49.11264731	7	0.008798227				
653	Glut	7	94886697	50.37959201	10	0.005639153	Inside	'3.2.2'	grmzm2g174396_t01	'minor CHO metabolism.trehalose.TPP'
654	Glut	7	142900670	81.10277074	5	0.006182641	Inside	'10.7'	grmzm2g413044_t01	'cell wall.modification'
655	Glut	7	153318373	92.800926	8	0.005690411				
656	Glut	8	6455489	18.09391822	6	0.00847514				
657	Glut	8	6456227	18.0946642	11	0.008664988				
658	Glut	8	7548635	19.78341505	71	0.007377193				
659	Glut	8	101278421	58.12094124	7	0.004952541	Inside	'26.12'	grmzm2g117365_t01	'misc.peroxidases'

660	Glut	8	103054530	58.74182186	12	0.007297413	Inside	'26.10'	grmzm2g096029_t01	'misc.cytochrome P450'
661	Glut	8	108849125	60.58213104	58	0.007826556	Inside	'30.5'	grmzm2g072089_t01	'signalling.G-proteins'
662	Glut	8	111162784	61.25050555	6	0.005962952				
663	Glut	9	147914070	105.0171122	7	-0.005016694	Inside	'30.2.11'	grmzm2g438840_t01	'signalling.receptor kinases.leucine rich repeat XI'
664	Glut	10	4806482	13.07619208	13	0.004785432				
665	Glut	10	4916937	13.82732142	5	0.005675285	Inside	'27.3.20'	grmzm2g016370_t01	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
666	Glut	10	107945494	44.01972245	13	-0.005346414	Inside	'26.1'	grmzm2g399530_t01	'misc.misc2'
667	Glut	10	121191348	47.87413076	6	-0.00534999				
668	Glut	10	143716606	81.33488617	5	0.005311941				
669	Glut	10	143720983	81.33864061	5	0.006129575	Inside	'30.2.17'	grmzm2g000633_t01	'signalling.receptor kinases.DUF 26'
670	Glut	10	145459551	86.83094884	6	0.00654061				
671	Glut	10	145674099	87.6872826	53	0.005786004				
672	Glut	10	146203278	89.79941527	6	0.005650134				
673	Glut	10	146744765	92.26833185	7	0.004535231				
674	Glut	10	148374079	101.4017084	12	0.006234528				
675	Mala	1	15026222	30.17736702	5	-0.00767141				
676	Mala	1	16018451	32.20888865	5	-0.010779957				
677	Mala	1	16018768	32.20944008	34	-0.010507566				

678	Mala	1	39323398	57.23255596	57	0.011761998				
679	Mala	1	40056302	57.91121791	14	0.007307404				
680	Mala	1	88319619	83.94252884	5	0.005107759				
681	Mala	1	90444879	84.51213232	6	0.007232955				
682	Mala	1	210010258	121.8475905	9	-0.007472494				
683	Mala	1	219597467	128.6680693	5	-0.010215717				
684	Mala	1	219599713	128.6689676	17	-0.008622717				
685	Mala	1	222370635	129.7771875	21	-0.010317833				
686	Mala	1	292093541	191.7018819	15	0.029138599				
687	Mala	1	295777277	199.3871057	5	0.021925596				
688	Mala	2	2111645	4.01866061	8	0.006346054				
689	Mala	2	2662790	6.10191746	5	0.012572964				
690	Mala	2	4313222	12.01705821	7	0.008065261				
691	Mala	2	4829815	13.98107797	14	0.007986073				
692	Mala	2	5064142	14.87195891	10	0.009403602				
693	Mala	2	5064288	14.87251398	29	0.009676366				
694	Mala	2	5564443	16.77403859	17	0.007030808	Inside	'27.3.3'	grmzm2g174917_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
695	Mala	2	38490452	66.37064702	10	-0.008181854				
696	Mala	2	53075256	72.33109749	67	-0.01005034				
697	Mala	2	121233141	77.09963877	6	-0.008726546				
698	Mala	2	187425746	99.07896093	34	0.006597118				
699	Mala	2	188442924	99.98704342	26	0.010380475				
700	Mala	2	190921710	102.1999719	13	0.007946425	Inside	'27.3.3'	grmzm2g170253_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
701	Mala	2	190922255	102.2004584	6	0.005818998	Inside	'27.3.3'	grmzm2g170253_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
702	Mala	2	208636969	118.3801568	72	-0.009940999				
703	Mala	3	28560505	53.70440674	76	0.012754816				
704	Mala	3	110591868	58.89150506	6	0.009305688				
705	Mala	3	197969185	105.1512436	6	0.008872874				

706	Mala	3	200646842	108.1602931	7	0.006749729				
707	Mala	3	207468446	116.9659734	5	0.007830782				
708	Mala	3	208722589	119.0297927	10	0.018556936				
709	Mala	3	208759190	119.072271	7	0.018809679				
710	Mala	3	213856232	126.6755216	29	-0.008429835	Inside	'1.5.1'	grmzm2g348512_t01	'PS.carbon concentrating mechanism.C4'
711	Mala	3	214330739	127.7703198	23	-0.007870489				
712	Mala	3	214355739	127.8009362	14	-0.007817618				
713	Mala	3	223533563	145.1258349	43	-0.006537456				
714	Mala	4	170999854	79.42178824	8	-0.017758613				
715	Mala	4	171775102	80.83509484	83	-0.010613833				
716	Mala	4	180344878	93.24990822	5	0.026764303	Inside	'33.99'	grmzm2g016948_t01	'development.unspecified'
717	Mala	5	2767759	7.538649577	9	-0.023022027				
718	Mala	5	4189784	13.29548628	8	-0.024817481				
719	Mala	5	5266701	18.78312331	16	-0.018541237				
720	Mala	5	25580476	54.40578016	17	0.006381893				
721	Mala	5	35870702	58.15768893	9	0.007312398				
722	Mala	5	159516767	75.22607915	59	0.006946802				
723	Mala	5	196990966	105.0448056	21	-0.006739831				
724	Mala	5	196991427	105.0451889	6	-0.007454933				
725	Mala	5	213281396	144.5097958	5	-0.007254868				
726	Mala	5	214193499	148.7600372	10	-0.005516584	Inside	'27.1.19'	grmzm2g150912_t01	'RNA.processing.ribonucleases'
727	Mala	6	2173089	-8.383242223	8	-0.007048492				
728	Mala	6	3682882	-6.670271784	7	-0.007945361	Inside	'26.10'	grmzm2g104877_t01	'misc.cytochrome P450'
729	Mala	6	6894842	-3.026068551	6	-0.005310972				
730	Mala	6	9251251	-0.35255042	21	-0.006131661	Inside	'33.99'	grmzm2g442170_t01	'development.unspecified'
731	Mala	6	160133599	84.08459515	7	-0.010156075				
732	Mala	6	161832235	87.63268966	6	-0.009770832	Inside	'26.2'	grmzm2g121237_t01	'misc.UDP glucosyl and glucoronyl transferases'
733	Mala	6	162218871	89.54447098	6	-0.006148267				

734	Mala	6	162665812	91.75443968	12	-0.008612649				
735	Mala	6	163284243	94.27967325	19	-0.005380966				
736	Mala	6	165585617	102.9436765	17	-0.006076029				
737	Mala	7	118340956	59.84562968	7	-0.012097666				
738	Mala	7	131033445	71.16406426	19	-0.009077321				
739	Mala	7	143058340	81.14259414	5	-0.006769154	Inside	'30.5'	grmzm2g131275_t01	'signalling.G-proteins'
740	Mala	7	145583488	83.49098005	9	-0.005789243	Inside	'26.2'	grmzm2g455075_t01	'misc.UDP glucosyl and glucoronyl transferases'
741	Mala	7	146746400	84.65040768	13	-0.007872159	Inside	'26.4.1'	grmzm2g325008_t02	'misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase'
742	Mala	7	163624094	115.764038	48	0.012940535	Inside	'30.3'	grmzm2g015703_t01	'signalling.calcium'
743	Mala	7	166492884	123.1295455	11	0.009047583				
744	Mala	7	166493179	123.1308276	67	0.011080937				
745	Mala	7	167073361	125.6523612	6	0.009385491				
746	Mala	7	167122054	125.8639863	17	0.012150093				
747	Mala	8	100197210	57.57868238	6	0.00790012				
748	Mala	8	108849390	60.58220759	51	0.005689455	Inside	'30.5'	grmzm2g072089_t01	'signalling.G-proteins'
749	Mala	8	120917873	65.51878959	5	0.008136638				
750	Mala	8	154959713	81.88784605	10	0.012371157				
751	Mala	8	159784012	88.41830479	12	0.012070302				
752	Mala	9	91767617	47.59229769	5	0.009468398				
753	Mala	9	109432591	53.84671075	14	0.010241133				
754	Mala	10	1210362	-2.349387514	15	-0.017276952				

755	Mala	10	1431221	-1.586267435	6	0.011410568	Inside	'26.16'	grmzm2g104655_t01	'misc.myrosinases-lectin-jacalin'
756	Mala	10	1467050	-1.462469767	16	0.006758966	Inside	'20.1'	grmzm2g400999_t01	'stress.biotic'
757	Mala	10	2275477	1.330836713	6	0.006068756				
758	Mala	10	2592048	2.424664387	5	0.008847718	Inside	'17.3.1.2.3'	grmzm2g068465_t01	'hormone metabolism.brassinosteroid.synthesis-degradation.sterols.CYP51'
759	Mala	10	4201480	8.961984916	5	0.006361453				
760	Mala	10	145447601	86.78325234	17	0.007756603				
761	Mala	10	145456506	86.81879521	5	0.008987877				
762	Mala	10	145674099	87.6872826	67	0.007733533				
763	Mala	10	145733506	87.92439606	8	0.009243772				
764	Nitr	1	5563538	9.70193737	75	0.003559647				
765	Nitr	1	51114082	65.50613364	11	0.003292823				
766	Nitr	1	60210415	71.99893136	5	0.002949116				
767	Nitr	1	63667791	73.22732147	7	0.00318244				
768	Nitr	1	199491006	112.8925649	7	-0.000697051				
769	Nitr	1	201845500	115.3791094	11	-0.000756257				
770	Nitr	1	201991158	115.4795854	6	-0.003767123				
771	Nitr	1	202621762	115.91	5	-0.0043	Inside	'8.2.9'	grmzm2g129513_t01	'TCA / org. transformation.other organic acid transformaitons.cyt MDH'
772	Nitr	1	207277145	119.465065	11	-0.000793889	Inside	'20.2.99'	grmzm2g363004_t01	'stress.abiotic.unspecified'
773	Nitr	1	207279145	119.4669916	8	-0.000840239				

774	Nitr	1	207313090	119.4996915	12	-0.000961106	Inside	'17.7.1.5'	grmzm2g148281_t01	'hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase'
775	Nitr	1	224410655	132.7669157	12	-0.0094014				
776	Nitr	1	232515055	138.1818938	6	0.011437559				
777	Nitr	1	233097149	138.4111567	9	0.012678888				
778	Nitr	1	249984566	148.2769963	25	0.000988754				
779	Nitr	1	254217830	150.9046175	9	0.040341299	Inside	'30.11'	grmzm2g172506_t01	'signalling.light'
780	Nitr	1	254218603	150.9052401	13	0.038373926	Inside	'30.11'	grmzm2g172506_t01	'signalling.light'
781	Nitr	1	256241409	152.3975751	16	1.893176617				
782	Nitr	1	256250277	152.4041229	6	-3.973615173				
783	Nitr	1	256300512	152.4470842	7	-0.373608989				
784	Nitr	1	257414838	153.4001486	40	-0.007243298				
785	Nitr	1	297905073	202.4622232	6	-0.001303846				
786	Nitr	2	3805	-5.496235757	26	0.001182912				
787	Nitr	2	2023274	3.619749446	24	0.001176073				
788	Nitr	2	2211917	4.471293489	10	0.001669864	Inside	'30.2.11'	grmzm2g452142_t01	'signalling.receptor kinases.leucine rich repeat XI'
789	Nitr	2	2491029	5.715556905	6	0.000821883				
790	Nitr	2	9387311	27.56530943	6	0.001306219				
791	Nitr	2	31005737	62.07871475	22	0.001211646				
792	Nitr	2	36815670	65.26831102	10	0.001463549				
793	Nitr	2	37323751	65.60272826	11	0.002275836				
794	Nitr	2	181079834	90.99646529	39	0.001816495				
795	Nitr	2	182483954	92.38830408	38	0.001818773				
796	Nitr	2	183983052	94.29078232	8	0.002369111	Inside	'27.3.99'	grmzm2g168163_t02	'RNA.regulation of transcription.unclassified'

797	Nitr	2	186765944	97.99865221	7	0.001224906				
798	Nitr	2	203303901	111.3475511	5	0.002210804				
799	Nitr	2	211231604	122.5790956	20	0.002091497				
800	Nitr	2	212538395	124.4779034	10	0.002047508				
801	Nitr	3	8109850	29.6995263	14	0.003636405				
802	Nitr	3	8678939	31.22826072	19	0.003500894				
803	Nitr	3	8924944	31.88908441	11	0.003569052				
804	Nitr	3	158547954	71.48562889	28	0.000938613				
805	Nitr	3	210217529	120.7696561	15	-0.000777862				
806	Nitr	3	212234516	123.2864138	11	-0.00092326				
807	Nitr	3	212247177	123.3022119	10	-0.000811602				
808	Nitr	3	212248108	123.3033736	27	-0.000852191				
809	Nitr	3	212248700	123.3041123	15	-0.000804228	Inside	'26.28'	grmzm2g047129_t02	'misc.GDSL-motif lipase'
810	Nitr	3	213848077	126.6554907	7	-0.000894249	Inside	'1.5.1'	grmzm2g348512_t03	'PS.carbon concentrating mechanism.C4'
811	Nitr	4	11351925	31.69382335	5	-0.003583568				
812	Nitr	4	11970641	33.81499619	6	-0.003758507				
813	Nitr	4	25849988	48.23626239	5	0.001059419	Inside	'34.13'	grmzm2g026459_t01	'transport.peptides and oligopeptides'
814	Nitr	4	25850469	48.23645002	7	0.001284805	Inside	'34.13'	grmzm2g026459_t01	'transport.peptides and oligopeptides'
815	Nitr	4	28177658	49.14422457	25	0.002716247				
816	Nitr	4	28839372	49.4032225	7	0.005200168				
817	Nitr	4	101964449	57.85755427	9	0.003029113				
818	Nitr	4	110010755	58.02556787	12	0.001209715				
819	Nitr	4	130200550	58.67643598	10	0.001469707				
820	Nitr	4	149531302	61.9954463	8	0.004684307				
821	Nitr	4	163054280	73.24125003	10	-0.002480041	Inside	'27.3.99'	grmzm2g141036_t01	'RNA.regulation of transcription.unclassified'
822	Nitr	4	163084391	73.26227648	17	-0.002987557				
823	Nitr	4	165718843	75.10190893	25	-0.003343143				

824	Nitr	4	166175217	75.86	5	-0.0009	Inside	'12.2.2'	grmzm2g036464_t01	'N-metabolism.ammonia metabolism.glutamine synthase'
825	Nitr	4	167831848	76.66597097	7	-0.002511466				
826	Nitr	4	170457980	78.38642641	8	-0.002662805	Inside	'30.5'	grmzm2g142806_t01	'signalling.G-proteins'
827	Nitr	4	177460609	88.85205365	6	-0.000971011				
828	Nitr	4	179532567	92.44677404	28	-0.002935932				
829	Nitr	4	242018406	128.094256	5	-0.026531277				
830	Nitr	4	242343398	129.4163957	6	0.793685036	Inside	'26.19'	grmzm2g101916_t01	'misc.plastocyanin-like'
831	Nitr	5	4862213	16.72130612	9	0.003196165				
832	Nitr	5	4925927	17.04607872	10	0.002167269				
833	Nitr	5	7664787	29.12019513	5	0.001140887				
834	Nitr	5	162808563	76.42708275	6	0.003808286				
835	Nitr	5	184229490	93.51868254	5	0.001723644				
836	Nitr	5	184794208	94.16914109	6	0.001178069				
837	Nitr	5	185030768	94.44161776	7	0.001440241				
838	Nitr	5	185056309	94.47103662	10	0.001491703				
839	Nitr	5	185687667	95.19825306	8	0.001158127	Inside	'29.4'	grmzm2g096753_t01	'protein.postranslational modification'
840	Nitr	5	185860200	95.39698157	5	0.000263629	Inside	'16.2.1.1'	grmzm2g074604_t02	'secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL'
841	Nitr	5	190089272	99.5622766	29	-0.023979728	Inside	'31.3'	grmzm2g160563_t01	'cell.cycle'
842	Nitr	5	190169366	99.64088567	25	-0.032819686				
843	Nitr	5	190751918	100.0087423	59	0.060946443				
844	Nitr	5	191728507	101.2378277	61	-0.033148662				
845	Nitr	5	205478714	119.252956	9	-0.001744117				
846	Nitr	5	205662825	119.8501543	20	-0.001468083				

847	Nitr	5	205964077	120.8273212	11	-0.000771887				
848	Nitr	5	207101210	124.0824263	25	-0.003509329				
849	Nitr	5	207118376	124.1210629	12	-0.000821003				
850	Nitr	5	207498927	124.9743369	13	-0.003573299				
851	Nitr	5	211861691	137.9485929	9	-0.00209302				
852	Nitr	6	78467563	11.02628868	8	0.00613447				
853	Nitr	6	92041721	18.74190429	8	-0.007360541				
854	Nitr	6	164046344	96.23353408	8	0.00311268				
855	Nitr	7	94080369	50.29845615	7	-0.002187415				
856	Nitr	7	97073633	50.59965001	5	-0.003762497				
857	Nitr	7	121206635	61.30136801	7	0.003846053				
858	Nitr	7	145280969	83.18936747	6	0.000758506	Inside	'27.3.11'	grmzm2g163095_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
859	Nitr	7	152493835	91.25002624	19	0.000787893				
860	Nitr	8	20733895	45.60822058	7	0.002081662				
861	Nitr	8	139383376	71.29644034	13	-0.004157906				
862	Nitr	8	147013249	76.63825194	16	0.004700156				
863	Nitr	8	150840981	79.70937466	9	0.002809057				
864	Nitr	8	160985585	90.37557478	10	-0.000844257				
865	Nitr	9	23279446	40.13731735	8	-0.000527851				
866	Nitr	9	23407123	40.42055726	5	-0.000732831				
867	Nitr	9	25029010	42.41502107	13	-0.000589684				
868	Nitr	9	121495902	60.17794088	5	-0.000866371				
869	Nitr	9	151011382	109.2060086	64	0.003263514	Inside	'1.2'	grmzm2g168281_t01	'PS.photorespiration'
870	Nitr	10	146509918	91.0233194	8	0.000766245				
871	Nitr	10	146628442	91.61626493	10	0.000710638				
872	Nitr	10	146744873	92.26893726	17	0.000679393				
873	Nitr	10	147132717	94.44305795	6	0.000722548				
874	Nitr	10	147981037	99.19844948	12	0.000848392				
875	Nitr	10	148513914	102.1855755	14	0.000913186	Inside	'23.4.99'	grmzm2g104918_t04	'nucleotide metabolism.phosphotransfer and pyrophosphatases.misc'
876	Prot	1	64910659	74.0301357	9	-0.006095916	Inside	'34.3'	grmzm2g306919_t01	'transport.amino acids'

877	Prot	1	64910976	74.03036785	33	-0.006371905	Inside	'34.3'	grmzm2g306919_t01	'transport.amino acids'
878	Prot	1	69196228	76.41372859	13	-0.006630505				
879	Prot	1	69271066	76.45177556	5	-0.007173736				
880	Prot	1	74985643	79.35701503	8	-0.015969066				
881	Prot	1	252882663	149.8292876	8	0.008583908				
882	Prot	2	20043374	50.80064207	26	-0.006974803				
883	Prot	2	185457136	96.16151574	6	0.006649714				
884	Prot	3	1187527	-0.271888706	19	0.008814859				
885	Prot	3	127883944	61.0242801	19	-0.009978835				
886	Prot	3	127884222	61.02430232	7	-0.008779638				
887	Prot	3	131786653	61.68464041	6	-0.014158624	Inside	'30.5'	grmzm2g084606_t01	'signalling.G-proteins'
888	Prot	3	179931178	91.94664886	37	-0.006464741				
889	Prot	3	186207858	97.81793168	13	-0.009426898				
890	Prot	3	186596173	98.06048224	5	-0.00757709				
891	Prot	3	188565185	99.29037279	6	-0.006679739	Inside	'17.5.3'	grmzm2g440529_t01	'hormone metabolism.ethylene.induced-regulated-responsive-activated'
892	Prot	3	203411410	111.3198505	6	-0.006026391				
893	Prot	3	212222986	123.2720269	21	-0.006839459				
894	Prot	3	212224642	123.2740932	16	-0.007350952				
895	Prot	3	213226535	125.1288155	17	-0.008878007				
896	Prot	3	213800913	126.5396432	5	-0.007297196				
897	Prot	3	213854238	126.6706238	9	-0.007474129	Inside	'1.5.1'	grmzm2g348512_t01	'PS.carbon concentrating mechanism.C4'
898	Prot	3	217611213	133.5696863	6	-0.008173794	Inside	'27.3.6'	grmzm2g081816_t03	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
899	Prot	4	168096468	76.74550042	5	-0.013008569				

900	Prot	4	227245511	112.6233194	44	0.009730652	Inside	'10.7'	grmzm2g112619_t01	'cell wall.modification'
901	Prot	4	230742777	113.8187579	6	0.008891322				
902	Prot	5	88557383	69.4927261	74	-0.007848454	Inside	'10.5.1.1'	grmzm2g134528_t01	'cell wall.cell wall proteins.AGPs.AGP'
903	Prot	5	91037740	69.69522773	20	-0.006780225				
904	Prot	5	186016180	95.57664385	5	-0.00735679				
905	Prot	5	187955512	97.81042264	8	-0.005429395				
906	Prot	5	189228254	98.86708725	21	-0.007553606				
907	Prot	5	203170982	112.0815943	20	-0.006893258				
908	Prot	5	205646722	119.7979212	18	-0.005971484	Inside	'17.2.2'	grmzm2g074267_t01	'hormone metabolism.auxin.signal transduction'
909	Prot	5	206043601	121.085272	6	-0.006353574				
910	Prot	5	208092874	126.5365424	6	-0.005967461	Inside	'27.3.6'	grmzm2g045883_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
911	Prot	6	22422464	7.104655221	26	-0.006334214				
912	Prot	6	35896471	8.2773635	5	-0.005965884				
913	Prot	6	72931425	10.26780431	14	-0.004869067				
914	Prot	6	72985636	10.2733065	9	-0.004940372	Inside	'27.1.19'	grmzm2g047265_t01	'RNA.processing.ribonucleases'
915	Prot	6	73021951	10.27699232	13	-0.0080408				
916	Prot	6	168683648	108.6048676	13	0.011314553				
917	Prot	6	168748906	108.622076	35	0.007222797				
918	Prot	7	5099065	21.78417429	9	-0.008417978	Inside	'31.1'	grmzm2g011800_t01	'cell.organisation'
919	Prot	7	33595519	47.99555999	10	0.00514782				

920	Prot	7	154247787	94.54909037	7	0.005825457	Inside	'30.2.3'	grmzm2g006505_t02	'signalling.receptor kinases.leucine rich repeat III'
921	Prot	7	157249277	100.7051801	14	0.006706373				
922	Prot	7	158036207	102.3366246	5	0.005791282				
923	Prot	7	159778542	106.10253	6	0.012461708				
924	Prot	7	168378312	131.3238192	8	-0.007477326				
925	Prot	8	21881574	47.44607971	10	0.011659826	Inside	'27.2'	grmzm2g032551_t01	'RNA.transcription'
926	Prot	8	108880988	60.59133569	5	0.008562491				
927	Prot	8	115683038	62.57820324	5	0.008392785				
928	Prot	8	117977083	63.86243699	51	0.01116072	Inside	'26.7'	grmzm2g142584_t01	'misc.oxidases - copper, flavone etc.'
929	Prot	8	129392376	68.26348656	8	0.009582417				
930	Prot	8	131868393	69.1089486	5	-0.007281874	Inside	'33.1'	grmzm2g005552_t01	'development.storage proteins'
931	Prot	8	161242940	90.87698678	53	-0.005415146				
932	Prot	8	170967906	124.4926125	15	-0.010060425				
933	Prot	9	73386482	45.90639706	5	-0.006073526				
934	Prot	9	75752943	46.01866137	10	-0.00678119				
935	Prot	9	86122013	46.66594904	22	-0.007718805				
936	Prot	9	98709960	49.58225494	8	-0.00680033	Inside	'10.6.2'	grmzm2g146523_t01	'cell wall.degradation.mannan-xylose-arabinose-fucose'
937	Prot	9	112772173	55.72841749	8	-0.006998869				
938	Prot	9	113322955	55.98017627	24	-0.006456001				
939	Prot	9	113731726	56.16702277	6	-0.00865215				
940	Prot	9	120621679	59.56922799	5	-0.00678539				
941	Prot	9	122100192	60.59870208	5	-0.007751436				
942	Prot	9	143538206	90.82527553	10	-0.007521104				
943	Prot	9	144829091	93.82411792	25	-0.004785192				
944	Prot	10	10440954	28.50645685	9	-0.008130968				
945	Prot	10	16919807	33.52470383	16	0.007567347				

946	Prot	10	147427851	96.09747813	13	0.004748578				
947	Prot	10	148213790	100.5031831	11	0.006813955				
948	Prot	10	148344527	101.23605	45	0.008225195				
949	Prot	10	148496242	102.0865123	5	0.007112842				
950	Star	1	7457814	13.94852432	86	-0.037258586				
951	Star	1	17278764	33.6621462	5	-0.041877285	Inside	'29.2.1.2.1.31'	grmzm2g145308_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.SA'
952	Star	1	21382731	37.73085137	29	-0.023301274				
953	Star	1	21383024	37.73112289	10	-0.022620507				
954	Star	1	42174991	59.32632563	11	0.051194392				
955	Star	1	45528222	61.4993069	7	0.044795124	Inside	'29.4'	ac208201.3_fgt002	'protein.postranslational modification'
956	Star	1	46715564	62.60388883	8	0.035909602				
957	Star	1	51113147	65.50551539	54	0.052957455				
958	Star	1	51531509	66.02023986	6	0.089385584				
959	Star	1	92753447	85.57176721	62	0.024022074				
960	Star	1	93661572	85.98563614	7	0.024453663				
961	Star	1	93667548	85.98835964	6	0.024126069				
962	Star	1	251149118	148.8823369	5	-0.048533652	Inside	'10.7'	grmzm2g103672_t01	'cell wall.modification'
963	Star	1	251176189	148.8964086	90	-0.057655015				
964	Star	1	292560966	192.501744	10	-0.071069046				
965	Star	2	5548326	16.71276385	15	-0.027020805				
966	Star	2	5548414	16.71309841	83	-0.028470515				
967	Star	2	21795122	52.9770168	8	-0.021390127	Inside	'10.2.2'	grmzm2g465188_t01	'cell wall.cellulose synthesis.COBRA'
968	Star	2	22808083	54.70986501	76	-0.029176947	Inside	'2.2.1.3.3'	grmzm2g394450_t01	'major CHO metabolism.degradation.sucrose.invertases.vacuolar'

969	Star	2	27790884	58.80007957	13	-0.032182719	Inside	'34.19.1'	grmzm2g178693_t01	'transport.Major Intrinsic Proteins.PIP'
970	Star	2	28788480	60.39948962	5	-0.024239309	Inside	'26.3'	grmzm2g012236_t01	'misc.gluco-, galacto- and mannosidases'
971	Star	2	28788620	60.39963767	12	-0.023889437	Inside	'26.3'	grmzm2g012236_t01	'misc.gluco-, galacto- and mannosidases'
972	Star	2	28960635	60.58154184	5	-0.030823242				
973	Star	2	28970761	60.59224999	8	-0.031083803				
974	Star	2	28972476	60.59406358	35	-0.02957084				
975	Star	2	107216168	76.50296846	7	-0.030529227				
976	Star	2	194191603	105.3998294	6	-0.020841194				
977	Star	2	201217096	109.0293094	10	-0.026005633	Inside	'30.2.17'	grmzm2g140231_t01	'signalling.receptor kinases.DUF 26'
978	Star	2	203650489	111.7689321	15	-0.025557901				
979	Star	2	205289573	113.7617273	5	-0.031413614				
980	Star	2	205289574	113.7617285	9	-0.027499236				
981	Star	2	214729037	127.4005253	5	-0.017802912				
982	Star	2	215881188	128.7144115	7	-0.017742045				
983	Star	2	217125385	130.3224898	5	-0.027701512				
984	Star	2	217810072	131.5466232	5	-0.0237361				
985	Star	3	3123500	9.745986067	7	0.038612596	Inside	'26.28'	grmzm2g085176_t01	'misc.GDSL-motif lipase'
986	Star	3	3780999	13.14827662	22	0.028169623				
987	Star	3	3836355	13.43472146	17	0.031403613				

988	Star	3	14416721	41.56032683	5	-0.028022937				
989	Star	3	17306447	45.29685092	89	-0.032281971	Inside	'15.2'	grmzm2g099340_t01	'metal handling.binding, chelation and storage'
990	Star	3	51981075	56.79858368	90	0.084784527				
991	Star	3	170725018	81.65819468	5	-0.07741098				
992	Star	3	178840635	90.20644881	8	0.036888541				
993	Star	3	192649685	100.9866632	10	-0.050036116	Inside	'17.2.3'	grmzm2g033359_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
994	Star	3	192874331	101.0880183	8	-0.042136484				
995	Star	3	192949443	101.1219071	9	-0.0571714				
996	Star	3	193619852	101.4802146	6	-0.049654665				
997	Star	3	193620690	101.4814585	27	-0.053595039				
998	Star	3	194144683	102.2592936	5	-0.038147905				
999	Star	4	24269222	47.52251807	66	0.054432733				
1000	Star	4	26928416	48.65692848	6	0.054001982				
1001	Star	4	63204562	55.58951138	5	-0.024189406				
1002	Star	4	116242442	58.15932573	10	-0.026678988				
1003	Star	4	194884222	103.0017383	8	-0.034945398				
1004	Star	4	194952409	103.053073	8	-0.027789043				
1005	Star	4	240714112	124.303751	25	-0.017633483				
1006	Star	4	245062382	140.1088204	5	-0.026856027				
1007	Star	4	245730715	144.0453722	15	-0.017329439				
1008	Star	4	245730944	144.0467211	11	-0.017442961				
1009	Star	4	245787531	144.3800244	15	-0.026106421				
1010	Star	4	246077836	146.0899515	5	-0.021761826				
1011	Star	5	1529458	1.89866854	11	-0.026956905				
1012	Star	5	1532216	1.906091195	16	-0.020171388				
1013	Star	5	1735588	2.453429899	6	-0.019083198				
1014	Star	5	1879182	2.839887002	5	-0.025793792				
1015	Star	5	20941271	51.30637712	10	-0.050307121	Inside	'28.1'	grmzm2g146041_t03	'DNA.synthesis/chromatin structure'
1016	Star	5	75996032	67.01800088	5	0.071648285	Inside	'27.3.60'	grmzm2g042278_t01	'RNA.regulation of transcription.NIN-like bZIP-related family'
1017	Star	5	96165401	69.92179085	29	0.054394768				

1018	Star	5	145308951	72.52912618	15	-0.06568065				
1019	Star	5	168868583	80.63961419	67	-0.073140188	Inside	'2.2.1.3.2'	grmzm2g139300_t01	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
1020	Star	5	171396511	83.30241817	34	0.023072258				
1021	Star	5	174165684	85.75501381	25	0.029476756				
1022	Star	5	174821506	86.48707371	5	0.027732203				
1023	Star	5	193444292	102.0960523	28	0.019728235				
1024	Star	5	195201674	103.5571638	6	0.019382462				
1025	Star	5	203772980	114.279637	34	0.032389813				
1026	Star	5	204520039	116.1433154	8	0.021779461				
1027	Star	5	205480420	119.2584897	23	0.024091119				
1028	Star	5	207749910	125.7434999	9	0.032228364				
1029	Star	6	25145461	7.801186431	11	-0.069037952				
1030	Star	6	118288607	43.43874583	32	-0.072025188	Inside	'30.2.99'	grmzm2g059634_t01	'signalling.receptor kinases.misc'
1031	Star	6	119252741	43.97152587	16	-0.049737056				
1032	Star	6	156368499	74.39513977	7	0.053819036				
1033	Star	6	166337059	105.4357129	22	-0.05306977				
1034	Star	6	166977847	107.6073304	44	-0.037821131				
1035	Star	7	18458794	44.19878603	5	-0.027460741				
1036	Star	7	20248668	44.70548997	38	-0.042578673				
1037	Star	7	20380953	44.78804553	7	-0.06171405				
1038	Star	7	21623347	45.56339066	5	-0.02739467	Inside	'34.12'	ac205008.4_fgt002	'transport.metal'
1039	Star	7	25948068	46.52566875	5	-0.043273669				
1040	Star	7	29953895	47.26241735	12	-0.028721815				
1041	Star	7	126449302	67.30732758	10	-0.021768781				
1042	Star	7	151507555	89.39729712	9	-0.032132802				
1043	Star	7	151913077	90.15766003	9	-0.079858825	Inside	'31.1'	grmzm2g057380_t01	'cell.organisation'
1044	Star	7	152316144	90.91580158	14	-0.058489035				
1045	Star	7	167105793	125.7933142	15	0.059219318				
1046	Star	7	168184709	130.4823997	13	0.045148368				

1047	Star	7	168193557	130.520854	5	0.036616985				
1048	Star	8	121670463	65.96008974	11	0.045441796				
1049	Star	8	121963051	66.1316561	6	0.042894621				
1050	Star	8	144585092	74.43452065	10	-0.055256199	Inside	'11.3'	grmzm2g177150_t01	'lipid metabolism.Phospholipid synthesis'
1051	Star	8	144767036	74.6069579	5	-0.056636807	Inside	'16.8.3'	grmzm2g013726_t01	'secondary metabolism.flavonoids.dihydroflavonols'
1052	Star	8	145553053	75.35190474	19	-0.047411963				
1053	Star	8	149499942	78.63341235	8	-0.058651712				
1054	Star	8	163958147	96.68361641	7	0.041224908				
1055	Star	8	164575505	99.62785513	54	0.021849064	Inside	'34.99'	grmzm2g033649_t01	'transport.misc'
1056	Star	8	164575577	99.62807455	6	0.025622402	Inside	'34.99'	grmzm2g033649_t01	'transport.misc'
1057	Star	8	170790378	123.8097673	5	0.018186972				
1058	Star	8	171107120	125.0290187	12	0.025903354				
1059	Star	8	171214220	125.4546422	15	0.023236917				
1060	Star	8	171235640	125.5397669	5	0.03304263	Inside	'33.1'	grmzm2g111472_t01	'development.storage proteins'
1061	Star	9	6999006	8.219780095	15	-0.070552837				
1062	Star	9	7182819	8.716269429	27	-0.043529797				
1063	Star	9	7188622	8.731943661	42	-0.041058477				
1064	Star	9	8451164	12.14214118	5	-0.047028655				
1065	Star	9	134402439	70.88375129	15	0.037960828	Inside	'31.1'	grmzm2g020982_t01	'cell.organisation'
1066	Star	9	134402663	70.88410046	6	0.036821304	Inside	'31.1'	grmzm2g020982_t01	'cell.organisation'
1067	Star	10	252732	-5.658225645	12	-0.051134421				

1068	Star	10	5058530	14.79019912	16	-0.06180889	Inside	'27.3.35'	grmzm2g366264_t01	'RNA.regulation of transcription.bZIP transcription factor family'
1069	Star	10	19566488	34.07832787	6	0.024937218				
1070	Star	10	24052625	35.28519133	6	-0.043928314				
1071	Star	10	25801766	35.75574637	8	0.085574049				
1072	Star	10	66920393	36.73131562	29	0.080127465				
1073	Star	10	89396968	41.46314855	33	0.05899755				
1074	Star	10	128172908	51.27327366	11	0.06244423				
1075	Star	10	129906986	52.44415722	5	0.052854061				
1076	Star	10	140767339	72.41844784	6	-0.032991889				
1077	Star	10	141976268	75.93807797	6	-0.020261715				
1078	Star	10	141976795	75.94005902	15	-0.022617226				
1079	Star	10	144909314	84.63476656	5	-0.022505092				
1080	Star	10	145742058	87.95852999	6	-0.025366805	Inside	'34.1'	grmzm2g006894_t02	'transport.p- and v-ATPases'
1081	Sucr	1	21442536	37.78627202	7	-0.039016626				
1082	Sucr	1	21449014	37.79227512	7	-0.03673907	Inside	'27.3.99'	grmzm2g004259_t01	'RNA.regulation of transcription.unclassified'
1083	Sucr	1	21560442	37.97512826	47	-0.038190551				
1084	Sucr	1	21688795	38.19316881	12	-0.036506395				
1085	Sucr	1	21689538	38.19443099	17	-0.081014671				
1086	Sucr	1	56544677	69.98493609	7	0.091004411				
1087	Sucr	1	69598189	76.61808194	8	0.06063527				
1088	Sucr	1	274645019	167.2992575	6	0.087168737				
1089	Sucr	2	2076282	3.859030239	6	-0.033975872				
1090	Sucr	2	3086016	6.851945591	12	-0.032332673				
1091	Sucr	2	16641157	44.04382336	15	-0.073754786				
1092	Sucr	2	22494974	54.03923714	9	-0.048242813				
1093	Sucr	2	28592546	60.19229134	29	-0.039020967	Inside	'31.1'	grmzm2g052644_t01	'cell.organisation'
1094	Sucr	2	28594174	60.19401294	7	-0.040826501	Inside	'31.1'	grmzm2g052644_t01	'cell.organisation'

1095	Sucr	2	28973324	60.59496034	16	-0.039233491				
1096	Sucr	3	13298136	40.11395447	19	-0.042921756				
1097	Sucr	3	16863398	44.72397195	35	-0.053561956				
1098	Sucr	3	16863598	44.72423056	21	-0.054013921				
1099	Sucr	3	20147626	48.97060192	5	-0.037039448				
1100	Sucr	3	110202362	58.86475128	7	0.123753616				
1101	Sucr	3	174587864	84.65461078	5	0.067483949				
1102	Sucr	3	221390629	140.2263942	10	-0.044839083	Inside	'34.3'	grmzm2g066428_t01	'transport.amino acids'
1103	Sucr	4	11976890	33.81581685	5	0.063333379				
1104	Sucr	4	12389613	33.87001839	25	0.073578644				
1105	Sucr	4	17655938	40.84317673	14	0.091223346				
1106	Sucr	4	49286057	55.14879543	6	-0.093785941				
1107	Sucr	4	60649130	55.4149908	15	-0.083392435				
1108	Sucr	4	110959949	58.04594151	5	-0.074747404				
1109	Sucr	4	140704850	60.02921307	7	-0.041801329				
1110	Sucr	4	173809531	84.19454361	9	-0.032604677				
1111	Sucr	4	173813253	84.2005901	5	-0.034242183				
1112	Sucr	4	173813260	84.20060147	28	-0.039007994				
1113	Sucr	4	175615429	86.62964208	5	-0.045120538	Inside	'27.3.3'	grmzm2g097081_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1114	Sucr	5	7403398	28.1227481	5	0.028118305	Inside	'1.1.1.2'	grmzm2g087435_t01	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
1115	Sucr	5	7568984	28.7329509	5	0.03044864	Inside	'29.4'	grmzm2g014618_t01	'protein.postranslational modification'
1116	Sucr	5	52480298	61.27077539	9	0.075988657				
1117	Sucr	5	68604010	65.0820323	8	0.067664981				
1118	Sucr	5	68606903	65.08331839	14	0.085965605				
1119	Sucr	5	73961139	66.43957914	7	-0.05697045				
1120	Sucr	5	76585969	67.18687192	15	-0.06624114				
1121	Sucr	5	80096521	67.90868619	6	-0.061436645	Inside	'10.6.1'	grmzm2g482256_t01	'cell wall.degradation.cellulases and beta -1,4-glucanases'

1122	Sucr	5	173340061	84.83341391	9	0.040041361	Inside	'26.7'	grmzm2g339523_t01	'misc.oxidases - copper, flavone etc.'
1123	Sucr	5	184390409	93.70403371	8	0.03379498				
1124	Sucr	5	184579203	93.9214921	6	0.048528702				
1125	Sucr	5	204093596	114.9003073	8	0.029700141				
1126	Sucr	5	204527912	116.1688529	7	0.036011734	Inside	'10.6.1'	grmzm2g151257_t01	'cell wall.degradation.cellulases and beta -1,4-glucanases'
1127	Sucr	6	120727054	44.61545648	5	-0.053699952				
1128	Sucr	6	120956190	44.6914035	8	-0.077855121	Inside	'27.3.99'	grmzm2g405498_t01	'RNA.regulation of transcription.unclassified'
1129	Sucr	6	125454322	46.41917569	67	-0.070562811	Inside	'30.3'	grmzm2g152040_t01	'signalling.calcium'
1130	Sucr	6	161584484	86.71512205	10	-0.089408624				
1131	Sucr	6	161899740	87.96647854	58	-0.077401595				
1132	Sucr	7	2586268	7.006474955	17	-0.036400236	Inside	'33.99'	grmzm2g341621_t01	'development.unspecified'
1133	Sucr	7	3570399	12.79412594	7	-0.060608629				
1134	Sucr	7	107347438	54.26102457	17	-0.042958657				
1135	Sucr	7	107748384	54.46470141	23	-0.048482794				
1136	Sucr	7	112739677	57.00023193	20	-0.052798268				
1137	Sucr	7	117566293	59.45210806	8	-0.045031015	Inside	'29.5.9'	grmzm2g095254_t01	'protein.degradation.AAA type'
1138	Sucr	7	140199828	78.55767933	6	0.050727731				
1139	Sucr	7	158146806	102.5659158	5	-0.076514492				
1140	Sucr	7	169562400	134.5167655	17	-0.03237163				
1141	Sucr	8	163333139	94.90114389	20	0.100296937				
1142	Sucr	8	164331901	98.88225877	17	0.036391177				
1143	Sucr	8	164401313	99.09699982	5	0.085464891	Inside	'20.2.99'	grmzm2g114057_t01	'stress.abiotic.unspecified'

1144	Sucr	8	164401324	99.09703335	20	0.065104941	Inside	'20.2.99'	grmzm2g114057_t01	'stress.abiotic.unspecified'
1145	Sucr	8	164401576	99.09780132	7	0.074809194	Inside	'20.2.99'	grmzm2g114057_t01	'stress.abiotic.unspecified'
1146	Sucr	8	168628318	113.9072651	19	0.03649192				
1147	Sucr	8	172057184	128.8248994	5	0.045679833	Inside	'1.1.2.2'	grmzm2g302639_t01	'PS.lightreaction.photosystem I.PSI polypeptide subunits'
1148	Sucr	8	172057190	128.8249236	9	0.044703695	Inside	'1.1.2.2'	grmzm2g302639_t01	'PS.lightreaction.photosystem I.PSI polypeptide subunits'
1149	Sucr	10	2166827	0.955425267	15	-0.093456643	Inside	'33.99'	grmzm2g127379_t01	'development.unspecified'
1150	Sucr	10	2698524	2.792564149	42	-0.098765758				
1151	Sucr	10	3240557	4.665416356	5	-0.076233214				
1152	Sucr	10	77488297	38.59893808	5	-0.053379979	Inside	'20.2.1'	grmzm2g001530_t01	'stress.abiotic.heat'
1153	Sucr	10	85544281	40.43156797	5	-0.03474644	Inside	'26.12'	grmzm2g394500_t01	'misc.peroxidases'
1154	Sucr	10	113451096	45.40733399	7	-0.04402236				
1155	Prin1	1	52690146	67.43745454	28	-0.325669425				
1156	Prin1	1	86713369	83.51202829	6	-0.361580066				
1157	Prin1	1	89352884	84.21946029	45	-0.377779862				
1158	Prin1	1	172752341	94.00861544	12	0.251503889	Inside	'29.5.11.4.3.2'	grmzm2g087608_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
1159	Prin1	1	173107592	94.12366453	7	0.364562902				

1160	Prin1	1	206686287	118.8958806	6	-0.243142768	Inside	'26.10'	grmzm2g089528_t01	'misc.cytochrome P450'
1161	Prin1	1	212358693	123.8826126	13	-0.187087297	Inside	'27.3.27'	grmzm2g152543_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
1162	Prin1	1	219369577	128.5769255	8	-0.230027518	Inside	'30.2.99'	grmzm2g154114_t01	'signalling.receptor kinases.misc'
1163	Prin1	1	221341695	129.3656668	18	-0.363923496	Inside	'27.4'	grmzm2g411041_t01	'RNA.RNA binding'
1164	Prin1	2	2211542	4.46960072	7	0.173420062	Inside	'30.2.11'	grmzm2g452142_t01	'signalling.receptor kinases.leucine rich repeat XI'
1165	Prin1	2	2211569	4.4697226	21	0.190449042	Inside	'30.2.11'	grmzm2g452142_t01	'signalling.receptor kinases.leucine rich repeat XI'
1166	Prin1	2	4299945	11.96658077	43	0.175516911				
1167	Prin1	2	4870077	14.13414888	6	0.185328555				
1168	Prin1	2	37249730	65.55400788	27	0.483745172				
1169	Prin1	2	38625981	66.45985177	6	0.393707078				
1170	Prin1	2	39794143	67.22873216	23	0.5113885	Inside	'34.3'	grmzm2g155491_t01	'transport.amino acids'
1171	Prin1	2	39879711	67.28505273	9	0.434301435				
1172	Prin1	2	185284281	95.94214858	24	0.238072478				
1173	Prin1	2	186269385	97.19232631	15	0.189950055				
1174	Prin1	2	186285785	97.21313925	13	0.19792386				

1175	Prin1	2	186766346	97.99944104	24	0.201406468	Inside	'27.3.6'	grmzm2g417597_t02	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
1176	Prin1	2	187583042	99.21938644	6	0.193767621				
1177	Prin1	2	208604410	118.3005988	5	-0.291990669				
1178	Prin1	3	6560146	25.42100729	9	0.224131566				
1179	Prin1	3	10019848	34.54290833	6	0.147532068				
1180	Prin1	3	10798853	36.10351096	5	0.15355804				
1181	Prin1	3	173210277	83.47025878	7	0.372725567				
1182	Prin1	3	176397560	87.31080195	31	0.329494913				
1183	Prin1	3	177498347	88.92648807	6	-0.320067184				
1184	Prin1	3	187651158	98.71945033	7	-0.295211159				
1185	Prin1	3	208541649	118.8197976	8	-0.369019896				
1186	Prin1	3	212248108	123.3033736	10	-0.263177037				
1187	Prin1	3	212248700	123.3041123	16	-0.250746746	Inside	'26.28'	grmzm2g047129_t02	'misc.GDSL-motif lipase'
1188	Prin1	3	213848298	126.6560335	53	-0.249180593				
1189	Prin1	3	213859916	126.6845705	6	-0.219255555				
1190	Prin1	4	31722606	50.95098413	20	0.217083693				
1191	Prin1	4	90652356	57.4372722	43	0.176560253				
1192	Prin1	4	176411838	87.58887022	6	-0.223703747				
1193	Prin1	4	176745377	87.99059847	6	-0.231675713	Inside	'12.1.1'	grmzm2g428027_t01	'N-metabolism.nitrate metabolism.NR'
1194	Prin1	4	177057759	88.36684435	37	-0.199910793				
1195	Prin1	4	177225650	88.56905925	19	-0.22500953				
1196	Prin1	4	177456322	88.84689021	5	-0.177386326				
1197	Prin1	4	243324592	133.223033	6	0.286380697	Inside	'18.1'	grmzm2g165966_t01	'Co-factor and vitamine metabolism.molybdenum cofactor'
1198	Prin1	5	1875087	2.828866055	9	0.198422919				
1199	Prin1	5	16786267	47.56865354	11	0.186128131				
1200	Prin1	5	18656090	49.4044948	5	0.231641756				
1201	Prin1	5	19607267	50.33047385	6	0.191852193	Inside	'34.99'	grmzm2g124938_t01	'transport.misc'
1202	Prin1	5	22228974	52.4036044	6	0.200210132				
1203	Prin1	5	22628739	52.93108894	19	0.179737138				

1204	Prin1	5	23032929	53.4644122		13	0.192543992				
1205	Prin1	5	26723660	54.83773092		5	0.181309457				
1206	Prin1	5	27926098	55.29207074		8	0.259427803				
1207	Prin1	5	205662825	119.8501543		5	-0.331878313				
1208	Prin1	5	205892823	120.5961956		20	-0.202211883				
1209	Prin1	5	206470516	122.4700502		8	-0.182601165				
1210	Prin1	5	207093116	124.0642086		6	-0.223961036	Inside	'27.3.3'	grmzm2g055204_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1211	Prin1	5	207103724	124.0880847		6	-0.211548066	Inside	'3.2.2'	grmzm2g055150_t01	'minor CHO metabolism.trehalose.TPP'
1212	Prin1	5	207325275	124.5867434		7	-0.207443465				
1213	Prin1	6	2898813	-7.559855335		7	-0.16547695				
1214	Prin1	6	5873783	-4.184534568		14	-0.194407963				
1215	Prin1	6	6894842	-3.026068551		14	-0.172667028				
1216	Prin1	6	8419109	-1.296676302		10	-0.156917082	Inside	'33.99'	grmzm2g061186_t01	'development.unspecified'
1217	Prin1	6	14792950	5.295348837		11	-0.186212199				
1218	Prin1	7	124476542	64.75250337		10	0.249817163				
1219	Prin1	7	153457755	93.06309404		13	0.245403				
1220	Prin1	7	156111925	98.3472492		7	0.241907825				
1221	Prin1	7	156185170	98.49909898		33	0.211508581				
1222	Prin1	7	159147927	104.6414159		9	0.180017249	Inside	'10.8.1'	grmzm2g037411_t01	'cell wall.pectin*esterases.PME'
1223	Prin1	7	159471791	105.3360113		5	0.203425704	Inside	'27.3.21'	grmzm2g169636_t01	'RNA.regulation of transcription.GRAS transcription factor family'
1224	Prin1	7	159471845	105.3361463		9	0.171827824	Inside	'27.3.21'	grmzm2g169636_t01	'RNA.regulation of transcription.GRAS transcription factor family'
1225	Prin1	7	160106822	106.9228459		9	0.206135369				

1226	Prin1	7	169415919	134.4048149	10	-0.207507404				
1227	Prin1	8	2087948	4.782267599	7	0.209648655				
1228	Prin1	8	4386420	11.24086841	11	0.365945724				
1229	Prin1	8	5283586	15.55733838	38	0.216233202	Inside	'10.8.1'	grmzm2g017555_t01	'cell wall.pectin*esterases.PME'
1230	Prin1	8	8255624	20.95732171	5	0.182206933	Inside	'27.3.67'	ac234160.1_fgt001	'RNA.regulation of transcription.putative transcription regulator'
1231	Prin1	8	8403455	21.19881565	12	0.37507853				
1232	Prin1	8	103054530	58.74182186	7	0.277385271	Inside	'26.10'	grmzm2g096029_t01	'misc.cytochrome P450'
1233	Prin1	8	105711842	59.67074769	21	0.237102288				
1234	Prin1	8	108389110	60.44924097	8	0.215129664				
1235	Prin1	8	108849125	60.58213104	19	0.325050069	Inside	'30.5'	grmzm2g072089_t01	'signalling.G-proteins'
1236	Prin1	8	111264320	61.27983748	5	0.202557625				
1237	Prin1	8	117142297	63.44621372	6	0.231321611				
1238	Prin1	8	117976115	63.86193872	6	0.224320933				
1239	Prin1	8	158510179	86.58550567	14	-0.190411215				
1240	Prin1	8	158697511	86.89047423	5	-0.249857512				
1241	Prin1	8	159893599	88.49652739	21	-0.181876531				
1242	Prin1	8	159898572	88.50016935	13	-0.17950465	Inside	'27.3.99'	grmzm2g461793_t01	'RNA.regulation of transcription.unclassified'
1243	Prin1	8	162773842	93.15571435	5	-0.176464664				
1244	Prin1	9	12785133	22.10483847	6	-0.158858265				
1245	Prin1	9	20668779	36.70158796	15	-0.209803433				
1246	Prin1	9	20780641	36.88056228	5	-0.183329952				
1247	Prin1	9	21433294	37.9247786	11	-0.168662562				
1248	Prin1	9	26434264	43.26084016	8	-0.174249746				
1249	Prin1	9	34855540	44.99799089	6	-0.212168913				

1250	Prin1	9	113108447	55.8821261	7	-0.307295112	Inside	'10.7'	grmzm2g073260_t01	'cell wall.modification'
1251	Prin1	9	144471186	92.93120956	15	-0.279214676				
1252	Prin1	9	144622187	93.27205089	19	-0.236362959				
1253	Prin1	9	146785494	99.6308883	11	-0.180210179				
1254	Prin1	10	3622484	6.02423381	5	0.18783093				
1255	Prin1	10	119575302	47.38384118	12	-0.204463112				
1256	Prin1	10	137172137	64.52401076	13	0.291125843				
1257	Prin1	10	140585346	71.90932116	6	0.416795748				
1258	Prin2	1	16528334	33.09583561	9	-0.148363759				
1259	Prin2	1	16774678	33.28332749	16	-0.148531763	Inside	'11.1.10'	grmzm2g445602_t01	'lipid metabolism.FA synthesis and FA elongation.beta ketoacyl CoA synthase'
1260	Prin2	1	17321663	33.69438463	6	-0.167753428				
1261	Prin2	1	21383024	37.73112289	14	-0.220900957				
1262	Prin2	1	21688795	38.19316881	19	-0.158781748				
1263	Prin2	1	21725760	38.25596337	8	-0.160463885				
1264	Prin2	1	46712396	62.60179969	12	0.205604085	Inside	'31.1'	grmzm2g104534_t01	'cell.organisation'
1265	Prin2	1	46752724	62.62839403	29	0.217392494				
1266	Prin2	1	48772229	63.96015846	7	0.183706966				
1267	Prin2	1	51413724	65.71798167	16	0.162964157				
1268	Prin2	1	51506627	65.97678122	7	0.17642016				
1269	Prin2	1	92753447	85.57176721	27	0.151936909				
1270	Prin2	1	228544370	135.6950109	18	-0.296287834	Inside	'31.1'	grmzm2g113202_t01	'cell.organisation'
1271	Prin2	1	229356638	136.3156268	6	-0.360908732				
1272	Prin2	1	241747994	142.5070084	6	-0.352944427				
1273	Prin2	1	244977165	144.1767876	5	-0.366739502	Inside	'34.15'	grmzm2g438960_t01	'transport.potassium'
1274	Prin2	1	245007633	144.1925424	9	-0.295276804				
1275	Prin2	1	252877501	149.8251302	6	-0.308540541				
1276	Prin2	1	253031255	149.9489621	5	-0.279689196				
1277	Prin2	1	253328929	150.1887057	6	-0.305359506				
1278	Prin2	2	4879221	14.16891319	10	-0.178554558				

1279	Prin2	2	5548572	16.71369911	43	-0.154491728				
1280	Prin2	2	5682220	17.22181151	5	-0.156996321				
1281	Prin2	2	26641159	57.94684499	18	-0.149499019				
1282	Prin2	2	27916738	59.06362357	30	-0.172361155				
1283	Prin2	2	28972476	60.59406358	25	-0.235153714				
1284	Prin2	2	34001062	63.56397414	13	-0.186467942	Inside	'20.1'	grmzm2g051943_t01	'stress.biotic'
1285	Prin2	2	34937097	64.04660572	9	0.335345874	Inside	'29.5.9'	grmzm2g138770_t01	'protein.degradation.AAA type'
1286	Prin2	2	81996078	75.87752354	6	-0.253830438				
1287	Prin2	2	124738310	77.33837071	9	-0.276512367				
1288	Prin2	2	124769416	77.34049122	25	-0.297074114				
1289	Prin2	3	2915029	8.667233227	5	-0.195341132	Inside	'17.2.3'	grmzm2g060991_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
1290	Prin2	3	3185414	10.0663659	10	-0.231447784				
1291	Prin2	3	3386685	11.10786166	18	-0.158579918	Inside	'26.28'	grmzm2g400929_t01	'misc.GDSL-motif lipase'
1292	Prin2	3	10750451	36.00654587	9	-0.164241331	Inside	'34.18'	grmzm2g051753_t01	'transport.unspecified anions'
1293	Prin2	3	10838771	36.18347982	6	-0.116432701				
1294	Prin2	3	13300926	40.11756205	6	-0.186344905				
1295	Prin2	3	13633702	40.54785389	18	-0.163225589				
1296	Prin2	3	13634126	40.54840214	12	-0.167661347				
1297	Prin2	3	14416721	41.56032683	26	-0.182957628				
1298	Prin2	3	17306447	45.29685092	9	-0.237524461	Inside	'15.2'	grmzm2g099340_t01	'metal handling.binding, chelation and storage'
1299	Prin2	3	19698629	48.39003196	8	-0.195530153				
1300	Prin2	3	19800505	48.52176145	5	-0.198444438				
1301	Prin2	3	51981075	56.79858368	23	0.417597478				

1302	Prin2	3	54021465	57.26319567	17	0.319862133				
1303	Prin2	3	106489882	58.60975416	5	0.31895293				
1304	Prin2	3	136646099	63.07155567	5	-0.237479608	Inside	'29.4'	grmzm2g010775_t01	'protein.postranslational modification'
1305	Prin2	3	171862276	82.33409418	6	0.513407834				
1306	Prin2	3	172148591	82.5754152	5	0.518185895				
1307	Prin2	3	173219900	83.47836954	15	0.538906436				
1308	Prin2	3	193922818	101.9299488	10	0.197939448				
1309	Prin2	3	198668625	105.7679086	5	0.17551164				
1310	Prin2	4	828147	2.931410178	7	0.187879628	Inside	'27.3.21'	grmzm2g073823_t01	'RNA.regulation of transcription.GRAS transcription factor family'
1311	Prin2	4	5696047	19.49225268	12	-0.299402936				
1312	Prin2	4	42018416	54.27865297	7	-0.145631996				
1313	Prin2	4	96251735	57.74714448	7	-0.124855363				
1314	Prin2	4	125186338	58.42286198	72	-0.130712371				
1315	Prin2	4	177668855	89.1123214	6	-0.18872756				
1316	Prin2	4	199778387	105.9507817	14	-0.193006416				
1317	Prin2	4	242574395	130.3125709	11	-0.281573519				
1318	Prin2	5	929964	0.282533564	43	-0.19293743				
1319	Prin2	5	1574000	2.018545222	10	-0.231021725				
1320	Prin2	5	1580722	2.036636261	5	-0.228448538	Inside	'33.99'	ac202974.3_fgt004	'development.unspecified'
1321	Prin2	5	1842198	2.740351301	7	-0.153703207	Inside	'20.2.1'	grmzm2g138511_t01	'stress.abiotic.heat'
1322	Prin2	5	2347751	4.958870956	12	-0.152516959	Inside	'27.3.8'	grmzm2g144188_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
1323	Prin2	5	7094245	26.093099	26	0.150251126				
1324	Prin2	5	10372835	33.33515135	9	0.176034799	Inside	'29.4.1.57'	grmzm2g158359_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
1325	Prin2	5	26734713	54.84190728	11	0.353426391				
1326	Prin2	5	73804215	66.39516104	21	0.292651485				
1327	Prin2	5	108262797	70.32363616	14	0.366236504				

1328	Prin2	5	143236820	72.10704824	7	0.356617661	Inside	'27.3.35'	grmzm2g158313_t01	'RNA.regulation of transcription.bZIP transcription factor family'
1329	Prin2	5	164299446	76.94625198	6	-0.300410103				
1330	Prin2	5	165991682	78.08035909	12	0.301900822				
1331	Prin2	5	169382477	81.27535729	5	-0.317414291				
1332	Prin2	5	188788930	98.54955746	8	0.15465899				
1333	Prin2	5	194052252	102.6015186	6	0.184420996				
1334	Prin2	5	203652758	113.8406769	6	0.258309313				
1335	Prin2	5	205472185	119.231778	50	0.148970386	Inside	'29.5.11.4.2'	grmzm2g053303_t01	'protein.degradation.ubiquitin.E3.RING'
1336	Prin2	5	207751210	125.7483283	10	0.22159592				
1337	Prin2	5	209217720	128.3485035	30	0.293163871				
1338	Prin2	5	209930161	130.9277607	5	0.227274598				
1339	Prin2	6	867384	-9.864659918	6	0.365645779				
1340	Prin2	6	1957524	-8.627816461	8	0.454475095				
1341	Prin2	6	118739798	43.69898027	13	-0.578903834				
1342	Prin2	6	119772986	44.24786955	73	-0.412080895				
1343	Prin2	6	120956190	44.6914035	7	-0.327835409	Inside	'27.3.99'	grmzm2g405498_t01	'RNA.regulation of transcription.unclassified'
1344	Prin2	6	165586711	102.9473046	27	-0.297375391				
1345	Prin2	6	165589669	102.9571143	8	-0.289894217				
1346	Prin2	6	165667455	103.215079	20	-0.261489914				
1347	Prin2	6	165667652	103.2157324	5	-0.237252512				
1348	Prin2	6	166076222	104.570689	13	-0.302483541				
1349	Prin2	7	5428540	23.50772999	34	-0.287429645				
1350	Prin2	7	22002213	45.79983088	10	-0.179913126	Inside	'27.3.3'	grmzm2g176175_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1351	Prin2	7	27302170	46.77471414	16	-0.174347347				
1352	Prin2	7	27327128	46.7793044	9	-0.205664769	Inside	'34.13'	grmzm2g156794_t01	'transport.peptides and oligopeptides'
1353	Prin2	7	29146881	47.11399196	45	-0.189498059				

1354	Prin2	7	124223168	64.44761155	10	-0.142549038				
1355	Prin2	7	156185236	98.49923581	6	-0.608676503				
1356	Prin2	7	156689760	99.54520289	27	-0.178439732				
1357	Prin2	7	166657242	123.8438631	41	0.243268708				
1358	Prin2	7	167223656	126.3055595	17	0.239027751				
1359	Prin2	7	168146779	130.3175518	8	0.250707874	Inside	'27.3.20'	ac155434.2_fgt005	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
1360	Prin2	7	168157307	130.3633076	7	0.263440613	Inside	'27.3.8'	ac155434.2_fgt006	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
1361	Prin2	8	10739260	27.73471036	6	-0.202260838				
1362	Prin2	8	103399576	58.8624408	6	0.15144341				
1363	Prin2	8	159090160	87.53999331	9	0.172388561				
1364	Prin2	8	160611990	89.64768912	20	0.195427349				
1365	Prin2	8	160612122	89.6479463	28	0.216705415				
1366	Prin2	8	164575465	99.62773322	5	0.134691981	Inside	'34.99'	grmzm2g033649_t01	'transport.misc'
1367	Prin2	8	170618195	123.1071582	8	0.141301951				
1368	Prin2	8	170786240	123.7938509	6	0.133385539				
1369	Prin2	8	173793234	135.8235771	8	0.119843765	Inside	'1.5.1'	grmzm2g118770_t01	'PS.carbon concentrating mechanism.C4'
1370	Prin2	8	173864083	136.1091964	9	0.124329055				
1371	Prin2	9	2701441	-3.388186607	59	-0.379560098	Inside	'27.3.20'	grmzm2g026833_t02	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
1372	Prin2	9	3689306	-0.719907238	18	-0.378505593				
1373	Prin2	9	7182819	8.716269429	14	-0.268943698				
1374	Prin2	9	109417983	53.84202072	8	0.254711069				
1375	Prin2	9	109658976	53.91939367	7	0.188444788				
1376	Prin2	9	117715320	57.64391617	6	0.137706712				
1377	Prin2	9	138570437	79.39501909	34	0.310626673	Inside	'20.1'	grmzm2g149798_t01	'stress.biotic'

1378	Prin2	10	5058530	14.79019912	46	-0.424128374	Inside	'27.3.35'	grmzm2g366264_t01	'RNA.regulation of transcription.bZIP transcription factor family'
1379	Prin2	10	5427445	17.07840286	12	-0.377394519				
1380	Prin2	10	6191195	21.4060557	6	-0.359938003	Inside	'27.3.18'	grmzm2g052515_t01	'RNA.regulation of transcription.E2F/DP transcription factor family'
1381	Prin2	10	9023970	24.98301526	9	-0.188824159				
1382	Prin2	10	22382517	34.8358978	9	0.185011049				
1383	Prin2	10	24154443	35.31258248	6	0.360806077				
1384	Prin2	10	79797589	39.13112595	6	0.260220052				
1385	Prin2	10	85540940	40.43084945	25	0.314408789				
1386	Prin2	10	86726870	40.71912634	15	0.304643229				
1387	Prin2	10	113194309	45.32268893	8	0.36996183	Inside	'27.1'	grmzm2g158300_t01	'RNA.processing'
1388	Prin2	10	133029713	57.10017332	5	-0.138816574				
1389	Prin2	10	142607850	78.31225962	6	-0.114292892				
1390	Prin2	10	142607858	78.31228969	7	-0.146722504				
1391	Prin2	10	142646940	78.45920294	5	-0.242947614				
1392	Prin2	10	143724295	81.34148153	8	-0.154720679	Inside	'30.2.24'	grmzm2g000620_t01	'signalling.receptor kinases.S-locus glycoprotein like'
1393	Prin2	10	144247405	82.22431479	10	-0.222878534				
1394	Prin2	10	144605053	83.42035782	8	-0.228222027				

Significant SNP Information										
SNP No.	**Trait**	**Chr**	**Physical Position (AGPv1)**	**Imputed cM on NAM Map**	**Resample Model Inclusion Probability**	**Average SNP effect**	**Distance to Gene**	**Bincode**	**Gene ID**	**Category**
1	AA	1	13935133	28.26096353	26	-0.085551628	-2201	'33.99'	grmzm2g123986_t01	'development.unspecified'

2	AA	1	16780363	33.28759975	31	-0.081912456	-4386	'11.1.10'	grmzm2g445602_t01	'lipid metabolism.FA synthesis and FA elongation.beta ketoacyl CoA synthase'
3	AA	1	33393305	52.652275	11	0.097059759	-1430	'34.3'	grmzm2g149481_t04	'transport.amino acids'
4	AA	1	165885858	91.92724657	9	0.091736639	-410789	'26.7'	grmzm2g369987_t01	'misc.oxidases - copper, flavone etc.'
5	AA	1	177389147	95.59351325	20	-0.098789746	-376086	'29.2.4'	ac199908.4_fgt002	'protein.synthesis.elongation'
6	AA	1	182391497	97.70267302	18	-0.094955313	-2273	'27.4'	grmzm2g110143_t01	'RNA.RNA binding'
7	AA	1	192608853	106.1391166	12	-0.107384883	-239795	'27.3'	grmzm2g179366_t01	'RNA.regulation of transcription'
8	AA	1	205585447	117.8354213	6	-0.061343453	-35648	'27.3.11'	grmzm2g179677_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
9	AA	1	205728648	117.9733694	10	-0.053004958	-101444	'25.9'	grmzm2g095579_t01	'C1-metabolism.dihydroneopterin aldolase'
10	AA	1	207120770	119.3144261	15	-0.061520606	-97318	'7.1.2'	grmzm2g122126_t01	'OPP.oxidative PP.6-phosphogluconolactonase'

11	AA	1	207135155	119.3282834	8	-0.073649634	-11302	'17.4.1'	grmzm2g348452_t01	'hormone metabolism.cytokinin.synthesis-degradation'
12	AA	1	208348395	120.4695879	10	-0.053930899	-3872	'33.99'	grmzm2g125557_t01	'development.unspecified'
13	AA	1	210147485	121.9613779	9	-0.073635914	-69318	'3.2.3'	grmzm2g079928_t01	'minor CHO metabolism.trehalose.potential TPS/TPP'
14	AA	1	211910691	123.4234132	9	-0.087541648	-5087	'4.2.4'	grmzm2g139360_t01	'glycolysis.plastid branch.phosphofructokinase (PFK)'
15	AA	1	218527234	128.2400336	6	-0.056062356	-63498	'34.99'	grmzm2g115635_t01	'transport.misc'
16	AA	2	3369867	8.460233144	8	0.081076721	-9429	'31.3'	grmzm2g047590_t03	'cell.cycle'
17	AA	2	4452933	12.54822136	11	0.119133386	-94242	'30.2.17'	grmzm2g363066_t01	'signalling.receptor kinases.DUF 26'
18	AA	2	5461777	16.38371574	10	0.080146925	-80220	'30.2.3'	grmzm2g055844_t01	'signalling.receptor kinases.leucine rich repeat III'
19	AA	2	6695031	20.19476759	27	0.044923744	-14118	'27.3.35'	grmzm2g131961_t01	'RNA.regulation of transcription.bZIP transcription factor family'

20	AA	2	10533238	30.11324699	5	0.050106955	-11750	'16.1.5'	grmzm2g049538_t01	'secondary metabolism.isoprenoids.terpenoids'
21	AA	2	11104224	31.84202766	21	0.071319845	-387	'29.4'	grmzm2g102088_t02	'protein.postranslational modification'
22	AA	2	13443804	37.94791551	22	0.054661567	-65666	'28.1'	ac195235.3_fgt003	'DNA.synthesis/chromatin structure'
23	AA	2	20521754	51.29525101	5	0.086430763	-37267	'27.3.3'	grmzm2g475678_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
24	AA	2	24175937	56.21986729	6	0.144114822	-214799	'31.2'	grmzm2g124371_t01	'cell.division'
25	AA	2	37317423	65.59856319	51	0.074663447	-6501	'29.5.11.1'	grmzm2g045117_t01	'protein.degradation.ubiquitin.ubiquitin'
26	AA	2	186765375	97.99753568	60	0.070644387	-40929	'20.2.1'	grmzm2g474367_t01	'stress.abiotic.heat'
27	AA	2	186894631	98.25116993	31	0.074688245	-47361	'27.3.57'	grmzm2g052908_t01	'RNA.regulation of transcription.JUMONJI family'
28	AA	2	209329786	120.0730566	6	0.043269516	-35133	'30.5'	grmzm2g128771_t01	'signalling.G-proteins'
29	AA	2	215989909	128.8383944	6	0.040326516	-77092	'34.99'	grmzm2g068220_t01	'transport.misc'

30	AA	2	217758767	131.4548964	10	0.05228333	-45009	'29.4.1.57'	grmzm2g349875_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
31	AA	3	106253820	58.5935399	18	0.080180593	-13791	'28.99'	grmzm2g351307_t01	'DNA.unspecified'
32	AA	3	136272706	62.99233029	6	0.116539144	-235077	'29.4'	grmzm2g027632_t01	'protein.postranslational modification'
33	AA	3	146217490	65.77990892	10	0.108646925	-534449	'30.3'	grmzm2g106945_t01	'signalling.calcium'
34	AA	3	170786664	81.70076623	6	0.085704188	-62304	'30.2.11'	grmzm2g167253_t01	'signalling.receptor kinases.leucine rich repeat XI'
35	AA	3	173982599	84.12121149	71	0.098605713	-44754	'11.8.3'	grmzm2g149617_t01	'lipid metabolism."exotics" (steroids, squalene etc).UDP-glucose:sterol glucosyltransferase'
36	AA	3	176799382	87.90057838	11	0.102983913	-142087	'16.2'	grmzm2g165192_t01	'secondary metabolism.phenylpropanoids'
37	AA	3	211702191	122.6221889	6	-0.041297758	-246240	'29.4'	grmzm2g150952_t01	'protein.postranslational modification'

38	AA	3	212222090	123.2709088	6	-0.046587836	-162233	'13.1.4.1'	grmzm2g004382_t01	'amino acid metabolism.synthesis.branched chain group.common'
39	AA	3	212226136	123.2759574	5	-0.06529147	-166279	'13.1.4.1'	grmzm2g004382_t01	'amino acid metabolism.synthesis.branched chain group.common'
40	AA	3	212726714	123.9011201	5	-0.044492619	-139	'34.15'	grmzm2g022915_t01	'transport.potassium'
41	AA	3	214950753	128.5482503	22	-0.045348234	-38970	'34.99'	grmzm2g000593_t02	'transport.misc'
42	AA	4	171000056	79.4221761	40	-0.050350535	-123565	'16.8.3'	grmzm2g099420_t01	'secondary metabolism.flavonoids.dihydroflavonols'
43	AA	4	171777409	80.83845057	9	-0.04494486	-5004	'29.5.11.4.2'	grmzm2g130002_t01	'protein.degradation.ubiquitin.E3.RING'
44	AA	4	171777978	80.83927823	30	-0.046656729	-5573	'29.5.11.4.2'	grmzm2g130002_t01	'protein.degradation.ubiquitin.E3.RING'
45	AA	4	172891786	82.70364317	8	-0.057980397	-7920	'29.2.1.2.2.39'	grmzm2g411764_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L39'
46	AA	4	238824264	119.1769941	5	-0.040095238	-9761	'31.2'	grmzm2g030542_t01	'cell.division'

47	AA	4	245327128	141.6682023	5	-0.092328356	-12766	'29.5.7'	grmzm2g006069_t01	'protein.degradation.metalloprotease'
48	AA	5	1122	-0.317541556	5	0.044960637				
49	AA	5	1049462	0.606846713	32	0.05132495	-2312	'26.22'	grmzm2g013042_t01	'misc.short chain dehydrogenase/reductase (SDR)'
50	AA	5	1621759	2.147079874	12	0.055070047	-6324	'11.1.13'	grmzm2g326195_t01	'lipid metabolism.FA synthesis and FA elongation.acyl-CoA binding protein'
51	AA	5	2598377	6.596313039	23	0.043582718	-3354	'16.8.3'	grmzm2g110952_t01	'secondary metabolism.flavonoids.dihydroflavonols'
52	AA	5	2608498	6.662437668	8	0.045011664	-1199	'16.8.3'	grmzm2g110881_t01	'secondary metabolism.flavonoids.dihydroflavonols'
53	AA	5	25375392	54.32828941	25	0.052640963	-90	'34.19.2'	grmzm2g305446_t02	'transport.Major Intrinsic Proteins.TIP'
54	AA	5	27056845	54.96362449	17	0.05259327	-90551	'13.2.6.2'	grmzm2g174145_t01	'amino acid metabolism.degradation.aromatic aa.tyrosine'
55	AA	5	27066959	54.96744605	6	0.0486529	-100665	'13.2.6.2'	grmzm2g174145_t01	'amino acid metabolism.degradation.aromatic aa.tyrosine'
56	AA	5	27983433	55.3137347	6	0.164199593	-11216	'13.2.3.5'	grmzm2g100360_t01	'amino acid metabolism.degradation.aspartate family.lysine'
57	AA	5	28303009	55.43448613	8	0.241124487	-2863	'28.99'	grmzm2g138744_t01	'DNA.unspecified'

58	AA	5	29915257	56.04367218	6	0.057108904	-1304	'29.2.1.2.2.23'	grmzm2g123495_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L23'
59	AA	5	30338901	56.28511551	23	0.221984742	-18381	'29.6'	grmzm2g458208_t01	'protein.folding'
60	AA	5	30990738	56.84135946	15	0.062976606	-24822	'29.5.11.3'	grmzm2g146374_t01	'protein.degradation.ubiquitin.E2'
61	AA	5	31224995	57.04126226	6	0.071656737	-4130	'27.3.67'	grmzm2g046438_t01	'RNA.regulation of transcription.putative transcription regulator'
62	AA	5	61094522	63.52954633	39	0.213909802	-101947	'27.3.35'	grmzm2g000171_t01	'RNA.regulation of transcription.bZIP transcription factor family'
63	AA	5	89493802	69.57132155	5	-0.046703904	-342485	'33.99'	grmzm2g131638_t01	'development.unspecified'
64	AA	5	185678096	95.1872289	9	-0.087360449	-81323	'27.3.25'	grmzm2g095904_t01	'RNA.regulation of transcription.MYB domain transcription factor family'

65	AA	5	191362737	100.706813	70	0.073417146	-11175	'27.3.3'	grmzm2g041839_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
66	AA	5	200532850	108.3793509	5	-0.123414326	-1320	'27.3.8'	grmzm2g140694_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
67	AA	5	202772744	110.6933233	16	-0.07001925	-1374	'30.5'	grmzm2g085049_t04	'signalling.G-proteins'
68	AA	5	204749015	116.8860416	7	0.083646321	-38969	'27.3.18'	grmzm2g378665_t01	'RNA.regulation of transcription.E2F/DP transcription factor family'
69	AA	5	206467622	122.460663	14	-0.121162674	-4066	'27.3.6'	grmzm2g036092_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
70	AA	5	207521465	125.022936	8	-0.056063751	-129402	'31.1'	grmzm2g061950_t01	'cell.organisation'
71	AA	5	207525531	125.0317036	16	-0.085116692	-133468	'31.1'	grmzm2g061950_t01	'cell.organisation'
72	AA	5	209222556	128.3660113	6	-0.173721735	-9430	'27.2'	grmzm2g055859_t01	'RNA.transcription'

73	AA	5	211196887	135.9702305	23	-0.069770475	-52434	'29.1.5'	grmzm2g478664_t01	'protein.aa activation.isoleucine-tRNA ligase'
74	AA	5	211196920	135.9703687	64	-0.080191679	-52467	'29.1.5'	grmzm2g478664_t01	'protein.aa activation.isoleucine-tRNA ligase'
75	AA	6	3992126	-6.319411877	5	-0.093170865	-114191	'27.3.27'	grmzm2g030325_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
76	AA	6	25737849	7.832137091	22	-0.098932689	-401027	'31.1'	grmzm2g037140_t01	'cell.organisation'
77	AA	6	31537911	8.165545093	17	-0.116422372	-148874	'29.5.11.4.2'	grmzm2g567897_t01	'protein.degradation.ubiquitin.E3.RING'
78	AA	6	79774320	11.21454839	11	-0.073829076	-22692	'20.1'	grmzm2g103033_t01	'stress.biotic'
79	AA	6	97578306	23.60510141	10	-0.064507888	-37737	'29.4'	grmzm2g018280_t01	'protein.postranslational modification'
80	AA	6	97988317	23.94996475	41	-0.052440749	-158913	'23.3.3'	grmzm2g162605_t03	'nucleotide metabolism.salvage.NUDIX hydrolases'
81	AA	6	98199018	24.12718696	9	-0.053340471	-60622	'34.15'	grmzm2g146760_t01	'transport.potassium'

82	AA	6	98204433	24.13174155	5	-0.05362577	-66037	'34.15'	grmzm2g146760_t01	'transport.potassium'
83	AA	6	98282571	24.19746402	8	-0.0579035	-3437	'27.3.38'	grmzm2g180654_t02	'RNA.regulation of transcription.AT-rich interaction domain containing transcription factor family'
84	AA	6	99986756	25.63086689	5	-0.061329207	-41187	'31.1'	grmzm2g112337_t03	'cell.organisation'
85	AA	6	110900537	37.5884191	5	-0.050221184	-91005	'29.5'	grmzm2g167733_t01	'protein.degradation'
86	AA	6	163949428	95.77601009	10	0.05979466	-4289	'29.5.11.3'	grmzm2g381709_t01	'protein.degradation.ubiquitin.E2'
87	AA	6	164286396	96.9462491	7	0.091622048	-4939	'24'	grmzm2g458607_t01	'Biodegradation of Xenobiotics'
88	AA	6	165260207	101.8645066	9	0.099911569	-5006	'34.2'	grmzm2g160430_t01	'transport.sugars'
89	AA	7	27056327	46.72949889	30	0.069854871	-395034	'23.2'	grmzm2g173063_t01	'nucleotide metabolism.degradation'
90	AA	7	28113557	46.92394381	6	0.042729427	-82741	'17.2.1'	grmzm2g003789_t01	'hormone metabolism.auxin.synthesis-degradation'
91	AA	7	28365776	46.97033173	8	0.044151146	-241637	'17.2.1'	grmzm2g016958_t01	'hormone metabolism.auxin.synthesis-degradation'

92	AA	7	37151920	48.23780461	7	0.043532305	-23688	'34.7'	grmzm2g139639_t01	'transport.phosphate'
93	AA	7	69012950	49.23292513	5	0.055519521	-849084	'30.2.11'	grmzm2g092604_t01	'signalling.receptor kinases.leucine rich repeat XI'
94	AA	7	83079854	49.85510044	8	0.04954641	-237227	'30.3'	grmzm2g140949_t01	'signalling.calcium'
95	AA	7	84174593	49.90284891	8	0.04989524	-471934	'26.10'	grmzm2g027041_t01	'misc.cytochrome P450'
96	AA	7	139404320	77.80580845	69	0.087922424	-68747	'31.1'	grmzm2g046186_t01	'cell.organisation'
97	AA	7	143287112	81.20148454	20	0.054812272	-104020	'20.1'	grmzm2g028713_t01	'stress.biotic'
98	AA	7	150564610	88.45717741	32	0.06982965	-6831	'30.2.24'	grmzm2g465999_t01	'signalling.receptor kinases.S-locus glycoprotein like'
99	AA	7	167987389	129.6248256	6	-0.118145535	-222236	'27.3.27'	grmzm2g430849_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
100	AA	7	169227583	134.2608759	5	-0.06723496	-10719	'27.3.66'	grmzm2g005732_t01	'RNA.regulation of transcription.Psudo ARR transcription factor family'

101	AA	8	103390158	58.85914851	73	0.067148754	-151198	'20.1'	grmzm2g047152_t01	'stress.biotic'
102	AA	8	117265267	63.49683053	11	0.076581176	-67450	'20.2.3'	ac204277.3_fgt006	'stress.abiotic.drought/salt'
103	AA	8	161883485	91.64355886	10	-0.044006499	-212095	'27.3.99'	grmzm2g001088_t01	'RNA.regulation of transcription.unclassified'
104	AA	8	161918620	91.67206646	11	-0.049289191	-32027	'27.3.55'	ac183950.2_fgt003	'RNA.regulation of transcription.HDA'
105	AA	8	161918881	91.67227822	36	-0.053035985	-32288	'27.3.55'	ac183950.2_fgt003	'RNA.regulation of transcription.HDA'
106	AA	8	161918960	91.67234232	7	-0.052130376	-32367	'27.3.55'	ac183950.2_fgt003	'RNA.regulation of transcription.HDA'
107	AA	8	163479600	95.34210376	11	-0.050996234	-41353	'29.5.5'	grmzm2g172829_t01	'protein.degradation.serine protease'
108	AA	8	170533744	122.5329248	12	-0.071952615	-8831	'26.8'	grmzm2g440003_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
109	AA	8	170538447	122.5649034	10	-0.073601987	-13534	'26.8'	grmzm2g440003_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
110	AA	8	170538683	122.5665081	58	-0.067975625	-13770	'26.8'	grmzm2g440003_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'

111	AA	9	5956414	5.403679997	8	-0.064234269	-105	'28.1'	grmzm2g093772_t01	'DNA.synthesis/chromatin structure'
112	AA	9	6999573	8.221311595	5	-0.059674728	-205967	'20.2.1'	grmzm2g097620_t01	'stress.abiotic.heat'
113	AA	9	7239482	8.869319404	9	-0.047569805	-97437	'31.1'	grmzm2g017257_t01	'cell.organisation'
114	AA	9	7239499	8.869365322	5	-0.043097808	-97454	'31.1'	grmzm2g017257_t01	'cell.organisation'
115	AA	9	9143611	13.42656327	6	-0.065774986	-36600	'17.5.1'	grmzm2g066358_t01	'hormone metabolism.ethylene.synthesis-degradation'
116	AA	9	9143948	13.42709594	23	-0.0560366	-297	'33.99'	grmzm2g088053_t01	'development.unspecified'
117	AA	9	20663923	36.69381857	30	-0.056366108	-1102	'26.13'	grmzm2g404897_t04	'misc.acid and other phosphatases'
118	AA	9	20665105	36.69570972	16	-0.062945098	-2284	'26.13'	grmzm2g404897_t04	'misc.acid and other phosphatases'
119	AA	9	20668477	36.70110477	32	-0.060619679	-2938	'34.2'	grmzm2g404965_t02	'transport.sugars'

120	AA	9	23215839	39.99840064	20	-0.058749345	-198908	'3.4.3'	grmzm2g010768_t01	'minor CHO metabolism.myo-inositol.InsP Synthases'
121	AA	9	86468357	46.72572703	12	-0.079201882	-1889	'20.2'	grmzm2g083655_t01	'stress.abiotic'
122	AA	9	116766687	57.30110688	5	0.11081529	-118	'29.5'	grmzm2g132238_t01	'protein.degradation'
123	AA	9	116766688	57.30110724	6	0.112627991	-119	'29.5'	grmzm2g132238_t01	'protein.degradation'
124	AA	9	133018761	68.62115268	53	-0.087203152	-45072	'9.1.2'	ac206223.3_fgt010	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
125	AA	9	135396489	72.43328428	16	-0.066126002	-12438	'28.1'	grmzm2g063151_t01	'DNA.synthesis/chromatin structure'
126	AA	9	140748270	85.13070924	14	0.115475213	-13160	'31.3.1'	grmzm2g393515_t01	'cell.cycle.peptidylprolyl isomerase'
127	AA	10	18523635	33.86783022	6	-0.110952691	-132048	'29.5'	grmzm2g015238_t01	'protein.degradation'

128	AA	10	99357506	43.32459092	9	-0.055016754	-118526	'7.1.1'	grmzm2g177077_t01	'OPP.oxidative PP.G6PD'
129	AA	10	102164870	43.55066643	36	-0.048664179	-5097	'29.5.11.4.2'	grmzm2g035899_t03	'protein.degradation.ubiquitin.E3.RING'
130	AA	10	102628153	43.57658233	13	-0.054721851	-435574	'33.99'	ac204711.3_fgt003	'development.unspecified'
131	AA	10	111326819	44.71918576	13	-0.049289342	-56084	'11.9.2.1'	grmzm2g153232_t01	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
132	AA	10	140890733	72.76364342	23	0.113234282	-16536	'10.7'	grmzm2g142857_t01	'cell wall.modification'
133	AA	10	143035801	79.92097141	6	0.075903997	-17469	'34.16'	grmzm2g148492_t01	'transport.ABC transporters and multidrug resistance systems'
134	AA	10	146203306	89.79952703	10	0.075504717	-2542	'26.2'	grmzm2g067424_t01	'misc.UDP glucosyl and glucoronyl transferases'
135	AA	10	146234149	89.92263189	71	0.074311201	-643	'27.3.99'	grmzm2g066981_t07	'RNA.regulation of transcription.unclassified'

136	AA	10	148094143	99.83248299	14	0.059544285	-2526	'27.3.67'	grmzm2g074107_t01	'RNA.regulation of transcription.putative transcription regulator'
137	AA	10	148490503	102.0543415	7	0.053929166	-431	'29.4'	grmzm2g104658_t01	'protein.postranslational modification'
138	AA	10	148496397	102.0873812	22	0.050154105	-6325	'29.4'	grmzm2g104658_t01	'protein.postranslational modification'
139	Chla	1	64135223	73.46224774	7	-1.078365591	-31100	'26.10'	grmzm2g459563_t01	'misc.cytochrome P450'
140	Chla	1	68902676	76.2644894	18	-1.11398638	-487854	'30.4.1'	grmzm2g111208_t01	'signalling.phosphinositides.phosphatidylinositol-4-phosphate 5-kinase'
141	Chla	1	70951065	77.30587192	7	-1.009978169	-16544	'7.1.1'	grmzm2g179521_t01	'OPP.oxidative PP.G6PD'
142	Chla	1	71560037	77.6154678	8	-1.079988686	-3479	'13.99'	grmzm2g096682_t02	'amino acid metabolism.misc'
143	Chla	1	114166513	89.09571398	6	-1.00096502	-118419	'29.5.11.4.2'	grmzm2g069070_t01	'protein.degradation.ubiquitin.E3.RING'

144	Chla	1	126428605	89.3753375	5	-1.429246348	-544181	'25'	grmzm2g421493_t01	'C1-metabolism'
145	Chla	1	139906399	89.5123698	6	-1.832781348	-65027	'17.5.1'	grmzm2g162158_t01	'hormone metabolism.ethylene.synthesis-degradation'
146	Chla	1	179696720	96.44277983	6	2.546725312	-190275	'24.2'	grmzm2g067028_t01	'Biodegradation of Xenobiotics.lactoylglutathione lyase'
147	Chla	1	280711700	175.6831083	16	-1.675800132	-52603	'10.2'	grmzm2g028286_t01	'cell wall.cellulose synthesis'
148	Chla	1	283540151	178.0419378	6	-1.065382143	-143465	'31.1'	grmzm2g568484_t01	'cell.organisation'
149	Chla	1	283829657	178.2988059	23	-1.082471106	-432971	'31.1'	grmzm2g568484_t01	'cell.organisation'
150	Chla	1	283830436	178.2994971	6	-1.062943975	-433750	'31.1'	grmzm2g568484_t01	'cell.organisation'
151	Chla	1	284054336	178.4981554	14	-1.146037697	-5982	'13.1.7.9'	grmzm2g058584_t01	'amino acid metabolism.synthesis.histidine.histidinol dehydrogenase'

152	Chla	2	1944162	3.262633877	5	0.896831894	-1230	'17.6.3'	grmzm2g068202_t01	'hormone metabolism.gibberelin induced-regulated-responsive-activated'
153	Chla	2	2021345	3.611041843	12	0.871536011	-14184	'1.1.1.1'	grmzm2g039996_t01	'PS.lightreaction.photosystem II.LHC-II'
154	Chla	2	2211569	4.4697226	48	0.962856414	-141542	'27.3.5'	grmzm2g040736_t01	'RNA.regulation of transcription.ARR'
155	Chla	2	3128671	6.982329207	6	0.876581025	-322	'27.3.20'	grmzm2g035370_t04	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
156	Chla	2	23800488	55.83244658	6	1.46067929	-104976	'21.1'	grmzm2g026656_t01	'redox.thioredoxin'
157	Chla	2	23881650	55.91619654	8	1.16323104	-77766	'34.16'	grmzm2g177812_t01	'transport.ABC transporters and multidrug resistance systems'
158	Chla	2	24284899	56.33230369	13	1.367200877	-33020	'27.3.25'	grmzm2g447090_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
159	Chla	2	24312309	56.3605877	7	1.310766647	-60430	'27.3.25'	grmzm2g447090_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
160	Chla	2	25437487	57.05362901	6	1.199994036	-127907	'29.3.4.99'	grmzm2g031360_t01	'protein.targeting.secretory pathway.unspecified'

161	Chla	2	25437559	57.05368243	5	1.144917046	-127979	'29.3.4.99'	grmzm2g031360_t01	'protein.targeting.secretory pathway.unspecified'
162	Chla	2	26691735	57.98437622	14	1.092321355	-39088	'17.1.3'	grmzm2g413887_t01	'hormone metabolism.abscisic acid.induced-regulated-responsive-activated'
163	Chla	2	26773008	58.04468695	6	0.928679226	-77292	'27.1'	grmzm2g171410_t01	'RNA.processing'
164	Chla	2	44156463	69.46377693	6	-2.024801273	-157155	'34.2'	grmzm2g061495_t01	'transport.sugars'
165	Chla	2	175505228	86.58930765	7	1.255193753	-20716	'29.5.11.4.2'	grmzm2g425965_t01	'protein.degradation.ubiquitin.E3.RING'
166	Chla	3	13632616	40.54644966	5	0.97166907	-6548	'27.2'	grmzm2g102664_t01	'RNA.transcription'
167	Chla	3	17328400	45.32523697	9	1.191986808	-21217	'15.2'	grmzm2g099340_t01	'metal handling.binding, chelation and storage'
168	Chla	3	20129322	48.94693416	8	1.760642777	-7237	'30.2.20'	grmzm2g013790_t01	'signalling.receptor kinases.wheat LRK10 like'
169	Chla	3	27862522	53.36115573	10	1.423867597	-158578	'29.4'	grmzm2g012472_t01	'protein.postranslational modification'

170	Chla	3	142821459	64.10032051	8	2.211347578	-35767	'29.3.3'	grmzm2g171390_t05	'protein.targeting.chloroplast'
171	Chla	3	176382057	87.28804733	7	2.673712072	-18885	'31.2'	grmzm2g007659_t01	'cell.division'
172	Chla	3	212248700	123.3041123	17	-1.457436983	-2158	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
173	Chla	3	213848077	126.6554907	48	-1.687766558	-44219	'26.2'	grmzm2g048010_t01	'misc.UDP glucosyl and glucoronyl transferases'
174	Chla	3	213848298	126.6560335	10	-1.668877969	-44440	'26.2'	grmzm2g048010_t01	'misc.UDP glucosyl and glucoronyl transferases'
175	Chla	3	213894582	126.7697196	24	-1.531651849	-34624	'1.5.1'	grmzm2g348512_t02	'PS.carbon concentrating mechanism.C4'
176	Chla	3	214166666	127.4380314	10	-1.452335655	-80589	'23.4.1'	grmzm2g125193_t01	'nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate kinase'
177	Chla	3	214171011	127.4487039	27	-1.512209361	-84934	'23.4.1'	grmzm2g125193_t01	'nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate kinase'
178	Chla	3	215371494	129.1375553	18	-1.61194824	-13200	'29.5.3'	grmzm2g042332_t01	'protein.degradation.cysteine protease'

179	Chla	3	215732765	129.6435644	14	-1.22775052	-52112	'27.3.69'	grmzm2g702253_t03	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
180	Chla	4	25857163	48.23906117	17	1.151000831	-5111	'34.13'	grmzm2g026459_t01	'transport.peptides and oligopeptides'
181	Chla	4	33663511	51.99288995	5	1.206422642	-136974	'7.2.2'	grmzm2g139550_t01	'OPP.non-reductive PP.transaldolase'
182	Chla	4	35498708	52.93310614	10	1.229496466	-83751	'27.3.6'	grmzm2g017586_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
183	Chla	4	36054065	53.09837236	5	1.000540179	-6122	'33.99'	grmzm2g111247_t01	'development.unspecified'
184	Chla	4	172424061	81.94381184	13	-3.771641365	-26213	'29.3.4.3'	grmzm2g178972_t01	'protein.targeting.secretory pathway.vacuole'
185	Chla	4	177225726	88.56915079	8	-1.412797811	-75966	'29.4'	grmzm2g158860_t02	'protein.postranslational modification'
186	Chla	4	177329556	88.69420796	10	-2.097767711	-5203	'27.3.67'	grmzm2g475583_t01	'RNA.regulation of transcription.putative transcription regulator'
187	Chla	4	177855845	90.07794504	8	-2.176405818	-9233	'27.3.3'	grmzm2g084457_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'

188	Chla	5	166987510	78.8793885	5	-2.122907288	-153446	'33.99'	grmzm2g099334_t01	'development.unspecified'
189	Chla	5	189389642	98.99515772	8	-1.297088271	-76276	'27.3.9'	grmzm2g140669_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
190	Chla	5	205646722	119.7979212	13	-1.057085938	-92306	'29.4'	grmzm2g127632_t01	'protein.postranslational modification'
191	Chla	5	205662084	119.8477507	30	-1.106120646	-12253	'17.2.2'	grmzm2g074267_t01	'hormone metabolism.auxin.signal transduction'
192	Chla	5	205842860	120.4341313	9	-1.314471195	-8384	'34.18.1'	grmzm2g105539_t01	'transport.unspecified anions.arsenite-transporting ATPase'
193	Chla	5	208092874	126.5365424	8	-1.242235214	-5948	'26.19'	grmzm2g045927_t01	'misc.plastocyanin-like'
194	Chla	5	208411778	126.7985254	6	-1.034251892	-66728	'20.2.1'	grmzm2g072300_t01	'stress.abiotic.heat'
195	Chla	5	212548689	141.0955085	7	-1.625212605	-9665	'21.2'	grmzm2g119782_t01	'redox.ascorbate and glutathione'
196	Chla	6	125640414	46.48436302	14	-2.050901443	-62488	'8.1.1.3'	grmzm2g159570_t01	'TCA / org. transformation.TCA.pyruvate DH.E3'

197	Chla	6	125640415	46.48436337	17	-2.07079645	-62489	'8.1.1.3'	grmzm2g159570_t01	'TCA / org. transformation.TCA.pyruvate DH.E3'
198	Chla	6	159559960	82.11064054	5	-0.859575964	-56867	'29.5.5'	grmzm2g331833_t01	'protein.degradation.serine protease'
199	Chla	7	33122197	47.86676722	19	1.636985743	-486602	'31.3.1'	grmzm2g092072_t01	'cell.cycle.peptidylprolyl isomerase'
200	Chla	7	35108196	48.14677419	7	2.022809364	-164805	'29.5.11.4.5.2'	grmzm2g109738_t01	'protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ'
201	Chla	7	35397449	48.15875943	7	1.157786171	-88567	'29.5.1'	grmzm2g076417_t01	'protein.degradation.subtilases'
202	Chla	7	42768959	48.86677354	5	0.867518993	-226886	'30.3'	grmzm2g433551_t01	'signalling.calcium'
203	Chla	7	125979602	66.69618807	7	2.632081769	-70577	'34.14'	grmzm2g090149_t01	'transport.unspecified cations'
204	Chla	7	157918090	102.0917472	6	1.307677429	-81602	'27.4'	grmzm2g068255_t01	'RNA.RNA binding'
205	Chla	8	8405589	21.20394308	18	1.770676205	-149874	'27.3.67'	ac234160.1_fgt001	'RNA.regulation of transcription.putative transcription regulator'

206	Chla	9	21661674	38.29017663	5	-1.285619712	-3078	'27.1'	grmzm2g115156_t01	'RNA.processing'
207	Chla	9	21670412	38.30415705	15	-1.744014465	-5027	'10.1.7'	grmzm2g115124_t01	'cell wall.precursor synthesis.GMD'
208	Chla	9	23215197	39.99779948	11	-1.046360749	-198266	'3.4.3'	grmzm2g010768_t01	'minor CHO metabolism.myo-inositol.InsP Synthases'
209	Chla	9	26434264	43.26084016	59	-1.065132951	-1131	'11.1.8'	grmzm2g393146_t03	'lipid metabolism.FA synthesis and FA elongation.acyl coa ligase'
210	Chla	10	143379980	80.93578714	10	1.736257572	-30629	'16.8.3'	grmzm2g431504_t01	'secondary metabolism.flavonoids.dihydroflavonols'
211	Chla	10	145845320	88.37068362	8	1.167874183	-103010	'34.1'	grmzm2g006894_t01	'transport.p- and v-ATPases'
212	Chla	10	148232936	100.610509	8	1.106911557	-20743	'34.15'	grmzm2g039797_t01	'transport.potassium'
213	Chla	10	148450393	101.8294985	36	1.201764063	-7791	'34.9'	grmzm2g177213_t01	'transport.metabolite transporters at the mitochondrial membrane'
214	Chla	10	148497003	102.0907782	6	1.10547339	-181	'29.4'	grmzm2g104658_t07	'protein.postranslational modification'

215	Chla	10	148499295	102.1036264	9	1.10891694	-2216	'29.4'	grmzm2g104658_t09	'protein.postranslational modification'
216	Chlb	1	97031439	87.3597852	18	0.627113181	-66195	'27.3.27'	grmzm2g082709_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
217	Chlb	1	101441507	87.90304019	5	0.237222688	-329169	'16.8.3'	grmzm2g068917_t01	'secondary metabolism.flavonoids.dihydroflavonols'
218	Chlb	1	103855930	88.27009228	13	0.528617492	-362145	'10.2.1'	grmzm2g436299_t01	'cell wall.cellulose synthesis.cellulose synthase'
219	Chlb	1	138458661	89.49765026	6	0.636936144	-881999	'27.3.39'	grmzm2g153594_t01	'RNA.regulation of transcription.AtSR Transcription Factor family'
220	Chlb	1	141762525	89.53124152	15	0.677150275	-94249	'27.2'	grmzm2g045668_t01	'RNA.transcription'
221	Chlb	1	146716486	89.58160975	18	37.87537959	-77548	'34.12'	grmzm2g057820_t01	'transport.metal'
222	Chlb	1	150498647	89.94777187	5	0.650291443	-205344	'33.99'	grmzm2g075456_t01	'development.unspecified'
223	Chlb	1	163239765	91.63742221	8	0.375622346	-591921	'10.3'	grmzm2g703790_t01	'cell wall.hemicellulose synthesis'

224	Chlb	1	181947110	97.49187685	6	-0.41770935	-2965	'26.19'	grmzm2g023847_t01	'misc.plastocyanin-like'
225	Chlb	1	187131514	101.742233	14	-0.546446647	-1085	'27.3.11'	grmzm2g445684_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
226	Chlb	1	202975799	116.1587985	10	-0.587258205	-83915	'10.7'	grmzm2g030531_t01	'cell wall.modification'
227	Chlb	1	205257253	117.519266	7	-0.562896571	-256995	'25.9'	grmzm2g015588_t01	'C1-metabolism.dihydroneopterin aldolase'
228	Chlb	1	225624776	133.6401321	12	-0.665556716	-17032	'19.2'	ac213521.3_fgt005	'tetrapyrrole synthesis.glu-tRNA reductase'
229	Chlb	1	228532522	135.6859584	17	-0.333710526	-5551	'17.1.3'	grmzm2g113167_t01	'hormone metabolism.abscisic acid.induced-regulated-responsive-activated'
230	Chlb	1	285864445	180.8598811	14	-1.175768963	-85704	'29.3.4.99'	grmzm2g120596_t01	'protein.targeting.secretory pathway.unspecified'
231	Chlb	1	291825337	191.0554431	5	1.628826253	-2579	'29.2.1.2.1.23'	ac225147.4_fgt002	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S23'
232	Chlb	1	294322791	196.7251432	76	0.398027959	-1237	'26.22'	grmzm2g156739_t01	'misc.short chain dehydrogenase/reductase (SDR)'

233	Chlb	1	294652893	197.2197826	22	-15.83957184	-7614	'20.2.1'	grmzm2g114673_t01	'stress.abiotic.heat'
234	Chlb	1	296022922	199.7554621	13	5.61697755	-88876	'33.99'	grmzm2g118014_t01	'development.unspecified'
235	Chlb	1	299894464	204.0221873	84	3.122396653	-81247	'30.5'	grmzm2g131939_t01	'signalling.G-proteins'
236	Chlb	2	5923229	18.30060959	6	-0.432741117	-21484	'34.18'	grmzm2g071119_t01	'transport.unspecified anions'
237	Chlb	2	6166067	18.83309554	9	-0.313343721	-2154	'34.16'	grmzm2g072850_t01	'transport.ABC transporters and multidrug resistance systems'
238	Chlb	2	69741938	75.18951102	10	0.13773773	-116268	'20.2.1'	ac235541.1_fgt002	'stress.abiotic.heat'
239	Chlb	2	148856409	80.60314611	22	8.071915262	-18560	'27.3.25'	grmzm2g032180_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
240	Chlb	2	149429597	80.70039502	22	-9.971712092	-62312	'29.3.4.3'	grmzm2g389362_t01	'protein.targeting.secretory pathway.vacuole'
241	Chlb	2	161877261	82.49985253	8	-4.135727968	-41635	'20.2.2'	ac210204.3_fgt002	'stress.abiotic.cold'

242	Chlb	2	172704855	85.0182288	5	0.153284287	-30872	'30.5'	grmzm2g039900_t01	'signalling.G-proteins'
243	Chlb	2	185915577	96.74331495	10	0.145544258	-4122	'29.5.5'	grmzm2g703293_t01	'protein.degradation.serine protease'
244	Chlb	2	186273082	97.1970181	7	0.137513277	-136321	'30.2.11'	ac233861.1_fgt001	'signalling.receptor kinases.leucine rich repeat XI'
245	Chlb	2	186375668	97.32720814	5	0.150539465	-754	'29.5.11.1'	grmzm2g353446_t01	'protein.degradation.ubiquitin.ubiquitin'
246	Chlb	2	191111571	102.3694697	8	0.135633799	-150052	'27.3.6'	grmzm2g107560_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
247	Chlb	2	192123634	103.2729858	11	0.120175148	-9108	'27.2'	grmzm2g034260_t01	'RNA.transcription'
248	Chlb	3	139536229	63.68477456	6	0.147217046	-293942	'20.1'	grmzm2g368151_t01	'stress.biotic'
249	Chlb	3	144468014	65.40015782	12	0.134612198	-2328	'27.3.5'	grmzm2g156019_t01	'RNA.regulation of transcription.ARR'

250	Chlb	3	147011536	66.05909566	44	0.123495734	-103171	'11.8'	grmzm2g347146_t01	'lipid metabolism."exotics" (steroids, squalene etc)'
251	Chlb	3	148514014	66.58736723	21	0.148804648	-132133	'17.4.1'	grmzm2g050997_t01	'hormone metabolism.cytokinin.synthesis-degradation'
252	Chlb	3	212765471	123.9963177	8	-0.336927049	-38896	'34.15'	grmzm2g022915_t01	'transport.potassium'
253	Chlb	3	216243829	131.9068925	14	-0.259823327	-2178	'27.3.46'	grmzm2g052991_t01	'RNA.regulation of transcription.DNA methyltransferases'
254	Chlb	4	10192700	27.53975118	5	-0.334206161	-180774	'30.2.11'	grmzm2g011896_t02	'signalling.receptor kinases.leucine rich repeat XI'
255	Chlb	4	10198136	27.55916751	33	-0.283755098	-2085	'30.2.11'	grmzm2g068398_t01	'signalling.receptor kinases.leucine rich repeat XI'
256	Chlb	4	10624506	29.08207781	6	-0.499306784	-107674	'1.1.5.2'	grmzm2g470653_t01	'PS.lightreaction.other electron carrier (ox/red).ferredoxin'
257	Chlb	4	154415397	65.4507691	5	-0.310092928	-62669	'29.5.11.4.2'	grmzm2g081829_t01	'protein.degradation.ubiquitin.E3.RING'
258	Chlb	4	157107343	68.51092069	5	-0.175013014	-63015	'27.3.20'	grmzm2g070865_t01	'RNA.regulation of transcription.G2-like transcription factor family, GARP'

259	Chlb	4	159175723	70.53286161	16	-0.172099323	-5436	'29.5.9'	grmzm2g069422_t01	'protein.degradation.AAA type'
260	Chlb	4	241996729	128.0064472	6	3.240118253	-5449	'17.2.3'	grmzm2g471304_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
261	Chlb	4	242374367	129.5365429	7	-2.331473365	-26749	'30.5'	grmzm2g101920_t01	'signalling.G-proteins'
262	Chlb	4	245553732	143.0029237	5	0.469486536	-119198	'29.6'	grmzm2g150337_t03	'protein.folding'
263	Chlb	5	2383652	5.193426861	6	-0.572992605	-330	'27.3.11'	grmzm2g002805_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
264	Chlb	5	6303981	23.51266789	6	0.790335738	-11201	'29.4'	grmzm2g034877_t01	'protein.postranslational modification'
265	Chlb	5	20023828	50.73599959	10	0.15378392	-76988	'16.1.5'	grmzm2g156748_t01	'secondary metabolism.isoprenoids.terpenoids'
266	Chlb	5	26723660	54.83773092	24	0.136021297	-473830	'26.10'	grmzm2g013082_t01	'misc.cytochrome P450'
267	Chlb	5	35357979	58.09472562	36	0.135646841	-336772	'34.9'	grmzm2g043182_t01	'transport.metabolite transporters at the mitochondrial membrane'
268	Chlb	5	45813768	59.90312559	5	0.138663161	-60098	'30.1.1'	grmzm2g057459_t01	'signalling.in sugar and nutrient physiology'

269	Chlb	6	162877409	92.80071368	5	0.254136304	-84434	'29.5.11.4.2'	grmzm2g320399_t01	'protein.degradation.ubiquitin.E3.RING'
270	Chlb	7	1921276	4.495740497	6	0.440671843	-123092	'26.13'	grmzm2g106600_t01	'misc.acid and other phosphatases'
271	Chlb	7	2047654	4.972450239	9	0.308546552	-64453	'27.3.67'	grmzm2g019879_t01	'RNA.regulation of transcription.putative transcription regulator'
272	Chlb	7	5043354	21.45653923	59	-0.623660171	-65874	'1.2.6'	grmzm2g040090_t02	'PS.photorespiration.hydroxypyruvate reductase'
273	Chlb	7	5299542	22.83360349	5	-0.725829344	-561	'34.2'	grmzm2g142063_t03	'transport.sugars'
274	Chlb	7	6484300	28.48085938	7	-0.385308166	-3347	'10.6.3'	grmzm2g032145_t03	'cell wall.degradation.pectate lyases and polygalacturonases'
275	Chlb	7	9145904	33.10358602	7	-0.455155264	-57306	'26.21'	grmzm2g046750_t01	'misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein'
276	Chlb	7	142898891	81.10232141	46	-0.930589021	-7412	'26.8'	grmzm2g111309_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
277	Chlb	7	151513769	89.4065889	57	2.205527693	-3032	'27.3.25'	grmzm2g031323_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
278	Chlb	7	152461246	91.18872855	6	0.1813481	-824	'34.2'	grmzm2g089493_t01	'transport.sugars'

279	Chlb	7	157011468	100.2121602	5	-1.389177806	-209189	'27.3.99'	grmzm2g090715_t01	'RNA.regulation of transcription.unclassified'
280	Chlb	7	157185116	100.5721631	5	-1.554880555	-103	'29.5.3'	grmzm2g036203_t01	'protein.degradation.cysteine protease'
281	Chlb	7	157532548	101.2924508	11	-1.522378582	-9296	'27.3.44'	grmzm2g313553_t01	'RNA.regulation of transcription.Chromatin Remodeling Factors'
282	Chlb	7	164316372	116.7981854	5	-0.786680562	-1620	'29.5.11.1'	grmzm2g055527_t01	'protein.degradation.ubiquitin.ubiquitin'
283	Chlb	7	167232557	126.3442442	8	0.152254886	-1209	'34.15'	grmzm2g166738_t01	'transport.potassium'
284	Chlb	7	167233412	126.3479602	14	0.1415427	-2064	'34.15'	grmzm2g166738_t01	'transport.potassium'
285	Chlb	8	926070	1.886736364	14	0.271650989	-58379	'19.9'	grmzm2g039396_t01	'tetrapyrrole synthesis.protoporphyrin IX oxidase'
286	Chlb	8	1359223	2.966202574	8	0.123826391	-38	'31.1'	grmzm2g042636_t01	'cell.organisation'
287	Chlb	8	99959295	57.50014689	6	-0.51065178	-12771	'28.99'	ac199379.4_fgt001	'DNA.unspecified'

288	Chlb	8	147589704	77.10076187	7	-0.197854431	-100178	'29.5'	grmzm2g000719_t01	'protein.degradation'
289	Chlb	8	147830284	77.29378758	5	-0.28678081	-2177	'28.1.1.4'	grmzm2g126917_t01	'DNA.synthesis/chromatin structure.retrotransposon/transposase.hat-like transposase'
290	Chlb	8	147830665	77.29409327	7	-0.289989168	-2558	'28.1.1.4'	grmzm2g126917_t01	'DNA.synthesis/chromatin structure.retrotransposon/transposase.hat-like transposase'
291	Chlb	8	152152815	80.797802	13	-0.348119811	-48527	'20.2.1'	grmzm2g469901_t01	'stress.abiotic.heat'
292	Chlb	9	8793952	12.87388515	8	-0.136620476	-161345	'27.3.52'	grmzm2g142072_t01	'RNA.regulation of transcription.Global transcription factor group'
293	Chlb	9	9141388	13.42304955	6	-0.254049865	-34377	'17.5.1'	grmzm2g066358_t01	'hormone metabolism.ethylene.synthesis-degradation'
294	Chlb	9	23231768	40.03154801	10	-0.113528991	-14079	'2.1.2.2'	grmzm2g024993_t01	'major CHO metabolism.synthesis.starch.starch synthase'
295	Chlb	9	25023438	42.41159442	6	-0.114018927	-3965	'20.1'	grmzm2g030051_t01	'stress.biotic'
296	Chlb	9	27036374	43.61692207	7	-0.146623845	-71307	'33.99'	grmzm2g168214_t01	'development.unspecified'

297	Chlb	9	64396713	45.73393561	5	-0.145382509	-257847	'27.3.6'	grmzm2g045109_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
298	Chlb	9	74140456	45.9421654	15	-2166.549455	-198434	'21.2.1'	grmzm2g141376_t01	'redox.ascorbate and glutathione.ascorbate'
299	Chlb	9	85978653	46.6412055	5	-0.164686897	-89656	'26.7'	grmzm2g019872_t01	'misc.oxidases - copper, flavone etc.'
300	Chlb	9	147213879	101.7957515	8	-0.318295344	-59698	'30.3'	grmzm2g120975_t01	'signalling.calcium'
301	Chlb	10	107950213	44.02050592	22	-0.311582186	-2996	'26.1'	grmzm2g399530_t01	'misc.misc2'
302	Chlb	10	118129854	47.02366267	15	-0.228236332	-262175	'23.5.2'	grmzm2g087180_t01	'nucleotide metabolism.deoxynucleotide metabolism.pseudouridine synthase'
303	Chlb	10	119651031	47.40080838	7	-0.115286868	-150952	'20.2.1'	grmzm2g346839_t01	'stress.abiotic.heat'
304	Chlb	10	129585091	52.11332474	32	0.256285226	-4047	'11.9.2.1'	grmzm2g377641_t01	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
305	Chlb	10	132147651	55.92474833	6	0.240383766	-502	'31.4'	grmzm2g040902_t01	'cell.vesicle transport'
306	Chlb	10	148943495	104.5936596	7	-0.338495455	-36125	'34.13'	grmzm2g011590_t01	'transport.peptides and oligopeptides'

307	Chlb	10	149647673	108.5410404	6	-0.456258788	-57680	'10.2'	grmzm2g178025_t01	'cell wall.cellulose synthesis'
308	Fruc	1	16386798	32.84963222	6	-0.013777599	-533	'20.2.99'	grmzm2g016443_t01	'stress.abiotic.unspecified'
309	Fruc	1	16770481	33.28017346	30	-0.015750944	-27721	'27.3.7'	grmzm2g445634_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
310	Fruc	1	16775647	33.28405569	10	-0.018370011	-32887	'27.3.7'	grmzm2g445634_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
311	Fruc	1	17461111	33.79917927	6	-0.014967229	-6444	'27.3.3'	ac206951.3_fgt016	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
312	Fruc	1	35272897	54.48195467	5	-0.029642508	-5161	'33.1'	grmzm2g030223_t01	'development.storage proteins'
313	Fruc	1	44348772	60.58908186	7	0.029290518	-11345	'29.7'	grmzm2g001079_t01	'protein.glycosylation'
314	Fruc	1	45121654	61.22096078	8	0.015684896	-157836	'11.2.3'	grmzm2g074401_t01	'lipid metabolism.FA desaturation.omega 3 desaturase'

315	Fruc	1	45567426	61.52614689	14	0.019975229	-3279	'34.9'	ac208201.3_fgt001	'transport.metabolite transporters at the mitochondrial membrane'
316	Fruc	1	46712396	62.60179969	5	0.013786727	-34913	'29.5.11.20'	grmzm2g104373_t01	'protein.degradation.ubiquitin.proteasom'
317	Fruc	1	57438776	70.59917107	14	0.013567425	-78818	'33.99'	grmzm2g107597_t01	'development.unspecified'
318	Fruc	1	95550141	86.84633266	14	0.034688611	-17787	'31.1'	grmzm2g379550_t01	'cell.organisation'
319	Fruc	2	3327524	8.176087352	9	-0.011446215	-108672	'2.2.1.3.2'	grmzm2g018692_t01	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
320	Fruc	2	3529245	9.556599097	7	-0.011598842	-126893	'30.3'	grmzm2g348909_t01	'signalling.calcium'
321	Fruc	2	3534327	9.591591385	10	-0.012952906	-131975	'30.3'	grmzm2g348909_t01	'signalling.calcium'
322	Fruc	2	3794582	10.51648703	20	-0.013392911	-22878	'29.4'	grmzm2g017654_t01	'protein.postranslational modification'

323	Fruc	2	4042572	11.15390606	18	-0.012020005	-3178	'30.2.17'	grmzm2g391741_t01	'signalling.receptor kinases.DUF 26'
324	Fruc	2	4663012	13.34691454	5	-0.011982641	-160	'29.4.1.57'	grmzm2g086577_t02	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
325	Fruc	2	34001062	63.56397414	5	-0.011897479	-26900	'20.1'	grmzm2g051921_t01	'stress.biotic'
326	Fruc	2	177151781	87.86279241	10	0.034341476	-69726	'27.3.29'	grmzm2g110242_t01	'RNA.regulation of transcription.TCP transcription factor family'
327	Fruc	2	177266143	87.95845923	6	0.046944656	-8092	'27.3.6'	grmzm2g176141_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
328	Fruc	2	181271307	91.1333845	7	0.046476341	-2251	'5.1'	grmzm2g130440_t02	'fermentation.LDH'
329	Fruc	3	3386685	11.10786166	29	-0.021944149	-29190	'29.3.4.4'	grmzm2g102795_t01	'protein.targeting.secretory pathway.plasma membrane'
330	Fruc	3	3903533	13.78234035	18	-0.016091322	-29382	'34.3'	grmzm2g146161_t01	'transport.amino acids'

331	Fruc	3	4856540	18.3470876	47	-0.014548164	-28145	'27.3.24'	grmzm2g471089_t01	'RNA.regulation of transcription.MADS box transcription factor family'
332	Fruc	3	49918968	56.54435347	26	-0.016411713	-219688	'34.16'	grmzm2g119894_t01	'transport.ABC transporters and multidrug resistance systems'
333	Fruc	3	171723196	82.25684086	47	0.040642762	-91194	'20.2.99'	grmzm2g060255_t01	'stress.abiotic.unspecified'
334	Fruc	3	172148591	82.5754152	7	0.064075885	-1652	'34.10'	grmzm2g037229_t01	'transport.nucleotides'
335	Fruc	3	173110658	83.38629476	18	0.042818427	-67819	'28.2'	grmzm2g002626_t01	'DNA.repair'
336	Fruc	3	173219900	83.47836954	11	0.066010087	-10226	'1.1.1.2'	grmzm2g077333_t01	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
337	Fruc	3	195593529	103.3189453	7	0.02012706	-79521	'23.1.1.3'	grmzm2g021704_t03	'nucleotide metabolism.synthesis.pyrimidine.dihydroorotase'
338	Fruc	3	196183579	103.6950757	5	0.011501099	-75396	'3.2.3'	grmzm2g304274_t01	'minor CHO metabolism.trehalose.potential TPS/TPP'
339	Fruc	3	219127882	135.874024	20	-0.018693012	-461	'29.5.3'	grmzm2g371628_t01	'protein.degradation.cysteine protease'

340	Fruc	3	221010928	139.3762734	18	-0.017339804	-2081	'26.24'	grmzm2g333775_t01	'misc.GCN5-related N-acetyltransferase'
341	Fruc	4	596627	2.14232426	45	0.025189271	-81396	'27.3.21'	grmzm2g018254_t01	'RNA.regulation of transcription.GRAS transcription factor family'
342	Fruc	4	101026208	57.83942086	5	-0.028462957	-385858	'29.3.1'	grmzm2g008497_t01	'protein.targeting.nucleus '
343	Fruc	4	109554972	58.01578487	6	-0.014600631	-223522	'27.3.35'	grmzm2g118870_t02	'RNA.regulation of transcription.bZIP transcription factor family'
344	Fruc	4	118225032	58.20188033	8	-0.015380681	-331981	'27.3.3'	grmzm2g139740_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
345	Fruc	4	121592260	58.27415502	6	-0.012488902	-97602	'24'	grmzm2g128219_t01	'Biodegradation of Xenobiotics'
346	Fruc	4	121913511	58.2810504	6	-0.014513129	-218457	'27.3.99'	grmzm2g069678_t01	'RNA.regulation of transcription.unclassified '
347	Fruc	4	122028538	58.28351935	8	-0.012822806	-26125	'29.5.11.4.2'	grmzm2g041344_t01	'protein.degradation.ubiquitin.E3.RING'
348	Fruc	4	125159697	58.42149244	5	-0.016269091	-6839	'30.7'	grmzm2g095397_t01	'signalling.14-3-3 proteins'

349	Fruc	4	139805548	59.87084184	6	-0.013396769	-336601	'30.5'	grmzm2g079817_t01	'signalling.G-proteins'
350	Fruc	4	144536877	60.82876771	5	-0.01193395	-48049	'29.5.11.3'	grmzm2g161545_t01	'protein.degradation.ubiquitin.E2'
351	Fruc	4	170738228	78.91944426	9	-0.027117788	-1766	'26.28'	grmzm2g384780_t01	'misc.GDSL-motif lipase'
352	Fruc	4	172300218	81.59892215	15	-0.0185491	-15126	'20.2.1'	grmzm2g054076_t01	'stress.abiotic.heat'
353	Fruc	4	240477479	123.4579602	5	-0.05014372	-32189	'29.4'	grmzm2g062683_t01	'protein.postranslational modification'
354	Fruc	5	1571929	2.012971503	16	-0.012617453	-131	'29.2.1.2.1.21'	grmzm2g125300_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S21'
355	Fruc	5	2279196	4.510973125	8	-0.011842701	-12128	'30.5'	grmzm2g144008_t01	'signalling.G-proteins'
356	Fruc	5	2358292	5.027739617	38	-0.013396885	-9114	'27.3.8'	grmzm2g144188_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
357	Fruc	5	2367917	5.090623676	8	-0.012236849	-2750	'27.3.67'	grmzm2g003068_t01	'RNA.regulation of transcription.putative transcription regulator'

358	Fruc	5	163819573	76.76334725		49	0.022715483	-1683	'28.1'	grmzm2g011631_t01	'DNA.synthesis/chromatin structure'
359	Fruc	5	166171297	78.20073394		5	0.023811543	-244497	'27.3.3'	grmzm2g047999_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
360	Fruc	5	204526436	116.1640652		41	0.018975985	-7287	'17.4.2'	grmzm2g151223_t02	'hormone metabolism.cytokinin.signal transduction'
361	Fruc	5	206993797	123.8406652		29	0.022620899	-925	'29.5.4'	grmzm2g335978_t02	'protein.degradation.aspartate protease'
362	Fruc	5	210780527	134.226701		7	0.0157951	-19553	'31.1'	grmzm2g385925_t01	'cell.organisation'
363	Fruc	5	214945363	152.2635928		8	0.024738523	-5270	'20.1'	grmzm2g013848_t01	'stress.biotic'
364	Fruc	6	83413352	12.31842953		47	-0.016984936	-1670	'11.8.1'	grmzm2g417009_t01	'lipid metabolism."exotics" (steroids, squalene etc).sphingolipids'
365	Fruc	6	93728026	20.25312295		19	-0.018294395	-1295	'29.5.11.4.5.2'	grmzm2g161610_t01	'protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ'
366	Fruc	6	117587976	42.56198959		5	-0.03397919	-81659	'27.3.7'	grmzm2g012717_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'

367	Fruc	6	119772986	44.24786955	23	-0.033796984	-90952	'26.19'	grmzm2g148624_t01	'misc.plastocyanin-like'
368	Fruc	6	124203584	45.80014821	9	-0.025280441	-40062	'1.3.1'	grmzm2g122563_t01	'PS.calvin cycle.rubisco large subunit'
369	Fruc	6	128598095	47.52042761	5	-0.033664993	-979	'31.1'	grmzm2g341155_t01	'cell.organisation'
370	Fruc	6	165119716	101.3985908	6	0.036582506	-1681	'29.5.4'	grmzm2g065757_t02	'protein.degradation.aspartate protease'
371	Fruc	6	166794282	106.9690738	8	-0.011678556	-2978	'31.2'	grmzm2g059037_t01	'cell.division'
372	Fruc	6	166794417	106.9695432	5	-0.01610415	-3113	'31.2'	grmzm2g059037_t01	'cell.division'
373	Fruc	7	6022883	26.56544125	7	-0.013079036	-55669	'27.4'	grmzm2g026614_t01	'RNA.RNA binding'
374	Fruc	7	9213492	33.2209742	16	-0.018141284	-66352	'28.1'	grmzm2g004301_t01	'DNA.synthesis/chromatin structure'
375	Fruc	7	20233795	44.69829015	10	-0.017981407	-72625	'29.3.4.99'	grmzm2g105996_t01	'protein.targeting.secretory pathway.unspecified'

376	Fruc	7	21622999	45.56317348	15	-0.018042126	-84794	'34.3'	grmzm2g173967_t01	'transport.amino acids'
377	Fruc	7	32630669	47.75472755	8	-0.017704491	-237974	'29.5.11.4.3.2'	grmzm2g012508_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
378	Fruc	7	84574592	49.92029539	9	-0.01885016	-67361	'30.2.99'	grmzm2g354615_t01	'signalling.receptor kinases.misc'
379	Fruc	7	86294238	49.99529999	25	-0.016277961	-89760	'34.16'	grmzm2g355523_t01	'transport.ABC transporters and multidrug resistance systems'
380	Fruc	7	86760483	50.01070124	5	-0.018393153	-76255	'18'	grmzm2g022837_t01	'Co-factor and vitamine metabolism'
381	Fruc	7	95364029	50.42762301	14	-0.019020479	-3782	'34.99'	grmzm2g176780_t01	'transport.misc'
382	Fruc	7	109178008	55.19093714	5	-0.016770261	-225062	'27.4'	grmzm2g042006_t02	'RNA.RNA binding'
383	Fruc	7	156688517	99.54262593	5	0.025852571	-7082	'27.3.11'	ac185108.3_fgt011	'RNA.regulation of transcription.C2H2 zinc finger family'
384	Fruc	9	2701441	-3.388186607	10	-0.03407797	-280728	'27.1.19'	grmzm2g016275_t01	'RNA.processing.ribonucleases'

385	Fruc	9	5619750	4.494331447	5	-0.026190353	-139829	'27.3.24'	grmzm2g152415_t01	'RNA.regulation of transcription.MADS box transcription factor family'
386	Fruc	9	9558874	14.08293641	31	-0.038288541	-41185	'27.3.11'	grmzm2g159402_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
387	Fruc	9	10186494	15.44407336	7	-0.018017282	-142075	'29.4.1.57'	grmzm2g055982_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
388	Fruc	9	21993322	38.82079896	27	-0.037006124	-9583	'27.3.25'	grmzm2g449056_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
389	Fruc	9	142204786	87.72532368	30	-0.022131324	-83140	'10.6.3'	grmzm2g034835_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
390	Fruc	9	143828279	91.48003191	5	-0.020830478	-34082	'20.2.3'	grmzm2g181551_t01	'stress.abiotic.drought/salt'
391	Fruc	9	145268207	95.10905936	8	-0.014832567	-4590	'27.3.22'	ac233899.1_fgt004	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
392	Fruc	10	5058530	14.79019912	28	-0.045641719	-2015	'13'	grmzm2g066496_t01	'amino acid metabolism'

393	Fruc	10	5258877	16.0525304	31	-0.045423584	-4552	'29.3.4.1'	grmzm2g113093_t01	'protein.targeting.secretory pathway.ER'
394	Fruc	10	5571203	17.95328644	17	-0.045237542	-31427	'27.1'	grmzm2g131120_t01	'RNA.processing'
395	Fruc	10	11480453	29.34116571	8	-0.038039626	-273511	'2.2.1.3.1'	grmzm2g040843_t01	'major CHO metabolism.degradation.sucrose.invertases.neutral'
396	Fruc	10	134630447	59.4071156	7	-0.017295414	-863	'29.5.11.4.2'	grmzm2g031280_t01	'protein.degradation.ubiquitin.E3.RING'
397	Fuma	1	195285519	108.2877857	22	0.010497833	-1708	'8.1.1.1'	grmzm2g043198_t01	'TCA / org. transformation.TCA.pyruvate DH.E1'
398	Fuma	1	195634638	108.6089505	6	0.010552372	-13265	'17.2.3'	grmzm2g020631_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
399	Fuma	1	196048817	109.0223788	6	0.007421199	-249	'31.4'	grmzm2g353483_t01	'cell.vesicle transport'
400	Fuma	1	205544235	117.795721	14	-0.006686224	-286271	'27.3.11'	grmzm2g104516_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
401	Fuma	1	205766088	118.0094361	13	-0.004995746	-138884	'25.9'	grmzm2g095579_t01	'C1-metabolism.dihydroneopterin aldolase'

402	Fuma	1	206425614	118.6447696	17	-0.005436419	-55079	'27.3.25'	grmzm2g084583_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
403	Fuma	1	207121477	119.3151072	6	-0.00753724	-98025	'7.1.2'	grmzm2g122126_t01	'OPP.oxidative PP.6-phosphogluconolactonase'
404	Fuma	1	208533778	120.6233059	7	-0.007359341	-2498	'16.2'	grmzm2g059465_t01	'secondary metabolism.phenylpropanoids'
405	Fuma	1	208593470	120.672802	13	-0.004806602	-1525	'17.2.3'	grmzm2g460861_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
406	Fuma	1	272244444	164.542002	10	0.003610726	-137417	'27.3.22'	grmzm2g396114_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
407	Fuma	1	272244581	164.5421084	19	0.003781599	-137554	'27.3.22'	grmzm2g396114_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
408	Fuma	1	289899574	186.9723092	6	0.002963805	-17296	'20.1'	grmzm2g402765_t01	'stress.biotic'
409	Fuma	2	5934701	18.32576495	5	0.014046764	-7458	'29.5.11'	grmzm2g070881_t01	'protein.degradation.ubiquitin'
410	Fuma	2	26788878	58.0564637	8	-0.007537765	-93162	'27.1'	grmzm2g171410_t01	'RNA.processing'

411	Fuma	2	40887517	67.93546257	5	-0.004119967	-2125	'31.2'	grmzm2g177070_t01	'cell.division'
412	Fuma	2	101178551	76.43228188	6	-0.003508264	-123480	'33.99'	grmzm2g149708_t01	'development.unspecified'
413	Fuma	2	126037868	77.45026254	6	-0.002840198	-394672	'29.5.11.4.3.2'	grmzm2g365677_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
414	Fuma	2	126357762	77.49091538	7	-0.003825335	-184159	'23.4.10'	grmzm2g001524_t01	'nucleotide metabolism.phosphotransfer and pyrophosphatases.nucleoside diphosphate kinase'
415	Fuma	2	128572754	77.77240149	5	0.006664527	-384	'12.1.1'	grmzm2g424659_t01	'N-metabolism.nitrate metabolism.NR'
416	Fuma	2	140085774	79.23550166	9	-0.003129574	-736	'29.5.11.1'	grmzm2g168829_t01	'protein.degradation.ubiquitin.ubiquitin'
417	Fuma	2	209368892	120.1686122	5	-0.003179256	-1096	'27.2'	grmzm2g086805_t01	'RNA.transcription'
418	Fuma	2	210076932	121.1450848	6	-0.005447489	-59	'31.4'	grmzm2g102903_t02	'cell.vesicle transport'
419	Fuma	3	27871359	53.36404037	8	-0.003866516	-167415	'29.4'	grmzm2g012472_t01	'protein.postranslational modification'

420	Fuma	3	223869464	146.0056611	18	0.010366321	-1856	'29.4'	grmzm2g061681_t02	'protein.postranslational modification'
421	Fuma	3	223869468	146.0056712	5	0.01094552	-1860	'29.4'	grmzm2g061681_t02	'protein.postranslational modification'
422	Fuma	4	3544388	12.18913098	8	-0.013932612	-134069	'34.14'	grmzm2g037342_t01	'transport.unspecified cations'
423	Fuma	4	4653906	15.97068346	12	-0.008852558	-40373	'34.2'	grmzm2g157057_t01	'transport.sugars'
424	Fuma	4	4655407	15.97579929	7	-0.008673224	-41874	'34.2'	grmzm2g157057_t01	'transport.sugars'
425	Fuma	4	168642940	76.90973825	5	-0.005552603	-39399	'17.2.3'	grmzm2g025671_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
426	Fuma	4	177728199	89.41877612	10	-0.003560153	-43695	'10.3'	grmzm2g471594_t01	'cell wall.hemicellulose synthesis'
427	Fuma	4	177733636	89.446853	10	-0.002949415	-49132	'10.3'	grmzm2g471594_t01	'cell wall.hemicellulose synthesis'

428	Fuma	4	179860377	92.79034271	8	-0.003276803	-139690	'27.3.99'	grmzm2g101518_t01	'RNA.regulation of transcription.unclassified'
429	Fuma	4	180517470	93.4957277	5	-0.002716131	-6587	'29.5.11'	grmzm2g025470_t01	'protein.degradation.ubiquitin'
430	Fuma	4	182201693	95.89453425	8	-0.004834603	-62211	'26.2'	grmzm2g021401_t01	'misc.UDP glucosyl and glucoronyl transferases'
431	Fuma	4	182528229	96.35961321	8	-0.003345301	-46446	'33.99'	grmzm2g111720_t02	'development.unspecified'
432	Fuma	4	182976299	96.99779073	7	-0.002979929	-164793	'27.3.99'	grmzm2g089876_t01	'RNA.regulation of transcription.unclassified'
433	Fuma	4	230346458	113.6832878	23	0.006178358	-125654	'27.3.6'	grmzm2g085751_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
434	Fuma	4	234235715	115.012717	20	0.005063297	-229	'30.11'	grmzm2g019358_t01	'signalling.light'
435	Fuma	4	244607562	137.8307023	33	-0.006210745	-31906	'31.1'	grmzm2g019838_t01	'cell.organisation'
436	Fuma	5	6670422	24.85176321	8	0.008168665	-119238	'27.3.32'	grmzm2g089696_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'

437	Fuma	5	6828578	25.41836288	5	0.002267897	-5713	'30.2.99'	grmzm2g072658_t01	'signalling.receptor kinases.misc'
438	Fuma	5	7550141	28.65678582	8	0.004885718	-30512	'31.4'	grmzm2g147046_t01	'cell.vesicle transport'
439	Fuma	5	9280217	30.80111555	6	0.003874816	-134301	'20.2.1'	grmzm2g129700_t02	'stress.abiotic.heat'
440	Fuma	5	10073594	32.64114173	7	0.003647227	-12829	'30.11'	grmzm2g181028_t01	'signalling.light'
441	Fuma	5	10073765	32.64153832	28	0.003494537	-13000	'30.11'	grmzm2g181028_t01	'signalling.light'
442	Fuma	5	10085671	32.66915111	5	0.00489814	-24906	'30.11'	grmzm2g181028_t01	'signalling.light'
443	Fuma	6	165445511	102.4790375	8	-0.005808279	-2460	'27.3.35'	grmzm2g011932_t05	'RNA.regulation of transcription.bZIP transcription factor family'
444	Fuma	7	57117438	49.15463724	6	-0.006367934	-229110	'31.4'	grmzm2g043758_t01	'cell.vesicle transport'
445	Fuma	7	129970942	70.62091409	6	-0.005265067	-6805	'27.4'	grmzm2g463359_t01	'RNA.RNA binding'

446	Fuma	7	159657824	105.8008762	37	0.003170054	-27580	'34.2'	grmzm2g377502_t01	'transport.sugars'
447	Fuma	7	162478003	113.1505321	5	0.004030903	-77858	'29.5.11.4.5.2'	ac195147.3_fgt001	'protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ'
448	Fuma	7	162478193	113.1514273	13	0.004228173	-78048	'29.5.11.4.5.2'	ac195147.3_fgt001	'protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ'
449	Fuma	7	162482540	113.1719093	13	0.003306758	-82395	'29.5.11.4.5.2'	ac195147.3_fgt001	'protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ'
450	Fuma	8	156139987	82.72693349	6	-0.00298176	-33486	'31.5.1'	grmzm2g435034_t01	'cell.cell death.plants'
451	Fuma	8	160438189	89.3463314	64	0.003362949	-118515	'10.5'	grmzm2g003493_t01	'cell wall.cell wall proteins'
452	Fuma	8	160597062	89.61860448	5	0.004068163	-17768	'27.3.99'	grmzm2g070898_t01	'RNA.regulation of transcription.unclassified'
453	Fuma	8	160929154	90.26562868	10	0.003237693	-13321	'30.2.11'	grmzm2g107484_t01	'signalling.receptor kinases.leucine rich repeat XI'
454	Fuma	10	89924492	41.55012521	6	0.006236087	-7043	'29.5.5'	grmzm2g063592_t01	'protein.degradation.serine protease'

455	Fuma	10	148039817	99.52795003	15	0.003588536	-6298	'11.1.13'	grmzm2g173636_t01	'lipid metabolism.FA synthesis and FA elongation.acyl-CoA binding protein'
456	Fuma	10	148043393	99.54799587	25	0.004260238	-9874	'11.1.13'	grmzm2g173636_t01	'lipid metabolism.FA synthesis and FA elongation.acyl-CoA binding protein'
457	Gluc	1	19427291	35.91876596	7	-0.027454867	-6397	'26.2'	grmzm2g039129_t01	'misc.UDP glucosyl and glucoronyl transferases'
458	Gluc	1	19427753	35.91919409	22	-0.037111842	-6859	'26.2'	grmzm2g039129_t01	'misc.UDP glucosyl and glucoronyl transferases'
459	Gluc	1	19745377	36.21353287	15	-0.032734262	-20670	'27.3.39'	grmzm2g447551_t02	'RNA.regulation of transcription.AtSR Transcription Factor family'
460	Gluc	1	19745402	36.21355604	13	-0.045012011	-20695	'27.3.39'	grmzm2g447551_t02	'RNA.regulation of transcription.AtSR Transcription Factor family'
461	Gluc	1	45048717	61.17102638	9	0.038550257	-84899	'11.2.3'	grmzm2g074401_t01	'lipid metabolism.FA desaturation.omega 3 desaturase'
462	Gluc	1	48047150	63.48200445	8	0.034229401	-214242	'31.1'	grmzm2g122965_t01	'cell.organisation'

463	Gluc	1	51070607	65.47738632	7	0.029008336	-257764	'33.99'	ac208571.4_fgt001	'development.unspecified'
464	Gluc	1	56261977	69.68972945	5	0.023260105	-85357	'30.2.11'	grmzm2g119850_t01	'signalling.receptor kinases.leucine rich repeat XI'
465	Gluc	1	155941648	90.6953495	7	0.038011307	-220544	'27.3.21'	grmzm2g179325_t01	'RNA.regulation of transcription.GRAS transcription factor family'
466	Gluc	1	219996077	128.8274919	14	0.047101374	-76064	'17.2.3'	ac217977.3_fgt001	'hormone metabolism.auxin.induced-regulated-responsive-activated'
467	Gluc	1	222371522	129.7775422	6	0.060501845	-20027	'29.5.11.4.3.2'	grmzm2g067626_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
468	Gluc	1	239603760	141.3379825	11	-0.05994586	-224044	'30.3'	grmzm2g070673_t01	'signalling.calcium'
469	Gluc	2	3583432	9.929705575	9	-0.023800048	-7688	'17.2.3'	grmzm2g365166_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
470	Gluc	2	3583516	9.930283959	21	-0.023735882	-7772	'17.2.3'	grmzm2g365166_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
471	Gluc	2	3980052	10.9932083	9	-0.020514387	-437	'34.3'	grmzm2g042933_t07	'transport.amino acids'
472	Gluc	2	4089979	11.27575825	6	-0.027570085	-50585	'30.2.17'	grmzm2g391741_t01	'signalling.receptor kinases.DUF 26'

473	Gluc	2	4154747	11.44223414	8	-0.02251602	-4133	'1.3.13'	grmzm2g039345_t01	'PS.calvin cycle.rubisco interacting'
474	Gluc	2	5500383	16.53049076	8	-0.031577515	-118826	'30.2.3'	grmzm2g055844_t01	'signalling.receptor kinases.leucine rich repeat III'
475	Gluc	2	21516360	52.5167576	7	-0.044827778	-6069	'34.13'	grmzm2g051179_t01	'transport.peptides and oligopeptides'
476	Gluc	2	21991139	53.30019341	33	-0.044813254	-152694	'30.5'	grmzm2g132055_t01	'signalling.G-proteins'
477	Gluc	2	21995485	53.30230537	23	-0.037693821	-2292	'27.3.9'	grmzm2g404973_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
478	Gluc	2	21996541	53.30281854	21	-0.033790264	-3348	'27.3.9'	grmzm2g404973_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
479	Gluc	2	61159379	74.01441319	8	-0.032013585	-391771	'29.5.11.4.2'	grmzm2g068590_t02	'protein.degradation.ubiquitin.E3.RING'
480	Gluc	2	160568992	82.32572371	9	-0.041399233	-100627	'31.3'	grmzm2g161382_t01	'cell.cycle'
481	Gluc	2	175895506	86.83396756	12	0.048831829	-69368	'11.1.20'	grmzm2g043501_t01	'lipid metabolism.FA synthesis and FA elongation.MCD'
482	Gluc	2	186768867	98.0043879	8	-0.035176619	-1542	'27.3.6'	grmzm2g417597_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'

483	Gluc	2	188188473	99.75988308	11	-0.03166046	-118565	'17.2.3'	grmzm2g150319_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
484	Gluc	3	1878568	3.303968086	7	-0.028976818	-32651	'34.19.2'	grmzm2g093090_t01	'transport.Major Intrinsic Proteins.TIP'
485	Gluc	3	1878573	3.303993959	5	-0.031384063	-32656	'34.19.2'	grmzm2g093090_t01	'transport.Major Intrinsic Proteins.TIP'
486	Gluc	3	1878755	3.304935735	5	-0.021125504	-32838	'34.19.2'	grmzm2g093090_t01	'transport.Major Intrinsic Proteins.TIP'
487	Gluc	3	4677417	17.51176627	6	-0.021815356	-4483	'26.2'	grmzm2g055313_t01	'misc.UDP glucosyl and glucoronyl transferases'
488	Gluc	3	10108659	34.7208259	23	-0.027274921	-34001	'34.16'	grmzm2g118243_t01	'transport.ABC transporters and multidrug resistance systems'
489	Gluc	3	10750452	36.00654788	19	-0.029665146	-119519	'26.2'	grmzm2g338465_t01	'misc.UDP glucosyl and glucoronyl transferases'
490	Gluc	3	13310374	40.12977866	10	-0.029446598	-9122	'34.19.2'	grmzm2g146627_t01	'transport.Major Intrinsic Proteins.TIP'

491	Gluc	3	13634107	40.54837757	8	-0.028513384	-8039	'27.2'	grmzm2g102664_t01	'RNA.transcription'
492	Gluc	3	16806728	44.65069551	9	-0.029377307	-33384	'16.2'	ac215260.3_fgt003	'secondary metabolism.phenylpropanoids'
493	Gluc	3	19194362	47.73799582	8	-0.033080281	-9397	'29.5.9'	grmzm2g088834_t01	'protein.degradation.AAA type'
494	Gluc	3	49808116	56.5306869	16	-0.031996718	-108836	'34.16'	grmzm2g119894_t01	'transport.ABC transporters and multidrug resistance systems'
495	Gluc	3	67958527	58.10223721	5	-0.033220713	-351421	'27.3.44'	grmzm2g015277_t01	'RNA.regulation of transcription.Chromatin Remodeling Factors'
496	Gluc	3	84984528	58.15869307	19	-0.053941727	-1317	'20.2.99'	grmzm2g343974_t01	'stress.abiotic.unspecified'
497	Gluc	3	126612628	60.92265927	13	-0.036596401	-64275	'20.2.99'	ac209744.3_fgt001	'stress.abiotic.unspecified'
498	Gluc	3	135511148	62.83074525	10	-0.032809231	-64544	'26.2'	grmzm2g174769_t01	'misc.UDP glucosyl and glucoronyl transferases'
499	Gluc	3	213286642	125.2764546	22	0.027989477	-95400	'27.3.12'	grmzm2g157927_t01	'RNA.regulation of transcription.C3H zinc finger family'

500	Gluc	3	223962036	146.2391988	22	0.049820979	-94428	'29.4'	grmzm2g061681_t02	'protein.postranslational modification'
501	Gluc	4	82547651	56.71433525	9	-0.032568459	-219607	'33.99'	grmzm2g146518_t01	'development.unspecified'
502	Gluc	4	93788979	57.69805012	9	-0.054449121	-19907	'34.13'	ac184794.2_fgt003	'transport.peptides and oligopeptides'
503	Gluc	4	94875017	57.72053661	9	-0.046879342	-317032	'30.2.25'	grmzm2g132591_t01	'signalling.receptor kinases.wall associated kinase'
504	Gluc	4	103678485	57.89068149	10	-0.02674891	-12819	'33.99'	grmzm2g168365_t02	'development.unspecified'
505	Gluc	4	110571777	58.03760973	7	-0.026815621	-84697	'1.1.3'	grmzm2g054687_t01	'PS.lightreaction.cytochrome b6/f'
506	Gluc	4	142457660	60.337891	31	-0.04524174	-262973	'23.3.2.1'	grmzm2g135132_t01	'nucleotide metabolism.salvage.nucleoside kinases.adenosine kinase'
507	Gluc	4	243115508	132.4118713	10	-0.035189308	-13861	'29.5.11.4.3.2'	grmzm2g166147_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'

508	Gluc	4	243119871	132.428798	9	-0.053005896	-3567	'27.3.22'	grmzm2g166041_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
509	Gluc	5	1571929	2.012971503	64	-0.030891034	-131	'29.2.1.2.1.21'	grmzm2g125300_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S21'
510	Gluc	5	2357601	5.023225032	15	-0.03524917	-8423	'27.3.8'	grmzm2g144188_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
511	Gluc	5	2358292	5.027739617	11	-0.034233745	-9114	'27.3.8'	grmzm2g144188_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
512	Gluc	5	7584397	28.79525161	9	0.05608891	-15192	'29.4'	grmzm2g014618_t01	'protein.postranslational modification'
513	Gluc	5	7815403	29.72899837	23	0.066760523	-75801	'29.3.4.2'	grmzm2g077295_t01	'protein.targeting.secretory pathway.golgi'
514	Gluc	5	10372835	33.33515135	6	0.037017755	-182827	'31.1'	grmzm2g152328_t01	'cell.organisation'
515	Gluc	5	10642005	33.95941932	32	0.047231589	-99030	'31.2'	grmzm2g131324_t01	'cell.division'
516	Gluc	5	11555355	36.07769085	9	0.04595894	-8454	'27.3.49'	grmzm2g162405_t01	'RNA.regulation of transcription.GeBP like'
517	Gluc	5	15080589	45.43333631	7	-0.041567563	-28137	'27.1'	grmzm2g420732_t01	'RNA.processing'

518	Gluc	5	15334088	45.78544974	26	-0.0335316	-4193	'31.1'	grmzm2g078612_t01	'cell.organisation'
519	Gluc	5	23315145	53.64866829	8	-0.048304577	-77757	'28.2'	grmzm2g060349_t01	'DNA.repair'
520	Gluc	5	36811132	58.27317542	5	-0.030458025	-124287	'30.3'	grmzm2g096228_t01	'signalling.calcium'
521	Gluc	5	36811154	58.27317812	24	-0.030783704	-124309	'30.3'	grmzm2g096228_t01	'signalling.calcium'
522	Gluc	5	37443804	58.32813065	7	-0.027227488	-196912	'27.4'	ac217556.3_fgt003	'RNA.RNA binding'
523	Gluc	5	38114919	58.37370611	5	-0.032853631	-226447	'11.1.1'	grmzm2g377341_t01	'lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation'
524	Gluc	5	88070567	69.41851202	9	-0.048661521	-174293	'27.1'	grmzm2g136599_t01	'RNA.processing'
525	Gluc	5	114204945	70.51015923	15	-0.037585673	-182325	'27.3.25'	grmzm2g159155_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
526	Gluc	5	149251475	73.13980408	9	-0.039233421	-768	'33.99'	grmzm2g108016_t01	'development.unspecified'

527	Gluc	5	163819573	76.76334725	6	0.03892669	-1683	'28.1'	grmzm2g011631_t01	'DNA.synthesis/chromatin structure'
528	Gluc	5	165729383	77.90457087	6	-0.068401599	-437510	'27.3.30'	grmzm2g084684_t01	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
529	Gluc	5	167871133	79.69575659	8	-0.063461483	-25140	'26.16'	grmzm2g038669_t01	'misc.myrosinases-lectin-jacalin'
530	Gluc	5	168259864	79.99109637	14	-0.054728927	-178993	'15.2'	grmzm2g113332_t01	'metal handling.binding, chelation and storage'
531	Gluc	5	168260887	79.99218626	6	-0.044931698	-180016	'15.2'	grmzm2g113332_t01	'metal handling.binding, chelation and storage'
532	Gluc	5	192568110	101.6096752	10	0.062349209	-3074	'31.1'	grmzm2g015127_t01	'cell.organisation'
533	Gluc	5	200083354	107.7054585	5	-0.035928509	-19886	'20.2.3'	grmzm2g415062_t01	'stress.abiotic.drought/salt'
534	Gluc	5	200531277	108.3769927	13	0.049459237	-115474	'21.2.1'	grmzm2g320307_t01	'redox.ascorbate and glutathione.ascorbate'
535	Gluc	5	201231896	109.0981131	11	-0.04069251	-25913	'20.2.1'	grmzm2g020040_t01	'stress.abiotic.heat'

536	Gluc	5	209935600	130.9474516	5	0.054968328	-9124	'29.5.9'	grmzm2g403454_t01	'protein.degradation.AAA type'
537	Gluc	5	212261524	139.7573696	29	0.03161962	-20262	'27.1.1'	grmzm2g080930_t01	'RNA.processing.splicing'
538	Gluc	5	213298320	144.5886587	7	0.03745947	-2778	'29.4'	grmzm2g180430_t01	'protein.postranslational modification'
539	Gluc	6	1331502	-9.338084147	17	0.048982117	-43973	'26.12'	grmzm2g098174_t01	'misc.peroxidases'
540	Gluc	6	1335665	-9.333360919	20	0.044914068	-31	'29.5.11.4.2'	grmzm2g423956_t01	'protein.degradation.ubiquitin.E3.RING'
541	Gluc	6	9189279	-0.422862181	10	0.0457043	-5373	'31.1'	grmzm2g066400_t01	'cell.organisation'
542	Gluc	6	49947554	8.548807235	13	0.050794602	-852925	'27.3.49'	grmzm2g392516_t01	'RNA.regulation of transcription.GeBP like'
543	Gluc	6	122728773	45.27892524	28	-0.090243045	-4430	'33.99'	grmzm2g071162_t01	'development.unspecified'
544	Gluc	6	123562319	45.55520364	14	-0.085892259	-108986	'29.2.1.2.2.523'	grmzm2g166659_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L23A'
545	Gluc	6	157445216	76.89711855	5	-0.059505241	-133994	'11.8.1'	grmzm2g163008_t01	'lipid metabolism."exotics" (steroids, squalene etc).sphingolipids'

546	Gluc	6	157953572	77.68801846	6	-0.050730304	-332	'29.3.4.1'	grmzm2g060324_t01	'protein.targeting.secretory pathway.ER'
547	Gluc	7	3665692	13.3545418	11	-0.043550162	-175257	'20.1'	grmzm2g465226_t01	'stress.biotic'
548	Gluc	7	20233795	44.69829015	5	-0.032821318	-72625	'29.3.4.99'	grmzm2g105996_t01	'protein.targeting.secretory pathway.unspecified'
549	Gluc	7	27327128	46.7793044	15	-0.031600786	-665835	'23.2'	grmzm2g173063_t01	'nucleotide metabolism.degradation'
550	Gluc	7	32868948	47.79855164	40	-0.03385516	-233353	'31.3.1'	grmzm2g092072_t01	'cell.cycle.peptidylprolyl isomerase'
551	Gluc	7	84574592	49.92029539	16	-0.03318546	-67361	'30.2.99'	grmzm2g354615_t01	'signalling.receptor kinases.misc'
552	Gluc	7	151684587	89.72788592	23	0.050943726	-59671	'29.3'	grmzm2g033493_t01	'protein.targeting'
553	Gluc	7	151704874	89.76604438	13	0.063838907	-79958	'29.3'	grmzm2g033493_t01	'protein.targeting'

554	Gluc	7	159106172	104.5548504	6	-0.033343837	-94883	'27.3.15'	grmzm2g384528_t01	'RNA.regulation of transcription.CCAAT box binding factor family, HAP3'
555	Gluc	7	166657242	123.8438631	13	0.046507086	-105055	'34.15'	grmzm2g020766_t01	'transport.potassium'
556	Gluc	7	167223656	126.3055595	5	0.04371809	-3846	'29.4'	grmzm2g166658_t01	'protein.postranslational modification'
557	Gluc	7	168146720	130.3172954	14	0.038042497	-9079	'29.3.1'	ac155434.2_fgt004	'protein.targeting.nucleus'
558	Gluc	7	168146779	130.3175518	16	0.050979889	-9138	'29.3.1'	ac155434.2_fgt004	'protein.targeting.nucleus'
559	Gluc	7	168259468	130.8073104	11	0.027577674	-67178	'27.3.19'	grmzm2g151811_t01	'RNA.regulation of transcription.EIN3-like(EIL) transcription factor family'
560	Gluc	7	168322280	131.0802981	6	0.034001816	-59905	'29.5.1'	grmzm2g059165_t01	'protein.degradation.subtilases'
561	Gluc	7	169418608	134.40687	6	0.032947988	-1317	'29.5.11.4.2'	grmzm2g440866_t01	'protein.degradation.ubiquitin.E3.RING'
562	Gluc	7	169612994	134.5554328	6	-0.060679509	-2569	'26.19'	grmzm2g086628_t01	'misc.plastocyanin-like'
563	Gluc	7	170074937	134.9084806	8	0.04615997	-28013	'13.1.6.1.2'	grmzm2g051129_t01	'amino acid metabolism.synthesis.aromatic aa.chorismate.3-dehydroquinate synthase'

564	Gluc	8	10208359	26.24898642	5	-0.026684796	-6556	'29.1.7'	grmzm2g140754_t01	'protein.aa activation.alanine-tRNA ligase'
565	Gluc	8	10978629	28.40458338	9	-0.025432862	-4989	'33.99'	grmzm2g049661_t01	'development.unspecified'
566	Gluc	8	13271527	33.98105	6	-0.027208471	-3957	'30.2.20'	grmzm2g171807_t01	'signalling.receptor kinases.wheat LRK10 like'
567	Gluc	8	15541604	37.97326272	22	-0.033735477	-23356	'29.5.11.4.2'	grmzm2g305901_t01	'protein.degradation.ubiquitin.E3.RING'
568	Gluc	8	17101531	39.8048484	7	-0.028932686	-58729	'27.3.30'	grmzm2g025215_t01	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
569	Gluc	8	17783857	40.90236227	24	-0.035698197	-69101	'27.1'	grmzm2g047949_t01	'RNA.processing'
570	Gluc	8	141607731	72.49035639	5	0.035922564	-18434	'26.28'	grmzm2g117754_t01	'misc.GDSL-motif lipase'
571	Gluc	8	160611990	89.64768912	7	0.033050154	-32696	'27.3.99'	grmzm2g070898_t01	'RNA.regulation of transcription.unclassified'
572	Gluc	8	161247986	90.88681804	17	0.025027089	-5246	'31.3.1'	grmzm2g031204_t01	'cell.cycle.peptidylprolyl isomerase'

573	Gluc	8	161456583	91.29323346	6	0.027119377	-82611	'33.99'	grmzm2g096169_t01	'development.unspecified'
574	Gluc	8	162617259	92.65142696	6	0.024273535	-16908	'28.2'	grmzm2g700757_t01	'DNA.repair'
575	Gluc	8	173914014	136.3104872	19	0.020511215	-35877	'30.3'	ac203173.3_fgt001	'signalling.calcium'
576	Gluc	9	2701441	-3.388186607	6	-0.065619148	-280728	'27.1.19'	grmzm2g016275_t01	'RNA.processing.ribonucleases'
577	Gluc	9	6998866	8.219401947	9	-0.027000187	-205260	'20.2.1'	grmzm2g097620_t01	'stress.abiotic.heat'
578	Gluc	9	7182819	8.716269429	28	-0.045797986	-40774	'31.1'	grmzm2g017257_t01	'cell.organisation'
579	Gluc	9	10186494	15.44407336	6	-0.034472041	-142075	'29.4.1.57'	grmzm2g055982_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
580	Gluc	9	26517167	43.30986818	6	0.044089609	-2690	'27.3.25'	grmzm2g044824_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
581	Gluc	9	26517266	43.30992673	33	0.044430659	-2789	'27.3.25'	grmzm2g044824_t01	'RNA.regulation of transcription.MYB domain transcription factor family'

582	Gluc	9	60088439	45.65313865	30	0.055300858	-297869	'13.1.6.4.1'	grmzm2g324297_t01	'amino acid metabolism.synthesis.aromatic aa.tyrosine.arogenate dehydrogenase \& prephenate dehydrogenase'
583	Gluc	9	144805016	93.75044572	11	0.03694982	-2034	'3.4.3'	grmzm2g004528_t01	'minor CHO metabolism.myo-inositol.InsP Synthases'
584	Gluc	10	5427445	17.07840286	48	-0.069028108	-60	'27.1.19'	grmzm2g065804_t01	'RNA.processing.ribonucleases'
585	Gluc	10	37230981	36.08777546	15	0.057220632	-4181	'26.27'	grmzm2g459370_t01	'misc.calcineurin-like phosphoesterase family protein'
586	Gluc	10	52110744	36.32411544	18	0.071276311	-52762	'28.1'	grmzm2g074818_t01	'DNA.synthesis/chromatin structure'
587	Gluc	10	76226092	38.27843109	8	0.042662267	-174913	'34.3'	grmzm2g078292_t01	'transport.amino acids'
588	Gluc	10	76332289	38.30539729	11	0.043798998	-5213	'27.3.67'	grmzm2g145130_t01	'RNA.regulation of transcription.putative transcription regulator'
589	Gluc	10	85540940	40.43084945	33	0.066852209	-54606	'29.4'	grmzm2g060798_t01	'protein.postranslational modification'
590	Gluc	10	138301683	66.29092836	9	-0.037590118	-163884	'3.5'	af466202.2_fgt007	'minor CHO metabolism.others'

591	Gluc	10	144247405	82.22431479	8	-0.040531525	-2506	'10.6.2'	grmzm2g136895_t01	'cell wall.degradation.mannan-xylose-arabinose-fucose'
592	Gluc	10	148193563	100.3897975	8	-0.046829239	-415	'28.2'	grmzm2g093623_t01	'DNA.repair'
593	Glut	1	52690146	67.43745454	13	-0.00764858	-34797	'27.3.19'	grmzm2g033570_t01	'RNA.regulation of transcription.EIN3-like(EIL) transcription factor family'
594	Glut	1	182943941	98.00929506	43	0.004651268	-192837	'27.4'	grmzm2g107163_t01	'RNA.RNA binding'
595	Glut	1	182944297	98.00949265	10	0.004698343	-193193	'27.4'	grmzm2g107163_t01	'RNA.RNA binding'
596	Glut	1	183661710	98.46017249	25	0.005469687	-4262	'34.99'	grmzm2g113840_t02	'transport.misc'
597	Glut	1	219467828	128.6162207	53	-0.006511624	-13460	'30.2.11'	grmzm2g136353_t01	'signalling.receptor kinases.leucine rich repeat XI'
598	Glut	1	220903481	129.1904047	5	-0.011601406	-17822	'1.5.1'	grmzm2g174107_t02	'PS.carbon concentrating mechanism.C4'
599	Glut	1	221341695	129.3656668	12	-0.009264172	-119609	'10.2.1'	grmzm2g044269_t01	'cell wall.cellulose synthesis.cellulose synthase'

600	Glut	1	277632495	170.2619536	14	0.010539017	-18814	'27.3.32'	grmzm2g008029_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
601	Glut	2	4153357	11.43866137	14	0.008070873	-2743	'1.3.13'	grmzm2g039345_t01	'PS.calvin cycle.rubisco interacting'
602	Glut	2	4153720	11.4395944	56	0.009484778	-3106	'1.3.13'	grmzm2g039345_t01	'PS.calvin cycle.rubisco interacting'
603	Glut	2	4299868	11.96628803	12	0.003568927	-25012	'17.5.2'	grmzm2g067463_t01	'hormone metabolism.ethylene.signal transduction'
604	Glut	2	12590485	36.29106182	5	-0.008475169	-9562	'29.2.1.2.2.12'	grmzm2g149649_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L12'
605	Glut	2	133606697	78.41212615	8	-0.005723744	-1115	'26.8'	grmzm2g053466_t08	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
606	Glut	2	185662626	96.4222994	8	0.005714311	-157937	'29.5.11'	grmzm2g137558_t01	'protein.degradation.ubiquitin'
607	Glut	2	186287170	97.21489693	11	0.00486937	-10581	'27.3.16'	grmzm2g022162_t01	'RNA.regulation of transcription.CCAAT box binding factor family, HAP5'
608	Glut	2	186556918	97.58848824	7	0.00560792	-12820	'29.5.11.4.1'	grmzm2g080439_t01	'protein.degradation.ubiquitin.E3.HECT'

609	Glut	2	186556997	97.58864326	38	0.004943913	-12899	'29.5.11.4.1'	grmzm2g080439_t01	'protein.degradation.ubiquitin.E3.HECT'
610	Glut	2	186558389	97.59137473	6	0.004850272	-14291	'29.5.11.4.1'	grmzm2g080439_t01	'protein.degradation.ubiquitin.E3.HECT'
611	Glut	2	186558494	97.59158077	8	0.005489912	-14396	'29.5.11.4.1'	grmzm2g080439_t01	'protein.degradation.ubiquitin.E3.HECT'
612	Glut	2	209437807	120.3370062	6	-0.006286015	-70011	'27.2'	grmzm2g086805_t01	'RNA.transcription'
613	Glut	2	210076624	121.1447377	5	-0.007333198	-36361	'26.12'	grmzm2g156257_t01	'misc.peroxidases'
614	Glut	2	233601849	155.7785003	5	-0.004272848	-56209	'27.3.20'	grmzm2g173882_t01	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
615	Glut	3	201451737	108.647491	5	-0.009148834	-156630	'27.3.32'	grmzm2g101405_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
616	Glut	3	209190519	119.5728622	8	-0.008009729	-34715	'29.2.1.2.2.518'	ac230013.2_fgt007	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L18A'
617	Glut	3	210306116	120.8801933	6	-0.016920822	-5739	'28.99'	grmzm2g173989_t03	'DNA.unspecified'
618	Glut	3	210710907	121.3852837	8	-0.017895411	-1120	'11.8.1'	grmzm2g003526_t01	'lipid metabolism."exotics" (steroids, squalene etc).sphingolipids'

619	Glut	3	210877159	121.5927298	12	-0.004934249	-167372	'11.8.1'	grmzm2g003526_t01	'lipid metabolism."exotics" (steroids, squalene etc).sphingolipids'
620	Glut	3	210988072	121.7311249	6	-0.016726602	-19176	'27.3.3'	grmzm2g160971_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
621	Glut	3	211148597	121.9314249	16	-0.005852378	-7703	'29.4'	grmzm2g118403_t01	'protein.postranslational modification'
622	Glut	3	212234516	123.2864138	7	-0.005205315	-174659	'13.1.4.1'	grmzm2g004382_t01	'amino acid metabolism.synthesis.branched chain group.common'
623	Glut	3	212718903	123.8908226	5	-0.004685377	-62927	'11.9.2.1'	grmzm2g153672_t01	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
624	Glut	3	213151216	124.9438117	7	-0.004725778	-206324	'34.8'	grmzm2g064473_t01	'transport.metabolite transporters at the envelope membrane'
625	Glut	3	213151324	124.944077	8	-0.004513687	-206432	'34.8'	grmzm2g064473_t01	'transport.metabolite transporters at the envelope membrane'
626	Glut	3	213890769	126.7603538	6	-0.010464009	-30811	'1.5.1'	grmzm2g348512_t02	'PS.carbon concentrating mechanism.C4'
627	Glut	3	215225785	128.93347	9	-0.005251452	-5347	'29.5.11.5'	grmzm2g064283_t01	'protein.degradation.ubiquitin.ubiquitin protease'

628	Glut	3	225244456	148.4971299	11	0.010839249	-51223	'20.2.4'	grmzm2g071154_t01	'stress.abiotic.touch/wounding'
629	Glut	3	228108627	153.4517969	9	-0.007734346	-13056	'27.1'	grmzm2g015592_t01	'RNA.processing'
630	Glut	4	113973202	58.11061842	7	0.012195634	-130029	'23.2'	grmzm2g106618_t01	'nucleotide metabolism.degradation'
631	Glut	4	114035361	58.11195261	27	0.009580393	-60128	'29.4'	grmzm2g130018_t01	'protein.postranslational modification'
632	Glut	4	114684938	58.12589523	19	0.012290204	-442195	'27.3.99'	grmzm2g140016_t01	'RNA.regulation of transcription.unclassified'
633	Glut	4	114784127	58.12802424	11	0.008190782	-541384	'27.3.99'	grmzm2g140016_t01	'RNA.regulation of transcription.unclassified'
634	Glut	4	177057914	88.36703104	8	-0.004129286	-311901	'12.1.1'	grmzm2g428027_t01	'N-metabolism.nitrate metabolism.NR'
635	Glut	4	177728199	89.41877612	7	-0.004671784	-43695	'10.3'	grmzm2g471594_t01	'cell wall.hemicellulose synthesis'

636	Glut	4	180521118	93.50092348	6	-0.003964857	-3260	'1.1.4.7'	grmzm2g025171_t01	'PS.lightreaction.ATP synthase.delta chain'
637	Glut	4	180521269	93.50113855	12	-0.003984467	-3411	'1.1.4.7'	grmzm2g025171_t01	'PS.lightreaction.ATP synthase.delta chain'
638	Glut	5	2188871	3.920842986	34	0.004382943	-1275	'34.2'	grmzm2g085301_t01	'transport.sugars'
639	Glut	5	2188935	3.921261124	7	0.004596176	-1339	'34.2'	grmzm2g085301_t01	'transport.sugars'
640	Glut	5	22628584	52.93088442	10	0.004845342	-7471	'27.3.99'	grmzm2g078379_t01	'RNA.regulation of transcription.unclassified'
641	Glut	5	24406989	53.96237944	33	0.005600127	-100832	'21.1'	grmzm2g090736_t01	'redox.thioredoxin'
642	Glut	5	26831469	54.87846643	28	0.004300894	-581639	'26.10'	grmzm2g013082_t01	'misc.cytochrome P450'
643	Glut	5	26968073	54.93008209	8	0.004561445	-1779	'13.2.6.2'	grmzm2g174145_t01	'amino acid metabolism.degradation.aromatic aa.tyrosine'

644	Glut	5	204624078	116.4807852	18	-0.008453086	-23326	'8.1.1.1'	grmzm2g140150_t01	'TCA / org. transformation.TCA.pyruvate DH.E1'
645	Glut	5	207099285	124.0780936	14	-0.005034335	-4736	'27.3.3'	grmzm2g055204_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
646	Glut	5	207830710	126.0436057	6	-0.005515777	-70804	'27.4'	grmzm2g303915_t02	'RNA.RNA binding'
647	Glut	5	208181590	126.6094235	22	-0.00481065	-25917	'33.99'	grmzm2g161175_t01	'development.unspecified'
648	Glut	5	211971359	138.4052511	12	-0.004321074	-6038	'11.3.5'	grmzm2g128214_t01	'lipid metabolism.Phospholipid synthesis.diacylglycerol kinase'
649	Glut	6	5873783	-4.184534568	5	-0.004487679	-224946	'13.99'	grmzm2g034404_t01	'amino acid metabolism.misc'
650	Glut	6	12079085	2.855833808	5	-0.006531182	-413099	'29.2.1.2.1.29'	grmzm2g060373_t03	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S29'
651	Glut	6	17417589	5.992091218	17	-0.007355935	-148645	'29.5.11.4.2'	grmzm2g101662_t01	'protein.degradation.ubiquitin.E3.RING'
652	Glut	7	46996523	49.11264731	7	0.008798227	-19190	'26.10'	grmzm2g435661_t01	'misc.cytochrome P450'
653	Glut	7	94886697	50.37959201	10	0.005639153	-41046	'28.99'	grmzm2g436649_t01	'DNA.unspecified'

654	Glut	7	142900670	81.10277074	5	0.006182641	-9191	'26.8'	grmzm2g111309_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
655	Glut	7	153318373	92.800926	8	0.005690411	-48233	'27.3.99'	grmzm2g081782_t01	'RNA.regulation of transcription.unclassified'
656	Glut	8	6455489	18.09391822	6	0.00847514	-7403	'13.1.5.3.1'	grmzm2g082185_t01	'amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL'
657	Glut	8	6456227	18.0946642	11	0.008664988	-8141	'13.1.5.3.1'	grmzm2g082185_t01	'amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL'
658	Glut	8	7548635	19.78341505	71	0.007377193	-74534	'3.5'	grmzm2g051842_t01	'minor CHO metabolism.others'
659	Glut	8	101278421	58.12094124	7	0.004952541	-232812	'27.4'	grmzm2g111596_t01	'RNA.RNA binding'
660	Glut	8	103054530	58.74182186	12	0.007297413	-11798	'27.3.37'	grmzm2g096064_t01	'RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family'
661	Glut	8	108849125	60.58213104	58	0.007826556	-37583	'30.5'	grmzm2g150724_t01	'signalling.G-proteins'
662	Glut	8	111162784	61.25050555	6	0.005962952	-209	'33.99'	grmzm2g179679_t01	'development.unspecified'

663	Glut	9	147914070	105.0171122	7	-0.005016694	-4364	'10.3'	grmzm2g137779_t01	'cell wall.hemicellulose synthesis'
664	Glut	10	4806482	13.07619208	13	0.004785432	-55832	'26.13'	grmzm2g434170_t01	'misc.acid and other phosphatases'
665	Glut	10	4916937	13.82732142	5	0.005675285	-166287	'26.13'	grmzm2g434170_t01	'misc.acid and other phosphatases'
666	Glut	10	107945494	44.01972245	13	-0.005346414	-215929	'20.1'	grmzm2g090441_t01	'stress.biotic'
667	Glut	10	121191348	47.87413076	6	-0.00534999	-81981	'20.2.1'	grmzm2g135608_t01	'stress.abiotic.heat'
668	Glut	10	143716606	81.33488617	5	0.005311941	-1695	'31.3'	grmzm2g000650_t01	'cell.cycle'
669	Glut	10	143720983	81.33864061	5	0.006129575	-6072	'31.3'	grmzm2g000650_t01	'cell.cycle'
670	Glut	10	145459551	86.83094884	6	0.00654061	-49	'18.3.2'	grmzm2g143480_t01	'Co-factor and vitamine metabolism.riboflavin.riboflavin synthase'

671	Glut	10	145674099	87.6872826	53	0.005786004	-3191	'30.11'	grmzm2g104268_t01	'signalling.light'
672	Glut	10	146203278	89.79941527	6	0.005650134	-2514	'26.2'	grmzm2g067424_t01	'misc.UDP glucosyl and glucoronyl transferases'
673	Glut	10	146744765	92.26833185	7	0.004535231	-3993	'31.1'	grmzm2g423861_t01	'cell.organisation'
674	Glut	10	148374079	101.4017084	12	0.006234528	-2242	'30.4.3'	grmzm2g406074_t01	'signalling.phosphinositides.bis(5''-nucleosyl)-tetraphosphatase'
675	Mala	1	15026222	30.17736702	5	-0.00767141	-640	'34.2.1'	grmzm2g034302_t01	'transport.sugars.sucrose'
676	Mala	1	16018451	32.20888865	5	-0.010779957	-77381	'26.8'	grmzm2g156486_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
677	Mala	1	16018768	32.20944008	34	-0.010507566	-77698	'26.8'	grmzm2g156486_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'

678	Mala	1	39323398	57.23255596	57	0.011761998	-39918	'26.8'	grmzm2g141799_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
679	Mala	1	40056302	57.91121791	14	0.007307404	-57119	'16.10'	grmzm2g305526_t01	'secondary metabolism.simple phenols'
680	Mala	1	88319619	83.94252884	5	0.005107759	-394993	'29.5.11.4.3.2'	grmzm2g079031_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
681	Mala	1	90444879	84.51213232	6	0.007232955	-439	'30.5'	grmzm2g071157_t01	'signalling.G-proteins'
682	Mala	1	210010258	121.8475905	9	-0.007472494	-1002	'30.2.11'	grmzm2g428554_t01	'signalling.receptor kinases.leucine rich repeat XI'
683	Mala	1	219597467	128.6680693	5	-0.010215717	-85238	'20.2.1'	grmzm2g047153_t01	'stress.abiotic.heat'
684	Mala	1	219599713	128.6689676	17	-0.008622717	-87484	'20.2.1'	grmzm2g047153_t01	'stress.abiotic.heat'
685	Mala	1	222370635	129.7771875	21	-0.010317833	-19140	'29.5.11.4.3.2'	grmzm2g067626_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
686	Mala	1	292093541	191.7018819	15	0.029138599	-11869	'27.3.11'	grmzm2g061897_t01	'RNA.regulation of transcription.C2H2 zinc finger family'

687	Mala	1	295777277	199.3871057	5	0.021925596	-4116	'9.1.1'	ac217358.3_fgt005	'mitochondrial electron transport / ATP synthesis.NADH-DH.complex I'
688	Mala	2	2111645	4.01866061	8	0.006346054	-41618	'27.3.5'	grmzm2g040736_t01	'RNA.regulation of transcription.ARR'
689	Mala	2	2662790	6.10191746	5	0.012572964	-40043	'30.3'	grmzm2g065012_t03	'signalling.calcium'
690	Mala	2	4313222	12.01705821	7	0.008065261	-41	'34.1'	grmzm2g019404_t01	'transport.p- and v-ATPases'
691	Mala	2	4829815	13.98107797	14	0.007986073	-141348	'34.18'	grmzm2g086920_t01	'transport.unspecified anions'
692	Mala	2	5064142	14.87195891	10	0.009403602	-3390	'13.2.3.1.1'	grmzm2g531230_t01	'amino acid metabolism.degradation.aspartate family.asparagine.L-asparaginase'
693	Mala	2	5064288	14.87251398	29	0.009676366	-3536	'13.2.3.1.1'	grmzm2g531230_t01	'amino acid metabolism.degradation.aspartate family.asparagine.L-asparaginase'
694	Mala	2	5564443	16.77403859	17	0.007030808	-44169	'33.99'	grmzm2g174784_t01	'development.unspecified'

695	Mala	2	38490452	66.37064702	10	-0.008181854	-150580	'29.5.11'	grmzm2g139846_t01	'protein.degradation.ubiquitin'
696	Mala	2	53075256	72.33109749	67	-0.01005034	-274404	'29.5.11.4.3.2'	grmzm2g541230_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
697	Mala	2	121233141	77.09963877	6	-0.008726546	-108524	'27.4'	grmzm2g435248_t01	'RNA.RNA binding'
698	Mala	2	187425746	99.07896093	34	0.006597118	-171106	'16.8.3'	grmzm2g078480_t01	'secondary metabolism.flavonoids.dihydroflavonols'
699	Mala	2	188442924	99.98704342	26	0.010380475	-24124	'29.2.1.2.2.32'	grmzm2g047971_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L32'
700	Mala	2	190921710	102.1999719	13	0.007946425	-9514	'31.1'	grmzm2g022032_t01	'cell.organisation'
701	Mala	2	190922255	102.2004584	6	0.005818998	-10059	'31.1'	grmzm2g022032_t01	'cell.organisation'
702	Mala	2	208636969	118.3801568	72	-0.009940999	-30560	'29.5.11.4.2'	grmzm2g358987_t01	'protein.degradation.ubiquitin.E3.RING'
703	Mala	3	28560505	53.70440674	76	0.012754816	-85335	'27.3.67'	grmzm2g075320_t01	'RNA.regulation of transcription.putative transcription regulator'
704	Mala	3	110591868	58.89150506	6	0.009305688	-241468	'29.4.1.57'	grmzm2g026203_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'

705	Mala	3	197969185	105.1512436	6	0.008872874	-167761	'31.1'	grmzm2g140455_t01	'cell.organisation'
706	Mala	3	200646842	108.1602931	7	0.006749729	-35	'27.4'	grmzm2g055276_t01	'RNA.RNA binding'
707	Mala	3	207468446	116.9659734	5	0.007830782	-162418	'16.2.1.3'	grmzm2g012233_t02	'secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL'
708	Mala	3	208722589	119.0297927	10	0.018556936	-10314	'27.3.4'	grmzm2g437460_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
709	Mala	3	208759190	119.072271	7	0.018809679	-46915	'27.3.4'	grmzm2g437460_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
710	Mala	3	213856232	126.6755216	29	-0.008429835	-52374	'26.2'	grmzm2g048010_t01	'misc.UDP glucosyl and glucoronyl transferases'
711	Mala	3	214330739	127.7703198	23	-0.007870489	-2029	'34.14'	grmzm2g099382_t01	'transport.unspecified cations'
712	Mala	3	214355739	127.8009362	14	-0.007817618	-59	'10.6.3'	grmzm2g037431_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
713	Mala	3	223533563	145.1258349	43	-0.006537456	-33379	'27.3.99'	grmzm2g002646_t01	'RNA.regulation of transcription.unclassified'
714	Mala	4	170999854	79.42178824	8	-0.017758613	-123363	'16.8.3'	grmzm2g099420_t01	'secondary metabolism.flavonoids.dihydroflavonols'

715	Mala	4	171775102	80.83509484	83	-0.010613833	-2697	'29.5.11.4.2'	grmzm2g130002_t01	'protein.degradation.ubiquitin.E3.RING'
716	Mala	4	180344878	93.24990822	5	0.026764303	-26662	'4.3.12'	grmzm2g021605_t01	'glycolysis.unclear/dually targeted.phosphoglycerate mutase'
717	Mala	5	2767759	7.538649577	9	-0.023022027	-75102	'16.8.3'	grmzm2g107076_t01	'secondary metabolism.flavonoids.dihydroflavonols'
718	Mala	5	4189784	13.29548628	8	-0.024817481	-39184	'27.3.25'	grmzm2g302549_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
719	Mala	5	5266701	18.78312331	16	-0.018541237	-31341	'34.4'	grmzm2g377555_t01	'transport.nitrate'
720	Mala	5	25580476	54.40578016	17	0.006381893	-204438	'34.19.2'	grmzm2g305446_t01	'transport.Major Intrinsic Proteins.TIP'
721	Mala	5	35870702	58.15768893	9	0.007312398	-12081	'29.4.1.57'	grmzm2g110968_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
722	Mala	5	159516767	75.22607915	59	0.006946802	-7921	'29.5.4'	grmzm2g411333_t01	'protein.degradation.aspartate protease'
723	Mala	5	196990966	105.0448056	21	-0.006739831	-56418	'29.5.11.4.2'	grmzm2g039725_t01	'protein.degradation.ubiquitin.E3.RING'

724	Mala	5	196991427	105.0451889	6	-0.007454933	-56879	'29.5.11.4.2'	grmzm2g039725_t01	'protein.degradation.ubiquitin.E3.RING'
725	Mala	5	213281396	144.5097958	5	-0.007254868	-6627	'29.5.11.4.2'	grmzm2g467756_t01	'protein.degradation.ubiquitin.E3.RING'
726	Mala	5	214193499	148.7600372	10	-0.005516584	-1364	'30.5'	grmzm2g150876_t01	'signalling.G-proteins'
727	Mala	6	2173089	-8.383242223	8	-0.007048492	-118322	'29.5'	grmzm2g313321_t01	'protein.degradation'
728	Mala	6	3682882	-6.670271784	7	-0.007945361	-30711	'29.5.11.4.2'	grmzm2g104769_t01	'protein.degradation.ubiquitin.E3.RING'
729	Mala	6	6894842	-3.026068551	6	-0.005310972	-189308	'29.5.11.4.2'	grmzm2g390009_t01	'protein.degradation.ubiquitin.E3.RING'
730	Mala	6	9251251	-0.35255042	21	-0.006131661	-55591	'29.2.1.2.2.80'	grmzm2g066460_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.P0'
731	Mala	6	160133599	84.08459515	7	-0.010156075	-6608	'29.5.11.4.3.2'	grmzm2g004592_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
732	Mala	6	161832235	87.63268966	6	-0.009770832	-53727	'28.1'	grmzm2g121186_t01	'DNA.synthesis/chromatin structure'
733	Mala	6	162218871	89.54447098	6	-0.006148267	-489	'20.2.1'	grmzm2g175089_t01	'stress.abiotic.heat'
734	Mala	6	162665812	91.75443968	12	-0.008612649	-714	'26.2'	grmzm2g059845_t01	'misc.UDP glucosyl and glucoronyl transferases'

735	Mala	6	163284243	94.27967325	19	-0.005380966	-371	'1.1.5.2'	grmzm2g481261_t01	'PS.lightreaction.other electron carrier (ox/red).ferredoxin'
736	Mala	6	165585617	102.9436765	17	-0.006076029	-85808	'30.11'	grmzm2g145556_t01	'signalling.light'
737	Mala	7	118340956	59.84562968	7	-0.012097666	-114501	'34.15'	grmzm2g088964_t01	'transport.potassium'
738	Mala	7	131033445	71.16406426	19	-0.009077321	-51423	'7.2.3'	grmzm2g083102_t01	'OPP.non-reductive PP.ribulose-phosphate 3-epimerase'
739	Mala	7	143058340	81.14259414	5	-0.006769154	-22803	'27.3.99'	grmzm2g007190_t01	'RNA.regulation of transcription.unclassified'
740	Mala	7	145583488	83.49098005	9	-0.005789243	-2637	'26.2'	grmzm2g155911_t01	'misc.UDP glucosyl and glucoronyl transferases'
741	Mala	7	146746400	84.65040768	13	-0.007872159	-37064	'14.2'	ac189750.4_fgt004	'S-assimilation.APR'
742	Mala	7	163624094	115.764038	48	0.012940535	-17529	'29.4'	grmzm2g013652_t01	'protein.postranslational modification'

743	Mala	7	166492884	123.1295455	11	0.009047583	-2523	'27.3.3'	grmzm2g307119_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
744	Mala	7	166493179	123.1308276	67	0.011080937	-2818	'27.3.3'	grmzm2g307119_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
745	Mala	7	167073361	125.6523612	6	0.009385491	-1066	'26.12'	grmzm2g126261_t01	'misc.peroxidases'
746	Mala	7	167122054	125.8639863	17	0.012150093	-13256	'29.4'	grmzm2g177050_t01	'protein.postranslational modification'
747	Mala	8	100197210	57.57868238	6	0.00790012	-153647	'11.1.5'	grmzm2g055667_t01	'lipid metabolism.FA synthesis and FA elongation.beta hydroxyacyl ACP dehydratase'
748	Mala	8	108849390	60.58220759	51	0.005689455	-37848	'30.5'	grmzm2g150724_t01	'signalling.G-proteins'
749	Mala	8	120917873	65.51878959	5	0.008136638	-43495	'27.3.17'	grmzm2g173198_t01	'RNA.regulation of transcription.CPP(Zn),CPP1-related transcription factor family'
750	Mala	8	154959713	81.88784605	10	0.012371157	-2361	'26.7'	grmzm2g017193_t01	'misc.oxidases - copper, flavone etc.'

751	Mala	8	159784012	88.41830479	12	0.012070302	-4318	'29.2.1.1.1.2.27'	grmzm2g145496_t01	'protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L27'
752	Mala	9	91767617	47.59229769	5	0.009468398	-117378	'27.3.71'	grmzm2g117935_t01	'RNA.regulation of transcription.SNF7'
753	Mala	9	109432591	53.84671075	14	0.010241133	-121520	'3.5'	grmzm2g144245_t01	'minor CHO metabolism.others'
754	Mala	10	1210362	-2.349387514	15	-0.017276952	-8498	'29.4'	grmzm2g430780_t01	'protein.postranslational modification'
755	Mala	10	1431221	-1.586267435	6	0.011410568	-22381	'29.5.1'	grmzm2g012062_t01	'protein.degradation.subtilases'
756	Mala	10	1467050	-1.462469767	16	0.006758966	-22947	'30.3'	grmzm2g104730_t01	'signalling.calcium'
757	Mala	10	2275477	1.330836713	6	0.006068756	-6178	'23.2'	grmzm2g431714_t01	'nucleotide metabolism.degradation'
758	Mala	10	2592048	2.424664387	5	0.008847718	-18	'17.3.1.2.3'	grmzm2g068465_t02	'hormone metabolism.brassinosteroid.synthesis-degradation.sterols.CYP51'
759	Mala	10	4201480	8.961984916	5	0.006361453	-8213	'29.5'	grmzm2g003750_t01	'protein.degradation'

760	Mala	10	145447601	86.78325234	17	0.007756603	-93217	'13.1.5.1.1'	grmzm2g009323_t01	'amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase'
761	Mala	10	145456506	86.81879521	5	0.008987877	-282	'18.3.2'	grmzm2g143480_t02	'Co-factor and vitamine metabolism.riboflavin.riboflavin synthase'
762	Mala	10	145674099	87.6872826	67	0.007733533	-3191	'30.11'	grmzm2g104268_t01	'signalling.light'
763	Mala	10	145733506	87.92439606	8	0.009243772	-5331	'30.2.17'	grmzm2g007477_t01	'signalling.receptor kinases.DUF 26'
764	Nitr	1	5563538	9.70193737	75	0.003559647	-47902	'29.4'	grmzm2g055575_t01	'protein.postranslational modification'
765	Nitr	1	51114082	65.50613364	11	0.003292823	-301239	'33.99'	ac208571.4_fgt001	'development.unspecified'
766	Nitr	1	60210415	71.99893136	5	0.002949116	-43502	'29.5.11.4.3.2'	grmzm2g378907_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
767	Nitr	1	63667791	73.22732147	7	0.00318244	-229	'26.12'	grmzm2g040638_t01	'misc.peroxidases'

768	Nitr	1	199491006	112.8925649	7	-0.000697051	-5829	'2.2.2.1'	grmzm2g070172_t01	'major CHO metabolism.degradation.starch.starch cleavage'
769	Nitr	1	201845500	115.3791094	11	-0.000756257	-56519	'27.3.3'	grmzm2g028386_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
770	Nitr	1	201991158	115.4795854	6	-0.003767123	-176	'30.2.3'	grmzm2g422373_t01	'signalling.receptor kinases.leucine rich repeat III'
771	Nitr	1	202621762	115.91	5	-0.0043	-81958	'27.3.27'	grmzm2g340305_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
772	Nitr	1	207277145	119.465065	11	-0.000793889	-153292	'17.4.1'	grmzm2g348452_t01	'hormone metabolism.cytokinin.synthesis-degradation'
773	Nitr	1	207279145	119.4669916	8	-0.000840239	-1952	'20.2.99'	grmzm2g363004_t01	'stress.abiotic.unspecified'
774	Nitr	1	207313090	119.4996915	12	-0.000961106	-10069	'20.2.99'	ac195794.3_fgt002	'stress.abiotic.unspecified'

775	Nitr	1	224410655	132.7669157	12	-0.0094014	-103813	'28.1'	grmzm2g168744_t01	'DNA.synthesis/chromatin structure'
776	Nitr	1	232515055	138.1818938	6	0.011437559	-163695	'30.3'	grmzm2g117763_t01	'signalling.calcium'
777	Nitr	1	233097149	138.4111567	9	0.012678888	-168640	'29.5.11.4.2'	grmzm2g343972_t01	'protein.degradation.ubiquitin.E3.RING'
778	Nitr	1	249984566	148.2769963	25	0.000988754	-19857	'27.3.25'	grmzm2g121570_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
779	Nitr	1	254217830	150.9046175	9	0.040341299	-26746	'29.4'	grmzm2g081915_t01	'protein.postranslational modification'
780	Nitr	1	254218603	150.9052401	13	0.038373926	-27519	'29.4'	grmzm2g081915_t01	'protein.postranslational modification'
781	Nitr	1	256241409	152.3975751	16	1.893176617	-142311	'29.4'	grmzm2g357081_t01	'protein.postranslational modification'
782	Nitr	1	256250277	152.4041229	6	-3.973615173	-2800	'27.3.50'	grmzm2g018414_t01	'RNA.regulation of transcription.General Transcription'

783	Nitr	1	256300512	152.4470842	7	-0.373608989	-53035	'27.3.50'	grmzm2g018414_t01	'RNA.regulation of transcription.General Transcription'
784	Nitr	1	257414838	153.4001486	40	-0.007243298	-31055	'34.12'	grmzm2g118821_t01	'transport.metal'
785	Nitr	1	297905073	202.4622232	6	-0.001303846	-55516	'27.1'	grmzm2g422649_t01	'RNA.processing'
786	Nitr	2	3805	-5.496235757	26	0.001182912				
787	Nitr	2	2023274	3.619749446	24	0.001176073	-16113	'1.1.1.1'	grmzm2g039996_t01	'PS.lightreaction.photosystem II.LHC-II'
788	Nitr	2	2211917	4.471293489	10	0.001669864	-141890	'27.3.5'	grmzm2g040736_t01	'RNA.regulation of transcription.ARR'
789	Nitr	2	2491029	5.715556905	6	0.000821883	-5964	'11.3.3'	grmzm2g104538_t01	'lipid metabolism.Phospholipid synthesis.phosphatidate cytidylyltransferase'
790	Nitr	2	9387311	27.56530943	6	0.001306219	-39933	'30.2.17'	grmzm2g165060_t01	'signalling.receptor kinases.DUF 26'
791	Nitr	2	31005737	62.07871475	22	0.001211646	-28612	'29.5.4'	grmzm2g333408_t01	'protein.degradation.aspartate protease'

792	Nitr	2	36815670	65.26831102	10	0.001463549	-9696	'6.2'	grmzm2g102183_t01	'gluconeogenese/ glyoxylate cycle.malate synthase'
793	Nitr	2	37323751	65.60272826	11	0.002275836	-12829	'29.5.11.1'	grmzm2g045117_t01	'protein.degradation.ubiquitin.ubiquitin'
794	Nitr	2	181079834	90.99646529	39	0.001816495	-428	'1.1.2.1'	grmzm2g117412_t01	'PS.lightreaction.photosystem I.LHC-I'
795	Nitr	2	182483954	92.38830408	38	0.001818773	-87084	'29.5'	grmzm2g065665_t01	'protein.degradation'
796	Nitr	2	183983052	94.29078232	8	0.002369111	-41357	'33.1'	grmzm2g123764_t01	'development.storage proteins'
797	Nitr	2	186765944	97.99865221	7	0.001224906	-41498	'20.2.1'	grmzm2g474367_t01	'stress.abiotic.heat'
798	Nitr	2	203303901	111.3475511	5	0.002210804	-101264	'16.8.2'	grmzm2g060011_t01	'secondary metabolism.flavonoids.chalcones'
799	Nitr	2	211231604	122.5790956	20	0.002091497	-41931	'20.1'	grmzm2g379770_t01	'stress.biotic'
800	Nitr	2	212538395	124.4779034	10	0.002047508	-28619	'29.4'	grmzm2g131554_t01	'protein.postranslational modification'
801	Nitr	3	8109850	29.6995263	14	0.003636405	-26893	'31.2'	grmzm2g576002_t01	'cell.division'
802	Nitr	3	8678939	31.22826072	19	0.003500894	-7	'20.1'	grmzm2g083797_t01	'stress.biotic'

803	Nitr	3	8924944	31.88908441	11	0.003569052	-10040	'28.1'	grmzm2g355381_t01	'DNA.synthesis/chromatin structure'
804	Nitr	3	158547954	71.48562889	28	0.000938613	-66241	'31.4'	grmzm2g436742_t01	'cell.vesicle transport'
805	Nitr	3	210217529	120.7696561	15	-0.000777862	-48203	'29.2.1.1.1.2.12'	grmzm2g360021_t01	'protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L12'
806	Nitr	3	212234516	123.2864138	11	-0.00092326	-174659	'13.1.4.1'	grmzm2g004382_t01	'amino acid metabolism.synthesis.branched chain group.common'
807	Nitr	3	212247177	123.3022119	10	-0.000811602	-635	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
808	Nitr	3	212248108	123.3033736	27	-0.000852191	-1566	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
809	Nitr	3	212248700	123.3041123	15	-0.000804228	-2158	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
810	Nitr	3	213848077	126.6554907	7	-0.000894249	-44219	'26.2'	grmzm2g048010_t01	'misc.UDP glucosyl and glucoronyl transferases'
811	Nitr	4	11351925	31.69382335	5	-0.003583568	-144988	'27.3.80'	grmzm2g068330_t01	'RNA.regulation of transcription.zf-HD'
812	Nitr	4	11970641	33.81499619	6	-0.003758507	-113036	'16.2'	grmzm2g017557_t01	'secondary metabolism.phenylpropanoids'

813	Nitr	4	25849988	48.23626239	5	0.001059419	-186185	'29.3.4.99'	grmzm2g147726_t02	'protein.targeting.secretory pathway.unspecified'
814	Nitr	4	25850469	48.23645002	7	0.001284805	-186666	'29.3.4.99'	grmzm2g147726_t02	'protein.targeting.secretory pathway.unspecified'
815	Nitr	4	28177658	49.14422457	25	0.002716247	-6686	'31.2'	grmzm2g125151_t01	'cell.division'
816	Nitr	4	28839372	49.4032225	7	0.005200168	-135	'27.3.22'	grmzm2g130442_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
817	Nitr	4	101964449	57.85755427	9	0.003029113	-148863	'27.3.73'	ac207890.3_fgt002	'RNA.regulation of transcription.Zn-finger(CCHC)'
818	Nitr	4	110010755	58.02556787	12	0.001209715	-679305	'27.3.35'	grmzm2g118870_t02	'RNA.regulation of transcription.bZIP transcription factor family'
819	Nitr	4	130200550	58.67643598	10	0.001469707	-3265	'31.4'	grmzm2g390691_t01	'cell.vesicle transport'
820	Nitr	4	149531302	61.9954463	8	0.004684307	-506860	'27.3.30'	grmzm2g063203_t01	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
821	Nitr	4	163054280	73.24125003	10	-0.002480041	-66034	'27.3.67'	grmzm2g411032_t01	'RNA.regulation of transcription.putative transcription regulator'

822	Nitr	4	163084391	73.26227648	17	-0.002987557	-29558	'27.3.99'	grmzm2g141036_t01	'RNA.regulation of transcription.unclassified'
823	Nitr	4	165718843	75.10190893	25	-0.003343143	-145301	'27.3.99'	grmzm2g444623_t02	'RNA.regulation of transcription.unclassified'
824	Nitr	4	166175217	75.86	5	-0.0009	-9468	'17.2.3'	grmzm2g015049_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
825	Nitr	4	167831848	76.66597097	7	-0.002511466	-500	'11.9.3.4'	grmzm2g045294_t01	'lipid metabolism.lipid degradation.lysophospholipases.phospholipase A2'
826	Nitr	4	170457980	78.38642641	8	-0.002662805	-151878	'15.2'	grmzm2g120964_t01	'metal handling.binding, chelation and storage'
827	Nitr	4	177460609	88.85205365	6	-0.000971011	-449	'27.3.3'	grmzm2g011110_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
828	Nitr	4	179532567	92.44677404	28	-0.002935932	-8453	'26.2'	grmzm2g383920_t01	'misc.UDP glucosyl and glucoronyl transferases'
829	Nitr	4	242018406	128.094256	5	-0.026531277	-17517	'13.2.5.3'	grmzm2g168888_t01	'amino acid metabolism.degradation.serine-glycine-cysteine group.cysteine'
830	Nitr	4	242343398	129.4163957	6	0.793685036	-3229	'26.19'	grmzm2g101872_t01	'misc.plastocyanin-like'

831	Nitr	5	4862213	16.72130612	9	0.003196165	-93667	'29.5.11.4.3.3'	ac155496.2_fgt009	'protein.degradation.ubiquitin.E3.SCF.cullin'
832	Nitr	5	4925927	17.04607872	10	0.002167269	-21244	'27.3.29'	grmzm2g089361_t01	'RNA.regulation of transcription.TCP transcription factor family'
833	Nitr	5	7664787	29.12019513	5	0.001140887	-95582	'29.4'	grmzm2g014618_t01	'protein.postranslational modification'
834	Nitr	5	162808563	76.42708275	6	0.003808286	-120194	'29.5.11.4.3.2'	grmzm2g011627_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
835	Nitr	5	184229490	93.51868254	5	0.001723644	-306984	'27.2'	grmzm2g043461_t02	'RNA.transcription'
836	Nitr	5	184794208	94.16914109	6	0.001178069	-47176	'29.5.11.4.2'	grmzm2g094602_t01	'protein.degradation.ubiquitin.E3.RING'
837	Nitr	5	185030768	94.44161776	7	0.001440241	-81869	'29.5.11.4.2'	grmzm2g362883_t01	'protein.degradation.ubiquitin.E3.RING'
838	Nitr	5	185056309	94.47103662	10	0.001491703	-107410	'29.5.11.4.2'	grmzm2g362883_t01	'protein.degradation.ubiquitin.E3.RING'
839	Nitr	5	185687667	95.19825306	8	0.001158127	-90894	'27.3.25'	grmzm2g095904_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
840	Nitr	5	185860200	95.39698157	5	0.000263629	-160417	'23.3.2.1'	grmzm2g540538_t01	'nucleotide metabolism.salvage.nucleoside kinases.adenosine kinase'

841	Nitr	5	190089272	99.5622766	29	-0.023979728	-21	'31.3'	grmzm2g160563_t02	'cell.cycle'
842	Nitr	5	190169366	99.64088567	25	-0.032819686	-78164	'31.3'	grmzm2g160563_t01	'cell.cycle'
843	Nitr	5	190751918	100.0087423	59	0.060946443	-44375	'27.3.3'	grmzm2g466044_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
844	Nitr	5	191728507	101.2378277	61	-0.033148662	-128	'11.9.4.5'	grmzm2g004752_t01	'lipid metabolism.lipid degradation.beta-oxidation.acyl-CoA thioesterase'
845	Nitr	5	205478714	119.252956	9	-0.001744117	-4714	'29.5.11.4.2'	grmzm2g053303_t01	'protein.degradation.ubiquitin.E3.RING'
846	Nitr	5	205662825	119.8501543	20	-0.001468083	-12994	'17.2.2'	grmzm2g074267_t01	'hormone metabolism.auxin.signal transduction'
847	Nitr	5	205964077	120.8273212	11	-0.000771887	-23060	'23.2'	grmzm2g114362_t01	'nucleotide metabolism.degradation'
848	Nitr	5	207101210	124.0824263	25	-0.003509329	-6661	'27.3.3'	grmzm2g055204_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
849	Nitr	5	207118376	124.1210629	12	-0.000821003	-9719	'26.2'	grmzm2g055124_t01	'misc.UDP glucosyl and glucoronyl transferases'

850	Nitr	5	207498927	124.9743369	13	-0.003573299	-106864	'31.1'	grmzm2g061950_t01	'cell.organisation'
851	Nitr	5	211861691	137.9485929	9	-0.00209302	-5262	'20.1'	grmzm2g008406_t01	'stress.biotic'
852	Nitr	6	78467563	11.02628868	8	0.00613447	-71172	'27.3.3'	grmzm2g119865_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
853	Nitr	6	92041721	18.74190429	8	-0.007360541	-52362	'27.3.26'	grmzm2g057408_t01	'RNA.regulation of transcription.MYB-related transcription factor family'
854	Nitr	6	164046344	96.23353408	8	0.00311268	-72666	'18'	grmzm2g085483_t01	'Co-factor and vitamine metabolism'
855	Nitr	7	94080369	50.29845615	7	-0.002187415	-149429	'15.2'	grmzm2g086066_t01	'metal handling.binding, chelation and storage'
856	Nitr	7	97073633	50.59965001	5	-0.003762497	-114832	'29.5.11.4.2'	grmzm2g030341_t01	'protein.degradation.ubiquitin.E3.RING'
857	Nitr	7	121206635	61.30136801	7	0.003846053	-43231	'11.9.4.5'	grmzm2g133836_t01	'lipid metabolism.lipid degradation.beta-oxidation.acyl-CoA thioesterase'
858	Nitr	7	145280969	83.18936747	6	0.000758506	-2769	'20.1'	grmzm2g163045_t01	'stress.biotic'

859	Nitr	7	152493835	91.25002624	19	0.000787893	-209	'29.4'	grmzm2g107565_t02	'protein.postranslational modification'
860	Nitr	8	20733895	45.60822058	7	0.002081662	-935	'29.4'	grmzm2g080588_t01	'protein.postranslational modification'
861	Nitr	8	139383376	71.29644034	13	-0.004157906	-7739	'16.2'	grmzm2g407949_t01	'secondary metabolism.phenylpropanoids'
862	Nitr	8	147013249	76.63825194	16	0.004700156	-46421	'20.2.2'	grmzm2g114538_t01	'stress.abiotic.cold'
863	Nitr	8	150840981	79.70937466	9	0.002809057	-11088	'20.1'	grmzm2g091973_t01	'stress.biotic'
864	Nitr	8	160985585	90.37557478	10	-0.000844257	-38122	'27.4'	grmzm2g042118_t01	'RNA.RNA binding'
865	Nitr	9	23279446	40.13731735	8	-0.000527851	-31291	'15'	grmzm2g171376_t01	'metal handling'
866	Nitr	9	23407123	40.42055726	5	-0.000732831	-158968	'15'	grmzm2g171376_t01	'metal handling'
867	Nitr	9	25029010	42.41502107	13	-0.000589684	-9537	'20.1'	grmzm2g030051_t01	'stress.biotic'

868	Nitr	9	121495902	60.17794088	5	-0.000866371	-145789	'20.1'	grmzm2g174286_t01	'stress.biotic'
869	Nitr	9	151011382	109.2060086	64	0.003263514	-11190	'27.3.44'	grmzm2g049168_t01	'RNA.regulation of transcription.Chromatin Remodeling Factors'
870	Nitr	10	146509918	91.0233194	8	0.000766245	-55566	'25.7'	grmzm2g106376_t01	'C1-metabolism.GTP cyclohydrolase I'
871	Nitr	10	146628442	91.61626493	10	0.000710638	-28101	'27.3.22'	grmzm2g028622_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
872	Nitr	10	146744873	92.26893726	17	0.000679393	-4101	'31.1'	grmzm2g423861_t01	'cell.organisation'
873	Nitr	10	147132717	94.44305795	6	0.000722548	-11231	'23.4.1'	grmzm2g150014_t01	'nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate kinase'
874	Nitr	10	147981037	99.19844948	12	0.000848392	-170	'27.3.8'	grmzm2g142718_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
875	Nitr	10	148513914	102.1855755	14	0.000913186	-5570	'33.99'	ac214046.4_fgt005	'development.unspecified'

876	Prot	1	64910659	74.0301357	9	-0.006095916	-10535	'8.1.7'	grmzm2g306945_t01	'TCA / org. transformation.TCA.succinate dehydrogenase'
877	Prot	1	64910976	74.03036785	33	-0.006371905	-10852	'8.1.7'	grmzm2g306945_t01	'TCA / org. transformation.TCA.succinate dehydrogenase'
878	Prot	1	69196228	76.41372859	13	-0.006630505	-191670	'11.8.4'	grmzm2g149224_t01	'lipid metabolism."exotics" (steroids, squalene etc).3-beta hydroxysteroid dehydrogenase/isomerase'
879	Prot	1	69271066	76.45177556	5	-0.007173736	-266508	'11.8.4'	grmzm2g149224_t01	'lipid metabolism."exotics" (steroids, squalene etc).3-beta hydroxysteroid dehydrogenase/isomerase'
880	Prot	1	74985643	79.35701503	8	-0.015969066	-1889	'33.99'	grmzm2g138710_t01	'development.unspecified'
881	Prot	1	252882663	149.8292876	8	0.008583908	-4271	'28.1'	grmzm2g043191_t01	'DNA.synthesis/chromatin structure'
882	Prot	2	20043374	50.80064207	26	-0.006974803	-357	'27.3.25'	grmzm2g105137_t01	'RNA.regulation of transcription.MYB domain transcription factor family'

883	Prot	2	185457136	96.16151574	6	0.006649714	-2959	'27.3.35'	grmzm2g137532_t01	'RNA.regulation of transcription.bZIP transcription factor family'
884	Prot	3	1187527	-0.271888706	19	0.008814859	-262839	'27.3.99'	grmzm2g461783_t01	'RNA.regulation of transcription.unclassified'
885	Prot	3	127883944	61.0242801	19	-0.009978835	-277970	'34.9'	grmzm2g447657_t01	'transport.metabolite transporters at the mitochondrial membrane'
886	Prot	3	127884222	61.02430232	7	-0.008779638	-278248	'34.9'	grmzm2g447657_t01	'transport.metabolite transporters at the mitochondrial membrane'
887	Prot	3	131786653	61.68464041	6	-0.014158624	-52957	'29.2.3'	grmzm2g084647_t01	'protein.synthesis.initiation'
888	Prot	3	179931178	91.94664886	37	-0.006464741	-2144	'34.12'	grmzm2g014454_t01	'transport.metal'
889	Prot	3	186207858	97.81793168	13	-0.009426898	-28487	'29.5.11.4.2'	ac213654.3_fgt001	'protein.degradation.ubiquitin.E3.RING'
890	Prot	3	186596173	98.06048224	5	-0.00757709	-4373	'29.5'	grmzm2g047274_t01	'protein.degradation'
891	Prot	3	188565185	99.29037279	6	-0.006679739	-212935	'27.3.11'	grmzm2g105224_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
892	Prot	3	203411410	111.3198505	6	-0.006026391	-49791	'16.1.2.9'	grmzm2g098569_t01	'secondary metabolism.isoprenoids.mevalonate pathway.farnesyl pyrophosphate synthetase'

893	Prot	3	212222986	123.2720269	21	-0.006839459	-163129	'13.1.4.1'	grmzm2g004382_t01	'amino acid metabolism.synthesis.branched chain group.common'
894	Prot	3	212224642	123.2740932	16	-0.007350952	-164785	'13.1.4.1'	grmzm2g004382_t01	'amino acid metabolism.synthesis.branched chain group.common'
895	Prot	3	213226535	125.1288155	17	-0.008878007	-35293	'27.3.12'	grmzm2g157927_t01	'RNA.regulation of transcription.C3H zinc finger family'
896	Prot	3	213800913	126.5396432	5	-0.007297196	-156736	'29.4'	grmzm2g088299_t01	'protein.postranslational modification'
897	Prot	3	213854238	126.6706238	9	-0.007474129	-50380	'26.2'	grmzm2g048010_t01	'misc.UDP glucosyl and glucoronyl transferases'
898	Prot	3	217611213	133.5696863	6	-0.008173794	-136	'27.3.6'	grmzm2g081816_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
899	Prot	4	168096468	76.74550042	5	-0.013008569	-14831	'29.2.3'	grmzm2g018947_t01	'protein.synthesis.initiation'
900	Prot	4	227245511	112.6233194	44	0.009730652	-112863	'29.4'	grmzm2g147026_t01	'protein.postranslational modification'

901	Prot	4	230742777	113.8187579	6	0.008891322	-48645	'29.4'	grmzm2g073788_t01	'protein.postranslational modification'
902	Prot	5	88557383	69.4927261	74	-0.007848454	-116887	'16.2.1.3'	grmzm2g075333_t01	'secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL'
903	Prot	5	91037740	69.69522773	20	-0.006780225	-139582	'27.4'	grmzm2g174785_t01	'RNA.RNA binding'
904	Prot	5	186016180	95.57664385	5	-0.00735679	-2254	'34'	grmzm2g068714_t01	'transport'
905	Prot	5	187955512	97.81042264	8	-0.005429395	-411	'21.1'	grmzm2g139803_t01	'redox.thioredoxin'
906	Prot	5	189228254	98.86708725	21	-0.007553606	-23431	'33.99'	grmzm2g409358_t01	'development.unspecified'
907	Prot	5	203170982	112.0815943	20	-0.006893258	-17977	'28.99'	grmzm2g018126_t01	'DNA.unspecified'

908	Prot	5	205646722	119.7979212	18	-0.005971484	-92306	'29.4'	grmzm2g127632_t01	'protein.postranslational modification'
909	Prot	5	206043601	121.085272	6	-0.006353574	-56780	'29.5.11.4.3.3'	grmzm2g380184_t01	'protein.degradation.ubiquitin.E3.SCF.cullin'
910	Prot	5	208092874	126.5365424	6	-0.005967461	-5948	'26.19'	grmzm2g045927_t01	'misc.plastocyanin-like'
911	Prot	6	22422464	7.104655221	26	-0.006334214	-86390	'4.1.16'	grmzm2g395569_t01	'glycolysis.cytosolic branch.phospho-enol-pyruvate carboxylase kinase (PPCK)'
912	Prot	6	35896471	8.2773635	5	-0.005965884	-23383	'29.4'	grmzm2g456423_t01	'protein.postranslational modification'
913	Prot	6	72931425	10.26780431	14	-0.004869067	-71749	'16.2'	grmzm2g362298_t01	'secondary metabolism.phenylpropanoids'
914	Prot	6	72985636	10.2733065	9	-0.004940372	-125960	'16.2'	grmzm2g362298_t01	'secondary metabolism.phenylpropanoids'
915	Prot	6	73021951	10.27699232	13	-0.0080408	-36020	'27.1.19'	grmzm2g047265_t01	'RNA.processing.ribonucleases'
916	Prot	6	168683648	108.6048676	13	0.011314553	-19134	'27.3.55'	grmzm2g367886_t01	'RNA.regulation of transcription.HDA'
917	Prot	6	168748906	108.622076	35	0.007222797	-65074	'34.9'	grmzm2g067877_t01	'transport.metabolite transporters at the mitochondrial membrane'

918	Prot	7	5099065	21.78417429	9	-0.008417978	-17896	'31.1'	grmzm2g093766_t01	'cell.organisation'
919	Prot	7	33595519	47.99555999	10	0.00514782	-13476	'20.1'	grmzm2g160265_t01	'stress.biotic'
920	Prot	7	154247787	94.54909037	7	0.005825457	-2282	'30.7'	grmzm2g305211_t01	'signalling.14-3-3 proteins'
921	Prot	7	157249277	100.7051801	14	0.006706373	-45332	'29.5.3'	grmzm2g049882_t01	'protein.degradation.cysteine protease'
922	Prot	7	158036207	102.3366246	5	0.005791282	-1527	'26.4'	grmzm2g131262_t02	'misc.beta 1,3 glucan hydrolases'
923	Prot	7	159778542	106.10253	6	0.012461708	-77328	'29.2.4'	grmzm2g031545_t01	'protein.synthesis.elongation'
924	Prot	7	168378312	131.3238192	8	-0.007477326	-39666	'27.1'	grmzm2g470461_t01	'RNA.processing'
925	Prot	8	21881574	47.44607971	10	0.011659826	-15911	'27.3.62'	grmzm2g032252_t01	'RNA.regulation of transcription.Nucleosome/chromatin assembly factor group'
926	Prot	8	108880988	60.59133569	5	0.008562491	-31108	'30.5'	grmzm2g072089_t01	'signalling.G-proteins'

927	Prot	8	115683038	62.57820324	5	0.008392785	-196269	'29.4'	grmzm2g035202_t01	'protein.postranslational modification'
928	Prot	8	117977083	63.86243699	51	0.01116072	-99957	'34.12'	grmzm2g138817_t01	'transport.metal'
929	Prot	8	129392376	68.26348656	8	0.009582417	-7407	'29.3.3'	grmzm2g034043_t01	'protein.targeting.chloroplast'
930	Prot	8	131868393	69.1089486	5	-0.007281874	-2333	'21.2.1'	grmzm2g005710_t01	'redox.ascorbate and glutathione.ascorbate'
931	Prot	8	161242940	90.87698678	53	-0.005415146	-200	'31.3.1'	grmzm2g031204_t01	'cell.cycle.peptidylprolyl isomerase'
932	Prot	8	170967906	124.4926125	15	-0.010060425	-20762	'29.5.7'	grmzm2g133249_t01	'protein.degradation.metalloprotease'
933	Prot	9	73386482	45.90639706	5	-0.006073526	-134278	'30.5'	grmzm2g018619_t01	'signalling.G-proteins'
934	Prot	9	75752943	46.01866137	10	-0.00678119	-187366	'27.3.6'	grmzm2g340177_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'

935	Prot	9	86122013	46.66594904	22	-0.007718805	-47007	'19.21'	grmzm2g157936_t01	'tetrapyrrole synthesis.heme oxygenase'
936	Prot	9	98709960	49.58225494	8	-0.00680033	-342523	'34.99'	grmzm2g143377_t01	'transport.misc'
937	Prot	9	112772173	55.72841749	8	-0.006998869	-71289	'10.7'	grmzm2g013671_t01	'cell wall.modification'
938	Prot	9	113322955	55.98017627	24	-0.006456001	-76302	'31.2'	ac191253.3_fgt004	'cell.division'
939	Prot	9	113731726	56.16702277	6	-0.00865215	-436	'13.2.2.2'	grmzm2g117956_t01	'amino acid metabolism.degradation.glutamate family.proline'
940	Prot	9	120621679	59.56922799	5	-0.00678539	-42612	'17.7.1.4'	grmzm2g415793_t01	'hormone metabolism.jasmonate.synthesis-degradation.allene oxidase cyclase'
941	Prot	9	122100192	60.59870208	5	-0.007751436	-108399	'29.4'	grmzm2g108309_t01	'protein.postranslational modification'
942	Prot	9	143538206	90.82527553	10	-0.007521104	-74129	'34.2'	grmzm2g137985_t01	'transport.sugars'
943	Prot	9	144829091	93.82411792	25	-0.004785192	-22827	'26.21'	grmzm2g004466_t01	'misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein'

944	Prot	10	10440954	28.50645685	9	-0.008130968	-59914	'29.4.1.56'	grmzm2g418432_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VI'
945	Prot	10	16919807	33.52470383	16	0.007567347	-208844	'20.2.1'	grmzm2g130127_t01	'stress.abiotic.heat'
946	Prot	10	147427851	96.09747813	13	0.004748578	-1150	'9.99'	grmzm2g092365_t03	'mitochondrial electron transport / ATP synthesis.unspecified'
947	Prot	10	148213790	100.5031831	11	0.006813955	-1597	'34.15'	grmzm2g039797_t01	'transport.potassium'
948	Prot	10	148344527	101.23605	45	0.008225195	-44946	'27.3.25'	grmzm2g478807_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
949	Prot	10	148496242	102.0865123	5	0.007112842	-6170	'29.4'	grmzm2g104658_t01	'protein.postranslational modification'
950	Star	1	7457814	13.94852432	86	-0.037258586	-4402	'27.3.27'	grmzm2g059428_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
951	Star	1	17278764	33.6621462	5	-0.041877285	-83731	'30.4'	grmzm2g097434_t01	'signalling.phosphinositides'
952	Star	1	21382731	37.73085137	29	-0.023301274	-196302	'10.1'	grmzm2g064841_t01	'cell wall.precursor synthesis'

953	Star	1	21383024	37.73112289	10	-0.022620507	-196595	'10.1'	grmzm2g064841_t01	'cell wall.precursor synthesis'
954	Star	1	42174991	59.32632563	11	0.051194392	-45014	'13.1.2.3.2'	grmzm2g044237_t01	'amino acid metabolism.synthesis.glutamate family.arginine.acetylglutamate kinase'
955	Star	1	45528222	61.4993069	7	0.044795124	-248164	'13.1.3.1'	grmzm2g053669_t01	'amino acid metabolism.synthesis.aspartate family.asparagine'
956	Star	1	46715564	62.60388883	8	0.035909602	-2482	'31.1'	grmzm2g104534_t01	'cell.organisation'
957	Star	1	51113147	65.50551539	54	0.052957455	-300304	'33.99'	ac208571.4_fgt001	'development.unspecified'
958	Star	1	51531509	66.02023986	6	0.089385584	-15801	'27.3.25'	grmzm2g070849_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
959	Star	1	92753447	85.57176721	62	0.024022074	-99005	'29.2.1.99.2.1185'	grmzm2g154487_t01	'protein.synthesis.ribosomal protein.unknown.large subunit.L18/L5'
960	Star	1	93661572	85.98563614	7	0.024453663	-282429	'27.3.9'	grmzm2g113098_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
961	Star	1	93667548	85.98835964	6	0.024126069	-288405	'27.3.9'	grmzm2g113098_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'

962	Star	1	251149118	148.8823369	5	-0.048533652	-18812	'30.2.25'	grmzm2g103610_t01	'signalling.receptor kinases.wall associated kinase'
963	Star	1	251176189	148.8964086	90	-0.057655015	-2474	'20.1'	grmzm2g081099_t01	'stress.biotic'
964	Star	1	292560966	192.501744	10	-0.071069046	-158	'29.4.1.57'	grmzm2g068117_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
965	Star	2	5548326	16.71276385	15	-0.027020805	-28052	'33.99'	grmzm2g174784_t01	'development.unspecified'
966	Star	2	5548414	16.71309841	83	-0.028470515	-28140	'33.99'	grmzm2g174784_t01	'development.unspecified'
967	Star	2	21795122	52.9770168	8	-0.021390127	-50745	'30.2.99'	grmzm2g168917_t01	'signalling.receptor kinases.misc'
968	Star	2	22808083	54.70986501	76	-0.029176947	-125949	'27.3.10'	grmzm2g054795_t01	'RNA.regulation of transcription.C2C2(Zn) YABBY family'
969	Star	2	27790884	58.80007957	13	-0.032182719	-36209	'31.1'	grmzm2g387389_t01	'cell.organisation'
970	Star	2	28788480	60.39948962	5	-0.024239309	-189580	'27.3.67'	grmzm2g052688_t01	'RNA.regulation of transcription.putative transcription regulator'

971	Star	2	28788620	60.39963767	12	-0.023889437	-189720	'27.3.67'	grmzm2g052688_t01	'RNA.regulation of transcription.putative transcription regulator'
972	Star	2	28960635	60.58154184	5	-0.030823242	-102237	'29.4'	grmzm2g032694_t01	'protein.postranslational modification'
973	Star	2	28970761	60.59224999	8	-0.031083803	-112363	'29.4'	grmzm2g032694_t01	'protein.postranslational modification'
974	Star	2	28972476	60.59406358	35	-0.02957084	-114078	'29.4'	grmzm2g032694_t01	'protein.postranslational modification'
975	Star	2	107216168	76.50296846	7	-0.030529227	-233414	'28.99'	grmzm2g053631_t01	'DNA.unspecified'
976	Star	2	194191603	105.3998294	6	-0.020841194	-199	'17.2.3'	grmzm2g156470_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
977	Star	2	201217096	109.0293094	10	-0.026005633	-56497	'30.2.17'	grmzm2g087625_t01	'signalling.receptor kinases.DUF 26'
978	Star	2	203650489	111.7689321	15	-0.025557901	-37827	'26.10'	grmzm2g031909_t01	'misc.cytochrome P450'
979	Star	2	205289573	113.7617273	5	-0.031413614	-87624	'9.1.2'	grmzm2g105207_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'

980	Star	2	205289574	113.7617285	9	-0.027499236	-87625	'9.1.2'	grmzm2g105207_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
981	Star	2	214729037	127.4005253	5	-0.017802912	-44435	'29.5.11.4.2'	grmzm2g402262_t01	'protein.degradation.ubiquitin.E3.RING'
982	Star	2	215881188	128.7144115	7	-0.017742045	-49386	'27.3.21'	grmzm2g425366_t01	'RNA.regulation of transcription.GRAS transcription factor family'
983	Star	2	217125385	130.3224898	5	-0.027701512	-7716	'10.8.1'	grmzm2g158240_t01	'cell wall.pectin*esterases.PME'
984	Star	2	217810072	131.5466232	5	-0.0237361	-18399	'7.1.2'	grmzm2g148769_t01	'OPP.oxidative PP.6-phosphogluconolactonase'
985	Star	3	3123500	9.745986067	7	0.038612596	-146144	'29.2.1.1.3.1.6'	grmzm2g026868_t01	'protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S6'
986	Star	3	3780999	13.14827662	22	0.028169623	-213	'26.10'	ac233853.1_fgt003	'misc.cytochrome P450'
987	Star	3	3836355	13.43472146	17	0.031403613	-40506	'34.15'	grmzm2g093313_t01	'transport.potassium'
988	Star	3	14416721	41.56032683	5	-0.028022937	-186199	'27.3.26'	grmzm2g163291_t01	'RNA.regulation of transcription.MYB-related transcription factor family'

989	Star	3	17306447	45.29685092	89	-0.032281971	-2219	'16.7'	grmzm2g541193_t01	'secondary metabolism.wax'
990	Star	3	51981075	56.79858368	90	0.084784527	-12830	'27.3.25'	grmzm2g158700_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
991	Star	3	170725018	81.65819468	5	-0.07741098	-658	'30.2.11'	grmzm2g167253_t01	'signalling.receptor kinases.leucine rich repeat XI'
992	Star	3	178840635	90.20644881	8	0.036888541	-27653	'27.3.99'	grmzm2g013463_t01	'RNA.regulation of transcription.unclassified'
993	Star	3	192649685	100.9866632	10	-0.050036116	-69958	'26.1'	grmzm2g089944_t01	'misc.misc2'
994	Star	3	192874331	101.0880183	8	-0.042136484	-15848	'26.19'	grmzm2g128531_t01	'misc.plastocyanin-like'
995	Star	3	192949443	101.1219071	9	-0.0571714	-90960	'26.19'	grmzm2g128531_t01	'misc.plastocyanin-like'
996	Star	3	193619852	101.4802146	6	-0.049654665	-251	'31.1'	grmzm2g016435_t01	'cell.organisation'
997	Star	3	193620690	101.4814585	27	-0.053595039	-1089	'31.1'	grmzm2g016435_t01	'cell.organisation'

998	Star	3	194144683	102.2592936	5	-0.038147905	-25644	'11.3.3'	grmzm2g452529_t01	'lipid metabolism.Phospholipid synthesis.phosphatidate cytidylyltransferase'
999	Star	4	24269222	47.52251807	66	0.054432733	-301899	'17.5.2'	ac213666.3_fgt003	'hormone metabolism.ethylene.signal transduction'
1000	Star	4	26928416	48.65692848	6	0.054001982	-51005	'29.5.11.4.3.2'	grmzm2g142043_t03	'protein.degradation.ubiquitin.E3.SCF.FBOX'
1001	Star	4	63204562	55.58951138	5	-0.024189406	-104473	'27.3.49'	grmzm2g423292_t01	'RNA.regulation of transcription.GeBP like'
1002	Star	4	116242442	58.15932573	10	-0.026678988	-19827	'29.5.11.4.3.2'	grmzm2g423663_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
1003	Star	4	194884222	103.0017383	8	-0.034945398	-20864	'29.5.11.4.2'	grmzm2g055643_t01	'protein.degradation.ubiquitin.E3.RING'
1004	Star	4	194952409	103.053073	8	-0.027789043	-184	'29.5.11.4.3.2'	grmzm2g302499_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
1005	Star	4	240714112	124.303751	25	-0.017633483	-201933	'28.2'	grmzm2g143462_t01	'DNA.repair'
1006	Star	4	245062382	140.1088204	5	-0.026856027	-3818	'30.6'	grmzm2g374088_t01	'signalling.MAP kinases'
1007	Star	4	245730715	144.0453722	15	-0.017329439	-54846	'20.2.1'	grmzm2g415007_t01	'stress.abiotic.heat'

1008	Star	4	245730944	144.0467211	11	-0.017442961	-55075	'20.2.1'	grmzm2g415007_t01	'stress.abiotic.heat'
1009	Star	4	245787531	144.3800244	15	-0.026106421	-48044	'21.6'	grmzm2g079348_t03	'redox.dismutases and catalases'
1010	Star	4	246077836	146.0899515	5	-0.021761826	-6829	'2.2.1.3.3'	grmzm2g463871_t01	'major CHO metabolism.degradation.sucrose.invertases.vacuolar'
1011	Star	5	1529458	1.89866854	11	-0.026956905	-34161	'29.2.1.2.1.4'	grmzm2g125271_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4'
1012	Star	5	1532216	1.906091195	16	-0.020171388	-36919	'29.2.1.2.1.4'	grmzm2g125271_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4'
1013	Star	5	1735588	2.453429899	6	-0.019083198	-4347	'11.9.2.1'	grmzm2g023049_t01	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
1014	Star	5	1879182	2.839887002	5	-0.025793792	-22687	'27.3.28'	grmzm2g138421_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
1015	Star	5	20941271	51.30637712	10	-0.050307121	-60679	'27.3.67'	grmzm2g024054_t01	'RNA.regulation of transcription.putative transcription regulator'
1016	Star	5	75996032	67.01800088	5	0.071648285	-864	'30.1.1'	grmzm2g042245_t01	'signalling.in sugar and nutrient physiology'

1017	Star	5	96165401	69.92179085	29	0.054394768	-131262	'29.4.1.57'	grmzm2g118939_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
1018	Star	5	145308951	72.52912618	15	-0.06568065	-187340	'29.4'	grmzm2g151916_t01	'protein.postranslational modification'
1019	Star	5	168868583	80.63961419	67	-0.073140188	-218438	'21.3'	grmzm2g074040_t01	'redox.heme'
1020	Star	5	171396511	83.30241817	34	0.023072258	-218132	'21.1'	grmzm2g007385_t01	'redox.thioredoxin'
1021	Star	5	174165684	85.75501381	25	0.029476756	-44515	'31.3'	ac212449.4_fgt004	'cell.cycle'
1022	Star	5	174821506	86.48707371	5	0.027732203	-2537	'26.2'	grmzm2g049798_t01	'misc.UDP glucosyl and glucoronyl transferases'
1023	Star	5	193444292	102.0960523	28	0.019728235	-49778	'27.3.99'	grmzm2g141503_t01	'RNA.regulation of transcription.unclassified'

1024	Star	5	195201674	103.5571638	6	0.019382462	-199033	'27.3.3'	grmzm2g137341_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1025	Star	5	203772980	114.279637	34	0.032389813	-45129	'20.1'	grmzm2g019317_t02	'stress.biotic'
1026	Star	5	204520039	116.1433154	8	0.021779461	-890	'17.4.2'	grmzm2g151223_t02	'hormone metabolism.cytokinin.signal transduction'
1027	Star	5	205480420	119.2584897	23	0.024091119	-6420	'29.5.11.4.2'	grmzm2g053303_t01	'protein.degradation.ubiquitin.E3.RING'
1028	Star	5	207749910	125.7434999	9	0.032228364	-137681	'29.2.1.1.1.2.29'	grmzm2g159554_t01	'protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L29'
1029	Star	6	25145461	7.801186431	11	-0.069037952	-21579	'23.4.99'	grmzm2g137930_t01	'nucleotide metabolism.phosphotransfer and pyrophosphatases.misc'
1030	Star	6	118288607	43.43874583	32	-0.072025188	-66879	'10.6.1'	grmzm2g455642_t01	'cell wall.degradation.cellulases and beta -1,4-glucanases'
1031	Star	6	119252741	43.97152587	16	-0.049737056	-47860	'31.1'	grmzm2g018823_t01	'cell.organisation'
1032	Star	6	156368499	74.39513977	7	0.053819036	-5054	'30.3'	grmzm2g305159_t01	'signalling.calcium'

1033	Star	6	166337059	105.4357129	22	-0.05306977	-2598	'27.3.26'	grmzm2g139174_t01	'RNA.regulation of transcription.MYB-related transcription factor family'
1034	Star	6	166977847	107.6073304	44	-0.037821131	-52799	'16.1.1.10'	grmzm2g163809_t01	'secondary metabolism.isoprenoids.non-mevalonate pathway.geranylgeranyl pyrophosphate synthase'
1035	Star	7	18458794	44.19878603	5	-0.027460741	-104907	'29.2.1.2.1.2'	grmzm2g168149_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S2'
1036	Star	7	20248668	44.70548997	38	-0.042578673	-9314	'27.3.69'	ac233961.1_fgt001	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
1037	Star	7	20380953	44.78804553	7	-0.06171405	-141599	'27.3.69'	ac233961.1_fgt001	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
1038	Star	7	21623347	45.56339066	5	-0.02739467	-85142	'34.3'	grmzm2g173967_t01	'transport.amino acids'
1039	Star	7	25948068	46.52566875	5	-0.043273669	-115635	'29.4'	grmzm2g050427_t01	'protein.postranslational modification'
1040	Star	7	29953895	47.26241735	12	-0.028721815	-84710	'26.24'	grmzm2g302778_t01	'misc.GCN5-related N-acetyltransferase'

1041	Star	7	126449302	67.30732758	10	-0.021768781	-21546	'13.1.7.2'	grmzm2g068862_t01	'amino acid metabolism.synthesis.histidine.bifunctional phosphoribosyl-ATP diphosphatase and phosphoribosyl-AMP cyclohydrolase'
1042	Star	7	151507555	89.39729712	9	-0.032132802	-33023	'34.3'	grmzm2g035893_t01	'transport.amino acids'
1043	Star	7	151913077	90.15766003	9	-0.079858825	-9221	'1.1.1.1'	grmzm2g057281_t01	'PS.lightreaction.photosystem II.LHC-II'
1044	Star	7	152316144	90.91580158	14	-0.058489035	-68253	'30.5'	grmzm2g335287_t01	'signalling.G-proteins'
1045	Star	7	167105793	125.7933142	15	0.059219318	-33498	'26.12'	grmzm2g126261_t01	'misc.peroxidases'
1046	Star	7	168184709	130.4823997	13	0.045148368	-577	'26.10'	grmzm2g425127_t01	'misc.cytochrome P450'
1047	Star	7	168193557	130.520854	5	0.036616985	-1267	'27.3.19'	grmzm2g151811_t01	'RNA.regulation of transcription.EIN3-like(EIL) transcription factor family'
1048	Star	8	121670463	65.96008974	11	0.045441796	-12451	'16.2'	ac209819.3_fgt005	'secondary metabolism.phenylpropanoids'

1049	Star	8	121963051	66.1316561	6	0.042894621	-189532	'29.5'	grmzm2g095955_t01	'protein.degradation'
1050	Star	8	144585092	74.43452065	10	-0.055256199	-55819	'19.30'	grmzm2g000739_t01	'tetrapyrrole synthesis.uroporphyrin-III C-methyltransferase'
1051	Star	8	144767036	74.6069579	5	-0.056636807	-2732	'9.6'	grmzm2g013712_t01	'mitochondrial electron transport / ATP synthesis.cytochrome c'
1052	Star	8	145553053	75.35190474	19	-0.047411963	-96772	'30.6'	grmzm2g375975_t01	'signalling.MAP kinases'
1053	Star	8	149499942	78.63341235	8	-0.058651712	-116	'29.5.4'	grmzm2g311680_t01	'protein.degradation.aspartate protease'
1054	Star	8	163958147	96.68361641	7	0.041224908	-14214	'10.3.2'	grmzm2g002023_t01	'cell wall.hemicellulose synthesis.glucuronoxylan'
1055	Star	8	164575505	99.62785513	54	0.021849064	-29769	'16.4.1'	grmzm2g338431_t01	'secondary metabolism.N misc.alkaloid-like'
1056	Star	8	164575577	99.62807455	6	0.025622402	-29841	'16.4.1'	grmzm2g338431_t01	'secondary metabolism.N misc.alkaloid-like'

1057	Star	8	170790378	123.8097673	5	0.018186972	-43298	'28.99'	grmzm2g004690_t01	'DNA.unspecified'
1058	Star	8	171107120	125.0290187	12	0.025903354	-103951	'30.2.17'	grmzm2g434363_t01	'signalling.receptor kinases.DUF 26'
1059	Star	8	171214220	125.4546422	15	0.023236917	-1566	'34.16'	grmzm2g111511_t01	'transport.ABC transporters and multidrug resistance systems'
1060	Star	8	171235640	125.5397669	5	0.03304263	-22986	'34.16'	grmzm2g111511_t01	'transport.ABC transporters and multidrug resistance systems'
1061	Star	9	6999006	8.219780095	15	-0.070552837	-205400	'20.2.1'	grmzm2g097620_t01	'stress.abiotic.heat'
1062	Star	9	7182819	8.716269429	27	-0.043529797	-40774	'31.1'	grmzm2g017257_t01	'cell.organisation'
1063	Star	9	7188622	8.731943661	42	-0.041058477	-46577	'31.1'	grmzm2g017257_t01	'cell.organisation'
1064	Star	9	8451164	12.14214118	5	-0.047028655	-126106	'26.2'	grmzm2g403740_t01	'misc.UDP glucosyl and glucoronyl transferases'

1065	Star	9	134402439	70.88375129	15	0.037960828	-23346	'34.21'	grmzm2g162426_t01	'transport.calcium'
1066	Star	9	134402663	70.88410046	6	0.036821304	-23570	'34.21'	grmzm2g162426_t01	'transport.calcium'
1067	Star	10	252732	-5.658225645	12	-0.051134421	-44477	'26.10'	grmzm2g179143_t01	'misc.cytochrome P450'
1068	Star	10	5058530	14.79019912	16	-0.06180889	-2015	'13'	grmzm2g066496_t01	'amino acid metabolism'
1069	Star	10	19566488	34.07832787	6	0.024937218	-40499	'13.2.6.3'	grmzm2g181227_t01	'amino acid metabolism.degradation.aromatic aa.tryptophan'
1070	Star	10	24052625	35.28519133	6	-0.043928314	-205553	'30.3'	grmzm2g176472_t01	'signalling.calcium'
1071	Star	10	25801766	35.75574637	8	0.085574049	-25049	'11.1.12'	grmzm2g149580_t01	'lipid metabolism.FA synthesis and FA elongation.ACP protein'
1072	Star	10	66920393	36.73131562	29	0.080127465	-192310	'30.2.17'	grmzm2g481531_t01	'signalling.receptor kinases.DUF 26'
1073	Star	10	89396968	41.46314855	33	0.05899755	-41782	'27.1.1'	grmzm2g039857_t01	'RNA.processing.splicing'
1074	Star	10	128172908	51.27327366	11	0.06244423	-28567	'34.99'	grmzm2g007481_t01	'transport.misc'

1075	Star	10	129906986	52.44415722	5	0.052854061	-56495	'29.5.11.4.2'	grmzm2g016487_t01	'protein.degradation.ubiquitin.E3.RING'
1076	Star	10	140767339	72.41844784	6	-0.032991889	-48678	'29.5.11.4.2'	grmzm2g140924_t01	'protein.degradation.ubiquitin.E3.RING'
1077	Star	10	141976268	75.93807797	6	-0.020261715	-86390	'19.3'	grmzm2g108125_t01	'tetrapyrrole synthesis.GSA'
1078	Star	10	141976795	75.94005902	15	-0.022617226	-86917	'19.3'	grmzm2g108125_t01	'tetrapyrrole synthesis.GSA'
1079	Star	10	144909314	84.63476656	5	-0.022505092	-757	'33.99'	grmzm2g076602_t01	'development.unspecified'
1080	Star	10	145742058	87.95852999	6	-0.025366805	-13883	'30.2.17'	grmzm2g007477_t01	'signalling.receptor kinases.DUF 26'
1081	Sucr	1	21442536	37.78627202	7	-0.039016626	-256107	'10.1'	grmzm2g064841_t01	'cell wall.precursor synthesis'
1082	Sucr	1	21449014	37.79227512	7	-0.03673907	-262585	'10.1'	grmzm2g064841_t01	'cell wall.precursor synthesis'

1083	Sucr	1	21560442	37.97512826	47	-0.038190551	-96448	'30.11'	grmzm2g004523_t01	'signalling.light'
1084	Sucr	1	21688795	38.19316881	12	-0.036506395	-18850	'17.5.2'	grmzm2g415251_t01	'hormone metabolism.ethylene.signal transduction'
1085	Sucr	1	21689538	38.19443099	17	-0.081014671	-19593	'17.5.2'	grmzm2g415251_t01	'hormone metabolism.ethylene.signal transduction'
1086	Sucr	1	56544677	69.98493609	7	0.091004411	-158735	'27.1'	grmzm2g063657_t01	'RNA.processing'
1087	Sucr	1	69598189	76.61808194	8	0.06063527	-169304	'20.1'	grmzm2g524711_t01	'stress.biotic'
1088	Sucr	1	274645019	167.2992575	6	0.087168737	-56161	'26.2'	grmzm2g074395_t01	'misc.UDP glucosyl and glucoronyl transferases'
1089	Sucr	2	2076282	3.859030239	6	-0.033975872	-6255	'27.3.5'	grmzm2g040736_t01	'RNA.regulation of transcription.ARR'
1090	Sucr	2	3086016	6.851945591	12	-0.032332673	-4139	'27.3.12'	grmzm2g071034_t01	'RNA.regulation of transcription.C3H zinc finger family'
1091	Sucr	2	16641157	44.04382336	15	-0.073754786	-3713	'34.99'	grmzm2g080992_t01	'transport.misc'
1092	Sucr	2	22494974	54.03923714	9	-0.048242813	-57435	'20.2.1'	grmzm2g070863_t01	'stress.abiotic.heat'

1093	Sucr	2	28592546	60.19229134	29	-0.039020967	-101820	'29.3.1'	grmzm2g002903_t01	'protein.targeting.nucleus'
1094	Sucr	2	28594174	60.19401294	7	-0.040826501	-103448	'29.3.1'	grmzm2g002903_t01	'protein.targeting.nucleus'
1095	Sucr	2	28973324	60.59496034	16	-0.039233491	-114926	'29.4'	grmzm2g032694_t01	'protein.postranslational modification'
1096	Sucr	3	13298136	40.11395447	19	-0.042921756	-68782	'21.1'	grmzm2g159145_t01	'redox.thioredoxin'
1097	Sucr	3	16863398	44.72397195	35	-0.053561956	-55597	'25'	ac215260.3_fgt004	'C1-metabolism'
1098	Sucr	3	16863598	44.72423056	21	-0.054013921	-55797	'25'	ac215260.3_fgt004	'C1-metabolism'
1099	Sucr	3	20147626	48.97060192	5	-0.037039448	-25541	'30.2.20'	grmzm2g013790_t01	'signalling.receptor kinases.wheat LRK10 like'
1100	Sucr	3	110202362	58.86475128	7	0.123753616	-19788	'20.1'	ac230011.2_fgt002	'stress.biotic'
1101	Sucr	3	174587864	84.65461078	5	0.067483949	-36815	'29.4'	grmzm2g074262_t01	'protein.postranslational modification'
1102	Sucr	3	221390629	140.2263942	10	-0.044839083	-74914	'29.5.11.4.3.2'	grmzm2g368767_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'

1103	Sucr	4	11976890	33.81581685	5	0.063333379	-119285	'16.2'	grmzm2g017557_t01	'secondary metabolism.phenylpropanoids'
1104	Sucr	4	12389613	33.87001839	25	0.073578644	-224118	'26.7'	grmzm2g110965_t01	'misc.oxidases - copper, flavone etc.'
1105	Sucr	4	17655938	40.84317673	14	0.091223346	-247787	'27.3.28'	grmzm2g106798_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
1106	Sucr	4	49286057	55.14879543	6	-0.093785941	-34613	'34.16'	grmzm2g031954_t01	'transport.ABC transporters and multidrug resistance systems'
1107	Sucr	4	60649130	55.4149908	15	-0.083392435	-37449	'16.1.5'	grmzm2g391312_t02	'secondary metabolism.isoprenoids.terpenoids'
1108	Sucr	4	110959949	58.04594151	5	-0.074747404	-260932	'29.5.11.4.2'	grmzm2g127690_t01	'protein.degradation.ubiquitin.E3.RING'
1109	Sucr	4	140704850	60.02921307	7	-0.041801329	-3582	'17.2.3'	grmzm2g118717_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
1110	Sucr	4	173809531	84.19454361	9	-0.032604677	-667232	'26.22'	grmzm2g316789_t01	'misc.short chain dehydrogenase/reductase (SDR)'
1111	Sucr	4	173813253	84.2005901	5	-0.034242183	-670954	'26.22'	grmzm2g316789_t01	'misc.short chain dehydrogenase/reductase (SDR)'

1112	Sucr	4	173813260	84.20060147	28	-0.039007994	-670961	'26.22'	grmzm2g316789_t01	'misc.short chain dehydrogenase/reductase (SDR)'
1113	Sucr	4	175615429	86.62964208	5	-0.045120538	-26961	'29.6'	grmzm2g091189_t01	'protein.folding'
1114	Sucr	5	7403398	28.1227481	5	0.028118305	-75359	'31.1'	grmzm2g460396_t01	'cell.organisation'
1115	Sucr	5	7568984	28.7329509	5	0.03044864	-49355	'31.4'	grmzm2g147046_t01	'cell.vesicle transport'
1116	Sucr	5	52480298	61.27077539	9	0.075988657	-162479	'26.28'	grmzm2g048904_t01	'misc.GDSL-motif lipase'
1117	Sucr	5	68604010	65.0820323	8	0.067664981	-21	'27.3.25'	grmzm2g088189_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1118	Sucr	5	68606903	65.08331839	14	0.085965605	-2914	'27.3.25'	grmzm2g088189_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1119	Sucr	5	73961139	66.43957914	7	-0.05697045	-34031	'13.1.6.5.2'	grmzm2g168791_t01	'amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate phosphoribosyltransferase'

1120	Sucr	5	76585969	67.18687192	15	-0.06624114	-57	'28.99'	grmzm2g319573_t01	'DNA.unspecified'
1121	Sucr	5	80096521	67.90868619	6	-0.061436645	-4132	'30.2.99'	grmzm2g093490_t01	'signalling.receptor kinases.misc'
1122	Sucr	5	173340061	84.83341391	9	0.040041361	-36413	'29.5.11.4.2'	grmzm2g460958_t01	'protein.degradation.ubiquitin.E3.RING'
1123	Sucr	5	184390409	93.70403371	8	0.03379498	-467903	'27.2'	grmzm2g043461_t02	'RNA.transcription'
1124	Sucr	5	184579203	93.9214921	6	0.048528702	-2643	'30.5'	grmzm2g148301_t01	'signalling.G-proteins'
1125	Sucr	5	204093596	114.9003073	8	0.029700141	-71121	'33.99'	grmzm2g090609_t01	'development.unspecified'
1126	Sucr	5	204527912	116.1688529	7	0.036011734	-8763	'17.4.2'	grmzm2g151223_t02	'hormone metabolism.cytokinin.signal transduction'
1127	Sucr	6	120727054	44.61545648	5	-0.053699952	-78750	'27.3.99'	grmzm2g110168_t01	'RNA.regulation of transcription.unclassified'
1128	Sucr	6	120956190	44.6914035	8	-0.077855121	-2697	'26.12'	grmzm2g104109_t01	'misc.peroxidases'

1129	Sucr	6	125454322	46.41917569	67	-0.070562811	-27104	'26.12'	grmzm2g450233_t01	'misc.peroxidases'
1130	Sucr	6	161584484	86.71512205	10	-0.089408624	-2734	'30.5'	grmzm2g090034_t01	'signalling.G-proteins'
1131	Sucr	6	161899740	87.96647854	58	-0.077401595	-6527	'23.1.2.2'	grmzm2g088995_t01	'nucleotide metabolism.synthesis.purine.GAR Synthetase'
1132	Sucr	7	2586268	7.006474955	17	-0.036400236	-26365	'27.3.12'	ac199624.4_fgt007	'RNA.regulation of transcription.C3H zinc finger family'
1133	Sucr	7	3570399	12.79412594	7	-0.060608629	-79964	'20.1'	grmzm2g465226_t01	'stress.biotic'
1134	Sucr	7	107347438	54.26102457	17	-0.042958657	-134133	'27.3.80'	grmzm2g071112_t01	'RNA.regulation of transcription.zf-HD'
1135	Sucr	7	107748384	54.46470141	23	-0.048482794	-184751	'20.2.3'	grmzm2g114706_t01	'stress.abiotic.drought/salt'
1136	Sucr	7	112739677	57.00023193	20	-0.052798268	-68289	'22.1.2'	grmzm2g060369_t01	'polyamine metabolism.synthesis.SAM decarboxylase'
1137	Sucr	7	117566293	59.45210806	8	-0.045031015	-268549	'27.3.11'	grmzm2g128212_t01	'RNA.regulation of transcription.C2H2 zinc finger family'

1138	Sucr	7	140199828	78.55767933	6	0.050727731	-5254	'26.19'	grmzm2g485559_t01	'misc.plastocyanin-like'
1139	Sucr	7	158146806	102.5659158	5	-0.076514492	-42193	'11.9.3.3'	grmzm2g017550_t01	'lipid metabolism.lipid degradation.lysophospholipases.glycerophosphodiester phosphodiesterase'
1140	Sucr	7	169562400	134.5167655	17	-0.03237163	-59463	'29.5.4'	grmzm2g420910_t01	'protein.degradation.aspartate protease'
1141	Sucr	8	163333139	94.90114389	20	0.100296937	-7825	'26.23'	grmzm2g080816_t01	'misc.rhodanese'
1142	Sucr	8	164331901	98.88225877	17	0.036391177	-33857	'20.2.1'	grmzm2g128248_t01	'stress.abiotic.heat'
1143	Sucr	8	164401313	99.09699982	5	0.085464891	-31457	'29.5.11.1'	grmzm2g114172_t01	'protein.degradation.ubiquitin.ubiquitin'
1144	Sucr	8	164401324	99.09703335	20	0.065104941	-31468	'29.5.11.1'	grmzm2g114172_t01	'protein.degradation.ubiquitin.ubiquitin'
1145	Sucr	8	164401576	99.09780132	7	0.074809194	-31720	'29.5.11.1'	grmzm2g114172_t01	'protein.degradation.ubiquitin.ubiquitin'
1146	Sucr	8	168628318	113.9072651	19	0.03649192	-760	'30.11'	grmzm2g135332_t01	'signalling.light'
1147	Sucr	8	172057184	128.8248994	5	0.045679833	-50309	'11.9.3.3'	grmzm2g153274_t01	'lipid metabolism.lipid degradation.lysophospholipases.glycerophosphodiester phosphodiesterase'

1148	Sucr	8	172057190	128.8249236	9	0.044703695	-50315	'11.9.3.3'	grmzm2g153274_t01	'lipid metabolism.lipid degradation.lysophospholipases.glycerophosphodiester phosphodiesterase'
1149	Sucr	10	2166827	0.955425267	15	-0.093456643	-18229	'29.6'	grmzm2g127393_t01	'protein.folding'
1150	Sucr	10	2698524	2.792564149	42	-0.098765758	-6647	'20.1'	grmzm2g356817_t02	'stress.biotic'
1151	Sucr	10	3240557	4.665416356	5	-0.076233214	-12409	'20.1'	grmzm2g443939_t02	'stress.biotic'
1152	Sucr	10	77488297	38.59893808	5	-0.053379979	-220547	'29.5.11.4.2'	grmzm2g305582_t01	'protein.degradation.ubiquitin.E3.RING'
1153	Sucr	10	85544281	40.43156797	5	-0.03474644	-3176	'26.12'	grmzm2g394500_t02	'misc.peroxidases'
1154	Sucr	10	113451096	45.40733399	7	-0.04402236	-135064	'13.1.6.3.1'	grmzm2g125923_t01	'amino acid metabolism.synthesis.aromatic aa.phenylalanine.arogenate dehydratase / prephenate dehydratase'
1155	Prin1	1	52690146	67.43745454	28	-0.325669425	-34797	'27.3.19'	grmzm2g033570_t01	'RNA.regulation of transcription.EIN3-like(EIL) transcription factor family'
1156	Prin1	1	86713369	83.51202829	6	-0.361580066	-47303	'2.1.2'	grmzm2g114772_t01	'major CHO metabolism.synthesis.starch'

1157	Prin1	1	89352884	84.21946029	45	-0.377779862	-42252	'29.4'	grmzm2g180916_t01	'protein.postranslational modification'
1158	Prin1	1	172752341	94.00861544	12	0.251503889	-51291	'33.99'	grmzm2g049201_t01	'development.unspecified'
1159	Prin1	1	173107592	94.12366453	7	0.364562902	-9718	'20.2.1'	grmzm2g003635_t01	'stress.abiotic.heat'
1160	Prin1	1	206686287	118.8958806	6	-0.243142768	-91322	'23.5.2'	grmzm2g037648_t01	'nucleotide metabolism.deoxynucleotide metabolism.pseudouridine synthase'
1161	Prin1	1	212358693	123.8826126	13	-0.187087297	-1907	'29.2.1.2.2.34'	grmzm2g152552_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L34'
1162	Prin1	1	219369577	128.5769255	8	-0.230027518	-73976	'28.99'	grmzm2g015925_t01	'DNA.unspecified'
1163	Prin1	1	221341695	129.3656668	18	-0.363923496	-119609	'10.2.1'	grmzm2g044269_t01	'cell wall.cellulose synthesis.cellulose synthase'
1164	Prin1	2	2211542	4.46960072	7	0.173420062	-141515	'27.3.5'	grmzm2g040736_t01	'RNA.regulation of transcription.ARR'
1165	Prin1	2	2211569	4.4697226	21	0.190449042	-141542	'27.3.5'	grmzm2g040736_t01	'RNA.regulation of transcription.ARR'

1166	Prin1	2	4299945	11.96658077	43	0.175516911	-25089	'17.5.2'	grmzm2g067463_t01	'hormone metabolism.ethylene.signal transduction'
1167	Prin1	2	4870077	14.13414888	6	0.185328555	-307	'31.4'	grmzm2g095308_t01	'cell.vesicle transport'
1168	Prin1	2	37249730	65.55400788	27	0.483745172	-63611	'27.3.20'	grmzm2g093832_t01	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
1169	Prin1	2	38625981	66.45985177	6	0.393707078	-197	'26.4'	grmzm2g447691_t02	'misc.beta 1,3 glucan hydrolases'
1170	Prin1	2	39794143	67.22873216	23	0.5113885	-282215	'4.3.6'	grmzm2g326631_t01	'glycolysis.unclear/dually targeted.fructose-2,6-bisphosphatase (Fru2,6BisPase)'
1171	Prin1	2	39879711	67.28505273	9	0.434301435	-84593	'34.3'	grmzm2g155491_t01	'transport.amino acids'
1172	Prin1	2	185284281	95.94214858	24	0.238072478	-38974	'27.3.59'	grmzm2g048411_t01	'RNA.regulation of transcription.Methyl binding domain proteins'
1173	Prin1	2	186269385	97.19232631	15	0.189950055	-132624	'30.2.11'	ac233861.1_fgt001	'signalling.receptor kinases.leucine rich repeat XI'
1174	Prin1	2	186285785	97.21313925	13	0.19792386	-9196	'27.3.16'	grmzm2g022162_t01	'RNA.regulation of transcription.CCAAT box binding factor family, HAP5'
1175	Prin1	2	186766346	97.99944104	24	0.201406468	-41900	'20.2.1'	grmzm2g474367_t01	'stress.abiotic.heat'
1176	Prin1	2	187583042	99.21938644	6	0.193767621	-12154	'19.6'	grmzm2g147955_t01	'tetrapyrrole synthesis.uroporphyrinogen III synthase'

1177	Prin1	2	208604410	118.3005988	5	-0.291990669	-80891	'25'	grmzm2g124919_t01	'C1-metabolism'
1178	Prin1	3	6560146	25.42100729	9	0.224131566	-9343	'29.2.1.2.1.4'	grmzm2g499197_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4'
1179	Prin1	3	10019848	34.54290833	6	0.147532068	-47297	'13.1.6.2'	grmzm2g029135_t01	'amino acid metabolism.synthesis.aromatic aa.phenylalanine and tyrosine'
1180	Prin1	3	10798853	36.10351096	5	0.15355804	-43117	'34.18'	grmzm2g051753_t01	'transport.unspecified anions'
1181	Prin1	3	173210277	83.47025878	7	0.372725567	-603	'1.1.1.2'	grmzm2g077333_t01	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
1182	Prin1	3	176397560	87.31080195	31	0.329494913	-34388	'31.2'	grmzm2g007659_t01	'cell.division'
1183	Prin1	3	177498347	88.92648807	6	-0.320067184	-50388	'27.3.25'	grmzm2g005112_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1184	Prin1	3	187651158	98.71945033	7	-0.295211159	-46363	'29.2.3'	grmzm2g113414_t01	'protein.synthesis.initiation'
1185	Prin1	3	208541649	118.8197976	8	-0.369019896	-35252	'29.5.11.4.3.2'	grmzm2g059799_t02	'protein.degradation.ubiquitin.E3.SCF.FBOX'

1186	Prin1	3	212248108	123.3033736	10	-0.263177037	-1566	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
1187	Prin1	3	212248700	123.3041123	16	-0.250746746	-2158	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
1188	Prin1	3	213848298	126.6560335	53	-0.249180593	-44440	'26.2'	grmzm2g048010_t01	'misc.UDP glucosyl and glucoronyl transferases'
1189	Prin1	3	213859916	126.6845705	6	-0.219255555	-63	'1.5.1'	grmzm2g348512_t03	'PS.carbon concentrating mechanism.C4'
1190	Prin1	4	31722606	50.95098413	20	0.217083693	-58091	'27.3.22'	grmzm2g048297_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
1191	Prin1	4	90652356	57.4372722	43	0.176560253	-14948	'10.2'	grmzm2g093999_t01	'cell wall.cellulose synthesis'
1192	Prin1	4	176411838	87.58887022	6	-0.223703747	-173143	'28.1'	grmzm2g115013_t01	'DNA.synthesis/chromatin structure'
1193	Prin1	4	176745377	87.99059847	6	-0.231675713	-5344	'30.11'	grmzm2g126795_t01	'signalling.light'
1194	Prin1	4	177057759	88.36684435	37	-0.199910793	-311746	'12.1.1'	grmzm2g428027_t01	'N-metabolism.nitrate metabolism.NR'

1195	Prin1	4	177225650	88.56905925	19	-0.22500953	-75890	'29.4'	grmzm2g158860_t02	'protein.postranslational modification'
1196	Prin1	4	177456322	88.84689021	5	-0.177386326	-82069	'29.5.3'	grmzm2g150153_t01	'protein.degradation.cysteine protease'
1197	Prin1	4	243324592	133.223033	6	0.286380697	-1333	'3.8.1'	grmzm2g165931_t01	'minor CHO metabolism.galactose.galactokinases'
1198	Prin1	5	1875087	2.828866055	9	0.198422919	-18592	'27.3.28'	grmzm2g138421_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
1199	Prin1	5	16786267	47.56865354	11	0.186128131	-58601	'34.22'	grmzm2g077828_t01	'transport.cyclic nucleotide or calcium regulated channels'
1200	Prin1	5	18656090	49.4044948	5	0.231641756	-1554	'27.4'	grmzm2g138572_t01	'RNA.RNA binding'
1201	Prin1	5	19607267	50.33047385	6	0.191852193	-27864	'34.99'	grmzm2g124918_t01	'transport.misc'
1202	Prin1	5	22228974	52.4036044	6	0.200210132	-61904	'27.2'	grmzm2g466938_t01	'RNA.transcription'
1203	Prin1	5	22628739	52.93108894	19	0.179737138	-7626	'27.3.99'	grmzm2g078379_t01	'RNA.regulation of transcription.unclassified'

1204	Prin1	5	23032929	53.4644122	13	0.192543992	-137586	'30.2.24'	grmzm2g330751_t01	'signalling.receptor kinases.S-locus glycoprotein like'
1205	Prin1	5	26723660	54.83773092	5	0.181309457	-473830	'26.10'	grmzm2g013082_t01	'misc.cytochrome P450'
1206	Prin1	5	27926098	55.29207074	8	0.259427803	-116540	'27.3.4'	grmzm2g159399_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
1207	Prin1	5	205662825	119.8501543	5	-0.331878313	-12994	'17.2.2'	grmzm2g074267_t01	'hormone metabolism.auxin.signal transduction'
1208	Prin1	5	205892823	120.5961956	20	-0.202211883	-47113	'34.19.2'	grmzm2g028325_t01	'transport.Major Intrinsic Proteins.TIP'
1209	Prin1	5	206470516	122.4700502	8	-0.182601165	-6960	'27.3.6'	grmzm2g036092_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
1210	Prin1	5	207093116	124.0642086	6	-0.223961036	-67701	'10.6.2'	grmzm2g035503_t01	'cell wall.degradation.mannan-xylose-arabinose-fucose'
1211	Prin1	5	207103724	124.0880847	6	-0.211548066	-9175	'27.3.3'	grmzm2g055204_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'

1212	Prin1	5	207325275	124.5867434	7	-0.207443465	-67992	'27.3.24'	grmzm2g044408_t01	'RNA.regulation of transcription.MADS box transcription factor family'
1213	Prin1	6	2898813	-7.559855335	7	-0.16547695	-170899	'31.4'	grmzm2g367941_t02	'cell.vesicle transport'
1214	Prin1	6	5873783	-4.184534568	14	-0.194407963	-224946	'13.99'	grmzm2g034404_t01	'amino acid metabolism.misc'
1215	Prin1	6	6894842	-3.026068551	14	-0.172667028	-189308	'29.5.11.4.2'	grmzm2g390009_t01	'protein.degradation.ubiquitin.E3.RING'
1216	Prin1	6	8419109	-1.296676302	10	-0.156917082	-6724	'33.99'	grmzm2g061186_t02	'development.unspecified'
1217	Prin1	6	14792950	5.295348837	11	-0.186212199	-599112	'30.2.17'	grmzm2g160853_t01	'signalling.receptor kinases.DUF 26'
1218	Prin1	7	124476542	64.75250337	10	0.249817163	-540	'27.3.6'	grmzm2g089501_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
1219	Prin1	7	153457755	93.06309404	13	0.245403	-4767	'26.19'	grmzm2g107562_t01	'misc.plastocyanin-like'
1220	Prin1	7	156111925	98.3472492	7	0.241907825	-38438	'9.1.2'	grmzm2g396397_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'

1221	Prin1	7	156185170	98.49909898	33	0.211508581	-1757	'11.9.2.1'	grmzm2g179777_t01	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
1222	Prin1	7	159147927	104.6414159	9	0.180017249	-2614	'27.3.67'	grmzm2g037444_t01	'RNA.regulation of transcription.putative transcription regulator'
1223	Prin1	7	159471791	105.3360113	5	0.203425704	-54049	'29.3.4.99'	grmzm2g121022_t01	'protein.targeting.secretory pathway.unspecified'
1224	Prin1	7	159471845	105.3361463	9	0.171827824	-54103	'29.3.4.99'	grmzm2g121022_t01	'protein.targeting.secretory pathway.unspecified'
1225	Prin1	7	160106822	106.9228459	9	0.206135369	-3287	'29.5.11.4.3.2'	grmzm2g054032_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
1226	Prin1	7	169415919	134.4048149	10	-0.207507404	-16584	'11.9.3.1'	grmzm2g140811_t01	'lipid metabolism.lipid degradation.lysophospholipases.phospholipase D'
1227	Prin1	8	2087948	4.782267599	7	0.209648655	-21167	'29.5.11.4.2'	grmzm2g417125_t01	'protein.degradation.ubiquitin.E3.RING'
1228	Prin1	8	4386420	11.24086841	11	0.365945724	-72264	'26.12'	grmzm2g037156_t01	'misc.peroxidases'
1229	Prin1	8	5283586	15.55733838	38	0.216233202	-10226	'31.4'	grmzm2g017329_t01	'cell.vesicle transport'
1230	Prin1	8	8255624	20.95732171	5	0.182206933	-9556	'27.3.67'	grmzm2g334457_t01	'RNA.regulation of transcription.putative transcription regulator'

1231	Prin1	8	8403455	21.19881565	12	0.37507853	-147740	'27.3.67'	ac234160.1_fgt001	'RNA.regulation of transcription.putative transcription regulator'
1232	Prin1	8	103054530	58.74182186	7	0.277385271	-11798	'27.3.37'	grmzm2g096064_t01	'RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family'
1233	Prin1	8	105711842	59.67074769	21	0.237102288	-70209	'29.5.2'	grmzm2g078468_t01	'protein.degradation.autophagy'
1234	Prin1	8	108389110	60.44924097	8	0.215129664	-154108	'27.3.32'	grmzm2g061408_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
1235	Prin1	8	108849125	60.58213104	19	0.325050069	-37583	'30.5'	grmzm2g150724_t01	'signalling.G-proteins'
1236	Prin1	8	111264320	61.27983748	5	0.202557625	-101745	'33.99'	grmzm2g179679_t01	'development.unspecified'
1237	Prin1	8	117142297	63.44621372	6	0.231321611	-123994	'28.1'	grmzm2g162112_t01	'DNA.synthesis/chromatin structure'
1238	Prin1	8	117976115	63.86193872	6	0.224320933	-98989	'34.12'	grmzm2g138817_t01	'transport.metal'
1239	Prin1	8	158510179	86.58550567	14	-0.190411215	-90849	'30.8'	grmzm2g423959_t01	'signalling.misc'
1240	Prin1	8	158697511	86.89047423	5	-0.249857512	-4815	'11.8.1.2'	grmzm2g010202_t01	'lipid metabolism."exotics" (steroids, squalene etc).sphingolipids.serine C-palmitoyltransferase'

1241	Prin1	8	159893599	88.49652739	21	-0.181876531	-20128	'26.27'	grmzm2g364863_t01	'misc.calcineurin-like phosphoesterase family protein'
1242	Prin1	8	159898572	88.50016935	13	-0.17950465	-25101	'26.27'	grmzm2g364863_t01	'misc.calcineurin-like phosphoesterase family protein'
1243	Prin1	8	162773842	93.15571435	5	-0.176464664	-156311	'11.9.2.1'	ac233916.1_fgt002	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
1244	Prin1	9	12785133	22.10483847	6	-0.158858265	-52684	'20.2.2'	grmzm2g079306_t01	'stress.abiotic.cold'
1245	Prin1	9	20668779	36.70158796	15	-0.209803433	-3240	'34.2'	grmzm2g404965_t02	'transport.sugars'
1246	Prin1	9	20780641	36.88056228	5	-0.183329952	-34504	'27.3.22'	grmzm2g134260_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
1247	Prin1	9	21433294	37.9247786	11	-0.168662562	-528328	'29.5.11.20'	grmzm2g374881_t01	'protein.degradation.ubiquitin.proteasom'
1248	Prin1	9	26434264	43.26084016	8	-0.174249746	-1131	'11.1.8'	grmzm2g393146_t03	'lipid metabolism.FA synthesis and FA elongation.acyl coa ligase'
1249	Prin1	9	34855540	44.99799089	6	-0.212168913	-130582	'29.5.11.4.2'	grmzm2g065612_t01	'protein.degradation.ubiquitin.E3.RING'
1250	Prin1	9	113108447	55.8821261	7	-0.307295112	-235865	'10.7'	grmzm2g059785_t01	'cell wall.modification'

1251	Prin1	9	144471186	92.93120956	15	-0.279214676	-231042	'29.2.1.1.1.1.10'	grmzm2g017957_t01	'protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S10'
1252	Prin1	9	144622187	93.27205089	19	-0.236362959	-981	'20.2.2'	grmzm2g096355_t01	'stress.abiotic.cold'
1253	Prin1	9	146785494	99.6308883	11	-0.180210179	-6230	'29.3.1'	ac149829.2_fgt003	'protein.targeting.nucleus'
1254	Prin1	10	3622484	6.02423381	5	0.18783093	-22975	'29.2.4'	grmzm2g129804_t01	'protein.synthesis.elongation'
1255	Prin1	10	119575302	47.38384118	12	-0.204463112	-75223	'20.2.1'	grmzm2g346839_t01	'stress.abiotic.heat'
1256	Prin1	10	137172137	64.52401076	13	0.291125843	-51956	'27.3.36'	ac209206.3_fgt011	'RNA.regulation of transcription.Argonaute'
1257	Prin1	10	140585346	71.90932116	6	0.416795748	-4690	'27.3.50'	grmzm2g129147_t01	'RNA.regulation of transcription.General Transcription'
1258	Prin2	1	16528334	33.09583561	9	-0.148363759	-104915	'29.4.1.57'	grmzm2g175164_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
1259	Prin2	1	16774678	33.28332749	16	-0.148531763	-31918	'27.3.7'	grmzm2g445634_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'

1260	Prin2	1	17321663	33.69438463	6	-0.167753428	-34007	'29.2.1.2.1.31'	grmzm2g145308_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.SA'
1261	Prin2	1	21383024	37.73112289	14	-0.220900957	-196595	'10.1'	grmzm2g064841_t01	'cell wall.precursor synthesis'
1262	Prin2	1	21688795	38.19316881	19	-0.158781748	-18850	'17.5.2'	grmzm2g415251_t01	'hormone metabolism.ethylene.signal transduction'
1263	Prin2	1	21725760	38.25596337	8	-0.160463885	-14292	'26.24'	grmzm2g114184_t01	'misc.GCN5-related N-acetyltransferase'
1264	Prin2	1	46712396	62.60179969	12	0.205604085	-34913	'29.5.11.20'	grmzm2g104373_t01	'protein.degradation.ubiquitin.proteasom'
1265	Prin2	1	46752724	62.62839403	29	0.217392494	-39642	'31.1'	grmzm2g104534_t01	'cell.organisation'
1266	Prin2	1	48772229	63.96015846	7	0.183706966	-92461	'20.2.1'	grmzm2g010000_t01	'stress.abiotic.heat'
1267	Prin2	1	51413724	65.71798167	16	0.162964157	-5640	'29.8'	grmzm2g084783_t01	'protein.assembly and cofactor ligation'
1268	Prin2	1	51506627	65.97678122	7	0.17642016	-61930	'2.2.1.3.1'	grmzm2g084940_t01	'major CHO metabolism.degradation.sucrose.invertases.neutral'
1269	Prin2	1	92753447	85.57176721	27	0.151936909	-99005	'29.2.1.99.2.1185'	grmzm2g154487_t01	'protein.synthesis.ribosomal protein.unknown.large subunit.L18/L5'

1270	Prin2	1	228544370	135.6950109	18	-0.296287834	-17399	'17.1.3'	grmzm2g113167_t01	'hormone metabolism.abscisic acid.induced-regulated-responsive-activated'
1271	Prin2	1	229356638	136.3156268	6	-0.360908732	-1937	'17.4.1'	grmzm2g404443_t01	'hormone metabolism.cytokinin.synthesis-degradation'
1272	Prin2	1	241747994	142.5070084	6	-0.352944427	-39800	'10.8.1'	grmzm2g019411_t01	'cell wall.pectin*esterases.PME'
1273	Prin2	1	244977165	144.1767876	5	-0.366739502	-77835	'34.15'	grmzm2g084486_t01	'transport.potassium'
1274	Prin2	1	245007633	144.1925424	9	-0.295276804	-29831	'34.15'	grmzm2g438960_t01	'transport.potassium'
1275	Prin2	1	252877501	149.8251302	6	-0.308540541	-73707	'34.99'	grmzm2g021055_t01	'transport.misc'
1276	Prin2	1	253031255	149.9489621	5	-0.279689196	-34757	'28.1'	grmzm2g099023_t01	'DNA.synthesis/chromatin structure'
1277	Prin2	1	253328929	150.1887057	6	-0.305359506	-141409	'29.4'	grmzm2g017089_t01	'protein.postranslational modification'
1278	Prin2	2	4879221	14.16891319	10	-0.178554558	-9451	'31.4'	grmzm2g095308_t01	'cell.vesicle transport'
1279	Prin2	2	5548572	16.71369911	43	-0.154491728	-28298	'33.99'	grmzm2g174784_t01	'development.unspecified'

1280	Prin2	2	5682220	17.22181151	5	-0.156996321	-107733	'29.5.11.4.2'	grmzm2g174926_t01	'protein.degradation.ubiquitin.E3.RING'
1281	Prin2	2	26641159	57.94684499	18	-0.149499019	-6089	'34.9'	grmzm2g114149_t01	'transport.metabolite transporters at the mitochondrial membrane'
1282	Prin2	2	27916738	59.06362357	30	-0.172361155	-15005	'27.3.4'	grmzm2g122614_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
1283	Prin2	2	28972476	60.59406358	25	-0.235153714	-114078	'29.4'	grmzm2g032694_t01	'protein.postranslational modification'
1284	Prin2	2	34001062	63.56397414	13	-0.186467942	-26900	'20.1'	grmzm2g051921_t01	'stress.biotic'
1285	Prin2	2	34937097	64.04660572	9	0.335345874	-39687	'34.13'	grmzm2g138731_t01	'transport.peptides and oligopeptides'
1286	Prin2	2	81996078	75.87752354	6	-0.253830438	-151865	'26.7'	grmzm2g028004_t01	'misc.oxidases - copper, flavone etc.'
1287	Prin2	2	124738310	77.33837071	9	-0.276512367	-59874	'29.5.5'	grmzm2g132154_t01	'protein.degradation.serine protease'

1288	Prin2	2	124769416	77.34049122	25	-0.297074114	-90980	'29.5.5'	grmzm2g132154_t01	'protein.degradation.serine protease'
1289	Prin2	3	2915029	8.667233227	5	-0.195341132	-3919	'17.2.3'	grmzm2g061005_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
1290	Prin2	3	3185414	10.0663659	10	-0.231447784	-53421	'27.3.69'	grmzm2g085266_t01	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
1291	Prin2	3	3386685	11.10786166	18	-0.158579918	-29190	'29.3.4.4'	grmzm2g102795_t01	'protein.targeting.secretory pathway.plasma membrane'
1292	Prin2	3	10750451	36.00654587	9	-0.164241331	-119518	'26.2'	grmzm2g338465_t01	'misc.UDP glucosyl and glucoronyl transferases'
1293	Prin2	3	10838771	36.18347982	6	-0.116432701	-83035	'34.18'	grmzm2g051753_t01	'transport.unspecified anions'
1294	Prin2	3	13300926	40.11756205	6	-0.186344905	-71572	'21.1'	grmzm2g159145_t01	'redox.thioredoxin'
1295	Prin2	3	13633702	40.54785389	18	-0.163225589	-7634	'27.2'	grmzm2g102664_t01	'RNA.transcription'

1296	Prin2	3	13634126	40.54840214	12	-0.167661347	-8058	'27.2'	grmzm2g102664_t01	'RNA.transcription'
1297	Prin2	3	14416721	41.56032683	26	-0.182957628	-186199	'27.3.26'	grmzm2g163291_t01	'RNA.regulation of transcription.MYB-related transcription factor family'
1298	Prin2	3	17306447	45.29685092	9	-0.237524461	-2219	'16.7'	grmzm2g541193_t01	'secondary metabolism.wax'
1299	Prin2	3	19698629	48.39003196	8	-0.195530153	-21856	'26.1'	grmzm2g169152_t02	'misc.misc2'
1300	Prin2	3	19800505	48.52176145	5	-0.198444438	-7709	'30.2.17'	grmzm2g094028_t01	'signalling.receptor kinases.DUF 26'
1301	Prin2	3	51981075	56.79858368	23	0.417597478	-12830	'27.3.25'	grmzm2g158700_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1302	Prin2	3	54021465	57.26319567	17	0.319862133	-36286	'27.3.99'	grmzm2g102014_t01	'RNA.regulation of transcription.unclassified'
1303	Prin2	3	106489882	58.60975416	5	0.31895293	-249853	'28.99'	grmzm2g351307_t01	'DNA.unspecified'
1304	Prin2	3	136646099	63.07155567	5	-0.237479608	-287899	'27.3.25'	grmzm2g041415_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1305	Prin2	3	171862276	82.33409418	6	0.513407834	-38074	'34.99'	grmzm2g081652_t01	'transport.misc'
1306	Prin2	3	172148591	82.5754152	5	0.518185895	-1652	'34.10'	grmzm2g037229_t01	'transport.nucleotides'

1307	Prin2	3	173219900	83.47836954	15	0.538906436	-10226	'1.1.1.2'	grmzm2g077333_t01	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
1308	Prin2	3	193922818	101.9299488	10	0.197939448	-28010	'29.3.4.99'	grmzm2g162274_t01	'protein.targeting.secretory pathway.unspecified'
1309	Prin2	3	198668625	105.7679086	5	0.17551164	-69220	'28.99'	grmzm2g330229_t01	'DNA.unspecified'
1310	Prin2	4	828147	2.931410178	7	0.187879628	-1090	'27.3.21'	grmzm2g073805_t01	'RNA.regulation of transcription.GRAS transcription factor family'
1311	Prin2	4	5696047	19.49225268	12	-0.299402936	-25394	'29.1.11'	grmzm2g169160_t01	'protein.aa activation.serine-tRNA ligase'
1312	Prin2	4	42018416	54.27865297	7	-0.145631996	-52167	'27.3.11'	grmzm2g377165_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
1313	Prin2	4	96251735	57.74714448	7	-0.124855363	-384209	'17.2.3'	grmzm2g131699_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
1314	Prin2	4	125186338	58.42286198	72	-0.130712371	-33480	'30.7'	grmzm2g095397_t01	'signalling.14-3-3 proteins'
1315	Prin2	4	177668855	89.1123214	6	-0.18872756	-1922	'33.99'	grmzm2g079353_t01	'development.unspecified'

1316	Prin2	4	199778387	105.9507817	14	-0.193006416	-37236	'29.5.11.4.2'	grmzm2g100913_t02	'protein.degradation.ubiquitin.E3.RING'
1317	Prin2	4	242574395	130.3125709	11	-0.281573519	-922	'11.3.2'	grmzm2g111319_t01	'lipid metabolism.Phospholipid synthesis.choline kinase'
1318	Prin2	5	929964	0.282533564	43	-0.19293743	-1418	'9.1.2'	grmzm2g082976_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
1319	Prin2	5	1574000	2.018545222	10	-0.231021725	-1899	'29.2.1.2.1.21'	grmzm2g125300_t02	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S21'
1320	Prin2	5	1580722	2.036636261	5	-0.228448538	-3445	'17.2.1'	grmzm2g125552_t04	'hormone metabolism.auxin.synthesis-degradation'
1321	Prin2	5	1842198	2.740351301	7	-0.153703207	-17853	'26.1'	grmzm2g133407_t01	'misc.misc2'
1322	Prin2	5	2347751	4.958870956	12	-0.152516959	-5480	'27.3.8'	grmzm2g144172_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
1323	Prin2	5	7094245	26.093099	26	0.150251126	-6870	'30.11'	grmzm2g129889_t01	'signalling.light'
1324	Prin2	5	10372835	33.33515135	9	0.176034799	-182827	'31.1'	grmzm2g152328_t01	'cell.organisation'

1325	Prin2	5	26734713	54.84190728	11	0.353426391	-484883	'26.10'	grmzm2g013082_t01	'misc.cytochrome P450'
1326	Prin2	5	73804215	66.39516104	21	0.292651485	-98624	'27.3.44'	grmzm2g524937_t01	'RNA.regulation of transcription.Chromatin Remodeling Factors'
1327	Prin2	5	108262797	70.32363616	14	0.366236504	-361129	'29.3.99'	grmzm2g072407_t01	'protein.targeting.unknown'
1328	Prin2	5	143236820	72.10704824	7	0.356617661	-15080	'30.3'	grmzm2g030945_t01	'signalling.calcium'
1329	Prin2	5	164299446	76.94625198	6	-0.300410103	-66466	'11.9.3.3'	grmzm2g018820_t01	'lipid metabolism.lipid degradation.lysophospholipases.glycerophosphodiester phosphodiesterase'
1330	Prin2	5	165991682	78.08035909	12	0.301900822	-64882	'27.3.3'	grmzm2g047999_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1331	Prin2	5	169382477	81.27535729	5	-0.317414291	-5351	'11.10.2'	grmzm2g092588_t01	'lipid metabolism.glycolipid synthesis.DGDG synthase'
1332	Prin2	5	188788930	98.54955746	8	0.15465899	-50964	'33.99'	grmzm2g315140_t01	'development.unspecified'
1333	Prin2	5	194052252	102.6015186	6	0.184420996	-213754	'27.3.20'	grmzm2g106185_t01	'RNA.regulation of transcription.G2-like transcription factor family, GARP'

1334	Prin2	5	203652758	113.8406769	6	0.258309313	-5454	'34.3'	grmzm2g020738_t01	'transport.amino acids'
1335	Prin2	5	205472185	119.231778	50	0.148970386	-63878	'31.1'	grmzm2g026560_t01	'cell.organisation'
1336	Prin2	5	207751210	125.7483283	10	0.22159592	-138981	'29.2.1.1.1.2.29'	grmzm2g159554_t01	'protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L29'
1337	Prin2	5	209217720	128.3485035	30	0.293163871	-4594	'27.2'	grmzm2g055859_t01	'RNA.transcription'
1338	Prin2	5	209930161	130.9277607	5	0.227274598	-3685	'29.5.9'	grmzm2g403454_t01	'protein.degradation.AAA type'
1339	Prin2	6	867384	-9.864659918	6	0.365645779	-73303	'26.1'	grmzm2g052825_t01	'misc.misc2'
1340	Prin2	6	1957524	-8.627816461	8	0.454475095	-91812	'27.3.12'	ac233871.1_fgt008	'RNA.regulation of transcription.C3H zinc finger family'
1341	Prin2	6	118739798	43.69898027	13	-0.578903834	-583	'30.3'	grmzm2g174315_t03	'signalling.calcium'
1342	Prin2	6	119772986	44.24786955	73	-0.412080895	-90952	'26.19'	grmzm2g148624_t01	'misc.plastocyanin-like'

1343	Prin2	6	120956190	44.6914035	7	-0.327835409	-2697	'26.12'	grmzm2g104109_t01	'misc.peroxidases'
1344	Prin2	6	165586711	102.9473046	27	-0.297375391	-86902	'30.11'	grmzm2g145556_t01	'signalling.light'
1345	Prin2	6	165589669	102.9571143	8	-0.289894217	-89860	'30.11'	grmzm2g145556_t01	'signalling.light'
1346	Prin2	6	165667455	103.215079	20	-0.261489914	-167646	'30.11'	grmzm2g145556_t01	'signalling.light'
1347	Prin2	6	165667652	103.2157324	5	-0.237252512	-167843	'30.11'	grmzm2g145556_t01	'signalling.light'
1348	Prin2	6	166076222	104.570689	13	-0.302483541	-15338	'29.2.1.2.1.12'	grmzm2g132929_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S12'
1349	Prin2	7	5428540	23.50772999	34	-0.287429645	-127863	'34.2'	grmzm2g142063_t01	'transport.sugars'

1350	Prin2	7	22002213	45.79983088	10	-0.179913126	-8939	'27.3.3'	grmzm2g176175_t02	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1351	Prin2	7	27302170	46.77471414	16	-0.174347347	-640877	'23.2'	grmzm2g173063_t01	'nucleotide metabolism.degradation'
1352	Prin2	7	27327128	46.7793044	9	-0.205664769	-665835	'23.2'	grmzm2g173063_t01	'nucleotide metabolism.degradation'
1353	Prin2	7	29146881	47.11399196	45	-0.189498059	-440042	'10.2.1'	grmzm2g177631_t01	'cell wall.cellulose synthesis.cellulose synthase'
1354	Prin2	7	124223168	64.44761155	10	-0.142549038	-75570	'27.3.35'	grmzm2g358796_t01	'RNA.regulation of transcription.bZIP transcription factor family'
1355	Prin2	7	156185236	98.49923581	6	-0.608676503	-1823	'11.9.2.1'	grmzm2g179777_t01	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
1356	Prin2	7	156689760	99.54520289	27	-0.178439732	-8325	'27.3.11'	ac185108.3_fgt011	'RNA.regulation of transcription.C2H2 zinc finger family'
1357	Prin2	7	166657242	123.8438631	41	0.243268708	-105055	'34.15'	grmzm2g020766_t01	'transport.potassium'
1358	Prin2	7	167223656	126.3055595	17	0.239027751	-3846	'29.4'	grmzm2g166658_t01	'protein.postranslational modification'

1359	Prin2	7	168146779	130.3175518	8	0.250707874	-9138	'29.3.1'	ac155434.2_fgt004	'protein.targeting.nucleus'
1360	Prin2	7	168157307	130.3633076	7	0.263440613	-10237	'27.3.20'	ac155434.2_fgt005	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
1361	Prin2	8	10739260	27.73471036	6	-0.202260838	-331436	'29.5.11.4.2'	grmzm2g003930_t01	'protein.degradation.ubiquitin.E3.RING'
1362	Prin2	8	103399576	58.8624408	6	0.15144341	-5146	'27.3.67'	grmzm2g087451_t01	'RNA.regulation of transcription.putative transcription regulator'
1363	Prin2	8	159090160	87.53999331	9	0.172388561	-6988	'27.1.2'	grmzm2g300375_t01	'RNA.processing.RNA helicase'
1364	Prin2	8	160611990	89.64768912	20	0.195427349	-32696	'27.3.99'	grmzm2g070898_t01	'RNA.regulation of transcription.unclassified'
1365	Prin2	8	160612122	89.6479463	28	0.216705415	-32828	'27.3.99'	grmzm2g070898_t01	'RNA.regulation of transcription.unclassified'
1366	Prin2	8	164575465	99.62773322	5	0.134691981	-29729	'16.4.1'	grmzm2g338431_t01	'secondary metabolism.N misc.alkaloid-like'
1367	Prin2	8	170618195	123.1071582	8	0.141301951	-24289	'11.8'	grmzm2g159643_t01	'lipid metabolism."exotics" (steroids, squalene etc)'
1368	Prin2	8	170786240	123.7938509	6	0.133385539	-39160	'28.99'	grmzm2g004690_t01	'DNA.unspecified'

1369	Prin2	8	173793234	135.8235771	8	0.119843765	-132232	'31.1'	grmzm2g124883_t01	'cell.organisation'
1370	Prin2	8	173864083	136.1091964	9	0.124329055	-39941	'10.8.1'	grmzm2g120779_t01	'cell wall.pectin*esterases.PME'
1371	Prin2	9	2701441	-3.388186607	59	-0.379560098	-280728	'27.1.19'	grmzm2g016275_t01	'RNA.processing.ribonucleases'
1372	Prin2	9	3689306	-0.719907238	18	-0.378505593	-89654	'17.2.2'	grmzm2g098643_t01	'hormone metabolism.auxin.signal transduction'
1373	Prin2	9	7182819	8.716269429	14	-0.268943698	-40774	'31.1'	grmzm2g017257_t01	'cell.organisation'
1374	Prin2	9	109417983	53.84202072	8	0.254711069	-106912	'3.5'	grmzm2g144245_t01	'minor CHO metabolism.others'
1375	Prin2	9	109658976	53.91939367	7	0.188444788	-107174	'20.2.1'	ac225193.3_fgt004	'stress.abiotic.heat'
1376	Prin2	9	117715320	57.64391617	6	0.137706712	-19785	'29.4'	ac217887.3_fgt001	'protein.postranslational modification'
1377	Prin2	9	138570437	79.39501909	34	0.310626673	-31425	'13.1.3.5.2'	grmzm2g104575_t01	'amino acid metabolism.synthesis.aspartate family.lysine.dihydrodipicolinate reductase'
1378	Prin2	10	5058530	14.79019912	46	-0.424128374	-2015	'13'	grmzm2g066496_t01	'amino acid metabolism'

1379	Prin2	10	5427445	17.07840286	12	-0.377394519	-60	'27.1.19'	grmzm2g065804_t01	'RNA.processing.ribonucleases'
1380	Prin2	10	6191195	21.4060557	6	-0.359938003	-69179	'28.1'	grmzm2g044317_t05	'DNA.synthesis/chromatin structure'
1381	Prin2	10	9023970	24.98301526	9	-0.188824159	-67484	'27.3.9'	grmzm2g118214_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
1382	Prin2	10	22382517	34.8358978	9	0.185011049	-65821	'10.2.1'	grmzm2g015886_t01	'cell wall.cellulose synthesis.cellulose synthase'
1383	Prin2	10	24154443	35.31258248	6	0.360806077	-307371	'30.3'	grmzm2g176472_t01	'signalling.calcium'
1384	Prin2	10	79797589	39.13112595	6	0.260220052	-242642	'27.2'	grmzm2g044306_t01	'RNA.transcription'
1385	Prin2	10	85540940	40.43084945	25	0.314408789	-54606	'29.4'	grmzm2g060798_t01	'protein.postranslational modification'
1386	Prin2	10	86726870	40.71912634	15	0.304643229	-116858	'29.4'	grmzm2g099002_t02	'protein.postranslational modification'
1387	Prin2	10	113194309	45.32268893	8	0.36996183	-91130	'20.2.3'	grmzm2g138937_t01	'stress.abiotic.drought/salt'

1388	Prin2	10	133029713	57.10017332	5	-0.138816574	-38470	'27.3.9'	grmzm2g054615_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
1389	Prin2	10	142607850	78.31225962	6	-0.114292892	-89150	'26.7'	grmzm2g396856_t02	'misc.oxidases - copper, flavone etc.'
1390	Prin2	10	142607858	78.31228969	7	-0.146722504	-89158	'26.7'	grmzm2g396856_t02	'misc.oxidases - copper, flavone etc.'
1391	Prin2	10	142646940	78.45920294	5	-0.242947614	-33448	'29.5.2'	grmzm2g419694_t01	'protein.degradation.autophagy'
1392	Prin2	10	143724295	81.34148153	8	-0.154720679	-2125	'30.2.17'	grmzm2g000633_t01	'signalling.receptor kinases.DUF 26'
1393	Prin2	10	144247405	82.22431479	10	-0.222878534	-2506	'10.6.2'	grmzm2g136895_t01	'cell wall.degradation.mannan-xylose-arabinose-fucose'
1394	Prin2	10	144605053	83.42035782	8	-0.228222027	-50952	'17.5.1'	grmzm2g127668_t01	'hormone metabolism.ethylene.synthesis-degradation'

Significant SNP Information										
SNP No.	Trait	Chr	Physical Position (AGPv1)	Imputed cM on NAM Map	Resample Model Inclusion Probability	Average SNP effect	Distance to Gene	Bincode	Gene ID	Category
1	AA	1	13935133	28.26096353	26	-0.085551628	35913	'11.3'	grmzm2g124042_t01	'lipid metabolism.Phospholipid synthesis'
2	AA	1	16780363	33.28759975	31	-0.081912456	175417	'26.7'	grmzm2g000427_t01	'misc.oxidases - copper, flavone etc.'
3	AA	1	33393305	52.652275	11	0.097059759	87487	'20.2.1'	grmzm2g448368_t01	'stress.abiotic.heat'
4	AA	1	165885858	91.92724657	9	0.091736639	36073	'28.1'	grmzm2g088613_t01	'DNA.synthesis/chromatin structure'
5	AA	1	177389147	95.59351325	20	-0.098789746	99723	'17.2.3'	grmzm2g422419_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
6	AA	1	182391497	97.70267302	18	-0.094955313	83060	'27.3.35'	ac186606.4_fgt003	'RNA.regulation of transcription.bZIP transcription factor family'
7	AA	1	192608853	106.1391166	12	-0.107384883	197459	'30.1'	grmzm2g703858_t01	'signalling.in sugar and nutrient physiology'
8	AA	1	205585447	117.8354213	6	-0.061343453	37422	'25.9'	grmzm2g095579_t01	'C1-metabolism.dihydroneopterin aldolase'
9	AA	1	205728648	117.9733694	10	-0.053004958	159819	'29.5.11.4.2'	grmzm2g112617_t01	'protein.degradation.ubiquitin.E3.RING'

10	AA	1	207120770	119.3144261	15	-0.061520606	241	'17.4.1'	grmzm2g348452_t02	'hormone metabolism.cytokinin.synthesis-degradation'
11	AA	1	207135155	119.3282834	8	-0.073649634	140185	'20.2.99'	grmzm2g363004_t01	'stress.abiotic.unspecified'
12	AA	1	208348395	120.4695879	10	-0.053930899	181373	'16.2'	grmzm2g059465_t01	'secondary metabolism.phenylpropanoids'
13	AA	1	210147485	121.9613779	9	-0.073635914	3578	'33.99'	grmzm2g059397_t01	'development.unspecified'
14	AA	1	211910691	123.4234132	9	-0.087541648	7666	'26.2'	grmzm2g139355_t01	'misc.UDP glucosyl and glucoronyl transferases'
15	AA	1	218527234	128.2400336	6	-0.056062356	270453	'27.4'	grmzm2g146111_t01	'RNA.RNA binding'
16	AA	2	3369867	8.460233144	8	0.081076721	5226	'27.3.22'	grmzm2g047448_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
17	AA	2	4452933	12.54822136	11	0.119133386	46523	'30.2.17'	grmzm2g059740_t01	'signalling.receptor kinases.DUF 26'

18	AA	2	5461777	16.38371574	10	0.080146925	54130	'33.99'	grmzm2g174784_t01	'development.unspecified'
19	AA	2	6695031	20.19476759	27	0.044923744	115956	'30.11'	grmzm2g159161_t01	'signalling.light'
20	AA	2	10533238	30.11324699	5	0.050106955	17911	'29.4'	grmzm2g098187_t02	'protein.postranslational modification'
21	AA	2	11104224	31.84202766	21	0.071319845	8029	'29.5.11.20'	grmzm2g102000_t01	'protein.degradation.ubiquitin.proteasom'
22	AA	2	13443804	37.94791551	22	0.054661567	30152	'27.3.99'	grmzm2g131280_t01	'RNA.regulation of transcription.unclassified'
23	AA	2	20521754	51.29525101	5	0.086430763	119197	'27.3.3'	grmzm2g055180_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
24	AA	2	24175937	56.21986729	6	0.144114822	73481	'27.3.25'	grmzm2g447090_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
25	AA	2	37317423	65.59856319	51	0.074663447	6542	'28.1'	grmzm2g044989_t01	'DNA.synthesis/chromatin structure'
26	AA	2	186765375	97.99753568	60	0.070644387	872	'27.3.6'	grmzm2g417597_t02	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'

27	AA	2	186894631	98.25116993	31	0.074688245	9354	'27.3.28'	grmzm2g126018_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
28	AA	2	209329786	120.0730566	6	0.043269516	299	'27.4'	grmzm2g077823_t01	'RNA.RNA binding'
29	AA	2	215989909	128.8383944	6	0.040326516	467	'30.2.11'	grmzm2g169681_t01	'signalling.receptor kinases.leucine rich repeat XI'
30	AA	2	217758767	131.4548964	10	0.05228333	28968	'7.1.2'	grmzm2g148769_t02	'OPP.oxidative PP.6-phosphogluconolactonase'
31	AA	3	106253820	58.5935399	18	0.080180593	379359	'29.5.11.4.2'	ac206768.3_fgt005	'protein.degradation.ubiquitin.E3.RING'
32	AA	3	136272706	62.99233029	6	0.116539144	84299	'27.3.25'	grmzm2g041415_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
33	AA	3	146217490	65.77990892	10	0.108646925	47433	'31.1'	grmzm2g039867_t01	'cell.organisation'
34	AA	3	170786664	81.70076623	6	0.085704188	3611	'29.7'	grmzm2g431006_t01	'protein.glycosylation'
35	AA	3	173982599	84.12121149	71	0.098605713	48888	'31.4'	grmzm2g178244_t01	'cell.vesicle transport'
36	AA	3	176799382	87.90057838	11	0.102983913	47758	'29.5.11.4.3.2'	grmzm2g125411_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'

37	AA	3	211702191	122.6221889	6	-0.041297758	37009	'8.1.4'	grmzm2g033515_t01	'TCA / org. transformation.TCA.IDH'
38	AA	3	212222090	123.2709088	6	-0.046587836	22506	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
39	AA	3	212226136	123.2759574	5	-0.06529147	18460	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
40	AA	3	212726714	123.9011201	5	-0.044492619	215929	'34.8'	grmzm2g064473_t01	'transport.metabolite transporters at the envelope membrane'
41	AA	3	214950753	128.5482503	22	-0.045348234	65376	'19.30'	grmzm2g105604_t01	'tetrapyrrole synthesis.uroporphyrin-III C-methyltransferase'
42	AA	4	171000056	79.4221761	40	-0.050350535	7838	'34.7'	grmzm2g466545_t01	'transport.phosphate'
43	AA	4	171777409	80.83845057	9	-0.04494486	2861	'2.1.2.2'	grmzm2g130043_t01	'major CHO metabolism.synthesis.starch.starch synthase'
44	AA	4	171777978	80.83927823	30	-0.046656729	2292	'2.1.2.2'	grmzm2g130043_t01	'major CHO metabolism.synthesis.starch.starch synthase'
45	AA	4	172891786	82.70364317	8	-0.057980397	4988	'29.4'	grmzm2g111491_t01	'protein.postranslational modification'

46	AA	4	238824264	119.1769941	5	-0.040095238	913	'10.6.3'	grmzm2g029566_t03	'cell wall.degradation.pectate lyases and polygalacturonases'
47	AA	4	245327128	141.6682023	5	-0.092328356	20431	'29.4.1.57'	grmzm2g025127_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
48	AA	5	1122	-0.317541556	5	0.044960637	457	'28.1'	grmzm2g356204_t01	'DNA.synthesis/chromatin structure'
49	AA	5	1049462	0.606846713	32	0.05132495	11455	'30.1'	grmzm2g012229_t01	'signalling.in sugar and nutrient physiology'
50	AA	5	1621759	2.147079874	12	0.055070047	2989	'29.3.3'	grmzm2g326272_t01	'protein.targeting.chloroplast'
51	AA	5	2598377	6.596313039	23	0.043582718	5950	'16.8.3'	grmzm2g110881_t04	'secondary metabolism.flavonoids.dihydroflavonols'
52	AA	5	2608498	6.662437668	8	0.045011664	81658	'16.8.3'	grmzm2g107076_t01	'secondary metabolism.flavonoids.dihydroflavonols'

53	AA	5	25375392	54.32828941	25	0.052640963	201693	'34.16'	grmzm2g177314_t01	'transport.ABC transporters and multidrug resistance systems'
54	AA	5	27056845	54.96362449	17	0.05259327	5051	'30.2.17'	grmzm2g102862_t01	'signalling.receptor kinases.DUF 26'
55	AA	5	27066959	54.96744605	6	0.0486529	189913	'27.3.50'	grmzm2g001887_t03	'RNA.regulation of transcription.General Transcription'
56	AA	5	27983433	55.3137347	6	0.164199593	85509	'29.2.3'	grmzm2g369939_t01	'protein.synthesis.initiation'
57	AA	5	28303009	55.43448613	8	0.241124487	196874	'27.3.1'	grmzm2g018336_t01	'RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing transcription factor family'
58	AA	5	29915257	56.04367218	6	0.057108904	138778	'27.1.1'	grmzm2g324540_t01	'RNA.processing.splicing'
59	AA	5	30338901	56.28511551	23	0.221984742	30144	'28.99'	grmzm2g132595_t01	'DNA.unspecified'
60	AA	5	30990738	56.84135946	15	0.062976606	142028	'31.1'	grmzm2g015861_t01	'cell.organisation'
61	AA	5	31224995	57.04126226	6	0.071656737	36825	'26.10'	grmzm2g122654_t01	'misc.cytochrome P450'

62	AA	5	61094522	63.52954633	39	0.213909802	35417	'29.4'	grmzm2g069970_t01	'protein.postranslational modification'
63	AA	5	89493802	69.57132155	5	-0.046703904	134590	'16.7'	grmzm2g083526_t01	'secondary metabolism.wax'
64	AA	5	185678096	95.1872289	9	-0.087360449	9409	'29.4'	grmzm2g096753_t01	'protein.postranslational modification'
65	AA	5	191362737	100.706813	70	0.073417146	23698	'34.19.2'	grmzm2g056908_t01	'transport.Major Intrinsic Proteins.TIP'
66	AA	5	200532850	108.3793509	5	-0.123414326	65284	'23.1.1.1'	grmzm2g147450_t01	'nucleotide metabolism.synthesis.pyrimidine.carbamoyl phosphate synthetase'
67	AA	5	202772744	110.6933233	16	-0.07001925	1104	'31.1'	grmzm2g382341_t01	'cell.organisation'
68	AA	5	204749015	116.8860416	7	0.083646321	10490	'26.28'	grmzm2g335280_t01	'misc.GDSL-motif lipase'
69	AA	5	206467622	122.460663	14	-0.121162674	142821	'21.4'	grmzm2g118366_t01	'redox.glutaredoxins'
70	AA	5	207521465	125.022936	8	-0.056063751	2581	'26.7'	grmzm2g059958_t01	'misc.oxidases - copper, flavone etc.'

71	AA	5	207525531	125.0317036	16	-0.085116692	31210	'20.2.3'	grmzm2g140893_t01	'stress.abiotic.drought/salt'
72	AA	5	209222556	128.3660113	6	-0.173721735	19237	'29.4'	grmzm2g058220_t01	'protein.postranslational modification'
73	AA	5	211196887	135.9702305	23	-0.069770475	32042	'29.5.1'	grmzm2g163749_t01	'protein.degradation.subtilases'
74	AA	5	211196920	135.9703687	64	-0.080191679	32009	'29.5.1'	grmzm2g163749_t01	'protein.degradation.subtilases'
75	AA	6	3992126	-6.319411877	5	-0.093170865	28316	'10.6.1'	grmzm2g009025_t01	'cell wall.degradation.cellulases and beta -1,4-glucanases'
76	AA	6	25737849	7.832137091	22	-0.098932689	1298673	'20.1'	grmzm2g454556_t01	'stress.biotic'
77	AA	6	31537911	8.165545093	17	-0.116422372	254806	'16.1.5'	grmzm2g451187_t01	'secondary metabolism.isoprenoids.terpenoids'
78	AA	6	79774320	11.21454839	11	-0.073829076	41338	'29.5.11.20'	grmzm2g120047_t01	'protein.degradation.ubiquitin.proteasom'
79	AA	6	97578306	23.60510141	10	-0.064507888	226232	'29.4.1.57'	grmzm2g162531_t03	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'

80	AA	6	97988317	23.94996475	41	-0.052440749	145359	'34.15'	grmzm2g146760_t01	'transport.potassium'
81	AA	6	98199018	24.12718696	9	-0.053340471	19651	'29.5.1'	grmzm2g073223_t01	'protein.degradation.subtilases'
82	AA	6	98204433	24.13174155	5	-0.05362577	14236	'29.5.1'	grmzm2g073223_t01	'protein.degradation.subtilases'
83	AA	6	98282571	24.19746402	8	-0.0579035	169857	'30.2.17'	grmzm2g082112_t01	'signalling.receptor kinases.DUF 26'
84	AA	6	99986756	25.63086689	5	-0.061329207	91970	'31.1'	grmzm2g092895_t01	'cell.organisation'
85	AA	6	110900537	37.5884191	5	-0.050221184	68	'27.3.11'	grmzm2g016744_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
86	AA	6	163949428	95.77601009	10	0.05979466	5983	'29.2.1.1.1.2.21'	grmzm2g085675_t01	'protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L21'
87	AA	6	164286396	96.9462491	7	0.091622048	8890	'27.3.30'	grmzm2g157219_t01	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
88	AA	6	165260207	101.8645066	9	0.099911569	43458	'18.7'	grmzm2g141252_t01	'Co-factor and vitamine metabolism.iron-sulphur clusters'
89	AA	7	27056327	46.72949889	30	0.069854871	269375	'34.13'	grmzm2g156794_t01	'transport.peptides and oligopeptides'

90	AA	7	28113557	46.92394381	6	0.042729427	2898	'17.2.1'	grmzm2g016958_t01	'hormone metabolism.auxin.synthesis-degradation'
91	AA	7	28365776	46.97033173	8	0.044151146	74629	'27.1'	grmzm2g144618_t01	'RNA.processing'
92	AA	7	37151920	48.23780461	7	0.043532305	412670	'27.3.11'	grmzm2g443109_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
93	AA	7	69012950	49.23292513	5	0.055519521	20987	'26.28'	grmzm2g101117_t01	'misc.GDSL-motif lipase'
94	AA	7	83079854	49.85510044	8	0.04954641	215855	'30.2.8.2'	grmzm2g011526_t01	'signalling.receptor kinases.leucine rich repeat VIII-2'
95	AA	7	84174593	49.90284891	8	0.04989524	309569	'30.2.99'	grmzm2g354621_t02	'signalling.receptor kinases.misc'
96	AA	7	139404320	77.80580845	69	0.087922424	233476	'34.1'	grmzm2g114704_t01	'transport.p- and v-ATPases'
97	AA	7	143287112	81.20148454	20	0.054812272	27741	'31.1'	grmzm2g117603_t01	'cell.organisation'
98	AA	7	150564610	88.45717741	32	0.06982965	62866	'10.2.1'	grmzm2g339645_t01	'cell wall.cellulose synthesis.cellulose synthase'

99	AA	7	167987389	129.6248256	6	-0.118145535	257	'33.99'	grmzm2g181605_t01	'development.unspecified'
100	AA	7	169227583	134.2608759	5	-0.06723496	158440	'13.1.3.5.5'	grmzm2g140824_t01	'amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate decarboxylase'
101	AA	8	103390158	58.85914851	73	0.067148754	409	'27.3.67'	grmzm2g087451_t01	'RNA.regulation of transcription.putative transcription regulator'
102	AA	8	117265267	63.49683053	11	0.076581176	7298	'27.3.99'	grmzm2g065566_t01	'RNA.regulation of transcription.unclassified'
103	AA	8	161883485	91.64355886	10	-0.044006499	672	'27.3.55'	ac183950.2_fgt003	'RNA.regulation of transcription.HDA'
104	AA	8	161918620	91.67206646	11	-0.049289191	66642	'29.5.11.4.2'	grmzm2g065893_t01	'protein.degradation.ubiquitin.E3.RING'
105	AA	8	161918881	91.67227822	36	-0.053035985	66381	'29.5.11.4.2'	grmzm2g065893_t01	'protein.degradation.ubiquitin.E3.RING'
106	AA	8	161918960	91.67234232	7	-0.052130376	66302	'29.5.11.4.2'	grmzm2g065893_t01	'protein.degradation.ubiquitin.E3.RING'
107	AA	8	163479600	95.34210376	11	-0.050996234	1042	'29.4'	grmzm2g472991_t04	'protein.postranslational modification'
108	AA	8	170533744	122.5329248	12	-0.071952615	9592	'27.3.11'	grmzm2g139160_t01	'RNA.regulation of transcription.C2H2 zinc finger family'

109	AA	8	170538447	122.5649034	10	-0.073601987	4889	'27.3.11'	grmzm2g139160_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
110	AA	8	170538683	122.5665081	58	-0.067975625	4653	'27.3.11'	grmzm2g139160_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
111	AA	9	5956414	5.403679997	8	-0.064234269	43386	'27.3.99'	grmzm2g019291_t01	'RNA.regulation of transcription.unclassified'
112	AA	9	6999573	8.221311595	5	-0.059674728	109097	'27.2'	grmzm2g017537_t01	'RNA.transcription'
113	AA	9	7239482	8.869319404	9	-0.047569805	87	'17.7.1.5'	grmzm2g000236_t01	'hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase'
114	AA	9	7239499	8.869365322	5	-0.043097808	70	'17.7.1.5'	grmzm2g000236_t01	'hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase'
115	AA	9	9143611	13.42656327	6	-0.065774986	178043	'31.3'	ac213896.2_fgt005	'cell.cycle'
116	AA	9	9143948	13.42709594	23	-0.0560366	177706	'31.3'	ac213896.2_fgt005	'cell.cycle'

117	AA	9	20663923	36.69381857	30	-0.056366108	77279	'29.4.1.59'	grmzm2g433433_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase IX'
118	AA	9	20665105	36.69570972	16	-0.062945098	76097	'29.4.1.59'	grmzm2g433433_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase IX'
119	AA	9	20668477	36.70110477	32	-0.060619679	72725	'29.4.1.59'	grmzm2g433433_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase IX'
120	AA	9	23215839	39.99840064	20	-0.058749345	16135	'27.3.27'	grmzm2g171395_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
121	AA	9	86468357	46.72572703	12	-0.079201882	150217	'27.2'	grmzm2g570791_t01	'RNA.transcription'
122	AA	9	116766687	57.30110688	5	0.11081529	47008	'29.5'	grmzm2g320206_t01	'protein.degradation'
123	AA	9	116766688	57.30110724	6	0.112627991	47007	'29.5'	grmzm2g320206_t01	'protein.degradation'
124	AA	9	133018761	68.62115268	53	-0.087203152	71041	'30.5'	grmzm2g078933_t01	'signalling.G-proteins'

125	AA	9	135396489	72.43328428	16	-0.066126002	1283	'31.4'	grmzm2g114126_t02	'cell.vesicle transport'
126	AA	9	140748270	85.13070924	14	0.115475213	81	'20.1'	grmzm2g393507_t02	'stress.biotic'
127	AA	10	18523635	33.86783022	6	-0.110952691	191354	'20.2.1'	grmzm2g068316_t01	'stress.abiotic.heat'
128	AA	10	99357506	43.32459092	9	-0.055016754	25855	'29.5.1'	grmzm2g157313_t01	'protein.degradation.subtilases'
129	AA	10	102164870	43.55066643	36	-0.048664179	27252	'33.99'	ac204711.3_fgt003	'development.unspecified'
130	AA	10	102628153	43.57658233	13	-0.054721851	464136	'27.3.99'	grmzm2g001265_t01	'RNA.regulation of transcription.unclassified'
131	AA	10	111326819	44.71918576	13	-0.049289342	279441	'9.5'	grmzm2g023194_t01	'mitochondrial electron transport / ATP synthesis.cytochrome c reductase'

132	AA	10	140890733	72.76364342	23	0.113234282	18825	'27.3.32'	grmzm2g091331_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
133	AA	10	143035801	79.92097141	6	0.075903997	14030	'29.4'	grmzm2g148506_t01	'protein.postranslational modification'
134	AA	10	146203306	89.79952703	10	0.075504717	21376	'18.1.1'	grmzm2g067176_t01	'Co-factor and vitamine metabolism.molybdenum cofactor.gephyrin'
135	AA	10	146234149	89.92263189	71	0.074311201	3423	'29.5.11.20'	grmzm2g368908_t01	'protein.degradation.ubiquitin.proteasom'
136	AA	10	148094143	99.83248299	14	0.059544285	8364	'11.1.8'	grmzm2g074759_t01	'lipid metabolism.FA synthesis and FA elongation.acyl coa ligase'
137	AA	10	148490503	102.0543415	7	0.053929166	2882	'29.4'	grmzm2g104658_t08	'protein.postranslational modification'
138	AA	10	148496397	102.0873812	22	0.050154105	4256	'29.5.11.4.3.2'	grmzm2g104882_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
139	Chla	1	64135223	73.46224774	7	-1.078365591	34467	'26.10'	grmzm2g084407_t01	'misc.cytochrome P450'

140	Chla	1	68902676	76.2644894	18	-1.11398638	236	'11.8.4'	grmzm2g009435_t01	'lipid metabolism."exotics" (steroids, squalene etc).3-beta hydroxysteroid dehydrogenase/isomerase'
141	Chla	1	70951065	77.30587192	7	-1.009978169	234962	'27.3.37'	grmzm2g060544_t01	'RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family'
142	Chla	1	71560037	77.6154678	8	-1.079988686	77821	'26.2'	ac177908.3_fgt002	'misc.UDP glucosyl and glucoronyl transferases'
143	Chla	1	114166513	89.09571398	6	-1.00096502	67003	'11.9.2.2'	grmzm2g110198_t01	'lipid metabolism.lipid degradation.lipases.acylglycerol lipase'
144	Chla	1	126428605	89.3753375	5	-1.429246348	1064	'29.2.1.2.1.4'	grmzm2g159228_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4'
145	Chla	1	139906399	89.5123698	6	-1.832781348	85909	'29.4.1.57'	grmzm2g004572_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
146	Chla	1	179696720	96.44277983	6	2.546725312	128594	'11.8'	grmzm2g093828_t01	'lipid metabolism."exotics" (steroids, squalene etc)'
147	Chla	1	280711700	175.6831083	16	-1.675800132	41478	'27.3.22'	grmzm2g135447_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'

148	Chla	1	283540151	178.0419378	6	-1.065382143	438718	'29.3.4.99'	grmzm2g361220_t01	'protein.targeting.secretory pathway.unspecified'
149	Chla	1	283829657	178.2988059	23	-1.082471106	149212	'29.3.4.99'	grmzm2g361220_t01	'protein.targeting.secretory pathway.unspecified'
150	Chla	1	283830436	178.2994971	6	-1.062943975	148433	'29.3.4.99'	grmzm2g361220_t01	'protein.targeting.secretory pathway.unspecified'
151	Chla	1	284054336	178.4981554	14	-1.146037697	1528	'7.3'	grmzm2g058760_t01	'OPP.electron transfer'
152	Chla	2	1944162	3.262633877	5	0.896831894	14386	'27.3.99'	grmzm2g068177_t01	'RNA.regulation of transcription.unclassified'
153	Chla	2	2021345	3.611041843	12	0.871536011	150	'30.11'	grmzm2g040115_t01	'signalling.light'
154	Chla	2	2211569	4.4697226	48	0.962856414	42543	'27.3.4'	grmzm2g078274_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
155	Chla	2	3128671	6.982329207	6	0.876581025	35163	'31.2'	grmzm2g119773_t01	'cell.division'
156	Chla	2	23800488	55.83244658	6	1.46067929	154339	'31.2'	grmzm2g124371_t01	'cell.division'

157	Chla	2	23881650	55.91619654	8	1.16323104	73177	'31.2'	grmzm2g124371_t01	'cell.division'
158	Chla	2	24284899	56.33230369	13	1.367200877	26939	'33.99'	grmzm2g434557_t01	'development.unspecified'
159	Chla	2	24312309	56.3605877	7	1.310766647	61877	'27.1.19'	grmzm2g064124_t01	'RNA.processing.ribonucleases'
160	Chla	2	25437487	57.05362901	6	1.199994036	226579	'33.99'	ac212859.3_fgt008	'development.unspecified'
161	Chla	2	25437559	57.05368243	5	1.144917046	226507	'33.99'	ac212859.3_fgt008	'development.unspecified'
162	Chla	2	26691735	57.98437622	14	1.092321355	681	'27.1'	grmzm2g171410_t01	'RNA.processing'
163	Chla	2	26773008	58.04468695	6	0.928679226	23344	'16.2'	grmzm2g362413_t01	'secondary metabolism.phenylpropanoids'
164	Chla	2	44156463	69.46377693	6	-2.024801273	41	'26.2'	grmzm2g009125_t01	'misc.UDP glucosyl and glucoronyl transferases'

165	Chla	2	175505228	86.58930765	7	1.255193753	5723	'21.2.1'	grmzm2g557799_t01	'redox.ascorbate and glutathione.ascorbate'
166	Chla	3	13632616	40.54644966	5	0.97166907	45498	'29.4'	grmzm2g129482_t01	'protein.postranslational modification'
167	Chla	3	17328400	45.32523697	9	1.191986808	44204	'16.7'	grmzm2g438938_t01	'secondary metabolism.wax'
168	Chla	3	20129322	48.94693416	8	1.760642777	26330	'20.2.1'	grmzm2g437100_t01	'stress.abiotic.heat'
169	Chla	3	27862522	53.36115573	10	1.423867597	7912	'29.5.11.4.2'	ac183315.4_fgt006	'protein.degradation.ubiquitin.E3.RING'
170	Chla	3	142821459	64.10032051	8	2.211347578	132510	'31.4'	grmzm2g016368_t01	'cell.vesicle transport'
171	Chla	3	176382057	87.28804733	7	2.673712072	45625	'11.3'	grmzm2g083195_t01	'lipid metabolism.Phospholipid synthesis'
172	Chla	3	212248700	123.3041123	17	-1.457436983	94418	'6.3'	grmzm2g466833_t01	'gluconeogenesis.Malate DH'
173	Chla	3	213848077	126.6554907	48	-1.687766558	40822	'1.5.1'	grmzm2g121878_t01	'PS.carbon concentrating mechanism.C4'

174	Chla	3	213848298	126.6560335	10	-1.668877969	40601	'1.5.1'	grmzm2g121878_t01	'PS.carbon concentrating mechanism.C4'
175	Chla	3	213894582	126.7697196	24	-1.531651849	55085	'27.3.69'	grmzm2g047695_t02	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
176	Chla	3	214166666	127.4380314	10	-1.452335655	106016	'27.3.25'	grmzm2g143328_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
177	Chla	3	214171011	127.4487039	27	-1.512209361	101671	'27.3.25'	grmzm2g143328_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
178	Chla	3	215371494	129.1375553	18	-1.61194824	37510	'26.10'	grmzm2g370745_t01	'misc.cytochrome P450'
179	Chla	3	215732765	129.6435644	14	-1.22775052	48141	'20.2.1'	grmzm2g089525_t01	'stress.abiotic.heat'
180	Chla	4	25857163	48.23906117	17	1.151000831	525	'29.5.11.4.5.2'	grmzm2g026724_t01	'protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ'
181	Chla	4	33663511	51.99288995	5	1.206422642	93904	'27.1.19'	grmzm2g394747_t01	'RNA.processing.ribonucleases'

182	Chla	4	35498708	52.93310614	10	1.229496466	95381	'27.3.65'	grmzm2g118205_t01	'RNA.regulation of transcription.Polycomb Group (PcG)'
183	Chla	4	36054065	53.09837236	5	1.000540179	91120	'31.4'	grmzm2g390489_t01	'cell.vesicle transport'
184	Chla	4	172424061	81.94381184	13	-3.771641365	38358	'30.3'	grmzm2g125838_t01	'signalling.calcium'
185	Chla	4	177225726	88.56915079	8	-1.412797811	89989	'27.3.67'	grmzm2g475583_t01	'RNA.regulation of transcription.putative transcription regulator'
186	Chla	4	177329556	88.69420796	10	-2.097767711	874	'17.2.3'	grmzm2g475683_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
187	Chla	4	177855845	90.07794504	8	-2.176405818	117764	'27.3.24'	grmzm2g370777_t01	'RNA.regulation of transcription.MADS box transcription factor family'
188	Chla	5	166987510	78.8793885	5	-2.122907288	16853	'30.2.17'	grmzm2g496370_t01	'signalling.receptor kinases.DUF 26'
189	Chla	5	189389642	98.99515772	8	-1.297088271	802	'27.3.7'	grmzm2g110541_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
190	Chla	5	205646722	119.7979212	13	-1.057085938	111140	'10.7'	grmzm2g105844_t01	'cell wall.modification'

191	Chla	5	205662084	119.8477507	30	-1.106120646	95778	'10.7'	grmzm2g105844_t01	'cell wall.modification'
192	Chla	5	205842860	120.4341313	9	-1.314471195	51773	'33.99'	grmzm2g100593_t01	'development.unspecified'
193	Chla	5	208092874	126.5365424	8	-1.242235214	26539	'29.5.11.4.2'	grmzm2g323013_t01	'protein.degradation.ubiquitin.E3.RING'
194	Chla	5	208411778	126.7985254	6	-1.034251892	45087	'29.6'	grmzm2g015784_t01	'protein.folding'
195	Chla	5	212548689	141.0955085	7	-1.625212605	15909	'29.2.3'	grmzm2g119691_t01	'protein.synthesis.initiation'
196	Chla	6	125640414	46.48436302	14	-2.050901443	80901	'26.28'	grmzm2g150187_t01	'misc.GDSL-motif lipase'
197	Chla	6	125640415	46.48436337	17	-2.07079645	80900	'26.28'	grmzm2g150187_t01	'misc.GDSL-motif lipase'
198	Chla	6	159559960	82.11064054	5	-0.859575964	72737	'20.2.99'	grmzm2g040517_t01	'stress.abiotic.unspecified'

199	Chla	7	33122197	47.86676722	19	1.636985743	169515	'26.21'	grmzm2g000221_t01	'misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein'
200	Chla	7	35108196	48.14677419	7	2.022809364	96849	'15.2'	grmzm2g042692_t01	'metal handling.binding, chelation and storage'
201	Chla	7	35397449	48.15875943	7	1.157786171	89645	'28.99'	grmzm2g364697_t01	'DNA.unspecified'
202	Chla	7	42768959	48.86677354	5	0.867518993	3169	'27.2'	grmzm2g146331_t01	'RNA.transcription'
203	Chla	7	125979602	66.69618807	7	2.632081769	83415	'20.2.1'	grmzm2g069651_t01	'stress.abiotic.heat'
204	Chla	7	157918090	102.0917472	6	1.307677429	12528	'30.5'	grmzm2g050501_t01	'signalling.G-proteins'
205	Chla	8	8405589	21.20394308	18	1.770676205	13355	'26.3'	ac234160.1_fgt003	'misc.gluco-, galacto- and mannosidases'
206	Chla	9	21661674	38.29017663	5	-1.285619712	2138	'10.1.7'	grmzm2g115124_t01	'cell wall.precursor synthesis.GMD'
207	Chla	9	21670412	38.30415705	15	-1.744014465	71062	'29.5.4'	grmzm2g144440_t01	'protein.degradation.aspartate protease'

208	Chla	9	23215197	39.99779948	11	-1.046360749	16777	'27.3.27'	grmzm2g171395_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
209	Chla	9	26434264	43.26084016	59	-1.065132951	63090	'20.2.1'	grmzm2g152373_t01	'stress.abiotic.heat'
210	Chla	10	143379980	80.93578714	10	1.736257572	329403	'31.3'	grmzm2g366270_t01	'cell.cycle'
211	Chla	10	145845320	88.37068362	8	1.167874183	1942	'27.3.28'	grmzm2g058588_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
212	Chla	10	148232936	100.610509	8	1.106911557	45256	'27.1.19'	grmzm2g177340_t01	'RNA.processing.ribonucleases'
213	Chla	10	148450393	101.8294985	36	1.201764063	34390	'13.1.4.4'	grmzm2g104613_t01	'amino acid metabolism.synthesis.branched chain group.leucine specific'
214	Chla	10	148497003	102.0907782	6	1.10547339	3650	'29.5.11.4.3.2'	grmzm2g104882_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
215	Chla	10	148499295	102.1036264	9	1.10891694	1358	'29.5.11.4.3.2'	grmzm2g104882_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
216	Chlb	1	97031439	87.3597852	18	0.627113181	154744	'20.2.1'	grmzm2g367023_t01	'stress.abiotic.heat'

217	Chlb	1	101441507	87.90304019	5	0.237222688	707312	'10.7'	grmzm2g070271_t01	'cell wall.modification'
218	Chlb	1	103855930	88.27009228	13	0.528617492	654699	'11.3.6'	grmzm2g132898_t01	'lipid metabolism.Phospholipid synthesis.choline-phosphate cytidylyltransferase'
219	Chlb	1	138458661	89.49765026	6	0.636936144	65479	'29.3.4.4'	grmzm2g014872_t01	'protein.targeting.secretory pathway.plasma membrane'
220	Chlb	1	141762525	89.53124152	15	0.677150275	787856	'27.4'	grmzm2g152526_t01	'RNA.RNA binding'
221	Chlb	1	146716486	89.58160975	18	37.87537959	89791	'33.99'	grmzm2g432850_t01	'development.unspecified'
222	Chlb	1	150498647	89.94777187	5	0.650291443	237911	'13.1.3.5.4'	grmzm2g130332_t01	'amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate epimerase'
223	Chlb	1	163239765	91.63742221	8	0.375622346	703536	'20.1'	grmzm2g443525_t01	'stress.biotic'
224	Chlb	1	181947110	97.49187685	6	-0.41770935	848	'27.4'	grmzm2g023591_t02	'RNA.RNA binding'
225	Chlb	1	187131514	101.742233	14	-0.546446647	71893	'30.3'	ac213857.4_fgt003	'signalling.calcium'

226	Chlb	1	202975799	116.1587985	10	-0.587258205	38265	'10.7'	grmzm2g106899_t01	'cell wall.modification'
227	Chlb	1	205257253	117.519266	7	-0.562896571	168	'27.3.11'	grmzm2g104516_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
228	Chlb	1	225624776	133.6401321	12	-0.665556716	79527	'30.4.1'	grmzm2g374973_t01	'signalling.phosphinositides.phosphatidylinositol-4-phosphate 5-kinase'
229	Chlb	1	228532522	135.6859584	17	-0.333710526	344103	'27.3.99'	grmzm2g014676_t01	'RNA.regulation of transcription.unclassified'
230	Chlb	1	285864445	180.8598811	14	-1.175768963	33886	'28.1'	grmzm2g371210_t01	'DNA.synthesis/chromatin structure'
231	Chlb	1	291825337	191.0554431	5	1.628826253	105497	'29.5'	grmzm2g155580_t01	'protein.degradation'
232	Chlb	1	294322791	196.7251432	76	0.398027959	3747	'11.3'	grmzm2g156729_t01	'lipid metabolism.Phospholipid synthesis'
233	Chlb	1	294652893	197.2197826	22	-15.83957184	213077	'29.3.3'	grmzm2g448523_t01	'protein.targeting.chloroplast'

234	Chlb	1	296022922	199.7554621	13	5.61697755	26029	'29.2.5'	grmzm2g304638_t01	'protein.synthesis.release'
235	Chlb	1	299894464	204.0221873	84	3.122396653	242700	'31.1'	grmzm2g160578_t01	'cell.organisation'
236	Chlb	2	5923229	18.30060959	6	-0.432741117	86894	'34.22'	grmzm2g023037_t01	'transport.cyclic nucleotide or calcium regulated channels'
237	Chlb	2	6166067	18.83309554	9	-0.313343721	10281	'27.3.6'	grmzm2g072820_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
238	Chlb	2	69741938	75.18951102	10	0.13773773	87347	'33.99'	grmzm2g179106_t01	'development.unspecified'
239	Chlb	2	148856409	80.60314611	22	8.071915262	27904	'27.3.32'	grmzm2g400559_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
240	Chlb	2	149429597	80.70039502	22	-9.971712092	264303	'29.4'	grmzm2g153675_t01	'protein.postranslational modification'
241	Chlb	2	161877261	82.49985253	8	-4.135727968	137361	'28.1.3'	grmzm2g442555_t01	'DNA.synthesis/chromatin structure.histone'
242	Chlb	2	172704855	85.0182288	5	0.153284287	102147	'26.2'	grmzm2g110816_t01	'misc.UDP glucosyl and glucoronyl transferases'
243	Chlb	2	185915577	96.74331495	10	0.145544258	45600	'29.4'	grmzm2g026065_t01	'protein.postranslational modification'

244	Chlb	2	186273082	97.1970181	7	0.137513277	18	'27.3.16'	grmzm2g022162_t01	'RNA.regulation of transcription.CCAAT box binding factor family, HAP5'
245	Chlb	2	186375668	97.32720814	5	0.150539465	132807	'20.2.1'	grmzm2g112165_t01	'stress.abiotic.heat'
246	Chlb	2	191111571	102.3694697	8	0.135633799	12708	'9.9'	grmzm2g530263_t01	'mitochondrial electron transport / ATP synthesis.F1-ATPase'
247	Chlb	2	192123634	103.2729858	11	0.120175148	64711	'31.1'	grmzm2g015395_t01	'cell.organisation'
248	Chlb	3	139536229	63.68477456	6	0.147217046	131110	'27.3.25'	grmzm2g369799_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
249	Chlb	3	144468014	65.40015782	12	0.134612198	106582	'31.2'	grmzm2g125642_t01	'cell.division'
250	Chlb	3	147011536	66.05909566	44	0.123495734	1717	'27.3.21'	grmzm2g082387_t01	'RNA.regulation of transcription.GRAS transcription factor family'
251	Chlb	3	148514014	66.58736723	21	0.148804648	157683	'11.5.2'	grmzm2g155348_t01	'lipid metabolism.glyceral metabolism.Glycerol-3-phosphate dehydrogenase (NAD
252	Chlb	3	212765471	123.9963177	8	-0.336927049	177172	'34.8'	grmzm2g064473_t01	'transport.metabolite transporters at the envelope membrane'

253	Chlb	3	216243829	131.9068925	14	-0.259823327	10027	'26.2'	grmzm2g053047_t01	'misc.UDP glucosyl and glucoronyl transferases'
254	Chlb	4	10192700	27.53975118	5	-0.334206161	9760	'27.3.99'	grmzm2g068331_t01	'RNA.regulation of transcription.unclassified'
255	Chlb	4	10198136	27.55916751	33	-0.283755098	4324	'27.3.99'	grmzm2g068331_t01	'RNA.regulation of transcription.unclassified'
256	Chlb	4	10624506	29.08207781	6	-0.499306784	9304	'20.1'	grmzm2g426306_t01	'stress.biotic'
257	Chlb	4	154415397	65.4507691	5	-0.310092928	83660	'31.1'	grmzm2g137029_t01	'cell.organisation'
258	Chlb	4	157107343	68.51092069	5	-0.175013014	3155	'31.4'	grmzm2g054354_t01	'cell.vesicle transport'
259	Chlb	4	159175723	70.53286161	16	-0.172099323	135692	'29.4'	grmzm2g110483_t01	'protein.postranslational modification'
260	Chlb	4	241996729	128.0064472	6	3.240118253	782	'13.2.5.3'	grmzm2g168888_t13	'amino acid metabolism.degradation.serine-glycine-cysteine group.cysteine'
261	Chlb	4	242374367	129.5365429	7	-2.331473365	95639	'29.5.11.1'	grmzm2g118637_t01	'protein.degradation.ubiquitin.ubiquitin'
262	Chlb	4	245553732	143.0029237	5	0.469486536	70	'27.2'	grmzm2g119393_t01	'RNA.transcription'

263	Chlb	5	2383652	5.193426861	6	-0.572992605	7015	'29.5.11.2'	grmzm2g002765_t02	'protein.degradation.ubiquitin.E1'
264	Chlb	5	6303981	23.51266789	6	0.790335738	567	'27.3.11'	grmzm2g035103_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
265	Chlb	5	20023828	50.73599959	10	0.15378392	60	'29.5.7'	grmzm2g062470_t01	'protein.degradation.metalloprotease'
266	Chlb	5	26723660	54.83773092	24	0.136021297	111423	'16.8.2'	grmzm2g477683_t01	'secondary metabolism.flavonoids.chalcones'
267	Chlb	5	35357979	58.09472562	36	0.135646841	10704	'29.5.11.4.3.2'	grmzm2g040182_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
268	Chlb	5	45813768	59.90312559	5	0.138663161	37674	'27.3.99'	grmzm2g148790_t01	'RNA.regulation of transcription.unclassified'
269	Chlb	6	162877409	92.80071368	5	0.254136304	22955	'17.4.1'	grmzm2g025429_t01	'hormone metabolism.cytokinin.synthesis-degradation'
270	Chlb	7	1921276	4.495740497	6	0.440671843	2128	'27.3.32'	grmzm2g018721_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
271	Chlb	7	2047654	4.972450239	9	0.308546552	33568	'27.3.24'	grmzm2g072582_t03	'RNA.regulation of transcription.MADS box transcription factor family'

272	Chlb	7	5043354	21.45653923	59	-0.623660171	31436	'30.4.1'	grmzm2g093705_t01	'signalling.phosphinositides.phosphatidylinositol-4-phosphate 5-kinase'
273	Chlb	7	5299542	22.83360349	5	-0.725829344	130930	'1.2.2'	grmzm2g129246_t01	'PS.photorespiration.glycolate oxydase'
274	Chlb	7	6484300	28.48085938	7	-0.385308166	259559	'17.3.1.1.1'	grmzm2g394968_t01	'hormone metabolism.brassinosteroid.synthesis-degradation.BRs.DET2'
275	Chlb	7	9145904	33.10358602	7	-0.455155264	67440	'27.3.17'	grmzm2g153754_t01	'RNA.regulation of transcription.CPP(Zn),CPP1-related transcription factor family'
276	Chlb	7	142898891	81.10232141	46	-0.930589021	196	'10.7'	grmzm2g413044_t01	'cell wall.modification'
277	Chlb	7	151513769	89.4065889	57	2.205527693	30683	'23.2'	grmzm2g036007_t01	'nucleotide metabolism.degradation'
278	Chlb	7	152461246	91.18872855	6	0.1813481	3469	'29.5.7'	ac213455.3_fgt008	'protein.degradation.metalloprotease'
279	Chlb	7	157011468	100.2121602	5	-1.389177806	1872	'17.2.3'	grmzm2g053338_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'

280	Chlb	7	157185116	100.5721631	5	-1.554880555	17355	'29.5.3'	grmzm2g049882_t01	'protein.degradation.cysteine protease'
281	Chlb	7	157532548	101.2924508	11	-1.522378582	299514	'27.4'	grmzm2g068255_t01	'RNA.RNA binding'
282	Chlb	7	164316372	116.7981854	5	-0.786680562	2495	'28.2'	grmzm2g356894_t01	'DNA.repair'
283	Chlb	7	167232557	126.3442442	8	0.152254886	131108	'3.8.2'	grmzm2g053554_t01	'minor CHO metabolism.galactose.alpha-galactosidases'
284	Chlb	7	167233412	126.3479602	14	0.1415427	130253	'3.8.2'	grmzm2g053554_t01	'minor CHO metabolism.galactose.alpha-galactosidases'
285	Chlb	8	926070	1.886736364	14	0.271650989	125736	'20.2.99'	grmzm2g103512_t01	'stress.abiotic.unspecified'
286	Chlb	8	1359223	2.966202574	8	0.123826391	74396	'31.4'	grmzm2g378906_t01	'cell.vesicle transport'
287	Chlb	8	99959295	57.50014689	6	-0.51065178	52151	'29.5.1'	grmzm2g055684_t01	'protein.degradation.subtilases'
288	Chlb	8	147589704	77.10076187	7	-0.197854431	91	'3.5'	grmzm2g178346_t01	'minor CHO metabolism.others'

289	Chlb	8	147830284	77.29378758		5	-0.28678081	79601	'27.3.22'	grmzm2g133972_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
290	Chlb	8	147830665	77.29409327		7	-0.289989168	79220	'27.3.22'	grmzm2g133972_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
291	Chlb	8	152152815	80.797802		13	-0.348119811	1266	'27.3.25'	grmzm2g003406_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
292	Chlb	9	8793952	12.87388515		8	-0.136620476	5123	'27.3.26'	grmzm2g371870_t01	'RNA.regulation of transcription.MYB-related transcription factor family'
293	Chlb	9	9141388	13.42304955		6	-0.254049865	134	'33.99'	grmzm2g088053_t01	'development.unspecified'
294	Chlb	9	23231768	40.03154801		10	-0.113528991	206	'27.3.27'	grmzm2g171395_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
295	Chlb	9	25023438	42.41159442		6	-0.114018927	16525	'30.2.16'	grmzm2g335052_t01	'signalling.receptor kinases.Catharanthus roseus-like RLK1'
296	Chlb	9	27036374	43.61692207		7	-0.146623845	1356	'29.2.1.2.2.9'	grmzm2g084739_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L9'
297	Chlb	9	64396713	45.73393561		5	-0.145382509	384975	'27.3.15'	grmzm2g121897_t01	'RNA.regulation of transcription.CCAAT box binding factor family, HAP3'

298	Chlb	9	74140456	45.9421654	15	-2166.549455	504839	'26.10'	grmzm2g138248_t01	'misc.cytochrome P450'
299	Chlb	9	85978653	46.6412055	5	-0.164686897	50748	'26.7'	grmzm2g099642_t01	'misc.oxidases - copper, flavone etc.'
300	Chlb	9	147213879	101.7957515	8	-0.318295344	9973	'29.4.1.57'	grmzm2g009869_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
301	Chlb	10	107950213	44.02050592	22	-0.311582186	96205	'33.99'	grmzm2g097106_t01	'development.unspecified'
302	Chlb	10	118129854	47.02366267	15	-0.228236332	41877	'27.3.6'	grmzm2g355469_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
303	Chlb	10	119651031	47.40080838	7	-0.115286868	5042	'27.3.30'	grmzm2g392168_t01	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
304	Chlb	10	129585091	52.11332474	32	0.256285226	47465	'27.1.20'	grmzm2g160473_t01	'RNA.processing.degradation dicer'
305	Chlb	10	132147651	55.92474833	6	0.240383766	13545	'26.2'	grmzm2g468661_t01	'misc.UDP glucosyl and glucoronyl transferases'
306	Chlb	10	148943495	104.5936596	7	-0.338495455	708	'29.3.1'	grmzm2g312026_t01	'protein.targeting.nucleus'
307	Chlb	10	149647673	108.5410404	6	-0.456258788				

308	Fruc	1	16386798	32.84963222	6	-0.013777599	31095	'29.4.1.57'	grmzm2g175164_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
309	Fruc	1	16770481	33.28017346	30	-0.015750944	1673	'11.1.10'	grmzm2g445602_t01	'lipid metabolism.FA synthesis and FA elongation.beta ketoacyl CoA synthase'
310	Fruc	1	16775647	33.28405569	10	-0.018370011	180133	'26.7'	grmzm2g000427_t01	'misc.oxidases - copper, flavone etc.'
311	Fruc	1	17461111	33.79917927	6	-0.014967229	105396	'33.99'	grmzm2g496991_t01	'development.unspecified'
312	Fruc	1	35272897	54.48195467	5	-0.029642508	18679	'20.1'	grmzm2g030422_t03	'stress.biotic'
313	Fruc	1	44348772	60.58908186	7	0.029290518	6195	'21.1'	grmzm2g073628_t01	'redox.thioredoxin'
314	Fruc	1	45121654	61.22096078	8	0.015684896	36601	'30.4.4'	grmzm2g114354_t01	'signalling.phosphinositides.phosphoinositide phospholipase C'
315	Fruc	1	45567426	61.52614689	14	0.019975229	19220	'29.4'	grmzm2g459824_t01	'protein.postranslational modification'
316	Fruc	1	46712396	62.60179969	5	0.013786727	40891	'27.1.1'	grmzm2g153450_t01	'RNA.processing.splicing'

317	Fruc	1	57438776	70.59917107	14	0.013567425	120153	'30.11'	grmzm2g158662_t01	'signalling.light'
318	Fruc	1	95550141	86.84633266	14	0.034688611	152072	'29.2.3'	grmzm2g174757_t01	'protein.synthesis.initiation'
319	Fruc	2	3327524	8.176087352	9	-0.011446215	26628	'31.3'	grmzm2g047590_t02	'cell.cycle'
320	Fruc	2	3529245	9.556599097	7	-0.011598842	14938	'16.8.3'	grmzm2g062396_t01	'secondary metabolism.flavonoids.dihydroflavonols'
321	Fruc	2	3534327	9.591591385	10	-0.012952906	9856	'16.8.3'	grmzm2g062396_t01	'secondary metabolism.flavonoids.dihydroflavonols'
322	Fruc	2	3794582	10.51648703	20	-0.013392911	51935	'34.16'	grmzm2g087201_t01	'transport.ABC transporters and multidrug resistance systems'
323	Fruc	2	4042572	11.15390606	18	-0.012020005	104796	'1.3.13'	grmzm2g039345_t01	'PS.calvin cycle.rubisco interacting'

324	Fruc	2	4663012	13.34691454	5	-0.011982641	12041	'30.11.1'	grmzm2g086801_t01	'signalling.light.COP9 signalosome'
325	Fruc	2	34001062	63.56397414	5	-0.011897479	1995	'20.1'	grmzm2g052175_t01	'stress.biotic'
326	Fruc	2	177151781	87.86279241	10	0.034341476	103361	'27.3.6'	grmzm2g176141_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
327	Fruc	2	177266143	87.95845923	6	0.046944656	358444	'29.4'	grmzm2g330049_t01	'protein.postranslational modification'
328	Fruc	2	181271307	91.1333845	7	0.046476341	81868	'26.10'	grmzm2g125482_t01	'misc.cytochrome P450'
329	Fruc	3	3386685	11.10786166	29	-0.021944149	16649	'27.3.52'	grmzm2g400907_t02	'RNA.regulation of transcription.Global transcription factor group'
330	Fruc	3	3903533	13.78234035	18	-0.016091322	39286	'17.6.1.13'	grmzm2g031432_t01	'hormone metabolism.gibberelin.synthesis-degradation.GA2 oxidase'
331	Fruc	3	4856540	18.3470876	47	-0.014548164	95949	'29.4'	grmzm2g477073_t01	'protein.postranslational modification'

332	Fruc	3	49918968	56.54435347	26	-0.016411713	285685	'29.4'	grmzm2g170120_t01	'protein.postranslational modification'
333	Fruc	3	171723196	82.25684086	47	0.040642762	1961	'1.2.5'	grmzm2g452630_t01	'PS.photorespiration.serine hydroxymethyltransferase'
334	Fruc	3	172148591	82.5754152	7	0.064075885	1267	'23.1.2.1'	grmzm2g339699_t01	'nucleotide metabolism.synthesis.purine.amidophosphoribosyltransferase'
335	Fruc	3	173110658	83.38629476	18	0.042818427	8042	'29.4'	grmzm2g110922_t01	'protein.postranslational modification'
336	Fruc	3	173219900	83.47836954	11	0.066010087	452174	'31.4'	grmzm2g439532_t01	'cell.vesicle transport'
337	Fruc	3	195593529	103.3189453	7	0.02012706	2132	'27.3.22'	grmzm2g314546_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
338	Fruc	3	196183579	103.6950757	5	0.011501099	3318	'3.2.3'	grmzm2g123277_t01	'minor CHO metabolism.trehalose.potential TPS/TPP'

339	Fruc	3	219127882	135.874024		20	-0.018693012	351	'29.4.1.59'	grmzm2g070961_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase IX'
340	Fruc	3	221010928	139.3762734		18	-0.017339804	8058	'10.5.3'	grmzm2g333811_t01	'cell wall.cell wall proteins.LRR'
341	Fruc	4	596627	2.14232426		45	0.025189271	12789	'27.3.11'	grmzm2g058868_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
342	Fruc	4	101026208	57.83942086		5	-0.028462957	783882	'27.3.73'	ac207890.3_fgt002	'RNA.regulation of transcription.Zn-finger(CCHC)'
343	Fruc	4	109554972	58.01578487		6	-0.014600631	734976	'29.2.1.2.2.14'	grmzm2g323971_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L14'
344	Fruc	4	118225032	58.20188033		8	-0.015380681	55874	'27.3.67'	grmzm2g009019_t02	'RNA.regulation of transcription.putative transcription regulator'
345	Fruc	4	121592260	58.27415502		6	-0.012488902	93412	'27.3.99'	grmzm2g069678_t01	'RNA.regulation of transcription.unclassified'
346	Fruc	4	121913511	58.2810504		6	-0.014513129	87386	'29.5.11.4.2'	grmzm2g041344_t01	'protein.degradation.ubiquitin.E3.RING'
347	Fruc	4	122028538	58.28351935		8	-0.012822806	118962	'18.3.1'	grmzm2g156803_t01	'Co-factor and vitamine metabolism.riboflavin.GTP cyclohydrolase II'

348	Fruc	4	125159697	58.42149244	5	-0.016269091	124040	'31.1'	grmzm2g145027_t01	'cell.organisation'
349	Fruc	4	139805548	59.87084184	6	-0.013396769	14614	'27.3.66'	grmzm2g020081_t01	'RNA.regulation of transcription.Psudo ARR transcription factor family'
350	Fruc	4	144536877	60.82876771	5	-0.01193395	142969	'16.5.1.3.3'	grmzm2g111225_t01	'secondary metabolism.sulfur-containing.glucosinolates.degradation.nitrilase'
351	Fruc	4	170738228	78.91944426	9	-0.027117788	17917	'29.4.1.57'	grmzm2g102163_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
352	Fruc	4	172300218	81.59892215	15	-0.0185491	585	'31.4'	grmzm2g054210_t01	'cell.vesicle transport'
353	Fruc	4	240477479	123.4579602	5	-0.05014372	27533	'28.2'	grmzm2g143462_t01	'DNA.repair'
354	Fruc	5	1571929	2.012971503	16	-0.012617453	1299	'17.2.1'	grmzm2g125552_t01	'hormone metabolism.auxin.synthesis-degradation'
355	Fruc	5	2279196	4.510973125	8	-0.011842701	8268	'29.4.1.57'	grmzm2g144042_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'

356	Fruc	5	2358292	5.027739617	38	-0.013396885	3764	'27.3.67'	grmzm2g003068_t01	'RNA.regulation of transcription.putative transcription regulator'
357	Fruc	5	2367917	5.090623676	8	-0.012236849	1502	'27.3.11'	grmzm2g002815_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
358	Fruc	5	163819573	76.76334725	49	0.022715483	1736	'17.2.3'	grmzm2g312274_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
359	Fruc	5	166171297	78.20073394	5	0.023811543	88984	'27.3.11'	grmzm2g320287_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
360	Fruc	5	204526436	116.1640652	41	0.018975985	1242	'10.6.1'	grmzm2g151257_t01	'cell wall.degradation.cellulases and beta -1,4-glucanases'
361	Fruc	5	206993797	123.8406652	29	0.022620899	7780	'33.99'	grmzm2g036286_t01	'development.unspecified'
362	Fruc	5	210780527	134.226701	7	0.0157951	163946	'27.3.67'	grmzm2g049194_t01	'RNA.regulation of transcription.putative transcription regulator'
363	Fruc	5	214945363	152.2635928	8	0.024738523	45426	'21.1'	grmzm2g003028_t01	'redox.thioredoxin'
364	Fruc	6	83413352	12.31842953	47	-0.016984936	100890	'20.2.3'	grmzm2g387935_t01	'stress.abiotic.drought/salt'
365	Fruc	6	93728026	20.25312295	19	-0.018294395	2352	'27.3.16'	grmzm2g161680_t01	'RNA.regulation of transcription.CCAAT box binding factor family, HAP5'
366	Fruc	6	117587976	42.56198959	5	-0.03397919	221907	'27.3.11'	grmzm2g435357_t01	'RNA.regulation of transcription.C2H2 zinc finger family'

367	Fruc	6	119772986	44.24786955	23	-0.033796984	121392	'30.1'	grmzm2g162788_t01	'signalling.in sugar and nutrient physiology'
368	Fruc	6	124203584	45.80014821	9	-0.025280441	191623	'11.8'	grmzm2g003064_t01	'lipid metabolism."exotics" (steroids, squalene etc)'
369	Fruc	6	128598095	47.52042761	5	-0.033664993	96115	'26.2'	grmzm2g458776_t01	'misc.UDP glucosyl and glucoronyl transferases'
370	Fruc	6	165119716	101.3985908	6	0.036582506	66369	'27.3.67'	grmzm2g128579_t03	'RNA.regulation of transcription.putative transcription regulator'
371	Fruc	6	166794282	106.9690738	8	-0.011678556	111528	'26.4'	grmzm2g163883_t01	'misc.beta 1,3 glucan hydrolases'
372	Fruc	6	166794417	106.9695432	5	-0.01610415	111393	'26.4'	grmzm2g163883_t01	'misc.beta 1,3 glucan hydrolases'

373	Fruc	7	6022883	26.56544125	7	-0.013079036	13738	'29.5.11.4.2'	grmzm2g029623_t01	'protein.degradation.ubiquitin.E3.RING'
374	Fruc	7	9213492	33.2209742	16	-0.018141284	13304	'10.5.3'	grmzm2g153741_t01	'cell wall.cell wall proteins.LRR'
375	Fruc	7	20233795	44.69829015	10	-0.017981407	2989	'27.3.69'	ac233961.1_fgt001	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
376	Fruc	7	21622999	45.56317348	15	-0.018042126	135788	'34.12'	grmzm2g093276_t01	'transport.metal'
377	Fruc	7	32630669	47.75472755	8	-0.017704491	3614	'31.3.1'	grmzm2g092072_t01	'cell.cycle.peptidylprolyl isomerase'
378	Fruc	7	84574592	49.92029539	9	-0.01885016	15252	'31.4'	grmzm2g360648_t01	'cell.vesicle transport'
379	Fruc	7	86294238	49.99529999	25	-0.016277961	102855	'29.4.1.57'	grmzm2g132184_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
380	Fruc	7	86760483	50.01070124	5	-0.018393153	31870	'9.9'	grmzm2g405751_t01	'mitochondrial electron transport / ATP synthesis.F1-ATPase'
381	Fruc	7	95364029	50.42762301	14	-0.019020479	977	'34.99'	grmzm2g176721_t01	'transport.misc'
382	Fruc	7	109178008	55.19093714	5	-0.016770261	409274	'30.5'	grmzm2g015349_t01	'signalling.G-proteins'

383	Fruc	7	156688517	99.54262593	5	0.025852571	50626	'26.22'	grmzm2g076981_t02	'misc.short chain dehydrogenase/reductase (SDR)'
384	Fruc	9	2701441	-3.388186607	10	-0.03407797	6507	'27.2'	grmzm2g180836_t01	'RNA.transcription'
385	Fruc	9	5619750	4.494331447	5	-0.026190353	334395	'28.1'	grmzm2g093772_t01	'DNA.synthesis/chromatin structure'
386	Fruc	9	9558874	14.08293641	31	-0.038288541	100236	'27.3.25'	grmzm2g005066_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
387	Fruc	9	10186494	15.44407336	7	-0.018017282	49289	'29.2.1.2.1.17'	grmzm2g086906_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S17'
388	Fruc	9	21993322	38.82079896	27	-0.037006124	45016	'4.1.13'	grmzm2g064302_t01	'glycolysis.cytosolic branch.enolase'
389	Fruc	9	142204786	87.72532368	30	-0.022131324	52062	'29.1.10'	grmzm2g143450_t01	'protein.aa activation.methionine-tRNA ligase'
390	Fruc	9	143828279	91.48003191	5	-0.020830478	184852	'33.1'	grmzm2g078441_t01	'development.storage proteins'
391	Fruc	9	145268207	95.10905936	8	-0.014832567	10980	'27.3.6'	ac233899.1_fgt002	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'

392	Fruc	10	5058530	14.79019912	28	-0.045641719	56738	'30.2.26'	grmzm2g051637_t01	'signalling.receptor kinases.crinkly like'
393	Fruc	10	5258877	16.0525304	31	-0.045423584	1765	'13.1.3.5.5'	grmzm2g020446_t01	'amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate decarboxylase'
394	Fruc	10	5571203	17.95328644	17	-0.045237542	119768	'34.3'	ac207755.3_fgt005	'transport.amino acids'
395	Fruc	10	11480453	29.34116571	8	-0.038039626	1754	'3.4.3'	grmzm2g392513_t01	'minor CHO metabolism.myo-inositol.InsP Synthases'
396	Fruc	10	134630447	59.4071156	7	-0.017295414	15764	'26.2'	grmzm2g031453_t01	'misc.UDP glucosyl and glucoronyl transferases'
397	Fuma	1	195285519	108.2877857	22	0.010497833	138707	'27.3.7'	grmzm2g159996_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
398	Fuma	1	195634638	108.6089505	6	0.010552372	5641	'27.3.3'	grmzm2g080565_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
399	Fuma	1	196048817	109.0223788	6	0.007421199	7116	'29.5.11.4.2'	grmzm2g053027_t01	'protein.degradation.ubiquitin.E3.RING'

400	Fuma	1	205544235	117.795721	14	-0.006686224	36816	'10.6.3'	grmzm2g154124_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
401	Fuma	1	205766088	118.0094361	13	-0.004995746	122379	'29.5.11.4.2'	grmzm2g112617_t01	'protein.degradation.ubiquitin.E3.RING'
402	Fuma	1	206425614	118.6447696	17	-0.005436419	20336	'20.1'	grmzm2g049057_t01	'stress.biotic'
403	Fuma	1	207121477	119.3151072	6	-0.00753724	153863	'20.2.99'	grmzm2g363004_t01	'stress.abiotic.unspecified'
404	Fuma	1	208533778	120.6233059	7	-0.007359341	2238	'20.2.1'	grmzm2g059502_t02	'stress.abiotic.heat'
405	Fuma	1	208593470	120.672802	13	-0.004806602	39346	'2.2.2.6'	grmzm2g053037_t01	'major CHO metabolism.degradation.starch.transporter'
406	Fuma	1	272244444	164.542002	10	0.003610726	67225	'20.1'	grmzm2g481194_t01	'stress.biotic'
407	Fuma	1	272244581	164.5421084	19	0.003781599	67088	'20.1'	grmzm2g481194_t01	'stress.biotic'
408	Fuma	1	289899574	186.9723092	6	0.002963805	2798	'27.3.99'	grmzm2g077079_t01	'RNA.regulation of transcription.unclassified'

409	Fuma	2	5934701	18.32576495	5	0.014046764	75422	'34.22'	grmzm2g023037_t01	'transport.cyclic nucleotide or calcium regulated channels'
410	Fuma	2	26788878	58.0564637	8	-0.007537765	7474	'16.2'	grmzm2g362413_t01	'secondary metabolism.phenylpropanoids'
411	Fuma	2	40887517	67.93546257	5	-0.004119967	71254	'30.2.99'	grmzm2g179268_t01	'signalling.receptor kinases.misc'
412	Fuma	2	101178551	76.43228188	6	-0.003508264	87613	'29.4.1.57'	grmzm2g463227_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
413	Fuma	2	126037868	77.45026254	6	-0.002840198	134222	'23.4.10'	grmzm2g001524_t01	'nucleotide metabolism.phosphotransfer and pyrophosphatases.nucleoside diphosphate kinase'
414	Fuma	2	126357762	77.49091538	7	-0.003825335	180624	'20.2.5'	grmzm2g046498_t01	'stress.abiotic.light'
415	Fuma	2	128572754	77.77240149	5	0.006664527	732083	'29.4'	grmzm2g416491_t01	'protein.postranslational modification'
416	Fuma	2	140085774	79.23550166	9	-0.003129574	177394	'29.5.11.4.3.2'	grmzm2g348855_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
417	Fuma	2	209368892	120.1686122	5	-0.003179256	84219	'3.2.2'	grmzm2g117564_t01	'minor CHO metabolism.trehalose.TPP'

418	Fuma	2	210076932	121.1450848	6	-0.005447489	52801	'27.3.25'	grmzm2g703373_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
419	Fuma	3	27871359	53.36404037	8	-0.003866516	37203	'34.19.3'	grmzm2g103214_t01	'transport.Major Intrinsic Proteins.NIP'
420	Fuma	3	223869464	146.0056611	18	0.010366321	89641	'21.1'	grmzm2g093436_t01	'redox.thioredoxin'
421	Fuma	3	223869468	146.0056712	5	0.01094552	89637	'21.1'	grmzm2g093436_t01	'redox.thioredoxin'
422	Fuma	4	3544388	12.18913098	8	-0.013932612	1313	'13.2.6.2'	grmzm2g006480_t01	'amino acid metabolism.degradation.aromatic aa.tyrosine'
423	Fuma	4	4653906	15.97068346	12	-0.008852558	11307	'29.2.1.2.2.57'	grmzm2g089830_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L7A'
424	Fuma	4	4655407	15.97579929	7	-0.008673224	9806	'29.2.1.2.2.57'	grmzm2g089830_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L7A'
425	Fuma	4	168642940	76.90973825	5	-0.005552603	1660	'27.3.67'	grmzm2g123887_t01	'RNA.regulation of transcription.putative transcription regulator'
426	Fuma	4	177728199	89.41877612	10	-0.003560153	11473	'10.3'	grmzm2g015983_t01	'cell wall.hemicellulose synthesis'

427	Fuma	4	177733636	89.446853		10	-0.002949415	6036	'10.3'	grmzm2g015983_t01	'cell wall.hemicellulose synthesis'
428	Fuma	4	179860377	92.79034271		8	-0.003276803	111398	'3.2.2'	grmzm2g151044_t01	'minor CHO metabolism.trehalose.TPP'
429	Fuma	4	180517470	93.4957277		5	-0.002716131	96128	'16.10'	grmzm2g169033_t01	'secondary metabolism.simple phenols'
430	Fuma	4	182201693	95.89453425		8	-0.004834603	78924	'30.2.99'	grmzm2g091632_t02	'signalling.receptor kinases.misc'
431	Fuma	4	182528229	96.35961321		8	-0.003345301	132850	'15.2'	grmzm2g325575_t01	'metal handling.binding, chelation and storage'
432	Fuma	4	182976299	96.99779073		7	-0.002979929	28429	'26.12'	ac197758.3_fgt004	'misc.peroxidases'
433	Fuma	4	230346458	113.6832878		23	0.006178358	84704	'30.3'	grmzm2g085022_t01	'signalling.calcium'
434	Fuma	4	234235715	115.012717		20	0.005063297	10161	'29.2.1.2.2.11'	grmzm2g018770_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L11'

435	Fuma	4	244607562	137.8307023	33	-0.006210745	5287	'27.3.35'	grmzm2g019106_t01	'RNA.regulation of transcription.bZIP transcription factor family'
436	Fuma	5	6670422	24.85176321	8	0.008168665	66746	'26.2'	grmzm2g030821_t01	'misc.UDP glucosyl and glucoronyl transferases'
437	Fuma	5	6828578	25.41836288	5	0.002267897	9656	'34.16'	grmzm2g072071_t01	'transport.ABC transporters and multidrug resistance systems'
438	Fuma	5	7550141	28.65678582	8	0.004885718	16933	'29.4'	grmzm2g014618_t01	'protein.postranslational modification'
439	Fuma	5	9280217	30.80111555	6	0.003874816	45660	'20.2.3'	grmzm2g164470_t01	'stress.abiotic.drought/salt'
440	Fuma	5	10073594	32.64114173	7	0.003647227	53346	'27.3.25'	grmzm2g455869_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
441	Fuma	5	10073765	32.64153832	28	0.003494537	53175	'27.3.25'	grmzm2g455869_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
442	Fuma	5	10085671	32.66915111	5	0.00489814	41269	'27.3.25'	grmzm2g455869_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
443	Fuma	6	165445511	102.4790375	8	-0.005808279	1687	'3.5'	grmzm2g011662_t01	'minor CHO metabolism.others'

444	Fuma	7	57117438	49.15463724	6	-0.006367934	311604	'26.28'	grmzm2g088919_t01	'misc.GDSL-motif lipase'
445	Fuma	7	129970942	70.62091409	6	-0.005265067	128832	'8.1.1.1'	grmzm2g128121_t01	'TCA / org. transformation.TCA.pyruvate DH.E1'
446	Fuma	7	159657824	105.8008762	37	0.003170054	1705	'29.5.11.20'	grmzm2g080549_t01	'protein.degradation.ubiquitin.proteasom'
447	Fuma	7	162478003	113.1505321	5	0.004030903	16072	'27.3.29'	grmzm2g180568_t01	'RNA.regulation of transcription.TCP transcription factor family'
448	Fuma	7	162478193	113.1514273	13	0.004228173	15882	'27.3.29'	grmzm2g180568_t01	'RNA.regulation of transcription.TCP transcription factor family'
449	Fuma	7	162482540	113.1719093	13	0.003306758	11535	'27.3.29'	grmzm2g180568_t01	'RNA.regulation of transcription.TCP transcription factor family'
450	Fuma	8	156139987	82.72693349	6	-0.00298176	1709	'1.1.5.3'	grmzm2g059191_t01	'PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase'
451	Fuma	8	160438189	89.3463314	64	0.003362949	2833	'26.17'	grmzm2g180335_t01	'misc.dynamin'

452	Fuma	8	160597062	89.61860448	5	0.004068163	25092	'23.3.3'	grmzm2g013060_t01	'nucleotide metabolism.salvage.NUDIX hydrolases'
453	Fuma	8	160929154	90.26562868	10	0.003237693	10379	'27.3.26'	grmzm2g107504_t01	'RNA.regulation of transcription.MYB-related transcription factor family'
454	Fuma	10	89924492	41.55012521	6	0.006236087	36850	'20.2.2'	grmzm2g367330_t01	'stress.abiotic.cold'
455	Fuma	10	148039817	99.52795003	15	0.003588536	6373	'29.5.2'	grmzm2g173682_t01	'protein.degradation.autophagy'
456	Fuma	10	148043393	99.54799587	25	0.004260238	2797	'29.5.2'	grmzm2g173682_t01	'protein.degradation.autophagy'
457	Gluc	1	19427291	35.91876596	7	-0.027454867	61046	'16.1'	grmzm2g097283_t01	'secondary metabolism.isoprenoids'
458	Gluc	1	19427753	35.91919409	22	-0.037111842	60584	'16.1'	grmzm2g097283_t01	'secondary metabolism.isoprenoids'
459	Gluc	1	19745377	36.21353287	15	-0.032734262	2983	'34.9'	grmzm2g147481_t01	'transport.metabolite transporters at the mitochondrial membrane'
460	Gluc	1	19745402	36.21355604	13	-0.045012011	2958	'34.9'	grmzm2g147481_t01	'transport.metabolite transporters at the mitochondrial membrane'
461	Gluc	1	45048717	61.17102638	9	0.038550257	67243	'16.8.1'	ac212219.3_fgt005	'secondary metabolism.flavonoids.anthocyanins'

462	Gluc	1	48047150	63.48200445	8	0.034229401	55161	'29.5.11.4.3.4'	grmzm2g162356_t01	'protein.degradation.ubiquitin.E3.SCF.RBX'
463	Gluc	1	51070607	65.47738632	7	0.029008336	45712	'9.1.2'	grmzm2g018941_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
464	Gluc	1	56261977	69.68972945	5	0.023260105	53491	'27.3.35'	grmzm2g062391_t01	'RNA.regulation of transcription.bZIP transcription factor family'
465	Gluc	1	155941648	90.6953495	7	0.038011307	260842	'6.9'	ac210816.3_fgt007	'gluconeogenese/glyoxylate cycle.isocitrate lyase'
466	Gluc	1	219996077	128.8274919	14	0.047101374	175158	'27.1.19'	grmzm2g101105_t01	'RNA.processing.ribonucleases'
467	Gluc	1	222371522	129.7775422	6	0.060501845	490	'29.5.9'	grmzm2g170982_t01	'protein.degradation.AAA type'
468	Gluc	1	239603760	141.3379825	11	-0.05994586	66143	'28.1'	grmzm2g017237_t01	'DNA.synthesis/chromatin structure'
469	Gluc	2	3583432	9.929705575	9	-0.023800048	1758	'17.2.3'	grmzm2g365162_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
470	Gluc	2	3583516	9.930283959	21	-0.023735882	1674	'17.2.3'	grmzm2g365162_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
471	Gluc	2	3980052	10.9932083	9	-0.020514387	2373	'29.2.5'	grmzm2g044011_t01	'protein.synthesis.release'

472	Gluc	2	4089979	11.27575825	6	-0.027570085	57389	'1.3.13'	grmzm2g039345_t01	'PS.calvin cycle.rubisco interacting'
473	Gluc	2	4154747	11.44223414	8	-0.02251602	6885	'3.5'	grmzm2g039588_t01	'minor CHO metabolism.others'
474	Gluc	2	5500383	16.53049076	8	-0.031577515	15524	'33.99'	grmzm2g174784_t01	'development.unspecified'
475	Gluc	2	21516360	52.5167576	7	-0.044827778	29670	'27.3.22'	grmzm2g351330_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
476	Gluc	2	21991139	53.30019341	33	-0.044813254	34	'27.3.9'	grmzm2g404973_t03	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
477	Gluc	2	21995485	53.30230537	23	-0.037693821	118804	'1.1.6'	grmzm2g109244_t01	'PS.lightreaction.NADH DH'
478	Gluc	2	21996541	53.30281854	21	-0.033790264	117748	'1.1.6'	grmzm2g109244_t01	'PS.lightreaction.NADH DH'
479	Gluc	2	61159379	74.01441319	8	-0.032013585	39101	'29.5.3'	grmzm2g122239_t01	'protein.degradation.cysteine protease'
480	Gluc	2	160568992	82.32572371	9	-0.041399233	263469	'30.2.3'	grmzm2g163724_t01	'signalling.receptor kinases.leucine rich repeat III'

481	Gluc	2	175895506	86.83396756	12	0.048831829	104436	'31.1'	grmzm2g009136_t01	'cell.organisation'
482	Gluc	2	186768867	98.0043879	8	-0.035176619	73501	'27.3.57'	grmzm2g052908_t01	'RNA.regulation of transcription.JUMONJI family'
483	Gluc	2	188188473	99.75988308	11	-0.03166046	33508	'9.1.2'	grmzm2g087312_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
484	Gluc	3	1878568	3.303968086	7	-0.028976818	3965	'29.4'	grmzm2g156035_t01	'protein.postranslational modification'
485	Gluc	3	1878573	3.303993959	5	-0.031384063	3960	'29.4'	grmzm2g156035_t01	'protein.postranslational modification'
486	Gluc	3	1878755	3.304935735	5	-0.021125504	3778	'29.4'	grmzm2g156035_t01	'protein.postranslational modification'
487	Gluc	3	4677417	17.51176627	6	-0.021815356	37710	'30.8'	grmzm2g357124_t01	'signalling.misc'
488	Gluc	3	10108659	34.7208259	23	-0.027274921	2203	'34.2'	grmzm2g429964_t01	'transport.sugars'
489	Gluc	3	10750452	36.00654788	19	-0.029665146	3267	'34.18'	grmzm2g051753_t02	'transport.unspecified anions'
490	Gluc	3	13310374	40.12977866	10	-0.029446598	65180	'34'	grmzm2g116053_t01	'transport'

491	Gluc	3	13634107	40.54837757	8	-0.028513384	44007	'29.4'	grmzm2g129482_t01	'protein.postranslational modification'
492	Gluc	3	16806728	44.65069551	9	-0.029377307	567	'25'	ac215260.3_fgt004	'C1-metabolism'
493	Gluc	3	19194362	47.73799582	8	-0.033080281	207619	'29.2.1.2.2.26'	grmzm2g327564_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L26'
494	Gluc	3	49808116	56.5306869	16	-0.031996718	396537	'29.4'	grmzm2g170120_t01	'protein.postranslational modification'
495	Gluc	3	67958527	58.10223721	5	-0.033220713	20464	'21.4'	grmzm2g110286_t01	'redox.glutaredoxins'
496	Gluc	3	84984528	58.15869307	19	-0.053941727	65318	'16.1.5'	ac214360.3_fgt001	'secondary metabolism.isoprenoids.terpenoids'
497	Gluc	3	126612628	60.92265927	13	-0.036596401	51156	'27.1.1'	grmzm2g162119_t01	'RNA.processing.splicing'
498	Gluc	3	135511148	62.83074525	10	-0.032809231	348	'8.1.1.2'	grmzm2g165176_t01	'TCA / org. transformation.TCA.pyruvate DH.E2'

499	Gluc	3	213286642	125.2764546	22	0.027989477	37906	'17.2.2'	grmzm2g126260_t02	'hormone metabolism.auxin.signal transduction'
500	Gluc	3	223962036	146.2391988	22	0.049820979	38215	'27.3.12'	grmzm2g422205_t01	'RNA.regulation of transcription.C3H zinc finger family'
501	Gluc	4	82547651	56.71433525	9	-0.032568459	264716	'15.2'	grmzm2g166711_t01	'metal handling.binding, chelation and storage'
502	Gluc	4	93788979	57.69805012	9	-0.054449121	23236	'34.99'	grmzm2g043075_t01	'transport.misc'
503	Gluc	4	94875017	57.72053661	9	-0.046879342	324483	'27.1.1'	grmzm2g011034_t01	'RNA.processing.splicing'
504	Gluc	4	103678485	57.89068149	10	-0.02674891	100683	'29.4'	grmzm2g378949_t01	'protein.postranslational modification'
505	Gluc	4	110571777	58.03760973	7	-0.026815621	125684	'29.5.11.4.2'	grmzm2g127690_t01	'protein.degradation.ubiquitin.E3.RING'
506	Gluc	4	142457660	60.337891	31	-0.04524174	26116	'16.2.1.1'	grmzm2g160541_t01	'secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL'
507	Gluc	4	243115508	132.4118713	10	-0.035189308	4881	'29.4'	grmzm2g166035_t01	'protein.postranslational modification'
508	Gluc	4	243119871	132.428798	9	-0.053005896	518	'29.4'	grmzm2g166035_t01	'protein.postranslational modification'

509	Gluc	5	1571929	2.012971503	64	-0.030891034	1299	'17.2.1'	grmzm2g125552_t01	'hormone metabolism.auxin.synthesis-degradation'
510	Gluc	5	2357601	5.023225032	15	-0.03524917	4455	'27.3.67'	grmzm2g003068_t01	'RNA.regulation of transcription.putative transcription regulator'
511	Gluc	5	2358292	5.027739617	11	-0.034233745	3764	'27.3.67'	grmzm2g003068_t01	'RNA.regulation of transcription.putative transcription regulator'
512	Gluc	5	7584397	28.79525161	9	0.05608891	77874	'14.1'	grmzm2g051270_t01	'S-assimilation.ATPS'
513	Gluc	5	7815403	29.72899837	23	0.066760523	1221	'31.3'	grmzm2g147814_t01	'cell.cycle'
514	Gluc	5	10372835	33.33515135	6	0.037017755	18639	'27.3.67'	grmzm2g408897_t01	'RNA.regulation of transcription.putative transcription regulator'
515	Gluc	5	10642005	33.95941932	32	0.047231589	20871	'30.6'	grmzm2g163217_t01	'signalling.MAP kinases'
516	Gluc	5	11555355	36.07769085	9	0.04595894	2509	'27.1.2'	grmzm2g123459_t01	'RNA.processing.RNA helicase'
517	Gluc	5	15080589	45.43333631	7	-0.041567563	15173	'27.3.67'	grmzm2g379428_t01	'RNA.regulation of transcription.putative transcription regulator'
518	Gluc	5	15334088	45.78544974	26	-0.0335316	915	'34.21'	grmzm2g340578_t01	'transport.calcium'

519	Gluc	5	23315145	53.64866829	8	-0.048304577	55948	'29.5'	grmzm2g422539_t01	'protein.degradation'
520	Gluc	5	36811132	58.27317542	5	-0.030458025	335265	'30.5'	grmzm2g122805_t01	'signalling.G-proteins'
521	Gluc	5	36811154	58.27317812	24	-0.030783704	335243	'30.5'	grmzm2g122805_t01	'signalling.G-proteins'
522	Gluc	5	37443804	58.32813065	7	-0.027227488	17734	'11.3'	grmzm2g005260_t01	'lipid metabolism.Phospholipid synthesis'
523	Gluc	5	38114919	58.37370611	5	-0.032853631	53769	'27.3.99'	grmzm2g436064_t01	'RNA.regulation of transcription.unclassified'
524	Gluc	5	88070567	69.41851202	9	-0.048661521	49109	'27.3.28'	grmzm2g111136_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
525	Gluc	5	114204945	70.51015923	15	-0.037585673	775936	'29.5.11.4.3.2'	grmzm2g069649_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
526	Gluc	5	149251475	73.13980408	9	-0.039233421	89010	'27.3.99'	grmzm2g019971_t01	'RNA.regulation of transcription.unclassified'
527	Gluc	5	163819573	76.76334725	6	0.03892669	1736	'17.2.3'	grmzm2g312274_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'

528	Gluc	5	165729383	77.90457087	6	-0.068401599	845	'27.3.3'	grmzm2g016434_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
529	Gluc	5	167871133	79.69575659	8	-0.063461483	8514	'2.1.2.3'	grmzm2g032628_t01	'major CHO metabolism.synthesis.starch.starch branching'
530	Gluc	5	168259864	79.99109637	14	-0.054728927	9174	'29.4'	grmzm2g038536_t01	'protein.postranslational modification'
531	Gluc	5	168260887	79.99218626	6	-0.044931698	8151	'29.4'	grmzm2g038536_t01	'protein.postranslational modification'
532	Gluc	5	192568110	101.6096752	10	0.062349209	29848	'34.99'	grmzm2g014977_t01	'transport.misc'
533	Gluc	5	200083354	107.7054585	5	-0.035928509	140	'27.3.6'	grmzm2g101350_t03	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
534	Gluc	5	200531277	108.3769927	13	0.049459237	66857	'23.1.1.1'	grmzm2g147450_t01	'nucleotide metabolism.synthesis.pyrimidine.carbamoyl phosphate synthetase'
535	Gluc	5	201231896	109.0981131	11	-0.04069251	122362	'29.5.5'	grmzm2g079352_t01	'protein.degradation.serine protease'
536	Gluc	5	209935600	130.9474516	5	0.054968328	529	'30.11'	grmzm2g104920_t01	'signalling.light'

537	Gluc	5	212261524	139.7573696	29	0.03161962	17396	'29.5.11.4.2'	grmzm2g122284_t01	'protein.degradation.ubiquitin.E3.RING'
538	Gluc	5	213298320	144.5886587	7	0.03745947	20740	'31.1'	grmzm2g180418_t01	'cell.organisation'
539	Gluc	6	1331502	-9.338084147	17	0.048982117	438	'29.5.11.4.2'	grmzm2g423956_t03	'protein.degradation.ubiquitin.E3.RING'
540	Gluc	6	1335665	-9.333360919	20	0.044914068	1362	'1.1.5.2'	grmzm2g122337_t01	'PS.lightreaction.other electron carrier (ox/red).ferredoxin'
541	Gluc	6	9189279	-0.422862181	10	0.0457043	282	'18.5.2.4'	grmzm2g066426_t01	'Co-factor and vitamine metabolism.folate & vitamine K.o-Succinyl-BenzoylCoa Synthetase'
542	Gluc	6	49947554	8.548807235	13	0.050794602	512668	'29.4'	grmzm2g145360_t01	'protein.postranslational modification'
543	Gluc	6	122728773	45.27892524	28	-0.090243045	74670	'30.3'	grmzm2g071100_t01	'signalling.calcium'
544	Gluc	6	123562319	45.55520364	14	-0.085892259	24435	'34.3'	grmzm2g148200_t01	'transport.amino acids'
545	Gluc	6	157445216	76.89711855	5	-0.059505241	29598	'10.7'	grmzm2g007708_t01	'cell wall.modification'
546	Gluc	6	157953572	77.68801846	6	-0.050730304	34606	'27.3.99'	grmzm2g032847_t01	'RNA.regulation of transcription.unclassified'

547	Gluc	7	3665692	13.3545418	11	-0.043550162	4647	'27.3.22'	grmzm2g028041_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
548	Gluc	7	20233795	44.69829015	5	-0.032821318	2989	'27.3.69'	ac233961.1_fgt001	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
549	Gluc	7	27327128	46.7793044	15	-0.031600786	64745	'33.99'	grmzm2g086757_t01	'development.unspecified'
550	Gluc	7	32868948	47.79855164	40	-0.03385516	422764	'26.21'	grmzm2g000221_t01	'misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein'
551	Gluc	7	84574592	49.92029539	16	-0.03318546	15252	'31.4'	grmzm2g360648_t01	'cell.vesicle transport'
552	Gluc	7	151684587	89.72788592	23	0.050943726	169523	'34.2'	grmzm2g019974_t01	'transport.sugars'
553	Gluc	7	151704874	89.76604438	13	0.063838907	149236	'34.2'	grmzm2g019974_t01	'transport.sugars'
554	Gluc	7	159106172	104.5548504	6	-0.033343837	34316	'27.3.67'	grmzm2g037444_t01	'RNA.regulation of transcription.putative transcription regulator'
555	Gluc	7	166657242	123.8438631	13	0.046507086	67872	'20.2.2'	grmzm2g364643_t01	'stress.abiotic.cold'

556	Gluc	7	167223656	126.3055595	5	0.04371809	3332	'34.15'	grmzm2g166738_t01	'transport.potassium'
557	Gluc	7	168146720	130.3172954	14	0.038042497	10144	'27.3.8'	ac155434.2_fgt006	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
558	Gluc	7	168146779	130.3175518	16	0.050979889	10085	'27.3.8'	ac155434.2_fgt006	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
559	Gluc	7	168259468	130.8073104	11	0.027577674	625	'29.5.1'	grmzm2g059165_t01	'protein.degradation.subtilases'
560	Gluc	7	168322280	131.0802981	6	0.034001816	10705	'27.1'	grmzm2g470461_t01	'RNA.processing'
561	Gluc	7	169418608	134.40687	6	0.032947988	70945	'27.3'	grmzm2g122116_t01	'RNA.regulation of transcription'
562	Gluc	7	169612994	134.5554328	6	-0.060679509	158800	'33.99'	grmzm2g032711_t02	'development.unspecified'
563	Gluc	7	170074937	134.9084806	8	0.04615997	63845	'17.1.1.1.10'	grmzm2g330848_t01	'hormone metabolism.abscisic acid.synthesis-degradation.synthesis.9-cis-epoxycarotenoid dioxygenase'
564	Gluc	8	10208359	26.24898642	5	-0.026684796	195798	'29.5.11.4.2'	grmzm2g003930_t01	'protein.degradation.ubiquitin.E3.RING'

565	Gluc	8	10978629	28.40458338	9	-0.025432862	8479	'33.99'	grmzm2g030384_t01	'development.unspecified'
566	Gluc	8	13271527	33.98105	6	-0.027208471	13787	'30.2.17'	grmzm2g172368_t01	'signalling.receptor kinases.DUF 26'
567	Gluc	8	15541604	37.97326272	22	-0.033735477	49349	'5.2'	grmzm2g038821_t01	'fermentation.PDC'
568	Gluc	8	17101531	39.8048484	7	-0.028932686	7086	'29.5'	grmzm2g162928_t01	'protein.degradation'
569	Gluc	8	17783857	40.90236227	24	-0.035698197	79627	'26.2'	grmzm2g457929_t01	'misc.UDP glucosyl and glucoronyl transferases'
570	Gluc	8	141607731	72.49035639	5	0.035922564	161506	'29.5.2'	grmzm2g005304_t01	'protein.degradation.autophagy'
571	Gluc	8	160611990	89.64768912	7	0.033050154	10164	'23.3.3'	grmzm2g013060_t01	'nucleotide metabolism.salvage.NUDIX hydrolases'
572	Gluc	8	161247986	90.88681804	17	0.025027089	13207	'27.3.6'	grmzm2g030762_t02	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
573	Gluc	8	161456583	91.29323346	6	0.027119377	35931	'27.3'	grmzm2g170941_t01	'RNA.regulation of transcription'

574	Gluc	8	162617259	92.65142696	6	0.024273535	171454	'28.1'	grmzm2g421829_t01	'DNA.synthesis/chromatin structure'
575	Gluc	8	173914014	136.3104872	19	0.020511215	1481	'30.2.11'	ac203173.3_fgt002	'signalling.receptor kinases.leucine rich repeat XI'
576	Gluc	9	2701441	-3.388186607	6	-0.065619148	6507	'27.2'	grmzm2g180836_t01	'RNA.transcription'
577	Gluc	9	6998866	8.219401947	9	-0.027000187	109804	'27.2'	grmzm2g017537_t01	'RNA.transcription'
578	Gluc	9	7182819	8.716269429	28	-0.045797986	56750	'17.7.1.5'	grmzm2g000236_t01	'hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase'
579	Gluc	9	10186494	15.44407336	6	-0.034472041	49289	'29.2.1.2.1.17'	grmzm2g086906_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S17'
580	Gluc	9	26517167	43.30986818	6	0.044089609	21521	'31.1'	grmzm2g136838_t01	'cell.organisation'
581	Gluc	9	26517266	43.30992673	33	0.044430659	21422	'31.1'	grmzm2g136838_t01	'cell.organisation'
582	Gluc	9	60088439	45.65313865	30	0.055300858	218331	'11.6'	grmzm2g025026_t01	'lipid metabolism.lipid transfer proteins etc'

583	Gluc	9	144805016	93.75044572	11	0.03694982	32253	'29.5.11.4.2'	grmzm2g004157_t01	'protein.degradation.ubiquitin.E3.RING'
584	Gluc	10	5427445	17.07840286	48	-0.069028108	16980	'27.3.35'	grmzm2g365754_t01	'RNA.regulation of transcription.bZIP transcription factor family'
585	Gluc	10	37230981	36.08777546	15	0.057220632	332073	'20.2.1'	grmzm2g117836_t01	'stress.abiotic.heat'
586	Gluc	10	52110744	36.32411544	18	0.071276311	1185032	'27.3.1'	grmzm2g405170_t01	'RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing transcription factor family'
587	Gluc	10	76226092	38.27843109	8	0.042662267	84	'11.1.13'	grmzm2g079908_t04	'lipid metabolism.FA synthesis and FA elongation.acyl-CoA binding protein'
588	Gluc	10	76332289	38.30539729	11	0.043798998	72244	'27.3.6'	grmzm2g042895_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
589	Gluc	10	85540940	40.43084945	33	0.066852209	45425	'26.12'	grmzm2g006727_t01	'misc.peroxidases'
590	Gluc	10	138301683	66.29092836	9	-0.037590118	12353	'11.1.8'	af466202.2_fgt012	'lipid metabolism.FA synthesis and FA elongation.acyl coa ligase'
591	Gluc	10	144247405	82.22431479	8	-0.040531525	33015	'27.2'	grmzm2g427031_t01	'RNA.transcription'
592	Gluc	10	148193563	100.3897975	8	-0.046829239	5178	'34.15'	grmzm2g093643_t01	'transport.potassium'

593	Glut	1	52690146	67.43745454	13	-0.00764858	22847	'26.21'	grmzm2g174680_t01	'misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein'
594	Glut	1	182943941	98.00929506	43	0.004651268	216	'34.13'	grmzm2g152555_t01	'transport.peptides and oligopeptides'
595	Glut	1	182944297	98.00949265	10	0.004698343	65017	'27.4'	ac233867.1_fgt004	'RNA.RNA binding'
596	Glut	1	183661710	98.46017249	25	0.005469687	25203	'28.99'	grmzm2g113899_t01	'DNA.unspecified'
597	Glut	1	219467828	128.6162207	53	-0.006511624	667	'23.3.3'	grmzm2g136426_t01	'nucleotide metabolism.salvage.NUDIX hydrolases'
598	Glut	1	220903481	129.1904047	5	-0.011601406	66180	'27.3.20'	grmzm2g113742_t01	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
599	Glut	1	221341695	129.3656668	12	-0.009264172	184041	'34.3'	grmzm2g149946_t01	'transport.amino acids'
600	Glut	1	277632495	170.2619536	14	0.010539017	5122	'34.8'	grmzm2g147589_t01	'transport.metabolite transporters at the envelope membrane'
601	Glut	2	4153357	11.43866137	14	0.008070873	8275	'3.5'	grmzm2g039588_t01	'minor CHO metabolism.others'

602	Glut	2	4153720	11.4395944	56	0.009484778	7912	'3.5'	grmzm2g039588_t01	'minor CHO metabolism.others'
603	Glut	2	4299868	11.96628803	12	0.003568927	6339	'34.1'	grmzm2g019404_t01	'transport.p- and v-ATPases'
604	Glut	2	12590485	36.29106182	5	-0.008475169	109481	'27.3.32'	grmzm2g024898_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
605	Glut	2	133606697	78.41212615	8	-0.005723744	63584	'27.3.57'	grmzm2g352947_t01	'RNA.regulation of transcription.JUMONJI family'
606	Glut	2	185662626	96.4222994	8	0.005714311	2562	'27.3.6'	grmzm2g009478_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
607	Glut	2	186287170	97.21489693	11	0.00486937	399	'34.99'	grmzm2g031837_t01	'transport.misc'
608	Glut	2	186556918	97.58848824	7	0.00560792	10606	'10.5.1.1'	grmzm2g081017_t01	'cell wall.cell wall proteins.AGPs.AGP'
609	Glut	2	186556997	97.58864326	38	0.004943913	10527	'10.5.1.1'	grmzm2g081017_t01	'cell wall.cell wall proteins.AGPs.AGP'
610	Glut	2	186558389	97.59137473	6	0.004850272	9135	'10.5.1.1'	grmzm2g081017_t01	'cell wall.cell wall proteins.AGPs.AGP'
611	Glut	2	186558494	97.59158077	8	0.005489912	9030	'10.5.1.1'	grmzm2g081017_t01	'cell wall.cell wall proteins.AGPs.AGP'
612	Glut	2	209437807	120.3370062	6	-0.006286015	15304	'3.2.2'	grmzm2g117564_t01	'minor CHO metabolism.trehalose.TPP'

613	Glut	2	210076624	121.1447377	5	-0.007333198	53109	'27.3.25'	grmzm2g703373_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
614	Glut	2	233601849	155.7785003	5	-0.004272848	14405	'8.1.7'	grmzm2g079888_t01	'TCA / org. transformation.TCA.succinate dehydrogenase'
615	Glut	3	201451737	108.647491	5	-0.009148834	237980	'31.1'	grmzm2g113319_t01	'cell.organisation'
616	Glut	3	209190519	119.5728622	8	-0.008009729	5234	'21.2'	grmzm2g024348_t01	'redox.ascorbate and glutathione'
617	Glut	3	210306116	120.8801933	6	-0.016920822	112218	'4.2.14'	grmzm2g152686_t01	'glycolysis.plastid branch.pyruvate kinase (PK)'
618	Glut	3	210710907	121.3852837	8	-0.017895411	255559	'27.3.3'	grmzm2g160971_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
619	Glut	3	210877159	121.5927298	12	-0.004934249	89307	'27.3.3'	grmzm2g160971_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
620	Glut	3	210988072	121.7311249	6	-0.016726602	146991	'29.4'	grmzm2g118403_t01	'protein.postranslational modification'

621	Glut	3	211148597	121.9314249	16	-0.005852378	32247	'27.3.32'	grmzm2g408462_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
622	Glut	3	212234516	123.2864138	7	-0.005205315	10080	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
623	Glut	3	212718903	123.8908226	5	-0.004685377	3621	'34.15'	grmzm2g022915_t01	'transport.potassium'
624	Glut	3	213151216	124.9438117	7	-0.004725778	3719	'27.3.69'	ac212898.2_fgt006	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
625	Glut	3	213151324	124.944077	8	-0.004513687	3611	'27.3.69'	ac212898.2_fgt006	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
626	Glut	3	213890769	126.7603538	6	-0.010464009	58898	'27.3.69'	grmzm2g047695_t02	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
627	Glut	3	215225785	128.93347	9	-0.005251452	36593	'26.13'	grmzm2g068690_t01	'misc.acid and other phosphatases'
628	Glut	3	225244456	148.4971299	11	0.010839249	49906	'31.1'	grmzm2g001981_t02	'cell.organisation'
629	Glut	3	228108627	153.4517969	9	-0.007734346	104550	'27.1.1'	grmzm2g078592_t01	'RNA.processing.splicing'

630	Glut	4	113973202	58.11061842	7	0.012195634	117232	'27.3.25'	grmzm2g059167_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
631	Glut	4	114035361	58.11195261	27	0.009580393	55073	'27.3.25'	grmzm2g059167_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
632	Glut	4	114684938	58.12589523	19	0.012290204	557504	'30.4'	grmzm2g171080_t01	'signalling.phosphinositides'
633	Glut	4	114784127	58.12802424	11	0.008190782	458315	'30.4'	grmzm2g171080_t01	'signalling.phosphinositides'
634	Glut	4	177057914	88.36703104	8	-0.004129286	66135	'20.1'	grmzm2g158811_t01	'stress.biotic'
635	Glut	4	177728199	89.41877612	7	-0.004671784	11473	'10.3'	grmzm2g015983_t01	'cell wall.hemicellulose synthesis'
636	Glut	4	180521118	93.50092348	6	-0.003964857	92480	'16.10'	grmzm2g169033_t01	'secondary metabolism.simple phenols'
637	Glut	4	180521269	93.50113855	12	-0.003984467	92329	'16.10'	grmzm2g169033_t01	'secondary metabolism.simple phenols'
638	Glut	5	2188871	3.920842986	34	0.004382943	1646	'29.2.1.1.3.2.30'	grmzm2g085336_t01	'protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S subunit.L30'

639	Glut	5	2188935	3.921261124	7	0.004596176	1582	'29.2.1.1.3.2.30'	grmzm2g085336_t01	'protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S subunit.L30'
640	Glut	5	22628584	52.93088442	10	0.004845342	588	'29.5.5'	grmzm2g082502_t01	'protein.degradation.serine protease'
641	Glut	5	24406989	53.96237944	33	0.005600127	73517	'26.1'	grmzm2g032910_t01	'misc.misc2'
642	Glut	5	26831469	54.87846643	28	0.004300894	3614	'16.8.2'	grmzm2g477683_t01	'secondary metabolism.flavonoids.chalcones'
643	Glut	5	26968073	54.93008209	8	0.004561445	93823	'30.2.17'	grmzm2g102862_t01	'signalling.receptor kinases.DUF 26'
644	Glut	5	204624078	116.4807852	18	-0.008453086	3280	'26.2'	grmzm2g142709_t01	'misc.UDP glucosyl and glucoronyl transferases'
645	Glut	5	207099285	124.0780936	14	-0.005034335	1942	'3.2.2'	grmzm2g055150_t01	'minor CHO metabolism.trehalose.TPP'
646	Glut	5	207830710	126.0436057	6	-0.005515777	883	'30.1.1'	grmzm2g081214_t01	'signalling.in sugar and nutrient physiology'
647	Glut	5	208181590	126.6094235	22	-0.00481065	154180	'29.5'	grmzm2g371795_t01	'protein.degradation'
648	Glut	5	211971359	138.4052511	12	-0.004321074	49314	'20.2.1'	grmzm2g040890_t01	'stress.abiotic.heat'

649	Glut	6	5873783	-4.184534568	5	-0.004487679	145507	'27.3.50'	grmzm2g019257_t01	'RNA.regulation of transcription.General Transcription'
650	Glut	6	12079085	2.855833808	5	-0.006531182	237506	'27.3.32'	grmzm2g143765_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
651	Glut	6	17417589	5.992091218	17	-0.007355935	109426	'26.3'	grmzm2g465617_t01	'misc.gluco-, galacto- and mannosidases'
652	Glut	7	46996523	49.11264731	7	0.008798227	15096	'16.2'	grmzm2g177424_t01	'secondary metabolism.phenylpropanoids'
653	Glut	7	94886697	50.37959201	10	0.005639153	149175	'9.7'	grmzm2g126408_t01	'mitochondrial electron transport / ATP synthesis.cytochrome c oxidase'
654	Glut	7	142900670	81.10277074	5	0.006182641	22269	'30.2.24'	grmzm2g413030_t01	'signalling.receptor kinases.S-locus glycoprotein like'
655	Glut	7	153318373	92.800926	8	0.005690411	31356	'29.5.7'	ac197013.3_fgt003	'protein.degradation.metalloprotease'
656	Glut	8	6455489	18.09391822	6	0.00847514	89221	'29.2.1.2.1.5'	grmzm2g156673_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S5'
657	Glut	8	6456227	18.0946642	11	0.008664988	88483	'29.2.1.2.1.5'	grmzm2g156673_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S5'
658	Glut	8	7548635	19.78341505	71	0.007377193	21940	'29.3.4.1'	grmzm2g078941_t01	'protein.targeting.secretory pathway.ER'

659	Glut	8	101278421	58.12094124	7	0.004952541	45822	'27.3.27'	grmzm2g104400_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
660	Glut	8	103054530	58.74182186	12	0.007297413	99819	'20.1'	grmzm2g017603_t01	'stress.biotic'
661	Glut	8	108849125	60.58213104	58	0.007826556	31652	'27.3.32'	grmzm2g449681_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
662	Glut	8	111162784	61.25050555	6	0.005962952	102802	'30.2.25'	grmzm2g061718_t01	'signalling.receptor kinases.wall associated kinase'
663	Glut	9	147914070	105.0171122	7	-0.005016694	13728	'27.3.9'	grmzm2g532534_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
664	Glut	10	4806482	13.07619208	13	0.004785432	108510	'27.3.20'	grmzm2g016370_t01	'RNA.regulation of transcription.G2-like transcription factor family, GARP'
665	Glut	10	4916937	13.82732142	5	0.005675285	11772	'26.10'	grmzm2g016264_t01	'misc.cytochrome P450'
666	Glut	10	107945494	44.01972245	13	-0.005346414	4236	'11.1.4'	grmzm2g099696_t01	'lipid metabolism.FA synthesis and FA elongation.ACP oxoacyl reductase'

667	Glut	10	121191348	47.87413076	6	-0.00534999	46628	'29.5.11.5'	grmzm2g036186_t01	'protein.degradation.ubiquitin.ubiquitin protease'
668	Glut	10	143716606	81.33488617	5	0.005311941	997	'30.2.17'	grmzm2g000633_t01	'signalling.receptor kinases.DUF 26'
669	Glut	10	143720983	81.33864061	5	0.006129575	1790	'30.2.24'	grmzm2g000620_t01	'signalling.receptor kinases.S-locus glycoprotein like'
670	Glut	10	145459551	86.83094884	6	0.00654061	30115	'34.18'	grmzm2g143402_t03	'transport.unspecified anions'
671	Glut	10	145674099	87.6872826	53	0.005786004	453	'17.5.2'	grmzm2g104260_t01	'hormone metabolism.ethylene.signal transduction'
672	Glut	10	146203278	89.79941527	6	0.005650134	21404	'18.1.1'	grmzm2g067176_t01	'Co-factor and vitamine metabolism.molybdenum cofactor.gephyrin'
673	Glut	10	146744765	92.26833185	7	0.004535231	309	'26.5'	grmzm2g125083_t01	'misc.acyl transferases'
674	Glut	10	148374079	101.4017084	12	0.006234528	11996	'30.4.3'	grmzm2g001905_t01	'signalling.phosphinositides.bis(5''-nucleosyl)-tetraphosphatase'
675	Mala	1	15026222	30.17736702	5	-0.00767141	58151	'27.3.6'	grmzm2g035156_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'

676	Mala	1	16018451	32.20888865	5	-0.010779957	50801	'27.3.3'	grmzm2g399072_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
677	Mala	1	16018768	32.20944008	34	-0.010507566	50484	'27.3.3'	grmzm2g399072_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
678	Mala	1	39323398	57.23255596	57	0.011761998	91097	'27.3.67'	grmzm2g119168_t01	'RNA.regulation of transcription.putative transcription regulator'
679	Mala	1	40056302	57.91121791	14	0.007307404	235662	'27.3.21'	grmzm2g049159_t01	'RNA.regulation of transcription.GRAS transcription factor family'
680	Mala	1	88319619	83.94252884	5	0.005107759	58893	'29.4'	grmzm2g392477_t01	'protein.postranslational modification'
681	Mala	1	90444879	84.51213232	6	0.007232955	325287	'13.2.2.2'	grmzm2g053720_t01	'amino acid metabolism.degradation. glutamate family.proline'
682	Mala	1	210010258	121.8475905	9	-0.007472494	40418	'31.2'	grmzm2g128605_t01	'cell.division'
683	Mala	1	219597467	128.6680693	5	-0.010215717	104121	'29.4'	grmzm2g032351_t01	'protein.postranslational modification'

684	Mala	1	219599713	128.6689676	17	-0.008622717	101875	'29.4'	grmzm2g032351_t01	'protein.postranslational modification'
685	Mala	1	222370635	129.7771875	21	-0.010317833	1377	'29.5.9'	grmzm2g170982_t01	'protein.degradation.AAA type'
686	Mala	1	292093541	191.7018819	15	0.029138599	2718	'27.3.11'	grmzm2g061626_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
687	Mala	1	295777277	199.3871057	5	0.021925596	63417	'26.22'	ac217358.3_fgt007	'misc.short chain dehydrogenase/reductase (SDR)'
688	Mala	2	2111645	4.01866061	8	0.006346054	97852	'30.2.11'	grmzm2g452142_t01	'signalling.receptor kinases.leucine rich repeat XI'
689	Mala	2	2662790	6.10191746	5	0.012572964	6023	'9.4'	grmzm2g010555_t01	'mitochondrial electron transport / ATP synthesis.alternative oxidase'
690	Mala	2	4313222	12.01705821	7	0.008065261	13790	'28.1'	grmzm2g314171_t01	'DNA.synthesis/chromatin structure'
691	Mala	2	4829815	13.98107797	14	0.007986073	6617	'28.1'	grmzm2g032977_t02	'DNA.synthesis/chromatin structure'
692	Mala	2	5064142	14.87195891	10	0.009403602	7583	'28.99'	grmzm2g082097_t01	'DNA.unspecified'

693	Mala	2	5064288	14.87251398	29	0.009676366	7437	'28.99'	grmzm2g082097_t01	'DNA.unspecified'
694	Mala	2	5564443	16.77403859	17	0.007030808	3595	'29.5.11.4.2'	grmzm2g174926_t01	'protein.degradation.ubiquitin.E3.RING'
695	Mala	2	38490452	66.37064702	10	-0.008181854	125815	'26.7'	grmzm2g147884_t01	'misc.oxidases - copper, flavone etc.'
696	Mala	2	53075256	72.33109749	67	-0.01005034	87822	'29.5.11.4.3.2'	grmzm2g014905_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
697	Mala	2	121233141	77.09963877	6	-0.008726546	46834	'29.3.4.2'	grmzm2g075680_t01	'protein.targeting.secretory pathway.golgi'
698	Mala	2	187425746	99.07896093	34	0.006597118	54226	'16.1.2.3'	grmzm2g058095_t01	'secondary metabolism.isoprenoids.mevalonate pathway.HMG-CoA reductase'
699	Mala	2	188442924	99.98704342	26	0.010380475	958	'27.3.6'	grmzm2g083504_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
700	Mala	2	190921710	102.1999719	13	0.007946425	38921	'27.3.6'	grmzm2g107560_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
701	Mala	2	190922255	102.2004584	6	0.005818998	38376	'27.3.6'	grmzm2g107560_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
702	Mala	2	208636969	118.3801568	72	-0.009940999	55417	'28.99'	grmzm2g056564_t01	'DNA.unspecified'

703	Mala	3	28560505	53.70440674	76	0.012754816	85679	'30.2.22'	grmzm2g355636_t01	'signalling.receptor kinases.proline extensin like'
704	Mala	3	110591868	58.89150506	6	0.009305688	39853	'26.2'	grmzm2g105991_t01	'misc.UDP glucosyl and glucoronyl transferases'
705	Mala	3	197969185	105.1512436	6	0.008872874	62723	'30.2.22'	ac211175.3_fgt005	'signalling.receptor kinases.proline extensin like'
706	Mala	3	200646842	108.1602931	7	0.006749729	73097	'27.3.28'	grmzm2g387993_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
707	Mala	3	207468446	116.9659734	5	0.007830782	3580	'24'	grmzm2g164674_t01	'Biodegradation of Xenobiotics'
708	Mala	3	208722589	119.0297927	10	0.018556936	73790	'30.2.17'	grmzm2g142207_t01	'signalling.receptor kinases.DUF 26'
709	Mala	3	208759190	119.072271	7	0.018809679	37189	'30.2.17'	grmzm2g142207_t01	'signalling.receptor kinases.DUF 26'
710	Mala	3	213856232	126.6755216	29	-0.008429835	32667	'1.5.1'	grmzm2g121878_t01	'PS.carbon concentrating mechanism.C4'

711	Mala	3	214330739	127.7703198	23	-0.007870489	21484	'10.6.3'	grmzm2g037431_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
712	Mala	3	214355739	127.8009362	14	-0.007817618	58715	'27.1'	grmzm2g132340_t01	'RNA.processing'
713	Mala	3	223533563	145.1258349	43	-0.006537456	14617	'26.28'	grmzm2g022279_t01	'misc.GDSL-motif lipase'
714	Mala	4	170999854	79.42178824	8	-0.017758613	8040	'34.7'	grmzm2g466545_t01	'transport.phosphate'
715	Mala	4	171775102	80.83509484	83	-0.010613833	5168	'2.1.2.2'	grmzm2g130043_t01	'major CHO metabolism.synthesis.starch.starch synthase'
716	Mala	4	180344878	93.24990822	5	0.026764303	79417	'29.5.4'	grmzm2g098583_t01	'protein.degradation.aspartate protease'
717	Mala	5	2767759	7.538649577	9	-0.023022027	11198	'21.99'	grmzm2g165270_t01	'redox.misc'
718	Mala	5	4189784	13.29548628	8	-0.024817481	467	'27.3.40'	grmzm2g152796_t01	'RNA.regulation of transcription.Aux/IAA family'
719	Mala	5	5266701	18.78312331	16	-0.018541237	2175	'1.1.2.2'	grmzm2g085646_t01	'PS.lightreaction.photosystem I.PSI polypeptide subunits'

720	Mala	5	25580476	54.40578016	17	0.006381893	74829	'29.5.11.4.2'	grmzm2g120933_t01	'protein.degradation.ubiquitin.E3.RING'
721	Mala	5	35870702	58.15768893	9	0.007312398	32733	'26.28'	grmzm2g087827_t01	'misc.GDSL-motif lipase'
722	Mala	5	159516767	75.22607915	59	0.006946802	253397	'21.1'	grmzm2g052402_t01	'redox.thioredoxin'
723	Mala	5	196990966	105.0448056	21	-0.006739831	26751	'29.3.4.99'	grmzm2g075253_t01	'protein.targeting.secretory pathway.unspecified'
724	Mala	5	196991427	105.0451889	6	-0.007454933	26290	'29.3.4.99'	grmzm2g075253_t01	'protein.targeting.secretory pathway.unspecified'
725	Mala	5	213281396	144.5097958	5	-0.007254868	4948	'29.4'	grmzm2g180430_t02	'protein.postranslational modification'
726	Mala	5	214193499	148.7600372	10	-0.005516584	4894	'29.4'	grmzm2g150932_t01	'protein.postranslational modification'
727	Mala	6	2173089	-8.383242223	8	-0.007048492	22535	'11.6'	grmzm2g118378_t01	'lipid metabolism.lipid transfer proteins etc'
728	Mala	6	3682882	-6.670271784	7	-0.007945361	191768	'27.3.27'	grmzm2g030325_t01	'RNA.regulation of transcription.NAC domain transcription factor family'

729	Mala	6	6894842	-3.026068551	6	-0.005310972	7826	'4.1.8'	grmzm2g180625_t01	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
730	Mala	6	9251251	-0.35255042	21	-0.006131661	309523	'30.11'	grmzm2g301803_t03	'signalling.light'
731	Mala	6	160133599	84.08459515	7	-0.010156075	2236	'27.3.12'	grmzm2g004795_t01	'RNA.regulation of transcription.C3H zinc finger family'
732	Mala	6	161832235	87.63268966	6	-0.009770832	3229	'28.1'	grmzm2g121262_t01	'DNA.synthesis/chromatin structure'
733	Mala	6	162218871	89.54447098	6	-0.006148267	3301	'34.99'	grmzm2g174990_t03	'transport.misc'
734	Mala	6	162665812	91.75443968	12	-0.008612649	7730	'27.3.3'	grmzm2g059939_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
735	Mala	6	163284243	94.27967325	19	-0.005380966	18263	'12.2.1'	grmzm2g375064_t01	'N-metabolism.ammonia metabolism.glutamate synthase'
736	Mala	6	165585617	102.9436765	17	-0.006076029	133380	'11.9.2.1'	ac231411.1_fgt011	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'

737	Mala	7	118340956	59.84562968	7	-0.012097666	352705	'27.3.11'	grmzm2g141031_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
738	Mala	7	131033445	71.16406426	19	-0.009077321	66256	'11.1.7'	grmzm2g143955_t01	'lipid metabolism.FA synthesis and FA elongation.ACP thioesterase'
739	Mala	7	143058340	81.14259414	5	-0.006769154	77047	'20.1'	grmzm2g397557_t01	'stress.biotic'
740	Mala	7	145583488	83.49098005	9	-0.005789243	22971	'27.3.28'	grmzm2g067624_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
741	Mala	7	146746400	84.65040768	13	-0.007872159	46919	'26.7'	grmzm2g076225_t01	'misc.oxidases - copper, flavone etc.'
742	Mala	7	163624094	115.764038	48	0.012940535	40018	'26.9'	grmzm2g109812_t01	'misc.glutathione S transferases'
743	Mala	7	166492884	123.1295455	11	0.009047583	48105	'34.15'	grmzm2g020766_t01	'transport.potassium'
744	Mala	7	166493179	123.1308276	67	0.011080937	47810	'34.15'	grmzm2g020766_t01	'transport.potassium'
745	Mala	7	167073361	125.6523612	6	0.009385491	33016	'29.4'	grmzm2g177050_t01	'protein.postranslational modification'

746	Mala	7	167122054	125.8639863	17	0.012150093	40729	'26.12'	grmzm2g042347_t01	'misc.peroxidases'
747	Mala	8	100197210	57.57868238	6	0.00790012	5257	'13.1.1.2.1'	grmzm2g033799_t01	'amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase'
748	Mala	8	108849390	60.58220759	51	0.005689455	31387	'27.3.32'	grmzm2g449681_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
749	Mala	8	120917873	65.51878959	5	0.008136638	118411	'10.5.3'	grmzm2g060213_t02	'cell wall.cell wall proteins.LRR'
750	Mala	8	154959713	81.88784605	10	0.012371157	64396	'11.8.2'	grmzm2g176301_t01	'lipid metabolism."exotics" (steroids, squalene etc).methylsterol monooxygenase'
751	Mala	8	159784012	88.41830479	12	0.012070302	19001	'29.5.11.4.3.2'	grmzm2g064954_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
752	Mala	9	91767617	47.59229769	5	0.009468398	80322	'29.5.11.20'	grmzm2g092975_t01	'protein.degradation.ubiquitin.proteasom'
753	Mala	9	109432591	53.84671075	14	0.010241133	112608	'27.3.67'	ac225193.3_fgt003	'RNA.regulation of transcription.putative transcription regulator'

754	Mala	10	1210362	-2.349387514	15	-0.017276952	972	'13.1.4.4.1'	grmzm2g130062_t01	'amino acid metabolism.synthesis.branched chain group.leucine specific.2-isopropylmalate synthase'
755	Mala	10	1431221	-1.586267435	6	0.011410568	2535	'16.2'	grmzm2g104710_t01	'secondary metabolism.phenylpropanoids'
756	Mala	10	1467050	-1.462469767	16	0.006758966	24539	'34.8'	grmzm2g178734_t01	'transport.metabolite transporters at the envelope membrane'
757	Mala	10	2275477	1.330836713	6	0.006068756	234464	'20.1'	grmzm2g004412_t01	'stress.biotic'
758	Mala	10	2592048	2.424664387	5	0.008847718	94004	'20.1'	grmzm2g356817_t01	'stress.biotic'
759	Mala	10	4201480	8.961984916	5	0.006361453	6138	'34.21'	grmzm2g004414_t01	'transport.calcium'
760	Mala	10	145447601	86.78325234	17	0.007756603	3545	'18.3.2'	grmzm2g143480_t01	'Co-factor and vitamine metabolism.riboflavin.riboflavin synthase'
761	Mala	10	145456506	86.81879521	5	0.008987877	33160	'34.18'	grmzm2g143402_t03	'transport.unspecified anions'
762	Mala	10	145674099	87.6872826	67	0.007733533	453	'17.5.2'	grmzm2g104260_t01	'hormone metabolism.ethylene.signal transduction'

763	Mala	10	145733506	87.92439606	8	0.009243772	1685	'34.1'	grmzm2g006894_t01	'transport.p- and v-ATPases'
764	Nitr	1	5563538	9.70193737	75	0.003559647	45127	'27.3.27'	grmzm2g025642_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
765	Nitr	1	51114082	65.50613364	11	0.003292823	2237	'9.1.2'	grmzm2g018941_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
766	Nitr	1	60210415	71.99893136	5	0.002949116	17955	'29.2.4'	grmzm2g000923_t01	'protein.synthesis.elongation'
767	Nitr	1	63667791	73.22732147	7	0.00318244	30179	'26.12'	grmzm2g004984_t01	'misc.peroxidases'
768	Nitr	1	199491006	112.8925649	7	-0.000697051	1925	'27.3.3'	grmzm2g369472_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
769	Nitr	1	201845500	115.3791094	11	-0.000756257	142924	'30.2.3'	grmzm2g422373_t01	'signalling.receptor kinases.leucine rich repeat III'
770	Nitr	1	201991158	115.4795854	6	-0.003767123	65461	'10.7'	grmzm2g309269_t01	'cell wall.modification'

771	Nitr	1	202621762	115.91	5	-0.0043	156054	'27.3.99'	grmzm2g139683_t01	'RNA.regulation of transcription.unclassified'
772	Nitr	1	207277145	119.465065	11	-0.000793889	25178	'20.2.99'	ac195794.3_fgt002	'stress.abiotic.unspecified'
773	Nitr	1	207279145	119.4669916	8	-0.000840239	23178	'20.2.99'	ac195794.3_fgt002	'stress.abiotic.unspecified'
774	Nitr	1	207313090	119.4996915	12	-0.000961106	1340	'17.7.1.5'	grmzm2g148281_t02	'hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase'
775	Nitr	1	224410655	132.7669157	12	-0.0094014	6518	'27.3.10'	grmzm2g167824_t01	'RNA.regulation of transcription.C2C2(Zn) YABBY family'
776	Nitr	1	232515055	138.1818938	6	0.011437559	18981	'28.1'	grmzm2g399212_t01	'DNA.synthesis/chromatin structure'
777	Nitr	1	233097149	138.4111567	9	0.012678888	59166	'29.5.11.4.2'	grmzm2g398198_t01	'protein.degradation.ubiquitin.E3.RING'
778	Nitr	1	249984566	148.2769963	25	0.000988754	38776	'27.3.99'	grmzm2g173425_t01	'RNA.regulation of transcription.unclassified'
779	Nitr	1	254217830	150.9046175	9	0.040341299	170083	'27.3.37'	grmzm2g017319_t01	'RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family'

780	Nitr	1	254218603	150.9052401	13	0.038373926	169310	'27.3.37'	grmzm2g017319_t01	'RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family'
781	Nitr	1	256241409	152.3975751	16	1.893176617	3351	'27.3.50'	grmzm2g018414_t01	'RNA.regulation of transcription.General Transcription'
782	Nitr	1	256250277	152.4041229	6	-3.973615173	122894	'20.2.3'	grmzm2g409093_t01	'stress.abiotic.drought/salt'
783	Nitr	1	256300512	152.4470842	7	-0.373608989	72659	'20.2.3'	grmzm2g409093_t01	'stress.abiotic.drought/salt'
784	Nitr	1	257414838	153.4001486	40	-0.007243298	20	'33.1'	grmzm2g067919_t01	'development.storage proteins'
785	Nitr	1	297905073	202.4622232	6	-0.001303846	103155	'30.5'	grmzm2g590033_t01	'signalling.G-proteins'
786	Nitr	2	3805	-5.496235757	26	0.001182912	84356	'31.4'	grmzm2g074530_t01	'cell.vesicle transport'
787	Nitr	2	2023274	3.619749446	24	0.001176073	4523	'31.8'	grmzm2g040247_t01	'cell.contractile vacuole'
788	Nitr	2	2211917	4.471293489	10	0.001669864	42195	'27.3.4'	grmzm2g078274_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
789	Nitr	2	2491029	5.715556905	6	0.000821883	29658	'29.5.3'	grmzm2g107187_t01	'protein.degradation.cysteine protease'

790	Nitr	2	9387311	27.56530943	6	0.001306219	8258	'30.2.11'	grmzm2g080041_t01	'signalling.receptor kinases.leucine rich repeat XI'
791	Nitr	2	31005737	62.07871475	22	0.001211646	33747	'30.2.11'	grmzm2g082191_t01	'signalling.receptor kinases.leucine rich repeat XI'
792	Nitr	2	36815670	65.26831102	10	0.001463549	28923	'31.2'	grmzm2g112072_t01	'cell.division'
793	Nitr	2	37323751	65.60272826	11	0.002275836	214	'28.1'	grmzm2g044989_t01	'DNA.synthesis/chromatin structure'
794	Nitr	2	181079834	90.99646529	39	0.001816495	23187	'27.3.7'	grmzm2g005954_t02	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
795	Nitr	2	182483954	92.38830408	38	0.001818773	824	'27.3.99'	grmzm2g090603_t01	'RNA.regulation of transcription.unclassified'
796	Nitr	2	183983052	94.29078232	8	0.002369111	4845	'29.5.5'	grmzm2g168196_t01	'protein.degradation.serine protease'
797	Nitr	2	186765944	97.99865221	7	0.001224906	303	'27.3.6'	grmzm2g417597_t02	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'

798	Nitr	2	203303901	111.3475511	5	0.002210804	10364	'26.7'	grmzm2g042660_t01	'misc.oxidases - copper, flavone etc.'
799	Nitr	2	211231604	122.5790956	20	0.002091497	22098	'34.2'	grmzm2g452930_t01	'transport.sugars'
800	Nitr	2	212538395	124.4779034	10	0.002047508	75099	'34.99'	grmzm2g070563_t01	'transport.misc'
801	Nitr	3	8109850	29.6995263	14	0.003636405	3991	'31.4'	grmzm2g015509_t01	'cell.vesicle transport'
802	Nitr	3	8678939	31.22826072	19	0.003500894	231	'20.2.1'	grmzm2g083810_t01	'stress.abiotic.heat'
803	Nitr	3	8924944	31.88908441	11	0.003569052	103716	'27.3.32'	grmzm2g151444_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
804	Nitr	3	158547954	71.48562889	28	0.000938613	6870	'27.3.99'	grmzm2g133428_t01	'RNA.regulation of transcription.unclassified'
805	Nitr	3	210217529	120.7696561	15	-0.000777862	81895	'28.99'	grmzm2g173989_t01	'DNA.unspecified'
806	Nitr	3	212234516	123.2864138	11	-0.00092326	10080	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
807	Nitr	3	212247177	123.3022119	10	-0.000811602	529	'26.28'	grmzm2g047129_t01	'misc.GDSL-motif lipase'

808	Nitr	3	212248108	123.3033736	27	-0.000852191	11	'26.28'	grmzm2g047129_t02	'misc.GDSL-motif lipase'
809	Nitr	3	212248700	123.3041123	15	-0.000804228	94418	'6.3'	grmzm2g466833_t01	'gluconeogenesis.Malate DH'
810	Nitr	3	213848077	126.6554907	7	-0.000894249	40822	'1.5.1'	grmzm2g121878_t01	'PS.carbon concentrating mechanism.C4'
811	Nitr	4	11351925	31.69382335	5	-0.003583568	108	'27.3.2'	grmzm2g008259_t01	'RNA.regulation of transcription.Alfin-like'
812	Nitr	4	11970641	33.81499619	6	-0.003758507	15538	'27.4'	grmzm2g010056_t02	'RNA.RNA binding'
813	Nitr	4	25849988	48.23626239	5	0.001059419	7700	'29.5.11.4.5.2'	grmzm2g026724_t01	'protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ'
814	Nitr	4	25850469	48.23645002	7	0.001284805	7219	'29.5.11.4.5.2'	grmzm2g026724_t01	'protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ'
815	Nitr	4	28177658	49.14422457	25	0.002716247	9566	'27.3.99'	grmzm2g426591_t01	'RNA.regulation of transcription.unclassified'
816	Nitr	4	28839372	49.4032225	7	0.005200168	130032	'27.1.19'	grmzm2g064868_t01	'RNA.processing.ribonucleases'

817	Nitr	4	101964449	57.85755427	9	0.003029113	163162	'34.10'	grmzm2g144254_t01	'transport.nucleotides'
818	Nitr	4	110010755	58.02556787	12	0.001209715	279193	'29.2.1.2.2.14'	grmzm2g323971_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L14'
819	Nitr	4	130200550	58.67643598	10	0.001469707	262479	'29.5.3'	grmzm2g139670_t01	'protein.degradation.cysteine protease'
820	Nitr	4	149531302	61.9954463	8	0.004684307	57230	'33.2'	grmzm2g100716_t01	'development.late embryogenesis abundant'
821	Nitr	4	163054280	73.24125003	10	-0.002480041	30403	'27.3.99'	grmzm2g168431_t01	'RNA.regulation of transcription.unclassified'
822	Nitr	4	163084391	73.26227648	17	-0.002987557	292	'27.3.99'	grmzm2g168431_t01	'RNA.regulation of transcription.unclassified'
823	Nitr	4	165718843	75.10190893	25	-0.003343143	145429	'29.5'	grmzm2g380457_t01	'protein.degradation'
824	Nitr	4	166175217	75.86	5	-0.0009	36325	'31.1'	grmzm2g136996_t01	'cell.organisation'
825	Nitr	4	167831848	76.66597097	7	-0.002511466	2055	'2.2.1.5'	grmzm2g045171_t01	'major CHO metabolism.degradation.sucrose.Susy'

826	Nitr	4	170457980	78.38642641	8	-0.002662805	5944	'27.3.40'	grmzm2g142768_t01	'RNA.regulation of transcription.Aux/IAA family'
827	Nitr	4	177460609	88.85205365	6	-0.000971011	80869	'29.1.15'	grmzm2g170313_t01	'protein.aa activation.proline-tRNA ligase'
828	Nitr	4	179532567	92.44677404	28	-0.002935932	52215	'20.2.3'	grmzm2g000764_t01	'stress.abiotic.drought/salt'
829	Nitr	4	242018406	128.094256	5	-0.026531277	6470	'30.2.17'	grmzm2g169020_t01	'signalling.receptor kinases.DUF 26'
830	Nitr	4	242343398	129.4163957	6	0.793685036	2086	'30.5'	grmzm2g101920_t01	'signalling.G-proteins'
831	Nitr	5	4862213	16.72130612	9	0.003196165	40910	'27.3.29'	grmzm2g089361_t01	'RNA.regulation of transcription.TCP transcription factor family'
832	Nitr	5	4925927	17.04607872	10	0.002167269	4371	'27.3.11'	grmzm2g089448_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
833	Nitr	5	7664787	29.12019513	5	0.001140887	15178	'29.4'	grmzm2g350844_t01	'protein.postranslational modification'
834	Nitr	5	162808563	76.42708275	6	0.003808286	57372	'31.1'	grmzm2g474531_t01	'cell.organisation'
835	Nitr	5	184229490	93.51868254	5	0.001723644	166972	'29.4'	grmzm2g463711_t01	'protein.postranslational modification'
836	Nitr	5	184794208	94.16914109	6	0.001178069	36189	'34.5'	grmzm2g028736_t01	'transport.ammonium'

837	Nitr	5	185030768	94.44161776	7	0.001440241	232883	'8.1.6'	grmzm2g064695_t01	'TCA / org. transformation.TCA.succinyl-CoA ligase'
838	Nitr	5	185056309	94.47103662	10	0.001491703	207342	'8.1.6'	grmzm2g064695_t01	'TCA / org. transformation.TCA.succinyl-CoA ligase'
839	Nitr	5	185687667	95.19825306	8	0.001158127	11103	'23.3.2.1'	grmzm2g540538_t01	'nucleotide metabolism.salvage.nucleoside kinases.adenosine kinase'
840	Nitr	5	185860200	95.39698157	5	0.000263629	1356	'16.2.1.1'	grmzm2g074604_t03	'secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL'
841	Nitr	5	190089272	99.5622766	29	-0.023979728	139380	'31.4'	grmzm2g171406_t01	'cell.vesicle transport'
842	Nitr	5	190169366	99.64088567	25	-0.032819686	59286	'31.4'	grmzm2g171406_t01	'cell.vesicle transport'
843	Nitr	5	190751918	100.0087423	59	0.060946443	96857	'17.5.2'	grmzm2g071844_t01	'hormone metabolism.ethylene.signal transduction'
844	Nitr	5	191728507	101.2378277	61	-0.033148662	4216	'11.9.4.5'	grmzm2g306566_t01	'lipid metabolism.lipid degradation.beta-oxidation.acyl-CoA thioesterase'

845	Nitr	5	205478714	119.252956	9	-0.001744117	11175	'27.3.25'	grmzm2g053396_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
846	Nitr	5	205662825	119.8501543	20	-0.001468083	95037	'10.7'	grmzm2g105844_t01	'cell wall.modification'
847	Nitr	5	205964077	120.8273212	11	-0.000771887	14845	'33.99'	grmzm2g380177_t01	'development.unspecified'
848	Nitr	5	207101210	124.0824263	25	-0.003509329	17	'3.2.2'	grmzm2g055150_t01	'minor CHO metabolism.trehalose.TPP'
849	Nitr	5	207118376	124.1210629	12	-0.000821003	772	'27.3.7'	grmzm2g041991_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
850	Nitr	5	207498927	124.9743369	13	-0.003573299	25119	'26.7'	grmzm2g059958_t01	'misc.oxidases - copper, flavone etc.'
851	Nitr	5	211861691	137.9485929	9	-0.00209302	18788	'29.5.11.4.2'	grmzm2g089466_t01	'protein.degradation.ubiquitin.E3.RING'

852	Nitr	6	78467563	11.02628868	8	0.00613447	288186	'27.3.40'	grmzm2g000158_t01	'RNA.regulation of transcription.Aux/IAA family'
853	Nitr	6	92041721	18.74190429	8	-0.007360541	27147	'18.1'	grmzm2g061821_t01	'Co-factor and vitamine metabolism.molybdenum cofactor'
854	Nitr	6	164046344	96.23353408	8	0.00311268	24836	'1.1.2.2'	grmzm2g451224_t01	'PS.lightreaction.photosystem I.PSI polypeptide subunits'
855	Nitr	7	94080369	50.29845615	7	-0.002187415	354	'21.2.1'	grmzm2g064106_t01	'redox.ascorbate and glutathione.ascorbate'
856	Nitr	7	97073633	50.59965001	5	-0.003762497	160838	'10.8.2'	grmzm2g113750_t01	'cell wall.pectin*esterases.acetyl esterase'
857	Nitr	7	121206635	61.30136801	7	0.003846053	23516	'24'	grmzm2g420786_t01	'Biodegradation of Xenobiotics'
858	Nitr	7	145280969	83.18936747	6	0.000758506	5515	'30.2.99'	grmzm2g163138_t01	'signalling.receptor kinases.misc'
859	Nitr	7	152493835	91.25002624	19	0.000787893	75899	'27.3.27'	grmzm2g179885_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
860	Nitr	8	20733895	45.60822058	7	0.002081662	128438	'27.3.27'	grmzm2g112681_t01	'RNA.regulation of transcription.NAC domain transcription factor family'

861	Nitr	8	139383376	71.29644034	13	-0.004157906	33360	'29.2.1.1.3.2.35'	grmzm2g423169_t01	'protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S subunit.L35'
862	Nitr	8	147013249	76.63825194	16	0.004700156	35582	'18.7'	grmzm2g064336_t01	'Co-factor and vitamine metabolism.iron-sulphur clusters'
863	Nitr	8	150840981	79.70937466	9	0.002809057	99103	'29.4'	grmzm2g518717_t01	'protein.postranslational modification'
864	Nitr	8	160985585	90.37557478	10	-0.000844257	225188	'31.4'	grmzm2g031352_t02	'cell.vesicle transport'
865	Nitr	9	23279446	40.13731735	8	-0.000527851	199835	'22.1.3'	grmzm2g396553_t01	'polyamine metabolism.synthesis.arginine decarboxylase'
866	Nitr	9	23407123	40.42055726	5	-0.000732831	72158	'22.1.3'	grmzm2g396553_t01	'polyamine metabolism.synthesis.arginine decarboxylase'
867	Nitr	9	25029010	42.41502107	13	-0.000589684	10953	'30.2.16'	grmzm2g335052_t01	'signalling.receptor kinases.Catharanthus roseus-like RLK1'
868	Nitr	9	121495902	60.17794088	5	-0.000866371	22322	'31.1'	grmzm2g343856_t01	'cell.organisation'

869	Nitr	9	151011382	109.2060086	64	0.003263514	14303	'16.8.4'	grmzm2g168355_t01	'secondary metabolism.flavonoids.flavonols'
870	Nitr	10	146509918	91.0233194	8	0.000766245	1082	'17.2.3'	grmzm2g442000_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
871	Nitr	10	146628442	91.61626493	10	0.000710638	28850	'27.3.4'	grmzm2g086949_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
872	Nitr	10	146744873	92.26893726	17	0.000679393	201	'26.5'	grmzm2g125083_t01	'misc.acyl transferases'
873	Nitr	10	147132717	94.44305795	6	0.000722548	989	'26.7'	grmzm2g150248_t02	'misc.oxidases - copper, flavone etc.'
874	Nitr	10	147981037	99.19844948	12	0.000848392	36945	'23.2'	grmzm2g173413_t01	'nucleotide metabolism.degradation'
875	Nitr	10	148513914	102.1855755	14	0.000913186	91418	'23.1.2.31'	grmzm2g136283_t01	'nucleotide metabolism.synthesis.purine.GMP synthetase'
876	Prot	1	64910659	74.0301357	9	-0.006095916	75579	'34.3'	grmzm2g127138_t01	'transport.amino acids'
877	Prot	1	64910976	74.03036785	33	-0.006371905	75262	'34.3'	grmzm2g127138_t01	'transport.amino acids'
878	Prot	1	69196228	76.41372859	13	-0.006630505	153059	'26.2'	grmzm2g123872_t01	'misc.UDP glucosyl and glucoronyl transferases'

879	Prot	1	69271066	76.45177556	5	-0.007173736	78221	'26.2'	grmzm2g123872_t01	'misc.UDP glucosyl and glucoronyl transferases'
880	Prot	1	74985643	79.35701503	8	-0.015969066	76392	'33.99'	grmzm2g075892_t01	'development.unspecified'
881	Prot	1	252882663	149.8292876	8	0.008583908	111731	'28.1'	grmzm2g099023_t01	'DNA.synthesis/chromatin structure'
882	Prot	2	20043374	50.80064207	26	-0.006974803	71742	'13.2.3.1.1'	grmzm2g139463_t01	'amino acid metabolism.degradation.aspartate family.asparagine.L-asparaginase'
883	Prot	2	185457136	96.16151574	6	0.006649714	33924	'27.3.6'	grmzm2g137541_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
884	Prot	3	1187527	-0.271888706	19	0.008814859	43949	'27.3.67'	ac233880.1_fgt005	'RNA.regulation of transcription.putative transcription regulator'
885	Prot	3	127883944	61.0242801	19	-0.009978835	273423	'29.4'	ac206425.3_fgt004	'protein.postranslational modification'
886	Prot	3	127884222	61.02430232	7	-0.008779638	273145	'29.4'	ac206425.3_fgt004	'protein.postranslational modification'
887	Prot	3	131786653	61.68464041	6	-0.014158624	92704	'29.2.1.2.1.9'	grmzm2g108348_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S9'
888	Prot	3	179931178	91.94664886	37	-0.006464741	8299	'28.99'	grmzm2g359230_t01	'DNA.unspecified'

889	Prot	3	186207858	97.81793168	13	-0.009426898	69471	'10.6.3'	ac213654.3_fgt006	'cell wall.degradation.pectate lyases and polygalacturonases'
890	Prot	3	186596173	98.06048224	5	-0.00757709	38992	'20.1'	grmzm2g047652_t01	'stress.biotic'
891	Prot	3	188565185	99.29037279	6	-0.006679739	4457	'11.8'	grmzm2g138800_t01	'lipid metabolism."exotics" (steroids, squalene etc)'
892	Prot	3	203411410	111.3198505	6	-0.006026391	94226	'34.99'	grmzm2g057283_t01	'transport.misc'
893	Prot	3	212222986	123.2720269	21	-0.006839459	21610	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
894	Prot	3	212224642	123.2740932	16	-0.007350952	19954	'16.7'	grmzm2g349407_t01	'secondary metabolism.wax'
895	Prot	3	213226535	125.1288155	17	-0.008878007	55830	'27.3.22'	grmzm2g126239_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
896	Prot	3	213800913	126.5396432	5	-0.007297196	1704	'26.2'	grmzm2g048010_t01	'misc.UDP glucosyl and glucoronyl transferases'
897	Prot	3	213854238	126.6706238	9	-0.007474129	34661	'1.5.1'	grmzm2g121878_t01	'PS.carbon concentrating mechanism.C4'
898	Prot	3	217611213	133.5696863	6	-0.008173794	7638	'28.99'	grmzm2g081924_t01	'DNA.unspecified'

899	Prot	4	168096468	76.74550042	5	-0.013008569	5907	'34.13'	grmzm2g019209_t01	'transport.peptides and oligopeptides'
900	Prot	4	227245511	112.6233194	44	0.009730652	127854	'26.16'	grmzm2g142037_t01	'misc.myrosinases-lectin-jacalin'
901	Prot	4	230742777	113.8187579	6	0.008891322	130027	'34.22'	grmzm2g148118_t01	'transport.cyclic nucleotide or calcium regulated channels'
902	Prot	5	88557383	69.4927261	74	-0.007848454	46768	'27.1'	grmzm2g058252_t01	'RNA.processing'
903	Prot	5	91037740	69.69522773	20	-0.006780225	43217	'29.4'	grmzm2g360455_t01	'protein.postranslational modification'
904	Prot	5	186016180	95.57664385	5	-0.00735679	4372	'34.22'	grmzm2g068904_t01	'transport.cyclic nucleotide or calcium regulated channels'
905	Prot	5	187955512	97.81042264	8	-0.005429395	5456	'27.3.3'	grmzm2g139765_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
906	Prot	5	189228254	98.86708725	21	-0.007553606	16596	'29.5.11.4.2'	grmzm2g409372_t01	'protein.degradation.ubiquitin.E3.RING'
907	Prot	5	203170982	112.0815943	20	-0.006893258	35767	'34.3'	grmzm2g161641_t01	'transport.amino acids'

908	Prot	5	205646722	119.7979212	18	-0.005971484	111140	'10.7'	grmzm2g105844_t01	'cell wall.modification'
909	Prot	5	206043601	121.085272	6	-0.006353574	14566	'27.3.29'	grmzm2g077755_t01	'RNA.regulation of transcription.TCP transcription factor family'
910	Prot	5	208092874	126.5365424	6	-0.005967461	26539	'29.5.11.4.2'	grmzm2g323013_t01	'protein.degradation.ubiquitin.E3.RING'
911	Prot	6	22422464	7.104655221	26	-0.006334214	488912	'30.2.17'	grmzm2g179270_t01	'signalling.receptor kinases.DUF 26'
912	Prot	6	35896471	8.2773635	5	-0.005965884	200355	'27.1.19'	grmzm2g124509_t01	'RNA.processing.ribonucleases'
913	Prot	6	72931425	10.26780431	14	-0.004869067	51246	'27.1.19'	grmzm2g047265_t01	'RNA.processing.ribonucleases'
914	Prot	6	72985636	10.2733065	9	-0.004940372	111093	'29.5.11.4.2'	grmzm2g430152_t01	'protein.degradation.ubiquitin.E3.RING'
915	Prot	6	73021951	10.27699232	13	-0.0080408	74778	'29.5.11.4.2'	grmzm2g430152_t01	'protein.degradation.ubiquitin.E3.RING'
916	Prot	6	168683648	108.6048676	13	0.011314553	124170	'27.3.25'	grmzm2g440349_t01	'RNA.regulation of transcription.MYB domain transcription factor family'

917	Prot	6	168748906	108.622076	35	0.007222797	58912	'27.3.25'	grmzm2g440349_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
918	Prot	7	5099065	21.78417429	9	-0.008417978	1869	'7.3'	grmzm2g011858_t01	'OPP.electron transfer'
919	Prot	7	33595519	47.99555999	10	0.00514782	68338	'20.1'	grmzm2g080547_t01	'stress.biotic'
920	Prot	7	154247787	94.54909037	7	0.005825457	17893	'34.2'	grmzm2g007909_t01	'transport.sugars'
921	Prot	7	157249277	100.7051801	14	0.006706373	24576	'29.4'	grmzm2g432796_t01	'protein.postranslational modification'
922	Prot	7	158036207	102.3366246	5	0.005791282	62508	'29.4.1.57'	grmzm2g017409_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
923	Prot	7	159778542	106.10253	6	0.012461708	2042	'30.11'	grmzm2g114461_t01	'signalling.light'
924	Prot	7	168378312	131.3238192	8	-0.007477326	31103	'3.1.1.2'	grmzm2g361984_t01	'minor CHO metabolism.raffinose family.galactinol synthases.putative'
925	Prot	8	21881574	47.44607971	10	0.011659826	27167	'29.2.3'	grmzm2g033283_t01	'protein.synthesis.initiation'

926	Prot	8	108880988	60.59133569	5	0.008562491	159905	'33.99'	grmzm2g101852_t01	'development.unspecified'
927	Prot	8	115683038	62.57820324	5	0.008392785	119756	'29.4.1.57'	grmzm2g090732_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
928	Prot	8	117977083	63.86243699	51	0.01116072	2390	'29.2.1.2.2.24'	grmzm2g142640_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L24'
929	Prot	8	129392376	68.26348656	8	0.009582417	111977	'27.3.22'	grmzm2g094241_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
930	Prot	8	131868393	69.1089486	5	-0.007281874	1759	'29.4'	grmzm2g005350_t01	'protein.postranslational modification'
931	Prot	8	161242940	90.87698678	53	-0.005415146	18253	'27.3.6'	grmzm2g030762_t02	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
932	Prot	8	170967906	124.4926125	15	-0.010060425	3673	'29.5.4'	grmzm2g133029_t01	'protein.degradation.aspartate protease'
933	Prot	9	73386482	45.90639706	5	-0.006073526	96108	'29.2.1.2.2.11'	grmzm2g001816_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L11'

934	Prot	9	75752943	46.01866137	10	-0.00678119	100423	'27.3.55'	grmzm2g008425_t01	'RNA.regulation of transcription.HDA'
935	Prot	9	86122013	46.66594904	22	-0.007718805	164316	'27.3.50'	grmzm2g058336_t01	'RNA.regulation of transcription.General Transcription'
936	Prot	9	98709960	49.58225494	8	-0.00680033	83560	'27.3.11'	grmzm2g436344_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
937	Prot	9	112772173	55.72841749	8	-0.006998869	98887	'10.7'	grmzm2g059785_t01	'cell wall.modification'
938	Prot	9	113322955	55.98017627	24	-0.006456001	431	'27.3.11'	grmzm2g152214_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
939	Prot	9	113731726	56.16702277	6	-0.00865215	12533	'10.8.2'	grmzm2g117999_t02	'cell wall.pectin*esterases.acetyl esterase'
940	Prot	9	120621679	59.56922799	5	-0.00678539	54616	'30.3'	grmzm2g047546_t04	'signalling.calcium'
941	Prot	9	122100192	60.59870208	5	-0.007751436	24620	'27.3.67'	grmzm2g127340_t01	'RNA.regulation of transcription.putative transcription regulator'
942	Prot	9	143538206	90.82527553	10	-0.007521104	8910	'10.6.2'	grmzm2g048375_t05	'cell wall.degradation.mannan-xylose-arabinose-fucose'

943	Prot	9	144829091	93.82411792	25	-0.004785192	8178	'29.5.11.4.2'	grmzm2g004157_t01	'protein.degradation.ubiquitin.E3.RING'
944	Prot	10	10440954	28.50645685	9	-0.008130968	190947	'34.3'	grmzm2g076593_t01	'transport.amino acids'
945	Prot	10	16919807	33.52470383	16	0.007567347	64360	'20.2.1'	grmzm2g170027_t01	'stress.abiotic.heat'
946	Prot	10	147427851	96.09747813	13	0.004748578	1997	'1.1.1.1'	grmzm2g092427_t01	'PS.lightreaction.photosystem II.LHC-II'
947	Prot	10	148213790	100.5031831	11	0.006813955	64402	'27.1.19'	grmzm2g177340_t01	'RNA.processing.ribonucleases'
948	Prot	10	148344527	101.23605	45	0.008225195	4374	'20.1'	grmzm2g406119_t01	'stress.biotic'
949	Prot	10	148496242	102.0865123	5	0.007112842	4411	'29.5.11.4.3.2'	grmzm2g104882_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
950	Star	1	7457814	13.94852432	86	-0.037258586	75819	'30.2.17'	grmzm2g410991_t02	'signalling.receptor kinases.DUF 26'
951	Star	1	17278764	33.6621462	5	-0.041877285	39171	'34.99'	grmzm2g115105_t01	'transport.misc'
952	Star	1	21382731	37.73085137	29	-0.023301274	63347	'27.3.99'	grmzm2g004259_t01	'RNA.regulation of transcription.unclassified'
953	Star	1	21383024	37.73112289	10	-0.022620507	63054	'27.3.99'	grmzm2g004259_t01	'RNA.regulation of transcription.unclassified'

954	Star	1	42174991	59.32632563	11	0.051194392	109965	'27.3.11'	grmzm2g048154_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
955	Star	1	45528222	61.4993069	7	0.044795124	33781	'34.9'	ac208201.3_fgt001	'transport.metabolite transporters at the mitochondrial membrane'
956	Star	1	46715564	62.60388883	8	0.035909602	37723	'27.1.1'	grmzm2g153450_t01	'RNA.processing.splicing'
957	Star	1	51113147	65.50551539	54	0.052957455	3172	'9.1.2'	grmzm2g018941_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
958	Star	1	51531509	66.02023986	6	0.089385584	118119	'3.1.1.2'	grmzm2g165919_t01	'minor CHO metabolism.raffinose family.galactinol synthases.putative'
959	Star	1	92753447	85.57176721	62	0.024022074	459526	'29.5.7'	grmzm2g317386_t01	'protein.degradation.metalloprotease'
960	Star	1	93661572	85.98563614	7	0.024453663	9642	'10.7'	grmzm2g021621_t02	'cell wall.modification'
961	Star	1	93667548	85.98835964	6	0.024126069	3666	'10.7'	grmzm2g021621_t02	'cell wall.modification'

962	Star	1	251149118	148.8823369	5	-0.048533652	22757	'20.1'	grmzm2g081099_t01	'stress.biotic'
963	Star	1	251176189	148.8964086	90	-0.057655015	13283	'13.2.2.3'	grmzm2g080828_t01	'amino acid metabolism.degradation.glutamate family.arginine'
964	Star	1	292560966	192.501744	10	-0.071069046	287	'10.7'	grmzm2g368886_t01	'cell wall.modification'
965	Star	2	5548326	16.71276385	15	-0.027020805	16078	'27.3.3'	grmzm2g174917_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
966	Star	2	5548414	16.71309841	83	-0.028470515	15990	'27.3.3'	grmzm2g174917_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
967	Star	2	21795122	52.9770168	8	-0.021390127	30205	'27.3.7'	grmzm2g131982_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
968	Star	2	22808083	54.70986501	76	-0.029176947	62966	'29.5.4'	grmzm2g003784_t01	'protein.degradation.aspartate protease'
969	Star	2	27790884	58.80007957	13	-0.032182719	109799	'27.3.4'	grmzm2g122614_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'

970	Star	2	28788480	60.39948962	5	-0.024239309	58573	'20.1'	grmzm2g032602_t01	'stress.biotic'
971	Star	2	28788620	60.39963767	12	-0.023889437	58433	'20.1'	grmzm2g032602_t01	'stress.biotic'
972	Star	2	28960635	60.58154184	5	-0.030823242	99412	'9.1.2'	grmzm2g141605_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
973	Star	2	28970761	60.59224999	8	-0.031083803	89286	'9.1.2'	grmzm2g141605_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
974	Star	2	28972476	60.59406358	35	-0.02957084	87571	'9.1.2'	grmzm2g141605_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
975	Star	2	107216168	76.50296846	7	-0.030529227	824	'8.1.1.1'	grmzm2g033894_t01	'TCA / org. transformation.TCA.pyruvate DH.E1'
976	Star	2	194191603	105.3998294	6	-0.020841194	40827	'17.2.3'	grmzm2g151656_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
977	Star	2	201217096	109.0293094	10	-0.026005633	65219	'29.2.1.1.3.2.28'	grmzm2g319634_t01	'protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S subunit.L28'

978	Star	2	203650489	111.7689321	15	-0.025557901	43040	'27.1'	grmzm2g099105_t01	'RNA.processing'
979	Star	2	205289573	113.7617273	5	-0.031413614	8694	'29.5.11.2'	grmzm2g129575_t01	'protein.degradation.ubiquitin.E1'
980	Star	2	205289574	113.7617285	9	-0.027499236	8693	'29.5.11.2'	grmzm2g129575_t01	'protein.degradation.ubiquitin.E1'
981	Star	2	214729037	127.4005253	5	-0.017802912	97107	'29.5.5'	grmzm2g387383_t01	'protein.degradation.serine protease'
982	Star	2	215881188	128.7144115	7	-0.017742045	29599	'34.99'	grmzm2g068220_t01	'transport.misc'
983	Star	2	217125385	130.3224898	5	-0.027701512	37889	'29.5.11.4.3.2'	grmzm2g048661_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'
984	Star	2	217810072	131.5466232	5	-0.0237361	68817	'27.4'	grmzm2g124809_t01	'RNA.RNA binding'
985	Star	3	3123500	9.745986067	7	0.038612596	192	'27.3.69'	grmzm2g085266_t01	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
986	Star	3	3780999	13.14827662	22	0.028169623	2780	'29.7'	grmzm2g093278_t01	'protein.glycosylation'

987	Star	3	3836355	13.43472146	17	0.031403613	35512	'34.3'	grmzm2g146161_t01	'transport.amino acids'
988	Star	3	14416721	41.56032683	5	-0.028022937	25363	'20.1'	grmzm2g062576_t01	'stress.biotic'
989	Star	3	17306447	45.29685092	89	-0.032281971	20778	'30.5'	grmzm2g166064_t01	'signalling.G-proteins'
990	Star	3	51981075	56.79858368	90	0.084784527	127495	'17.5.1'	grmzm2g363893_t01	'hormone metabolism.ethylene.synthesis-degradation'
991	Star	3	170725018	81.65819468	5	-0.07741098	65257	'29.7'	grmzm2g431006_t01	'protein.glycosylation'
992	Star	3	178840635	90.20644881	8	0.036888541	17640	'27.3.32'	grmzm2g178671_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
993	Star	3	192649685	100.9866632	10	-0.050036116	42671	'23.4.99'	grmzm2g052816_t01	'nucleotide metabolism.phosphotransfer and pyrophosphatases.misc'
994	Star	3	192874331	101.0880183	8	-0.042136484	88999	'26.4'	grmzm2g162768_t01	'misc.beta 1,3 glucan hydrolases'

995	Star	3	192949443	101.1219071	9	-0.0571714	13887	'26.4'	grmzm2g162768_t01	'misc.beta 1,3 glucan hydrolases'
996	Star	3	193619852	101.4802146	6	-0.049654665	18058	'27.3.67'	grmzm2g015881_t01	'RNA.regulation of transcription.putative transcription regulator'
997	Star	3	193620690	101.4814585	27	-0.053595039	17220	'27.3.67'	grmzm2g015881_t01	'RNA.regulation of transcription.putative transcription regulator'
998	Star	3	194144683	102.2592936	5	-0.038147905	2909	'27.3.8'	grmzm2g394973_t01	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'
999	Star	4	24269222	47.52251807	66	0.054432733	205777	'17.5.3'	grmzm2g101480_t01	'hormone metabolism.ethylene.induced-regulated-responsive-activated'
1000	Star	4	26928416	48.65692848	6	0.054001982	19119	'1.1.1.2'	grmzm2g174984_t01	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
1001	Star	4	63204562	55.58951138	5	-0.024189406	67970	'27.3.29'	grmzm2g062711_t01	'RNA.regulation of transcription.TCP transcription factor family'
1002	Star	4	116242442	58.15932573	10	-0.026678988	632941	'27.3.5'	grmzm2g096171_t01	'RNA.regulation of transcription.ARR'
1003	Star	4	194884222	103.0017383	8	-0.034945398	12238	'34.14'	grmzm2g401874_t01	'transport.unspecified cations'

1004	Star	4	194952409	103.053073	8	-0.027789043	48973	'20.1'	grmzm2g050959_t01	'stress.biotic'
1005	Star	4	240714112	124.303751	25	-0.017633483	52492	'29.5.11'	grmzm2g037185_t01	'protein.degradation.ubiquitin'
1006	Star	4	245062382	140.1088204	5	-0.026856027	42239	'31.1'	grmzm2g169871_t01	'cell.organisation'
1007	Star	4	245730715	144.0453722	15	-0.017329439	4805	'21.6'	grmzm2g079348_t01	'redox.dismutases and catalases'
1008	Star	4	245730944	144.0467211	11	-0.017442961	4576	'21.6'	grmzm2g079348_t01	'redox.dismutases and catalases'
1009	Star	4	245787531	144.3800244	15	-0.026106421	60132	'33.99'	grmzm2g010372_t01	'development.unspecified'
1010	Star	4	246077836	146.0899515	5	-0.021761826	66707	'27.3.30'	grmzm2g037128_t02	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
1011	Star	5	1529458	1.89866854	11	-0.026956905	7573	'29.4.1.56'	grmzm2g148962_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VI'
1012	Star	5	1532216	1.906091195	16	-0.020171388	4815	'29.4.1.56'	grmzm2g148962_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VI'

1013	Star	5	1735588	2.453429899	6	-0.019083198	24507	'21.4'	grmzm2g053378_t01	'redox.glutaredoxins'
1014	Star	5	1879182	2.839887002	5	-0.025793792	3659	'28.1'	grmzm2g398668_t01	'DNA.synthesis/chromatin structure'
1015	Star	5	20941271	51.30637712	10	-0.050307121	489	'27.3.44'	grmzm2g146041_t04	'RNA.regulation of transcription.Chromatin Remodeling Factors'
1016	Star	5	75996032	67.01800088	5	0.071648285	42717	'29.4.1.57'	grmzm2g398559_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
1017	Star	5	96165401	69.92179085	29	0.054394768	287647	'27.3.99'	grmzm2g119921_t01	'RNA.regulation of transcription.unclassified'
1018	Star	5	145308951	72.52912618	15	-0.06568065	375787	'31.4'	grmzm2g372812_t01	'cell.vesicle transport'
1019	Star	5	168868583	80.63961419	67	-0.073140188	54819	'29.6'	grmzm2g039089_t01	'protein.folding'
1020	Star	5	171396511	83.30241817	34	0.023072258	188322	'28.2'	grmzm2g139031_t01	'DNA.repair'
1021	Star	5	174165684	85.75501381	25	0.029476756	52182	'29.5.11.4.2'	grmzm2g331253_t01	'protein.degradation.ubiquitin.E3.RING'
1022	Star	5	174821506	86.48707371	5	0.027732203	5443	'30.11'	grmzm2g105400_t01	'signalling.light'

1023	Star	5	193444292	102.0960523	28	0.019728235	76235	'27.3.62'	grmzm2g013821_t01	'RNA.regulation of transcription.Nucleosome/chromatin assembly factor group'
1024	Star	5	195201674	103.5571638	6	0.019382462	57099	'10.1.10'	grmzm2g072911_t01	'cell wall.precursor synthesis.UDP-glucose 4,6-dehydratase'
1025	Star	5	203772980	114.279637	34	0.032389813	4519	'29.3.4.99'	grmzm2g089454_t01	'protein.targeting.secretory pathway.unspecified'
1026	Star	5	204520039	116.1433154	8	0.021779461	7639	'10.6.1'	grmzm2g151257_t01	'cell wall.degradation.cellulases and beta -1,4-glucanases'
1027	Star	5	205480420	119.2584897	23	0.024091119	9469	'27.3.25'	grmzm2g053396_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1028	Star	5	207749910	125.7434999	9	0.032228364	1083	'27.4'	grmzm2g303915_t01	'RNA.RNA binding'
1029	Star	6	25145461	7.801186431	11	-0.069037952	24877	'28.1.3'	grmzm2g448458_t01	'DNA.synthesis/chromatin structure.histone'
1030	Star	6	118288607	43.43874583	32	-0.072025188	6156	'33.99'	grmzm2g164308_t01	'development.unspecified'
1031	Star	6	119252741	43.97152587	16	-0.049737056	181387	'29.4'	grmzm2g159953_t01	'protein.postranslational modification'

1032	Star	6	156368499	74.39513977	7	0.053819036	32885	'26.4'	grmzm2g088951_t01	'misc.beta 1,3 glucan hydrolases'
1033	Star	6	166337059	105.4357129	22	-0.05306977	7973	'31.4'	grmzm2g438895_t01	'cell.vesicle transport'
1034	Star	6	166977847	107.6073304	44	-0.037821131	11484	'29.5.5'	grmzm2g159016_t01	'protein.degradation.serine protease'
1035	Star	7	18458794	44.19878603	5	-0.027460741	28908	'10.2.1'	grmzm2g424832_t01	'cell wall.cellulose synthesis.cellulose synthase'
1036	Star	7	20248668	44.70548997	38	-0.042578673	418915	'33.99'	ac212570.3_fgt006	'development.unspecified'
1037	Star	7	20380953	44.78804553	7	-0.06171405	286630	'33.99'	ac212570.3_fgt006	'development.unspecified'
1038	Star	7	21623347	45.56339066	5	-0.02739467	135440	'34.12'	grmzm2g093276_t01	'transport.metal'
1039	Star	7	25948068	46.52566875	5	-0.043273669	39876	'2.1.2.1'	grmzm2g144002_t01	'major CHO metabolism.synthesis.starch.AGPase'

1040	Star	7	29953895	47.26241735	12	-0.028721815	38416	'33.2'	grmzm2g053637_t01	'development.late embryogenesis abundant'
1041	Star	7	126449302	67.30732758	10	-0.021768781	2413	'29.5.11.4.1'	grmzm2g181378_t01	'protein.degradation.ubiquitin.E3.HECT'
1042	Star	7	151507555	89.39729712	9	-0.032132802	1643	'27.3.25'	grmzm2g031323_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1043	Star	7	151913077	90.15766003	9	-0.079858825	12823	'11.8.1'	grmzm2g057475_t01	'lipid metabolism."exotics" (steroids, squalene etc).sphingolipids'
1044	Star	7	152316144	90.91580158	14	-0.058489035	56984	'27.3.42'	grmzm2g434301_t02	'RNA.regulation of transcription.Bromodomain proteins'
1045	Star	7	167105793	125.7933142	15	0.059219318	584	'29.4'	grmzm2g177050_t01	'protein.postranslational modification'
1046	Star	7	168184709	130.4823997	13	0.045148368	5553	'27.3.19'	grmzm2g151811_t01	'RNA.regulation of transcription.EIN3-like(EIL) transcription factor family'
1047	Star	7	168193557	130.520854	5	0.036616985	66536	'29.5.1'	grmzm2g059165_t01	'protein.degradation.subtilases'
1048	Star	8	121670463	65.96008974	11	0.045441796	21053	'27.3.8'	ac209819.3_fgt009	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'

1049	Star	8	121963051	66.1316561	6	0.042894621	23142	'27.3.37'	ac234149.1_fgt002	'RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family'
1050	Star	8	144585092	74.43452065	10	-0.055256199	64095	'29.4.1.55'	grmzm2g017386_t02	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase V'
1051	Star	8	144767036	74.6069579	5	-0.056636807	38988	'10.6.3'	grmzm2g179696_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
1052	Star	8	145553053	75.35190474	19	-0.047411963	136731	'34.8'	grmzm2g050003_t01	'transport.metabolite transporters at the envelope membrane'
1053	Star	8	149499942	78.63341235	8	-0.058651712	7548	'28.1'	grmzm2g052296_t01	'DNA.synthesis/chromatin structure'
1054	Star	8	163958147	96.68361641	7	0.041224908	11592	'27.3.27'	grmzm2g092759_t01	'RNA.regulation of transcription.NAC domain transcription factor family'
1055	Star	8	164575505	99.62785513	54	0.021849064	16931	'27.3.25'	grmzm2g405094_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1056	Star	8	164575577	99.62807455	6	0.025622402	16859	'27.3.25'	grmzm2g405094_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1057	Star	8	170790378	123.8097673	5	0.018186972	138833	'29.5.7'	grmzm2g133249_t01	'protein.degradation.metalloprotease'

1058	Star	8	171107120	125.0290187	12	0.025903354	8056	'17.4.1'	grmzm2g024476_t01	'hormone metabolism.cytokinin.synthesis-degradation'
1059	Star	8	171214220	125.4546422	15	0.023236917	20943	'33.1'	grmzm2g111472_t01	'development.storage proteins'
1060	Star	8	171235640	125.5397669	5	0.03304263	4349	'26.2'	grmzm2g111428_t01	'misc.UDP glucosyl and glucoronyl transferases'
1061	Star	9	6999006	8.219780095	15	-0.070552837	109664	'27.2'	grmzm2g017537_t01	'RNA.transcription'
1062	Star	9	7182819	8.716269429	27	-0.043529797	56750	'17.7.1.5'	grmzm2g000236_t01	'hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase'
1063	Star	9	7188622	8.731943661	42	-0.041058477	50947	'17.7.1.5'	grmzm2g000236_t01	'hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase'
1064	Star	9	8451164	12.14214118	5	-0.047028655	149948	'27.3.22'	grmzm2g062318_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
1065	Star	9	134402439	70.88375129	15	0.037960828	80058	'10.1.5'	grmzm2g347717_t01	'cell wall.precursor synthesis.UXS'
1066	Star	9	134402663	70.88410046	6	0.036821304	79834	'10.1.5'	grmzm2g347717_t01	'cell wall.precursor synthesis.UXS'

1067	Star	10	252732	-5.658225645	12	-0.051134421	130394	'26.10'	grmzm2g135536_t01	'misc.cytochrome P450'
1068	Star	10	5058530	14.79019912	16	-0.06180889	56738	'30.2.26'	grmzm2g051637_t01	'signalling.receptor kinases.crinkly like'
1069	Star	10	19566488	34.07832787	6	0.024937218	19288	'30.4.5'	grmzm2g006206_t01	'signalling.phosphinositides.inositol-1,3,4-trisphosphate 5/6-kinase'
1070	Star	10	24052625	35.28519133	6	-0.043928314	390904	'21.1'	grmzm2g141848_t01	'redox.thioredoxin'
1071	Star	10	25801766	35.75574637	8	0.085574049	163401	'13.1.6.1.10'	grmzm2g014376_t01	'amino acid metabolism.synthesis.aromatic aa.chorismate.dehydroquinate/shikimate dehydrogenase'
1072	Star	10	66920393	36.73131562	29	0.080127465	212540	'27.3.1'	grmzm2g423393_t01	'RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing transcription factor family'
1073	Star	10	89396968	41.46314855	33	0.05899755	15206	'33.99'	grmzm2g339820_t01	'development.unspecified'
1074	Star	10	128172908	51.27327366	11	0.06244423	30487	'34.15'	grmzm2g000261_t01	'transport.potassium'
1075	Star	10	129906986	52.44415722	5	0.052854061	20956	'26.3'	grmzm2g031628_t01	'misc.gluco-, galacto- and mannosidases'

1076	Star	10	140767339	72.41844784	6	-0.032991889	105575	'10.7'	grmzm2g142857_t01	'cell wall.modification'
1077	Star	10	141976268	75.93807797	6	-0.020261715	31348	'15.2'	grmzm2g354855_t01	'metal handling.binding, chelation and storage'
1078	Star	10	141976795	75.94005902	15	-0.022617226	30821	'15.2'	grmzm2g354855_t01	'metal handling.binding, chelation and storage'
1079	Star	10	144909314	84.63476656	5	-0.022505092	22430	'31.3'	grmzm2g546369_t01	'cell.cycle'
1080	Star	10	145742058	87.95852999	6	-0.025366805	105204	'27.3.28'	grmzm2g058588_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
1081	Sucr	1	21442536	37.78627202	7	-0.039016626	3542	'27.3.99'	grmzm2g004259_t01	'RNA.regulation of transcription.unclassified'
1082	Sucr	1	21449014	37.79227512	7	-0.03673907	9475	'29.5.11.4.2'	grmzm2g004422_t01	'protein.degradation.ubiquitin.E3.RING'
1083	Sucr	1	21560442	37.97512826	47	-0.038190551	31998	'17.5.2'	ac200038.4_fgt011	'hormone metabolism.ethylene.signal transduction'
1084	Sucr	1	21688795	38.19316881	12	-0.036506395	21240	'26.24'	grmzm2g114184_t01	'misc.GCN5-related N-acetyltransferase'
1085	Sucr	1	21689538	38.19443099	17	-0.081014671	20497	'26.24'	grmzm2g114184_t01	'misc.GCN5-related N-acetyltransferase'

1086	Sucr	1	56544677	69.98493609	7	0.091004411	113019	'19.7'	grmzm2g044074_t02	'tetrapyrrole synthesis.uroporphyrinogen decarboxylase'
1087	Sucr	1	69598189	76.61808194	8	0.06063527	17432	'29.4.1.57'	grmzm2g142390_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
1088	Sucr	1	274645019	167.2992575	6	0.087168737	5834	'29.4'	grmzm2g131629_t01	'protein.postranslational modification'
1089	Sucr	2	2076282	3.859030239	6	-0.033975872	133215	'30.2.11'	grmzm2g452142_t01	'signalling.receptor kinases.leucine rich repeat XI'
1090	Sucr	2	3086016	6.851945591	12	-0.032332673	313	'29.1.4'	grmzm2g071333_t01	'protein.aa activation.leucine-tRNA ligase'
1091	Sucr	2	16641157	44.04382336	15	-0.073754786	10096	'31.1'	grmzm2g081032_t01	'cell.organisation'
1092	Sucr	2	22494974	54.03923714	9	-0.048242813	2409	'30.2.99'	grmzm2g062471_t01	'signalling.receptor kinases.misc'
1093	Sucr	2	28592546	60.19229134	29	-0.039020967	2135	'27.3.67'	grmzm2g052688_t01	'RNA.regulation of transcription.putative transcription regulator'
1094	Sucr	2	28594174	60.19401294	7	-0.040826501	507	'27.3.67'	grmzm2g052688_t01	'RNA.regulation of transcription.putative transcription regulator'

1095	Sucr	2	28973324	60.59496034	16	-0.039233491	86723	'9.1.2'	grmzm2g141605_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
1096	Sucr	3	13298136	40.11395447	19	-0.042921756	248	'34.19.2'	grmzm2g146627_t01	'transport.Major Intrinsic Proteins.TIP'
1097	Sucr	3	16863398	44.72397195	35	-0.053561956	4617	'20.1'	ac215260.3_fgt001	'stress.biotic'
1098	Sucr	3	16863598	44.72423056	21	-0.054013921	4417	'20.1'	ac215260.3_fgt001	'stress.biotic'
1099	Sucr	3	20147626	48.97060192	5	-0.037039448	8026	'20.2.1'	grmzm2g437100_t01	'stress.abiotic.heat'
1100	Sucr	3	110202362	58.86475128	7	0.123753616	122264	'20.2.4'	grmzm2g028665_t01	'stress.abiotic.touch/wounding'
1101	Sucr	3	174587864	84.65461078	5	0.067483949	101677	'27.3.26'	grmzm2g027914_t01	'RNA.regulation of transcription.MYB-related transcription factor family'
1102	Sucr	3	221390629	140.2263942	10	-0.044839083	16918	'34.3'	grmzm2g476954_t01	'transport.amino acids'
1103	Sucr	4	11976890	33.81581685	5	0.063333379	9289	'27.4'	grmzm2g010056_t02	'RNA.RNA binding'
1104	Sucr	4	12389613	33.87001839	25	0.073578644	226873	'27.1'	grmzm2g030463_t01	'RNA.processing'

1105	Sucr	4	17655938	40.84317673	14	0.091223346	69362	'26.8'	grmzm2g173105_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
1106	Sucr	4	49286057	55.14879543	6	-0.093785941	238546	'27.3.67'	grmzm2g173479_t01	'RNA.regulation of transcription.putative transcription regulator'
1107	Sucr	4	60649130	55.4149908	15	-0.083392435	118072	'31.3.1'	grmzm2g049525_t01	'cell.cycle.peptidylprolyl isomerase'
1108	Sucr	4	110959949	58.04594151	5	-0.074747404	453213	'11.3'	ac217811.3_fgt002	'lipid metabolism.Phospholipid synthesis'
1109	Sucr	4	140704850	60.02921307	7	-0.041801329	555464	'29.4'	grmzm2g162637_t01	'protein.postranslational modification'
1110	Sucr	4	173809531	84.19454361	9	-0.032604677	47484	'29.4'	grmzm2g135073_t01	'protein.postranslational modification'
1111	Sucr	4	173813253	84.2005901	5	-0.034242183	43762	'29.4'	grmzm2g135073_t01	'protein.postranslational modification'
1112	Sucr	4	173813260	84.20060147	28	-0.039007994	43755	'29.4'	grmzm2g135073_t01	'protein.postranslational modification'

1113	Sucr	4	175615429	86.62964208	5	-0.045120538	118213	'10.6.3'	grmzm2g047414_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
1114	Sucr	5	7403398	28.1227481	5	0.028118305	873	'27.3.63'	grmzm2g087482_t01	'RNA.regulation of transcription.PHD finger transcription factor'
1115	Sucr	5	7568984	28.7329509	5	0.03044864	93287	'14.1'	grmzm2g051270_t01	'S-assimilation.ATPS'
1116	Sucr	5	52480298	61.27077539	9	0.075988657	30430	'26.12'	grmzm2g142011_t02	'misc.peroxidases'
1117	Sucr	5	68604010	65.0820323	8	0.067664981	3265	'33.99'	grmzm2g389155_t01	'development.unspecified'
1118	Sucr	5	68606903	65.08331839	14	0.085965605	372	'33.99'	grmzm2g389155_t01	'development.unspecified'
1119	Sucr	5	73961139	66.43957914	7	-0.05697045	243055	'29.5.11.4.2'	grmzm2g072142_t01	'protein.degradation.ubiquitin.E3.RING'
1120	Sucr	5	76585969	67.18687192	15	-0.06624114	287731	'17.8.1'	grmzm2g303419_t01	'hormone metabolism.salicylic acid.synthesis-degradation'
1121	Sucr	5	80096521	67.90868619	6	-0.061436645	23270	'27.3.67'	grmzm2g425774_t01	'RNA.regulation of transcription.putative transcription regulator'

1122	Sucr	5	173340061	84.83341391		9	0.040041361	107050	'27.3.3'	grmzm2g087040_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1123	Sucr	5	184390409	93.70403371		8	0.03379498	6053	'29.4'	grmzm2g463711_t01	'protein.postranslational modification'
1124	Sucr	5	184579203	93.9214921		6	0.048528702	597	'21.4'	grmzm2g148387_t01	'redox.glutaredoxins'
1125	Sucr	5	204093596	114.9003073		8	0.029700141	2446	'29.5'	grmzm2g090981_t01	'protein.degradation'
1126	Sucr	5	204527912	116.1688529		7	0.036011734	70954	'8.1.1.1'	grmzm2g140150_t01	'TCA / org. transformation.TCA.pyruvate DH.E1'
1127	Sucr	6	120727054	44.61545648		5	-0.053699952	159637	'27.3.99'	grmzm2g174129_t01	'RNA.regulation of transcription.unclassified'
1128	Sucr	6	120956190	44.6914035		8	-0.077855121	105351	'23.1.2.9'	grmzm2g164665_t01	'nucleotide metabolism.synthesis.purine.AICAR transformylase'
1129	Sucr	6	125454322	46.41917569		67	-0.070562811	1745	'30.3'	grmzm2g152040_t02	'signalling.calcium'
1130	Sucr	6	161584484	86.71512205		10	-0.089408624	14608	'31.1'	grmzm2g445423_t01	'cell.organisation'
1131	Sucr	6	161899740	87.96647854		58	-0.077401595	65874	'27.3.6'	grmzm2g094892_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'

1132	Sucr	7	2586268	7.006474955	17	-0.036400236	1170	'29.6'	grmzm2g043383_t01	'protein.folding'
1133	Sucr	7	3570399	12.79412594	7	-0.060608629	99940	'27.3.22'	grmzm2g028041_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
1134	Sucr	7	107347438	54.26102457	17	-0.042958657	108249	'27.3.80'	grmzm2g161315_t01	'RNA.regulation of transcription.zf-HD'
1135	Sucr	7	107748384	54.46470141	23	-0.048482794	9704	'34.2'	grmzm2g029153_t01	'transport.sugars'
1136	Sucr	7	112739677	57.00023193	20	-0.052798268	168812	'33.99'	grmzm2g041175_t01	'development.unspecified'
1137	Sucr	7	117566293	59.45210806	8	-0.045031015	529	'29.4'	grmzm2g396350_t01	'protein.postranslational modification'
1138	Sucr	7	140199828	78.55767933	6	0.050727731	137104	'26.7'	grmzm2g041394_t01	'misc.oxidases - copper, flavone etc.'
1139	Sucr	7	158146806	102.5659158	5	-0.076514492	55878	'26.8'	grmzm2g151801_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'

1140	Sucr	7	169562400	134.5167655	17	-0.03237163	38864	'29.2.1.2.1.4'	grmzm2g086656_t01	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4'
1141	Sucr	8	163333139	94.90114389	20	0.100296937	99019	'29.5.5'	grmzm2g172829_t01	'protein.degradation.serine protease'
1142	Sucr	8	164331901	98.88225877	17	0.036391177	34241	'29.5.11.1'	grmzm2g114172_t01	'protein.degradation.ubiquitin.ubiquitin'
1143	Sucr	8	164401313	99.09699982	5	0.085464891	15381	'1.2.5'	grmzm2g113959_t01	'PS.photorespiration.serine hydroxymethyltransferase'
1144	Sucr	8	164401324	99.09703335	20	0.065104941	15370	'1.2.5'	grmzm2g113959_t01	'PS.photorespiration.serine hydroxymethyltransferase'
1145	Sucr	8	164401576	99.09780132	7	0.074809194	15118	'1.2.5'	grmzm2g113959_t01	'PS.photorespiration.serine hydroxymethyltransferase'
1146	Sucr	8	168628318	113.9072651	19	0.03649192	81970	'20.2.99'	grmzm2g169695_t01	'stress.abiotic.unspecified'

1147	Sucr	8	172057184	128.8248994	5	0.045679833	8995	'27.3.17'	grmzm2g104246_t01	'RNA.regulation of transcription.CPP(Zn),CPP1-related transcription factor family'
1148	Sucr	8	172057190	128.8249236	9	0.044703695	8989	'27.3.17'	grmzm2g104246_t01	'RNA.regulation of transcription.CPP(Zn),CPP1-related transcription factor family'
1149	Sucr	10	2166827	0.955425267	15	-0.093456643	9229	'1.1.5.3'	grmzm2g320305_t01	'PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase'
1150	Sucr	10	2698524	2.792564149	42	-0.098765758	11584	'30.11'	grmzm2g058531_t01	'signalling.light'
1151	Sucr	10	3240557	4.665416356	5	-0.076233214	49388	'20.1'	grmzm2g349565_t01	'stress.biotic'
1152	Sucr	10	77488297	38.59893808	5	-0.053379979	386121	'26.8'	grmzm2g078906_t01	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
1153	Sucr	10	85544281	40.43156797	5	-0.03474644	42084	'26.12'	grmzm2g006727_t01	'misc.peroxidases'
1154	Sucr	10	113451096	45.40733399	7	-0.04402236	57318	'28.1'	grmzm2g147390_t01	'DNA.synthesis/chromatin structure'
1155	Prin1	1	52690146	67.43745454	28	-0.325669425	22847	'26.21'	grmzm2g174680_t01	'misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein'

1156	Prin1	1	86713369	83.51202829	6	-0.361580066	39984	'26.7'	grmzm2g425719_t01	'misc.oxidases - copper, flavone etc.'
1157	Prin1	1	89352884	84.21946029	45	-0.377779862	50645	'30.3'	grmzm2g107575_t01	'signalling.calcium'
1158	Prin1	1	172752341	94.00861544	12	0.251503889	56380	'27.1.2'	grmzm2g107984_t01	'RNA.processing.RNA helicase'
1159	Prin1	1	173107592	94.12366453	7	0.364562902	73759	'27.3.14'	grmzm2g361842_t01	'RNA.regulation of transcription.CCAAT box binding factor family, HAP2'
1160	Prin1	1	206686287	118.8958806	6	-0.243142768	113757	'27.3.11'	grmzm2g042407_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
1161	Prin1	1	212358693	123.8826126	13	-0.187087297	24411	'29.5'	grmzm2g152485_t01	'protein.degradation'
1162	Prin1	1	219369577	128.5769255	8	-0.230027518	29974	'27.3.69'	grmzm2g074094_t02	'RNA.regulation of transcription.SET-domain transcriptional regulator family'
1163	Prin1	1	221341695	129.3656668	18	-0.363923496	184041	'34.3'	grmzm2g149946_t01	'transport.amino acids'
1164	Prin1	2	2211542	4.46960072	7	0.173420062	42570	'27.3.4'	grmzm2g078274_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
1165	Prin1	2	2211569	4.4697226	21	0.190449042	42543	'27.3.4'	grmzm2g078274_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'

1166	Prin1	2	4299945	11.96658077	43	0.175516911	6262	'34.1'	grmzm2g019404_t01	'transport.p- and v-ATPases'
1167	Prin1	2	4870077	14.13414888	6	0.185328555	9259	'34.6'	grmzm2g395114_t01	'transport.sulphate'
1168	Prin1	2	37249730	65.55400788	27	0.483745172	2987	'33.99'	grmzm2g063163_t01	'development.unspecified'
1169	Prin1	2	38625981	66.45985177	6	0.393707078	50517	'17.5.1'	grmzm2g121700_t04	'hormone metabolism.ethylene.synthesis-degradation'
1170	Prin1	2	39794143	67.22873216	23	0.5113885	91213	'27.1'	grmzm2g027571_t01	'RNA.processing'
1171	Prin1	2	39879711	67.28505273	9	0.434301435	5645	'27.1'	grmzm2g027571_t01	'RNA.processing'
1172	Prin1	2	185284281	95.94214858	24	0.238072478	169068	'27.3.35'	grmzm2g137532_t01	'RNA.regulation of transcription.bZIP transcription factor family'
1173	Prin1	2	186269385	97.19232631	15	0.189950055	3715	'27.3.16'	grmzm2g022162_t01	'RNA.regulation of transcription.CCAAT box binding factor family, HAP5'
1174	Prin1	2	186285785	97.21313925	13	0.19792386	1784	'34.99'	grmzm2g031837_t01	'transport.misc'
1175	Prin1	2	186766346	97.99944104	24	0.201406468	76022	'27.3.57'	grmzm2g052908_t01	'RNA.regulation of transcription.JUMONJI family'

1176	Prin1	2	187583042	99.21938644	6	0.193767621	147197	'27.3.59'	grmzm2g025095_t01	'RNA.regulation of transcription.Methyl binding domain proteins'
1177	Prin1	2	208604410	118.3005988	5	-0.291990669	585	'29.5.11.4.2'	grmzm2g358987_t01	'protein.degradation.ubiquitin.E3.RING'
1178	Prin1	3	6560146	25.42100729	9	0.224131566	37842	'4.3.4'	grmzm2g132069_t01	'glycolysis.unclear/dually targeted.phosphofructokinase (PFK)'
1179	Prin1	3	10019848	34.54290833	6	0.147532068	44682	'34.16'	grmzm2g118243_t01	'transport.ABC transporters and multidrug resistance systems'
1180	Prin1	3	10798853	36.10351096	5	0.15355804	198338	'26.10'	grmzm2g138750_t01	'misc.cytochrome P450'
1181	Prin1	3	173210277	83.47025878	7	0.372725567	461797	'31.4'	grmzm2g439532_t01	'cell.vesicle transport'
1182	Prin1	3	176397560	87.31080195	31	0.329494913	30122	'11.3'	grmzm2g083195_t01	'lipid metabolism.Phospholipid synthesis'
1183	Prin1	3	177498347	88.92648807	6	-0.320067184	161011	'26.21'	grmzm2g065557_t01	'misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein'
1184	Prin1	3	187651158	98.71945033	7	-0.295211159	66284	'10.6.3'	ac233851.1_fgt011	'cell wall.degradation.pectate lyases and polygalacturonases'

1185	Prin1	3	208541649	118.8197976	8	-0.369019896	664	'27.3.22'	grmzm2g002548_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
1186	Prin1	3	212248108	123.3033736	10	-0.263177037	11	'26.28'	grmzm2g047129_t02	'misc.GDSL-motif lipase'
1187	Prin1	3	212248700	123.3041123	16	-0.250746746	94418	'6.3'	grmzm2g466833_t01	'gluconeogenesis.Malate DH'
1188	Prin1	3	213848298	126.6560335	53	-0.249180593	5541	'1.5.1'	grmzm2g348512_t03	'PS.carbon concentrating mechanism.C4'
1189	Prin1	3	213859916	126.6845705	6	-0.219255555	28983	'1.5.1'	grmzm2g121878_t01	'PS.carbon concentrating mechanism.C4'
1190	Prin1	4	31722606	50.95098413	20	0.217083693	280734	'31.1'	ac203909.3_fgt006	'cell.organisation'
1191	Prin1	4	90652356	57.4372722	43	0.176560253	164194	'6.3'	grmzm2g068455_t01	'gluconeogenesis.Malate DH'
1192	Prin1	4	176411838	87.58887022	6	-0.223703747	2298	'27.3.11'	grmzm2g121151_t01	'RNA.regulation of transcription.C2H2 zinc finger family'

1193	Prin1	4	176745377	87.99059847	6	-0.231675713	378672	'20.1'	grmzm2g158811_t01	'stress.biotic'
1194	Prin1	4	177057759	88.36684435	37	-0.199910793	66290	'20.1'	grmzm2g158811_t01	'stress.biotic'
1195	Prin1	4	177225650	88.56905925	19	-0.22500953	90065	'27.3.67'	grmzm2g475583_t01	'RNA.regulation of transcription.putative transcription regulator'
1196	Prin1	4	177456322	88.84689021	5	-0.177386326	2470	'27.3.3'	grmzm2g011110_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1197	Prin1	4	243324592	133.223033	6	0.286380697	51080	'16.1.5'	grmzm2g065494_t01	'secondary metabolism.isoprenoids.terpenoids'
1198	Prin1	5	1875087	2.828866055	9	0.198422919	7754	'28.1'	grmzm2g398668_t01	'DNA.synthesis/chromatin structure'
1199	Prin1	5	16786267	47.56865354	11	0.186128131	159981	'29.2.3'	grmzm2g018943_t01	'protein.synthesis.initiation'
1200	Prin1	5	18656090	49.4044948	5	0.231641756	9698	'10.5.5'	grmzm2g087326_t01	'cell wall.cell wall proteins.RGP'
1201	Prin1	5	19607267	50.33047385	6	0.191852193	173070	'27.3.6'	grmzm2g001724_t03	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'

1202	Prin1	5	22228974	52.4036044	6	0.200210132	272	'30.2.99'	grmzm2g166719_t01	'signalling.receptor kinases.misc'
1203	Prin1	5	22628739	52.93108894	19	0.179737138	433	'29.5.5'	grmzm2g082502_t01	'protein.degradation.serine protease'
1204	Prin1	5	23032929	53.4644122	13	0.192543992	96191	'31.1'	grmzm2g026800_t01	'cell.organisation'
1205	Prin1	5	26723660	54.83773092	5	0.181309457	111423	'16.8.2'	grmzm2g477683_t01	'secondary metabolism.flavonoids.chalcones'
1206	Prin1	5	27926098	55.29207074	8	0.259427803	20280	'34'	grmzm2g462081_t01	'transport'
1207	Prin1	5	205662825	119.8501543	5	-0.331878313	95037	'10.7'	grmzm2g105844_t01	'cell wall.modification'
1208	Prin1	5	205892823	120.5961956	20	-0.202211883	1810	'33.99'	grmzm2g100593_t01	'development.unspecified'
1209	Prin1	5	206470516	122.4700502	8	-0.182601165	139927	'21.4'	grmzm2g118366_t01	'redox.glutaredoxins'
1210	Prin1	5	207093116	124.0642086	6	-0.223961036	8111	'3.2.2'	grmzm2g055150_t01	'minor CHO metabolism.trehalose.TPP'

1211	Prin1	5	207103724	124.0880847	6	-0.211548066	3583	'26.2'	grmzm2g055124_t01	'misc.UDP glucosyl and glucoronyl transferases'
1212	Prin1	5	207325275	124.5867434	7	-0.207443465	11730	'34.15'	grmzm2g375116_t01	'transport.potassium'
1213	Prin1	6	2898813	-7.559855335	7	-0.16547695	2045	'11.9.3'	grmzm2g023335_t01	'lipid metabolism.lipid degradation.lysophospholipases'
1214	Prin1	6	5873783	-4.184534568	14	-0.194407963	145507	'27.3.50'	grmzm2g019257_t01	'RNA.regulation of transcription.General Transcription'
1215	Prin1	6	6894842	-3.026068551	14	-0.172667028	7826	'4.1.8'	grmzm2g180625_t01	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
1216	Prin1	6	8419109	-1.296676302	10	-0.156917082	280289	'27.3.99'	grmzm2g060057_t01	'RNA.regulation of transcription.unclassified'
1217	Prin1	6	14792950	5.295348837	11	-0.186212199	368729	'27.3.30'	grmzm2g016637_t01	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
1218	Prin1	7	124476542	64.75250337	10	0.249817163	1292	'17.2.3'	grmzm2g089854_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'
1219	Prin1	7	153457755	93.06309404	13	0.245403	321100	'27.3.10'	grmzm2g046829_t01	'RNA.regulation of transcription.C2C2(Zn) YABBY family'
1220	Prin1	7	156111925	98.3472492	7	0.241907825	52249	'34.1'	grmzm2g479163_t01	'transport.p- and v-ATPases'

1221	Prin1	7	156185170	98.49909898	33	0.211508581	16515	'34.1'	grmzm2g411916_t01	'transport.p- and v-ATPases'
1222	Prin1	7	159147927	104.6414159	9	0.180017249	128734	'29.2.1.2.1.3'	grmzm2g093902_t04	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S3'
1223	Prin1	7	159471791	105.3360113	5	0.203425704	86267	'29.2.1.2.2.527'	grmzm2g030731_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L27A'
1224	Prin1	7	159471845	105.3361463	9	0.171827824	86213	'29.2.1.2.2.527'	grmzm2g030731_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L27A'
1225	Prin1	7	160106822	106.9228459	9	0.206135369	17498	'27.3.3'	grmzm2g060876_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1226	Prin1	7	169415919	134.4048149	10	-0.207507404	55	'29.5.11.4.2'	grmzm2g440866_t01	'protein.degradation.ubiquitin.E3.RING'
1227	Prin1	8	2087948	4.782267599	7	0.209648655	8185	'13.1.7.2'	grmzm2g082214_t01	'amino acid metabolism.synthesis.histidine.bifunctional phosphoribosyl-ATP diphosphatase and phosphoribosyl-AMP cyclohydrolase'
1228	Prin1	8	4386420	11.24086841	11	0.365945724	16856	'10.5.4'	grmzm2g006734_t01	'cell wall.cell wall proteins.HRGP'
1229	Prin1	8	5283586	15.55733838	38	0.216233202	157660	'3.2.3'	grmzm2g416836_t01	'minor CHO metabolism.trehalose.potential TPS/TPP'

1230	Prin1	8	8255624	20.95732171	5	0.182206933	163320	'26.3'	ac234160.1_fgt003	'misc.gluco-, galacto- and mannosidases'
1231	Prin1	8	8403455	21.19881565	12	0.37507853	15489	'26.3'	ac234160.1_fgt003	'misc.gluco-, galacto- and mannosidases'
1232	Prin1	8	103054530	58.74182186	7	0.277385271	99819	'20.1'	grmzm2g017603_t01	'stress.biotic'
1233	Prin1	8	105711842	59.67074769	21	0.237102288	2318	'1.5.1'	grmzm2g097457_t03	'PS.carbon concentrating mechanism.C4'
1234	Prin1	8	108389110	60.44924097	8	0.215129664	223750	'34.99'	grmzm2g312198_t01	'transport.misc'
1235	Prin1	8	108849125	60.58213104	19	0.325050069	31652	'27.3.32'	grmzm2g449681_t01	'RNA.regulation of transcription.WRKY domain transcription factor family'
1236	Prin1	8	111264320	61.27983748	5	0.202557625	1266	'30.2.25'	grmzm2g061718_t01	'signalling.receptor kinases.wall associated kinase'
1237	Prin1	8	117142297	63.44621372	6	0.231321611	54716	'20.2.3'	ac204277.3_fgt006	'stress.abiotic.drought/salt'

1238	Prin1	8	117976115	63.86193872	6	0.224320933	180	'26.7'	grmzm2g142584_t01	'misc.oxidases - copper, flavone etc.'
1239	Prin1	8	158510179	86.58550567	14	-0.190411215	81429	'11.3'	grmzm2g002135_t01	'lipid metabolism.Phospholipid synthesis'
1240	Prin1	8	158697511	86.89047423	5	-0.249857512	109822	'27.3.4'	grmzm2g116557_t01	'RNA.regulation of transcription.ARF, Auxin Response Factor family'
1241	Prin1	8	159893599	88.49652739	21	-0.181876531	198	'27.3.99'	grmzm2g461793_t01	'RNA.regulation of transcription.unclassified'
1242	Prin1	8	159898572	88.50016935	13	-0.17950465	194146	'17.4.2'	grmzm2g423456_t01	'hormone metabolism.cytokinin.signal transduction'
1243	Prin1	8	162773842	93.15571435	5	-0.176464664	14871	'28.1'	grmzm2g421829_t01	'DNA.synthesis/chromatin structure'
1244	Prin1	9	12785133	22.10483847	6	-0.158858265	14297	'30.11'	grmzm2g067053_t01	'signalling.light'
1245	Prin1	9	20668779	36.70158796	15	-0.209803433	72423	'29.4.1.59'	grmzm2g433433_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase IX'
1246	Prin1	9	20780641	36.88056228	5	-0.183329952	4999	'27.3.22'	grmzm2g106276_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'

1247	Prin1	9	21433294	37.9247786	11	-0.168662562	84952	'26.14'	grmzm2g114098_t01	'misc.oxygenases'
1248	Prin1	9	26434264	43.26084016	8	-0.174249746	63090	'20.2.1'	grmzm2g152373_t01	'stress.abiotic.heat'
1249	Prin1	9	34855540	44.99799089	6	-0.212168913	33435	'34.3'	grmzm2g150406_t01	'transport.amino acids'
1250	Prin1	9	113108447	55.8821261	7	-0.307295112	68610	'10.7'	grmzm2g094990_t01	'cell wall.modification'
1251	Prin1	9	144471186	92.93120956	15	-0.279214676	1648	'34.6'	grmzm2g342907_t01	'transport.sulphate'
1252	Prin1	9	144622187	93.27205089	19	-0.236362959	100601	'33.99'	grmzm2g028039_t02	'development.unspecified'
1253	Prin1	9	146785494	99.6308883	11	-0.180210179	533	'27.3.6'	ac149829.2_fgt004	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
1254	Prin1	10	3622484	6.02423381	5	0.18783093	1653	'29.5.11.4.2'	grmzm2g467576_t01	'protein.degradation.ubiquitin.E3.RING'
1255	Prin1	10	119575302	47.38384118	12	-0.204463112	80771	'27.3.30'	grmzm2g392168_t01	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'

1256	Prin1	10	137172137	64.52401076	13	0.291125843	98040	'34.14'	grmzm2g455171_t01	'transport.unspecified cations'
1257	Prin1	10	140585346	71.90932116	6	0.416795748	76614	'27.3.30'	grmzm2g415229_t01	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
1258	Prin2	1	16528334	33.09583561	9	-0.148363759	16588	'28.1'	grmzm2g017254_t01	'DNA.synthesis/chromatin structure'
1259	Prin2	1	16774678	33.28332749	16	-0.148531763	181102	'26.7'	grmzm2g000427_t01	'misc.oxidases - copper, flavone etc.'
1260	Prin2	1	17321663	33.69438463	6	-0.167753428	21476	'29.2.3'	grmzm2g115182_t01	'protein.synthesis.initiation'
1261	Prin2	1	21383024	37.73112289	14	-0.220900957	63054	'27.3.99'	grmzm2g004259_t01	'RNA.regulation of transcription.unclassified'
1262	Prin2	1	21688795	38.19316881	19	-0.158781748	21240	'26.24'	grmzm2g114184_t01	'misc.GCN5-related N-acetyltransferase'
1263	Prin2	1	21725760	38.25596337	8	-0.160463885	29740	'30.11'	grmzm2g114055_t01	'signalling.light'
1264	Prin2	1	46712396	62.60179969	12	0.205604085	40891	'27.1.1'	grmzm2g153450_t01	'RNA.processing.splicing'

1265	Prin2	1	46752724	62.62839403	29	0.217392494	563	'27.1.1'	grmzm2g153450_t01	'RNA.processing.splicing'
1266	Prin2	1	48772229	63.96015846	7	0.183706966	36480	'11.1.8'	grmzm2g013783_t01	'lipid metabolism.FA synthesis and FA elongation.acyl coa ligase'
1267	Prin2	1	51413724	65.71798167	16	0.162964157	20752	'2.2.1.3.1'	grmzm2g084940_t01	'major CHO metabolism.degradation.sucrose.invertases.neutral'
1268	Prin2	1	51506627	65.97678122	7	0.17642016	6810	'27.3.25'	grmzm2g070849_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1269	Prin2	1	92753447	85.57176721	27	0.151936909	459526	'29.5.7'	grmzm2g317386_t01	'protein.degradation.metalloprotease'
1270	Prin2	1	228544370	135.6950109	18	-0.296287834	332255	'27.3.99'	grmzm2g014676_t01	'RNA.regulation of transcription.unclassified'
1271	Prin2	1	229356638	136.3156268	6	-0.360908732	161565	'27.3.50'	grmzm2g131577_t01	'RNA.regulation of transcription.General Transcription'
1272	Prin2	1	241747994	142.5070084	6	-0.352944427	100384	'10.2'	grmzm2g115772_t01	'cell wall.cellulose synthesis'
1273	Prin2	1	244977165	144.1767876	5	-0.366739502	158902	'27.3.25'	ac217264.3_fgt005	'RNA.regulation of transcription.MYB domain transcription factor family'

1274	Prin2	1	245007633	144.1925424	9	-0.295276804	128434	'27.3.25'	ac217264.3_fgt005	'RNA.regulation of transcription.MYB domain transcription factor family'
1275	Prin2	1	252877501	149.8251302	6	-0.308540541	116893	'28.1'	grmzm2g099023_t01	'DNA.synthesis/chromatin structure'
1276	Prin2	1	253031255	149.9489621	5	-0.279689196	126804	'33.99'	grmzm2g031120_t01	'development.unspecified'
1277	Prin2	1	253328929	150.1887057	6	-0.305359506	120443	'27.3.41'	grmzm2g098063_t01	'RNA.regulation of transcription.B3 transcription factor family'
1278	Prin2	2	4879221	14.16891319	10	-0.178554558	115	'34.6'	grmzm2g395114_t01	'transport.sulphate'
1279	Prin2	2	5548572	16.71369911	43	-0.154491728	15832	'27.3.3'	grmzm2g174917_t01	'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family'
1280	Prin2	2	5682220	17.22181151	5	-0.156996321	82350	'29.5.11.4.2'	grmzm2g066169_t01	'protein.degradation.ubiquitin.E3.RING'
1281	Prin2	2	26641159	57.94684499	18	-0.149499019	6232	'17.1.3'	grmzm2g114153_t01	'hormone metabolism.abscisic acid.induced-regulated-responsive-activated'
1282	Prin2	2	27916738	59.06362357	30	-0.172361155	8595	'13.2.3.5'	grmzm2g471931_t01	'amino acid metabolism.degradation.aspartate family.lysine'

1283	Prin2	2	28972476	60.59406358	25	-0.235153714	87571	'9.1.2'	grmzm2g141605_t01	'mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear'
1284	Prin2	2	34001062	63.56397414	13	-0.186467942	1995	'20.1'	grmzm2g052175_t01	'stress.biotic'
1285	Prin2	2	34937097	64.04660572	9	0.335345874	74139	'29.4.1.57'	grmzm2g051984_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
1286	Prin2	2	81996078	75.87752354	6	-0.253830438	142550	'13.2.3.2'	grmzm2g125310_t01	'amino acid metabolism.degradation.aspartate family.threonine'
1287	Prin2	2	124738310	77.33837071	9	-0.276512367	321557	'30.2.99'	grmzm2g301355_t01	'signalling.receptor kinases.misc'
1288	Prin2	2	124769416	77.34049122	25	-0.297074114	290451	'30.2.99'	grmzm2g301355_t01	'signalling.receptor kinases.misc'
1289	Prin2	3	2915029	8.667233227	5	-0.195341132	3441	'33.99'	grmzm2g060974_t01	'development.unspecified'
1290	Prin2	3	3185414	10.0663659	10	-0.231447784	4509	'17.2.2'	grmzm2g001566_t01	'hormone metabolism.auxin.signal transduction'

1291	Prin2	3	3386685	11.10786166	18	-0.158579918	16649	'27.3.52'	grmzm2g400907_t02	'RNA.regulation of transcription.Global transcription factor group'
1292	Prin2	3	10750451	36.00654587	9	-0.164241331	3268	'34.18'	grmzm2g051753_t02	'transport.unspecified anions'
1293	Prin2	3	10838771	36.18347982	6	-0.116432701	158420	'26.10'	grmzm2g138750_t01	'misc.cytochrome P450'
1294	Prin2	3	13300926	40.11756205	6	-0.186344905	74628	'34'	grmzm2g116053_t01	'transport'
1295	Prin2	3	13633702	40.54785389	18	-0.163225589	44412	'29.4'	grmzm2g129482_t01	'protein.postranslational modification'
1296	Prin2	3	13634126	40.54840214	12	-0.167661347	43988	'29.4'	grmzm2g129482_t01	'protein.postranslational modification'
1297	Prin2	3	14416721	41.56032683	26	-0.182957628	25363	'20.1'	grmzm2g062576_t01	'stress.biotic'
1298	Prin2	3	17306447	45.29685092	9	-0.237524461	20778	'30.5'	grmzm2g166064_t01	'signalling.G-proteins'
1299	Prin2	3	19698629	48.39003196	8	-0.195530153	2081	'30.2.17'	grmzm2g467671_t01	'signalling.receptor kinases.DUF 26'

1300	Prin2	3	19800505	48.52176145	5	-0.198444438	105632	'30.2.17'	grmzm2g412760_t01	'signalling.receptor kinases.DUF 26'
1301	Prin2	3	51981075	56.79858368	23	0.417597478	127495	'17.5.1'	grmzm2g363893_t01	'hormone metabolism.ethylene.synthesis-degradation'
1302	Prin2	3	54021465	57.26319567	17	0.319862133	105966	'27.3.25'	grmzm2g051256_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1303	Prin2	3	106489882	58.60975416	5	0.31895293	143297	'29.5.11.4.2'	ac206768.3_fgt005	'protein.degradation.ubiquitin.E3.RING'
1304	Prin2	3	136646099	63.07155567	5	-0.237479608	235598	'3.8.2'	grmzm2g402368_t01	'minor CHO metabolism.galactose.alpha-galactosidases'
1305	Prin2	3	171862276	82.33409418	6	0.513407834	6467	'27.3.25'	grmzm2g160838_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1306	Prin2	3	172148591	82.5754152	5	0.518185895	1267	'23.1.2.1'	grmzm2g339699_t01	'nucleotide metabolism.synthesis.purine.amidophosphoribosyl transferase'
1307	Prin2	3	173219900	83.47836954	15	0.538906436	452174	'31.4'	grmzm2g439532_t01	'cell.vesicle transport'

1308	Prin2	3	193922818	101.9299488	10	0.197939448	180454	'11.3.3'	grmzm2g452529_t01	'lipid metabolism.Phospholipid synthesis.phosphatidate cytidylyltransferase'
1309	Prin2	3	198668625	105.7679086	5	0.17551164	209448	'33.99'	grmzm2g022625_t03	'development.unspecified'
1310	Prin2	4	828147	2.931410178	7	0.187879628	13616	'27.3.21'	grmzm2g163427_t01	'RNA.regulation of transcription.GRAS transcription factor family'
1311	Prin2	4	5696047	19.49225268	12	-0.299402936	83431	'34.16'	grmzm2g421495_t01	'transport.ABC transporters and multidrug resistance systems'
1312	Prin2	4	42018416	54.27865297	7	-0.145631996	61572	'20.1'	grmzm2g304049_t01	'stress.biotic'
1313	Prin2	4	96251735	57.74714448	7	-0.124855363	596253	'24'	grmzm2g064193_t01	'Biodegradation of Xenobiotics'
1314	Prin2	4	125186338	58.42286198	72	-0.130712371	97399	'31.1'	grmzm2g145027_t01	'cell.organisation'
1315	Prin2	4	177668855	89.1123214	6	-0.18872756	1203	'12.1.2'	grmzm2g079381_t05	'N-metabolism.nitrate metabolism.nitrite reductase'

1316	Prin2	4	199778387	105.9507817	14	-0.193006416	79155	'30.3'	grmzm2g332660_t01	'signalling.calcium'
1317	Prin2	4	242574395	130.3125709	11	-0.281573519	3590	'20.1'	grmzm2g410963_t01	'stress.biotic'
1318	Prin2	5	929964	0.282533564	43	-0.19293743	7785	'28.1.3'	grmzm2g028955_t01	'DNA.synthesis/chromatin structure.histone'
1319	Prin2	5	1574000	2.018545222	10	-0.231021725	783	'17.2.1'	grmzm2g125552_t03	'hormone metabolism.auxin.synthesis-degradation'
1320	Prin2	5	1580722	2.036636261	5	-0.228448538	1523	'29.2.1.2.2.99'	grmzm2g125784_t01	'protein.synthesis.ribosomal protein.eukaryotic.60S subunit.unknown'
1321	Prin2	5	1842198	2.740351301	7	-0.153703207	7308	'27.3.28'	grmzm2g138421_t01	'RNA.regulation of transcription.SBP,Squamosa promoter binding protein family'
1322	Prin2	5	2347751	4.958870956	12	-0.152516959	8604	'34.99'	grmzm2g003108_t01	'transport.misc'
1323	Prin2	5	7094245	26.093099	26	0.150251126	7400	'27.3.54'	grmzm2g129817_t03	'RNA.regulation of transcription.Histone acetyltransferases'
1324	Prin2	5	10372835	33.33515135	9	0.176034799	18639	'27.3.67'	grmzm2g408897_t01	'RNA.regulation of transcription.putative transcription regulator'

1325	Prin2	5	26734713	54.84190728	11	0.353426391	100370	'16.8.2'	grmzm2g477683_t01	'secondary metabolism.flavonoids.chalcones'
1326	Prin2	5	73804215	66.39516104	21	0.292651485	109286	'34.12'	grmzm2g168747_t01	'transport.metal'
1327	Prin2	5	108262797	70.32363616	14	0.366236504	998325	'26.10'	grmzm2g045319_t01	'misc.cytochrome P450'
1328	Prin2	5	143236820	72.10704824	7	0.356617661	124991	'3.6'	grmzm2g111529_t01	'minor CHO metabolism.callose'
1329	Prin2	5	164299446	76.94625198	6	-0.300410103	26700	'29.4.1.57'	grmzm2g137468_t01	'protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII'
1330	Prin2	5	165991682	78.08035909	12	0.301900822	268599	'27.3.11'	grmzm2g320287_t01	'RNA.regulation of transcription.C2H2 zinc finger family'
1331	Prin2	5	169382477	81.27535729	5	-0.317414291	85025	'29.5.11.4.2'	grmzm2g071484_t01	'protein.degradation.ubiquitin.E3.RING'
1332	Prin2	5	188788930	98.54955746	8	0.15465899	170393	'17.2.3'	grmzm2g391596_t01	'hormone metabolism.auxin.induced-regulated-responsive-activated'

1333	Prin2	5	194052252	102.6015186	6	0.184420996	134834	'27.3.6'	grmzm2g144097_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
1334	Prin2	5	203652758	113.8406769	6	0.258309313	560	'27.3.6'	grmzm2g317450_t01	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
1335	Prin2	5	205472185	119.231778	50	0.148970386	17704	'27.3.25'	grmzm2g053396_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1336	Prin2	5	207751210	125.7483283	10	0.22159592	80383	'30.1.1'	grmzm2g081214_t01	'signalling.in sugar and nutrient physiology'
1337	Prin2	5	209217720	128.3485035	30	0.293163871	24073	'29.4'	grmzm2g058220_t01	'protein.postranslational modification'
1338	Prin2	5	209930161	130.9277607	5	0.227274598	5968	'30.11'	grmzm2g104920_t01	'signalling.light'
1339	Prin2	6	867384	-9.864659918	6	0.365645779	369074	'10.6.3'	grmzm2g004435_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
1340	Prin2	6	1957524	-8.627816461	8	0.454475095	35346	'26.18'	ac186577.3_fgt006	'misc.invertase/pectin methylesterase inhibitor family protein'
1341	Prin2	6	118739798	43.69898027	13	-0.578903834	1033	'30.3'	grmzm2g174315_t02	'signalling.calcium'

1342	Prin2	6	119772986	44.24786955	73	-0.412080895	121392	'30.1'	grmzm2g162788_t01	'signalling.in sugar and nutrient physiology'
1343	Prin2	6	120956190	44.6914035	7	-0.327835409	105351	'23.1.2.9'	grmzm2g164665_t01	'nucleotide metabolism.synthesis.purine.AICAR transformylase'
1344	Prin2	6	165586711	102.9473046	27	-0.297375391	132286	'11.9.2.1'	ac231411.1_fgt011	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
1345	Prin2	6	165589669	102.9571143	8	-0.289894217	129328	'11.9.2.1'	ac231411.1_fgt011	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
1346	Prin2	6	165667455	103.215079	20	-0.261489914	51542	'11.9.2.1'	ac231411.1_fgt011	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
1347	Prin2	6	165667652	103.2157324	5	-0.237252512	51345	'11.9.2.1'	ac231411.1_fgt011	'lipid metabolism.lipid degradation.lipases.triacylglycerol lipase'
1348	Prin2	6	166076222	104.570689	13	-0.302483541	96501	'27.3.9'	grmzm2g325850_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
1349	Prin2	7	5428540	23.50772999	34	-0.287429645	1932	'1.2.2'	grmzm2g129246_t01	'PS.photorespiration.glycolate oxydase'
1350	Prin2	7	22002213	45.79983088	10	-0.179913126	140251	'27.3.71'	grmzm2g431900_t01	'RNA.regulation of transcription.SNF7'

1351	Prin2	7	27302170	46.77471414	16	-0.174347347	23532	'34.13'	grmzm2g156794_t01	'transport.peptides and oligopeptides'
1352	Prin2	7	27327128	46.7793044	9	-0.205664769	64745	'33.99'	grmzm2g086757_t01	'development.unspecified'
1353	Prin2	7	29146881	47.11399196	45	-0.189498059	5436	'34.12'	grmzm2g147560_t01	'transport.metal'
1354	Prin2	7	124223168	64.44761155	10	-0.142549038	148496	'29.5.11'	ac225205.3_fgt003	'protein.degradation.ubiquitin'
1355	Prin2	7	156185236	98.49923581	6	-0.608676503	16449	'34.1'	grmzm2g411916_t01	'transport.p- and v-ATPases'
1356	Prin2	7	156689760	99.54520289	27	-0.178439732	49383	'26.22'	grmzm2g076981_t02	'misc.short chain dehydrogenase/reductase (SDR)'
1357	Prin2	7	166657242	123.8438631	41	0.243268708	67872	'20.2.2'	grmzm2g364643_t01	'stress.abiotic.cold'
1358	Prin2	7	167223656	126.3055595	17	0.239027751	3332	'34.15'	grmzm2g166738_t01	'transport.potassium'
1359	Prin2	7	168146779	130.3175518	8	0.250707874	10085	'27.3.8'	ac155434.2_fgt006	'RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family'

1360	Prin2	7	168157307	130.3633076	7	0.263440613	25193	'26.10'	grmzm2g425127_t01	'misc.cytochrome P450'
1361	Prin2	8	10739260	27.73471036	6	-0.202260838	132779	'34.16'	grmzm2g119345_t01	'transport.ABC transporters and multidrug resistance systems'
1362	Prin2	8	103399576	58.8624408	6	0.15144341	34765	'16.1.2.7'	grmzm2g145029_t01	'secondary metabolism.isoprenoids.mevalonate pathway.isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase'
1363	Prin2	8	159090160	87.53999331	9	0.172388561	3852	'26.2'	grmzm2g134308_t02	'misc.UDP glucosyl and glucoronyl transferases'
1364	Prin2	8	160611990	89.64768912	20	0.195427349	10164	'23.3.3'	grmzm2g013060_t01	'nucleotide metabolism.salvage.NUDIX hydrolases'
1365	Prin2	8	160612122	89.6479463	28	0.216705415	10032	'23.3.3'	grmzm2g013060_t01	'nucleotide metabolism.salvage.NUDIX hydrolases'
1366	Prin2	8	164575465	99.62773322	5	0.134691981	16971	'27.3.25'	grmzm2g405094_t01	'RNA.regulation of transcription.MYB domain transcription factor family'
1367	Prin2	8	170618195	123.1071582	8	0.141301951	5058	'20.2.99'	grmzm2g106690_t01	'stress.abiotic.unspecified'
1368	Prin2	8	170786240	123.7938509	6	0.133385539	142971	'29.5.7'	grmzm2g133249_t01	'protein.degradation.metalloprotease'

1369	Prin2	8	173793234	135.8235771	8	0.119843765	2576	'29.5'	grmzm2g118806_t01	'protein.degradation'
1370	Prin2	8	173864083	136.1091964	9	0.124329055	12896	'30.3'	ac203173.3_fgt001	'signalling.calcium'
1371	Prin2	9	2701441	-3.388186607	59	-0.379560098	6507	'27.2'	grmzm2g180836_t01	'RNA.transcription'
1372	Prin2	9	3689306	-0.719907238	18	-0.378505593	84069	'2.2.1.1'	grmzm2g072091_t01	'major CHO metabolism.degradation.sucrose.fructokinase'
1373	Prin2	9	7182819	8.716269429	14	-0.268943698	56750	'17.7.1.5'	grmzm2g000236_t01	'hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase'
1374	Prin2	9	109417983	53.84202072	8	0.254711069	127216	'27.3.67'	ac225193.3_fgt003	'RNA.regulation of transcription.putative transcription regulator'
1375	Prin2	9	109658976	53.91939367	7	0.188444788	32637	'26.13'	grmzm2g007754_t01	'misc.acid and other phosphatases'
1376	Prin2	9	117715320	57.64391617	6	0.137706712	78991	'10.8.1'	grmzm2g314663_t01	'cell wall.pectin*esterases.PME'
1377	Prin2	9	138570437	79.39501909	34	0.310626673	10685	'20.1'	grmzm2g149809_t01	'stress.biotic'

1378	Prin2	10	5058530	14.79019912	46	-0.424128374	56738	'30.2.26'	grmzm2g051637_t01	'signalling.receptor kinases.crinkly like'
1379	Prin2	10	5427445	17.07840286	12	-0.377394519	16980	'27.3.35'	grmzm2g365754_t01	'RNA.regulation of transcription.bZIP transcription factor family'
1380	Prin2	10	6191195	21.4060557	6	-0.359938003	84745	'27.3.22'	grmzm2g060050_t01	'RNA.regulation of transcription.HB,Homeobox transcription factor family'
1381	Prin2	10	9023970	24.98301526	9	-0.188824159	56220	'27.3.9'	grmzm2g324131_t01	'RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family'
1382	Prin2	10	22382517	34.8358978	9	0.185011049	28293	'10.6.3'	grmzm2g113815_t01	'cell wall.degradation.pectate lyases and polygalacturonases'
1383	Prin2	10	24154443	35.31258248	6	0.360806077	289086	'21.1'	grmzm2g141848_t01	'redox.thioredoxin'
1384	Prin2	10	79797589	39.13112595	6	0.260220052	33428	'34.13'	grmzm2g086496_t01	'transport.peptides and oligopeptides'
1385	Prin2	10	85540940	40.43084945	25	0.314408789	45425	'26.12'	grmzm2g006727_t01	'misc.peroxidases'
1386	Prin2	10	86726870	40.71912634	15	0.304643229	194374	'29.5.11.4.3.2'	grmzm2g028014_t01	'protein.degradation.ubiquitin.E3.SCF.FBOX'

1387	Prin2	10	113194309	45.32268893	8	0.36996183	119976	'13.1.6.3.1'	grmzm2g125923_t01	'amino acid metabolism.synthesis.aromatic aa.phenylalanine.arogenate dehydratase / prephenate dehydratase'
1388	Prin2	10	133029713	57.10017332	5	-0.138816574	93976	'27.3.7'	grmzm2g098442_t01	'RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family'
1389	Prin2	10	142607850	78.31225962	6	-0.114292892	1640	'29.5.2'	grmzm2g419694_t01	'protein.degradation.autophagy'
1390	Prin2	10	142607858	78.31228969	7	-0.146722504	1632	'29.5.2'	grmzm2g419694_t01	'protein.degradation.autophagy'
1391	Prin2	10	142646940	78.45920294	5	-0.242947614	401	'2.1.2.2'	grmzm2g121612_t01	'major CHO metabolism.synthesis.starch.starch synthase'
1392	Prin2	10	143724295	81.34148153	8	-0.154720679	43851	'17.1.1.1.10'	ac188128.3_fgt002	'hormone metabolism.abscisic acid.synthesis-degradation.synthesis.9-cis-epoxycarotenoid dioxygenase'
1393	Prin2	10	144247405	82.22431479	10	-0.222878534	33015	'27.2'	grmzm2g427031_t01	'RNA.transcription'

1394	Prin2	10	144605053	83.42035782		8	-0.228222027	21295	'11.1.3'	grmzm2g003190_t01	'lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase'

ning or adjacent to detected SNPs

to functional categories
acids; Prot, protein; Prin1: principal component 1; Prin2: principal component 2.

Predicted Gene Containing SNP
Description
'moderately similar to (260) AT1G34670 | Symbols: AtMYB93 | AtMYB93 (myb domain protein 93); DNA binding / transcription factor | chr1:12709128-12710423 FORWARDmoderately similar to (201) ODO1_PETHY ODORANT1 protein (MYB-like protein ODO1) - Petunia hybrida (Petunia)moderately similar to (286) loc_os08g37970 12008.m07782 protein myb-like DNA-binding domain containing protein, expressed seq=cds; coord=1:182542564..182543903:-1; parent_gene=GRMZM2G110135'
'moderately similar to (483) AT3G23820 | Symbols: GAE6 | GAE6 (UDP-D-GLUCURONATE 4-EPIMERASE 6); UDP-glucuronate 4-epimerase/ catalytic | chr3:8603645-8605027 FORWARDhighly similar to (659) loc_os08g41440 12008.m08122 protein NAD-dependent epimerase/dehydratase family protein, putative, expressed seq=cds; coord=1:192730986..192732596:-1; parent_gene=GRMZM2G161233'
'highly similar to (884) AT1G09890 | Symbols: | lyase | chr1:3214237-3217386 REVERSEnearly identical (1221) loc_os08g44020 12008.m080048 protein lyase, putative, expressed seq=cds; coord=1:206155710..206160274:-1; parent_gene=GRMZM2G154124'
'moderately similar to (255) AT4G32300 | Symbols: SD2-5 | SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase | chr4:15599970-15602435 FORWARDweakly similar to (172) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (568) loc_os04g56110 12004.m35493 protein ATP binding protein, putative, expressed seq=cds; coord=2:4464619..4466714:-1; parent_gene=GRMZM2G076212'

'highly similar to (613) AT2G24360 | Symbols: | serine/threonine/tyrosine kinase, putative | chr2:10364742-10366075 REVERSEweakly similar to (116) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (771) loc_os04g51950 12004.m10090 protein serine/threonine protein kinase, putative, expressed seq=cds; coord=2:11197500..11203331:1; parent_gene=GRMZM2G102088'

'moderately similar to (379) AT5G06839 | Symbols: | bZIP family transcription factor | chr5:2120911-2126217 FORWARDmoderately similar to (319) TGA21_TOBAC TGACG-sequence-specific DNA-binding protein TGA-2.1 (TGA2.1) - Nicotiana tabacum (Common tobacco)highly similar to (656) loc_os09g31390 12009.m22141 protein DNA binding protein, putative, expressed seq=cds; coord=2:189820806..189829874:-1; parent_gene=GRMZM2G125934'

'moderately similar to (230) AT5G58900 | Symbols: | myb family transcription factor | chr5:23783275-23784667 REVERSEmoderately similar to (342) loc_os01g63460 12001.m12462 protein MYB transcription factor, putative, expressed seq=cds; coord=3:178553778..178555626:1; parent_gene=GRMZM2G125522'

'moderately similar to (439) AT1G06520 | Symbols: ATGPAT1, GPAT1 | GPAT1 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 1); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase | chr1:1994170-1996067 REVERSEhighly similar to (736) loc_os01g44069 12001.m10665 protein glycerol-3-phosphate acyltransferase 1, putative, expressed seq=cds; coord=3:216522432..216528663:-1; parent_gene=GRMZM2G065203'

'weakly similar to (133) AT5G25190 | Symbols: | ethylene-responsive element-binding protein, putative | chr5:8707007-8707655 REVERSEweakly similar to (174) loc_os02g55380 12002.m10564 protein ethylene response factor 1, putative, expressed seq=cds; coord=4:173800132..173801383:1; parent_gene=GRMZM2G111415' 'highly similar to (570) AT3G47570 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr3:17527611-17530748 FORWARDmoderately similar to (298) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1077) loc_os01g05960 12001.m07227 protein ATP binding protein, putative, expressed seq=cds; coord=4:239702248..239706103:-1; parent_gene=GRMZM2G322348'

'moderately similar to (284) AT5G58490 | Symbols: | cinnamoyl-CoA reductase family | chr5:23643068-23644455 FORWARDweakly similar to (125) DFRA_VITVI Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Vitis vinifera (Grape)moderately similar to (352) loc_os03g60380 12003.m10928 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=5:2594160..2603545:-1; parent_gene=GRMZM2G110881'

'moderately similar to (248) AT5G58490 | Symbols: | cinnamoyl-CoA reductase family | chr5:23643068-23644455 FORWARDweakly similar to (143) DFRA_DIACA Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Dianthus caryophyllus (Carnation) (Clove pink)moderately similar to (261) loc_os03g60380 12003.m10928 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=5:2604483..2606065:-1; parent_gene=GRMZM2G410865'

'moderately similar to (272) AT1G17810 | Symbols: BETA-TIP | BETA-TIP (BETA-TONOPLAST INTRINSIC PROTEIN); water channel | chr1:6130209-6131442 FORWARDmoderately similar to (379) TIP31_ORYSA Probable aquaporin TIP3.1 (Tonoplast intrinsic protein 3.1) (OsTIP3.1) - Oryza sativa (Rice)moderately similar to (379) loc_os10g35050 12010.m06328 protein aquaporin TIP3.1, putative, expressed seq=cds; coord=5:25511080..25512421:1; parent_gene=GRMZM2G305446'

'weakly similar to (123) AT1G56120 | Symbols: | kinase | chr1:20987288-20993072 REVERSEmoderately similar to (243) loc_os11g28104 12011.m06728 protein protein kinase, putative, expressed seq=cds; coord=5:27198279..27204222:-1; parent_gene=GRMZM2G102862'

'weakly similar to (125) AT1G04500 | Symbols: | zinc finger CONSTANS-related | chr1:1221757-1224235 REVERSEmoderately similar to (315) loc_os10g32900 12010.m065283 protein CCT motif family protein, expressed seq=cds; coord=5:30600307..30602869:-1; parent_gene=GRMZM2G123550'

'weakly similar to (114) AT4G35840 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr4:16981083-16982266 FORWARDweakly similar to (198) loc_os06g50370 12006.m09561 protein RING-H2 finger protein ATL2B, putative, expressed seq=cds; coord=5:61801847..61803639:1; parent_gene=GRMZM2G069923' 'highly similar to (738) AT1G62830 | Symbols: LDL1, SWP1, ATSWP1 | LDL1 (LSD1-LIKE1); amine oxidase/ electron carrier/ oxidoreductase | chr1:23264638-23267172 REVERSEweakly similar to (107) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)nearly identical (1155) loc_os02g51880 12002.m10219 protein amine oxidase/ oxidoreductase, putative, expressed seq=cds; coord=5:208426880..208429748:1; parent_gene=GRMZM2G059958'

'moderately similar to (382) AT5G14180 | Symbols: MPL1 | MPL1 (MYZUS PERSICAE-INDUCED LIPASE 1); catalytic | chr5:4571442-4574413 REVERSEhighly similar to (595) loc_os06g42860 12006.m08816 protein gastric triacylglycerol lipase precursor, putative, expressed seq=cds; coord=6:97382174..97384634:-1; parent_gene=GRMZM2G322892'

'nearly identical (1598) AT5G42390 | Symbols: | metalloendopeptidase | chr5:16945308-16952647 FORWARDnearly identical (2070) loc_os06g41990 12006.m32119 protein metalloendopeptidase, putative, expressed seq=cds; coord=6:98000549..98014552:1; parent_gene=GRMZM2G073312'

'nearly identical (1598) AT5G42390 | Symbols: | metalloendopeptidase | chr5:16945308-16952647 FORWARDnearly identical (2070) loc_os06g41990 12006.m32119 protein metalloendopeptidase, putative, expressed seq=cds; coord=6:98000549..98014552:1; parent_gene=GRMZM2G073312'

'moderately similar to (393) AT2G17410 | Symbols: | ARID/BRIGHT DNA-binding domain-containing protein | chr2:7559869-7563474 FORWARDhighly similar to (562) loc_os06g41730 12006.m31901 protein ARID/BRIGHT DNA binding domain containing protein, expressed seq=cds; coord=6:98085270..98091283:-1; parent_gene=GRMZM2G180654' 'highly similar to (748) AT1G19440 | Symbols: KCS4 | KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups | chr1:6729119-6730669 FORWARDhighly similar to (858) loc_os05g49290 12005.m27982 protein acyltransferase, putative, expressed seq=cds; coord=6:165162158..165164637:-1; parent_gene=GRMZM2G160417'

'moderately similar to (220) AT3G57880 | Symbols: | C2 domain-containing protein | chr3:21431198-21433519 REVERSEmoderately similar to (252) loc_os07g30020 12007.m07273 protein phosphoribosylanthranilate transferase, putative, expressed seq=cds; coord=7:148849994..148855647:-1; parent_gene=GRMZM2G416484'

'highly similar to (755) AT1G02730 | Symbols: ATCSLD5, CSLD5 | ATCSLD5; 1,4-beta-D-xylan synthase/ cellulose synthase | chr1:594697-598473 REVERSEnearly identical (1262) loc_os07g36690 12007.m07919 protein CSLF2 - cellulose synthase-like family F; beta1,3;1,4 glucan synthase, expressed seq=cds; coord=7:156222296..156226604:-1; parent_gene=GRMZM2G103972'

'weakly similar to (122) AT5G48930 | Symbols: HCT | HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase | chr5:19836654-19838092 REVERSEweakly similar to (115) HCBT1_DIACA Anthranilate N-benzoyltransferase protein 1 (EC 2.3.1.144) (Anthranilate N-hydroxycinnamoyl/benzoyltransferase 1) - Dianthus caryophyllus (Carnation) (Clove pink)highly similar to (553) loc_os09g37180 12009.m06666 protein anthranilate N-benzoyltransferase protein 1, putative, expressed seq=cds; coord=7:174995238..174996574:-1; parent_gene=GRMZM2G307437'

'moderately similar to (488) AT2G13620 | Symbols: ATCHX15, CHX15 | ATCHX15; monovalent cation:proton antiporter/ sodium:hydrogen antiporter | chr2:5678006-5680621 FORWARDnearly identical (1223) loc_os05g39600 12005.m08138 protein ATCHX15, putative, expressed seq=cds; coord=8:118670851..118676392:1; parent_gene=GRMZM2G366851'

'very weakly similar to (85.5) loc_os07g39960 12007.m08238 protein zinc finger, C2H2 type family protein seq=cds; coord=8:163179500..163179916:1; parent_gene=AC183950.2_FG002' 'moderately similar to (328) AT1G21890 | Symbols: | nodulin MtN21 family protein | chr1:7682808-7685581 REVERSEmoderately similar to (478) loc_os06g10750 12006.m05792 protein nodulin protein, putative, expressed seq=cds; coord=9:8432717..8434846:-1; parent_gene=GRMZM2G088053'

'moderately similar to (264) AT1G75050 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to other organism; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Thaumatin, conserved site (InterPro:IPR017949), Thaumatin, pathogenesis-related (InterPro:IPR001938); BEST Arabidopsis thaliana protein match is: ATLP-3 (TAIR:AT1G75030.1); Has 1070 Blast hits to 1056 proteins in 144 species: Archae - 0; Bacteria - 18; Metazoa - 48; Fungi - 48; Plants - 944; Viruses - 4; Other Eukaryotes - 8 (source: NCBI BLink). | chr1:28180116-28181062 FORWARDmoderately similar to (201) TP1A_MALDO Thaumatin-like protein 1a precursor (Allergen Mal d 2) (Mdtl1) (Pathogenesis-related protein 5a) (PR-5a) - Malus domestica (Apple) (Malus sylvestris)moderately similar to (370) loc_os03g13070 12003.m06753 protein pathogenesis-related protein 5 precursor, putative seq=cds; coord=9:145169132..145170513:-1; parent_gene=GRMZM2G393507'

'moderately similar to (254) AT3G23730 | Symbols: | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative | chr3:8550222-8551248 FORWARDmoderately similar to (246) BRU1_SOYBN Brassinosteroid-regulated protein BRU1 precursor - Glycine max (Soybean)moderately similar to (327) loc_os08g13980 12008.m05523 protein xyloglucan endotransglucosylase/hydrolase protein 15 precursor, putative, expressed seq=cds; coord=10:141250965..141252692:1; parent_gene=GRMZM2G091303' 'moderately similar to (423) AT2G17700 | Symbols: | protein kinase family protein | chr2:7685778-7689278 REVERSEweakly similar to (115) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (679) loc_os04g59000 12004.m10778 protein ATP binding protein, putative, expressed seq=cds; coord=10:148973414..148980886:-1; parent_gene=GRMZM2G104658'

'moderately similar to (266) AT5G17540 | Symbols: | transferase family protein | chr5:5782061-5783682 REVERSEweakly similar to (109) HCBT1_DIACA Anthranilate N-benzoyltransferase protein 1 (EC 2.3.1.144) (Anthranilate N-hydroxycinnamoyl/benzoyltransferase 1) - Dianthus caryophyllus (Carnation) (Clove pink)highly similar to (546) loc_os10g11980 12010.m04516 protein transferase family protein, expressed seq=cds; coord=1:115337828..115339542:-1; parent_gene=GRMZM2G107851'

'very weakly similar to (84.7) AT2G34730 | Symbols: | myosin heavy chain-related | chr2:14654611-14657443 FORWARDhighly similar to (842) loc_os03g57110 12003.m35440 protein expressed protein seq=cds; coord=1:285132040..285136056:-1; parent_gene=GRMZM2G058734'

'highly similar to (934) AT2G02220 | Symbols: ATPSKR1, PSKR1 | PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase | chr2:584098-587124 REVERSEhighly similar to (910) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1459) loc_os04g57630 12004.m10648 protein phytosulfokine receptor precursor, putative, expressed seq=cds; coord=2:2222100..2225911:1; parent_gene=GRMZM2G452142'

'weakly similar to (188) AT5G06800 | Symbols: | myb family transcription factor | chr5:2103374-2105680 FORWARDmoderately similar to (379) loc_os04g56990 12004.m101684 protein transfactor, putative, expressed seq=cds; coord=2:3105142..3108209:1; parent_gene=GRMZM2G035370' 'highly similar to (679) AT1G17840 | Symbols: WBC11, ABCG11, DSO, COF1, ATWBC11 | WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter | chr1:6142870-6145894 FORWARDweakly similar to (115) PDR3_TOBAC Pleiotropic drug resistance protein 3 (NtPDR3) - Nicotiana tabacum (Common tobacco)highly similar to (753) loc_os04g44610 12004.m09420 protein ABC transporter C05D10.3 in chromosome III, putative, expressed seq=cds; coord=2:23874538..23877737:-1; parent_gene=GRMZM2G177812'

'weakly similar to (181) AT1G21140 | Symbols: | nodulin, putative | chr1:7404464-7405066 FORWARDweakly similar to (125) NO21_SOYBN Nodulin 21 (N-21) - Glycine max (Soybean)moderately similar to (204) loc_os04g59020 12004.m10780 protein integral membrane protein, expressed seq=cds; coord=2:24387828..24389072:1; parent_gene=GRMZM2G434557'

'weakly similar to (190) IAAS_ORYSA Alpha-amylase/subtilisin inhibitor precursor (RASI) - Oryza sativa (Rice)weakly similar to (190) loc_os04g44470 12004.m09406 protein alpha-amylase/subtilisin inhibitor, putative, expressed seq=cds; coord=2:26769801..26771736:1; parent_gene=GRMZM2G474575'

'highly similar to (564) loc_os01g05660 12001.m150482 protein expressed protein seq=cds; coord=3:17580074..17584970:1; parent_gene=GRMZM2G166064'

'weakly similar to (178) AT1G28600 | Symbols: | lipase, putative | chr1:10051604-10053073 REVERSEvery weakly similar to (86.7) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)weakly similar to (194) loc_os01g42730 12001.m10537 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=3:213800866..213804340:-1; parent_gene=GRMZM2G047129'

'moderately similar to (241) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (341) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215431519..215437533:-1; parent_gene=GRMZM2G348512'

'moderately similar to (241) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (341) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215431519..215437533:-1; parent_gene=GRMZM2G348512'

'moderately similar to (201) AT1G70410 | Symbols: ATBCA4, BCA4 | carbonic anhydrase, putative / carbonate dehydratase, putative | chr1:26534167-26537457 REVERSEmoderately similar to (275) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (273) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215466579..215468759:-1; parent_gene=GRMZM2G121878'

'moderately similar to (270) AT5G14700 | Symbols: | cinnamoyl-CoA reductase-related | chr5:4740502-4743327 REVERSEvery weakly similar to (82.4) DFRA_MAIZE Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Zea mays (Maize)moderately similar to (499) loc_os01g45200 12001.m10725 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=3:215757514..215764384:1; parent_gene=GRMZM2G029547'

'moderately similar to (270) AT5G14700 | Symbols: | cinnamoyl-CoA reductase-related | chr5:4740502-4743327 REVERSEvery weakly similar to (82.4) DFRA_MAIZE Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Zea mays (Maize)moderately similar to (499) loc_os01g45200 12001.m10725 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=3:215757514..215764384:1; parent_gene=GRMZM2G029547'

'highly similar to (758) AT3G28860 | Symbols: ATMDR1, ATMDR11, PGP19, MDR11, MDR1, ATPGP19, ABCB19, ATABCB19 | ABCB19; ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter | chr3:10870287-10877286 REVERSEhighly similar to (689) MDR_ORYSA Putative multidrug resistance protein (P-glycoprotein) - Oryza sativa (Rice)nearly identical (1565) loc_os08g05710 12008.m04714 protein multidrug resistance protein 12, putative, expressed seq=cds; coord=4:33816544..33821596:-1; parent_gene=GRMZM2G441722'

'moderately similar to (223) AT5G45160 | Symbols: | root hair defective 3 GTP-binding (RHD3) family protein | chr5:18264991-18270035 FORWARDmoderately similar to (315) loc_os12g41170 12012.m07899 protein protein SEY1, putative, expressed seq=cds; coord=4:36216954..36264537:1; parent_gene=GRMZM2G407913'

'highly similar to (790) AT1G73590 | Symbols: PIN1, ATPIN1 | PIN1 (PIN-FORMED 1); transporter | chr1:27659772-27662876 FORWARDnearly identical (1019) PIN1_ORYSA Auxin efflux carrier component 1 (OsPIN1) (Ethylene insensitive root 1 homolog) - Oryza sativa (Rice)nearly identical (1019) loc_os02g50960 12002.m33866 protein auxin efflux carrier component 1, putative, expressed seq=cds; coord=5:206727149..206730565:1; parent_gene=GRMZM2G074267' 'moderately similar to (213) AT5G37810 | Symbols: NIP4;1, NLM4 | NIP4;1 (NOD26-LIKE INTRINSIC PROTEIN 4;1); water channel | chr5:15045232-15047807 FORWARDmoderately similar to (473) LSI1_ORYSA Silicon transporter LSI1 (Low silicon protein 1) - Oryza sativa (Rice)moderately similar to (473) loc_os02g51110 12002.m10145 protein aquaporin NIP4.2, putative, expressed seq=cds; coord=5:206922588..206926444:1; parent_gene=GRMZM2G028325'

'very weakly similar to (90.1) AT1G22490 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr1:7938448-7940489 REVERSEmoderately similar to (243) loc_os02g52190 12002.m10250 protein DNA binding protein, putative, expressed seq=cds; coord=5:208895710..208901046:-1; parent_gene=GRMZM2G045883'

'moderately similar to (219) loc_os05g45480 12005.m08673 protein arabinogalactan protein, putative, expressed seq=cds; coord=6:159437488..159438613:-1; parent_gene=GRMZM2G043035'

'highly similar to (716) AT1G32900 | Symbols: | starch synthase, putative | chr1:11920582-11923506 REVERSEnearly identical (1076) SSG1_MAIZE Granule-bound starch synthase 1, chloroplast precursor (EC 2.4.1.242) (Granule-bound starch synthase I) (GBSS-I) - Zea mays (Maize)highly similar to (933) loc_os06g04200 12006.m31969 protein granule-bound starch synthase 1, chloroplast precursor, putative, expressed seq=cds; coord=9:23256308..23260236:-1; parent_gene=GRMZM2G024993'

'weakly similar to (125) AT2G17700 | Symbols: | protein kinase family protein | chr2:7685778-7689278 REVERSEweakly similar to (189) loc_os04g59000 12004.m10778 protein ATP binding protein, putative, expressed seq=cds; coord=10:148978659..148981143:-1; parent_gene=GRMZM2G104658' 'nearly identical (1507) AT3G19960 | Symbols: ATM1 | ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor | chr3:6949787-6956736 FORWARDnearly identical (1802) loc_os10g34710 12010.m06298 protein myosin-2 heavy chain, non muscle, putative, expressed seq=cds; coord=1:229190070..229205919:-1; parent_gene=GRMZM2G113202'

'weakly similar to (156) loc_os03g61570 12003.m11038 protein expressed protein seq=cds; coord=1:295768837..295770331:1; parent_gene=GRMZM2G114775'

'moderately similar to (224) AT3G08850 | Symbols: RAPTOR1B, ATRAPTOR1B, RAPTOR1 | RAPTOR1; nucleotide binding / protein binding | chr3:2686978-2694911 REVERSEweakly similar to (111) ADO1_ORYSA Adagio-like protein 1 - Oryza sativa (Rice)moderately similar to (417) loc_os12g01916 12012.m27002 protein bcpLH protein, putative, expressed seq=cds; coord=2:152219219..152236923:1; parent_gene=GRMZM2G444808'

'highly similar to (518) AT3G61880 | Symbols: CYP78A9 | CYP78A9 (CYTOCHROME P450 78A9); monooxygenase/ oxygen binding | chr3:22906114-22907890 REVERSEmoderately similar to (495) C78A3_SOYBN Cytochrome P450 78A3 (EC 1.14.-.-) - Glycine max (Soybean)highly similar to (718) loc_os09g35940 12009.m06545 protein cytochrome P450 78A3, putative, expressed seq=cds; coord=2:195035853..195038235:-1; parent_gene=GRMZM2G034471' 'highly similar to (604) AT5G65700 | Symbols: BAM1 | BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase | chr5:26281826-26284945 FORWARDweakly similar to (179) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (645) loc_os11g12620 12011.m05454 protein receptor protein kinase CLAVATA1 precursor, putative, expressed seq=cds; coord=4:10216533..10222046:1; parent_gene=GRMZM2G068398'

'weakly similar to (104) AT5G15210 | Symbols: ATHB30, ZFHD3 | ATHB30 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 30); DNA binding / transcription factor | chr5:4937874-4938689 REVERSEmoderately similar to (213) loc_os02g47770 12002.m09811 protein zinc finger homeodomain protein 1, putative, expressed seq=cds; coord=4:160125950..160128076:-1; parent_gene=GRMZM2G069365'

'moderately similar to (304) AT1G75880 | Symbols: | family II extracellular lipase 1 (EXL1) | chr1:28490564-28492298 FORWARDmoderately similar to (248) APG_BRANA Anter-specific proline-rich protein APG (Protein CEX) (Fragment) - Brassica napus (Rape)moderately similar to (499) loc_os06g24404 12006.m091692 protein anther-specific proline-rich protein APG precursor, putative, expressed seq=cds; coord=7:5037195..5039353:1; parent_gene=GRMZM2G060866'

'highly similar to (695) AT1G30220 | Symbols: ATINT2, INT2 | INT2 (INOSITOL TRANSPORTER 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter | chr1:10632957-10635439 REVERSEweakly similar to (124) STC_RICCO Sugar carrier protein C - Ricinus communis (Castor bean)highly similar to (787) loc_os07g05640 12007.m05028 protein proton myo-inositol cotransporter, putative, expressed seq=cds; coord=7:5335384..5337829:1; parent_gene=GRMZM2G142063' 'very weakly similar to (87.8) AT1G09530 | Symbols: PIF3, POC1, PAP3 | PIF3 (PHYTOCHROME INTERACTING FACTOR 3); DNA binding / protein binding / transcription factor/ transcription regulator | chr1:3077216-3079367 FORWARDmoderately similar to (259) loc_os01g18290 12001.m42972 protein basic helix-loop-helix dimerisation region bHLH, putative, expressed seq=cds; coord=8:935667..938714:1; parent_gene=GRMZM2G387528'

'moderately similar to (327) AT2G34480 | Symbols: | 60S ribosomal protein L18A (RPL18aB) | chr2:14532916-14534161 REVERSEmoderately similar to (352) RL18A_ORYSA 60S ribosomal protein L18a - Oryza sativa (Rice)moderately similar to (360) loc_os05g49030 12005.m08974 protein 60S ribosomal protein L18a, putative, expressed seq=cds; coord=8:149220935..149222561:-1; parent_gene=GRMZM2G126928'

'moderately similar to (327) AT2G34480 | Symbols: | 60S ribosomal protein L18A (RPL18aB) | chr2:14532916-14534161 REVERSEmoderately similar to (352) RL18A_ORYSA 60S ribosomal protein L18a - Oryza sativa (Rice)moderately similar to (360) loc_os05g49030 12005.m08974 protein 60S ribosomal protein L18a, putative, expressed seq=cds; coord=8:149220935..149222561:-1; parent_gene=GRMZM2G126928'

'moderately similar to (320) AT2G26670 | Symbols: ATHO1, HO1, TED4, GUN2, HY6 | TED4 (REVERSAL OF THE DET PHENOTYPE 4); heme oxygenase (decyclizing) | chr2:11341816-11343394 FORWARDmoderately similar to (393) loc_os06g40080 12006.m08545 protein heme oxygenase 1, putative, expressed seq=cds; coord=9:88918347..88927536:-1; parent_gene=GRMZM2G101004'

'moderately similar to (374) AT1G24360 | Symbols: | 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase | chr1:8640820-8643283 FORWARDmoderately similar to (397) FABG3_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 3, chloroplast precursor (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 3) - Brassica napus (Rape)moderately similar to (476) loc_os04g30760 12004.m08180 protein 3-oxoacyl-reductase, chloroplast precursor, putative, expressed seq=cds; coord=10:108122298..108130104:1; parent_gene=GRMZM2G099696' 'highly similar to (714) AT2G26250 | Symbols: FDH, KCS10 | KCS10 (3-KETOACYL-COA SYNTHASE 10); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups | chr2:11170799-11173059 REVERSEhighly similar to (929) loc_os03g08360 12003.m35563 protein fiddlehead-like protein, putative, expressed seq=cds; coord=1:16822675..16826498:1; parent_gene=GRMZM2G445602'

'very weakly similar to (81.6) AT1G72360 | Symbols: | ethylene-responsive element-binding protein, putative | chr1:27241904-27242777 FORWARDvery weakly similar to (83.2) ERF1_ORYSA Ethylene-responsive transcription factor 1 (Ethylene-responsive element-binding factor 1) (EREBP-1) (OsEREBP1) - Oryza sativa (Rice)weakly similar to (144) loc_os03g08500 12003.m06358 protein ethylene-responsive element binding protein 2, putative, expressed seq=cds; coord=1:17526391..17527311:-1; parent_gene=AC206951.3_FG017'

'moderately similar to (384) AT3G11180 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr3:3504249-3506688 FORWARDmoderately similar to (204) LDOX_MALDO Leucoanthocyanidin dioxygenase (EC 1.14.11.19) (LDOX) (Leucocyanidin oxygenase) (Leucoanthocyanidin hydroxylase) (Anthocyanidin synthase) - Malus domestica (Apple) (Malus sylvestris)highly similar to (520) loc_os03g18030 12003.m101308 protein leucoanthocyanidin dioxygenase, putative, expressed seq=cds; coord=1:44955003..44960551:-1; parent_gene=AC212219.3_FG005'

'weakly similar to (198) AT2G38440 | Symbols: ITB1, SCAR2, DIS3, WAVE4, ATSCAR2 | SCAR2 (SCAR HOMOLOG 2) | chr2:16095550-16100851 FORWARDweakly similar to (192) SCRL1_ORYSA SCAR-like protein 1 - Oryza sativa (Rice)highly similar to (598) loc_os03g18710 12003.m07292 protein expressed protein seq=cds; coord=1:46576198..46582130:-1; parent_gene=GRMZM2G104534'

'weakly similar to (124) loc_os03g22270 12003.m78861 protein auxin-repressed protein, putative, expressed seq=cds; coord=1:57296569..57299181:-1; parent_gene=GRMZM2G073755'

'moderately similar to (432) AT3G07270 | Symbols: | GTP cyclohydrolase I | chr3:2314005-2317059 FORWARDhighly similar to (603) loc_os04g56710 12004.m10558 protein GTP cyclohydrolase I 1, putative, expressed seq=cds; coord=2:3541475..3547749:1; parent_gene=GRMZM2G062420'

'moderately similar to (432) AT3G07270 | Symbols: | GTP cyclohydrolase I | chr3:2314005-2317059 FORWARDhighly similar to (603) loc_os04g56710 12004.m10558 protein GTP cyclohydrolase I 1, putative, expressed seq=cds; coord=2:3541475..3547749:1; parent_gene=GRMZM2G062420' 'moderately similar to (404) AT2G18890 | Symbols: | protein kinase family protein | chr2:8184027-8185673 FORWARDweakly similar to (195) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (572) loc_os04g56060 12004.m10497 protein BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed seq=cds; coord=2:4670163..4677087:1; parent_gene=GRMZM2G086577'

'moderately similar to (321) AT2G43590 | Symbols: | chitinase, putative | chr2:18081592-18082749 REVERSEhighly similar to (515) CHIA_MAIZE Endochitinase A precursor (EC 3.2.1.14) (Seed chitinase A) - Zea mays (Maize)moderately similar to (377) loc_os04g41680 12004.m09144 protein endochitinase A precursor, putative, expressed seq=cds; coord=2:33534101..33535449:1; parent_gene=GRMZM2G051943'

'weakly similar to (119) AT1G70760 | Symbols: CRR23 | CRR23 ((chlororespiratory reduction 23) | chr1:26687267-26688201 FORWARDweakly similar to (198) loc_os05g28090 12005.m07096 protein expressed protein seq=cds; coord=2:180163167..180166298:-1; parent_gene=GRMZM2G176129'

'moderately similar to (283) AT1G54100 | Symbols: ALDH7B4 | ALDH7B4 (Aldehyde Dehydrogenase 7B4); 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase | chr1:20195435-20198853 REVERSEmoderately similar to (292) AL7A1_MALDO Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin-1) (Matured fruit 60 kDa protein) (MF-60) - Malus domestica (Apple) (Malus sylvestris)moderately similar to (346) loc_os09g26880 12009.m22098 protein aldehyde dehydrogenase family 7 member A1, putative, expressed seq=cds; coord=2:184131308..184138715:-1; parent_gene=GRMZM2G130440'

'moderately similar to (275) AT1G28600 | Symbols: | lipase, putative | chr1:10051604-10053073 REVERSEweakly similar to (151) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)highly similar to (561) loc_os01g11620 12001.m07778 protein esterase precursor, putative, expressed seq=cds; coord=3:3430959..3432894:-1; parent_gene=GRMZM2G400929'

'nearly identical (1013) AT1G53140 | Symbols: | dynamin family protein | chr1:19799271-19802441 FORWARDnearly identical (1394) loc_os01g54420 12001.m11606 protein ATP binding protein, putative, expressed seq=cds; coord=3:197386891..197392522:-1; parent_gene=GRMZM2G010306' 'moderately similar to (215) AT4G30550 | Symbols: | glutamine amidotransferase class-I domain-containing protein | chr4:14925618-14926713 FORWARDmoderately similar to (302) loc_os02g08270 12002.m06173 protein defense-related protein, putative, expressed seq=cds; coord=4:234873379..234874456:-1; parent_gene=GRMZM2G062716'

'moderately similar to (258) AT2G28950 | Symbols: ATEXPA6, ATEXP6, ATHEXP ALPHA 1.8 | ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN A6) | chr2:12431840-12433482 REVERSEmoderately similar to (293) EXPA7_ORYSA Expansin-A7 precursor (OsEXPA7) (Alpha-expansin-7) (OsEXP7) (OsaEXPa1.26) - Oryza sativa (Rice)moderately similar to (293) loc_os03g60720 12003.m10961 protein alpha-expansin 6 precursor, putative, expressed seq=cds; coord=5:2274980..2275954:1; parent_gene=GRMZM2G445169'

'moderately similar to (366) AT3G46450 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr3:17093297-17095319 REVERSEhighly similar to (694) loc_os03g60610 12003.m101547 protein CRAL/TRIO domain containing protein, expressed seq=cds; coord=5:2350263..2356801:1; parent_gene=GRMZM2G003108'

'weakly similar to (177) AT5G59890 | Symbols: ADF4, ATADF4 | ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding | chr5:24123107-24123596 FORWARDmoderately similar to (275) ADF3_MAIZE Actin-depolymerizing factor 3 (ADF 3) (ZmABP3) (ZmADF3) - Zea mays (Maize)moderately similar to (223) loc_os03g60590 12003.m101135 protein actin-depolymerizing factor 3, putative, expressed seq=cds; coord=5:2362323..2364777:-1; parent_gene=GRMZM2G002825'

'moderately similar to (456) AT5G10080 | Symbols: | aspartyl protease family protein | chr5:3150843-3153380 FORWARDvery weakly similar to (85.9) ASP1_ORYSA Aspartic proteinase Asp1 precursor (EC 3.4.23.-) (OsAsp1) (OSAP1) (Nucellin-like protein) - Oryza sativa (Rice)highly similar to (796) loc_os02g51540 12002.m10187 protein pepsin A, putative, expressed seq=cds; coord=5:208060721..208065128:1; parent_gene=GRMZM2G335978' 'weakly similar to (102) AT1G26310 | Symbols: CAL, CAL1, agl10 | CAL (CAULIFLOWER); DNA binding / transcription factor | chr1:9100330-9103510 REVERSEweakly similar to (127) MAD30_ORYSA MADS-box transcription factor 30 (OsMADS30) - Oryza sativa (Rice)weakly similar to (127) loc_os06g45650 12006.m09093 protein MADS-box transcription factor 30, putative, expressed seq=cds; coord=6:93493646..93495861:-1; parent_gene=GRMZM2G161666'

'highly similar to (555) AT1G68530 | Symbols: CUT1, POP1, CER6, G2, KCS6 | KCS6 (3-KETOACYL-COA SYNTHASE 6); catalytic/ transferase, transferring acyl groups other than amino-acyl groups | chr1:25713600-25714733 REVERSEhighly similar to (794) loc_os06g14810 12006.m06196 protein 3-ketoacyl-CoA synthase, putative, expressed seq=cds; coord=6:117452361..117454400:1; parent_gene=GRMZM2G168304'

'moderately similar to (222) AT1G62300 | Symbols: WRKY6, ATWRKY6 | WRKY6; transcription factor | chr1:23016887-23019155 REVERSEmoderately similar to (380) loc_os05g49210 12005.m08991 protein OsWRKY43 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=6:165021433..165023895:1; parent_gene=GRMZM2G366795'

'moderately similar to (280) AT4G14770 | Symbols: TCX2, ATTCX2 | TCX2 (TESMIN/TSO1-LIKE CXC 2); transcription factor | chr4:8481522-8484825 REVERSEhighly similar to (861) loc_os07g07974 12007.m05257 protein TSO1, putative, expressed seq=cds; coord=7:9327103..9332339:1; parent_gene=GRMZM2G153754'

'highly similar to (583) AT4G30110 | Symbols: HMA2 | HMA2; cadmium-transporting ATPase | chr4:14720253-14724577 REVERSEvery weakly similar to (87.8) PMA4_NICPL Plasma membrane ATPase 4 (EC 3.6.3.6) (Proton pump 4) - Nicotiana plumbaginifolia (Leadwort-leaved tobacco)highly similar to (774) loc_os07g12900 12007.m05742 protein cadmium/zinc-transporting ATPase 2, putative seq=cds; coord=7:21633432..21636570:1; parent_gene=AC205008.4_FG002'

'weakly similar to (183) AT2G20570 | Symbols: GPRI1, GLK1 | GPRI1 (GBF'S PRO-RICH REGION-INTERACTING FACTOR 1); transcription factor/ transcription regulator | chr2:8855486-8857522 FORWARDmoderately similar to (384) loc_os06g24070 12006.m31875 protein transcription factor ZmGLK1, putative, expressed seq=cds; coord=9:2711408..2713807:-1; parent_gene=GRMZM2G026833' moderately similar to (384) AT5G65140 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr5:26020411-26022077 REVERSEmoderately similar to (486) loc_os06g11840 12006.m05901 protein expressed protein seq=cds; coord=9:5654343..5657317:-1; parent_gene=GRMZM2G080354'

'weakly similar to (183) AT1G12410 | Symbols: CLPR2, NCLPP2, CLP2 | CLP2 (CLP PROTEASE PROTEOLYTIC SUBUNIT 2); serine-type endopeptidase | chr1:4223099-4224954 FORWARDvery weakly similar to (87.4) CLPP_CHLVU ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp) - Chlorella vulgaris (Green alga)moderately similar to (265) loc_os06g04530 12006.m05183 protein ATP-dependent Clp protease proteolytic subunit 2, putative, expressed seq=cds; coord=9:22055173..22056303:-1; parent_gene=GRMZM2G148106'

'moderately similar to (325) AT1G08320 | Symbols: | bZIP family transcription factor | chr1:2622113-2627451 REVERSEmoderately similar to (303) TGA21_TOBAC TGACG-sequence-specific DNA-binding protein TGA-2.1 (TGA2.1) - Nicotiana tabacum (Common tobacco)moderately similar to (409) loc_os12g05680 12012.m04561 protein transcription factor HBP-1b, putative, expressed seq=cds; coord=10:5530500..5533143:-1; parent_gene=GRMZM2G366264'

'moderately similar to (338) AT2G31450 | Symbols: ATNTH1 | endonuclease-related | chr2:13401318-13404134 REVERSEmoderately similar to (475) loc_os11g16580 12011.m05743 protein endonuclease III-like protein 1, putative, expressed seq=cds; coord=10:5730941..5734533:1; parent_gene=GRMZM2G113228' 'moderately similar to (291) AT3G03440 | Symbols: | armadillo/beta-catenin repeat family protein | chr3:815709-818568 FORWARDmoderately similar to (412) loc_os01g02200 12001.m06862 protein ubiquitin-protein ligase, putative, expressed seq=cds; coord=3:28221287..28223015:1; parent_gene=AC183315.4_FG006'

'very weakly similar to (100) AT5G59720 | Symbols: HSP18.2 | HSP18.2 (heat shock protein 18.2) | chr5:24062632-24063117 FORWARDweakly similar to (103) HSP11_PEA 18.1 kDa class I heat shock protein (HSP 18.1) - Pisum sativum (Garden pea)weakly similar to (155) loc_os02g03570 12002.m05707 protein 18.3 kDa class I heat shock protein, putative, expressed seq=cds; coord=4:238985398..238986190:1; parent_gene=GRMZM2G324956' 'very weakly similar to (94.4) AT1G78860 | Symbols: | curculin-like (mannose-binding) lectin family protein | chr1:29646168-29647499 REVERSEvery weakly similar to (89.7) EP1G_DAUCA Epidermis-specific secreted glycoprotein EP1 precursor (52/54 kDa medium protein) - Daucus carota (Carrot)highly similar to (540) loc_os01g72810 12001.m13314 protein secreted glycoprotein, putative, expressed seq=cds; coord=8:157452514..157453996:-1; parent_gene=GRMZM2G059299'

'highly similar to (806) AT5G64220 | Symbols: | calmodulin-binding protein | chr5:25686434-25691903 FORWARDnearly identical (1520) loc_os03g09100 12003.m06416 protein calmodulin-binding transcription activator 2, putative, expressed seq=cds; coord=1:19789491..19814550:-1; parent_gene=GRMZM2G447551'

'highly similar to (806) AT5G64220 | Symbols: | calmodulin-binding protein | chr5:25686434-25691903 FORWARDnearly identical (1520) loc_os03g09100 12003.m06416 protein calmodulin-binding transcription activator 2, putative, expressed seq=cds; coord=1:19789491..19814550:-1; parent_gene=GRMZM2G447551'

'weakly similar to (182) AT2G28490 | Symbols: | cupin family protein | chr2:12178812-12180983 REVERSEmoderately similar to (454) loc_os03g21790 12003.m07583 protein cupin family protein, expressed seq=cds; coord=1:56160677..56162858:-1; parent_gene=GRMZM2G054916' weakly similar to (138) AT2G32990 | Symbols: AtGH9B8 | AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds | chr2:14003361-14005844 FORWARDweakly similar to (154) GUN22_ORYSA Endoglucanase 22 precursor (EC 3.2.1.4) (Endo-1,4-beta glucanase 22) (OsGLU11) - Oryza sativa (Rice)weakly similar to (154) loc_os09g23084 12009.m05465 protein endoglucanase 1 precursor, putative, expressed seq=cds; coord=2:178811871..178813335:-1; parent_gene=GRMZM2G703265'

'highly similar to (822) AT1G15460 | Symbols: ATBOR4, BOR4 | BOR4 (REQUIRES HIGH BORON 4); anion exchanger | chr1:5310196-5313376 REVERSEnearly identical (1013) loc_os01g08020 12001.m07427 protein boron transporter-like protein 2, putative, expressed seq=cds; coord=3:10934126..10940345:-1; parent_gene=GRMZM2G051753'

'weakly similar to (178) AT2G01430 | Symbols: ATHB17, ATHB-17 | ATHB17 (ARABIDOPSIS THALIANA HOMEOBOX-LEUCINE ZIPPER PROTEIN 17); transcription factor | chr2:187798-190369 REVERSEmoderately similar to (291) loc_os01g45570 12001.m10759 protein homeobox-leucine zipper protein ATHB-4, putative, expressed seq=cds; coord=3:214857327..214861719:1; parent_gene=GRMZM2G126239'

'moderately similar to (490) AT1G53300 | Symbols: TTL1 | TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN LIKE 1); binding | chr1:19879726-19882375 FORWARDhighly similar to (828) loc_os01g42960 12001.m10559 protein electron transporter, putative, expressed seq=cds; coord=3:225545980..225550303:1; parent_gene=GRMZM2G093436' 'very weakly similar to (99.0) AT4G16780 | Symbols: ATHB-2, HAT4, ATHB2 | ATHB-2 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 2); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription factor | chr4:9449291-9450604 FORWARDweakly similar to (129) loc_os02g05640 12002.m05912 protein homeobox-leucine zipper protein ATHB-4, putative seq=cds; coord=4:237502428..237504286:-1; parent_gene=GRMZM2G166041'

moderately similar to (366) AT3G46450 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr3:17093297-17095319 REVERSEhighly similar to (694) loc_os03g60610 12003.m101547 protein CRAL/TRIO domain containing protein, expressed seq=cds; coord=5:2350263..2356801:1; parent_gene=GRMZM2G003108'

'moderately similar to (366) AT3G46450 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr3:17093297-17095319 REVERSEhighly similar to (694) loc_os03g60610 12003.m101547 protein CRAL/TRIO domain containing protein, expressed seq=cds; coord=5:2350263..2356801:1; parent_gene=GRMZM2G003108'

'highly similar to (962) AT1G66150 | Symbols: TMK1 | TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase | chr1:24631503-24634415 FORWARDmoderately similar to (209) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1318) loc_os03g50810 12003.m10067 protein receptor protein kinase TMK1 precursor, putative, expressed seq=cds; coord=5:10414656..10418698:1; parent_gene=GRMZM2G158359'

'weakly similar to (120) AT1G31320 | Symbols: LBD4 | LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4) | chr1:11213107-11214032 FORWARDweakly similar to (180) loc_os03g45750 12003.m09600 protein LOB domain protein 12, putative, expressed seq=cds; coord=5:15187010..15189734:-1; parent_gene=GRMZM2G079185'

'nearly identical (1060) AT5G35750 | Symbols: AHK2 | AHK2 (ARABIDOPSIS HISTIDINE KINASE 2); cytokinin receptor/ osmosensor/ protein histidine kinase | chr5:13911743-13916337 REVERSEweakly similar to (154) ETR1_BRAOL Ethylene receptor (EC 2.7.13.3) - Brassica oleracea (Wild cabbage)nearly identical (1503) loc_os10g21810 12010.m65482 protein histidine kinase 3, putative, expressed seq=cds; coord=5:38752228..38809303:1; parent_gene=GRMZM2G158252' 'weakly similar to (122) AT3G09980 | Symbols: | unknown protein | chr3:3069358-3071145 FORWARDmoderately similar to (202) loc_os02g32650 12002.m33393 protein expressed protein seq=cds; coord=5:168449383..168450781:-1; parent_gene=GRMZM2G045188'

'weakly similar to (144) AT5G62940 | Symbols: | Dof-type zinc finger domain-containing protein | chr5:25257183-25258504 REVERSEweakly similar to (119) PBF_MAIZE Dof zinc finger protein PBF (Prolamin box-binding factor) - Zea mays (Maize)moderately similar to (360) loc_os02g47810 12002.m09815 protein dof domain, zinc finger family protein, expressed seq=cds; coord=5:201381499..201385596:-1; parent_gene=GRMZM2G140694'

'very weakly similar to (98.2) loc_os02g48140 12002.m100336 protein 17.4 kDa class I heat shock protein 3, putative, expressed seq=cds; coord=5:202095278..202096275:1; parent_gene=GRMZM2G481605'

highly similar to (953) AT2G18700 | Symbols: ATTPS11, TPS11, ATTPSB | ATTPS11; transferase, transferring glycosyl groups | chr2:8109043-8111799 FORWARDnearly identical (1372) loc_os02g54820 12002.m33906 protein trehalose-6-phosphate synthase, putative, expressed seq=cds; coord=5:213055055..213058997:1; parent_gene=GRMZM2G122231'

'moderately similar to (377) AT1G71980 | Symbols: | protease-associated zinc finger (C3HC4-type RING finger) family protein | chr1:27098250-27099881 FORWARDhighly similar to (561) loc_os03g07130 12003.m101101 protein RING finger protein 13, putative, expressed seq=cds; coord=6:1334626..1338778:1; parent_gene=GRMZM2G423956'

moderately similar to (451) AT1G32450 | Symbols: NRT1.5 | NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter | chr1:11715337-11719807 REVERSEmoderately similar to (434) loc_os02g46460 12002.m09683 protein peptide transporter PTR2, putative, expressed seq=cds; coord=7:25089776..25092351:-1; parent_gene=GRMZM2G156794' 'moderately similar to (214) AT3G04030 | Symbols: | myb family transcription factor | chr3:1042920-1044574 REVERSEmoderately similar to (284) loc_os07g48596 12007.m09071 protein MYR1, putative, expressed seq=cds; coord=7:173817875..173820052:-1; parent_gene=AC155434.2_FG005'

'moderately similar to (214) AT3G04030 | Symbols: | myb family transcription factor | chr3:1042920-1044574 REVERSEmoderately similar to (284) loc_os07g48596 12007.m09071 protein MYR1, putative, expressed seq=cds; coord=7:173817875..173820052:-1; parent_gene=AC155434.2_FG005'

'highly similar to (971) AT5G56040 | Symbols: | leucine-rich repeat protein kinase, putative | chr5:22695050-22698410 FORWARDmoderately similar to (420) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1647) loc_os01g07560 12001.m07382 protein receptor-like protein kinase precursor, putative, expressed seq=cds; coord=8:17058192..17062569:1; parent_gene=GRMZM2G463493'

'moderately similar to (435) AT3G24460 | Symbols: | TMS membrane family protein / tumour differentially expressed (TDE) family protein | chr3:8886160-8889717 REVERSEhighly similar to (586) loc_os01g08460 12001.m07471 protein TMS membrane protein/tumour differentially expressed protein containing protein, expressed seq=cds; coord=8:18892547..18898086:-1; parent_gene=GRMZM2G088356'

'moderately similar to (356) AT1G05800 | Symbols: DGL | DGL (DONGLE); triacylglycerol lipase | chr1:1741204-1742619 FORWARDmoderately similar to (436) loc_os01g67430 12001.m12847 protein triacylglycerol lipase, putative, expressed seq=cds; coord=8:163911970..163913352:-1; parent_gene=AC233916.1_FG002'

'weakly similar to (183) AT2G20570 | Symbols: GPRI1, GLK1 | GPRI1 (GBF'S PRO-RICH REGION-INTERACTING FACTOR 1); transcription factor/ transcription regulator | chr2:8855486-8857522 FORWARDmoderately similar to (384) loc_os06g24070 12006.m31875 protein transcription factor ZmGLK1, putative, expressed seq=cds; coord=9:2711408..2713807:-1; parent_gene=GRMZM2G026833' 'very weakly similar to (86.7) AT5G64080 | Symbols: | protease inhibitor/seed storage/lipid transfer protein (LTP) family protein | chr5:25645475-25646638 REVERSEweakly similar to (140) loc_os03g09230 12003.m35062 protein xylogen protein 1, putative, expressed seq=cds; coord=9:149245864..149247159:1; parent_gene=GRMZM2G004466'

'moderately similar to (216) AT3G19090 | Symbols: | RNA-binding protein, putative | chr3:6601466-6603709 FORWARDmoderately similar to (393) loc_os03g36900 12003.m08805 protein RNA binding protein, putative, expressed seq=cds; coord=1:221945123..221947755:1; parent_gene=GRMZM2G411041'

'weakly similar to (107) AT3G50410 | Symbols: OBP1 | OBP1 (OBF BINDING PROTEIN 1); DNA binding / protein binding / transcription factor | chr3:18709872-18710633 FORWARDweakly similar to (144) MNB1A_MAIZE Dof zinc finger protein MNB1A - Zea mays (Maize)moderately similar to (215) loc_os09g29960 12009.m06147 protein dof zinc finger protein MNB1A, putative, expressed seq=cds; coord=2:188526058..188527888:-1; parent_gene=GRMZM2G009406' 'weakly similar to (179) AT4G18260 | Symbols: | cytochrome B561-related | chr4:10093524-10097337 REVERSEmoderately similar to (261) loc_os05g49040 12005.m27467 protein expressed protein seq=cds; coord=3:210748854..210750807:1; parent_gene=GRMZM2G024448'

moderately similar to (245) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (340) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215469087..215473931:-1; parent_gene=GRMZM2G121878'

'weakly similar to (125) AT5G53040 | Symbols: | RWP-RK domain-containing protein | chr5:21506967-21507948 REVERSEmoderately similar to (218) loc_os01g37100 12001.m10005 protein RWP-RK domain containing protein, expressed seq=cds; coord=3:226822416..226824199:-1; parent_gene=GRMZM2G071322'

'highly similar to (568) AT3G22880 | Symbols: ATDMC1, DMC1, ARLIM15 | DMC1 (DISRUPTION OF MEIOTIC CONTROL 1); ATP binding / DNA binding / DNA-dependent ATPase/ damaged DNA binding / nucleoside-triphosphatase/ nucleotide binding / protein binding | chr3:8097948-8100740 REVERSEhighly similar to (606) DMC1_LILLO Meiotic recombination protein DMC1 homolog - Lilium longiflorum (Trumpet lily)highly similar to (654) loc_os11g04954 12011.m079904 protein meiotic recombination protein DMC1, putative, expressed seq=cds; coord=3:229673847..229678762:-1; parent_gene=GRMZM2G109618'

'weakly similar to (140) AT5G60340 | Symbols: | maoC-like dehydratase domain-containing protein | chr5:24273879-24275891 REVERSEweakly similar to (189) loc_os05g09370 12005.m27729 protein carbohydrate kinase, PfkB, putative, expressed seq=cds; coord=5:2184671..2186446:-1; parent_gene=GRMZM2G085320' 'weakly similar to (140) AT5G60340 | Symbols: | maoC-like dehydratase domain-containing protein | chr5:24273879-24275891 REVERSEweakly similar to (189) loc_os05g09370 12005.m27729 protein carbohydrate kinase, PfkB, putative, expressed seq=cds; coord=5:2184671..2186446:-1; parent_gene=GRMZM2G085320'

'very weakly similar to (95.5) AT4G37780 | Symbols: MYB87, ATMYB87 | MYB87 (MYB DOMAIN PROTEIN 87); DNA binding / transcription factor | chr4:17758404-17759526 REVERSEvery weakly similar to (84.3) MYB2_PHYPA Myb-related protein Pp2 - Physcomitrella patens (Moss)weakly similar to (132) loc_os10g35660 12010.m06386 protein P-type R2R3 Myb protein, putative seq=cds; coord=5:24542797..24544221:1; parent_gene=GRMZM2G392823'

'moderately similar to (240) AT4G33905 | Symbols: | peroxisomal membrane protein 22 kDa, putative | chr4:16254065-16255592 REVERSEmoderately similar to (341) loc_os12g32330 12012.m07038 protein mpv17 / PMP22 family protein, expressed seq=cds; coord=6:22666535..22670670:-1; parent_gene=GRMZM2G166537'

'moderately similar to (370) AT4G39770 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr4:18449138-18451218 REVERSEmoderately similar to (459) loc_os09g20390 12009.m22232 protein expressed protein seq=cds; coord=7:100324179..100326266:-1; parent_gene=GRMZM2G174396'

'moderately similar to (377) AT2G36870 | Symbols: | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative | chr2:15472869-15474630 REVERSEmoderately similar to (218) XTH_TOBAC Probable xyloglucan endotransglucosylase/hydrolase protein precursor (EC 2.4.1.207) - Nicotiana tabacum (Common tobacco)highly similar to (537) loc_os07g29750 12007.m07246 protein xyloglucan endotransglucosylase/hydrolase protein 32 precursor, putative, expressed seq=cds; coord=7:148463792..148465550:1; parent_gene=GRMZM2G413044'

'moderately similar to (278) AT5G06730 | Symbols: | peroxidase, putative | chr5:2080207-2081621 REVERSEmoderately similar to (276) PER2_CUCSA Peroxidase 2 (EC 1.11.1.7) (CUP2) (Fragment) - Cucumis sativus (Cucumber)moderately similar to (358) loc_os03g13180 12003.m06764 protein peroxidase 54 precursor, putative, expressed seq=cds; coord=8:102488133..102490149:1; parent_gene=GRMZM2G117365' 'moderately similar to (414) AT1G11680 | Symbols: CYP51G1, EMB1738, CYP51A2, CYP51 | CYP51G1 (CYTOCHROME P450 51G1); oxygen binding / sterol 14-demethylase | chr1:3938925-3940585 FORWARDmoderately similar to (421) CP51_SORBI Cytochrome P450 51 (EC 1.14.13.70) (CYPLI) (P450-LIA1) (Obtusifoliol 14-alpha demethylase) - Sorghum bicolor (Sorghum) (Sorghum vulgare)moderately similar to (477) loc_os05g34380 12005.m07669 protein cytochrome P450 51, putative seq=cds; coord=8:104279166..104281118:-1; parent_gene=GRMZM2G096029'

'moderately similar to (248) AT3G07880 | Symbols: | Rho GDP-dissociation inhibitor family protein | chr3:2514175-2515544 FORWARDmoderately similar to (348) loc_os01g68540 12001.m12957 protein rho GDP-dissociation inhibitor 1, putative, expressed seq=cds; coord=8:110181330..110183162:-1; parent_gene=GRMZM2G072089'

'nearly identical (1043) AT4G28650 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr4:14144155-14147276 REVERSEmoderately similar to (407) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1607) loc_os03g05140 12003.m06038 protein receptor-like protein kinase 5 precursor, putative, expressed seq=cds; coord=9:152256777..152260287:-1; parent_gene=GRMZM2G438840'

'weakly similar to (189) AT1G25550 | Symbols: | myb family transcription factor | chr1:8976644-8977942 FORWARDmoderately similar to (290) loc_os02g22020 12002.m07440 protein DNA binding protein, putative, expressed seq=cds; coord=10:5384582..5386647:1; parent_gene=GRMZM2G016370'

'moderately similar to (280) AT1G13080 | Symbols: CYP71B2 | CYP71B2 (CYTOCHROME P450 71B2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr1:4459493-4460807 FORWARDmoderately similar to (432) C71C2_MAIZE Cytochrome P450 71C2 (EC 1.14.-.-) (Benzoxazineless 3) - Zea mays (Maize)moderately similar to (452) loc_os08g01510 12008.m04299 protein cytochrome P450 71C4, putative, expressed seq=cds; coord=10:108117921..108119785:1; parent_gene=GRMZM2G399530'

'moderately similar to (394) AT4G23180 | Symbols: CRK10, RLK4 | CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr4:12138171-12140780 FORWARDmoderately similar to (203) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (523) loc_os04g53994 12004.m10292 protein ATP binding protein, putative, expressed seq=cds; coord=10:144138641..144143208:-1; parent_gene=GRMZM2G000633' 'weakly similar to (101) AT5G67190 | Symbols: | AP2 domain-containing transcription factor, putative | chr5:26809135-26809689 REVERSEweakly similar to (168) loc_os04g55520 12004.m10443 protein dehydration responsive element binding protein, putative, expressed seq=cds; coord=2:5562976..5564647:1; parent_gene=GRMZM2G174917'

'moderately similar to (248) AT1G01180 | Symbols: | unknown protein | chr1:75633-77446 FORWARDmoderately similar to (397) loc_os09g34320 12009.m06481 protein expressed protein seq=cds; coord=2:193842347..193843862:-1; parent_gene=GRMZM2G170253'

'moderately similar to (248) AT1G01180 | Symbols: | unknown protein | chr1:75633-77446 FORWARDmoderately similar to (397) loc_os09g34320 12009.m06481 protein expressed protein seq=cds; coord=2:193842347..193843862:-1; parent_gene=GRMZM2G170253'

'moderately similar to (260) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (338) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (331) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215424737..215427767:-1; parent_gene=GRMZM2G348512'

'weakly similar to (110) loc_os02g51550 12002.m10188 protein expressed protein seq=cds; coord=4:181258192..181259808:-1; parent_gene=GRMZM2G016948'

'highly similar to (717) AT3G04480 | Symbols: | endoribonuclease | chr3:1193988-1197320 REVERSE seq=cds; coord=5:215011519..215016709:-1; parent_gene=GRMZM2G150912'

'moderately similar to (211) AT1G64940 | Symbols: CYP89A6 | CYP89A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr1:24123789-24125324 FORWARDweakly similar to (163) C77A1_SOLME Cytochrome P450 77A1 (EC 1.14.-.-) (CYPLXXVIIA1) (P-450EG6) (Fragment) - Solanum melongena (Eggplant) (Aubergine)moderately similar to (240) loc_os06g22340 12006.m06888 protein cytochrome P450 89A2, putative, expressed seq=cds; coord=6:3677020..3678837:1; parent_gene=GRMZM2G104877'

'moderately similar to (229) AT3G51280 | Symbols: | male sterility MS5, putative | chr3:19037229-19038781 FORWARDhighly similar to (808) loc_os08g03620 12008.m04506 protein TPR Domain containing protein seq=cds; coord=6:9148014..9152540:-1; parent_gene=GRMZM2G442170'

'highly similar to (775) AT5G04500 | Symbols: | glycosyltransferase family protein 47 | chr5:1283604-1286155 FORWARDnearly identical (1256) loc_os05g46260 12005.m08751 protein expressed protein seq=cds; coord=6:161715219..161719692:1; parent_gene=GRMZM2G121237' 'moderately similar to (399) AT4G00460 | Symbols: ATROPGEF3, ROPGEF3 | Rho guanyl-nucleotide exchange factor | chr4:211146-213094 REVERSEhighly similar to (696) loc_os07g29780 12007.m07249 protein pollen-specific kinase partner protein, putative, expressed seq=cds; coord=7:148620567..148623468:-1; parent_gene=GRMZM2G131275'

moderately similar to (250) AT3G21800 | Symbols: UGT71B8 | UGT71B8 (UDP-GLUCOSYL TRANSFERASE 71B8); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ transferase, transferring glycosyl groups | chr3:7680243-7681685 REVERSEweakly similar to (147) ZOX_PHAVU Zeatin O-xylosyltransferase (EC 2.4.2.40) (Zeatin O-beta-D-xylosyltransferase) - Phaseolus vulgaris (Kidney bean) (French bean)moderately similar to (429) loc_os07g32010 12007.m07467 protein anthocyanidin 5,3-O-glucosyltransferase, putative, expressed seq=cds; coord=7:151193308..151195193:1; parent_gene=GRMZM2G455075'

'moderately similar to (386) AT2G01630 | Symbols: | glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative | chr2:279564-281955 REVERSEweakly similar to (166) E13B_WHEAT Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-endoglucanase) - Triticum aestivum (Wheat)highly similar to (645) loc_os07g32600 12007.m28981 protein glucan endo-1,3-beta-glucosidase 3 precursor, putative, expressed seq=cds; coord=7:152391511..152397214:1; parent_gene=GRMZM2G325008'

'highly similar to (830) AT2G41140 | Symbols: CRK1, ATCRK1, ATCBK3 | CRK1 (CDPK-RELATED KINASE 1); calcium ion binding / calcium-dependent protein serine/threonine phosphatase/ calmodulin-dependent protein kinase/ kinase | chr2:17150492-17153378 FORWARDhighly similar to (778) CRK_DAUCA CDPK-related protein kinase (EC 2.7.11.1) (PK421) - Daucus carota (Carrot)highly similar to (984) loc_os07g44710 12007.m08692 protein CDPK-related protein kinase, putative, expressed seq=cds; coord=7:169249410..169255466:-1; parent_gene=GRMZM2G015703'

'moderately similar to (248) AT3G07880 | Symbols: | Rho GDP-dissociation inhibitor family protein | chr3:2514175-2515544 FORWARDmoderately similar to (348) loc_os01g68540 12001.m12957 protein rho GDP-dissociation inhibitor 1, putative, expressed seq=cds; coord=8:110181330..110183162:-1; parent_gene=GRMZM2G072089' 'moderately similar to (284) AT5G10530 | Symbols: | lectin protein kinase, putative | chr5:3324978-3326933 REVERSEweakly similar to (177) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)moderately similar to (438) loc_os09g16950 12009.m04955 protein protein kinase, putative, expressed seq=cds; coord=10:1915531..1918048:1; parent_gene=GRMZM2G104655'

'weakly similar to (142) AT5G24090 | Symbols: | acidic endochitinase (CHIB1) | chr5:8143805-8145153 REVERSEmoderately similar to (285) XIP1_ORYSA Xylanase inhibitor protein 1 precursor (Class III chitinase homolog a) (RIXI protein) - Oryza sativa (Rice)moderately similar to (285) loc_os11g47580 12011.m08558 protein xylanase inhibitor protein 1 precursor, putative, expressed seq=cds; coord=10:1980938..1982242:1; parent_gene=GRMZM2G400999'

'highly similar to (761) AT1G11680 | Symbols: CYP51G1, EMB1738, CYP51A2, CYP51 | CYP51G1 (CYTOCHROME P450 51G1); oxygen binding / sterol 14-demethylase | chr1:3938925-3940585 FORWARDhighly similar to (911) CP51_SORBI Cytochrome P450 51 (EC 1.14.13.70) (CYPLI) (P450-LIA1) (Obtusifoliol 14-alpha demethylase) - Sorghum bicolor (Sorghum) (Sorghum vulgare)highly similar to (862) loc_os11g32240 12011.m07126 protein cytochrome P450 51, putative, expressed seq=cds; coord=10:3062645..3066771:-1; parent_gene=GRMZM2G068465'

'highly similar to (625) AT5G58330 | Symbols: | malate dehydrogenase (NADP), chloroplast, putative | chr5:23580010-23582287 REVERSEhighly similar to (791) MDHP_MAIZE Malate dehydrogenase [NADP], chloroplast precursor (EC 1.1.1.82) (NADP-MDH) - Zea mays (Maize)highly similar to (697) loc_os08g44810 12008.m08453 protein malate dehydrogenase 1, chloroplast precursor, putative, expressed seq=cds; coord=1:203170067..203174226:-1; parent_gene=GRMZM2G129513'

'weakly similar to (101) AT5G20630 | Symbols: GLP3, GLP3A, GLP3B, ATGER3, GER3 | GER3 (GERMIN 3); oxalate oxidase | chr5:6975315-6975950 REVERSEweakly similar to (103) GLP1_SINAL Germin-like protein 1 precursor - Sinapis alba (White mustard) (Brassica hirta)weakly similar to (114) loc_os08g35750 12008.m07564 protein germin-like protein 1 precursor, putative, expressed seq=cds; coord=1:207865153..207865778:-1; parent_gene=GRMZM2G363004' 'highly similar to (552) AT2G06050 | Symbols: OPR3 | OPR3 (OPDA-REDUCTASE 3); 12-oxophytodienoate reductase | chr2:2359240-2361971 REVERSEhighly similar to (717) loc_os08g35740 12008.m080177 protein 12-oxophytodienoate reductase 3, putative, expressed seq=cds; coord=1:207901911..207905956:-1; parent_gene=GRMZM2G148281'

'moderately similar to (374) AT4G37590 | Symbols: NPY5 | NPY5 (NAKED PINS IN YUC MUTANTS 5); protein binding / signal transducer | chr4:17663080-17665299 REVERSEmoderately similar to (204) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)highly similar to (552) loc_os03g41350 12003.m34896 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=1:255150622..255155140:1; parent_gene=GRMZM2G172506'

'moderately similar to (374) AT4G37590 | Symbols: NPY5 | NPY5 (NAKED PINS IN YUC MUTANTS 5); protein binding / signal transducer | chr4:17663080-17665299 REVERSEmoderately similar to (204) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)highly similar to (552) loc_os03g41350 12003.m34896 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=1:255150622..255155140:1; parent_gene=GRMZM2G172506'

'highly similar to (934) AT2G02220 | Symbols: ATPSKR1, PSKR1 | PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase | chr2:584098-587124 REVERSEhighly similar to (910) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1459) loc_os04g57630 12004.m10648 protein phytosulfokine receptor precursor, putative, expressed seq=cds; coord=2:2222100..2225911:1; parent_gene=GRMZM2G452142'

'moderately similar to (363) AT3G19130 | Symbols: ATRBP47B | ATRBP47B (RNA-binding protein 47B); RNA binding | chr3:6611398-6613823 REVERSEvery weakly similar to (82.4) ROC1_NICSY 29 kDa ribonucleoprotein A, chloroplast precursor (CP29A) - Nicotiana sylvestris (Wood tobacco)highly similar to (520) loc_os09g28810 12009.m06032 protein expressed protein seq=cds; coord=2:186893618..186898382:1; parent_gene=GRMZM2G168163' 'weakly similar to (178) AT1G28600 | Symbols: | lipase, putative | chr1:10051604-10053073 REVERSEvery weakly similar to (86.7) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)weakly similar to (194) loc_os01g42730 12001.m10537 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=3:213800866..213804340:-1; parent_gene=GRMZM2G047129'

'moderately similar to (241) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (341) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215431519..215437533:-1; parent_gene=GRMZM2G348512'

'moderately similar to (317) AT1G33440 | Symbols: | proton-dependent oligopeptide transport (POT) family protein | chr1:12127712-12130327 REVERSEmoderately similar to (423) loc_os04g36040 12004.m08693 protein peptide transporter PTR2, putative, expressed seq=cds; coord=4:25983954..25985905:1; parent_gene=GRMZM2G026459'

'moderately similar to (317) AT1G33440 | Symbols: | proton-dependent oligopeptide transport (POT) family protein | chr1:12127712-12130327 REVERSEmoderately similar to (423) loc_os04g36040 12004.m08693 protein peptide transporter PTR2, putative, expressed seq=cds; coord=4:25983954..25985905:1; parent_gene=GRMZM2G026459'

'moderately similar to (329) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEhighly similar to (549) loc_os02g48860 12002.m09920 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=4:163962237..163964018:1; parent_gene=GRMZM2G141036' 'highly similar to (676) AT5G37600 | Symbols: ATGSR1, GLN1;1, GSR 1 | ATGSR1; copper ion binding / glutamate-ammonia ligase | chr5:14933574-14935656 REVERSEhighly similar to (733) GLNA3_MAIZE Glutamine synthetase root isozyme 3 (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS112) - Zea mays (Maize)highly similar to (714) loc_os02g50240 12002.m33860 protein glutamine synthetase root isozyme 3, putative, expressed seq=cds; coord=4:167081372..167084703:-1; parent_gene=GRMZM2G036464'

'highly similar to (618) AT2G30710 | Symbols: | RabGAP/TBC domain-containing protein | chr2:13086147-13088991 REVERSEhighly similar to (792) loc_os09g34040 12009.m06453 protein TBC1 domain family member 22A, putative, expressed seq=cds; coord=4:171362826..171367336:1; parent_gene=GRMZM2G142806'

'weakly similar to (108) AT3G20570 | Symbols: | plastocyanin-like domain-containing protein | chr3:7186754-7187453 REVERSEweakly similar to (155) loc_os02g06670 12002.m06015 protein early nodulin 20 precursor, putative, expressed seq=cds; coord=4:236730981..236732351:-1; parent_gene=GRMZM2G101916'

'moderately similar to (207) AT3G04530 | Symbols: PPCK2, PEPCK2 | PPCK2; kinase/ protein serine/threonine kinase | chr3:1221546-1222456 FORWARDweakly similar to (153) CDPK2_ORYSA Calcium-dependent protein kinase, isoform 2 (EC 2.7.11.1) (CDPK 2) - Oryza sativa (Rice)moderately similar to (419) loc_os02g41580 12002.m09194 protein calcium-dependent protein kinase 2, putative, expressed seq=cds; coord=5:186505821..186507490:1; parent_gene=GRMZM2G096753'

highly similar to (800) AT3G53260 | Symbols: PAL2, ATPAL2 | PAL2; phenylalanine ammonia-lyase | chr3:19744256-19746619 REVERSEhighly similar to (966) PAL1_ORYSA Phenylalanine ammonia-lyase (EC 4.3.1.5) - Oryza sativa (Rice)highly similar to (966) loc_os02g41630 12002.m33418 protein phenylalanine ammonia-lyase, putative, expressed seq=cds; coord=5:186677171..186679442:-1; parent_gene=GRMZM2G074604'

'weakly similar to (147) AT5G07450 | Symbols: CYCP4;3 | CYCP4;3 (cyclin p4;3); cyclin-dependent protein kinase | chr5:2358418-2359253 REVERSEmoderately similar to (227) loc_os02g43550 12002.m09390 protein nuc-1 negative regulatory protein preg, putative, expressed seq=cds; coord=5:195401851..195404340:1; parent_gene=GRMZM2G160563' 'weakly similar to (147) AT1G48590 | Symbols: | C2 domain-containing protein | chr1:17962979-17964274 FORWARDmoderately similar to (244) loc_os07g31830 12007.m07449 protein GTPase activating protein, putative, expressed seq=cds; coord=7:150889841..150897264:1; parent_gene=GRMZM2G163095'

'moderately similar to (402) AT4G17360 | Symbols: | formyltetrahydrofolate deformylase/ hydroxymethyl-, formyl- and related transferase/ methyltransferase | chr4:9703698-9705468 REVERSEhighly similar to (533) loc_os03g01222 12003.m35587 protein formyltetrahydrofolate deformylase, putative, expressed seq=cds; coord=9:155451718..155453474:-1; parent_gene=GRMZM2G168281'

'moderately similar to (367) AT2G46860 | Symbols: AtPPa3 | AtPPa3 (Arabidopsis thaliana pyrophosphorylase 3); inorganic diphosphatase/ pyrophosphatase | chr2:19253843-19255060 FORWARDmoderately similar to (423) IPYR_MAIZE Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase) - Zea mays (Maize)moderately similar to (409) loc_os04g59040 12004.m101703 protein soluble inorganic pyrophosphatase, putative, expressed seq=cds; coord=10:148996189..148998596:-1; parent_gene=GRMZM2G104918'

'moderately similar to (268) AT3G13620 | Symbols: | amino acid permease family protein | chr3:4450904-4452556 REVERSEmoderately similar to (377) loc_os03g25840 12003.m07929 protein cationic amino acid transporter, putative, expressed seq=cds; coord=1:64885893..64889912:-1; parent_gene=GRMZM2G306919' 'moderately similar to (268) AT3G13620 | Symbols: | amino acid permease family protein | chr3:4450904-4452556 REVERSEmoderately similar to (377) loc_os03g25840 12003.m07929 protein cationic amino acid transporter, putative, expressed seq=cds; coord=1:64885893..64889912:-1; parent_gene=GRMZM2G306919'

'highly similar to (612) AT3G54190 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G38630.1); Has 77 Blast hits to 77 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink). | chr3:20061759-20063880 REVERSEhighly similar to (757) loc_os12g31440 12012.m06953 protein expressed protein seq=cds; coord=3:135500443..135510945:1; parent_gene=GRMZM2G084606'

'weakly similar to (162) AT1G61660 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr1:22754603-22756171 REVERSEmoderately similar to (372) loc_os01g57580 12001.m11909 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=3:190314296..190317061:1; parent_gene=GRMZM2G440529'

'moderately similar to (260) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (338) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (331) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215424737..215427767:-1; parent_gene=GRMZM2G348512'

'very weakly similar to (100) AT3G21330 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr3:7507720-7508841 FORWARDvery weakly similar to (80.9) LAX_ORYSA Transcription factor LAX PANICLE - Oryza sativa (Rice)weakly similar to (143) loc_os01g38610 12001.m10144 protein DNA binding protein, putative, expressed seq=cds; coord=3:219182141..219184295:-1; parent_gene=GRMZM2G081816' moderately similar to (260) AT4G28850 | Symbols: | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative | chr4:14244336-14245781 FORWARDmoderately similar to (236) BRU1_SOYBN Brassinosteroid-regulated protein BRU1 precursor - Glycine max (Soybean)moderately similar to (421) loc_os02g17900 12002.m07034 protein xyloglucan endotransglucosylase/hydrolase protein 26 precursor, putative, expressed seq=cds; coord=4:221631043..221632262:-1; parent_gene=GRMZM2G112619'

weakly similar to (119) loc_os06g44660 12006.m08993 protein fasciclin-like arabinogalactan protein 8 precursor, putative, expressed seq=cds; coord=5:89287541..89288511:1; parent_gene=GRMZM2G134528'

'highly similar to (790) AT1G73590 | Symbols: PIN1, ATPIN1 | PIN1 (PIN-FORMED 1); transporter | chr1:27659772-27662876 FORWARDnearly identical (1019) PIN1_ORYSA Auxin efflux carrier component 1 (OsPIN1) (Ethylene insensitive root 1 homolog) - Oryza sativa (Rice)nearly identical (1019) loc_os02g50960 12002.m33866 protein auxin efflux carrier component 1, putative, expressed seq=cds; coord=5:206727149..206730565:1; parent_gene=GRMZM2G074267'

'very weakly similar to (90.1) AT1G22490 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr1:7938448-7940489 REVERSEmoderately similar to (243) loc_os02g52190 12002.m10250 protein DNA binding protein, putative, expressed seq=cds; coord=5:208895710..208901046:-1; parent_gene=GRMZM2G045883'

'weakly similar to (181) AT2G43190 | Symbols: | ribonuclease P family protein | chr2:17956220-17957833 FORWARDmoderately similar to (438) loc_os05g39530 12005.m083751 protein ribonuclease P/ ribonuclease, putative, expressed seq=cds; coord=6:74035080..74038340:-1; parent_gene=GRMZM2G047265'

'weakly similar to (110) AT2G34730 | Symbols: | myosin heavy chain-related | chr2:14654611-14657443 FORWARDhighly similar to (712) loc_os07g05390 12007.m05003 protein expressed protein seq=cds; coord=7:5086583..5093575:-1; parent_gene=GRMZM2G011800' 'moderately similar to (226) AT1G68400 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr1:25646401-25648916 REVERSEweakly similar to (136) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (712) loc_os07g38640 12007.m08109 protein receptor-kinase isolog, 5 partial, putative, expressed seq=cds; coord=7:159907257..159909577:-1; parent_gene=GRMZM2G006505'

'weakly similar to (177) AT5G45540 | Symbols: | unknown protein | chr5:18458294-18460705 REVERSEmoderately similar to (385) loc_os10g11310 12010.m065239 protein expressed protein seq=cds; coord=8:21845748..21848205:1; parent_gene=GRMZM2G032551'

'highly similar to (684) AT3G13390 | Symbols: sks11 | sks11 (SKU5 Similar 11); copper ion binding / oxidoreductase | chr3:4351401-4353289 REVERSEhighly similar to (686) NTP3_TOBAC Pollen-specific protein NTP303 precursor - Nicotiana tabacum (Common tobacco)highly similar to (927) loc_os05g40740 12005.m083761 protein pollen-specific protein NTP303 precursor, putative, expressed seq=cds; coord=8:119369178..119371841:-1; parent_gene=GRMZM2G142584'

'moderately similar to (447) AT2G28680 | Symbols: | cupin family protein | chr2:12303118-12304747 REVERSEvery weakly similar to (97.8) GLUA2_ORYSA Glutelin type-A 2 precursor (Glutelin type II) [Contains: Glutelin type-A 2 acidic chain; Glutelin type-A 2 basic chain] - Oryza sativa (Rice)highly similar to (549) loc_os05g02520 12005.m27675 protein legumin-like protein, putative, expressed seq=cds; coord=8:133178452..133180059:1; parent_gene=GRMZM2G005552'

highly similar to (619) AT5G64570 | Symbols: XYL4, ATBXL4 | XYL4; hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase | chr5:25810227-25813309 REVERSEmoderately similar to (290) XYNB_PRUPE Putative beta-D-xylosidase (EC 3.2.1.-) (PpAz152) (Fragment) - Prunus persica (Peach)nearly identical (1204) loc_os11g47350 12011.m08515 protein beta-D-xylosidase, putative seq=cds; coord=9:101686324..101689087:1; parent_gene=GRMZM2G146523' 'moderately similar to (382) AT1G72370 | Symbols: P40, AP40, RP40, RPSAA | P40; structural constituent of ribosome | chr1:27243148-27244842 REVERSEmoderately similar to (406) RSSA_SOYBN 40S ribosomal protein SA (p40) - Glycine max (Soybean)moderately similar to (477) loc_os03g08440 12003.m35048 protein 40S ribosomal protein SA, putative, expressed seq=cds; coord=1:17325366..17335709:-1; parent_gene=GRMZM2G145308'

'moderately similar to (299) AT2G30020 | Symbols: | protein phosphatase 2C, putative / PP2C, putative | chr2:12814437-12815904 FORWARDmoderately similar to (469) loc_os03g18150 12003.m07240 protein protein phosphatase 2C isoform epsilon, putative, expressed seq=cds; coord=1:45366147..45367585:1; parent_gene=AC208201.3_FG002'

moderately similar to (236) AT2G45110 | Symbols: ATEXPB4, EXPB4, ATHEXP BETA 1.1 | ATEXPB4 (ARABIDOPSIS THALIANA EXPANSIN B4) | chr2:18599575-18601237 FORWARDmoderately similar to (412) EXB12_ORYSA Expansin-B12 precursor (OsEXPB12) (Beta-expansin-12) (OsaEXPb1.17) - Oryza sativa (Rice)moderately similar to (414) loc_os03g44290 12003.m35332 protein beta-expansin 4 precursor, putative, expressed seq=cds; coord=1:251136916..251138525:1; parent_gene=GRMZM2G103672'

'moderately similar to (461) AT3G02210 | Symbols: COBL1 | COBL1 (COBRA-LIKE PROTEIN 1 PRECURSOR) | chr3:409352-411478 REVERSEhighly similar to (597) COBL7_ORYSA COBRA-like 7 protein precursor (BRITTLE CULM1-like 3 protein) - Oryza sativa (Rice)moderately similar to (456) loc_os05g32110 12005.m083711 protein COBRA-like protein 4 precursor, putative, expressed seq=cds; coord=2:21872675..21874781:-1; parent_gene=GRMZM2G465188'

'highly similar to (716) AT1G62660 | Symbols: | beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar | chr1:23199949-23203515 FORWARDnearly identical (1191) INV1_MAIZE Beta-fructofuranosidase 1 precursor (EC 3.2.1.26) (Sucrose 1) (Invertase 1) - Zea mays (Maize)highly similar to (956) loc_os04g45290 12004.m35180 protein beta-fructofuranosidase 1 precursor, putative, expressed seq=cds; coord=2:22880766..22885337:-1; parent_gene=GRMZM2G394450' 'moderately similar to (473) AT2G37170 | Symbols: PIP2B, PIP2;2 | PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel | chr2:15613624-15614791 REVERSEhighly similar to (525) PIP23_ORYSA Probable aquaporin PIP2.3 (Plasma membrane intrinsic protein 2.3) (OsPIP2.3) - Oryza sativa (Rice)highly similar to (525) loc_os04g44060 12004.m09364 protein aquaporin PIP2.3, putative, expressed seq=cds; coord=2:27867805..27870068:-1; parent_gene=GRMZM2G178693'

highly similar to (543) AT1G61820 | Symbols: BGLU46 | BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds | chr1:22836707-22838444 FORWARDmoderately similar to (374) BGLC_MAIZE Beta-glucosidase, chloroplast precursor (EC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucoside glucohydrolase) - Zea mays (Maize)highly similar to (647) loc_os04g43360 12004.m101583 protein beta-glucosidase, chloroplast precursor, putative, expressed seq=cds; coord=2:28861517..28871313:-1; parent_gene=GRMZM2G012236'

highly similar to (543) AT1G61820 | Symbols: BGLU46 | BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds | chr1:22836707-22838444 FORWARDmoderately similar to (374) BGLC_MAIZE Beta-glucosidase, chloroplast precursor (EC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucoside glucohydrolase) - Zea mays (Maize)highly similar to (647) loc_os04g43360 12004.m101583 protein beta-glucosidase, chloroplast precursor, putative, expressed seq=cds; coord=2:28861517..28871313:-1; parent_gene=GRMZM2G012236'

'moderately similar to (401) AT4G23310 | Symbols: | receptor-like protein kinase, putative | chr4:12185737-12188763 FORWARDweakly similar to (200) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (692) loc_os07g35370 12007.m07793 protein receptor-like protein kinase homolog RK20-1, putative, expressed seq=cds; coord=2:204116816..204119629:-1; parent_gene=GRMZM2G140231'

'moderately similar to (298) AT5G45910 | Symbols: | GDSL-motif lipase/hydrolase family protein | chr5:18620420-18622264 REVERSEweakly similar to (135) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)highly similar to (574) loc_os01g11650 12001.m42621 protein esterase precursor, putative, expressed seq=cds; coord=3:3209208..3210849:1; parent_gene=GRMZM2G085176'

'seq=cds; coord=3:17605685..17606666:1; parent_gene=GRMZM2G099340'

'highly similar to (837) AT2G14960 | Symbols: GH3.1 | GH3.1 | chr2:6451659-6453670 REVERSEnearly identical (1033) GH32_ORYSA Probable indole-3-acetic acid-amido synthetase GH3.2 (EC 6.3.2.-) (Auxin-responsive GH3-like protein 2) (OsGH3-2) - Oryza sativa (Rice)nearly identical (1033) loc_os01g55940 12001.m11750 protein indole-3-acetic acid-amido synthetase GH3.2, putative, expressed seq=cds; coord=3:194424615..194428239:-1; parent_gene=GRMZM2G033359'

'highly similar to (888) AT1G03750 | Symbols: CHR9 | SWI2 (SWITCH 2); ATP binding / DNA binding / helicase/ nucleic acid binding | chr1:937920-941068 FORWARDweakly similar to (130) ISW2_ORYSA Probable chromatin remodelling complex ATPase chain (EC 3.6.1.-) (ISW2-like) (Sucrose nonfermenting protein 2 homolog) - Oryza sativa (Rice)nearly identical (1074) loc_os05g15890 12005.m27751 protein ATP binding protein, putative, expressed seq=cds; coord=5:21030962..21046194:1; parent_gene=GRMZM2G146041'

'moderately similar to (340) AT1G64530 | Symbols: | RWP-RK domain-containing protein | chr1:23959820-23962896 FORWARDmoderately similar to (424) loc_os02g04340 12002.m05783 protein NIN-like protein 2, putative, expressed seq=cds; coord=5:76682569..76685854:-1; parent_gene=GRMZM2G042278' 'highly similar to (642) AT3G52600 | Symbols: AtcwINV2 | AtcwINV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds | chr3:19507080-19508833 REVERSEnearly identical (1174) INVA_MAIZE Beta-fructofuranosidase, cell wall isozyme precursor (EC 3.2.1.26) (Sucrose hydrolase) (Invertase) - Zea mays (Maize)highly similar to (927) loc_os02g33110 12002.m100224 protein beta-fructofuranosidase, insoluble isoenzyme 1 precursor, putative, expressed seq=cds; coord=5:169454598..169459090:1; parent_gene=GRMZM2G139300'

'weakly similar to (167) AT2G01660 | Symbols: PDLP6 | PDLP6 (PLASMODESMATA-LOCATED PROTEIN 6) | chr2:291717-292496 REVERSEmoderately similar to (363) loc_os06g14280 12006.m06143 protein secretory protein-like, putative, expressed seq=cds; coord=6:118147444..118150871:1; parent_gene=GRMZM2G059634'

'highly similar to (583) AT4G30110 | Symbols: HMA2 | HMA2; cadmium-transporting ATPase | chr4:14720253-14724577 REVERSEvery weakly similar to (87.8) PMA4_NICPL Plasma membrane ATPase 4 (EC 3.6.3.6) (Proton pump 4) - Nicotiana plumbaginifolia (Leadwort-leaved tobacco)highly similar to (774) loc_os07g12900 12007.m05742 protein cadmium/zinc-transporting ATPase 2, putative seq=cds; coord=7:21633432..21636570:1; parent_gene=AC205008.4_FG002'

'nearly identical (1143) AT5G54280 | Symbols: ATM2, ATMYOS1, ATM4 | ATM2 (ARABIDOPSIS THALIANA MYOSIN 2); motor | chr5:22039606-22045592 REVERSEnearly identical (1733) loc_os07g37560 12007.m28992 protein myosin-5C, putative, expressed seq=cds; coord=7:157571319..157580965:-1; parent_gene=GRMZM2G057380' 'moderately similar to (440) AT1G06520 | Symbols: ATGPAT1, GPAT1 | GPAT1 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 1); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase | chr1:1994170-1996067 REVERSEhighly similar to (758) loc_os01g44069 12001.m10665 protein glycerol-3-phosphate acyltransferase 1, putative, expressed seq=cds; coord=8:145960909..145968749:1; parent_gene=GRMZM2G177150'

'moderately similar to (427) AT5G42800 | Symbols: DFR, TT3, M318 | DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase | chr5:17164296-17165864 REVERSEhighly similar to (574) DFRA_MAIZE Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Zea mays (Maize)moderately similar to (392) loc_os01g44260 12001.m10683 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=8:146110828..146112451:1; parent_gene=GRMZM2G013726'

'moderately similar to (389) AT4G09160 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr4:5839761-5842158 FORWARDhighly similar to (623) loc_os01g65380 12001.m12651 protein patellin-5, putative, expressed seq=cds; coord=8:165856036..165859140:-1; parent_gene=GRMZM2G033649'

'moderately similar to (389) AT4G09160 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr4:5839761-5842158 FORWARDhighly similar to (623) loc_os01g65380 12001.m12651 protein patellin-5, putative, expressed seq=cds; coord=8:165856036..165859140:-1; parent_gene=GRMZM2G033649'

'moderately similar to (283) AT4G17650 | Symbols: | aromatic-rich family protein | chr4:9827749-9829443 FORWARDmoderately similar to (368) loc_os01g56560 12001.m11813 protein protein COQ10 A, mitochondrial precursor, putative, expressed seq=cds; coord=8:172486699..172489943:1; parent_gene=GRMZM2G111472'

'highly similar to (704) AT3G12360 | Symbols: ITN1 | ITN1 (INCREASED TOLERANCE TO NACL); protein binding | chr3:3934146-3936495 FORWARDhighly similar to (951) loc_os03g17240 12003.m07154 protein protein binding protein, putative, expressed seq=cds; coord=9:138798239..138801359:-1; parent_gene=GRMZM2G020982'

'highly similar to (704) AT3G12360 | Symbols: ITN1 | ITN1 (INCREASED TOLERANCE TO NACL); protein binding | chr3:3934146-3936495 FORWARDhighly similar to (951) loc_os03g17240 12003.m07154 protein protein binding protein, putative, expressed seq=cds; coord=9:138798239..138801359:-1; parent_gene=GRMZM2G020982'

'moderately similar to (325) AT1G08320 | Symbols: | bZIP family transcription factor | chr1:2622113-2627451 REVERSEmoderately similar to (303) TGA21_TOBAC TGACG-sequence-specific DNA-binding protein TGA-2.1 (TGA2.1) - Nicotiana tabacum (Common tobacco)moderately similar to (409) loc_os12g05680 12012.m04561 protein transcription factor HBP-1b, putative, expressed seq=cds; coord=10:5530500..5533143:-1; parent_gene=GRMZM2G366264'

'nearly identical (1538) AT4G30190 | Symbols: AHA2, PMA2 | AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism | chr4:14770820-14775920 REVERSEnearly identical (1693) PMA1_ORYSA Plasma membrane ATPase (EC 3.6.3.6) (Proton pump) - Oryza sativa (Rice)nearly identical (1693) loc_os04g56160 12004.m101441 protein plasma membrane ATPase, putative, expressed seq=cds; coord=10:146179978..146186537:1; parent_gene=GRMZM2G006894'

'weakly similar to (152) AT3G59650 | Symbols: | mitochondrial ribosomal protein L51/S25/CI-B8 family protein | chr3:22033216-22033928 FORWARDweakly similar to (182) loc_os03g10930 12003.m06545 protein mitochondrial ribosomal protein L43, putative, expressed seq=cds; coord=1:21456899..21461749:1; parent_gene=GRMZM2G004259'

'weakly similar to (175) AT2G33385 | Symbols: arpc2b | arpc2b (actin-related protein C2B); structural molecule | chr2:14147604-14149769 REVERSEmoderately similar to (350) loc_os04g43290 12004.m101581 protein ARPC2B, putative, expressed seq=cds; coord=2:28671052..28673189:-1; parent_gene=GRMZM2G052644'

'weakly similar to (175) AT2G33385 | Symbols: arpc2b | arpc2b (actin-related protein C2B); structural molecule | chr2:14147604-14149769 REVERSEmoderately similar to (350) loc_os04g43290 12004.m101581 protein ARPC2B, putative, expressed seq=cds; coord=2:28671052..28673189:-1; parent_gene=GRMZM2G052644' 'moderately similar to (304) AT5G15240 | Symbols: | amino acid transporter family protein | chr5:4947762-4950211 FORWARDhighly similar to (542) loc_os01g41420 12001.m10409 protein amino acid permease, putative, expressed seq=cds; coord=3:222949367..222951117:-1; parent_gene=GRMZM2G066428'

'very weakly similar to (91.7) AT1G19210 | Symbols: | AP2 domain-containing transcription factor, putative | chr1:6626973-6627530 REVERSEweakly similar to (199) loc_os02g54050 12002.m10434 protein transcriptional factor TINY, putative, expressed seq=cds; coord=4:176528249..176529362:1; parent_gene=GRMZM2G097081'

'weakly similar to (158) AT1G05385 | Symbols: | photosystem II 11 kDa protein-related | chr1:1582747-1583648 REVERSEmoderately similar to (206) loc_os03g53640 12003.m10335 protein expressed protein seq=cds; coord=5:7442570..7443838:1; parent_gene=GRMZM2G087435'

'moderately similar to (375) AT3G22750 | Symbols: | protein kinase, putative | chr3:8037364-8039096 REVERSEhighly similar to (538) loc_os03g53410 12003.m10311 protein ATMRK1, putative, expressed seq=cds; coord=5:7587329..7589198:-1; parent_gene=GRMZM2G014618'

'highly similar to (597) AT2G32990 | Symbols: AtGH9B8 | AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds | chr2:14003361-14005844 FORWARDhighly similar to (760) GUN5_ORYSA Endoglucanase 5 precursor (EC 3.2.1.4) (Endo-1,4-beta glucanase 5) - Oryza sativa (Rice)highly similar to (760) loc_os02g05744 12002.m05922 protein endoglucanase 1 precursor, putative, expressed seq=cds; coord=5:80803727..80807409:-1; parent_gene=GRMZM2G482256' 'weakly similar to (157) AT4G15760 | Symbols: MO1 | MO1 (MONOOXYGENASE 1); electron carrier/ oxidoreductase | chr4:8972785-8974548 REVERSEmoderately similar to (220) loc_os02g35320 12002.m08620 protein oxidoreductase, putative, expressed seq=cds; coord=5:174126967..174128883:-1; parent_gene=GRMZM2G339523'

'highly similar to (606) AT2G32990 | Symbols: AtGH9B8 | AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds | chr2:14003361-14005844 FORWARDhighly similar to (809) GUN7_ORYSA Endoglucanase 7 precursor (EC 3.2.1.4) (Endo-1,4-beta glucanase 7) (OsGLU10) - Oryza sativa (Rice)highly similar to (809) loc_os02g50490 12002.m10083 protein endoglucanase 1 precursor, putative, expressed seq=cds; coord=5:205562436..205565933:1; parent_gene=GRMZM2G151257'

'moderately similar to (273) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEmoderately similar to (481) loc_os06g20140 12006.m06671 protein aspartic proteinase nepenthesin-1 precursor, putative seq=cds; coord=6:120916323..120918370:-1; parent_gene=GRMZM2G405498'

'highly similar to (572) AT3G17470 | Symbols: ATCRSH | RelA/SpoT domain-containing protein / calcium-binding EF-hand family protein | chr3:5979868-5981968 FORWARDhighly similar to (816) loc_os05g06890 12005.m05216 protein relA-SpoT like protein RSH4, putative, expressed seq=cds; coord=6:125187387..125190276:-1; parent_gene=GRMZM2G152040'

'highly similar to (560) AT3G06430 | Symbols: EMB2750 | EMB2750 (embryo defective 2750) | chr3:1956658-1958240 REVERSEweakly similar to (128) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (701) loc_os03g19650 12003.m35185 protein PPR2, putative, expressed seq=cds; coord=7:2581533..2584327:-1; parent_gene=GRMZM2G341621'

'moderately similar to (301) AT5G57480 | Symbols: | AAA-type ATPase family protein | chr5:23279406-23280968 REVERSEhighly similar to (660) loc_os09g27340 12009.m05886 protein ATP binding protein, putative seq=cds; coord=7:122985316..122987123:1; parent_gene=GRMZM2G095254'

'weakly similar to (187) AT1G44760 | Symbols: | universal stress protein (USP) family protein | chr1:16896894-16898427 REVERSEmoderately similar to (248) loc_os01g65440 12001.m12655 protein universal stress protein family protein, expressed seq=cds; coord=8:165713440..165715862:-1; parent_gene=GRMZM2G114057' 'weakly similar to (187) AT1G44760 | Symbols: | universal stress protein (USP) family protein | chr1:16896894-16898427 REVERSEmoderately similar to (248) loc_os01g65440 12001.m12655 protein universal stress protein family protein, expressed seq=cds; coord=8:165713440..165715862:-1; parent_gene=GRMZM2G114057'

'weakly similar to (187) AT1G44760 | Symbols: | universal stress protein (USP) family protein | chr1:16896894-16898427 REVERSEmoderately similar to (248) loc_os01g65440 12001.m12655 protein universal stress protein family protein, expressed seq=cds; coord=8:165713440..165715862:-1; parent_gene=GRMZM2G114057'

'weakly similar to (130) loc_os01g55570 12001.m43202 protein thylakoid membrane phosphoprotein 14 kda, chloroplast precursor, putative, expressed seq=cds; coord=8:173408069..173410516:-1; parent_gene=GRMZM2G302639'

'weakly similar to (130) loc_os01g55570 12001.m43202 protein thylakoid membrane phosphoprotein 14 kda, chloroplast precursor, putative, expressed seq=cds; coord=8:173408069..173410516:-1; parent_gene=GRMZM2G302639'

'moderately similar to (233) AT3G15510 | Symbols: ATNAC2, ANAC056, NARS1 | ATNAC2 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 2); transcription factor | chr3:5243696-5245037 FORWARDmoderately similar to (223) NAC68_ORYSA NAC domain-containing protein 68 (ONAC068) - Oryza sativa (Rice)moderately similar to (286) loc_os11g03300 12011.m04526 protein NAC domain transcription factor, putative, expressed seq=cds; coord=10:2679313..2681402:-1; parent_gene=GRMZM2G127379'

'weakly similar to (135) AT5G45420 | Symbols: | myb family transcription factor | chr5:18405668-18406597 REVERSEmoderately similar to (235) loc_os08g06240 12008.m04763 protein dnajc2 protein, putative, expressed seq=cds; coord=10:77673604..77678581:-1; parent_gene=GRMZM2G001530'

'weakly similar to (194) AT4G33420 | Symbols: | peroxidase, putative | chr4:16084856-16086105 FORWARDweakly similar to (170) PER1_ARAHY Cationic peroxidase 1 precursor (EC 1.11.1.7) (PNPC1) - Arachis hypogaea (Peanut)highly similar to (504) loc_os05g04380 12005.m27687 protein peroxidase 1 precursor, putative, expressed seq=cds; coord=10:85640717..85645627:1; parent_gene=GRMZM2G394500'

'weakly similar to (172) loc_os12g03440 12012.m04342 protein F-box domain containing protein, expressed seq=cds; coord=1:172875290..172877007:-1; parent_gene=GRMZM2G087608' 'moderately similar to (478) AT4G12320 | Symbols: CYP706A6 | CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr4:7314939-7316647 REVERSEmoderately similar to (308) C75A2_SOLME Flavonoid 3',5'-hydroxylase (EC 1.14.13.88) (F3'5'H) (Cytochrome P450 75A2) (CYPLXXVA2) (P-450EG1) - Solanum melongena (Eggplant) (Aubergine)highly similar to (709) loc_os08g43440 12008.m08318 protein flavonoid 3-monooxygenase, putative, expressed seq=cds; coord=1:207274164..207276641:1; parent_gene=GRMZM2G089528'

'moderately similar to (323) AT1G26870 | Symbols: FEZ, ANAC009 | FEZ (FEZ); transcription factor | chr1:9312856-9314983 FORWARDweakly similar to (187) NAC68_ORYSA NAC domain-containing protein 68 (ONAC068) - Oryza sativa (Rice)highly similar to (518) loc_os08g33910 12008.m07381 protein NAC domain-containing protein 9, putative, expressed seq=cds; coord=1:212951664..212953388:-1; parent_gene=GRMZM2G152543'

'weakly similar to (108) AT5G46080 | Symbols: | protein kinase family protein | chr5:18689723-18690721 REVERSEmoderately similar to (315) loc_os08g28890 12008.m06894 protein ATP binding protein, putative, expressed seq=cds; coord=1:219974839..219976008:-1; parent_gene=GRMZM2G154114'

'moderately similar to (216) AT3G19090 | Symbols: | RNA-binding protein, putative | chr3:6601466-6603709 FORWARDmoderately similar to (393) loc_os03g36900 12003.m08805 protein RNA binding protein, putative, expressed seq=cds; coord=1:221945123..221947755:1; parent_gene=GRMZM2G411041'

'highly similar to (934) AT2G02220 | Symbols: ATPSKR1, PSKR1 | PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase | chr2:584098-587124 REVERSEhighly similar to (910) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1459) loc_os04g57630 12004.m10648 protein phytosulfokine receptor precursor, putative, expressed seq=cds; coord=2:2222100..2225911:1; parent_gene=GRMZM2G452142'

'highly similar to (934) AT2G02220 | Symbols: ATPSKR1, PSKR1 | PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase | chr2:584098-587124 REVERSEhighly similar to (910) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1459) loc_os04g57630 12004.m10648 protein phytosulfokine receptor precursor, putative, expressed seq=cds; coord=2:2222100..2225911:1; parent_gene=GRMZM2G452142'

'highly similar to (537) AT5G23810 | Symbols: AAP7 | AAP7; amino acid transmembrane transporter | chr5:8028461-8030138 FORWARDhighly similar to (704) loc_os04g39489 12004.m35579 protein AAP7, putative, expressed seq=cds; coord=2:39327335..39330173:1; parent_gene=GRMZM2G155491'

'weakly similar to (119) loc_os09g31300 12009.m22140 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=2:189701055..189703654:1; parent_gene=GRMZM2G417597'

'weakly similar to (178) AT1G28600 | Symbols: | lipase, putative | chr1:10051604-10053073 REVERSEvery weakly similar to (86.7) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)weakly similar to (194) loc_os01g42730 12001.m10537 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=3:213800866..213804340:-1; parent_gene=GRMZM2G047129'

'nearly identical (1232) AT1G77760 | Symbols: NIA1, GNR1, NR1 | NIA1 (NITRATE REDUCTASE 1); nitrate reductase | chr1:29236005-29239367 REVERSEnearly identical (1540) NIA7_HORVU Nitrate reductase [NAD(P)H] (EC 1.7.1.2) - Hordeum vulgare (Barley)nearly identical (1573) loc_os02g53130 12002.m10342 protein nitrate reductase, putative, expressed seq=cds; coord=4:177655913..177659763:1; parent_gene=GRMZM2G428027'

'weakly similar to (129) AT2G43760 | Symbols: | molybdopterin biosynthesis MoaE family protein | chr2:18133276-18133872 FORWARDweakly similar to (188) loc_os02g04740 12002.m05822 protein molybdenum cofactor synthesis protein 2 large subunit, putative, expressed seq=cds; coord=4:237711634..237712667:-1; parent_gene=GRMZM2G165966'

'moderately similar to (330) AT2G20840 | Symbols: | secretory carrier membrane protein (SCAMP) family protein | chr2:8971925-8974400 REVERSEmoderately similar to (418) loc_os03g38600 12003.m08954 protein SCAMP37, putative seq=cds; coord=5:19709117..19712463:-1; parent_gene=GRMZM2G124938' 'weakly similar to (132) AT1G78080 | Symbols: RAP2.4 | RAP2.4 (related to AP2 4); DNA binding / transcription factor | chr1:29364790-29365794 FORWARDmoderately similar to (202) loc_os02g51670 12002.m10198 protein AP2 domain-containing protein, putative, expressed seq=cds; coord=5:208162767..208165707:1; parent_gene=GRMZM2G055204'

'moderately similar to (407) AT4G39770 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr4:18449138-18451218 REVERSEhighly similar to (521) loc_os02g51680 12002.m10199 protein expressed protein seq=cds; coord=5:208172385..208174899:1; parent_gene=GRMZM2G055150'

'highly similar to (675) AT5G08560 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:2771104-2773827 REVERSEhighly similar to (986) loc_os02g19210 12002.m07164 protein WD-repeat protein 26, putative, expressed seq=cds; coord=6:8380046..8400603:1; parent_gene=GRMZM2G061186'

'moderately similar to (350) AT5G55590 | Symbols: QRT1 | QRT1 (QUARTET 1); pectinesterase | chr5:22519911-22521699 FORWARDweakly similar to (169) PME3_CITSI Pectinesterase-3 precursor (EC 3.1.1.11) (Pectin methylesterase 3) (PE 3) - Citrus sinensis (Sweet orange)highly similar to (565) loc_os07g41650 12007.m08401 protein pectinesterase VGDH2 precursor, putative, expressed seq=cds; coord=7:164829922..164833174:-1; parent_gene=GRMZM2G037411'

'moderately similar to (253) AT3G13840 | Symbols: | scarecrow transcription factor family protein | chr3:4555305-4556837 REVERSEmoderately similar to (261) NSP1_MEDTR Nodulation signaling pathway 1 protein - Medicago truncatula (Barrel medic)moderately similar to (457) loc_os03g29480 12003.m08221 protein nodulation signaling pathway 1 protein, putative, expressed seq=cds; coord=7:165156675..165158312:1; parent_gene=GRMZM2G169636'

'moderately similar to (253) AT3G13840 | Symbols: | scarecrow transcription factor family protein | chr3:4555305-4556837 REVERSEmoderately similar to (261) NSP1_MEDTR Nodulation signaling pathway 1 protein - Medicago truncatula (Barrel medic)moderately similar to (457) loc_os03g29480 12003.m08221 protein nodulation signaling pathway 1 protein, putative, expressed seq=cds; coord=7:165156675..165158312:1; parent_gene=GRMZM2G169636' 'moderately similar to (460) AT3G05620 | Symbols: | pectinesterase family protein | chr3:1629658-1631766 REVERSEmoderately similar to (426) PME_PRUPE Pectinesterase PPE8B precursor (EC 3.1.1.11) (Pectin methylesterase) (PE) - Prunus persica (Peach)highly similar to (779) loc_os01g15039 12001.m08104 protein pectinesterase PPE8B precursor, putative, expressed seq=cds; coord=8:5329655..5332095:1; parent_gene=GRMZM2G017555'

'moderately similar to (249) AT1G70060 | Symbols: SNL4 | SNL4 (SIN3-LIKE 4) | chr1:26383789-26389568 FORWARDmoderately similar to (338) loc_os01g01960 12001.m06838 protein paired amphipathic helix repeat family protein, expressed seq=cds; coord=8:8136058..8139636:-1; parent_gene=AC234160.1_FG001'

'moderately similar to (414) AT1G11680 | Symbols: CYP51G1, EMB1738, CYP51A2, CYP51 | CYP51G1 (CYTOCHROME P450 51G1); oxygen binding / sterol 14-demethylase | chr1:3938925-3940585 FORWARDmoderately similar to (421) CP51_SORBI Cytochrome P450 51 (EC 1.14.13.70) (CYPLI) (P450-LIA1) (Obtusifoliol 14-alpha demethylase) - Sorghum bicolor (Sorghum) (Sorghum vulgare)moderately similar to (477) loc_os05g34380 12005.m07669 protein cytochrome P450 51, putative seq=cds; coord=8:104279166..104281118:-1; parent_gene=GRMZM2G096029'

'moderately similar to (248) AT3G07880 | Symbols: | Rho GDP-dissociation inhibitor family protein | chr3:2514175-2515544 FORWARDmoderately similar to (348) loc_os01g68540 12001.m12957 protein rho GDP-dissociation inhibitor 1, putative, expressed seq=cds; coord=8:110181330..110183162:-1; parent_gene=GRMZM2G072089'

'moderately similar to (280) AT1G23280 | Symbols: | MAK16 protein-related | chr1:8260865-8262650 REVERSEmoderately similar to (362) loc_os07g16950 12007.m079650 protein MAK16-like protein RBM13, putative, expressed seq=cds; coord=8:161187376..161192709:-1; parent_gene=GRMZM2G461793' 'weakly similar to (197) AT1G65680 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2) | chr1:24427266-24428399 FORWARDmoderately similar to (293) EXPB6_ORYSA Expansin-B6 precursor (OsEXPB6) (Beta-expansin-6) (OsaEXPb1.8) - Oryza sativa (Rice)moderately similar to (293) loc_os10g40700 12010.m06838 protein beta-expansin 1a precursor, putative, expressed seq=cds; coord=9:116679986..116681453:1; parent_gene=GRMZM2G073260'

'highly similar to (714) AT2G26250 | Symbols: FDH, KCS10 | KCS10 (3-KETOACYL-COA SYNTHASE 10); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups | chr2:11170799-11173059 REVERSEhighly similar to (929) loc_os03g08360 12003.m35563 protein fiddlehead-like protein, putative, expressed seq=cds; coord=1:16822675..16826498:1; parent_gene=GRMZM2G445602'

'weakly similar to (198) AT2G38440 | Symbols: ITB1, SCAR2, DIS3, WAVE4, ATSCAR2 | SCAR2 (SCAR HOMOLOG 2) | chr2:16095550-16100851 FORWARDweakly similar to (192) SCRL1_ORYSA SCAR-like protein 1 - Oryza sativa (Rice)highly similar to (598) loc_os03g18710 12003.m07292 protein expressed protein seq=cds; coord=1:46576198..46582130:-1; parent_gene=GRMZM2G104534'

'nearly identical (1507) AT3G19960 | Symbols: ATM1 | ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor | chr3:6949787-6956736 FORWARDnearly identical (1802) loc_os10g34710 12010.m06298 protein myosin-2 heavy chain, non muscle, putative, expressed seq=cds; coord=1:229190070..229205919:-1; parent_gene=GRMZM2G113202'

'highly similar to (632) AT4G13420 | Symbols: HAK5, ATHAK5 | HAK5 (HIGH AFFINITY K 'moderately similar to (321) AT2G43590 | Symbols: | chitinase, putative | chr2:18081592-18082749 REVERSEhighly similar to (515) CHIA_MAIZE Endochitinase A precursor (EC 3.2.1.14) (Seed chitinase A) - Zea mays (Maize)moderately similar to (377) loc_os04g41680 12004.m09144 protein endochitinase A precursor, putative, expressed seq=cds; coord=2:33534101..33535449:1; parent_gene=GRMZM2G051943'

'moderately similar to (485) AT5G40010 | Symbols: AATP1 | AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding | chr5:16020218-16021762 REVERSEhighly similar to (649) loc_os12g44190 12012.m08190 protein ATPase 3, putative, expressed seq=cds; coord=2:34473212..34475281:-1; parent_gene=GRMZM2G138770'

'highly similar to (609) AT2G46370 | Symbols: JAR1, FIN219 | JAR1 (JASMONATE RESISTANT 1); ATP binding / adenylyltransferase/ catalytic/ jasmonate-amino synthetase | chr2:19034579-19036369 FORWARDhighly similar to (719) GH312_ORYSA Probable indole-3-acetic acid-amido synthetase GH3.12 (EC 6.3.2.-) (Auxin-responsive GH3-like protein 12) (OsGH3-12) - Oryza sativa (Rice)highly similar to (796) loc_os01g12160 12001.m07831 protein indole-3-acetic acid-amido synthetase GH3.3, putative, expressed seq=cds; coord=3:2949994..2952747:-1; parent_gene=GRMZM2G060991'

'moderately similar to (275) AT1G28600 | Symbols: | lipase, putative | chr1:10051604-10053073 REVERSEweakly similar to (151) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)highly similar to (561) loc_os01g11620 12001.m07778 protein esterase precursor, putative, expressed seq=cds; coord=3:3430959..3432894:-1; parent_gene=GRMZM2G400929'

'highly similar to (822) AT1G15460 | Symbols: ATBOR4, BOR4 | BOR4 (REQUIRES HIGH BORON 4); anion exchanger | chr1:5310196-5313376 REVERSEnearly identical (1013) loc_os01g08020 12001.m07427 protein boron transporter-like protein 2, putative, expressed seq=cds; coord=3:10934126..10940345:-1; parent_gene=GRMZM2G051753'

'seq=cds; coord=3:17605685..17606666:1; parent_gene=GRMZM2G099340'

'moderately similar to (261) AT1G71860 | Symbols: PTP1, ATPTP1 | PTP1 (PROTEIN TYROSINE PHOSPHATASE 1); protein tyrosine phosphatase | chr1:27026866-27028675 FORWARDmoderately similar to (409) loc_os12g07590 12012.m073780 protein receptor-type tyrosine-protein phosphatase S precursor, putative, expressed seq=cds; coord=3:140409749..140417545:1; parent_gene=GRMZM2G010775'

'moderately similar to (327) AT2G37650 | Symbols: | scarecrow-like transcription factor 9 (SCL9) | chr2:15792623-15794779 FORWARDweakly similar to (147) CIGR2_ORYSA Chitin-inducible gibberellin-responsive protein 2 - Oryza sativa (Rice)highly similar to (558) loc_os11g47900 12011.m08587 protein chitin-inducible gibberellin-responsive protein 2, putative, expressed seq=cds; coord=4:829955..831938:-1; parent_gene=GRMZM2G073823'

'weakly similar to (197) loc_os03g62020 12003.m11081 protein harpin-induced protein, putative, expressed seq=cds; coord=5:1576579..1577232:-1; parent_gene=AC202974.3_FG004'

'highly similar to (506) AT5G49580 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:20123823-20126813 REVERSEhighly similar to (883) loc_os03g61730 12003.m11054 protein heat shock protein binding protein, putative, expressed seq=cds; coord=5:1829665..1838651:-1; parent_gene=GRMZM2G138511'

'very weakly similar to (98.2) AT2G37590 | Symbols: ATDOF2.4, DOF2.4 | Dof-type zinc finger domain-containing protein | chr2:15769292-15770497 FORWARDweakly similar to (157) loc_os03g60630 12003.m10953 protein expressed protein seq=cds; coord=5:2343761..2345249:-1; parent_gene=GRMZM2G144188'

'highly similar to (962) AT1G66150 | Symbols: TMK1 | TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase | chr1:24631503-24634415 FORWARDmoderately similar to (209) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1318) loc_os03g50810 12003.m10067 protein receptor protein kinase TMK1 precursor, putative, expressed seq=cds; coord=5:10414656..10418698:1; parent_gene=GRMZM2G158359' 'weakly similar to (160) AT3G58120 | Symbols: ATBZIP61, BZIP61 | BZIP61; DNA binding / transcription activator/ transcription factor | chr3:21521289-21523078 REVERSEvery weakly similar to (85.9) RF2A_ORYSA Transcription factor RF2a - Oryza sativa (Rice)moderately similar to (225) loc_os02g14910 12002.m06735 protein bZIP transcription factor family protein, expressed seq=cds; coord=5:143972500..143974231:-1; parent_gene=GRMZM2G158313'

'moderately similar to (248) AT5G40250 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:16086056-16087186 FORWARDmoderately similar to (472) loc_os02g50930 12002.m10127 protein RING-H2 finger protein ATL5I, putative, expressed seq=cds; coord=5:206555179..206557068:1; parent_gene=GRMZM2G053303'

'moderately similar to (273) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEmoderately similar to (481) loc_os06g20140 12006.m06671 protein aspartic proteinase nepenthesin-1 precursor, putative seq=cds; coord=6:120916323..120918370:-1; parent_gene=GRMZM2G405498'

'moderately similar to (261) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDweakly similar to (147) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (499) loc_os07g13170 12007.m29109 protein floral homeotic protein, putative, expressed seq=cds; coord=7:22004372..22015553:1; parent_gene=GRMZM2G176175'

'moderately similar to (451) AT1G32450 | Symbols: NRT1.5 | NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter | chr1:11715337-11719807 REVERSEmoderately similar to (434) loc_os02g46460 12002.m09683 protein peptide transporter PTR2, putative, expressed seq=cds; coord=7:25089776..25092351:-1; parent_gene=GRMZM2G156794'

'moderately similar to (214) AT3G04030 | Symbols: | myb family transcription factor | chr3:1042920-1044574 REVERSEmoderately similar to (284) loc_os07g48596 12007.m09071 protein MYR1, putative, expressed seq=cds; coord=7:173817875..173820052:-1; parent_gene=AC155434.2_FG005'

'weakly similar to (131) AT5G39660 | Symbols: CDF2 | CDF2 (CYCLING DOF FACTOR 2); DNA binding / protein binding / transcription factor | chr5:15878920-15880712 FORWARDvery weakly similar to (92.8) MNB1A_MAIZE Dof zinc finger protein MNB1A - Zea mays (Maize)moderately similar to (399) loc_os07g48570 12007.m09068 protein expressed protein seq=cds; coord=7:173806883..173808319:-1; parent_gene=AC155434.2_FG006'

'moderately similar to (389) AT4G09160 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr4:5839761-5842158 FORWARDhighly similar to (623) loc_os01g65380 12001.m12651 protein patellin-5, putative, expressed seq=cds; coord=8:165856036..165859140:-1; parent_gene=GRMZM2G033649'

'highly similar to (875) AT2G19900 | Symbols: ATNADP-ME1 | ATNADP-ME1 (NADP-malic enzyme 1); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP

'weakly similar to (183) AT2G20570 | Symbols: GPRI1, GLK1 | GPRI1 (GBF'S PRO-RICH REGION-INTERACTING FACTOR 1); transcription factor/ transcription regulator | chr2:8855486-8857522 FORWARDmoderately similar to (384) loc_os06g24070 12006.m31875 protein transcription factor ZmGLK1, putative, expressed seq=cds; coord=9:2711408..2713807:-1; parent_gene=GRMZM2G026833'

'moderately similar to (292) AT4G38660 | Symbols: | thaumatin, putative | chr4:18066448-18067792 REVERSEmoderately similar to (232) TLP1_PRUPE Thaumatin-like protein 1 precursor (PpAZ44) - Prunus persica (Peach)moderately similar to (380) loc_os03g14030 12003.m06846 protein thaumatin-like protein 1 precursor, putative, expressed seq=cds; coord=9:143050607..143053350:1; parent_gene=GRMZM2G149798' 'moderately similar to (325) AT1G08320 | Symbols: | bZIP family transcription factor | chr1:2622113-2627451 REVERSEmoderately similar to (303) TGA21_TOBAC TGACG-sequence-specific DNA-binding protein TGA-2.1 (TGA2.1) - Nicotiana tabacum (Common tobacco)moderately similar to (409) loc_os12g05680 12012.m04561 protein transcription factor HBP-1b, putative, expressed seq=cds; coord=10:5530500..5533143:-1; parent_gene=GRMZM2G366264'

'moderately similar to (326) AT2G36010 | Symbols: E2F3, ATE2FA | E2F3 (E2F TRANSCRIPTION FACTOR 3); DNA binding / transcription factor | chr2:15119688-15122893 FORWARDhighly similar to (674) loc_os12g06200 12012.m26841 protein transcription factor E2F2, putative, expressed seq=cds; coord=10:6659332..6664025:-1; parent_gene=GRMZM2G052515'

'weakly similar to (145) AT3G19330 | Symbols: | polyadenylate-binding protein-related / PABP-related | chr3:6699423-6700772 FORWARD seq=cds; coord=10:113394167..113395746:-1; parent_gene=GRMZM2G158300'

'highly similar to (641) AT4G21380 | Symbols: ARK3 | ARK3 (A. THALIANA RECEPTOR KINASE 3); kinase/ transmembrane receptor protein serine/threonine kinase | chr4:11389219-11393090 REVERSEmoderately similar to (299) SLSG6_BRAOL S-locus-specific glycoprotein S6 precursor (SLSG-6) - Brassica oleracea (Wild cabbage)nearly identical (1018) loc_os04g54070 12004.m10299 protein receptor-like kinase, putative, expressed seq=cds; coord=10:144143811..144147098:1; parent_gene=GRMZM2G000620'

First Predicted Gene to Left

Description

'moderately similar to (264) AT5G48850 | Symbols: ATSDI1 | ATSDI1 (SULPHUR DEFICIENCY-INDUCED 1); binding | chr5:19805576-19807699 REVERSEmoderately similar to (398) loc_os03g06970 12003.m06214 protein pollenless3, putative, expressed seq=cds; coord=1:13991176..13993273:-1; parent_gene=GRMZM2G123986' 'highly similar to (714) AT2G26250 | Symbols: FDH, KCS10 | KCS10 (3-KETOACYL-COA SYNTHASE 10); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups | chr2:11170799-11173059 REVERSEhighly similar to (929) loc_os03g08360 12003.m35563 protein fiddlehead-like protein, putative, expressed seq=cds; coord=1:16822675..16826498:1; parent_gene=GRMZM2G445602'

'moderately similar to (266) AT2G21050 | Symbols: | amino acid permease, putative | chr2:9034289-9036439 FORWARDmoderately similar to (252) LAX5_MEDTR Auxin transporter-like protein 5 (AUX1-like protein 5) (MtLAX5) - Medicago truncatula (Barrel medic)moderately similar to (277) loc_os03g14080 12003.m06851 protein auxin transporter-like protein 3, putative, expressed seq=cds; coord=1:33317596..33321228:1; parent_gene=GRMZM2G149481'

'very weakly similar to (100) AT3G24200 | Symbols: | FAD binding / monooxygenase/ oxidoreductase/ oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen | chr3:8748095-8751166 REVERSEweakly similar to (158) loc_os03g62260 12003.m11104 protein monooxygenase/ oxidoreductase, putative, expressed seq=cds; coord=1:165614250..165617511:1; parent_gene=GRMZM2G369987'

'very weakly similar to (83.6) loc_os04g20920 12004.m07245 protein transcription regulator, putative, expressed seq=cds; coord=1:177148034..177150936:1; parent_gene=AC199908.4_FG002'

'weakly similar to (163) AT5G64200 | Symbols: ATSC35, SC35 | ATSC35; RNA binding / nucleic acid binding / nucleotide binding | chr5:25681849-25683553 REVERSEweakly similar to (187) loc_os08g37960 12008.m26517 protein splicing factor, arginine/serine-rich 2, putative, expressed seq=cds; coord=1:182538397..182541456:-1; parent_gene=GRMZM2G110143'

'weakly similar to (196) AT1G14685 | Symbols: BPC2, BBR/BPC2, ATBPC2 | BPC2 (BASIC PENTACYSTEINE 2); DNA binding / transcription factor | chr1:5043086-5043925 FORWARDmoderately similar to (236) loc_os10g02584 12010.m065191 protein GAGA-binding protein, putative, expressed seq=cds; coord=1:192490099..192492652:-1; parent_gene=GRMZM2G179366'

'moderately similar to (337) AT2G02070 | Symbols: AtIDD5 | AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding | chr2:505523-509154 FORWARDhighly similar to (571) loc_os08g44050 12008.m26786 protein INDETERMINATE-related protein 1, putative, expressed seq=cds; coord=1:206117307..206124458:1; parent_gene=GRMZM2G179677'

'weakly similar to (157) AT3G11750 | Symbols: | dihydroneopterin aldolase, putative | chr3:3715071-3715904 REVERSEmoderately similar to (206) loc_os09g38759 12009.m50203 protein dihydroneopterin aldolase, putative, expressed seq=cds; coord=1:206197528..206201863:1; parent_gene=GRMZM2G095579'

'moderately similar to (324) AT5G24400 | Symbols: emb2024 | emb2024 (embryo defective 2024); 6-phosphogluconolactonase/ catalytic | chr5:8330532-8331784 REVERSEmoderately similar to (418) loc_os09g35970 12009.m06548 protein 6-phosphogluconolactonase, putative, expressed seq=cds; coord=1:207611046..207613075:-1; parent_gene=GRMZM2G122126' 'moderately similar to (485) AT5G21482 | Symbols: CKX7, ATCKX5 | CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase | chr5:7226842-7230052 FORWARDmoderately similar to (321) CKX1_MAIZE Cytokinin dehydrogenase 1 precursor (EC 1.5.99.12) (Cytokinin oxidase 1) (CKO 1) (COX 1) (ZmCKX1) - Zea mays (Maize)highly similar to (706) loc_os08g35860 12008.m07575 protein cytokinin dehydrogenase 7, putative, expressed seq=cds; coord=1:207708925..207713476:1; parent_gene=GRMZM2G348452'

'very weakly similar to (96.7) loc_os08g35190 12008.m26509 protein auxin-repressed protein, putative, expressed seq=cds; coord=1:208963692..208966672:1; parent_gene=GRMZM2G125557'

'highly similar to (745) AT2G18700 | Symbols: ATTPS11, TPS11, ATTPSB | ATTPS11; transferase, transferring glycosyl groups | chr2:8109043-8111799 FORWARDnearly identical (1055) loc_os08g34580 12008.m26506 protein trehalose-6-phosphate synthase, putative, expressed seq=cds; coord=1:210663759..210667488:-1; parent_gene=GRMZM2G079928'

'moderately similar to (315) AT2G22480 | Symbols: PFK5 | PFK5 (PHOSPHOFRUCTOKINASE 5); 6-phosphofructokinase | chr2:9545670-9548414 FORWARDmoderately similar to (454) loc_os08g34050 12008.m07394 protein 6-phosphofructokinase 2, putative seq=cds; coord=1:212484786..212489531:1; parent_gene=GRMZM2G139360'

'highly similar to (809) AT5G62890 | Symbols: | permease, putative | chr5:25243723-25246748 FORWARDhighly similar to (972) loc_os08g32500 12008.m07244 protein permease, putative, expressed seq=cds; coord=1:219063550..219067715:1; parent_gene=GRMZM2G115635'

'very weakly similar to (84.7) AT2G18040 | Symbols: PIN1AT | PIN1AT (PEPTIDYLPROLYL CIS/TRANS ISOMERASE, NIMA-INTERACTING 1); peptidyl-prolyl cis-trans isomerase | chr2:7842346-7843537 FORWARDvery weakly similar to (85.9) PIN1_MALDO Peptidyl-prolyl cis-trans isomerase 1 (EC 5.2.1.8) (Rotamase Pin1) (PPIase Pin1) (MdPin1) - Malus domestica (Apple) (Malus sylvestris)weakly similar to (136) loc_os04g56800 12004.m10567 protein peptidyl-prolyl cis-trans isomerase 1, putative, expressed seq=cds; coord=2:3366755..3369670:1; parent_gene=GRMZM2G047590'

'moderately similar to (245) AT1G34300 | Symbols: | lectin protein kinase family protein | chr1:12503450-12505939 FORWARDweakly similar to (177) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (556) loc_os04g56120 12004.m10503 protein receptor-like kinase, putative, expressed seq=cds; coord=2:4369756..4371294:-1; parent_gene=GRMZM2G363066'

'moderately similar to (494) AT5G67200 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr5:26813893-26816555 REVERSEweakly similar to (149) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1002) loc_os04g55620 12004.m10453 protein receptor kinase, putative, expressed seq=cds; coord=2:5374131..5380129:1; parent_gene=GRMZM2G055844'

'moderately similar to (340) AT5G10030 | Symbols: TGA4, OBF4 | TGA4 (TGACG MOTIF-BINDING FACTOR 4); DNA binding / calmodulin binding / transcription factor | chr5:3137648-3139295 REVERSEmoderately similar to (321) TGA1A_TOBAC TGACG-sequence-specific DNA-binding protein TGA-1A (TGA1a) (ASF-1 protein) - Nicotiana tabacum (Common tobacco)highly similar to (515) loc_os04g54474 12004.m101669 protein transcription factor TGA4, putative, expressed seq=cds; coord=2:6717922..6723608:1; parent_gene=GRMZM2G131961' 'moderately similar to (385) AT1G79460 | Symbols: GA2, KS, ATKS | GA2 (GA REQUIRING 2); ent-kaurene synthase | chr1:29890568-29894436 FORWARDmoderately similar to (363) KSB_CUCMA Ent-kaurene synthase B, chloroplast precursor (EC 4.2.3.19) (KSB) - Cucurbita maxima (Pumpkin) (Winter squash)highly similar to (588) loc_os04g52210 12004.m10116 protein ent-kaurene synthase B, chloroplast precursor, putative, expressed seq=cds; coord=2:10596796..10605493:1; parent_gene=GRMZM2G049538'

'highly similar to (613) AT2G24360 | Symbols: | serine/threonine/tyrosine kinase, putative | chr2:10364742-10366075 REVERSEweakly similar to (116) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (771) loc_os04g51950 12004.m10090 protein serine/threonine protein kinase, putative, expressed seq=cds; coord=2:11197500..11201569:1; parent_gene=GRMZM2G102088'

'weakly similar to (105) loc_os03g32526 12003.m08494 protein expressed protein seq=cds; coord=2:13459177..13467511:-1; parent_gene=AC195235.3_FG003'

'weakly similar to (117) AT5G47230 | Symbols: ERF5, ATERF-5, ATERF5 | ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcription activator/ transcription factor | chr5:19180072-19180974 FORWARDweakly similar to (110) ERF5_TOBAC Ethylene-responsive transcription factor 5 (Ethylene-responsive element-binding factor 5 homolog) (EREBP-4) (NtERF4) - Nicotiana tabacum (Common tobacco)weakly similar to (176) loc_os04g46250 12004.m09575 protein AP2 domain containing protein, expressed seq=cds; coord=2:20563651..20564721:-1; parent_gene=GRMZM2G475678'

'nearly identical (1071) AT1G76950 | Symbols: PRAF1 | PRAF1; Ran GTPase binding / chromatin binding / zinc ion binding | chr1:28906952-28911325 FORWARDnearly identical (1565) loc_os04g58960 12004.m10775 protein ran GTPase binding protein, putative, expressed seq=cds; coord=2:24030713..24037024:-1; parent_gene=GRMZM2G124371'

'weakly similar to (129) AT5G14360 | Symbols: | ubiquitin family protein | chr5:4631038-4631641 FORWARDweakly similar to (167) loc_os02g38410 12002.m08929 protein BCL-2 binding anthanogene-1, putative, expressed seq=cds; coord=2:36824114..36825732:-1; parent_gene=GRMZM2G045117'

'weakly similar to (139) loc_os12g32986 12012.m27011 protein heat shock protein 83, putative, expressed seq=cds; coord=2:189610974..189617149:1; parent_gene=GRMZM2G474367'

'moderately similar to (434) AT3G20810 | Symbols: | transcription factor jumonji (jmjC) domain-containing protein | chr3:7275814-7278182 FORWARDhighly similar to (523) loc_os09g31380 12009.m06252 protein conserved hypothetical protein seq=cds; coord=2:189777176..189782078:1; parent_gene=GRMZM2G052908'

'moderately similar to (317) AT2G44610 | Symbols: RAB6, ATRABH1B, ATRAB6A, RAB6A | RAB6A; GTP binding / protein binding | chr2:18411778-18413883 REVERSEweakly similar to (135) RGP2_ORYSA Ras-related protein RGP2 (GTP-binding regulatory protein RGP2) - Oryza sativa (Rice)moderately similar to (318) loc_os07g31370 12007.m07406 protein ras-related protein Rab-6A, putative, expressed seq=cds; coord=2:212301578..212321626:1; parent_gene=GRMZM2G128771'

'highly similar to (572) AT5G50300 | Symbols: | xanthine/uracil/vitamin C permease family protein | chr5:20466492-20468084 REVERSEhighly similar to (792) loc_os11g24060 12011.m06332 protein transmembrane transport protein-like, putative, expressed seq=cds; coord=2:218937924..218939954:1; parent_gene=GRMZM2G068220' 'moderately similar to (415) AT3G23750 | Symbols: | leucine-rich repeat family protein / protein kinase family protein | chr3:8558332-8561263 FORWARDmoderately similar to (201) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1155) loc_os11g26130 12011.m06534 protein receptor protein kinase TMK1 precursor, putative, expressed seq=cds; coord=2:220750945..220758496:1; parent_gene=GRMZM2G349875'

'very weakly similar to (94.7) AT1G52950 | Symbols: | replication protein-related | chr1:19725483-19728007 FORWARDmoderately similar to (207) loc_os07g02230 12007.m04695 protein retrotransposon protein, putative, unclassified, expressed seq=cds; coord=3:88916116..88921100:1; parent_gene=GRMZM2G351307'

'moderately similar to (244) AT5G21170 | Symbols: | 5'-AMP-activated protein kinase beta-2 subunit, putative | chr5:7205718-7208239 FORWARDmoderately similar to (343) loc_os03g20340 12003.m07444 protein SNF1-related protein kinase regulatory subunit beta-1, putative, expressed seq=cds; coord=3:139808606..139811549:-1; parent_gene=GRMZM2G027632'

'weakly similar to (147) AT1G24620 | Symbols: | polcalcin, putative / calcium-binding pollen allergen, putative | chr1:8723893-8724453 REVERSEweakly similar to (111) CALM_CHLRE Calmodulin (CaM) - Chlamydomonas reinhardtiimoderately similar to (254) loc_os01g72100 12001.m13246 protein polcalcin Jun o 2, putative, expressed seq=cds; coord=3:149552437..149553876:1; parent_gene=GRMZM2G106945'

'highly similar to (853) AT1G72180 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr1:27164074-27167204 FORWARDmoderately similar to (416) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1417) loc_os01g65650 12001.m12674 protein receptor-like protein kinase 5 precursor, putative, expressed seq=cds; coord=3:172374935..172378448:-1; parent_gene=GRMZM2G167253'

'highly similar to (678) AT1G43620 | Symbols: | UDP-glucose:sterol glucosyltransferase, putative | chr1:16425654-16429500 REVERSEnearly identical (1015) loc_os01g64750 12001.m12589 protein sterol 3-beta-glucosyltransferase, putative, expressed seq=cds; coord=3:175571565..175589373:-1; parent_gene=GRMZM2G149617'

'moderately similar to (439) AT5G01210 | Symbols: | transferase family protein | chr5:84554-85981 FORWARDvery weakly similar to (82.0) HCBT1_DIACA Anthranilate N-benzoyltransferase protein 1 (EC 2.3.1.144) (Anthranilate N-hydroxycinnamoyl/benzoyltransferase 1) - Dianthus caryophyllus (Carnation) (Clove pink)highly similar to (776) loc_os01g63480 12001.m12464 protein AER, putative, expressed seq=cds; coord=3:178409357..178411316:-1; parent_gene=GRMZM2G165192'

'highly similar to (650) AT5G53450 | Symbols: ORG1 | ORG1 (OBP3-responsive gene 1); ATP binding / kinase/ protein kinase | chr5:21689444-21692242 FORWARDhighly similar to (938) loc_os01g46720 12001.m10869 protein protein kinase domain containing protein, expressed seq=cds; coord=3:213005290..213017220:-1; parent_gene=GRMZM2G150952' 'highly similar to (868) AT3G58610 | Symbols: | ketol-acid reductoisomerase | chr3:21671561-21674639 FORWARDhighly similar to (858) ILV5_PEA Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) - Pisum sativum (Garden pea)highly similar to (920) loc_os01g46380 12001.m10836 protein ketol-acid reductoisomerase, chloroplast precursor, putative, expressed seq=cds; coord=3:213623450..213627174:-1; parent_gene=GRMZM2G004382'

'highly similar to (868) AT3G58610 | Symbols: | ketol-acid reductoisomerase | chr3:21671561-21674639 FORWARDhighly similar to (858) ILV5_PEA Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) - Pisum sativum (Garden pea)highly similar to (920) loc_os01g46380 12001.m10836 protein ketol-acid reductoisomerase, chloroplast precursor, putative, expressed seq=cds; coord=3:213623450..213627174:-1; parent_gene=GRMZM2G004382'

'highly similar to (627) AT2G26650 | Symbols: AKT1, ATAKT1 | AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel | chr2:11331965-11336444 REVERSEhighly similar to (824) AKT1_ORYSA Potassium channel AKT1 (OsAKT1) - Oryza sativa (Rice)highly similar to (824) loc_os01g45990 12001.m10798 protein potassium channel AKT1, putative, expressed seq=cds; coord=3:214273957..214280038:1; parent_gene=GRMZM2G022915'

'very weakly similar to (98.6) AT3G23550 | Symbols: | MATE efflux family protein | chr3:8448435-8450649 REVERSEweakly similar to (124) loc_os07g01750 12007.m04654 protein transparent testa 12 protein, putative, expressed seq=cds; coord=3:216484840..216488798:-1; parent_gene=GRMZM2G000593'

'moderately similar to (323) AT1G15950 | Symbols: CCR1, IRX4, ATCCR1 | CCR1 (CINNAMOYL COA REDUCTASE 1); cinnamoyl-CoA reductase | chr1:5478855-5481949 FORWARDweakly similar to (171) DFRA_MAIZE Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Zea mays (Maize)highly similar to (513) loc_os02g56460 12002.m10668 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=4:171783871..171785676:-1; parent_gene=GRMZM2G099420'

'highly similar to (694) AT5G60710 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24410953-24414849 REVERSEnearly identical (1189) loc_os02g56280 12002.m10651 protein protein binding protein, putative, expressed seq=cds; coord=4:172685051..172689834:1; parent_gene=GRMZM2G130002'

'highly similar to (694) AT5G60710 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24410953-24414849 REVERSEnearly identical (1189) loc_os02g56280 12002.m10651 protein protein binding protein, putative, expressed seq=cds; coord=4:172685051..172689834:1; parent_gene=GRMZM2G130002'

'weakly similar to (104) AT4G31985 | Symbols: | 60S ribosomal protein L39 (RPL39C) | chr4:15469931-15470366 FORWARDweakly similar to (112) RL39_ORYSA 60S ribosomal protein L39 - Oryza sativa (Rice)weakly similar to (112) loc_os02g55390 12002.m100783 protein 60S ribosomal protein L39, putative, expressed seq=cds; coord=4:173792258..173793051:-1; parent_gene=GRMZM2G411764'

'moderately similar to (339) AT5G48330 | Symbols: | regulator of chromosome condensation (RCC1) family protein | chr5:19585989-19587729 FORWARDhighly similar to (577) loc_os02g10380 12002.m06336 protein regulator of chromosome condensation like, putative, expressed seq=cds; coord=4:233209443..233212350:1; parent_gene=GRMZM2G030542' 'moderately similar to (393) AT5G42320 | Symbols: | metallocarboxypeptidase/ zinc ion binding | chr5:16918651-16920845 REVERSEhighly similar to (655) loc_os02g02710 12002.m33511 protein carboxypeptidase A, putative, expressed seq=cds; coord=4:239686593..239692358:-1; parent_gene=GRMZM2G006069'

'moderately similar to (260) AT3G01980 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr3:327747-328833 REVERSEmoderately similar to (390) loc_os03g63290 12003.m11197 protein alcohol dehydrogenases, putative, expressed seq=cds; coord=5:1044358..1047150:1; parent_gene=GRMZM2G013042'

'moderately similar to (350) AT3G05420 | Symbols: ACBP4 | ACBP4 (ACYL-COA BINDING PROTEIN 4); acyl-CoA binding | chr3:1561880-1567047 FORWARDmoderately similar to (434) loc_os03g61930 12003.m35507 protein acyl-CoA binding protein, putative, expressed seq=cds; coord=5:1608613..1611742:1; parent_gene=GRMZM2G326195'

'weakly similar to (106) AT5G58490 | Symbols: | cinnamoyl-CoA reductase family | chr5:23643068-23644455 FORWARDweakly similar to (135) loc_os03g60380 12003.m10928 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=5:2593504..2594875:1; parent_gene=GRMZM2G110952'

'moderately similar to (324) AT5G58490 | Symbols: | cinnamoyl-CoA reductase family | chr5:23643068-23644455 FORWARDweakly similar to (157) DFRA_DIACA Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Dianthus caryophyllus (Carnation) (Clove pink)moderately similar to (412) loc_os03g60380 12003.m10928 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=5:2594137..2603606:-1; parent_gene=GRMZM2G110881'

'very weakly similar to (90.1) TIP31_ORYSA Probable aquaporin TIP3.1 (Tonoplast intrinsic protein 3.1) (OsTIP3.1) - Oryza sativa (Rice)very weakly similar to (90.1) loc_os10g35050 12010.m06328 protein aquaporin TIP3.1, putative, expressed seq=cds; coord=5:25511080..25511685:1; parent_gene=GRMZM2G305446'

'weakly similar to (108) AT1G77670 | Symbols: | aminotransferase class I and II family protein | chr1:29189043-29190901 REVERSEmoderately similar to (301) loc_os10g34350 12010.m06261 protein kynurenine--oxoglutarate transaminase 1, putative, expressed seq=cds; coord=5:27099256..27102677:1; parent_gene=GRMZM2G174145'

'weakly similar to (108) AT1G77670 | Symbols: | aminotransferase class I and II family protein | chr1:29189043-29190901 REVERSEmoderately similar to (301) loc_os10g34350 12010.m06261 protein kynurenine--oxoglutarate transaminase 1, putative, expressed seq=cds; coord=5:27099256..27102677:1; parent_gene=GRMZM2G174145'

'moderately similar to (337) AT2G37210 | Symbols: | Encodes a protein of unknown function. It has been crystallized and shown to be structurally almost identical to the protein encoded by At5g11950. | chr2:15624253-15626834 REVERSEmoderately similar to (387) loc_os10g33900 12010.m06219 protein carboxy-lyase, putative, expressed seq=cds; coord=5:28109811..28112194:-1; parent_gene=GRMZM2G100360'

'moderately similar to (213) AT4G35220 | Symbols: | cyclase family protein | chr4:16752636-16753966 FORWARDmoderately similar to (271) loc_os09g02270 12009.m03600 protein cyclase, putative, expressed seq=cds; coord=5:28436619..28440123:1; parent_gene=GRMZM2G138744' 'moderately similar to (277) AT3G04400 | Symbols: emb2171 | emb2171 (embryo defective 2171); structural constituent of ribosome | chr3:1167339-1168308 FORWARDmoderately similar to (274) RL23_TOBAC 60S ribosomal protein L23 - Nicotiana tabacum (Common tobacco)moderately similar to (279) loc_os10g32920 12010.m06128 protein 60S ribosomal protein L23, putative, expressed seq=cds; coord=5:30596598..30600002:1; parent_gene=GRMZM2G123495'

'highly similar to (603) AT3G23990 | Symbols: HSP60, HSP60-3B | HSP60 (HEAT SHOCK PROTEIN 60); ATP binding | chr3:8669013-8672278 FORWARDhighly similar to (684) CH61_MAIZE Chaperonin CPN60-1, mitochondrial precursor (HSP60-1) - Zea mays (Maize)highly similar to (652) loc_os10g32550 12010.m06092 protein chaperonin CPN60-1, mitochondrial precursor, putative, expressed seq=cds; coord=5:31002750..31006569:-1; parent_gene=GRMZM2G458208'

'moderately similar to (219) AT1G63800 | Symbols: UBC5 | UBC5 (ubiquitin-conjugating enzyme 5); ubiquitin-protein ligase | chr1:23667888-23669003 REVERSEmoderately similar to (218) UBC4_WHEAT Ubiquitin-conjugating enzyme E2-23 kDa (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) - Triticum aestivum (Wheat)moderately similar to (244) loc_os10g31000 12010.m21788 protein ubiquitin-conjugating enzyme E2-21 kDa 1, putative, expressed seq=cds; coord=5:31648146..31651787:-1; parent_gene=GRMZM2G146374'

'weakly similar to (106) loc_os10g30719 12010.m05931 protein myb-like DNA-binding domain containing protein, expressed seq=cds; coord=5:31901583..31906914:-1; parent_gene=GRMZM2G046438'

'weakly similar to (196) AT4G35040 | Symbols: | bZIP transcription factor family protein | chr4:16680821-16681805 FORWARDmoderately similar to (378) loc_os06g50310 12006.m09555 protein DNA binding protein, putative, expressed seq=cds; coord=5:61696485..61700292:1; parent_gene=GRMZM2G000171'

'highly similar to (731) AT3G19240 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046) Vacuolar import and degradation, Vid27-related (InterPro:IPR013863); BEST Arabidopsis thaliana protein match is: dem protein-related / defective embryo and meristems protein-related (TAIR:AT4G33400.1); Has 206 Blast hits to 202 proteins in 88 species: Archae - 0; Bacteria - 0; Metazoa - 11; Fungi - 117; Plants - 38; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink). | chr3:6664383-6666423 FORWARDnearly identical (1075) loc_os02g08190 12002.m06165 protein protein CYPRO4, putative, expressed seq=cds; coord=5:89859666..89864514:-1; parent_gene=GRMZM2G131638'

'moderately similar to (232) AT3G23250 | Symbols: MYB15, ATY19, ATMYB15 | MYB15 (MYB DOMAIN PROTEIN 15); DNA binding / transcription factor | chr3:8309742-8310624 FORWARDmoderately similar to (285) MYB4_ORYSA Myb-related protein Myb4 (OsMyb4) (Transcription factor RLTR1) - Oryza sativa (Rice)moderately similar to (322) loc_os02g41510 12002.m09187 protein myb-related protein Myb4, putative, expressed seq=cds; coord=5:186413823..186415077:-1; parent_gene=GRMZM2G095904' 'weakly similar to (128) AT2G44940 | Symbols: | AP2 domain-containing transcription factor TINY, putative | chr2:18537294-18538181 FORWARDvery weakly similar to (83.6) ERF1_ORYSA Ethylene-responsive transcription factor 1 (Ethylene-responsive element-binding factor 1) (EREBP-1) (OsEREBP1) - Oryza sativa (Rice)weakly similar to (169) loc_os04g46410 12004.m09590 protein dehydration-responsive element-binding protein 1B, putative, expressed seq=cds; coord=5:191851620..191853237:1; parent_gene=GRMZM2G041839'

'weakly similar to (144) AT5G62940 | Symbols: | Dof-type zinc finger domain-containing protein | chr5:25257183-25258504 REVERSEweakly similar to (119) PBF_MAIZE Dof zinc finger protein PBF (Prolamin box-binding factor) - Zea mays (Maize)moderately similar to (360) loc_os02g47810 12002.m09815 protein dof domain, zinc finger family protein, expressed seq=cds; coord=5:201381499..201385596:-1; parent_gene=GRMZM2G140694'

'moderately similar to (241) AT3G07880 | Symbols: | Rho GDP-dissociation inhibitor family protein | chr3:2514175-2515544 FORWARDmoderately similar to (268) loc_os02g48730 12002.m09907 protein rho GDP-dissociation inhibitor 1, putative, expressed seq=cds; coord=5:203617123..203618504:1; parent_gene=GRMZM2G085049'

'moderately similar to (320) AT3G48160 | Symbols: DEL1, E2L3, E2FE | DEL1 (DP-E2F-LIKE 1); DNA binding / transcription factor | chr3:17783641-17785846 FORWARDhighly similar to (548) loc_os02g50630 12002.m10097 protein transcription regulator of the cell cycle TaE2Fe, putative, expressed seq=cds; coord=5:205783382..205786772:-1; parent_gene=GRMZM2G378665'

'very weakly similar to (100) AT1G26945 | Symbols: KDR | KDR (KIDARI); transcription regulator | chr1:9351571-9352474 FORWARDweakly similar to (155) loc_os02g51320 12002.m10166 protein DNA binding protein, putative, expressed seq=cds; coord=5:207504983..207506597:-1; parent_gene=GRMZM2G036092'

'moderately similar to (385) AT5G65020 | Symbols: ANNAT2 | ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding | chr5:25974366-25975554 FORWARDmoderately similar to (343) ANX4_FRAAN Annexin-like protein RJ4 - Fragaria ananassa (Strawberry)highly similar to (566) loc_os02g51750 12002.m10206 protein annexin-like protein RJ4, putative, expressed seq=cds; coord=5:208194750..208197747:1; parent_gene=GRMZM2G061950'

'moderately similar to (385) AT5G65020 | Symbols: ANNAT2 | ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding | chr5:25974366-25975554 FORWARDmoderately similar to (343) ANX4_FRAAN Annexin-like protein RJ4 - Fragaria ananassa (Strawberry)highly similar to (566) loc_os02g51750 12002.m10206 protein annexin-like protein RJ4, putative, expressed seq=cds; coord=5:208194750..208197747:1; parent_gene=GRMZM2G061950'

'moderately similar to (299) ATCG00170 | Symbols: RPOC2 | RNA polymerase beta' subunit-2 | chrC:15938-20068 REVERSEnearly identical (1103) RPOC2_MAIZE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6) (PEP) (Plastid-encoded RNA polymerase beta" subunit) (RNA polymerase beta" subunit) - Zea mays (Maize)highly similar to (578) loc_osp1g00260 11562.m00015 protein RNA polymerase beta" chain seq=cds; coord=5:210010750..210014897:1; parent_gene=GRMZM2G055859' 'highly similar to (786) AT5G49030 | Symbols: OVA2 | OVA2 (ovule abortion 2); ATP binding / aminoacyl-tRNA ligase/ isoleucine-tRNA ligase/ nucleotide binding | chr5:19876365-19882291 REVERSEhighly similar to (969) loc_os02g53770 12002.m33899 protein isoleucyl-tRNA synthetase, putative, expressed seq=cds; coord=5:211898501..211913266:1; parent_gene=GRMZM2G478664'

'highly similar to (786) AT5G49030 | Symbols: OVA2 | OVA2 (ovule abortion 2); ATP binding / aminoacyl-tRNA ligase/ isoleucine-tRNA ligase/ nucleotide binding | chr5:19876365-19882291 REVERSEhighly similar to (969) loc_os02g53770 12002.m33899 protein isoleucyl-tRNA synthetase, putative, expressed seq=cds; coord=5:211898501..211913266:1; parent_gene=GRMZM2G478664'

'moderately similar to (282) AT2G02450 | Symbols: ANAC035 | ANAC035 (Arabidopsis NAC domain containing protein 35); transcription factor | chr2:648044-650649 FORWARDweakly similar to (172) NAC48_ORYSA NAC domain-containing protein 48 (ONAC048) - Oryza sativa (Rice)moderately similar to (355) loc_os08g02160 12008.m04362 protein NAC domain-containing protein 68, putative, expressed seq=cds; coord=6:3869561..3872846:1; parent_gene=GRMZM2G030325'

'moderately similar to (228) AT5G59890 | Symbols: ADF4, ATADF4 | ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding | chr5:24123107-24123596 FORWARDmoderately similar to (231) ADF1_PETHY Actin-depolymerizing factor 1 (ADF 1) - Petunia hybrida (Petunia)moderately similar to (254) loc_os05g02250 12005.m64199 protein expressed protein seq=cds; coord=6:35896131..35897803:-1; parent_gene=GRMZM2G037140'

'moderately similar to (211) AT3G46620 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr3:17178837-17180024 REVERSEmoderately similar to (351) loc_os05g01940 12005.m04730 protein zinc finger, RING-type, putative, expressed seq=cds; coord=6:38792335..38794002:-1; parent_gene=GRMZM2G567897'

'weakly similar to (107) loc_os06g07130 12006.m05437 protein SHR5-receptor-like kinase, putative, expressed seq=cds; coord=6:80901468..80907416:1; parent_gene=GRMZM2G103033'

'moderately similar to (494) AT1G62400 | Symbols: HT1 | HT1 (high leaf temperature 1); kinase/ protein serine/threonine/tyrosine kinase | chr1:23090243-23091529 FORWARDvery weakly similar to (100) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (621) loc_os06g43030 12006.m08833 protein HT1 protein kinase, putative, expressed seq=cds; coord=6:97343332..97346122:-1; parent_gene=GRMZM2G018280'

'moderately similar to (233) AT5G47650 | Symbols: ATNUDT2, ATNUDX2 | ATNUDT2 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 2); ADP-ribose diphosphatase/ NAD or NADH binding / hydrolase | chr5:19310391-19312084 REVERSEmoderately similar to (357) loc_os06g42790 12006.m32122 protein nudix hydrolase 2, putative, expressed seq=cds; coord=6:97631102..97634957:1; parent_gene=GRMZM2G162605'

'nearly identical (1068) AT1G70300 | Symbols: KUP6 | KUP6; potassium ion transmembrane transporter | chr1:26477993-26481233 REVERSEnearly identical (1291) HAK10_ORYSA Potassium transporter 10 (OsHAK10) - Oryza sativa (Rice)nearly identical (1291) loc_os06g42030 12006.m08735 protein potassium transporter 10, putative, expressed seq=cds; coord=6:97941833..97946553:1; parent_gene=GRMZM2G146760'

'nearly identical (1068) AT1G70300 | Symbols: KUP6 | KUP6; potassium ion transmembrane transporter | chr1:26477993-26481233 REVERSEnearly identical (1291) HAK10_ORYSA Potassium transporter 10 (OsHAK10) - Oryza sativa (Rice)nearly identical (1291) loc_os06g42030 12006.m08735 protein potassium transporter 10, putative, expressed seq=cds; coord=6:97941833..97946553:1; parent_gene=GRMZM2G146760'

'moderately similar to (397) AT2G17410 | Symbols: | ARID/BRIGHT DNA-binding domain-containing protein | chr2:7559869-7563474 FORWARDhighly similar to (566) loc_os06g41730 12006.m31901 protein ARID/BRIGHT DNA binding domain containing protein, expressed seq=cds; coord=6:98085264..98091283:-1; parent_gene=GRMZM2G180654'

'highly similar to (675) AT5G55230 | Symbols: ATMAP65-1, MAP65-1 | ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); microtubule binding | chr5:22402716-22405182 FORWARDhighly similar to (834) loc_os06g40840 12006.m08619 protein microtubule-associated protein MAP65-1a, putative, expressed seq=cds; coord=6:99761240..99767447:-1; parent_gene=GRMZM2G112337'

'weakly similar to (110) AT1G55360 | Symbols: | unknown protein | chr1:20666526-20668502 REVERSEmoderately similar to (261) loc_os06g45920 12006.m09120 protein ZmEBE-1 protein, putative seq=cds; coord=6:108857961..108860755:1; parent_gene=GRMZM2G167733'

'highly similar to (711) AT2G33770 | Symbols: UBC24, ATUBC24, PHO2 | PHO2 (PHOSPHATE 2); ubiquitin-protein ligase | chr2:14277785-14281482 REVERSEnearly identical (1309) loc_os05g48390 12005.m08910 protein ubiquitin conjugating enzyme, putative, expressed seq=cds; coord=6:163843112..163847600:-1; parent_gene=GRMZM2G381709'

'moderately similar to (486) AT5G19580 | Symbols: | glyoxal oxidase-related | chr5:6607595-6609517 REVERSEhighly similar to (895) loc_os05g48520 12005.m08923 protein glyoxal oxidase, putative, expressed seq=cds; coord=6:164181429..164183918:1; parent_gene=GRMZM2G458607'

'highly similar to (580) AT1G75220 | Symbols: | integral membrane protein, putative | chr1:28229412-28232606 REVERSEweakly similar to (164) STC_RICCO Sugar carrier protein C - Ricinus communis (Castor bean)highly similar to (710) loc_os05g49270 12005.m08997 protein solute carrier family 2, facilitated glucose transporter member 8, putative, expressed seq=cds; coord=6:165151948..165157662:1; parent_gene=GRMZM2G160430'

'weakly similar to (150) AT5G28050 | Symbols: | cytidine/deoxycytidylate deaminase family protein | chr5:10044209-10045484 REVERSEweakly similar to (161) loc_os07g14150 12007.m079579 protein cytidine/deoxycytidylate deaminase family protein, putative, expressed seq=cds; coord=7:24368445..24370041:1; parent_gene=GRMZM2G173063'

'moderately similar to (406) AT3G02875 | Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugat hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase | chr3:631993-633859 FORWARDhighly similar to (558) loc_os07g14590 12007.m05904 protein IAA-amino acid hydrolase ILR1 precursor, putative, expressed seq=cds; coord=7:25812344..25817942:1; parent_gene=GRMZM2G003789'

'moderately similar to (464) AT3G02875 | Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugat hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase | chr3:631993-633859 FORWARDhighly similar to (640) loc_os07g14590 12007.m05904 protein IAA-amino acid hydrolase ILR1 precursor, putative, expressed seq=cds; coord=7:25903581..25911265:1; parent_gene=GRMZM2G016958' 'highly similar to (630) AT2G38940 | Symbols: ATPT2, PHT1;4 | ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter | chr2:16258500-16260104 FORWARDhighly similar to (649) loc_os04g10750 12004.m101431 protein inorganic phosphate transporter 1-5, putative, expressed seq=cds; coord=7:34925082..34926916:-1; parent_gene=GRMZM2G139639'

'nearly identical (1162) AT3G13380 | Symbols: BRL3 | BRL3 (BRI1-LIKE 3); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase | chr3:4347240-4350734 FORWARDmoderately similar to (456) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1795) loc_os09g12240 12009.m04486 protein serine/threonine-protein kinase BRI1-like 1 precursor, putative, expressed seq=cds; coord=7:79095632..79100094:-1; parent_gene=GRMZM2G092604'

'weakly similar to (161) AT1G56340 | Symbols: CRT1 | CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding | chr1:21090022-21092630 REVERSEweakly similar to (193) CALR_MAIZE Calreticulin precursor - Zea mays (Maize)weakly similar to (189) loc_os07g14270 12007.m29118 protein calreticulin precursor, putative, expressed seq=cds; coord=7:93853570..93863210:1; parent_gene=GRMZM2G140949'

'weakly similar to (160) AT3G26230 | Symbols: CYP71B24 | CYP71B24; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr3:9598200-9599892 REVERSEweakly similar to (191) C71D8_SOYBN Cytochrome P450 71D8 (EC 1.14.-.-) (P450 CP7) - Glycine max (Soybean)moderately similar to (232) loc_os09g36080 12009.m06558 protein cytochrome P450 71A2, putative, expressed seq=cds; coord=7:94644611..94646428:1; parent_gene=GRMZM2G027041'

'weakly similar to (121) AT5G51720 | Symbols: | unknown protein | chr5:21009645-21010227 FORWARDweakly similar to (132) loc_os07g28400 12007.m07112 protein kinesin like protein, putative, expressed seq=cds; coord=7:144904996..144907474:-1; parent_gene=GRMZM2G046186'

'moderately similar to (290) AT3G14470 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4857940-4861104 FORWARDnearly identical (1321) loc_os07g29820 12007.m07253 protein NBS-LRR disease resistance protein, putative, expressed seq=cds; coord=7:148734857..148747797:-1; parent_gene=GRMZM2G028713'

'highly similar to (711) AT4G27290 | Symbols: | ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding | chr4:13666281-13669202 FORWARDmoderately similar to (351) SLSG3_BRAOL S-locus-specific glycoprotein S13 precursor (SLSG-13) (Fragment) - Brassica oleracea (Wild cabbage)nearly identical (1172) loc_os07g36544 12007.m07905 protein serine/threonine-protein kinase receptor precursor, putative, expressed seq=cds; coord=7:156111748..156116073:-1; parent_gene=GRMZM2G465999'

'moderately similar to (241) AT3G15510 | Symbols: ATNAC2, ANAC056, NARS1 | ATNAC2 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 2); transcription factor | chr3:5243696-5245037 FORWARDmoderately similar to (229) NAC48_ORYSA NAC domain-containing protein 48 (ONAC048) - Oryza sativa (Rice)moderately similar to (406) loc_os07g48450 12007.m29337 protein NAC domain-containing protein 18, putative, expressed seq=cds; coord=7:173514759..173517298:-1; parent_gene=GRMZM2G430849'

'moderately similar to (295) PRR37_ORYSA Two-component response regulator-like PRR37 (Pseudo-response regulator 37) (OsPRR37) - Oryza sativa (Rice)moderately similar to (295) loc_os07g49460 12007.m079806 protein two-component response regulator-like PRR37, putative, expressed seq=cds; coord=7:174982376..174985250:1; parent_gene=GRMZM2G005732' 'moderately similar to (379) AT3G14470 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4857940-4861104 FORWARDnearly identical (1194) loc_os05g34220 12005.m27824 protein disease resistance protein, putative, expressed seq=cds; coord=8:104460886..104464505:-1; parent_gene=GRMZM2G047152'

'moderately similar to (310) AT2G40280 | Symbols: | dehydration-responsive family protein | chr2:16825707-16828300 REVERSEmoderately similar to (459) loc_os05g39520 12005.m08130 protein ankyrin-like protein, putative, expressed seq=cds; coord=8:118529129..118653539:-1; parent_gene=AC204277.3_FG006'

'moderately similar to (266) AT1G07840 | Symbols: | leucine zipper factor-related | chr1:2424603-2426131 FORWARDmoderately similar to (378) loc_os01g68310 12001.m12933 protein expressed protein seq=cds; coord=8:162963891..162967617:1; parent_gene=GRMZM2G001088'

'very weakly similar to (87.0) HD2C_MAIZE Histone deacetylase 2c (HD2c) (Zm-HD2c) - Zea mays (Maize)very weakly similar to (87.4) loc_os05g51830 12005.m09245 protein histone deacetylase 2b, putative, expressed seq=cds; coord=8:163180384..163182820:1; parent_gene=AC183950.2_FG003'

'very weakly similar to (87.0) HD2C_MAIZE Histone deacetylase 2c (HD2c) (Zm-HD2c) - Zea mays (Maize)very weakly similar to (87.4) loc_os05g51830 12005.m09245 protein histone deacetylase 2b, putative, expressed seq=cds; coord=8:163180384..163182820:1; parent_gene=AC183950.2_FG003'

'very weakly similar to (87.0) HD2C_MAIZE Histone deacetylase 2c (HD2c) (Zm-HD2c) - Zea mays (Maize)very weakly similar to (87.4) loc_os05g51830 12005.m09245 protein histone deacetylase 2b, putative, expressed seq=cds; coord=8:163180384..163182820:1; parent_gene=AC183950.2_FG003'

'highly similar to (550) AT5G53350 | Symbols: CLPX | CLPX; ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding | chr5:21644060-21647503 FORWARDhighly similar to (840) loc_os01g66330 12001.m12741 protein ATP-dependent Clp protease ATP-binding subunit clpX, putative, expressed seq=cds; coord=8:164810797..164816886:1; parent_gene=GRMZM2G172829'

'weakly similar to (192) AT2G23620 | Symbols: ATMES1, MES1 | MES1 (METHYL ESTERASE 1); hydrolase, acting on ester bonds / methyl indole-3-acetate esterase/ methyl jasmonate esterase/ methyl salicylate esterase | chr2:10047462-10049248 REVERSEweakly similar to (173) PIR7A_ORYSA Probable esterase PIR7A (EC 3.1.-.-) - Oryza sativa (Rice)moderately similar to (357) loc_os01g57770 12001.m11926 protein polyneuridine-aldehyde esterase precursor, putative, expressed seq=cds; coord=8:171784918..171786870:-1; parent_gene=GRMZM2G440003'

'weakly similar to (192) AT2G23620 | Symbols: ATMES1, MES1 | MES1 (METHYL ESTERASE 1); hydrolase, acting on ester bonds / methyl indole-3-acetate esterase/ methyl jasmonate esterase/ methyl salicylate esterase | chr2:10047462-10049248 REVERSEweakly similar to (173) PIR7A_ORYSA Probable esterase PIR7A (EC 3.1.-.-) - Oryza sativa (Rice)moderately similar to (357) loc_os01g57770 12001.m11926 protein polyneuridine-aldehyde esterase precursor, putative, expressed seq=cds; coord=8:171784918..171786870:-1; parent_gene=GRMZM2G440003'

'weakly similar to (192) AT2G23620 | Symbols: ATMES1, MES1 | MES1 (METHYL ESTERASE 1); hydrolase, acting on ester bonds / methyl indole-3-acetate esterase/ methyl jasmonate esterase/ methyl salicylate esterase | chr2:10047462-10049248 REVERSEweakly similar to (173) PIR7A_ORYSA Probable esterase PIR7A (EC 3.1.-.-) - Oryza sativa (Rice)moderately similar to (357) loc_os01g57770 12001.m11926 protein polyneuridine-aldehyde esterase precursor, putative, expressed seq=cds; coord=8:171784918..171786870:-1; parent_gene=GRMZM2G440003' 'highly similar to (505) AT5G65090 | Symbols: MRH3, BST1, DER4 | BST1 (BRISTLED 1); hydrolase/ inositol or phosphatidylinositol phosphatase | chr5:26004837-26006656 FORWARDhighly similar to (706) loc_os06g11920 12006.m05909 protein hydrolase/ inositol or phosphatidylinositol phosphatase, putative, expressed seq=cds; coord=9:6006293..6008457:-1; parent_gene=GRMZM2G093772'

'weakly similar to (109) AT1G28210 | Symbols: ATJ1 | ATJ1; heat shock protein binding / nucleic acid binding / unfolded protein binding / zinc ion binding | chr1:9854598-9859977 FORWARDweakly similar to (149) loc_os06g11440 12006.m32015 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=9:6826102..6839564:-1; parent_gene=GRMZM2G097620'

'nearly identical (1504) AT5G65460 | Symbols: | kinesin motor protein-related | chr5:26161831-26169001 REVERSEweakly similar to (138) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiihighly similar to (894) loc_os06g11380 12006.m05855 protein ATP binding protein, putative, expressed seq=cds; coord=9:7186959..7210629:-1; parent_gene=GRMZM2G017257'

'nearly identical (1504) AT5G65460 | Symbols: | kinesin motor protein-related | chr5:26161831-26169001 REVERSEweakly similar to (138) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiihighly similar to (894) loc_os06g11380 12006.m05855 protein ATP binding protein, putative, expressed seq=cds; coord=9:7186959..7210629:-1; parent_gene=GRMZM2G017257'

'moderately similar to (255) AT1G06620 | Symbols: | 2-oxoglutarate-dependent dioxygenase, putative | chr1:2025618-2027094 FORWARDmoderately similar to (217) DV4H_CATRO Desacetoxyvindoline 4-hydroxylase (EC 1.14.11.20) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)moderately similar to (290) loc_os03g48430 12003.m09851 protein 1-aminocyclopropane-1-carboxylate oxidase, putative, expressed seq=cds; coord=9:8469357..8471020:1; parent_gene=GRMZM2G066358'

'moderately similar to (328) AT1G21890 | Symbols: | nodulin MtN21 family protein | chr1:7682808-7685581 REVERSEmoderately similar to (478) loc_os06g10750 12006.m05792 protein nodulin protein, putative, expressed seq=cds; coord=9:8432717..8434846:-1; parent_gene=GRMZM2G088053'

'moderately similar to (462) AT5G20070 | Symbols: ATNUDT19, ATNUDX19 | ATNUDX19 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 19); hydrolase/ metal ion binding | chr5:6779893-6782308 FORWARDhighly similar to (622) loc_os06g04910 12006.m05220 protein hydrolase, NUDIX family protein, expressed seq=cds; coord=9:20740530..20746313:1; parent_gene=GRMZM2G404897'

'moderately similar to (462) AT5G20070 | Symbols: ATNUDT19, ATNUDX19 | ATNUDX19 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 19); hydrolase/ metal ion binding | chr5:6779893-6782308 FORWARDhighly similar to (622) loc_os06g04910 12006.m05220 protein hydrolase, NUDIX family protein, expressed seq=cds; coord=9:20740530..20746313:1; parent_gene=GRMZM2G404897'

'moderately similar to (362) AT5G61520 | Symbols: | hexose transporter, putative | chr5:24739358-24740833 REVERSEmoderately similar to (432) HEX6_RICCO Hexose carrier protein HEX6 - Ricinus communis (Castor bean)highly similar to (507) loc_os06g04900 12006.m05219 protein hexose carrier protein HEX6, putative, expressed seq=cds; coord=9:20747007..20749031:1; parent_gene=GRMZM2G404965' 'moderately similar to (311) AT2G22240 | Symbols: ATMIPS2, MIPS2 | MIPS2 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase | chr2:9451901-9453375 REVERSEmoderately similar to (324) INO1_MAIZE Inositol-3-phosphate synthase (EC 5.5.1.4) (Myo-inositol-1-phosphate synthase) (MI-1-P synthase) (IPS) - Zea mays (Maize)moderately similar to (318) loc_os03g09250 12003.m35064 protein inositol-3-phosphate synthase, putative, expressed seq=cds; coord=9:23062831..23063984:-1; parent_gene=GRMZM2G010768'

'weakly similar to (166) AT5G20150 | Symbols: ATSPX1, SPX1 | SPX1 (SPX DOMAIN GENE 1) | chr5:6802429-6803367 FORWARDmoderately similar to (211) loc_os06g40120 12006.m08548 protein IDS4-like protein, putative, expressed seq=cds; coord=9:89392972..89394125:-1; parent_gene=GRMZM2G083655'

'weakly similar to (191) AT1G02170 | Symbols: LOL3, ATMCPB1, MCP1B, AMC1, ATMC1 | AMC1 (METACASPASE 1); cysteine-type endopeptidase | chr1:411883-413426 FORWARDmoderately similar to (276) loc_os03g27120 12003.m08043 protein LOL3, putative, expressed seq=cds; coord=9:120365364..120366799:-1; parent_gene=GRMZM2G132238'

'weakly similar to (191) AT1G02170 | Symbols: LOL3, ATMCPB1, MCP1B, AMC1, ATMC1 | AMC1 (METACASPASE 1); cysteine-type endopeptidase | chr1:411883-413426 FORWARDmoderately similar to (276) loc_os03g27120 12003.m08043 protein LOL3, putative, expressed seq=cds; coord=9:120365364..120366799:-1; parent_gene=GRMZM2G132238'

'weakly similar to (103) AT5G18800 | Symbols: | NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein | chr5:6267304-6268393 FORWARDweakly similar to (124) loc_os03g18420 12003.m07265 protein NADH-ubiquinone oxidoreductase 19 kDa subunit, putative, expressed seq=cds; coord=9:137344168..137344612:-1; parent_gene=AC206223.3_FG010'

'moderately similar to (304) AT1G07540 | Symbols: TRFL2 | TRFL2 (TRF-LIKE 2); DNA binding | chr1:2318433-2321048 REVERSEhighly similar to (901) loc_os03g16700 12003.m101292 protein initiator-binding protein, putative, expressed seq=cds; coord=9:139744606..139748920:-1; parent_gene=GRMZM2G063151'

'weakly similar to (130) AT3G62030 | Symbols: ROC4 | peptidyl-prolyl cis-trans isomerase, chloroplast / cyclophilin / rotamase / cyclosporin A-binding protein (ROC4) | chr3:22973004-22975139 FORWARDweakly similar to (118) CYPB_VICFA Peptidyl-prolyl cis-trans isomerase, chloroplast precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) (CYP B) - Vicia faba (Broad bean)weakly similar to (150) loc_os01g18210 12001.m08363 protein peptidyl-prolyl cis-trans isomerase, chloroplast precursor, putative, expressed seq=cds; coord=9:145151242..145156208:-1; parent_gene=GRMZM2G393515'

'nearly identical (1120) AT1G76140 | Symbols: | serine-type endopeptidase/ serine-type peptidase | chr1:28571187-28574852 FORWARDnearly identical (1320) loc_os01g01830 12001.m06826 protein prolyl endopeptidase, putative, expressed seq=cds; coord=10:18333983..18347671:-1; parent_gene=GRMZM2G015238' 'highly similar to (863) AT5G13110 | Symbols: G6PD2 | G6PD2 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 2); glucose-6-phosphate dehydrogenase | chr5:4158952-4161640 FORWARDhighly similar to (862) G6PDC_TOBAC Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor (EC 1.1.1.49) (G6PD) - Nicotiana tabacum (Common tobacco)highly similar to (993) loc_os07g22350 12007.m06520 protein glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor, putative, expressed seq=cds; coord=10:99364726..99371326:1; parent_gene=GRMZM2G177077'

'weakly similar to (132) AT5G66160 | Symbols: ATRMR1, RMR1 | JR700; peptidase/ protein binding / zinc ion binding | chr5:26445198-26446878 FORWARDweakly similar to (130) loc_os03g07130 12003.m101101 protein RING finger protein 13, putative, expressed seq=cds; coord=10:102285674..102287561:-1; parent_gene=GRMZM2G035899'

'weakly similar to (115) AT2G21045 | Symbols: | INVOLVED IN: aging; EXPRESSED IN: hypocotyl, root; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66170.2); Has 1919 Blast hits to 1917 proteins in 542 species: Archae - 34; Bacteria - 1258; Metazoa - 17; Fungi - 21; Plants - 115; Viruses - 0; Other Eukaryotes - 474 (source: NCBI BLink). | chr2:9027858-9028805 FORWARDweakly similar to (102) DIN1_RAPSA Senescence-associated protein DIN1 - Raphanus sativus (Radish)weakly similar to (173) loc_os04g17660 12004.m35123 protein senescence-associated protein DIN1, putative, expressed seq=cds; coord=10:102318701..102320375:-1; parent_gene=AC204711.3_FG003'

'weakly similar to (171) AT3G14075 | Symbols: | lipase class 3 family protein | chr3:4663819-4666338 REVERSEmoderately similar to (220) loc_os02g54010 12002.m10430 protein triacylglycerol lipase, putative, expressed seq=cds; coord=10:111437426..111441085:1; parent_gene=GRMZM2G153232'

'moderately similar to (313) AT4G30270 | Symbols: MERI5B, MERI-5, SEN4 | MERI5B (meristem-5); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase | chr4:14819445-14820448 REVERSEmoderately similar to (300) BRU1_SOYBN Brassinosteroid-regulated protein BRU1 precursor - Glycine max (Soybean)moderately similar to (436) loc_os04g51460 12004.m10042 protein xyloglucan endotransglucosylase/hydrolase protein 15 precursor, putative, expressed seq=cds; coord=10:141234026..141235309:1; parent_gene=GRMZM2G142857'

'moderately similar to (319) AT1G63270 | Symbols: ATNAP10 | ATNAP10; transporter | chr1:23469664-23470353 REVERSEmoderately similar to (358) loc_os04g53550 12004.m10248 protein cytochrome c biogenesis ATP-binding export protein ccmA-like, putative seq=cds; coord=10:143421871..143422992:-1; parent_gene=GRMZM2G148492'

'weakly similar to (160) AT3G53160 | Symbols: UGT73C7 | UGT73C7 (UDP-glucosyl transferase 73C7); UDP-glycosyltransferase/ transferase, transferring glycosyl groups | chr3:19702485-19703957 REVERSEweakly similar to (126) ZOX_PHAVU Zeatin O-xylosyltransferase (EC 2.4.2.40) (Zeatin O-beta-D-xylosyltransferase) - Phaseolus vulgaris (Kidney bean) (French bean)moderately similar to (380) loc_os03g46400 12003.m09658 protein flavonol-3-O-glycoside-7-O-glucosyltransferase 1, putative, expressed seq=cds; coord=10:146643280..146645035:1; parent_gene=GRMZM2G067424'

'weakly similar to (198) AT5G03500 | Symbols: | transcription coactivator | chr5:876673-877660 REVERSEmoderately similar to (253) loc_os04g56640 12004.m35500 protein cofactor required for Sp1 transcriptional activation subunit 9, putative, expressed seq=cds; coord=10:146675877..146677777:-1; parent_gene=GRMZM2G066981' 'very weakly similar to (97.8) AT3G61310 | Symbols: | DNA-binding family protein | chr3:22690799-22692445 REVERSEmoderately similar to (326) loc_os04g58730 12004.m35526 protein DNA binding protein, putative, expressed seq=cds; coord=10:148640860..148643787:-1; parent_gene=GRMZM2G074107'

'moderately similar to (253) AT1G49180 | Symbols: | protein kinase family protein | chr1:18184840-18187444 REVERSEweakly similar to (128) CDPK_DAUCA Calcium-dependent protein kinase (EC 2.7.11.1) (CDPK) - Daucus carota (Carrot)moderately similar to (409) loc_os04g58990 12004.m10777 protein MAP/microtubule affinity-regulating kinase 4, putative, expressed seq=cds; coord=10:148972118..148974136:-1; parent_gene=GRMZM2G104658'

'moderately similar to (253) AT1G49180 | Symbols: | protein kinase family protein | chr1:18184840-18187444 REVERSEweakly similar to (128) CDPK_DAUCA Calcium-dependent protein kinase (EC 2.7.11.1) (CDPK) - Daucus carota (Carrot)moderately similar to (409) loc_os04g58990 12004.m10777 protein MAP/microtubule affinity-regulating kinase 4, putative, expressed seq=cds; coord=10:148972118..148974136:-1; parent_gene=GRMZM2G104658'

'moderately similar to (494) AT2G46950 | Symbols: CYP709B2 | CYP709B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr2:19289466-19291541 REVERSEmoderately similar to (365) C72A1_CATRO Cytochrome P450 72A1 (EC 1.3.3.9) (CYPLXXII) (Secologanin synthase) (SLS) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)highly similar to (694) loc_os03g25480 12003.m07897 protein cytochrome P450 72A1, putative, expressed seq=cds; coord=1:64079848..64082498:1; parent_gene=GRMZM2G459563'

'nearly identical (1603) AT3G14270 | Symbols: | phosphatidylinositol-4-phosphate 5-kinase family protein | chr3:4754624-4761185 FORWARDnearly identical (2592) loc_os03g28140 12003.m08138 protein 1-phosphatidylinositol-4-phosphate 5-kinase/ zinc ion binding protein, putative, expressed seq=cds; coord=1:69541657..69552704:-1; parent_gene=GRMZM2G111208'

'highly similar to (829) AT5G35790 | Symbols: G6PD1 | G6PD1 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 1); glucose-6-phosphate dehydrogenase | chr5:13956879-13959686 REVERSEhighly similar to (838) G6PDC_SOLTU Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor (EC 1.1.1.49) (G6PD) - Solanum tuberosum (Potato)highly similar to (895) loc_os03g29950 12003.m35274 protein glucose-6-phosphate 1-dehydrogenase, chloroplast precursor, putative, expressed seq=cds; coord=1:72093978..72113326:1; parent_gene=GRMZM2G179521'

'highly similar to (546) AT1G69040 | Symbols: ACR4 | ACR4 (ACT REPEAT 4); amino acid binding | chr1:25957843-25960079 FORWARDhighly similar to (662) loc_os03g29980 12003.m34884 protein ACR4, putative, expressed seq=cds; coord=1:72701780..72704900:1; parent_gene=GRMZM2G096682'

'very weakly similar to (95.9) AT2G35930 | Symbols: PUB23 | PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase | chr2:15083101-15084336 REVERSEmoderately similar to (291) loc_os10g03440 12010.m03761 protein avr9/Cf-9 rapidly elicited protein 74, putative seq=cds; coord=1:115218400..115219880:1; parent_gene=GRMZM2G069070' 'moderately similar to (395) AT2G16370 | Symbols: THY-1 | THY-1 (THYMIDYLATE SYNTHASE 1); dihydrofolate reductase/ thymidylate synthase | chr2:7082038-7084333 REVERSEhighly similar to (543) DRTS_MAIZE Bifunctional dihydrofolate reductase-thymidylate synthase (DHFR-TS) [Includes: Dihydrofolate reductase (EC 1.5.1.3); Thymidylate synthase (EC 2.1.1.45)] - Zea mays (Maize)moderately similar to (489) loc_os11g29390 12011.m06849 protein bifunctional dihydrofolate reductase-thymidylate synthase, putative, expressed seq=cds; coord=1:127019050..127023309:-1; parent_gene=GRMZM2G421493'

'moderately similar to (283) AT5G54000 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr5:21917776-21919064 REVERSEweakly similar to (186) FLS_PETHY Flavonol synthase/flavanone 3-hydroxylase (EC 1.14.11.23) (EC 1.14.11.9) (FLS) - Petunia hybrida (Petunia)moderately similar to (464) loc_os02g17940 12002.m100171 protein leucoanthocyanidin dioxygenase, putative, expressed seq=cds; coord=1:140918675..140920524:1; parent_gene=GRMZM2G162158'

'moderately similar to (231) AT5G57040 | Symbols: | lactoylglutathione lyase family protein / glyoxalase I family protein | chr5:23084035-23085116 REVERSEmoderately similar to (268) loc_os07g06660 12007.m29075 protein glyoxalase/bleomycin resistance protein/dioxygenase, putative, expressed seq=cds; coord=1:179641676..179643591:-1; parent_gene=GRMZM2G067028'

'highly similar to (787) AT4G07960 | Symbols: ATCSLC12, CSLC12 | ATCSLC12 (CELLULOSE-SYNTHASE LIKE C12); cellulose synthase/ transferase, transferring glycosyl groups | chr4:4802628-4805114 REVERSEhighly similar to (862) loc_os07g03260 12007.m04797 protein CSLC10 - cellulose synthase-like family C seq=cds; coord=1:281644459..281648331:-1; parent_gene=GRMZM2G028286'

'very weakly similar to (88.2) AT2G31200 | Symbols: ADF6, ATADF6 | ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); actin binding | chr2:13294171-13294948 FORWARDvery weakly similar to (87.4) ADF_VITVI Actin-depolymerizing factor (ADF) - Vitis vinifera (Grape)very weakly similar to (100) loc_os03g56790 12003.m10595 protein actin-depolymerizing factor 6, putative, expressed seq=cds; coord=1:284469074..284477533:1; parent_gene=GRMZM2G568484'

'very weakly similar to (88.2) AT2G31200 | Symbols: ADF6, ATADF6 | ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); actin binding | chr2:13294171-13294948 FORWARDvery weakly similar to (87.4) ADF_VITVI Actin-depolymerizing factor (ADF) - Vitis vinifera (Grape)very weakly similar to (100) loc_os03g56790 12003.m10595 protein actin-depolymerizing factor 6, putative, expressed seq=cds; coord=1:284469074..284477533:1; parent_gene=GRMZM2G568484'

'very weakly similar to (88.2) AT2G31200 | Symbols: ADF6, ATADF6 | ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); actin binding | chr2:13294171-13294948 FORWARDvery weakly similar to (87.4) ADF_VITVI Actin-depolymerizing factor (ADF) - Vitis vinifera (Grape)very weakly similar to (100) loc_os03g56790 12003.m10595 protein actin-depolymerizing factor 6, putative, expressed seq=cds; coord=1:284469074..284477533:1; parent_gene=GRMZM2G568484'

'highly similar to (700) AT5G63890 | Symbols: ATHDH | ATHDH (HISTIDINOL DEHYDROGENASE); histidinol dehydrogenase | chr5:25565600-25568104 REVERSEhighly similar to (788) HISX_ORYSA Histidinol dehydrogenase, chloroplast precursor (EC 1.1.1.23) (HDH) - Oryza sativa (Rice)highly similar to (788) loc_os01g13190 12001.m07929 protein histidinol dehydrogenase, chloroplast precursor, putative, expressed seq=cds; coord=1:285124791..285129572:-1; parent_gene=GRMZM2G058584'

'seq=cds; coord=2:1954640..1955535:1; parent_gene=GRMZM2G068202'

'moderately similar to (388) AT1G15820 | Symbols: LHCB6, CP24 | LHCB6 (LIGHT HARVESTING COMPLEX PSII SUBUNIT 6); chlorophyll binding | chr1:5446685-5447676 REVERSEmoderately similar to (388) CB4_SPIOL Chlorophyll a-b binding protein CP24, chloroplast precursor - Spinacia oleracea (Spinach)moderately similar to (405) loc_os04g38410 12004.m08831 protein chlorophyll a-b binding protein CP24, chloroplast precursor, putative, expressed seq=cds; coord=2:2018212..2019764:-1; parent_gene=GRMZM2G039996'

'weakly similar to (135) AT3G48100 | Symbols: ARR5, ATRR2, IBC6 | ARR5 (ARABIDOPSIS RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator | chr3:17759112-17760740 REVERSEweakly similar to (189) loc_os04g57720 12004.m10657 protein OsRR6 - Rice type-A response regulator, expressed seq=cds; coord=2:2081848..2082630:-1; parent_gene=GRMZM2G040736'

'weakly similar to (194) AT5G06800 | Symbols: | myb family transcription factor | chr5:2103374-2105680 FORWARDmoderately similar to (384) loc_os04g56990 12004.m101684 protein transfactor, putative, expressed seq=cds; coord=2:3105844..3108209:1; parent_gene=GRMZM2G035370'

'very weakly similar to (100) FTRV_MAIZE Ferredoxin-thioredoxin reductase, variable chain (FTR-V) (Ferredoxin-thioredoxin reductase subunit A) (FTR-A) - Zea mays (Maize)weakly similar to (122) loc_os04g44650 12004.m09424 protein ferredoxin-thioredoxin reductase, variable chain, putative, expressed seq=cds; coord=2:23767850..23771398:1; parent_gene=GRMZM2G026656'

'highly similar to (992) AT1G17840 | Symbols: WBC11, ABCG11, DSO, COF1, ATWBC11 | WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter | chr1:6142870-6145894 FORWARDweakly similar to (164) PDR4_ORYSA Pleiotropic drug resistance protein 4 - Oryza sativa (Rice)nearly identical (1204) loc_os04g44610 12004.m09420 protein ABC transporter C05D10.3 in chromosome III, putative, expressed seq=cds; coord=2:23874520..23879770:-1; parent_gene=GRMZM2G177812'

'highly similar to (640) AT3G15130 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:5097153-5099222 REVERSEweakly similar to (104) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (998) loc_os04g58980 12004.m10776 protein EMB2261, putative, expressed seq=cds; coord=2:24360634..24363095:1; parent_gene=GRMZM2G447090'

'highly similar to (640) AT3G15130 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:5097153-5099222 REVERSEweakly similar to (104) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (998) loc_os04g58980 12004.m10776 protein EMB2261, putative, expressed seq=cds; coord=2:24360634..24363095:1; parent_gene=GRMZM2G447090'

'highly similar to (712) AT4G24550 | Symbols: | clathrin adaptor complexes medium subunit family protein | chr4:12675873-12678903 FORWARDhighly similar to (832) loc_os07g42810 12007.m29006 protein AP-4 complex subunit mu-1, putative, expressed seq=cds; coord=2:25377862..25389131:-1; parent_gene=GRMZM2G031360' 'highly similar to (712) AT4G24550 | Symbols: | clathrin adaptor complexes medium subunit family protein | chr4:12675873-12678903 FORWARDhighly similar to (832) loc_os07g42810 12007.m29006 protein AP-4 complex subunit mu-1, putative, expressed seq=cds; coord=2:25377862..25389131:-1; parent_gene=GRMZM2G031360'

'weakly similar to (143) AT5G23370 | Symbols: | GRAM domain-containing protein / ABA-responsive protein-related | chr5:7863542-7864201 REVERSEmoderately similar to (293) loc_os04g44500 12004.m09409 protein FIP1, putative, expressed seq=cds; coord=2:26730259..26731532:1; parent_gene=GRMZM2G413887'

'moderately similar to (376) AT3G52210 | Symbols: | mRNA capping enzyme family protein | chr3:19367035-19369293 FORWARDhighly similar to (541) MCES2_ORYSA mRNA cap guanine-N7 methyltransferase 2 (EC 2.1.1.56) (mRNA (guanine-N(7)-)-methyltransferase 2) (mRNA cap methyltransferase 2) - Oryza sativa (Rice)highly similar to (541) loc_os02g54000 12002.m10429 protein S-adenosylmethionine-dependent methyltransferase/ catalytic, putative, expressed seq=cds; coord=2:26771301..26774601:-1; parent_gene=GRMZM2G171410'

'weakly similar to (120) AT1G34580 | Symbols: | monosaccharide transporter, putative | chr1:12660631-12663553 FORWARDvery weakly similar to (92.8) STC_RICCO Sugar carrier protein C - Ricinus communis (Castor bean)weakly similar to (132) loc_os04g37980 12004.m08787 protein sugar transport protein 5, putative, expressed seq=cds; coord=2:43482588..43483408:-1; parent_gene=GRMZM2G061495'

'weakly similar to (130) AT3G47820 | Symbols: | armadillo/beta-catenin repeat family protein / U-box domain-containing protein | chr3:17644434-17645963 FORWARDmoderately similar to (338) loc_os09g21740 12009.m05381 protein ubiquitin-protein ligase, putative, expressed seq=cds; coord=2:178382551..178384466:-1; parent_gene=GRMZM2G425965'

'moderately similar to (410) loc_os02g43750 12002.m09409 protein transcription initiation factor, putative, expressed seq=cds; coord=3:13846717..13865900:-1; parent_gene=GRMZM2G102664'

'seq=cds; coord=3:17605685..17606666:1; parent_gene=GRMZM2G099340'

'moderately similar to (409) AT1G25390 | Symbols: | protein kinase family protein | chr1:8906640-8908800 REVERSEmoderately similar to (222) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (631) loc_os01g04409 12001.m07075 protein OsWAK1 - OsWAK receptor-like cytoplasmic kinase (OsWAK-RLCK), expressed seq=cds; coord=3:20399610..20409348:1; parent_gene=GRMZM2G013790'

'weakly similar to (123) AT1G30270 | Symbols: CIPK23, SnRK3.23, ATCIPK23, LKS1 | CIPK23 (CBL-INTERACTING PROTEIN KINASE 23); kinase/ protein binding / protein serine/threonine kinase | chr1:10655270-10658524 FORWARDweakly similar to (108) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)weakly similar to (134) loc_os07g05620 12007.m29069 protein CIPK-like protein 1, putative, expressed seq=cds; coord=3:28055973..28058891:-1; parent_gene=GRMZM2G012472' 'highly similar to (714) AT1G44446 | Symbols: CH1, ATCAO, CAO | CH1 (CHLORINA 1); chlorophyllide a oxygenase | chr1:16849132-16851152 REVERSEhighly similar to (876) CAO_ORYSA Chlorophyllide a oxygenase, chloroplast precursor (EC 1.13.12.14) (Chlorophyll a oxygenase) (Chlorophyll b synthase) - Oryza sativa (Rice)highly similar to (876) loc_os10g41780 12010.m21805 protein chlorophyllide a oxygenase, chloroplast precursor, putative, expressed seq=cds; coord=3:146605798..146608649:1; parent_gene=GRMZM2G171390'

'moderately similar to (335) AT2G29680 | Symbols: CDC6, ATCDC6 | CDC6 (CELL DIVISION CONTROL 6) | chr2:12689586-12692854 FORWARDhighly similar to (549) loc_os01g63710 12001.m42760 protein cell division control protein 6, putative, expressed seq=cds; coord=3:178059283..178062665:-1; parent_gene=GRMZM2G007659'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'highly similar to (538) AT4G16745 | Symbols: | exostosin family protein | chr4:9412185-9414053 FORWARDhighly similar to (709) loc_os01g45350 12001.m10738 protein limonene cyclase like protein, putative, expressed seq=cds; coord=3:215380332..215382314:-1; parent_gene=GRMZM2G048010'

'highly similar to (538) AT4G16745 | Symbols: | exostosin family protein | chr4:9412185-9414053 FORWARDhighly similar to (709) loc_os01g45350 12001.m10738 protein limonene cyclase like protein, putative, expressed seq=cds; coord=3:215380332..215382314:-1; parent_gene=GRMZM2G048010'

'moderately similar to (260) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (338) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (331) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215425032..215437638:-1; parent_gene=GRMZM2G348512'

'moderately similar to (404) AT5G63400 | Symbols: ADK1 | ADK1 (ADENYLATE KINASE 1); ATP binding / adenylate kinase/ nucleobase, nucleoside, nucleotide kinase | chr5:25393502-25394817 REVERSEmoderately similar to (439) KAD2_ORYSA Adenylate kinase B (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Oryza sativa (Rice)moderately similar to (439) loc_os11g20790 12011.m06153 protein adenylate kinase B, putative, expressed seq=cds; coord=3:215654139..215663757:-1; parent_gene=GRMZM2G125193'

'moderately similar to (404) AT5G63400 | Symbols: ADK1 | ADK1 (ADENYLATE KINASE 1); ATP binding / adenylate kinase/ nucleobase, nucleoside, nucleotide kinase | chr5:25393502-25394817 REVERSEmoderately similar to (439) KAD2_ORYSA Adenylate kinase B (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Oryza sativa (Rice)moderately similar to (439) loc_os11g20790 12011.m06153 protein adenylate kinase B, putative, expressed seq=cds; coord=3:215654139..215663757:-1; parent_gene=GRMZM2G125193'

'weakly similar to (147) loc_os10g24954 12010.m05448 protein ulp1 protease family, C-terminal catalytic domain containing protein seq=cds; coord=3:216932802..216935071:1; parent_gene=GRMZM2G042332' 'weakly similar to (196) AT2G23740 | Symbols: | nucleic acid binding / transcription factor/ zinc ion binding | chr2:10098213-10103229 FORWARDmoderately similar to (283) loc_os02g47900 12002.m09824 protein SET domain protein SDG117, putative, expressed seq=cds; coord=3:217256382..217257668:1; parent_gene=GRMZM2G702253'

'moderately similar to (317) AT1G33440 | Symbols: | proton-dependent oligopeptide transport (POT) family protein | chr1:12127712-12130327 REVERSEmoderately similar to (423) loc_os04g36040 12004.m08693 protein peptide transporter PTR2, putative, expressed seq=cds; coord=4:25983954..25985905:1; parent_gene=GRMZM2G026459'

'moderately similar to (379) AT1G12230 | Symbols: | transaldolase, putative | chr1:4148050-4150708 FORWARDmoderately similar to (470) loc_os08g05830 12008.m80251 protein transaldolase, putative, expressed seq=cds; coord=4:33662889..33690509:1; parent_gene=GRMZM2G139550'

'weakly similar to (148) AT5G54680 | Symbols: ILR3 | ILR3 (iaa-leucine resistant3); DNA binding / transcription factor | chr5:22217270-22218993 FORWARDmoderately similar to (307) loc_os08g04390 12008.m26570 protein bHLH transcription factor, putative, expressed seq=cds; coord=4:35575487..35578048:1; parent_gene=GRMZM2G017586'

'highly similar to (654) AT5G08560 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:2771104-2773827 REVERSEhighly similar to (943) loc_os02g19210 12002.m07164 protein WD-repeat protein 26, putative, expressed seq=cds; coord=4:36204069..36211034:1; parent_gene=GRMZM2G111247'

'weakly similar to (176) AT1G32410 | Symbols: | vacuolar protein sorting 55 family protein / VPS55 family protein | chr1:11694398-11695297 FORWARDmoderately similar to (248) loc_os02g55980 12002.m10622 protein vacuolar protein sorting 55 containing protein, expressed seq=cds; coord=4:173302471..173307033:1; parent_gene=GRMZM2G178972'

'moderately similar to (343) AT4G08500 | Symbols: MEKK1, ATMEKK1, MAPKKK8, ARAKIN | MEKK1 (MAP KINASE KINASE KINASE 1); DNA binding / MAP kinase kinase kinase/ kinase/ kinase binding / protein binding | chr4:5404272-5407062 REVERSEweakly similar to (117) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)moderately similar to (393) loc_os03g15570 12003.m06994 protein mitogen-activated protein kinase 1, putative, expressed seq=cds; coord=4:178052009..178063510:-1; parent_gene=GRMZM2G158860'

'moderately similar to (399) AT1G77800 | Symbols: | PHD finger family protein | chr1:29253800-29260190 FORWARDhighly similar to (842) loc_os02g52960 12002.m10326 protein PHD-finger family protein, expressed seq=cds; coord=4:178229465..178238103:1; parent_gene=GRMZM2G475583'

'weakly similar to (133) loc_os02g51300 12002.m10164 protein protein BABY BOOM 2, putative, expressed seq=cds; coord=4:178758748..178760362:-1; parent_gene=GRMZM2G084457' 'highly similar to (510) AT1G12910 | Symbols: ATAN11, LWD1 | ATAN11 (ANTHOCYANIN11); nucleotide binding | chr1:4395114-4396154 REVERSEhighly similar to (622) loc_os02g32430 12002.m08336 protein WD40 repeat protein, putative, expressed seq=cds; coord=5:167430904..167433315:-1; parent_gene=GRMZM2G099334'

'weakly similar to (140) AT5G66320 | Symbols: | zinc finger (GATA type) family protein | chr5:26496208-26497309 REVERSEweakly similar to (163) loc_os02g43150 12002.m100295 protein GATA zinc finger family protein, expressed seq=cds; coord=5:189973035..189975037:1; parent_gene=GRMZM2G140669'

'highly similar to (612) AT1G73660 | Symbols: | protein kinase family protein | chr1:27692247-27696718 REVERSEvery weakly similar to (97.8) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1146) loc_os02g50970 12002.m33450 protein protein kinase domain containing protein, expressed seq=cds; coord=5:206622614..206635150:-1; parent_gene=GRMZM2G127632'

'highly similar to (790) AT1G73590 | Symbols: PIN1, ATPIN1 | PIN1 (PIN-FORMED 1); transporter | chr1:27659772-27662876 FORWARDnearly identical (1019) PIN1_ORYSA Auxin efflux carrier component 1 (OsPIN1) (Ethylene insensitive root 1 homolog) - Oryza sativa (Rice)nearly identical (1019) loc_os02g50960 12002.m33866 protein auxin efflux carrier component 1, putative, expressed seq=cds; coord=5:206727149..206730565:1; parent_gene=GRMZM2G074267'

'highly similar to (509) AT3G10350 | Symbols: | anion-transporting ATPase family protein | chr3:3208310-3210678 FORWARDhighly similar to (585) loc_os02g51100 12002.m10144 protein arsenical pump-driving ATPase, putative, expressed seq=cds; coord=5:206910875..206915210:-1; parent_gene=GRMZM2G105539'

'weakly similar to (106) AT1G72230 | Symbols: | plastocyanin-like domain-containing protein | chr1:27188287-27189093 FORWARDweakly similar to (116) BCP_PEA Blue copper protein precursor - Pisum sativum (Garden pea)weakly similar to (150) loc_os02g52180 12002.m10249 protein uclacyanin-2 precursor, putative, expressed seq=cds; coord=5:208891470..208892610:-1; parent_gene=GRMZM2G045927'

'weakly similar to (126) AT5G16650 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:5463446-5465075 REVERSEmoderately similar to (236) loc_os02g52270 12002.m10258 protein chaperone protein dnaJ, putative, expressed seq=cds; coord=5:209147684..209150734:-1; parent_gene=GRMZM2G072300'

'weakly similar to (138) AT2G24940 | Symbols: AtMAPR2 | AtMAPR2 (Arabidopsis thaliana membrane-associated progesterone binding protein 2); heme binding | chr2:10609447-10609749 FORWARDweakly similar to (192) loc_os02g55060 12002.m100058 protein membrane steroid-binding protein 1, putative, expressed seq=cds; coord=5:213336713..213337573:1; parent_gene=GRMZM2G119782'

'moderately similar to (223) AT1G48030 | Symbols: mtLPD1 | mtLPD1 (mitochondrial lipoamide dehydrogenase 1); ATP binding / dihydrolipoyl dehydrogenase | chr1:17717432-17719141 REVERSEmoderately similar to (219) DLDH_PEA Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase) (Pyruvate dehydrogenase complex E3 subunit) (PDC-E3) (E3) (Glycine cleavage system L protein) - Pisum sativum (Garden pea)moderately similar to (249) loc_os05g06750 12005.m05202 protein dihydrolipoyl dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=6:125308128..125311064:-1; parent_gene=GRMZM2G159570' 'moderately similar to (223) AT1G48030 | Symbols: mtLPD1 | mtLPD1 (mitochondrial lipoamide dehydrogenase 1); ATP binding / dihydrolipoyl dehydrogenase | chr1:17717432-17719141 REVERSEmoderately similar to (219) DLDH_PEA Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase) (Pyruvate dehydrogenase complex E3 subunit) (PDC-E3) (E3) (Glycine cleavage system L protein) - Pisum sativum (Garden pea)moderately similar to (249) loc_os05g06750 12005.m05202 protein dihydrolipoyl dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=6:125308128..125311064:-1; parent_gene=GRMZM2G159570'

'very weakly similar to (96.7) AT1G33360 | Symbols: | ATP-dependent Clp protease ATP-binding subunit ClpX, putative | chr1:12092111-12095789 FORWARDmoderately similar to (218) loc_os05g45750 12005.m27930 protein ATP-dependent Clp protease ATP-binding subunit clpX, putative, expressed seq=cds; coord=6:159379755..159386097:-1; parent_gene=GRMZM2G331833'

'weakly similar to (160) AT4G34960 | Symbols: | peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative | chr4:16648865-16650646 FORWARDweakly similar to (102) CYPH_MAIZE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) - Zea mays (Maize)weakly similar to (175) loc_os09g36670 12009.m06616 protein peptidyl-prolyl cis-trans isomerase CYP19-4 precursor, putative, expressed seq=cds; coord=7:30423336..30427964:1; parent_gene=GRMZM2G092072'

'weakly similar to (178) AT3G06190 | Symbols: ATBPM2, BPM2 | BPM2 (BTB-POZ AND MATH DOMAIN 2); protein binding | chr3:1874577-1876575 REVERSEmoderately similar to (359) loc_os06g45730 12006.m09101 protein speckle-type POZ protein, putative, expressed seq=cds; coord=7:32734580..32736140:1; parent_gene=GRMZM2G109738'

'highly similar to (651) AT1G20160 | Symbols: ATSBT5.2 | ATSBT5.2; identical protein binding / serine-type endopeptidase | chr1:6990852-6993737 REVERSEhighly similar to (966) loc_os09g30458 12009.m06202 protein subtilisin-like protein, putative, expressed seq=cds; coord=7:33098345..33101631:-1; parent_gene=GRMZM2G076417'

'weakly similar to (126) AT1G56340 | Symbols: CRT1 | CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding | chr1:21090022-21092630 REVERSEweakly similar to (144) CALR_MAIZE Calreticulin precursor - Zea mays (Maize)weakly similar to (146) loc_os07g14270 12007.m29118 protein calreticulin precursor, putative, expressed seq=cds; coord=7:40334576..40341507:1; parent_gene=GRMZM2G433551'

'moderately similar to (477) AT1G79610 | Symbols: ATNHX6, NHX6 | sodium proton exchanger, putative (NHX6) | chr1:29953089-29957070 REVERSEmoderately similar to (468) loc_os09g11450 12009.m04407 protein sodium/hydrogen exchanger family protein, expressed seq=cds; coord=7:131642734..131652194:1; parent_gene=GRMZM2G090149'

'moderately similar to (271) AT3G04500 | Symbols: | RNA recognition motif (RRM)-containing protein | chr3:1212065-1213795 REVERSEmoderately similar to (320) loc_os08g45240 12008.m62038 protein expressed protein seq=cds; coord=7:163512342..163516768:1; parent_gene=GRMZM2G068255'

'moderately similar to (249) AT1G70060 | Symbols: SNL4 | SNL4 (SIN3-LIKE 4) | chr1:26383789-26389568 FORWARDmoderately similar to (338) loc_os01g01960 12001.m06838 protein paired amphipathic helix repeat family protein, expressed seq=cds; coord=8:8136058..8139636:-1; parent_gene=AC234160.1_FG001' 'moderately similar to (207) AT4G34730 | Symbols: | ribosome-binding factor A family protein | chr4:16570019-16571274 REVERSEmoderately similar to (243) loc_os06g04610 12006.m05191 protein ribosome-binding factor A, chloroplast precursor, putative, expressed seq=cds; coord=9:21714338..21720944:1; parent_gene=GRMZM2G115156'

'highly similar to (550) AT3G51160 | Symbols: MUR1, MUR_1, GMD2 | MUR1 (MURUS 1); GDP-mannose 4,6-dehydratase | chr3:19007232-19008353 REVERSEhighly similar to (639) loc_os06g04620 12006.m05192 protein GDP-mannose 4,6 dehydratase 2, putative, expressed seq=cds; coord=9:21726160..21727733:1; parent_gene=GRMZM2G115124'

'moderately similar to (311) AT2G22240 | Symbols: ATMIPS2, MIPS2 | MIPS2 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase | chr2:9451901-9453375 REVERSEmoderately similar to (324) INO1_MAIZE Inositol-3-phosphate synthase (EC 5.5.1.4) (Myo-inositol-1-phosphate synthase) (MI-1-P synthase) (IPS) - Zea mays (Maize)moderately similar to (318) loc_os03g09250 12003.m35064 protein inositol-3-phosphate synthase, putative, expressed seq=cds; coord=9:23062831..23063984:-1; parent_gene=GRMZM2G010768'

'highly similar to (679) AT5G35930 | Symbols: | AMP-dependent synthetase and ligase family protein | chr5:14067197-14074404 REVERSEnearly identical (1253) loc_os06g02160 12006.m091577 protein AMP-binding enzyme family protein, expressed seq=cds; coord=9:26478641..26484651:1; parent_gene=GRMZM2G393146'

'moderately similar to (252) AT1G61720 | Symbols: BAN | BAN (BANYULS); oxidoreductase | chr1:22791326-22792757 REVERSEmoderately similar to (208) DFRA_MAIZE Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Zea mays (Maize)moderately similar to (378) loc_os04g53920 12004.m10284 protein leucoanthocyanidin reductase, putative seq=cds; coord=10:143752078..143754011:1; parent_gene=GRMZM2G431504'

'nearly identical (1538) AT4G30190 | Symbols: AHA2, PMA2 | AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism | chr4:14770820-14775920 REVERSEnearly identical (1693) PMA1_ORYSA Plasma membrane ATPase (EC 3.6.3.6) (Proton pump) - Oryza sativa (Rice)nearly identical (1693) loc_os04g56160 12004.m101441 protein plasma membrane ATPase, putative, expressed seq=cds; coord=10:146179462..146186581:1; parent_gene=GRMZM2G006894'

'very weakly similar to (80.9) AT4G00630 | Symbols: KEA2, ATKEA2 | KEA2; potassium ion transmembrane transporter/ potassium:hydrogen antiporter | chr4:261655-267789 REVERSEvery weakly similar to (94.7) loc_os04g58620 12004.m10744 protein KEA1, putative, expressed seq=cds; coord=10:148570662..148572508:-1; parent_gene=GRMZM2G039797'

'moderately similar to (365) AT4G27940 | Symbols: ATMTM1, MTM1 | mitochondrial substrate carrier family protein | chr4:13904745-13907036 FORWARDhighly similar to (527) loc_os01g12470 12001.m07861 protein mitochondrial carrier protein CGI-69, putative, expressed seq=cds; coord=10:148922929..148926666:-1; parent_gene=GRMZM2G177213'

'moderately similar to (423) AT2G17700 | Symbols: | protein kinase family protein | chr2:7685778-7689278 REVERSEweakly similar to (115) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (679) loc_os04g59000 12004.m10778 protein ATP binding protein, putative, expressed seq=cds; coord=10:148973414..148980886:-1; parent_gene=GRMZM2G104658' 'weakly similar to (125) AT2G17700 | Symbols: | protein kinase family protein | chr2:7685778-7689278 REVERSEweakly similar to (189) loc_os04g59000 12004.m10778 protein ATP binding protein, putative, expressed seq=cds; coord=10:148978659..148981143:-1; parent_gene=GRMZM2G104658'

'moderately similar to (244) AT4G17980 | Symbols: anac071 | anac071 (Arabidopsis NAC domain containing protein 71); transcription factor | chr4:9978850-9980038 REVERSEweakly similar to (191) NAC74_ORYSA NAC domain-containing protein 74 (ONAC074) - Oryza sativa (Rice)moderately similar to (353) loc_os10g42130 12010.m06969 protein ANAC071, putative, expressed seq=cds; coord=1:98096125..98097592:1; parent_gene=GRMZM2G082709'

'weakly similar to (197) AT2G23910 | Symbols: | cinnamoyl-CoA reductase-related | chr2:10177902-10179789 FORWARDvery weakly similar to (89.4) DFRA_MAIZE Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Zea mays (Maize)moderately similar to (360) loc_os10g42620 12010.m07015 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=1:102244449..102248245:1; parent_gene=GRMZM2G068917'

'nearly identical (1743) AT3G03050 | Symbols: CSLD3, KJK, ATCSLD3 | CSLD3 (CELLULOSE SYNTHASE-LIKE D3); cellulose synthase/ transferase, transferring glycosyl groups | chr3:687873-691629 FORWARDnearly identical (1914) loc_os10g42750 12010.m07027 protein CSLD1 - cellulose synthase-like family D, expressed seq=cds; coord=1:104608860..104612984:1; parent_gene=GRMZM2G436299'

'highly similar to (571) AT5G64220 | Symbols: | calmodulin-binding protein | chr5:25686434-25691903 FORWARDnearly identical (1273) loc_os10g22950 12010.m05301 protein calmodulin-binding transcription activator 2, putative, expressed seq=cds; coord=1:138637289..138645028:-1; parent_gene=GRMZM2G153594'

'moderately similar to (348) AT1G03280 | Symbols: | transcription initiation factor IIE (TFIIE) alpha subunit family protein / general transcription factor TFIIE family protein | chr1:803635-806758 FORWARDmoderately similar to (489) loc_os08g25460 12008.m06562 protein RNA polymerase II transcription factor/ transcription initiation factor, putative, expressed seq=cds; coord=1:142703238..142720304:-1; parent_gene=GRMZM2G045668'

'moderately similar to (286) AT5G26820 | Symbols: ATIREG3 | ATIREG3 (IRON-REGULATED PROTEIN 3) | chr5:9433858-9437005 FORWARDmoderately similar to (489) loc_os12g37530 12012.m26930 protein expressed protein seq=cds; coord=1:147720182..147724862:-1; parent_gene=GRMZM2G057820'

'weakly similar to (126) AT1G70670 | Symbols: | caleosin-related family protein | chr1:26644830-26645970 FORWARDweakly similar to (174) loc_os06g14350 12006.m71422 protein calcium binding EF-hand protein, putative, expressed seq=cds; coord=1:150224146..150226388:-1; parent_gene=GRMZM2G075456'

'weakly similar to (107) AT1G14110 | Symbols: FUT9, ATFUT9 | FUT9 (FUCOSYLTRANSFERASE 9); fucosyltransferase | chr1:4830297-4831915 FORWARDweakly similar to (109) FUT1_PEA Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1) - Pisum sativum (Garden pea)weakly similar to (146) loc_os06g10920 12006.m05809 protein fucosyltransferase 8, putative, expressed seq=cds; coord=1:162790043..162791359:-1; parent_gene=GRMZM2G703790' 'very weakly similar to (90.5) AT2G32300 | Symbols: UCC1 | UCC1 (UCLACYANIN 1); copper ion binding / electron carrier | chr2:13722510-13723464 FORWARDvery weakly similar to (97.8) BCP_PEA Blue copper protein precursor - Pisum sativum (Garden pea)weakly similar to (108) loc_os08g37670 12008.m07752 protein blue copper protein precursor, putative, expressed seq=cds; coord=1:182095259..182096377:-1; parent_gene=GRMZM2G023847'

'moderately similar to (333) AT3G57670 | Symbols: NTT | NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding | chr3:21370936-21373121 FORWARDmoderately similar to (434) loc_os08g39390 12008.m07920 protein zinc finger protein, putative, expressed seq=cds; coord=1:187269130..187271929:1; parent_gene=GRMZM2G445684'

'moderately similar to (281) AT2G37640 | Symbols: ATEXPA3, ATEXP3, ATHEXP ALPHA 1.9, EXP3 | EXP3 | chr2:15788077-15789812 REVERSEmoderately similar to (400) EXP32_ORYSA Expansin-A32 precursor (OsEXPA32) (Alpha-expansin-32) (OsEXP32) (OsaEXPa1.30) - Oryza sativa (Rice)moderately similar to (400) loc_os08g44790 12008.m08451 protein alpha-expansin 3 precursor, putative, expressed seq=cds; coord=1:203442486..203444246:1; parent_gene=GRMZM2G030531'

'weakly similar to (160) AT3G11750 | Symbols: | dihydroneopterin aldolase, putative | chr3:3715071-3715904 REVERSEmoderately similar to (204) loc_os09g38759 12009.m50203 protein dihydroneopterin aldolase, putative, expressed seq=cds; coord=1:205574134..205574917:-1; parent_gene=GRMZM2G015588'

'highly similar to (630) AT1G58290 | Symbols: HEMA1 | HEMA1; glutamyl-tRNA reductase | chr1:21624028-21626051 REVERSEhighly similar to (808) HEM1_ORYSA Glutamyl-tRNA reductase, chloroplast precursor (EC 1.2.1.70) (GluTR) - Oryza sativa (Rice)highly similar to (808) loc_os10g35840 12010.m06402 protein glutamyl-tRNA reductase, chloroplast precursor, putative, expressed seq=cds; coord=1:226217182..226220470:1; parent_gene=AC213521.3_FG005'

'weakly similar to (187) AT5G23370 | Symbols: | GRAM domain-containing protein / ABA-responsive protein-related | chr5:7863542-7864201 REVERSEmoderately similar to (335) loc_os10g34730 12010.m06300 protein FIP1, putative, expressed seq=cds; coord=1:229187112..229188270:1; parent_gene=GRMZM2G113167'

'moderately similar to (350) AT1G11890 | Symbols: SEC22, ATSEC22 | SEC22; transporter | chr1:4011509-4012835 FORWARDmoderately similar to (372) loc_os06g09850 12006.m32005 protein 25.3 kDa vesicle transport protein, putative, expressed seq=cds; coord=1:286858004..286864584:1; parent_gene=GRMZM2G120596'

'moderately similar to (277) AT5G02960 | Symbols: | 40S ribosomal protein S23 (RPS23B) | chr5:693280-694396 REVERSEmoderately similar to (281) RS23_FRAAN 40S ribosomal protein S23 (S12) - Fragaria ananassa (Strawberry)moderately similar to (288) loc_os03g60400 12003.m10930 protein 40S ribosomal protein S23, putative, expressed seq=cds; coord=1:292879723..292882219:-1; parent_gene=AC225147.4_FG002'

'moderately similar to (261) AT2G47140 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr2:19350970-19352059 REVERSEmoderately similar to (242) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (422) loc_os03g61740 12003.m11055 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=1:295436901..295438003:-1; parent_gene=GRMZM2G156739' 'weakly similar to (114) AT3G06778 | Symbols: | heat shock protein binding / unfolded protein binding | chr3:2140249-2141437 REVERSEmoderately similar to (215) loc_os03g61550 12003.m11036 protein dnaJ domain containing protein, expressed seq=cds; coord=1:295760264..295761728:1; parent_gene=GRMZM2G114673'

'moderately similar to (406) AT5G17440 | Symbols: | LUC7 N_terminus domain-containing protein | chr5:5749849-5753415 FORWARDmoderately similar to (466) loc_os03g62640 12003.m35644 protein RNA-binding protein Luc7-like 2, putative, expressed seq=cds; coord=1:297048516..297054513:-1; parent_gene=GRMZM2G118014'

'moderately similar to (302) AT5G45130 | Symbols: ATRAB5A, ATRABF2A, RABF2A, RAB5A, RHA1, ATRAB-F2A, RAB-F2A | RHA1 (RAB HOMOLOG 1); GTP binding | chr5:18244495-18246060 FORWARDmoderately similar to (287) RHN1_NICPL Ras-related protein RHN1 - Nicotiana plumbaginifolia (Leadwort-leaved tobacco)moderately similar to (363) loc_os03g46390 12003.m09657 protein ras-related protein RHN1, putative, expressed seq=cds; coord=1:300872153..300884599:-1; parent_gene=GRMZM2G131939'

'moderately similar to (305) AT5G33280 | Symbols: | chloride channel-like (CLC) protein, putative | chr5:12549280-12552305 FORWARDmoderately similar to (402) loc_os04g55210 12004.m10413 protein chloride channel-like protein CLC-g, putative, expressed seq=cds; coord=2:5901687..5904448:-1; parent_gene=GRMZM2G071119'

'nearly identical (1791) AT3G28860 | Symbols: ATMDR1, ATMDR11, PGP19, MDR11, MDR1, ATPGP19, ABCB19, ATABCB19 | ABCB19; ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter | chr3:10870287-10877286 REVERSEhighly similar to (962) MDR_ORYSA Putative multidrug resistance protein (P-glycoprotein) - Oryza sativa (Rice)nearly identical (1887) loc_os04g38570 12004.m101543 protein multidrug resistance protein 11, putative, expressed seq=cds; coord=2:6171190..6178089:1; parent_gene=GRMZM2G072850'

'moderately similar to (421) AT5G53150 | Symbols: | heat shock protein binding / unfolded protein binding | chr5:21554935-21557202 FORWARDnearly identical (1088) loc_os04g31940 12004.m08293 protein heat shock protein binding protein, putative, expressed seq=cds; coord=2:69703892..69707982:-1; parent_gene=AC235541.1_FG002'

'weakly similar to (110) AT5G12870 | Symbols: ATMYB46, MYB46 | MYB46 (MYB DOMAIN PROTEIN 46); DNA binding / transcription factor | chr5:4062939-4064939 REVERSEweakly similar to (109) MYBC_MAIZE Anthocyanin regulatory C1 protein - Zea mays (Maize)weakly similar to (122) loc_os01g07430 12001.m07369 protein anthocyanin regulatory C1 protein, putative seq=cds; coord=2:151638006..151638689:-1; parent_gene=GRMZM2G032180'

'highly similar to (961) AT3G52850 | Symbols: VSR1, BP-80, ATELP, VSR-1, BP80, BP80B, ATELP1, ATVSR1 | VSR1 (VACUOLAR SORTING RECEPTOR HOMOLOG 1); amino-terminal vacuolar sorting propeptide binding | chr3:19587999-19591690 FORWARDhighly similar to (907) VSR1_PEA Vacuolar sorting receptor 1 precursor (BP-80) (80 kDa proaleurein-binding protein) - Pisum sativum (Garden pea)nearly identical (1150) loc_os11g02464 12011.m80128 protein vacuolar sorting receptor 1 precursor, putative, expressed seq=cds; coord=2:152168102..152171963:-1; parent_gene=GRMZM2G389362'

'weakly similar to (154) AT5G23950 | Symbols: | C2 domain-containing protein | chr5:8082789-8083448 FORWARDmoderately similar to (243) loc_os09g39770 12009.m06914 protein C2 domain containing protein, expressed seq=cds; coord=2:164667085..164668830:-1; parent_gene=AC210204.3_FG002' 'moderately similar to (395) AT5G60860 | Symbols: AtRABA1f | AtRABA1f (Arabidopsis Rab GTPase homolog A1f); GTP binding | chr5:24484750-24485565 FORWARDmoderately similar to (385) RB11B_TOBAC Ras-related protein Rab11B - Nicotiana tabacum (Common tobacco)moderately similar to (422) loc_os09g15790 12009.m04840 protein ras-related protein Rab11B, putative, expressed seq=cds; coord=2:175516690..175519184:1; parent_gene=GRMZM2G039900'

'moderately similar to (353) AT2G35770 | Symbols: scpl28 | scpl28 (serine carboxypeptidase-like 28); serine-type carboxypeptidase | chr2:15034179-15036497 REVERSEmoderately similar to (364) CBP23_HORVU Serine carboxypeptidase II-3 precursor (EC 3.4.16.6) (CP-MII.3) [Contains: Serine carboxypeptidase II-3 chain A; Serine carboxypeptidase II-3 chain B] - Hordeum vulgare (Barley)moderately similar to (452) loc_os09g28830 12009.m06034 protein serine carboxypeptidase, putative seq=cds; coord=2:188817047..188819624:1; parent_gene=GRMZM2G703293'

'nearly identical (1037) AT4G26540 | Symbols: | kinase | chr4:13394673-13398028 REVERSEmoderately similar to (338) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1429) loc_os09g30190 12009.m06170 protein receptor-like protein kinase precursor, putative, expressed seq=cds; coord=2:189087675..189091198:1; parent_gene=AC233861.1_FG001'

'moderately similar to (220) loc_os09g30390 12009.m06190 protein conserved hypothetical protein seq=cds; coord=2:189309162..189309722:1; parent_gene=GRMZM2G353446'

'very weakly similar to (81.3) AT1G32640 | Symbols: ATMYC2, RD22BP1, JAI1, JIN1, MYC2, ZBF1 | MYC2; DNA binding / transcription activator/ transcription factor | chr1:11799042-11800913 REVERSEmoderately similar to (204) loc_os09g34330 12009.m06482 protein transcription factor AtMYC2, putative seq=cds; coord=2:193882051..193882939:-1; parent_gene=GRMZM2G107560'

'moderately similar to (242) AT1G26665 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: RNA polymerase II mediator complex protein-related (TAIR:AT5G41910.1); Has 223 Blast hits to 223 proteins in 105 species: Archae - 0; Bacteria - 0; Metazoa - 112; Fungi - 83; Plants - 24; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink). | chr1:9214510-9215426 FORWARDmoderately similar to (280) loc_os09g35920 12009.m22176 protein mediator complex subunit 10 CG5057-PA, putative, expressed seq=cds; coord=2:195046778..195052829:1; parent_gene=GRMZM2G034260'

'weakly similar to (162) AT3G44220 | Symbols: | harpin-induced family protein / HIN1 family protein / harpin-responsive family protein | chr3:15928216-15929645 FORWARDmoderately similar to (289) loc_os12g06260 12012.m04617 protein VAMP protein SEC22, putative, expressed seq=cds; coord=3:143060865..143062237:-1; parent_gene=GRMZM2G368151'

'weakly similar to (157) AT3G57040 | Symbols: ARR9, ATRR4 | ARR9 (RESPONSE REGULATOR 9); transcription regulator/ two-component response regulator | chr3:21110059-21111228 FORWARDweakly similar to (192) loc_os01g72330 12001.m13268 protein OsRR4 - Rice type-A response regulator, expressed seq=cds; coord=3:148239120..148241018:-1; parent_gene=GRMZM2G156019' 'weakly similar to (151) AT2G03760 | Symbols: ST, ATST1, RAR047, ST1 | ST; brassinosteroid sulfotransferase/ sulfotransferase | chr2:1149475-1150455 REVERSEmoderately similar to (214) loc_os09g38239 12009.m06769 protein flavonol sulfotransferase-like, putative, expressed seq=cds; coord=3:150720894..150721526:-1; parent_gene=GRMZM2G347146'

'highly similar to (652) AT2G41510 | Symbols: ATCKX1, CKX1 | CKX1 (CYTOKININ OXIDASE/DEHYDROGENASE 1); cytokinin dehydrogenase | chr2:17314626-17316861 FORWARDmoderately similar to (404) CKX1_MAIZE Cytokinin dehydrogenase 1 precursor (EC 1.5.99.12) (Cytokinin oxidase 1) (CKO 1) (COX 1) (ZmCKX1) - Zea mays (Maize)highly similar to (865) loc_os01g71310 12001.m13174 protein cytokinin dehydrogenase 1 precursor, putative, expressed seq=cds; coord=3:152201140..152203793:-1; parent_gene=GRMZM2G050997'

'highly similar to (627) AT2G26650 | Symbols: AKT1, ATAKT1 | AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel | chr2:11331965-11336444 REVERSEhighly similar to (824) AKT1_ORYSA Potassium channel AKT1 (OsAKT1) - Oryza sativa (Rice)highly similar to (824) loc_os01g45990 12001.m10798 protein potassium channel AKT1, putative, expressed seq=cds; coord=3:214273957..214280038:1; parent_gene=GRMZM2G022915'

'weakly similar to (196) AT5G15380 | Symbols: DRM1 | DRM1 (domains rearranged methylase 1); DNA (cytosine-5-)-methyltransferase | chr5:4991347-4994826 FORWARDmoderately similar to (232) loc_os03g02010 12003.m34978 protein DNA cytosine methyltransferase Zmet3, putative, expressed seq=cds; coord=3:217806255..217809492:1; parent_gene=GRMZM2G052991'

'highly similar to (803) AT1G72180 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr1:27164074-27167204 FORWARDmoderately similar to (404) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1344) loc_os11g12530 12011.m05445 protein receptor-like protein kinase 5 precursor, putative, expressed seq=cds; coord=4:10031958..10037921:-1; parent_gene=GRMZM2G011896'

'highly similar to (604) AT5G65700 | Symbols: BAM1 | BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase | chr5:26281826-26284945 FORWARDweakly similar to (179) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (645) loc_os11g12620 12011.m05454 protein receptor protein kinase CLAVATA1 precursor, putative, expressed seq=cds; coord=4:10216533..10222046:1; parent_gene=GRMZM2G068398'

'moderately similar to (201) AT4G32590 | Symbols: | ferredoxin-related | chr4:15721417-15722781 FORWARDmoderately similar to (207) loc_os05g48160 12005.m27636 protein electron carrier/ electron transporter/ iron ion binding protein, putative, expressed seq=cds; coord=4:10541116..10542827:1; parent_gene=GRMZM2G470653'

'moderately similar to (340) AT1G63170 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:23425574-23427073 FORWARDmoderately similar to (465) loc_os02g45240 12002.m09563 protein protein binding protein, putative, expressed seq=cds; coord=4:155224624..155229873:-1; parent_gene=GRMZM2G081829'

'weakly similar to (120) AT1G32240 | Symbols: KAN2 | KAN2 (KANADI 2); DNA binding / transcription factor | chr1:11625882-11630355 REVERSEmoderately similar to (207) loc_os02g46940 12002.m09730 protein KAN, putative, expressed seq=cds; coord=4:158068289..158073370:1; parent_gene=GRMZM2G070865' 'moderately similar to (241) AT2G18330 | Symbols: | AAA-type ATPase family protein | chr2:7965829-7968915 FORWARDmoderately similar to (274) loc_os02g47760 12002.m09810 protein ATPase family AAA domain-containing protein 3, putative, expressed seq=cds; coord=4:160120609..160122543:1; parent_gene=GRMZM2G069422'

'very weakly similar to (97.1) loc_os02g07110 12002.m06058 protein OsSAUR6 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=4:236378470..236379262:-1; parent_gene=GRMZM2G471304'

'weakly similar to (161) loc_os02g06660 12002.m06014 protein desiccation-associated protein, putative seq=cds; coord=4:236733466..236735600:-1; parent_gene=GRMZM2G101920'

'moderately similar to (225) AT1G20810 | Symbols: | immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein | chr1:7232025-7233367 FORWARDmoderately similar to (299) loc_os02g02550 12002.m05604 protein peptidyl-prolyl cis-trans isomerase, FKBP-type family protein, expressed seq=cds; coord=4:239783229..239789117:-1; parent_gene=GRMZM2G150337'

'weakly similar to (129) loc_os03g60560 12003.m10945 protein ZFP16-2, putative, expressed seq=cds; coord=5:2378330..2379629:-1; parent_gene=GRMZM2G002805'

'moderately similar to (360) AT5G66850 | Symbols: MAPKKK5 | MAPKKK5; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr5:26695965-26699159 REVERSEvery weakly similar to (91.3) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)highly similar to (734) loc_os03g55560 12003.m35425 protein MAPKKK5, putative, expressed seq=cds; coord=5:6279965..6303438:1; parent_gene=GRMZM2G034877'

'very weakly similar to (90.9) loc_os11g18340 12011.m05910 protein cycloartenol synthase, putative seq=cds; coord=5:20097280..20098552:-1; parent_gene=GRMZM2G156748'

'highly similar to (670) AT5G23190 | Symbols: CYP86B1 | CYP86B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr5:7803478-7805659 REVERSEweakly similar to (114) C97B2_SOYBN Cytochrome P450 97B2 (EC 1.14.-.-) - Glycine max (Soybean)highly similar to (830) loc_os10g34480 12010.m06272 protein cytochrome P450 86A2, putative, expressed seq=cds; coord=5:26443691..26446113:1; parent_gene=GRMZM2G013082'

'moderately similar to (270) AT1G72820 | Symbols: | mitochondrial substrate carrier family protein | chr1:27403457-27404506 FORWARDmoderately similar to (371) loc_os10g25830 12010.m05527 protein mitochondrial carrier-like protein, putative, expressed seq=cds; coord=5:35709682..35711264:1; parent_gene=GRMZM2G043182'

'nearly identical (1023) AT1G05200 | Symbols: ATGLR3.4, GLR3.4, GLUR3 | ATGLR3.4; intracellular ligand-gated ion channel | chr1:1505642-1509002 FORWARDhighly similar to (890) GLR31_ORYSA Glutamate receptor 3.1 precursor (Ligand-gated ion channel 3.1) - Oryza sativa (Rice)nearly identical (1448) loc_os06g46670 12006.m32152 protein glutamate receptor 3.4 precursor, putative, expressed seq=cds; coord=5:46423968..46428629:1; parent_gene=GRMZM2G057459' 'nearly identical (1153) AT3G18290 | Symbols: EMB2454 | EMB2454 (embryo defective 2454); protein binding / zinc ion binding | chr3:6274308-6280174 FORWARDnearly identical (1343) loc_os05g47780 12005.m27952 protein CHY zinc finger family protein, expressed seq=cds; coord=6:162682754..162690139:1; parent_gene=GRMZM2G320399'

'highly similar to (742) AT1G13900 | Symbols: | calcineurin-like phosphoesterase family protein | chr1:4753494-4755554 REVERSEweakly similar to (160) NPP_HORVU Nucleotide pyrophosphatase/phosphodiesterase (EC 3.-.-.-) (Fragments) - Hordeum vulgare (Barley)nearly identical (1072) loc_os07g02090 12007.m04683 protein hydrolase/ protein serine/threonine phosphatase, putative, expressed seq=cds; coord=7:1789556..1794539:-1; parent_gene=GRMZM2G106600'

'moderately similar to (361) AT5G61150 | Symbols: VIP4 | VIP4 (VERNALIZATION INDEPENDENCE 4); protein binding | chr5:24603846-24607528 REVERSEhighly similar to (701) loc_os07g01880 12007.m04666 protein VIP4, putative, expressed seq=cds; coord=7:1971639..1979556:1; parent_gene=GRMZM2G019879'

'weakly similar to (124) AT1G12550 | Symbols: | oxidoreductase family protein | chr1:4274649-4275831 FORWARDweakly similar to (160) loc_os04g01674 12004.m05484 protein glyoxylate reductase, putative, expressed seq=cds; coord=7:4964407..4965801:-1; parent_gene=GRMZM2G040090'

'very weakly similar to (97.4) loc_os07g05640 12007.m05028 protein proton myo-inositol cotransporter, putative, expressed seq=cds; coord=7:5335384..5336133:1; parent_gene=GRMZM2G142063'

'weakly similar to (101) AT5G25610 | Symbols: RD22 | RD22; nutrient reservoir | chr5:8914498-8916684 REVERSEmoderately similar to (217) loc_os02g18690 12002.m07112 protein BURP domain containing protein, expressed seq=cds; coord=7:6570622..6574976:1; parent_gene=GRMZM2G032145'

'very weakly similar to (94.0) AT3G22620 | Symbols: | protease inhibitor/seed storage/lipid transfer protein (LTP) family protein | chr3:8008615-8009415 FORWARDweakly similar to (115) loc_os07g07920 12007.m05252 protein lipid binding protein, putative, expressed seq=cds; coord=7:9201072..9202357:1; parent_gene=GRMZM2G046750'

'moderately similar to (382) AT4G34880 | Symbols: | amidase family protein | chr4:16615549-16617424 FORWARDhighly similar to (588) loc_os04g10460 12004.m06299 protein amidase, putative, expressed seq=cds; coord=7:148453586..148456184:-1; parent_gene=GRMZM2G111309'

'moderately similar to (266) AT4G21440 | Symbols: ATMYB102, ATM4 | ATMYB102 (ARABIDOPSIS MYB-LIKE 102); DNA binding / transcription factor | chr4:11418425-11419652 REVERSEmoderately similar to (215) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (355) loc_os07g37210 12007.m07971 protein MYB transcription factor, putative, expressed seq=cds; coord=7:157167150..157168689:-1; parent_gene=GRMZM2G031323'
'weakly similar to (137) loc_os07g37850 12007.m08034 protein expressed protein seq=cds; coord=7:158126216..158127461:-1; parent_gene=GRMZM2G089493'

'highly similar to (524) AT5G43100 | Symbols: | aspartyl protease family protein | chr5:17299264-17302718 FORWARDvery weakly similar to (99.4) ASP1_ORYSA Aspartic proteinase Asp1 precursor (EC 3.4.23.-) (OsAsp1) (OSAP1) (Nucellin-like protein) - Oryza sativa (Rice)highly similar to (662) loc_os07g40260 12007.m29392 protein pepsin A, putative, expressed seq=cds; coord=7:162417514..162430709:-1; parent_gene=GRMZM2G090715'

'weakly similar to (197) AT1G06260 | Symbols: | cysteine proteinase, putative | chr1:1916449-1917585 FORWARDweakly similar to (176) ACTN_ACTCH Actinidain precursor (EC 3.4.22.14) (Actinidin) (Allergen Act c 1) - Actinidia chinensis (Kiwi) (Yangtao)moderately similar to (245) loc_os09g21370 12009.m05344 protein cysteine proteinase EP-B 1 precursor, putative, expressed seq=cds; coord=7:162839856..162841296:-1; parent_gene=GRMZM2G036203'

'highly similar to (521) AT5G07810 | Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing protein | chr5:2491412-2498484 REVERSEhighly similar to (875) loc_os07g40730 12007.m079739 protein ATP binding protein, putative, expressed seq=cds; coord=7:163214920..163233302:1; parent_gene=GRMZM2G313553'

'weakly similar to (129) AT5G57860 | Symbols: | ubiquitin family protein | chr5:23437991-23438474 FORWARDweakly similar to (149) loc_os03g24920 12003.m07835 protein ubiquitin-like protein, putative, expressed seq=cds; coord=7:170026036..170029198:1; parent_gene=GRMZM2G055527'

'nearly identical (1079) AT2G40540 | Symbols: KT2, ATKT2, SHY3, KUP2, ATKUP2, TRK2 | KT2 (POTASSIUM TRANSPORTER 2); potassium ion transmembrane transporter | chr2:16931445-16934516 FORWARDnearly identical (1287) HAK9_ORYSA Probable potassium transporter 9 (OsHAK9) - Oryza sativa (Rice)nearly identical (1287) loc_os07g48130 12007.m079793 protein potassium transporter 9, putative, expressed seq=cds; coord=7:172935556..172939916:-1; parent_gene=GRMZM2G166738'

'nearly identical (1079) AT2G40540 | Symbols: KT2, ATKT2, SHY3, KUP2, ATKUP2, TRK2 | KT2 (POTASSIUM TRANSPORTER 2); potassium ion transmembrane transporter | chr2:16931445-16934516 FORWARDnearly identical (1287) HAK9_ORYSA Probable potassium transporter 9 (OsHAK9) - Oryza sativa (Rice)nearly identical (1287) loc_os07g48130 12007.m079793 protein potassium transporter 9, putative, expressed seq=cds; coord=7:172935556..172939916:-1; parent_gene=GRMZM2G166738'

'highly similar to (724) AT4G01690 | Symbols: PPOX, HEMG1, PPO1 | PPOX; protoporphyrinogen oxidase | chr4:729929-732309 FORWARDhighly similar to (720) PPOC_TOBAC Protoporphyrinogen oxidase, chloroplast precursor (EC 1.3.3.4) (PPO I) (Protoporphyrinogen IX oxidase isozyme I) (PPX I) - Nicotiana tabacum (Common tobacco)highly similar to (856) loc_os01g18320 12001.m08374 protein protoporphyrinogen oxidase, chloroplast precursor, putative, expressed seq=cds; coord=8:876212..882478:-1; parent_gene=GRMZM2G039396'

'highly similar to (843) AT5G12250 | Symbols: TUB6 | TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton | chr5:3961317-3962971 REVERSEhighly similar to (852) TBB5_MAIZE Tubulin beta-5 chain (Beta-5 tubulin) - Zea mays (Maize)highly similar to (852) loc_os01g18050 12001.m08347 protein tubulin beta-1 chain, putative, expressed seq=cds; coord=8:1370962..1373972:-1; parent_gene=GRMZM2G042636'

'weakly similar to (141) loc_os12g26850 12012.m06503 protein retrotransposon protein, putative, unclassified, expressed seq=cds; coord=8:101141998..101143439:1; parent_gene=AC199379.4_FG001' 'moderately similar to (277) AT5G46390 | Symbols: | peptidase S41 family protein | chr5:18816612-18819148 FORWARDmoderately similar to (385) loc_os01g47450 12001.m10940 protein carboxyl-terminal-processing protease precursor, putative, expressed seq=cds; coord=8:148790959..148795942:1; parent_gene=GRMZM2G000719'

'weakly similar to (101) TRA1_MAIZE Putative AC transposase (ORFA) - Zea mays (Maize)weakly similar to (105) loc_os10g14230 12010.m04671 protein transposon protein, putative, unclassified seq=cds; coord=8:149218592..149219079:1; parent_gene=GRMZM2G126917'

'weakly similar to (101) TRA1_MAIZE Putative AC transposase (ORFA) - Zea mays (Maize)weakly similar to (105) loc_os10g14230 12010.m04671 protein transposon protein, putative, unclassified seq=cds; coord=8:149218592..149219079:1; parent_gene=GRMZM2G126917'

'moderately similar to (375) AT4G39150 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr4:18233651-18235740 REVERSEmoderately similar to (474) loc_os01g50700 12001.m11251 protein dehydrin family protein, expressed seq=cds; coord=8:153407824..153413500:1; parent_gene=GRMZM2G469901'

'nearly identical (1107) AT4G08350 | Symbols: GTA02, GTA2 | GTA2 (GLOBAL TRANSCRIPTION FACTOR GROUP A2); structural constituent of ribosome / transcription elongation regulator/ transcription factor | chr4:5286351-5292072 FORWARDnearly identical (1303) loc_os06g10620 12006.m05780 protein transcription elongation factor SPT5 homolog 1, putative, expressed seq=cds; coord=9:8943775..8956824:1; parent_gene=GRMZM2G142072'

'moderately similar to (255) AT1G06620 | Symbols: | 2-oxoglutarate-dependent dioxygenase, putative | chr1:2025618-2027094 FORWARDmoderately similar to (217) DV4H_CATRO Desacetoxyvindoline 4-hydroxylase (EC 1.14.11.20) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)moderately similar to (290) loc_os03g48430 12003.m09851 protein 1-aminocyclopropane-1-carboxylate oxidase, putative, expressed seq=cds; coord=9:8469357..8471020:1; parent_gene=GRMZM2G066358'

'highly similar to (716) AT1G32900 | Symbols: | starch synthase, putative | chr1:11920582-11923506 REVERSEnearly identical (1076) SSG1_MAIZE Granule-bound starch synthase 1, chloroplast precursor (EC 2.4.1.242) (Granule-bound starch synthase I) (GBSS-I) - Zea mays (Maize)highly similar to (933) loc_os06g04200 12006.m31969 protein granule-bound starch synthase 1, chloroplast precursor, putative, expressed seq=cds; coord=9:23256308..23260236:-1; parent_gene=GRMZM2G024993'

'moderately similar to (263) AT1G50180 | Symbols: | disease resistance protein (CC-NBS-LRR class), putative | chr1:18584235-18587136 FORWARDhighly similar to (522) loc_os10g10360 12010.m065236 protein NBS-LRR disease resistance protein, putative, expressed seq=cds; coord=9:25062949..25065642:-1; parent_gene=GRMZM2G030051'

'moderately similar to (231) AT3G30340 | Symbols: | nodulin MtN21 family protein | chr3:11956626-11958969 FORWARDmoderately similar to (440) loc_os06g01840 12006.m31822 protein nodulin-like protein, putative, expressed seq=cds; coord=9:27017282..27019536:-1; parent_gene=GRMZM2G168214' 'moderately similar to (226) AT5G53210 | Symbols: SPCH | SPCH (SPEECHLESS); DNA binding / transcription factor | chr5:21586606-21588941 REVERSEmoderately similar to (318) loc_os06g33450 12006.m07882 protein DNA binding protein, putative, expressed seq=cds; coord=9:67071379..67075188:-1; parent_gene=GRMZM2G045109'

'highly similar to (689) AT5G21105 | Symbols: | L-ascorbate oxidase/ copper ion binding / oxidoreductase | chr5:7174321-7177409 FORWARDhighly similar to (729) ASO_CUCSA L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) (ASO) - Cucumis sativus (Cucumber)highly similar to (915) loc_os06g37080 12006.m08243 protein L-ascorbate oxidase precursor, putative, expressed seq=cds; coord=9:77544305..77549474:1; parent_gene=GRMZM2G141376'

'moderately similar to (307) AT5G17000 | Symbols: | NADP-dependent oxidoreductase, putative | chr5:5584983-5586991 REVERSEhighly similar to (520) loc_os06g40070 12006.m08544 protein NADP-dependent oxidoreductase P2, putative, expressed seq=cds; coord=9:88798886..88800768:-1; parent_gene=GRMZM2G019872'

'moderately similar to (466) AT1G20760 | Symbols: | calcium-binding EF hand family protein | chr1:7209515-7214773 FORWARDnearly identical (1343) loc_os03g03830 12003.m05915 protein calcium ion binding protein, putative, expressed seq=cds; coord=9:151488003..151502416:-1; parent_gene=GRMZM2G120975'

'moderately similar to (280) AT1G13080 | Symbols: CYP71B2 | CYP71B2 (CYTOCHROME P450 71B2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr1:4459493-4460807 FORWARDmoderately similar to (432) C71C2_MAIZE Cytochrome P450 71C2 (EC 1.14.-.-) (Benzoxazineless 3) - Zea mays (Maize)moderately similar to (452) loc_os08g01510 12008.m04299 protein cytochrome P450 71C4, putative, expressed seq=cds; coord=10:108117921..108119785:1; parent_gene=GRMZM2G399530'

'weakly similar to (104) AT5G14460 | Symbols: | pseudouridine synthase/ transporter | chr5:4660239-4662543 REVERSEweakly similar to (110) loc_os05g01750 12005.m04712 protein pseudouridylate synthase/ transporter, putative, expressed seq=cds; coord=10:118034725..118039344:-1; parent_gene=GRMZM2G087180'

'weakly similar to (176) AT4G10250 | Symbols: ATHSP22.0 | ATHSP22.0 | chr4:6370537-6371124 FORWARDweakly similar to (185) HSP41_SOYBN 22.0 kDa class IV heat shock protein precursor - Glycine max (Soybean)moderately similar to (227) loc_os04g36750 12004.m08715 protein 22.0 kDa class IV heat shock protein precursor, putative, expressed seq=cds; coord=10:119759011..119760065:1; parent_gene=GRMZM2G346839'

'moderately similar to (300) AT4G13550 | Symbols: | triacylglycerol lipase | chr4:7871251-7876160 REVERSEhighly similar to (700) loc_os04g43030 12004.m09267 protein triacylglycerol lipase, putative, expressed seq=cds; coord=10:129921387..129931446:1; parent_gene=GRMZM2G377641'

'moderately similar to (324) AT1G51740 | Symbols: SYP81, ATUFE1, ATSYP81, UFE1 | SYP81 (SYNTAXIN OF PLANTS 81); SNAP receptor/ protein binding | chr1:19189063-19191188 FORWARDmoderately similar to (437) loc_os04g44810 12004.m09438 protein syntaxin 81, putative, expressed seq=cds; coord=10:132507829..132511210:1; parent_gene=GRMZM2G040902'

'moderately similar to (319) AT1G22550 | Symbols: | proton-dependent oligopeptide transport (POT) family protein | chr1:7966608-7968552 REVERSEmoderately similar to (422) loc_os04g59480 12004.m10824 protein POT family protein, expressed seq=cds; coord=10:149370031..149391434:1; parent_gene=GRMZM2G011590' 'highly similar to (684) AT5G49720 | Symbols: ATGH9A1, DEC, KOR, RSW2, IRX2, KOR1 | ATGH9A1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9A1); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds | chr5:20197765-20200168 REVERSEnearly identical (1052) GUN12_ORYSA Endoglucanase 12 (EC 3.2.1.4) (Endo-1,4-beta glucanase 12) (OsGLU3) - Oryza sativa (Rice)nearly identical (1041) loc_os04g41970 12004.m09171 protein glycoside transferase, six-hairpin, subgroup, putative, expressed seq=cds; coord=10:150090477..150093383:-1; parent_gene=GRMZM2G178025'

'weakly similar to (181) AT1G10460 | Symbols: GLP7 | GLP7 (GERMIN-LIKE PROTEIN 7); manganese ion binding / nutrient reservoir | chr1:3439578-3440231 REVERSEweakly similar to (140) RHRE_PEA Rhicadhesin receptor precursor (Germin-like protein) - Pisum sativum (Garden pea)moderately similar to (320) loc_os03g08150 12003.m06324 protein germin-like protein subfamily 1 member 1 precursor, putative, expressed seq=cds; coord=1:16436083..16436786:1; parent_gene=GRMZM2G016443'

'weakly similar to (143) loc_os03g08330 12003.m06342 protein ZIM motif family protein, expressed seq=cds; coord=1:16792359..16793281:1; parent_gene=GRMZM2G445634'

'weakly similar to (143) loc_os03g08330 12003.m06342 protein ZIM motif family protein, expressed seq=cds; coord=1:16792359..16793281:1; parent_gene=GRMZM2G445634'

'very weakly similar to (90.9) AT1G72360 | Symbols: | ethylene-responsive element-binding protein, putative | chr1:27241904-27242777 FORWARDweakly similar to (138) loc_os03g08500 12003.m06358 protein ethylene-responsive element binding protein 2, putative, expressed seq=cds; coord=1:17519643..17520458:-1; parent_gene=AC206951.3_FG016'

'moderately similar to (374) AT3G54950 | Symbols: PLP7, PLA IIIA | PLA IIIA (PATATIN-LIKE PROTEIN 6) | chr3:20359076-20360774 REVERSEhighly similar to (671) loc_os03g14950 12003.m06932 protein patatin-like protein 3, putative, expressed seq=cds; coord=1:35214345..35216784:1; parent_gene=GRMZM2G030223'

'weakly similar to (118) AT2G37090 | Symbols: IRX9 | IRX9 (IRREGULAR XYLEM 9); transferase, transferring glycosyl groups / xylosyltransferase | chr2:15587671-15589223 REVERSEmoderately similar to (272) loc_os03g17850 12003.m07210 protein beta3-glucuronyltransferase, putative, expressed seq=cds; coord=1:44176429..44177881:1; parent_gene=GRMZM2G001079'

'highly similar to (518) AT5G05580 | Symbols: FAD8 | FAD8 (FATTY ACID DESATURASE 8); omega-3 fatty acid desaturase | chr5:1664331-1666345 FORWARDhighly similar to (531) FAD3C_SOYBN Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-) - Glycine max (Soybean)highly similar to (570) loc_os03g18070 12003.m07232 protein omega-3 fatty acid desaturase, chloroplast precursor, putative, expressed seq=cds; coord=1:44800825..44803738:-1; parent_gene=GRMZM2G074401' 'moderately similar to (484) AT5G01340 | Symbols: | mitochondrial substrate carrier family protein | chr5:143240-144561 REVERSEhighly similar to (553) loc_os03g18160 12003.m07241 protein tricarboxylate transport protein, mitochondrial precursor, putative, expressed seq=cds; coord=1:45400061..45402643:1; parent_gene=AC208201.3_FG001'

'highly similar to (743) AT4G29040 | Symbols: RPT2a | RPT2a (regulatory particle AAA-ATPase 2a); ATPase | chr4:14312369-14314386 FORWARDhighly similar to (783) PRS4_ORYSA 26S protease regulatory subunit 4 homolog (TAT-binding protein homolog 2) - Oryza sativa (Rice)highly similar to (794) loc_os03g18690 12003.m07290 protein 26S protease regulatory subunit 4, putative, expressed seq=cds; coord=1:46542947..46546531:1; parent_gene=GRMZM2G104373'

'weakly similar to (162) AT4G15920 | Symbols: | INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink). | chr4:9030742-9033343 REVERSEmoderately similar to (304) loc_os03g22200 12003.m101337 protein cytochrome c oxidoreductase, putative, expressed seq=cds; coord=1:57246486..57249614:1; parent_gene=GRMZM2G107597'

'moderately similar to (217) AT5G51600 | Symbols: PLE, ATMAP65-3, MAP65-3 | PLE (PLEIADE); microtubule binding | chr5:20961061-20964080 REVERSEmoderately similar to (363) loc_os01g49200 12001.m11107 protein microtubule-associated protein, putative, expressed seq=cds; coord=1:96660606..96664702:-1; parent_gene=GRMZM2G379550'

'highly similar to (540) AT1G55120 | Symbols: ATFRUCT5 | ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5); hydrolase, hydrolyzing O-glycosyl compounds / levanase | chr1:20566983-20569165 FORWARDhighly similar to (897) INV6_ORYSA Beta-fructofuranosidase, insoluble isoenzyme 6 precursor (EC 3.2.1.26) (Sucrose hydrolase 6) (Invertase 6) (Cell wall beta-fructosidase 6) (OsCIN6) - Oryza sativa (Rice)highly similar to (897) loc_os04g56920 12004.m10579 protein beta-fructofuranosidase, insoluble isoenzyme 6 precursor, putative, expressed seq=cds; coord=2:3229044..3231455:1; parent_gene=GRMZM2G018692'

'moderately similar to (224) AT1G19870 | Symbols: iqd32 | iqd32 (IQ-domain 32); calmodulin binding | chr1:6895400-6898539 REVERSEhighly similar to (811) loc_os04g56740 12004.m35501 protein IQ calmodulin-binding motif family protein, expressed seq=cds; coord=2:3409613..3414955:-1; parent_gene=GRMZM2G348909'

'moderately similar to (224) AT1G19870 | Symbols: iqd32 | iqd32 (IQ-domain 32); calmodulin binding | chr1:6895400-6898539 REVERSEhighly similar to (811) loc_os04g56740 12004.m35501 protein IQ calmodulin-binding motif family protein, expressed seq=cds; coord=2:3409613..3414955:-1; parent_gene=GRMZM2G348909'

'nearly identical (1563) AT3G13530 | Symbols: MAPKKK7, MAP3KE1 | MAPKKK7; ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr3:4411934-4419320 REVERSEweakly similar to (134) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)nearly identical (2130) loc_os04g56530 12004.m10542 protein MAPKKK7, putative, expressed seq=cds; coord=2:3775744..3804915:1; parent_gene=GRMZM2G017654' 'moderately similar to (318) AT1G56120 | Symbols: | kinase | chr1:20987288-20993072 REVERSEmoderately similar to (214) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (646) loc_os04g56360 12004.m10526 protein protein kinase, putative seq=cds; coord=2:4050541..4053702:-1; parent_gene=GRMZM2G391741'

'moderately similar to (404) AT2G18890 | Symbols: | protein kinase family protein | chr2:8184027-8185673 FORWARDweakly similar to (195) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (570) loc_os04g56060 12004.m10497 protein BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed seq=cds; coord=2:4669997..4675455:1; parent_gene=GRMZM2G086577'

'moderately similar to (300) AT3G54420 | Symbols: ATEP3, ATCHITIV, CHIV | ATEP3; chitinase | chr3:20145935-20147034 FORWARDmoderately similar to (370) CHIA_MAIZE Endochitinase A precursor (EC 3.2.1.14) (Seed chitinase A) - Zea mays (Maize)moderately similar to (343) loc_os04g41680 12004.m09144 protein endochitinase A precursor, putative, expressed seq=cds; coord=2:33507060..33508210:1; parent_gene=GRMZM2G051921'

'weakly similar to (105) AT3G18550 | Symbols: BRC1, TCP18, ATTCP18 | BRC1 (BRANCHED 1); transcription factor | chr3:6383769-6385604 FORWARDweakly similar to (192) loc_os09g24480 12009.m05602 protein teosinte-branched one, putative seq=cds; coord=2:179980551..179982009:1; parent_gene=GRMZM2G110242'

'weakly similar to (146) AT1G68810 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr1:25861289-25862882 FORWARDmoderately similar to (253) loc_os09g24490 12009.m05603 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=2:180155096..180158005:-1; parent_gene=GRMZM2G176141'

'highly similar to (769) AT1G54100 | Symbols: ALDH7B4 | ALDH7B4 (Aldehyde Dehydrogenase 7B4); 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase | chr1:20195435-20198853 REVERSEhighly similar to (785) AL7A1_MALDO Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin-1) (Matured fruit 60 kDa protein) (MF-60) - Malus domestica (Apple) (Malus sylvestris)highly similar to (902) loc_os09g26880 12009.m22098 protein aldehyde dehydrogenase family 7 member A1, putative, expressed seq=cds; coord=2:184127551..184138715:-1; parent_gene=GRMZM2G130440'

'highly similar to (515) AT2G30050 | Symbols: | transducin family protein / WD-40 repeat family protein | chr2:12825540-12826448 FORWARDhighly similar to (616) loc_os02g04320 12002.m33334 protein SEC13-related protein, putative, expressed seq=cds; coord=3:3399286..3402872:-1; parent_gene=GRMZM2G102795'

'highly similar to (695) AT2G34960 | Symbols: CAT5 | CAT5 (CATIONIC AMINO ACID TRANSPORTER 5); L-glutamate transmembrane transporter/ L-lysine transmembrane transporter/ arginine transmembrane transporter/ cationic amino acid transmembrane transporter | chr2:14744175-14745884 REVERSEhighly similar to (887) loc_os01g11160 12001.m07736 protein cationic amino acid transporter 4, putative, expressed seq=cds; coord=3:3923176..3925460:1; parent_gene=GRMZM2G146161' 'weakly similar to (160) AT4G18960 | Symbols: AG | AG (AGAMOUS); DNA binding / transcription factor | chr4:10383917-10388272 FORWARDmoderately similar to (226) MADS3_ORYSA MADS-box transcription factor 3 (OsMADS3) (Protein AGAMOUS-like) (RMADS222) - Oryza sativa (Rice)moderately similar to (226) loc_os01g10504 12001.m150506 protein MADS-box transcription factor 3, putative, expressed seq=cds; coord=3:4861529..4865955:-1; parent_gene=GRMZM2G471089'

'nearly identical (1523) AT2G47000 | Symbols: MDR4, PGP4, ABCB4, ATPGP4 | ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase | chr2:19310008-19314750 REVERSEhighly similar to (892) MDR_ORYSA Putative multidrug resistance protein (P-glycoprotein) - Oryza sativa (Rice)nearly identical (2004) loc_os01g18670 12001.m08406 protein multidrug resistance protein 17, putative, expressed seq=cds; coord=3:50093119..50099618:-1; parent_gene=GRMZM2G119894'

'weakly similar to (195) AT1G44760 | Symbols: | universal stress protein (USP) family protein | chr1:16896894-16898427 REVERSEmoderately similar to (267) loc_os01g65440 12001.m12655 protein universal stress protein family protein, expressed seq=cds; coord=3:173280370..173283530:-1; parent_gene=GRMZM2G060255'

'moderately similar to (209) AT4G38730 | Symbols: | unknown protein | chr4:18080484-18082305 REVERSEmoderately similar to (247) loc_os01g65310 12001.m12644 protein non-imprinted in Prader-Willi/Angelman syndrome region protein 1homolog, putative, expressed seq=cds; coord=3:173795427..173798467:1; parent_gene=GRMZM2G037229'

'weakly similar to (172) AT5G64520 | Symbols: XRCC2 | XRCC2 | chr5:25788069-25789884 FORWARDmoderately similar to (214) loc_os01g64990 12001.m43303 protein GPI transamidase subunit PIG-U family protein, expressed seq=cds; coord=3:174688276..174694367:-1; parent_gene=GRMZM2G002626'

'moderately similar to (273) AT1G44575 | Symbols: NPQ4, PSBS | NPQ4 (NONPHOTOCHEMICAL QUENCHING); chlorophyll binding / xanthophyll binding | chr1:16871768-16872548 FORWARDmoderately similar to (286) PSBS_SPIOL Photosystem II 22 kDa protein, chloroplast precursor (CP22) - Spinacia oleracea (Spinach)moderately similar to (305) loc_os01g64960 12001.m150788 protein photosystem II 22 kDa protein, chloroplast precursor, putative, expressed seq=cds; coord=3:174825201..174827787:-1; parent_gene=GRMZM2G077333'

'moderately similar to (384) AT4G22930 | Symbols: PYR4, DHOASE | PYR4 (PYRIMIDIN 4); dihydroorotase/ hydrolase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides | chr4:12019315-12021200 FORWARDmoderately similar to (442) loc_os01g54370 12001.m11601 protein dihydroorotase, mitochondrial precursor, putative, expressed seq=cds; coord=3:197320789..197322601:1; parent_gene=GRMZM2G021704'

'nearly identical (1189) AT1G06410 | Symbols: ATTPS7, TPS7, ATTPSA | ATTPS7; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase | chr1:1955413-1958153 FORWARDnearly identical (1538) loc_os01g54560 12001.m150713 protein trehalose synthase, putative, expressed seq=cds; coord=3:197889969..197905140:-1; parent_gene=GRMZM2G304274'

'weakly similar to (132) loc_os10g24954 12010.m05448 protein ulp1 protease family, C-terminal catalytic domain containing protein seq=cds; coord=3:220693706..220701719:-1; parent_gene=GRMZM2G371628' 'weakly similar to (130) AT2G32020 | Symbols: | GCN5-related N-acetyltransferase (GNAT) family protein | chr2:13631193-13631744 REVERSEmoderately similar to (231) loc_os03g46200 12003.m09640 protein acetyltransferase, GNAT family protein, expressed seq=cds; coord=3:222582855..222584403:1; parent_gene=GRMZM2G333775'

'moderately similar to (367) AT2G37650 | Symbols: | scarecrow-like transcription factor 9 (SCL9) | chr2:15792623-15794779 FORWARDweakly similar to (197) CIGR2_ORYSA Chitin-inducible gibberellin-responsive protein 2 - Oryza sativa (Rice)highly similar to (536) loc_os11g47890 12011.m08586 protein SCARECROW-like protein, putative, expressed seq=cds; coord=4:513060..515231:-1; parent_gene=GRMZM2G018254'

'highly similar to (751) AT2G31660 | Symbols: SAD2, URM9 | SAD2 (SUPER SENSITIVE TO ABA AND DROUGHT2); binding / protein transporter | chr2:13464519-13471353 FORWARDhighly similar to (886) loc_os02g27470 12002.m07891 protein importin-7, putative, expressed seq=cds; coord=4:93254018..93267787:1; parent_gene=GRMZM2G008497'

'weakly similar to (142) AT5G04840 | Symbols: | bZIP protein | chr5:1406005-1407648 FORWARDmoderately similar to (413) loc_os02g33560 12002.m08449 protein expressed protein seq=cds; coord=4:110523604..110529675:-1; parent_gene=GRMZM2G118870'

'very weakly similar to (82.8) AT1G71450 | Symbols: | AP2 domain-containing transcription factor, putative | chr1:26927088-26927639 FORWARDweakly similar to (182) loc_os02g35240 12002.m08612 protein dehydration-responsive element-binding protein 1A, putative seq=cds; coord=4:119082526..119083116:-1; parent_gene=GRMZM2G139740'

'moderately similar to (213) AT1G47480 | Symbols: | hydrolase | chr1:17417623-17419296 FORWARDvery weakly similar to (82.8) GID1_ORYSA Gibberellin receptor GID1 (EC 3.-.-.-) (Gibberellin-insensitive dwarf protein 1) (Protein GIBBERELLIN INSENSITIVE DWARF1) - Oryza sativa (Rice)moderately similar to (431) loc_os02g35940 12002.m08682 protein gibberellin receptor GID1L2, putative, expressed seq=cds; coord=4:122677472..122678792:1; parent_gene=GRMZM2G128219'

'moderately similar to (353) AT1G47500 | Symbols: ATRBP47C' | ATRBP47C' (RNA-binding protein 47C'); RNA binding | chr1:17432682-17434805 FORWARDvery weakly similar to (86.3) ROC1_NICSY 29 kDa ribonucleoprotein A, chloroplast precursor (CP29A) - Nicotiana sylvestris (Wood tobacco)highly similar to (527) loc_os04g37690 12004.m35140 protein nucleic acid binding protein, putative, expressed seq=cds; coord=4:122869806..122879188:1; parent_gene=GRMZM2G069678'

'weakly similar to (108) AT4G33565 | Symbols: | protein binding / zinc ion binding | chr4:16136821-16137924 FORWARDweakly similar to (175) loc_os02g36330 12002.m08720 protein RING-H2 finger protein ATL1O, putative, expressed seq=cds; coord=4:123185031..123186547:-1; parent_gene=GRMZM2G041344'

'very weakly similar to (82.8) AT4G24210 | Symbols: SLY1 | SLY1 (SLEEPY1) | chr4:12563658-12564113 FORWARDweakly similar to (148) GID2_ORYSA F-box protein GID2 (Gibberellin-insensitive dwarf protein 2) (Protein GIBBERELLIN INSENSITIVE DWARF2) - Oryza sativa (Rice)very weakly similar to (87.4) loc_os04g3887
12004.m35150 protein 14-3-3-like protein GF14-6, putative, expressed seq=cds; coord=4:126342399..126344503:1; parent_gene=GRMZM2G095397'

'highly similar to (578) AT5G19320 | Symbols: RANGAP2 | RANGAP2 (RAN GTPASE ACTIVATING PROTEIN 2); RAN GTPase activator | chr5:6505310-6506947 REVERSEhighly similar to (842) loc_os05g46560 12005.m27945 protein ran GTPase activating protein, putative, expressed seq=cds; coord=4:140347561..140350401:1; parent_gene=GRMZM2G079817'

'moderately similar to (308) AT5G25760 | Symbols: PEX4 | PEX4 (PEROXIN4); protein binding / ubiquitin-protein ligase | chr5:8967983-8969173 FORWARDweakly similar to (113) UBC2_MEDSA Ubiquitin-conjugating enzyme E2-17 kDa (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) - Medicago sativa (Alfalfa)moderately similar to (320) loc_os02g42314 12002.m33306 protein ubiquitin-conjugating enzyme E2 16, putative, expressed seq=cds; coord=4:145368230..145371847:-1; parent_gene=GRMZM2G161545'

'moderately similar to (460) AT5G33370 | Symbols: | GDSL-motif lipase/hydrolase family protein | chr5:12602864-12604670 REVERSEweakly similar to (169) APG_BRANA Anter-specific proline-rich protein APG (Protein CEX) (Fragment) - Brassica napus (Rape)highly similar to (576) loc_os02g57110 12002.m10733 protein anther-specific proline-rich protein APG precursor, putative, expressed seq=cds; coord=4:171632768..171634757:1; parent_gene=GRMZM2G384780'

'moderately similar to (473) AT1G80030 | Symbols: | DNAJ heat shock protein, putative | chr1:30105398-30108873 REVERSEweakly similar to (119) DNJH_CUCSA DnaJ protein homolog (DNAJ-1) - Cucumis sativus (Cucumber)highly similar to (576) loc_os02g56040 12002.m10628 protein chaperone protein dnaJ, putative, expressed seq=cds; coord=4:173181520..173194277:-1; parent_gene=GRMZM2G054076'

'moderately similar to (407) AT1G79640 | Symbols: | ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr1:29966913-29971387 REVERSEweakly similar to (134) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)highly similar to (611) loc_os02g08240 12002.m06170 protein STE20/SPS1-related proline-alanine-rich protein kinase, putative, expressed seq=cds; coord=4:234834311..234841928:1; parent_gene=GRMZM2G062683'

'weakly similar to (144) AT5G27700 | Symbols: | structural constituent of ribosome | chr5:9807541-9808048 REVERSEweakly similar to (164) RS21_MAIZE 40S ribosomal protein S21 - Zea mays (Maize)weakly similar to (145) loc_os03g46490 12003.m09669 protein 40S ribosomal protein S21, putative seq=cds; coord=5:1565057..1568105:-1; parent_gene=GRMZM2G125300'

'moderately similar to (371) AT1G07410 | Symbols: ATRABA2B, RAB-A2B, ATRAB-A2B | ATRABA2B (ARABIDOPSIS RAB GTPASE HOMOLOG A2B); GTP binding / GTPase/ protein binding | chr1:2276270-2277154 FORWARDmoderately similar to (377) RB11C_LOTJA Ras-related protein Rab11C - Lotus japonicusmoderately similar to (407) loc_os03g60870 12003.m10974 protein ras-related protein Rab11A, putative, expressed seq=cds; coord=5:2259484..2263375:-1; parent_gene=GRMZM2G144008'

'very weakly similar to (98.2) AT2G37590 | Symbols: ATDOF2.4, DOF2.4 | Dof-type zinc finger domain-containing protein | chr2:15769292-15770497 FORWARDweakly similar to (157) loc_os03g60630 12003.m10953 protein expressed protein seq=cds; coord=5:2343761..2345249:-1; parent_gene=GRMZM2G144188'

'moderately similar to (270) AT1G75560 | Symbols: | zinc knuckle (CCHC-type) family protein | chr1:28371420-28372717 REVERSEmoderately similar to (389) loc_os03g60600 12003.m10949 protein cellular nucleic acid-binding protein, putative, expressed seq=cds; coord=5:2358363..2361474:1; parent_gene=GRMZM2G003068' 'nearly identical (1519) AT1G08260 | Symbols: EMB529 | TIL1 (TILTED 1); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding / zinc ion binding | chr1:2590944-2606892 FORWARDnearly identical (1981) loc_os02g30800 12002.m08223 protein DNA polymerase family B, exonuclease domain containing protein, expressed seq=cds; coord=5:164340015..164361538:1; parent_gene=GRMZM2G011631'

'weakly similar to (102) AT5G13910 | Symbols: LEP | LEP (LEAFY PETIOLE); DNA binding / transcription factor | chr5:4482450-4483085 REVERSEweakly similar to (195) loc_os02g32040 12002.m08297 protein AP2 domain containing protein seq=cds; coord=5:166514893..166515834:1; parent_gene=GRMZM2G047999'

'highly similar to (580) AT2G01830 | Symbols: WOL, CRE1, WOL1, AHK4, ATCRE1 | WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase | chr2:363332-367429 REVERSEvery weakly similar to (92.4) ETR1_BRAOL Ethylene receptor (EC 2.7.13.3) - Brassica oleracea (Wild cabbage)highly similar to (800) loc_os02g50480 12002.m10082 protein histidine kinase 1, putative, expressed seq=cds; coord=5:205544166..205551400:1; parent_gene=GRMZM2G151223'

'weakly similar to (132) AT5G10080 | Symbols: | aspartyl protease family protein | chr5:3150843-3153380 FORWARDmoderately similar to (201) loc_os02g51540 12002.m10187 protein pepsin A, putative, expressed seq=cds; coord=5:208060698..208061885:1; parent_gene=GRMZM2G335978'

'highly similar to (983) AT5G06670 | Symbols: | ATP binding / microtubule motor | chr5:2048243-2055019 REVERSEmoderately similar to (247) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiinearly identical (1517) loc_os02g53520 12002.m10381 protein ATP binding protein, putative, expressed seq=cds; coord=5:211512773..211530461:-1; parent_gene=GRMZM2G385925'

'moderately similar to (234) AT1G72300 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr1:27217679-27220966 REVERSEmoderately similar to (204) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)moderately similar to (336) loc_os02g05940 12002.m05942 protein phytosulfokine receptor precursor, putative, expressed seq=cds; coord=5:215846665..215848735:1; parent_gene=GRMZM2G013848'

'moderately similar to (215) AT3G58490 | Symbols: | phosphatidic acid phosphatase family protein / PAP2 family protein | chr3:21633362-21635057 FORWARDmoderately similar to (278) loc_os03g59070 12003.m10808 protein phosphoric ester hydrolase, putative, expressed seq=cds; coord=6:84569693..84573555:1; parent_gene=GRMZM2G417009'

'weakly similar to (109) AT5G19000 | Symbols: ATBPM1 | ATBPM1 (BTB-POZ and MATH domain 1); protein binding | chr5:6342563-6344641 FORWARDweakly similar to (187) loc_os06g14060 12006.m32038 protein speckle-type POZ protein, putative, expressed seq=cds; coord=6:93490896..93493178:-1; parent_gene=GRMZM2G161610'

'moderately similar to (233) AT1G25440 | Symbols: | zinc finger (B-box type) family protein | chr1:8933939-8935284 REVERSEmoderately similar to (472) loc_os06g15330 12006.m06246 protein zinc finger protein CONSTANS-LIKE 16, putative, expressed seq=cds; coord=6:117370662..117372555:1; parent_gene=GRMZM2G012717' 'weakly similar to (104) AT4G30590 | Symbols: | plastocyanin-like domain-containing protein | chr4:14935760-14936469 REVERSEweakly similar to (180) loc_os06g17730 12006.m06485 protein blue copper protein precursor, putative, expressed seq=cds; coord=6:119641904..119642938:1; parent_gene=GRMZM2G148624'

'moderately similar to (238) ATCG00490 | Symbols: RBCL | large subunit of RUBISCO. Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds. | chrC:54958-56397 FORWARDmoderately similar to (257) RBL_SACOF Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39) (RuBisCO large subunit) - Saccharum officinarum (Sugarcane)moderately similar to (252) loc_os01g58020 12001.m11949 protein ribulose bisphosphate carboxylase large chain precursor, putative seq=cds; coord=6:123912807..123913530:1; parent_gene=GRMZM2G122563'

'very weakly similar to (82.4) AT2G31820 | Symbols: | ankyrin repeat family protein | chr2:13530350-13532562 FORWARDmoderately similar to (284) loc_os09g12480 12009.m04511 protein conserved hypothetical protein seq=cds; coord=6:128318222..128323167:-1; parent_gene=GRMZM2G341155'

'highly similar to (728) AT1G11910 | Symbols: | aspartyl protease family protein | chr1:4017119-4019874 REVERSEhighly similar to (876) ASPR1_ORYSA Aspartic proteinase oryzasin-1 precursor (EC 3.4.23.-) - Oryza sativa (Rice)highly similar to (876) loc_os05g49200 12005.m27639 protein aspartic proteinase oryzasin-1 precursor, putative, expressed seq=cds; coord=6:165013896..165020047:1; parent_gene=GRMZM2G065757'

'moderately similar to (353) AT5G05490 | Symbols: SYN1, DIF1 | SYN1 (SYNAPTIC 1) | chr5:1624712-1629144 FORWARDhighly similar to (754) loc_os05g50410 12005.m083823 protein sister chromatid cohesion 1 protein 1, putative, expressed seq=cds; coord=6:166595022..166626902:1; parent_gene=GRMZM2G059037'

'moderately similar to (353) AT5G05490 | Symbols: SYN1, DIF1 | SYN1 (SYNAPTIC 1) | chr5:1624712-1629144 FORWARDhighly similar to (754) loc_os05g50410 12005.m083823 protein sister chromatid cohesion 1 protein 1, putative, expressed seq=cds; coord=6:166595022..166626902:1; parent_gene=GRMZM2G059037'

'moderately similar to (224) AT3G52380 | Symbols: CP33, PDE322 | CP33; RNA binding | chr3:19421619-19422855 FORWARDmoderately similar to (206) ROC5_NICSY 33 kDa ribonucleoprotein, chloroplast precursor - Nicotiana sylvestris (Wood tobacco)moderately similar to (305) loc_os07g06450 12007.m05106 protein ribonucleoprotein, chloroplast precursor, putative, expressed seq=cds; coord=7:6067559..6069626:-1; parent_gene=GRMZM2G026614'

'highly similar to (630) AT2G32010 | Symbols: | endonuclease/exonuclease/phosphatase family protein | chr2:13625344-13628081 FORWARDhighly similar to (911) loc_os07g07950 12007.m29082 protein type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2, putative, expressed seq=cds; coord=7:9255254..9260899:-1; parent_gene=GRMZM2G004301'

'moderately similar to (361) AT2G47170 | Symbols: ARF1A1C | ARF1A1C; GTP binding / phospholipase activator/ protein binding | chr2:19367264-19368518 FORWARDmoderately similar to (355) ARF_VIGUN ADP-ribosylation factor - Vigna unguiculata (Cowpea)moderately similar to (365) loc_os07g12200 12007.m05673 protein ADP-ribosylation factor 1, putative, expressed seq=cds; coord=7:20165377..20168407:1; parent_gene=GRMZM2G105996' 'moderately similar to (355) AT3G11900 | Symbols: ANT1 | ANT1 (AROMATIC AND NEUTRAL TRANSPORTER 1); amino acid transmembrane transporter/ aromatic amino acid transmembrane transporter/ neutral amino acid transmembrane transporter | chr3:3758523-3760103 FORWARDhighly similar to (568) loc_os07g12770 12007.m05729 protein ANT1, putative, expressed seq=cds; coord=7:21546705..21550608:-1; parent_gene=GRMZM2G173967'

'moderately similar to (255) loc_os12g37110 12012.m07496 protein ribosomal RNA apurinic site specific lyase, putative, expressed seq=cds; coord=7:30147128..30148775:1; parent_gene=GRMZM2G012508'

'moderately similar to (250) AT1G05700 | Symbols: | leucine-rich repeat protein kinase, putative | chr1:1709796-1713245 FORWARDweakly similar to (125) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)moderately similar to (439) loc_os09g19140 12009.m05122 protein senescence-induced receptor-like serine/threonine-protein kinase precursor, putative seq=cds; coord=7:95446340..95451284:-1; parent_gene=GRMZM2G354615'

'highly similar to (979) AT3G47780 | Symbols: ATATH6, ATH6 | ATATH6; ATPase, coupled to transmembrane movement of substances / transporter | chr3:17624500-17628972 FORWARDvery weakly similar to (98.2) CYSA_MESVI Probable sulfate/thiosulfate import ATP-binding protein cysA (EC 3.6.3.25) (Sulfate-transporting ATPase) - Mesostigma viridenearly identical (1293) loc_os08g30770 12008.m07077 protein ATATH6, putative, expressed seq=cds; coord=7:97161861..97168183:1; parent_gene=GRMZM2G355523'

'highly similar to (547) AT1G18870 | Symbols: ICS2 | ICS2 (ISOCHORISMATE SYNTHASE 2); isochorismate synthase | chr1:6515746-6519176 FORWARDhighly similar to (506) ICS_CATRO Isochorismate synthase, chloroplast precursor (EC 5.4.4.2) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)highly similar to (862) loc_os09g19734 12009.m50200 protein isochorismate synthase 1, chloroplast precursor, putative, expressed seq=cds; coord=7:97622762..97626689:1; parent_gene=GRMZM2G022837'

'moderately similar to (451) AT1G78130 | Symbols: UNE2 | UNE2 (unfertilized embryo sac 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter | chr1:29400171-29401814 FORWARDhighly similar to (581) loc_os08g31670 12008.m07161 protein carbohydrate transporter/ sugar porter/ transporter, putative, expressed seq=cds; coord=7:100796427..100799442:1; parent_gene=GRMZM2G176780'

'weakly similar to (130) loc_os09g24954 12009.m22237 protein double-stranded RNA binding motif family protein, expressed seq=cds; coord=7:114354289..114358224:1; parent_gene=GRMZM2G042006'

'very weakly similar to (95.1) AT5G04340 | Symbols: C2H2, CZF2, ZAT6 | ZAT6 (ZINC FINGER OF ARABIDOPSIS THALIANA 6); nucleic acid binding / transcription factor/ zinc ion binding | chr5:1216321-1217037 REVERSEvery weakly similar to (82.8) ZFP1_WHEAT Zinc-finger protein 1 (WZF1) - Triticum aestivum (Wheat)weakly similar to (137) loc_os07g40080 12007.m08250 protein zinc-finger protein 1, putative, expressed seq=cds; coord=7:162313242..162313838:1; parent_gene=AC185108.3_FG011'

'weakly similar to (191) AT1G24090 | Symbols: | RNase H domain-containing protein | chr1:8520834-8524690 FORWARDmoderately similar to (281) loc_os06g13010 12006.m06017 protein nucleic acid binding protein, putative, expressed seq=cds; coord=9:2485121..2487554:-1; parent_gene=GRMZM2G016275' 'moderately similar to (207) AT1G77980 | Symbols: AGL66 | AGL66 (AGAMOUS-LIKE 66); transcription factor | chr1:29315212-29317067 REVERSEvery weakly similar to (91.3) AGL8_SINAL Agamous-like MADS-box protein AGL8 homolog (MADS B) - Sinapis alba (White mustard) (Brassica hirta)moderately similar to (301) loc_os06g11970 12006.m05914 protein MADS-box protein AGL66, putative, expressed seq=cds; coord=9:5511653..5517241:1; parent_gene=GRMZM2G152415'

'very weakly similar to (92.8) AT2G41940 | Symbols: ZFP8 | ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding | chr2:17507556-17508329 FORWARDweakly similar to (147) loc_os02g53530 12002.m10382 protein zinc finger protein, putative, expressed seq=cds; coord=9:9595102..9599382:-1; parent_gene=GRMZM2G159402'

'moderately similar to (429) AT2G05940 | Symbols: | protein kinase, putative | chr2:2287514-2289270 REVERSEmoderately similar to (218) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (616) loc_os06g10160 12006.m05734 protein protein kinase APK1A, chloroplast precursor, putative, expressed seq=cds; coord=9:10125256..10127926:1; parent_gene=GRMZM2G055982'

'weakly similar to (116) MYB4_ORYSA Myb-related protein Myb4 (OsMyb4) (Transcription factor RLTR1) - Oryza sativa (Rice)weakly similar to (116) loc_os04g43680 12004.m09327 protein myb-related protein Myb4, putative, expressed seq=cds; coord=9:22045463..22046431:-1; parent_gene=GRMZM2G449056'

'moderately similar to (322) AT3G07970 | Symbols: QRT2 | QRT2 (QUARTET 2); polygalacturonase | chr3:2541006-2543370 FORWARDmoderately similar to (334) PGLR_ACTCH Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) - Actinidia chinensis (Kiwi) (Yangtao)highly similar to (559) loc_os03g11760 12003.m06628 protein polygalacturonase precursor, putative, expressed seq=cds; coord=9:146528352..146530720:-1; parent_gene=GRMZM2G034835'

'very weakly similar to (98.6) AT2G41430 | Symbols: ERD15, LSR1, CID1 | ERD15 (EARLY RESPONSIVE TO DEHYDRATION 15); protein binding | chr2:17269736-17270314 FORWARDweakly similar to (189) loc_os03g23010 12003.m35608 protein expressed protein seq=cds; coord=9:148225279..148226869:1; parent_gene=GRMZM2G181551'

'very weakly similar to (89.0) AT4G40060 | Symbols: ATHB16, ATHB-16 | ATHB16 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 16); sequence-specific DNA binding / transcription activator/ transcription factor | chr4:18571682-18572774 REVERSEweakly similar to (107) loc_os03g08960 12003.m06402 protein homeodomain-leucine zipper transcription factor TaHDZipI-1, putative, expressed seq=cds; coord=9:149646070..149647584:1; parent_gene=AC233899.1_FG004'

'moderately similar to (323) AT5G04740 | Symbols: | ACT domain-containing protein | chr5:1368713-1371391 REVERSEmoderately similar to (415) loc_os12g05650 12012.m04558 protein ACT domain containing protein, expressed seq=cds; coord=10:5523751..5529199:-1; parent_gene=GRMZM2G066496' 'highly similar to (664) AT5G03940 | Symbols: FFC, 54CP, CPSRP54, SRP54CP | CPSRP54 (CHLOROPLAST SIGNAL RECOGNITION PARTICLE 54 KDA SUBUNIT); 7S RNA binding / GTP binding / mRNA binding / signal sequence binding | chr5:1060265-1063257 REVERSEmoderately similar to (207) SR541_HORVU Signal recognition particle 54 kDa protein 1 (SRP54) - Hordeum vulgare (Barley)highly similar to (803) loc_os11g05556 12011.m61754 protein signal recognition particle 54 kDa protein, chloroplast precursor, putative, expressed seq=cds; coord=10:5737001..5744526:-1; parent_gene=GRMZM2G113093'

'moderately similar to (214) AT1G08370 | Symbols: DCP1, ATDCP1 | DCP1 (decapping 1); m7G(5')pppN diphosphatase/ protein homodimerization | chr1:2638355-2640367 FORWARDmoderately similar to (269) loc_os11g05650 12011.m04762 protein dcp1-like decapping family protein, expressed seq=cds; coord=10:6009679..6012460:1; parent_gene=GRMZM2G131120'

'highly similar to (848) AT5G22510 | Symbols: | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr5:7474974-7477479 REVERSEnearly identical (1092) loc_os02g32730 12002.m08366 protein alkaline/neutral invertase, putative, expressed seq=cds; coord=10:300426..310885:-1; parent_gene=GRMZM2G040843'

'weakly similar to (121) AT1G76410 | Symbols: ATL8 | ATL8; protein binding / zinc ion binding | chr1:28668915-28669472 FORWARDvery weakly similar to (89.0) EL5_ORYSA E3 ubiquitin-protein ligase EL5 (EC 6.3.2.-) - Oryza sativa (Rice)weakly similar to (166) loc_os02g46100 12002.m09647 protein RING-H2 finger protein ATL1R, putative, expressed seq=cds; coord=10:134991961..134992953:-1; parent_gene=GRMZM2G031280'

'highly similar to (588) AT5G50850 | Symbols: MAB1 | MAB1 (MACCI-BOU); catalytic/ pyruvate dehydrogenase (acetyl-transferring) | chr5:20689671-20692976 FORWARDhighly similar to (576) ODPB_PEA Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B) - Pisum sativum (Garden pea)highly similar to (653) loc_os08g42410 12008.m080219 protein pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor, putative, expressed seq=cds; coord=1:195400126..195416505:1; parent_gene=GRMZM2G043198'

'highly similar to (542) AT1G60710 | Symbols: ATB2 | ATB2; oxidoreductase | chr1:22355073-22356627 REVERSEhighly similar to (508) IN22_MAIZE IN2-2 protein - Zea mays (Maize)highly similar to (607) loc_os04g26910 12004.m07816 protein auxin-induced protein PCNT115, putative, expressed seq=cds; coord=1:195752951..195756226:-1; parent_gene=GRMZM2G020631'

'very weakly similar to (89.4) AT5G50380 | Symbols: ATEXO70F1 | ATEXO70F1 (exocyst subunit EXO70 family protein F1); protein binding | chr5:20516382-20518433 REVERSEmoderately similar to (346) loc_os01g28600 12001.m09300 protein exo70 exocyst complex subunit family protein, expressed seq=cds; coord=1:196193577..196195939:1; parent_gene=GRMZM2G353483'

'weakly similar to (104) loc_os08g44190 12008.m08392 protein zinc finger protein 2, putative, expressed seq=cds; coord=1:205832080..205832623:1; parent_gene=GRMZM2G104516'

'weakly similar to (157) AT3G11750 | Symbols: | dihydroneopterin aldolase, putative | chr3:3715071-3715904 REVERSEmoderately similar to (206) loc_os09g38759 12009.m50203 protein dihydroneopterin aldolase, putative, expressed seq=cds; coord=1:206197528..206201863:1; parent_gene=GRMZM2G095579' 'moderately similar to (264) AT4G38620 | Symbols: ATMYB4, MYB4 | MYB4; DNA binding / transcription factor | chr4:18053866-18054876 FORWARDmoderately similar to (447) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (341) loc_os08g43550 12008.m08329 protein myb-related protein Zm38, putative, expressed seq=cds; coord=1:206858424..206859706:1; parent_gene=GRMZM2G084583'

'moderately similar to (324) AT5G24400 | Symbols: emb2024 | emb2024 (embryo defective 2024); 6-phosphogluconolactonase/ catalytic | chr5:8330532-8331784 REVERSEmoderately similar to (418) loc_os09g35970 12009.m06548 protein 6-phosphogluconolactonase, putative, expressed seq=cds; coord=1:207611046..207613075:-1; parent_gene=GRMZM2G122126'

'weakly similar to (132) AT4G35160 | Symbols: | O-methyltransferase family 2 protein | chr4:16730989-16732808 REVERSEmoderately similar to (293) ZRP4_MAIZE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT) - Zea mays (Maize)moderately similar to (344) loc_os06g16960 12006.m06409 protein O-methyltransferase ZRP4, putative seq=cds; coord=1:209119391..209120903:1; parent_gene=GRMZM2G059465'

'weakly similar to (130) loc_os08g35110 12008.m07500 protein OsSAUR33 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=1:209180557..209181568:1; parent_gene=GRMZM2G460861'

'moderately similar to (378) AT2G23760 | Symbols: BLH4, SAW2 | BLH4 (BEL1-LIKE HOMEODOMAIN 4); DNA binding / transcription factor | chr2:10107951-10112736 REVERSEhighly similar to (771) loc_os03g52239 12003.m101484 protein homeodomain protein JUBEL1, putative, expressed seq=cds; coord=1:273091163..273101408:-1; parent_gene=GRMZM2G396114'

'moderately similar to (378) AT2G23760 | Symbols: BLH4, SAW2 | BLH4 (BEL1-LIKE HOMEODOMAIN 4); DNA binding / transcription factor | chr2:10107951-10112736 REVERSEhighly similar to (771) loc_os03g52239 12003.m101484 protein homeodomain protein JUBEL1, putative, expressed seq=cds; coord=1:273091163..273101408:-1; parent_gene=GRMZM2G396114'

'weakly similar to (160) AT2G21110 | Symbols: | disease resistance-responsive family protein | chr2:9050290-9050850 REVERSEmoderately similar to (224) loc_os03g59440 12003.m10842 protein disease resistance response like protein, putative, expressed seq=cds; coord=1:290937052..290937639:1; parent_gene=GRMZM2G402765'

'moderately similar to (390) AT2G12550 | Symbols: | ubiquitin-associated (UBA)/TS-N domain-containing protein | chr2:5114881-5118486 FORWARDhighly similar to (630) loc_os04g55150 12004.m35482 protein UBA/TS-N domain containing protein, expressed seq=cds; coord=2:5925456..5929946:-1; parent_gene=GRMZM2G070881'

'moderately similar to (376) AT3G52210 | Symbols: | mRNA capping enzyme family protein | chr3:19367035-19369293 FORWARDhighly similar to (541) MCES2_ORYSA mRNA cap guanine-N7 methyltransferase 2 (EC 2.1.1.56) (mRNA (guanine-N(7)-)-methyltransferase 2) (mRNA cap methyltransferase 2) - Oryza sativa (Rice)highly similar to (541) loc_os02g54000 12002.m10429 protein S-adenosylmethionine-dependent methyltransferase/ catalytic, putative, expressed seq=cds; coord=2:26771301..26774601:-1; parent_gene=GRMZM2G171410' 'moderately similar to (449) AT3G02450 | Symbols: | cell division protein ftsH, putative | chr3:502876-505030 REVERSEmoderately similar to (261) FTSH_ORYSA Cell division protease ftsH homolog, chloroplast precursor (EC 3.4.24.-) - Oryza sativa (Rice)highly similar to (650) loc_os04g39190 12004.m08908 protein cell division protein ftsH homolog 4, putative, expressed seq=cds; coord=2:40408933..40420447:1; parent_gene=GRMZM2G177070'

'highly similar to (577) AT5G67320 | Symbols: HOS15 | HOS15 (high expression of osmotically responsive genes 15) | chr5:26857268-26860974 FORWARDweakly similar to (121) PF20_CHLRE Flagellar WD repeat protein PF20 - Chlamydomonas reinhardtiihighly similar to (919) loc_os07g22220 12007.m06507 protein F-box-like/WD-repeat-containing protein TBL1XR1-A, putative, expressed seq=cds; coord=2:104729978..104750595:-1; parent_gene=GRMZM2G149708'

'weakly similar to (166) loc_os10g25210 12010.m065256 protein F-box protein interaction domain containing protein, expressed seq=cds; coord=2:128405636..128407367:1; parent_gene=GRMZM2G365677'

'moderately similar to (236) AT4G23900 | Symbols: | nucleoside diphosphate kinase 4 (NDK4) | chr4:12424505-12426318 FORWARDmoderately similar to (231) NDK4_SPIOL Nucleoside diphosphate kinase 4, chloroplast precursor (EC 2.7.4.6) (Nucleoside diphosphate kinase IV) (NDK IV) (NDP kinase IV) (NDPK IV) (Nucleoside diphosphate kinase III) - Spinacia oleracea (Spinach)moderately similar to (238) loc_os05g51700 12005.m083838 protein nucleoside diphosphate kinase 4, chloroplast precursor, putative, expressed seq=cds; coord=2:128936549..128937471:1; parent_gene=GRMZM2G001524'

'very weakly similar to (89.7) NIA7_HORVU Nitrate reductase [NAD(P)H] (EC 1.7.1.2) - Hordeum vulgare (Barley)very weakly similar to (88.6) loc_os02g53130 12002.m10342 protein nitrate reductase, putative, expressed seq=cds; coord=2:131344453..131348267:-1; parent_gene=GRMZM2G424659'

'weakly similar to (190) AT5G03240 | Symbols: UBQ3 | UBQ3 (POLYUBIQUITIN 3); protein binding | chr5:771976-772896 REVERSEweakly similar to (190) loc_os06g46770 12006.m091761 protein polyubiquitin containing 7 ubiquitin monomers, putative, expressed seq=cds; coord=2:142864156..142865649:-1; parent_gene=GRMZM2G168829'

'weakly similar to (189) AT5G08565 | Symbols: | positive transcription elongation factor/ zinc ion binding | chr5:2775964-2777154 FORWARDmoderately similar to (223) loc_os07g43060 12007.m08534 protein transcription elongation factor SPT4 homolog 1, putative, expressed seq=cds; coord=2:212361624..212366846:-1; parent_gene=GRMZM2G086805'

'moderately similar to (377) AT3G17440 | Symbols: NPSN13, ATNPSN13 | NPSN13 (NOVEL PLANT SNARE 13) | chr3:5970153-5972290 REVERSEmoderately similar to (464) loc_os07g44350 12007.m08656 protein novel plant SNARE 11, putative, expressed seq=cds; coord=2:213095980..213099205:-1; parent_gene=GRMZM2G102903'

'weakly similar to (123) AT1G30270 | Symbols: CIPK23, SnRK3.23, ATCIPK23, LKS1 | CIPK23 (CBL-INTERACTING PROTEIN KINASE 23); kinase/ protein binding / protein serine/threonine kinase | chr1:10655270-10658524 FORWARDweakly similar to (108) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)weakly similar to (134) loc_os07g05620 12007.m29069 protein CIPK-like protein 1, putative, expressed seq=cds; coord=3:28055973..28058891:-1; parent_gene=GRMZM2G012472' 'highly similar to (984) AT1G22870 | Symbols: | protein kinase family protein | chr1:8089501-8094173 FORWARDnearly identical (1259) loc_os01g42950 12001.m43091 protein ATP binding protein, putative, expressed seq=cds; coord=3:225446387..225454476:1; parent_gene=GRMZM2G061681'

'highly similar to (984) AT1G22870 | Symbols: | protein kinase family protein | chr1:8089501-8094173 FORWARDnearly identical (1259) loc_os01g42950 12001.m43091 protein ATP binding protein, putative, expressed seq=cds; coord=3:225446387..225454476:1; parent_gene=GRMZM2G061681'

'moderately similar to (376) AT5G27150 | Symbols: NHX1, ATNHX, AT-NHX1, ATNHX1 | NHX1 (NA

'moderately similar to (429) AT3G18830 | Symbols: ATPLT5 | ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann | chr3:6489000-6491209 REVERSEweakly similar to (134) STC_RICCO Sugar carrier protein C - Ricinus communis (Castor bean)highly similar to (642) loc_os11g41850 12011.m08023 protein sugar transporter family protein, putative, expressed seq=cds; coord=4:4601041..4602806:1; parent_gene=GRMZM2G157057'

'moderately similar to (429) AT3G18830 | Symbols: ATPLT5 | ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann | chr3:6489000-6491209 REVERSEweakly similar to (134) STC_RICCO Sugar carrier protein C - Ricinus communis (Castor bean)highly similar to (642) loc_os11g41850 12011.m08023 protein sugar transporter family protein, putative, expressed seq=cds; coord=4:4601041..4602806:1; parent_gene=GRMZM2G157057'

'highly similar to (676) AT3G03810 | Symbols: EDA30 | EDA30 (embryo sac development arrest 30) | chr3:972190-975901 REVERSEnearly identical (1014) loc_os05g04190 12005.m083565 protein auxin-independent growth promoter protein, putative, expressed seq=cds; coord=4:169505982..169512726:-1; parent_gene=GRMZM2G025671'

'highly similar to (503) AT2G03220 | Symbols: FT1, ATFUT1, ATFT1, MUR2 | FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups | chr2:970401-972353 REVERSEhighly similar to (513) FUT1_PEA Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1) - Pisum sativum (Garden pea)highly similar to (697) loc_os02g52630 12002.m10293 protein fucosyltransferase 7, putative, expressed seq=cds; coord=4:178596383..178598254:-1; parent_gene=GRMZM2G471594'

'highly similar to (503) AT2G03220 | Symbols: FT1, ATFUT1, ATFT1, MUR2 | FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups | chr2:970401-972353 REVERSEhighly similar to (513) FUT1_PEA Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1) - Pisum sativum (Garden pea)highly similar to (697) loc_os02g52630 12002.m10293 protein fucosyltransferase 7, putative, expressed seq=cds; coord=4:178596383..178598254:-1; parent_gene=GRMZM2G471594'

'moderately similar to (294) AT4G39870 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TLDc (InterPro:IPR006571); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G05590.2); Has 2018 Blast hits to 1865 proteins in 220 species: Archae - 0; Bacteria - 39; Metazoa - 1002; Fungi - 279; Plants - 129; Viruses - 34; Other Eukaryotes - 535 (source: NCBI BLink). | chr4:18502234-18504275 FORWARDhighly similar to (525) loc_os02g51770 12002.m33456 protein TLD family protein, expressed seq=cds; coord=4:180630485..180634437:-1; parent_gene=GRMZM2G101518'

'weakly similar to (158) AT1G22050 | Symbols: MUB6 | MUB6 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 6 PRECURSOR) | chr1:7771897-7772843 FORWARDmoderately similar to (230) MUB3_ORYSA Membrane-anchored ubiquitin-fold protein 3 precursor (Membrane-anchored ub-fold protein 3) (OsMUB3) - Oryza sativa (Rice)moderately similar to (230) loc_os02g51500 12002.m34032 protein NTGP5, putative, expressed seq=cds; coord=4:181420387..181424633:1; parent_gene=GRMZM2G025470'

'moderately similar to (236) AT4G22580 | Symbols: | exostosin family protein | chr4:11889382-11890689 REVERSEvery weakly similar to (99.8) KATAM_ORYSA Xyloglucan galactosyltransferase KATAMARI1 homolog (EC 2.4.1.-) - Oryza sativa (Rice)moderately similar to (339) loc_os10g40559 12010.m06823 protein xyloglucan galactosyltransferase KATAMARI 1, putative, expressed seq=cds; coord=4:183063050..183066593:1; parent_gene=GRMZM2G021401'

'highly similar to (539) AT2G45260 | Symbols: | unknown protein | chr2:18664661-18665938 REVERSEhighly similar to (735) loc_os10g23220 12010.m21871 protein expressed protein seq=cds; coord=4:183405528..183408894:-1; parent_gene=GRMZM2G111720'

'weakly similar to (143) AT5G37055 | Symbols: ATSWC6, SEF | SEF (SERRATED LEAVES AND EARLY FLOWERING) | chr5:14641634-14642387 REVERSEweakly similar to (199) loc_os03g25260 12003.m07868 protein zinc finger HIT domain-containing protein 1, putative, expressed seq=cds; coord=4:183736182..183738617:-1; parent_gene=GRMZM2G089876'

'moderately similar to (247) AT5G53210 | Symbols: SPCH | SPCH (SPEECHLESS); DNA binding / transcription factor | chr5:21586606-21588941 REVERSEmoderately similar to (361) loc_os02g15760 12002.m06819 protein DNA binding protein, putative seq=cds; coord=4:224623490..224627055:1; parent_gene=GRMZM2G085751'

'highly similar to (754) AT4G18810 | Symbols: | binding / catalytic/ transcription repressor | chr4:10322622-10325735 REVERSEhighly similar to (941) loc_os02g13970 12002.m77732 protein UOS1, putative, expressed seq=cds; coord=4:228626363..228632489:1; parent_gene=GRMZM2G019358'

'moderately similar to (289) AT5G40160 | Symbols: EMB506 | EMB506 (embryo defective 506); protein binding | chr5:16062726-16064301 REVERSEmoderately similar to (369) loc_os06g13000 12006.m06016 protein ankyrin repeat protein, chloroplast precursor, putative, expressed seq=cds; coord=4:238951331..238953642:1; parent_gene=GRMZM2G019838'

'moderately similar to (444) AT3G29185 | Symbols: | unknown protein | chr3:11155092-11157207 REVERSEhighly similar to (536) loc_os03g55164 12003.m101731 protein OsWRKY4 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=5:6575335..6578215:-1; parent_gene=GRMZM2G089696' 'highly similar to (691) AT3G02130 | Symbols: RPK2, TOAD2 | RPK2 (RECEPTOR-LIKE PROTEIN KINASE 2); ATP binding / kinase/ protein serine/threonine kinase | chr3:381224-384181 FORWARDmoderately similar to (292) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (961) loc_os03g54900 12003.m35418 protein phytosulfokine receptor precursor, putative, expressed seq=cds; coord=5:6858359..6862072:1; parent_gene=GRMZM2G072658'

'moderately similar to (323) AT3G22845 | Symbols: | emp24/gp25L/p24 protein-related | chr3:8087373-8088550 FORWARDmoderately similar to (377) loc_os03g53310 12003.m10303 protein suppressor/enhancer of lin-12 protein 9 precursor, putative, expressed seq=cds; coord=5:7598126..7603275:1; parent_gene=GRMZM2G147046'

'weakly similar to (192) AT4G07990 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr4:4825650-4829608 REVERSEmoderately similar to (339) loc_os03g51830 12003.m10163 protein heat shock protein binding protein, putative, expressed seq=cds; coord=5:9187793..9192085:-1; parent_gene=GRMZM2G129700'

'nearly identical (1406) AT1G09570 | Symbols: PHYA, FHY2, FRE1, HY8 | PHYA (PHYTOCHROME A); G-protein coupled photoreceptor/ protein histidine kinase/ red or far-red light photoreceptor/ signal transducer | chr1:3095498-3098892 REVERSEnearly identical (2126) PHYA1_MAIZE Phytochrome A - Zea mays (Maize)nearly identical (1915) loc_os03g51030 12003.m101474 protein phytochrome A, putative, expressed seq=cds; coord=5:10101047..10106758:-1; parent_gene=GRMZM2G181028'

'nearly identical (1406) AT1G09570 | Symbols: PHYA, FHY2, FRE1, HY8 | PHYA (PHYTOCHROME A); G-protein coupled photoreceptor/ protein histidine kinase/ red or far-red light photoreceptor/ signal transducer | chr1:3095498-3098892 REVERSEnearly identical (2126) PHYA1_MAIZE Phytochrome A - Zea mays (Maize)nearly identical (1915) loc_os03g51030 12003.m101474 protein phytochrome A, putative, expressed seq=cds; coord=5:10101047..10106758:-1; parent_gene=GRMZM2G181028'

'nearly identical (1406) AT1G09570 | Symbols: PHYA, FHY2, FRE1, HY8 | PHYA (PHYTOCHROME A); G-protein coupled photoreceptor/ protein histidine kinase/ red or far-red light photoreceptor/ signal transducer | chr1:3095498-3098892 REVERSEnearly identical (2126) PHYA1_MAIZE Phytochrome A - Zea mays (Maize)nearly identical (1915) loc_os03g51030 12003.m101474 protein phytochrome A, putative, expressed seq=cds; coord=5:10101047..10106758:-1; parent_gene=GRMZM2G181028'

'very weakly similar to (90.1) AT2G46270 | Symbols: GBF3 | GBF3 (G-BOX BINDING FACTOR 3); sequence-specific DNA binding / transcription factor | chr2:19000859-19002901 FORWARDvery weakly similar to (93.6) CPRF1_PETCR Common plant regulatory factor CPRF-1 - Petroselinum crispum (Parsley) (Petroselinum hortense)weakly similar to (168) loc_os05g49420 12005.m09012 protein G-box-binding factor 3, putative, expressed seq=cds; coord=6:165343365..165345512:1; parent_gene=GRMZM2G011932'

'weakly similar to (173) AT4G18060 | Symbols: | clathrin binding | chr4:10027668-10029662 REVERSEmoderately similar to (233) loc_os07g32460 12007.m07511 protein clathrin binding protein, putative, expressed seq=cds; coord=7:52837501..52840130:-1; parent_gene=GRMZM2G043758'

'very weakly similar to (89.0) AT3G03920 | Symbols: | Gar1 RNA-binding region family protein | chr3:1009123-1010379 REVERSEvery weakly similar to (97.8) loc_os11g37080 12011.m07556 protein h/ACA ribonucleoprotein complex subunit 1-like protein 1, putative, expressed seq=cds; coord=7:135694991..135698715:-1; parent_gene=GRMZM2G463359' 'very weakly similar to (85.5) AT2G16120 | Symbols: | mannitol transporter, putative | chr2:6996727-6998441 REVERSEweakly similar to (148) loc_os11g41840 12011.m08022 protein arabinose-proton symporter, putative seq=cds; coord=7:165314232..165315737:1; parent_gene=GRMZM2G377502'

'weakly similar to (162) AT5G19000 | Symbols: ATBPM1 | ATBPM1 (BTB-POZ and MATH domain 1); protein binding | chr5:6342563-6344641 FORWARDmoderately similar to (239) loc_os08g41240 12008.m08102 protein ATBPM1, putative seq=cds; coord=7:168107563..168108606:1; parent_gene=AC195147.3_FG001'

'weakly similar to (162) AT5G19000 | Symbols: ATBPM1 | ATBPM1 (BTB-POZ and MATH domain 1); protein binding | chr5:6342563-6344641 FORWARDmoderately similar to (239) loc_os08g41240 12008.m08102 protein ATBPM1, putative seq=cds; coord=7:168107563..168108606:1; parent_gene=AC195147.3_FG001'

'weakly similar to (162) AT5G19000 | Symbols: ATBPM1 | ATBPM1 (BTB-POZ and MATH domain 1); protein binding | chr5:6342563-6344641 FORWARDmoderately similar to (239) loc_os08g41240 12008.m08102 protein ATBPM1, putative seq=cds; coord=7:168107563..168108606:1; parent_gene=AC195147.3_FG001'

'highly similar to (724) AT4G24290 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: NSL1 (necrotic spotted lesions 1) (TAIR:AT1G28380.1); Has 150 Blast hits to 149 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 41; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink). | chr4:12594856-12597815 FORWARDhighly similar to (931) loc_os07g07194 12007.m66713 protein MAC/Perforin domain containing protein, expressed seq=cds; coord=8:157413485..157419964:-1; parent_gene=GRMZM2G435034'

'moderately similar to (439) AT3G48530 | Symbols: KING1 | KING1 (SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA 1) | chr3:17987559-17989592 FORWARDhighly similar to (671) loc_os01g69240 12001.m13024 protein AKIN gamma, putative, expressed seq=cds; coord=8:161621236..161623147:1; parent_gene=GRMZM2G003493'

'moderately similar to (265) AT3G57170 | Symbols: | N-acetylglucosaminyl transferase component family protein / Gpi1 family protein | chr3:21159620-21162259 REVERSEweakly similar to (187) loc_os05g22370 12005.m27768 protein N-acetylglucosaminyl transferase component, putative, expressed seq=cds; coord=8:161880772..161882765:1; parent_gene=GRMZM2G070898'

'moderately similar to (380) AT5G07280 | Symbols: EMS1, EXS | EMS1 (EXCESS MICROSPOROCYTES1); kinase/ transmembrane receptor protein kinase | chr5:2285088-2288666 FORWARDmoderately similar to (315) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (904) loc_os01g68870 12001.m43349 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed seq=cds; coord=8:162190503..162207903:-1; parent_gene=GRMZM2G107484'

'highly similar to (789) AT2G47940 | Symbols: DEGP2 | DEGP2; serine-type endopeptidase/ serine-type peptidase | chr2:19618372-19622164 REVERSEhighly similar to (980) loc_os05g05480 12005.m27701 protein protease Do-like 2, chloroplast precursor, putative, expressed seq=cds; coord=10:89988812..90000754:-1; parent_gene=GRMZM2G063592' 'weakly similar to (156) AT4G27780 | Symbols: ACBP2 | ACBP2 (ACYL-COA BINDING PROTEIN ACBP 2); acyl-CoA binding / lead ion binding | chr4:13847774-13849629 FORWARDmoderately similar to (248) loc_os04g58550 12004.m10737 protein acyl-CoA-binding domain-containing protein 6, putative, expressed seq=cds; coord=10:148514945..148517583:-1; parent_gene=GRMZM2G173636'

'weakly similar to (156) AT4G27780 | Symbols: ACBP2 | ACBP2 (ACYL-COA BINDING PROTEIN ACBP 2); acyl-CoA binding / lead ion binding | chr4:13847774-13849629 FORWARDmoderately similar to (248) loc_os04g58550 12004.m10737 protein acyl-CoA-binding domain-containing protein 6, putative, expressed seq=cds; coord=10:148514945..148517583:-1; parent_gene=GRMZM2G173636'

'weakly similar to (188) AT3G21750 | Symbols: UGT71B1 | UGT71B1 (UDP-GLUCOSYL TRANSFERASE 71B1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups | chr3:7664565-7665986 FORWARDvery weakly similar to (85.1) ZOX_PHAVU Zeatin O-xylosyltransferase (EC 2.4.2.40) (Zeatin O-beta-D-xylosyltransferase) - Phaseolus vulgaris (Kidney bean) (French bean)moderately similar to (423) loc_os07g32020 12007.m07468 protein anthocyanidin 3-O-glucosyltransferase, putative, expressed seq=cds; coord=1:19489549..19492878:1; parent_gene=GRMZM2G039129'

'weakly similar to (188) AT3G21750 | Symbols: UGT71B1 | UGT71B1 (UDP-GLUCOSYL TRANSFERASE 71B1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups | chr3:7664565-7665986 FORWARDvery weakly similar to (85.1) ZOX_PHAVU Zeatin O-xylosyltransferase (EC 2.4.2.40) (Zeatin O-beta-D-xylosyltransferase) - Phaseolus vulgaris (Kidney bean) (French bean)moderately similar to (423) loc_os07g32020 12007.m07468 protein anthocyanidin 3-O-glucosyltransferase, putative, expressed seq=cds; coord=1:19489549..19492878:1; parent_gene=GRMZM2G039129'

'highly similar to (578) AT5G64220 | Symbols: | calmodulin-binding protein | chr5:25686434-25691903 FORWARDnearly identical (1259) loc_os03g09100 12003.m06416 protein calmodulin-binding transcription activator 2, putative, expressed seq=cds; coord=1:19789491..19793759:-1; parent_gene=GRMZM2G447551'

'highly similar to (578) AT5G64220 | Symbols: | calmodulin-binding protein | chr5:25686434-25691903 FORWARDnearly identical (1259) loc_os03g09100 12003.m06416 protein calmodulin-binding transcription activator 2, putative, expressed seq=cds; coord=1:19789491..19793759:-1; parent_gene=GRMZM2G447551'

'highly similar to (518) AT5G05580 | Symbols: FAD8 | FAD8 (FATTY ACID DESATURASE 8); omega-3 fatty acid desaturase | chr5:1664331-1666345 FORWARDhighly similar to (531) FAD3C_SOYBN Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-) - Glycine max (Soybean)highly similar to (570) loc_os03g18070 12003.m07232 protein omega-3 fatty acid desaturase, chloroplast precursor, putative, expressed seq=cds; coord=1:44800825..44803738:-1; parent_gene=GRMZM2G074401'

'highly similar to (601) AT2G47500 | Symbols: | ATP binding / microtubule motor | chr2:19493247-19497882 FORWARDvery weakly similar to (98.2) K125_TOBAC 125 kDa kinesin-related protein - Nicotiana tabacum (Common tobacco)highly similar to (807) loc_os03g18980 12003.m07316 protein kinesin-4, putative, expressed seq=cds; coord=1:47699083..47705236:-1; parent_gene=GRMZM2G122965' 'moderately similar to (229) AT1G56500 | Symbols: | haloacid dehalogenase-like hydrolase family protein | chr1:21159775-21167092 FORWARDmoderately similar to (349) loc_os03g19760 12003.m35188 protein NHL repeat protein, putative, expressed seq=cds; coord=1:50700350..50712129:1; parent_gene=AC208571.4_FG001'

'highly similar to (966) AT3G56370 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr3:20899403-20902390 REVERSEmoderately similar to (334) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1484) loc_os03g21730 12003.m07577 protein receptor-like protein kinase precursor, putative, expressed seq=cds; coord=1:56073143..56077145:1; parent_gene=GRMZM2G119850'

'moderately similar to (447) AT2G37650 | Symbols: | scarecrow-like transcription factor 9 (SCL9) | chr2:15792623-15794779 FORWARDmoderately similar to (207) CIGR2_ORYSA Chitin-inducible gibberellin-responsive protein 2 - Oryza sativa (Rice)highly similar to (708) loc_os12g38490 12012.m07635 protein chitin-inducible gibberellin-responsive protein 1, putative, expressed seq=cds; coord=1:155675315..155678789:1; parent_gene=GRMZM2G179325'

'weakly similar to (117) AT3G07390 | Symbols: AIR12 | AIR12; extracellular matrix structural constituent | chr3:2365452-2366273 FORWARDmoderately similar to (203) loc_os08g41290 12008.m08107 protein AIR12, putative, expressed seq=cds; coord=1:220523997..220524734:-1; parent_gene=AC217977.3_FG001'

'moderately similar to (409) loc_os10g37570 12010.m06544 protein F-box domain containing protein, expressed seq=cds; coord=1:222945692..222947391:-1; parent_gene=GRMZM2G067626'

'weakly similar to (187) AT4G14750 | Symbols: IQD19 | IQD19 (IQ-domain 19); calmodulin binding | chr4:8470449-8471903 FORWARDmoderately similar to (314) loc_os10g28420 12010.m05722 protein IQ calmodulin-binding motif family protein seq=cds; coord=1:240038938..240040880:1; parent_gene=GRMZM2G070673'

'weakly similar to (110) loc_os04g56690 12004.m10556 protein OsSAUR23 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=2:3587683..3588347:1; parent_gene=GRMZM2G365166'

'weakly similar to (110) loc_os04g56690 12004.m10556 protein OsSAUR23 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=2:3587683..3588347:1; parent_gene=GRMZM2G365166'

'highly similar to (504) AT5G23810 | Symbols: AAP7 | AAP7; amino acid transmembrane transporter | chr5:8028461-8030138 FORWARDhighly similar to (740) loc_os04g56470 12004.m101680 protein AAP7, putative, expressed seq=cds; coord=2:3935621..3938281:-1; parent_gene=GRMZM2G042933'

'moderately similar to (318) AT1G56120 | Symbols: | kinase | chr1:20987288-20993072 REVERSEmoderately similar to (214) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (646) loc_os04g56360 12004.m10526 protein protein kinase, putative seq=cds; coord=2:4050541..4053702:-1; parent_gene=GRMZM2G391741'

'moderately similar to (294) AT1G73110 | Symbols: | ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative | chr1:27494344-27496844 REVERSEmoderately similar to (202) RCA_MAIZE Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase) (RA) - Zea mays (Maize)moderately similar to (344) loc_os04g56320 12004.m10522 protein ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor, putative, expressed seq=cds; coord=2:4159971..4163217:1; parent_gene=GRMZM2G039345'

'moderately similar to (494) AT5G67200 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr5:26813893-26816555 REVERSEweakly similar to (149) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1002) loc_os04g55620 12004.m10453 protein receptor kinase, putative, expressed seq=cds; coord=2:5374131..5380129:1; parent_gene=GRMZM2G055844'

'highly similar to (873) AT5G53550 | Symbols: YSL3, ATYSL3 | YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter | chr5:21756081-21758776 FORWARDnearly identical (1098) loc_os04g45860 12004.m101436 protein transposon protein, putative, unclassified, expressed seq=cds; coord=2:21633846..21638619:-1; parent_gene=GRMZM2G051179'

'very weakly similar to (84.0) loc_os03g17540 12003.m101301 protein TBC domain containing protein, expressed seq=cds; coord=2:21912102..21916408:1; parent_gene=GRMZM2G132055'

'weakly similar to (140) AT5G66320 | Symbols: | zinc finger (GATA type) family protein | chr5:26496208-26497309 REVERSEmoderately similar to (204) loc_os04g45650 12004.m35556 protein expressed protein seq=cds; coord=2:22068797..22071156:-1; parent_gene=GRMZM2G404973'

'weakly similar to (140) AT5G66320 | Symbols: | zinc finger (GATA type) family protein | chr5:26496208-26497309 REVERSEmoderately similar to (204) loc_os04g45650 12004.m35556 protein expressed protein seq=cds; coord=2:22068797..22071156:-1; parent_gene=GRMZM2G404973'

'very weakly similar to (89.7) loc_os04g33030 12004.m08399 protein inhibitor of apoptosis-like protein, putative, expressed seq=cds; coord=2:60874838..60875855:-1; parent_gene=GRMZM2G068590'

'very weakly similar to (92.4) AT4G34160 | Symbols: CYCD3;1, CYCD3 | CYCD3;1 (CYCLIN D3;1); cyclin-dependent protein kinase regulator/ protein binding | chr4:16357903-16359304 FORWARDmoderately similar to (213) loc_os09g02360 12009.m03608 protein cyclin delta-3, putative, expressed seq=cds; coord=2:163317840..163320224:1; parent_gene=GRMZM2G161382'

'highly similar to (513) AT4G04320 | Symbols: | malonyl-CoA decarboxylase family protein | chr4:2113565-2116525 FORWARDhighly similar to (728) loc_os09g23070 12009.m05464 protein malonyl-CoA decarboxylase, mitochondrial precursor, putative, expressed seq=cds; coord=2:178716947..178725990:-1; parent_gene=GRMZM2G043501'

'weakly similar to (162) AT2G42280 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr2:17611891-17613163 REVERSEmoderately similar to (219) loc_os09g31300 12009.m22140 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=2:189701055..189703654:1; parent_gene=GRMZM2G417597' 'moderately similar to (379) AT3G21190 | Symbols: | unknown protein | chr3:7432579-7434543 REVERSEhighly similar to (593) loc_os09g32320 12009.m06320 protein expressed protein seq=cds; coord=2:191000059..191004274:-1; parent_gene=GRMZM2G150319'

'weakly similar to (172) AT2G25810 | Symbols: TIP4;1 | TIP4;1 (tonoplast intrinsic protein 4;1); water channel | chr2:11012658-11013906 FORWARDmoderately similar to (270) TIP43_ORYSA Probable aquaporin TIP4.3 (Tonoplast intrinsic protein 4.3) (OsTIP4.3) - Oryza sativa (Rice)moderately similar to (270) loc_os01g13120 12001.m07922 protein aquaporin TIP4.1, putative, expressed seq=cds; coord=3:1847906..1849027:-1; parent_gene=GRMZM2G093090'

'weakly similar to (172) AT2G25810 | Symbols: TIP4;1 | TIP4;1 (tonoplast intrinsic protein 4;1); water channel | chr2:11012658-11013906 FORWARDmoderately similar to (270) TIP43_ORYSA Probable aquaporin TIP4.3 (Tonoplast intrinsic protein 4.3) (OsTIP4.3) - Oryza sativa (Rice)moderately similar to (270) loc_os01g13120 12001.m07922 protein aquaporin TIP4.1, putative, expressed seq=cds; coord=3:1847906..1849027:-1; parent_gene=GRMZM2G093090'

'weakly similar to (172) AT2G25810 | Symbols: TIP4;1 | TIP4;1 (tonoplast intrinsic protein 4;1); water channel | chr2:11012658-11013906 FORWARDmoderately similar to (270) TIP43_ORYSA Probable aquaporin TIP4.3 (Tonoplast intrinsic protein 4.3) (OsTIP4.3) - Oryza sativa (Rice)moderately similar to (270) loc_os01g13120 12001.m07922 protein aquaporin TIP4.1, putative, expressed seq=cds; coord=3:1847906..1849027:-1; parent_gene=GRMZM2G093090'

'moderately similar to (452) AT3G15350 | Symbols: | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein | chr3:5167250-5168882 FORWARDhighly similar to (561) loc_os01g10440 12001.m07665 protein xylosyltransferase oxt, putative, expressed seq=cds; coord=3:4706836..4710494:1; parent_gene=GRMZM2G055313'

'nearly identical (1256) AT2G26910 | Symbols: PDR4, ATPDR4 | PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances | chr2:11481623-11487874 FORWARDnearly identical (1686) PDR6_ORYSA Pleiotropic drug resistance protein 6 - Oryza sativa (Rice)nearly identical (1060) loc_os02g11760 12002.m06425 protein PDR5-like ABC transporter, putative, expressed seq=cds; coord=3:10273100..10283228:1; parent_gene=GRMZM2G118243'

'moderately similar to (385) AT2G36800 | Symbols: DOGT1, UGT73C5 | DOGT1 (DON-GLUCOSYLTRANSFERASE 1); UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transf | chr2:15423493-15424980 REVERSEweakly similar to (190) CZOG_SORBI Putative cis-zeatin O-glucosyltransferase (EC 2.4.1.215) - Sorghum bicolor (Sorghum) (Sorghum vulgare)highly similar to (681) loc_os10g09990 12010.m04338 protein cytokinin-O-glucosyltransferase 3, putative, expressed seq=cds; coord=3:10843334..10845067:1; parent_gene=GRMZM2G338465'

'moderately similar to (228) AT2G25810 | Symbols: TIP4;1 | TIP4;1 (tonoplast intrinsic protein 4;1); water channel | chr2:11012658-11013906 FORWARDmoderately similar to (287) TIP42_ORYSA Probable aquaporin TIP4.2 (Tonoplast intrinsic protein 4.2) (OsTIP4.2) - Oryza sativa (Rice)moderately similar to (287) loc_os01g13130 12001.m07923 protein aquaporin TIP4.1, putative, expressed seq=cds; coord=3:13529209..13532077:1; parent_gene=GRMZM2G146627'

'moderately similar to (410) loc_os02g43750 12002.m09409 protein transcription initiation factor, putative, expressed seq=cds; coord=3:13846717..13865900:-1; parent_gene=GRMZM2G102664'

'moderately similar to (209) AT5G48930 | Symbols: HCT | HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase | chr5:19836654-19838092 REVERSEweakly similar to (182) HCBT1_DIACA Anthranilate N-benzoyltransferase protein 1 (EC 2.3.1.144) (Anthranilate N-hydroxycinnamoyl/benzoyltransferase 1) - Dianthus caryophyllus (Carnation) (Clove pink)moderately similar to (429) loc_os08g43040 12008.m26780 protein anthranilate N-benzoyltransferase protein 1, putative, expressed seq=cds; coord=3:17019972..17021399:1; parent_gene=AC215260.3_FG003'

'moderately similar to (451) AT2G27600 | Symbols: SKD1, VPS4 | SKD1 (SUPPRESSOR OF K

'nearly identical (1523) AT2G47000 | Symbols: MDR4, PGP4, ABCB4, ATPGP4 | ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase | chr2:19310008-19314750 REVERSEhighly similar to (892) MDR_ORYSA Putative multidrug resistance protein (P-glycoprotein) - Oryza sativa (Rice)nearly identical (2004) loc_os01g18670 12001.m08406 protein multidrug resistance protein 17, putative, expressed seq=cds; coord=3:50093119..50099618:-1; parent_gene=GRMZM2G119894'

'weakly similar to (116) AT5G18620 | Symbols: CHR17 | CHR17 (CHROMATIN REMODELING FACTOR17); ATP binding / DNA binding / DNA-dependent ATPase/ helicase/ hydrolase, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding / nucleosome binding | chr5:6196190-6202058 REVERSEweakly similar to (137) ISW2_ORYSA Probable chromatin remodelling complex ATPase chain (EC 3.6.1.-) (ISW2-like) (Sucrose nonfermenting protein 2 homolog) - Oryza sativa (Rice)weakly similar to (137) loc_os01g27040 12001.m09155 protein chromatin remodelling complex ATPase chain, putative, expressed seq=cds; coord=3:68357930..68359191:1; parent_gene=GRMZM2G015277'

'very weakly similar to (98.2) AT1G72610 | Symbols: GLP1, ATGER1, GER1 | GER1 (GERMIN-LIKE PROTEIN 1); oxalate oxidase | chr1:27339302-27339928 REVERSEvery weakly similar to (95.1) AB19A_PRUPE Auxin-binding protein ABP19a precursor - Prunus persica (Peach)weakly similar to (105) loc_os08g35760 12008.m07565 protein auxin-binding protein ABP20 precursor, putative, expressed seq=cds; coord=3:110255712..110257286:1; parent_gene=GRMZM2G343974'

'weakly similar to (180) AT2G47710 | Symbols: | universal stress protein (USP) family protein | chr2:19555045-19555956 REVERSEmoderately similar to (246) loc_os12g36630 12012.m07449 protein fiber protein Fb19, putative, expressed seq=cds; coord=3:130262812..130263752:1; parent_gene=AC209744.3_FG001'

'weakly similar to (169) AT2G44120 | Symbols: | 60S ribosomal protein L7 (RPL7C) | chr2:18249227-18250417 REVERSEweakly similar to (187) loc_os08g13690 12008.m05494 protein 60S ribosomal protein L7-1, putative, expressed seq=cds; coord=3:139217403..139225950:-1; parent_gene=GRMZM2G174769'

'weakly similar to (174) AT1G68200 | Symbols: | zinc finger (CCCH-type) family protein | chr1:25562118-25563948 FORWARDmoderately similar to (234) loc_os01g45730 12001.m10773 protein nucleic acid binding protein, putative seq=cds; coord=3:214751394..214753488:1; parent_gene=GRMZM2G157927' 'highly similar to (984) AT1G22870 | Symbols: | protein kinase family protein | chr1:8089501-8094173 FORWARDnearly identical (1259) loc_os01g42950 12001.m43091 protein ATP binding protein, putative, expressed seq=cds; coord=3:225446387..225454476:1; parent_gene=GRMZM2G061681'

'moderately similar to (392) AT5G12100 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:3911388-3913838 FORWARDmoderately similar to (270) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (718) loc_os08g31110 12008.m07109 protein fertility restorer, putative, expressed seq=cds; coord=4:75017798..75020292:1; parent_gene=GRMZM2G146518'

'moderately similar to (318) AT3G16180 | Symbols: | proton-dependent oligopeptide transport (POT) family protein | chr3:5481477-5484943 REVERSEmoderately similar to (495) loc_os11g23890 12011.m06314 protein peptide transporter PTR2, putative seq=cds; coord=4:86443074..86444800:1; parent_gene=AC184794.2_FG003'

'moderately similar to (226) AT1G21230 | Symbols: WAK5 | WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase | chr1:7429980-7432346 FORWARDweakly similar to (159) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)moderately similar to (443) loc_os10g09620 12010.m04304 protein OsWAK108 - OsWAK receptor-like protein kinase, expressed seq=cds; coord=4:87222023..87233713:1; parent_gene=GRMZM2G132591'

'moderately similar to (266) AT5G13170 | Symbols: SAG29 | SAG29 (SENESCENCE-ASSOCIATED PROTEIN 29) chr5:4181331-4183171 REVERSEmoderately similar to (387) loc_os02g30910 12002.m08234 protein MTN3, putative, expressed seq=cds; coord=4:96310957..96312854:1; parent_gene=GRMZM2G168365'

'moderately similar to (442) ATMG00220 | Symbols: COB | Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript. | chrM:60235-61416 FORWARDmoderately similar to (461) CYB_MAIZE Cytochrome b - Zea mays (Maize)moderately similar to (461) loc_osm1g00480 11706.m00041 protein Apocytochrome b seq=cds; coord=4:111680559..111685048:-1; parent_gene=GRMZM2G054687'

'highly similar to (577) AT5G03300 | Symbols: ADK2 | ADK2 (ADENOSINE KINASE 2); adenosine kinase/ copper ion binding / kinase | chr5:796573-798997 FORWARDmoderately similar to (474) ADK_PHYPA Adenosine kinase (EC 2.7.1.20) (AK) (Adenosine 5'-phosphotransferase) - Physcomitrella patens (Moss)highly similar to (646) loc_os02g41590 12002.m09195 protein adenosine kinase 2, putative, expressed seq=cds; coord=4:143082898..143087846:-1; parent_gene=GRMZM2G135132'

'weakly similar to (167) AT5G57360 | Symbols: ZTL, LKP1, ADO1, FKL2 | ZTL (ZEITLUPE); protein binding / ubiquitin-protein ligase | chr5:23241597-23244415 FORWARDweakly similar to (178) ADO1_ORYSA Adagio-like protein 1 - Oryza sativa (Rice)weakly similar to (178) loc_os06g47890 12006.m32164 protein adagio protein 1, putative, expressed seq=cds; coord=4:237488619..237489629:-1; parent_gene=GRMZM2G166147' 'very weakly similar to (99.0) AT4G16780 | Symbols: ATHB-2, HAT4, ATHB2 | ATHB-2 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 2); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription factor | chr4:9449291-9450604 FORWARDweakly similar to (129) loc_os02g05640 12002.m05912 protein homeobox-leucine zipper protein ATHB-4, putative seq=cds; coord=4:237502428..237504286:-1; parent_gene=GRMZM2G166041'

'weakly similar to (144) AT5G27700 | Symbols: | structural constituent of ribosome | chr5:9807541-9808048 REVERSEweakly similar to (164) RS21_MAIZE 40S ribosomal protein S21 - Zea mays (Maize)weakly similar to (145) loc_os03g46490 12003.m09669 protein 40S ribosomal protein S21, putative seq=cds; coord=5:1565057..1568105:-1; parent_gene=GRMZM2G125300'

'very weakly similar to (98.2) AT2G37590 | Symbols: ATDOF2.4, DOF2.4 | Dof-type zinc finger domain-containing protein | chr2:15769292-15770497 FORWARDweakly similar to (157) loc_os03g60630 12003.m10953 protein expressed protein seq=cds; coord=5:2343761..2345249:-1; parent_gene=GRMZM2G144188'

'very weakly similar to (98.2) AT2G37590 | Symbols: ATDOF2.4, DOF2.4 | Dof-type zinc finger domain-containing protein | chr2:15769292-15770497 FORWARDweakly similar to (157) loc_os03g60630 12003.m10953 protein expressed protein seq=cds; coord=5:2343761..2345249:-1; parent_gene=GRMZM2G144188'

'moderately similar to (375) AT3G22750 | Symbols: | protein kinase, putative | chr3:8037364-8039096 REVERSEhighly similar to (538) loc_os03g53410 12003.m10311 protein ATMRK1, putative, expressed seq=cds; coord=5:7587329..7589198:-1; parent_gene=GRMZM2G014618'

'highly similar to (840) AT5G43670 | Symbols: | transport protein, putative | chr5:17539025-17541733 REVERSEnearly identical (1272) loc_os03g53140 12003.m35407 protein protein transport protein Sec23A, putative, expressed seq=cds; coord=5:7775738..7779579:-1; parent_gene=GRMZM2G077295'

'highly similar to (747) AT3G12110 | Symbols: ACT11 | ACT11 (actin-11); structural constituent of cytoskeleton | chr3:3858116-3859609 FORWARDhighly similar to (758) ACT1_ORYSA Actin-1 - Oryza sativa (Rice)highly similar to (758) loc_os03g50890 12003.m10074 protein actin-1, putative, expressed seq=cds; coord=5:10223674..10226373:-1; parent_gene=GRMZM2G152328'

'moderately similar to (430) AT4G12790 | Symbols: | ATP-binding family protein | chr4:7517280-7518892 REVERSEhighly similar to (506) loc_os03g50620 12003.m101469 protein ATP binding protein, putative, expressed seq=cds; coord=5:10583966..10588381:1; parent_gene=GRMZM2G131324'

'moderately similar to (269) loc_os03g50110 12003.m10006 protein expressed protein seq=cds; coord=5:11590629..11592307:1; parent_gene=GRMZM2G162405'

'weakly similar to (119) AT4G33630 | Symbols: EX1 | EX1 (EXECUTER1) | chr4:16155560-16159094 FORWARDweakly similar to (152) loc_os01g01790 12001.m42829 protein expressed protein seq=cds; coord=5:15142195..15154928:-1; parent_gene=GRMZM2G420732' 'moderately similar to (223) AT5G05620 | Symbols: TUBG2, ATGCP2, GCP2 | GCP2 (GAMMA-TUBULIN COMPLEX PROTEIN 2); GTP binding / GTPase/ structural molecule | chr5:1679340-1681719 FORWARDmoderately similar to (229) TBG2_MAIZE Tubulin gamma-2 chain (Gamma-2 tubulin) - Zea mays (Maize)moderately similar to (225) loc_os05g06450 12005.m27549 protein tubulin gamma-2 chain, putative, expressed seq=cds; coord=5:15437689..15443735:-1; parent_gene=GRMZM2G078612'

'highly similar to (617) AT5G54090 | Symbols: | DNA mismatch repair MutS family protein | chr5:21948283-21952550 REVERSEhighly similar to (874) loc_os10g36530 12010.m06463 protein mutS domain V family protein, expressed seq=cds; coord=5:23337364..23367111:-1; parent_gene=GRMZM2G060349'

'weakly similar to (187) AT3G50360 | Symbols: ATCEN2, CEN1 | ATCEN2 (CENTRIN2); calcium ion binding | chr3:18674421-18675502 FORWARDweakly similar to (158) CATR_CHLRE Caltractin (Centrin) (20 kDa calcium-binding protein) - Chlamydomonas reinhardtiimoderately similar to (242) loc_os10g25010 12010.m05452 protein caltractin, putative, expressed seq=cds; coord=5:37374885..37376902:-1; parent_gene=GRMZM2G096228'

'weakly similar to (187) AT3G50360 | Symbols: ATCEN2, CEN1 | ATCEN2 (CENTRIN2); calcium ion binding | chr3:18674421-18675502 FORWARDweakly similar to (158) CATR_CHLRE Caltractin (Centrin) (20 kDa calcium-binding protein) - Chlamydomonas reinhardtiimoderately similar to (242) loc_os10g25010 12010.m05452 protein caltractin, putative, expressed seq=cds; coord=5:37374885..37376902:-1; parent_gene=GRMZM2G096228'

'weakly similar to (153) loc_os10g08570 12010.m04205 protein RNA recognition motif family protein, expressed seq=cds; coord=5:37931456..37936949:-1; parent_gene=AC217556.3_FG003'

'nearly identical (3229) AT1G36160 | Symbols: ACC1, AT-ACC1, EMB22, GK, PAS3 | ACC1 (ACETYL-COENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase | chr1:13534196-13543773 FORWARDmoderately similar to (228) MCCA_SOYBN Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial precursor (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 1) (MCCase subunit alpha) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit alpha) - Glycine max (Soybean)nearly identical (3953) loc_os10g21910 12010.m65459 protein acetyl-coenzyme A carboxylase ACC1A, putative, expressed seq=cds; coord=5:38567212..38578529:-1; parent_gene=GRMZM2G377341'

'moderately similar to (442) AT2G47420 | Symbols: | dimethyladenosine transferase, putative | chr2:19457574-19458777 FORWARDhighly similar to (605) loc_os10g10434 12010.m04378 protein dimethyladenosine transferase, putative, expressed seq=cds; coord=5:88606055..88608547:1; parent_gene=GRMZM2G136599'

'moderately similar to (232) AT2G47210 | Symbols: | myb family transcription factor | chr2:19379039-19382204 FORWARDmoderately similar to (291) loc_os05g46330 12005.m08758 protein DNA methyltransferase 1-associated protein 1, putative, expressed seq=cds; coord=5:114740551..114771064:-1; parent_gene=GRMZM2G159155'

'moderately similar to (229) AT1G65480 | Symbols: FT | FT (FLOWERING LOCUS T); phosphatidylethanolamine binding / protein binding | chr1:24331510-24333689 FORWARDweakly similar to (184) CET1_TOBAC CEN-like protein 1 - Nicotiana tabacum (Common tobacco)moderately similar to (315) loc_os02g13830 12002.m06629 protein OsFTL13 - Rice FT-Like13 homogous to Arabidopsis Flowering Locus T gene seq=cds; coord=5:149997592..149998908:-1; parent_gene=GRMZM2G108016' 'nearly identical (1519) AT1G08260 | Symbols: EMB529 | TIL1 (TILTED 1); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding / zinc ion binding | chr1:2590944-2606892 FORWARDnearly identical (1981) loc_os02g30800 12002.m08223 protein DNA polymerase family B, exonuclease domain containing protein, expressed seq=cds; coord=5:164340015..164361538:1; parent_gene=GRMZM2G011631'

'moderately similar to (201) AT2G33550 | Symbols: | gt-2-related | chr2:14210180-14211487 REVERSEmoderately similar to (280) loc_os02g31160 12002.m08259 protein conserved hypothetical protein seq=cds; coord=5:165851119..165855227:-1; parent_gene=GRMZM2G084684'

'moderately similar to (299) AT5G03700 | Symbols: | PAN domain-containing protein | chr5:965874-967322 REVERSEvery weakly similar to (86.3) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (647) loc_os02g32620 12002.m08355 protein D-mannose binding lectin family protein, expressed seq=cds; coord=5:168428378..168430248:1; parent_gene=GRMZM2G038669'

'weakly similar to (114) AT3G56240 | Symbols: CCH | CCH (COPPER CHAPERONE); copper chaperone | chr3:20863460-20864402 REVERSEweakly similar to (119) loc_os02g32814 12002.m08373 protein heavy metal-associated domain containing protein, expressed seq=cds; coord=5:168671806..168673715:1; parent_gene=GRMZM2G113332'

'weakly similar to (114) AT3G56240 | Symbols: CCH | CCH (COPPER CHAPERONE); copper chaperone | chr3:20863460-20864402 REVERSEweakly similar to (119) loc_os02g32814 12002.m08373 protein heavy metal-associated domain containing protein, expressed seq=cds; coord=5:168671806..168673715:1; parent_gene=GRMZM2G113332'

'moderately similar to (224) AT4G25590 | Symbols: ADF7 | ADF7 (actin depolymerizing factor 7); actin binding | chr4:13059137-13060050 REVERSEmoderately similar to (239) ADF_LILLO Actin-depolymerizing factor (ADF) - Lilium longiflorum (Trumpet lily)moderately similar to (263) loc_os02g44470 12002.m09487 protein actin-depolymerizing factor, putative, expressed seq=cds; coord=5:193084737..193087687:-1; parent_gene=GRMZM2G015127'

'moderately similar to (231) AT5G14430 | Symbols: | dehydration-responsive protein-related | chr5:4653092-4655741 FORWARDmoderately similar to (304) loc_os06g47294 12006.m91847 protein ankyrin like protein, putative, expressed seq=cds; coord=5:200912768..200917534:-1; parent_gene=GRMZM2G415062'

'highly similar to (598) AT3G27820 | Symbols: ATMDAR4, MDAR4 | MDAR4 (MONODEHYDROASCORBATE REDUCTASE 4); monodehydroascorbate reductase (NADH) | chr3:10315249-10317881 FORWARDmoderately similar to (436) MDARS_CUCSA Monodehydroascorbate reductase, seedling isozyme (EC 1.6.5.4) (MDAR seedling) (Ascorbate free radical reductase seedling) (AFR reductase seedling) - Cucumis sativus (Cucumber)highly similar to (760) loc_os02g47800 12002.m09814 protein monodehydroascorbate reductase, cytoplasmic isoform 2, putative, expressed seq=cds; coord=5:201264863..201269869:-1; parent_gene=GRMZM2G320307'

'highly similar to (993) AT4G16660 | Symbols: | heat shock protein 70, putative / HSP70, putative | chr4:9377225-9381232 FORWARDmoderately similar to (216) BIP4_TOBAC Luminal-binding protein 4 precursor (BiP 4) (78 kDa glucose-regulated protein homolog 4) (GRP 78-4) - Nicotiana tabacum (Common tobacco)nearly identical (1311) loc_os02g48110 12002.m09845 protein oxygen-regulated protein precursor, putative, expressed seq=cds; coord=5:202050924..202059781:1; parent_gene=GRMZM2G020040' 'weakly similar to (157) AT2G46620 | Symbols: | AAA-type ATPase family protein | chr2:19139071-19140546 REVERSEmoderately similar to (280) loc_os03g02330 12003.m05775 protein ATP binding protein, putative, expressed seq=cds; coord=5:210728409..210730929:-1; parent_gene=GRMZM2G403454'

'very weakly similar to (100) AT4G31580 | Symbols: SRZ-22, SRZ22, RSZP22 | SRZ-22; protein binding | chr4:15306983-15308064 FORWARDweakly similar to (120) loc_os02g54770 12002.m33468 protein splicing factor, arginine/serine-rich 7, putative, expressed seq=cds; coord=5:213034925..213038562:-1; parent_gene=GRMZM2G080930'

'moderately similar to (348) AT2G25620 | Symbols: | protein phosphatase 2C, putative / PP2C, putative | chr2:10903154-10904978 REVERSEhighly similar to (585) loc_os02g55560 12002.m100396 protein DNA-binding protein phosphatase 2C, putative, expressed seq=cds; coord=5:214092148..214098979:1; parent_gene=GRMZM2G180430'

'moderately similar to (250) AT1G48110 | Symbols: ECT7 | ECT7 (evolutionarily conserved C-terminal region 7) | chr1:17770339-17772806 REVERSEhighly similar to (732) loc_os01g22630 12001.m42647 protein YT521-B-like family protein, expressed seq=cds; coord=6:1281657..1287910:1; parent_gene=GRMZM2G098174'

'moderately similar to (377) AT1G71980 | Symbols: | protease-associated zinc finger (C3HC4-type RING finger) family protein | chr1:27098250-27099881 FORWARDhighly similar to (561) loc_os03g07130 12003.m101101 protein RING finger protein 13, putative, expressed seq=cds; coord=6:1334626..1338778:1; parent_gene=GRMZM2G423956'

'weakly similar to (171) AT2G34730 | Symbols: | myosin heavy chain-related | chr2:14654611-14657443 FORWARDhighly similar to (645) loc_os09g04810 12009.m50204 protein myosin heavy chain, putative, expressed seq=cds; coord=6:9190508..9194532:-1; parent_gene=GRMZM2G066400'

'moderately similar to (228) loc_os09g01140 12009.m60283 protein expressed protein seq=cds; coord=6:19962512..19966575:-1; parent_gene=GRMZM2G392516'

'highly similar to (555) AT5G48730 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:19763152-19765136 FORWARDweakly similar to (127) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (807) loc_os06g07550 12006.m05478 protein PPR2, putative, expressed seq=cds; coord=6:122582429..122585001:1; parent_gene=GRMZM2G071162'

'weakly similar to (161) AT3G55280 | Symbols: RPL23AB | RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome | chr3:20500667-20501519 FORWARDweakly similar to (167) RL23A_TOBAC 60S ribosomal protein L23a (L25) - Nicotiana tabacum (Common tobacco)weakly similar to (180) loc_os04g42270 12004.m35367 protein 60S ribosomal protein L23a, putative, expressed seq=cds; coord=6:123201350..123203341:1; parent_gene=GRMZM2G166659'

'moderately similar to (263) AT1G14290 | Symbols: SBH2 | SBH2 (SPHINGOID BASE HYDROXYLASE 2); catalytic/ sphingosine hydroxylase | chr1:4880307-4881784 REVERSEmoderately similar to (300) loc_os06g22490 12006.m06903 protein protein SUR2, putative seq=cds; coord=6:157166978..157168162:-1; parent_gene=GRMZM2G163008' 'highly similar to (653) AT1G48900 | Symbols: | signal recognition particle 54 kDa protein 3 / SRP54 (SRP-54C) | chr1:18085031-18087743 REVERSEhighly similar to (698) SR542_HORVU Signal recognition particle 54 kDa protein 2 (SRP54) - Hordeum vulgare (Barley)highly similar to (696) loc_os01g56600 12001.m11817 protein signal recognition particle 54 kDa protein 2, putative, expressed seq=cds; coord=6:157823781..157828193:-1; parent_gene=GRMZM2G060324'

'weakly similar to (143) AT5G57625 | Symbols: | allergen V5/Tpx-1-related family protein | chr5:23337865-23338577 FORWARDweakly similar to (177) PR13_HORVU Pathogenesis-related protein PRB1-3 precursor (PR-1B) (HV-8) - Hordeum vulgare (Barley)weakly similar to (194) loc_os07g03710 12007.m04841 protein pathogenesis-related protein PRB1-3 precursor, putative, expressed seq=cds; coord=7:3483732..3484794:1; parent_gene=GRMZM2G465226'

'moderately similar to (361) AT2G47170 | Symbols: ARF1A1C | ARF1A1C; GTP binding / phospholipase activator/ protein binding | chr2:19367264-19368518 FORWARDmoderately similar to (355) ARF_VIGUN ADP-ribosylation factor - Vigna unguiculata (Cowpea)moderately similar to (365) loc_os07g12200 12007.m05673 protein ADP-ribosylation factor 1, putative, expressed seq=cds; coord=7:20165377..20168407:1; parent_gene=GRMZM2G105996'

'weakly similar to (150) AT5G28050 | Symbols: | cytidine/deoxycytidylate deaminase family protein | chr5:10044209-10045484 REVERSEweakly similar to (161) loc_os07g14150 12007.m079579 protein cytidine/deoxycytidylate deaminase family protein, putative, expressed seq=cds; coord=7:24368445..24370041:1; parent_gene=GRMZM2G173063'

'weakly similar to (160) AT4G34960 | Symbols: | peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative | chr4:16648865-16650646 FORWARDweakly similar to (102) CYPH_MAIZE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) - Zea mays (Maize)weakly similar to (175) loc_os09g36670 12009.m06616 protein peptidyl-prolyl cis-trans isomerase CYP19-4 precursor, putative, expressed seq=cds; coord=7:30423336..30427964:1; parent_gene=GRMZM2G092072'

'moderately similar to (250) AT1G05700 | Symbols: | leucine-rich repeat protein kinase, putative | chr1:1709796-1713245 FORWARDweakly similar to (125) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)moderately similar to (439) loc_os09g19140 12009.m05122 protein senescence-induced receptor-like serine/threonine-protein kinase precursor, putative seq=cds; coord=7:95446340..95451284:-1; parent_gene=GRMZM2G354615'

'moderately similar to (336) AT2G20890 | Symbols: PSB29, THF1 | PSB29 | chr2:8987783-8989185 FORWARDmoderately similar to (417) THF1_ORYSA Protein THYLAKOID FORMATION1, chloroplast precursor Oryza sativa (Rice)moderately similar to (417) loc_os07g37250 12007.m07975 protein chloroplast-localized Ptr ToxA-binding protein1, putative, expressed seq=cds; coord=7:157278232..157282868:-1; parent_gene=GRMZM2G033493'

'moderately similar to (336) AT2G20890 | Symbols: PSB29, THF1 | PSB29 | chr2:8987783-8989185 FORWARDmoderately similar to (417) THF1_ORYSA Protein THYLAKOID FORMATION1, chloroplast precursor Oryza sativa (Rice)moderately similar to (417) loc_os07g37250 12007.m07975 protein chloroplast-localized Ptr ToxA-binding protein1, putative, expressed seq=cds; coord=7:157278232..157282868:-1; parent_gene=GRMZM2G033493'

'moderately similar to (206) AT4G14540 | Symbols: NF-YB3 | NF-YB3 (NUCLEAR FACTOR Y, SUBUNIT B3); transcription factor | chr4:8344663-8345148 FORWARDweakly similar to (185) NFYB_MAIZE Nuclear transcription factor Y subunit B (NF-YB) (CAAT-box DNA-binding protein subunit B) - Zea mays (Maize)moderately similar to (226) loc_os03g29970 12003.m08258 protein nuclear transcription factor Y subunit B-3, putative, expressed seq=cds; coord=7:164694042..164695458:-1; parent_gene=GRMZM2G384528'

'nearly identical (1023) AT3G02050 | Symbols: KUP3, ATKUP3, ATKT4 | KUP3 (K

'highly similar to (580) AT5G58380 | Symbols: CIPK10, PKS2, SIP1, SNRK3.8 | SIP1 (SOS3-INTERACTING PROTEIN 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr5:23597092-23598531 REVERSEmoderately similar to (454) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)highly similar to (744) loc_os07g48100 12007.m09025 protein CBL-interacting serine/threonine-protein kinase 15, putative, expressed seq=cds; coord=7:172925400..172928378:-1; parent_gene=GRMZM2G166658'

'moderately similar to (308) AT1G55545 | Symbols: | unknown protein | chr1:20738987-20743049 REVERSEmoderately similar to (387) loc_os07g48602 12007.m66702 protein EMB1011, putative, expressed seq=cds; coord=7:173827304..173838463:-1; parent_gene=AC155434.2_FG004'

'moderately similar to (308) AT1G55545 | Symbols: | unknown protein | chr1:20738987-20743049 REVERSEmoderately similar to (387) loc_os07g48602 12007.m66702 protein EMB1011, putative, expressed seq=cds; coord=7:173827304..173838463:-1; parent_gene=AC155434.2_FG004'

'moderately similar to (311) AT3G20770 | Symbols: EIN3 | EIN3 (ETHYLENE-INSENSITIVE3); transcription factor chr3:7260702-7262588 REVERSEmoderately similar to (433) loc_os07g48630 12007.m29024 protein ETHYLENE-INSENSITIVE3-like 1 protein, putative, expressed seq=cds; coord=7:173951359..173953387:-1; parent_gene=GRMZM2G151811'

'moderately similar to (447) AT3G14067 | Symbols: | subtilase family protein | chr3:4658421-4660754 REVERSEhighly similar to (798) loc_os07g48650 12007.m09076 protein xylem serine proteinase 1 precursor, putative, expressed seq=cds; coord=7:174029436..174031718:1; parent_gene=GRMZM2G059165'

'weakly similar to (187) AT2G17730 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:7704142-7705312 FORWARDmoderately similar to (202) loc_os06g50370 12006.m09561 protein RING-H2 finger protein ATL2B, putative, expressed seq=cds; coord=7:175204235..175205552:1; parent_gene=GRMZM2G440866'

'very weakly similar to (90.1) AT2G32300 | Symbols: UCC1 | UCC1 (UCLACYANIN 1); copper ion binding / electron carrier | chr2:13722510-13723464 FORWARDvery weakly similar to (89.7) BCP_PEA Blue copper protein precursor - Pisum sativum (Garden pea)weakly similar to (147) loc_os09g36940 12009.m06643 protein blue copper binding protein, putative, expressed seq=cds; coord=7:175397827..175398686:1; parent_gene=GRMZM2G086628'

'moderately similar to (458) AT5G66120 | Symbols: | 3-dehydroquinate synthase, putative | chr5:26431516-26433649 REVERSEhighly similar to (510) loc_os09g36800 12009.m06629 protein 3-dehydroquinate synthase, putative, expressed seq=cds; coord=7:175831402..175835185:1; parent_gene=GRMZM2G051129' 'moderately similar to (311) AT3G16565 | Symbols: | ATP binding / alanine-tRNA ligase/ ligase, forming aminoacyl-tRNA and related compounds / nucleic acid binding / nucleotide binding | chr3:5640531-5642675 REVERSEmoderately similar to (409) loc_os01g03030 12001.m06942 protein alanyl-tRNA synthetase, putative, expressed seq=cds; coord=8:10082012..10085602:-1; parent_gene=GRMZM2G140754'

'weakly similar to (196) loc_os01g03170 12001.m06956 protein seven in absentia protein family protein, expressed seq=cds; coord=8:10855642..10857439:1; parent_gene=GRMZM2G049661'

'moderately similar to (449) AT1G18390 | Symbols: | ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr1:6327463-6329935 FORWARDmoderately similar to (222) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (698) loc_os01g04409 12001.m07075 protein OsWAK1 - OsWAK receptor-like cytoplasmic kinase (OsWAK-RLCK), expressed seq=cds; coord=8:13203175..13210491:1; parent_gene=GRMZM2G171807'

'weakly similar to (125) AT2G37150 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:15603748-15605988 REVERSEmoderately similar to (425) loc_os01g06590 12001.m42872 protein protein containing C-terminal RING-finger, putative, expressed seq=cds; coord=8:15468054..15475632:-1; parent_gene=GRMZM2G305901'

'weakly similar to (147) AT5G14540 | Symbols: | proline-rich family protein | chr5:4687333-4689624 REVERSEhighly similar to (557) loc_os01g07520 12001.m07378 protein proline-rich protein, putative, expressed seq=cds; coord=8:16994084..16999444:-1; parent_gene=GRMZM2G025215'

'nearly identical (1420) AT2G06990 | Symbols: HEN2 | HEN2 (hua enhancer 2); ATP-dependent helicase/ RNA helicase | chr2:2895135-2900909 FORWARDnearly identical (1658) loc_os11g07500 12011.m079953 protein helicase C6F12.16c, putative, expressed seq=cds; coord=8:18967013..18976088:1; parent_gene=GRMZM2G047949'

'moderately similar to (345) AT2G27360 | Symbols: | lipase, putative | chr2:11706233-11707905 FORWARDweakly similar to (184) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)highly similar to (678) loc_os01g42730 12001.m10537 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=8:142977440..142982997:1; parent_gene=GRMZM2G117754'

'moderately similar to (265) AT3G57170 | Symbols: | N-acetylglucosaminyl transferase component family protein / Gpi1 family protein | chr3:21159620-21162259 REVERSEweakly similar to (187) loc_os05g22370 12005.m27768 protein N-acetylglucosaminyl transferase component, putative, expressed seq=cds; coord=8:161880772..161882765:1; parent_gene=GRMZM2G070898'

'moderately similar to (214) AT3G25220 | Symbols: FKBP15-1 | FKBP15-1; FK506 binding / peptidyl-prolyl cis-trans isomerase | chr3:9182691-9184463 FORWARDmoderately similar to (203) FKB15_VICFA FK506-binding protein 2 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (15 kDa FKBP) (FKBP-15) - Vicia faba (Broad bean)moderately similar to (248) loc_os01g68710 12001.m150820 protein FK506-binding protein 2-1 precursor, putative, expressed seq=cds; coord=8:162534879..162538967:1; parent_gene=GRMZM2G031204' 'highly similar to (568) AT4G25360 | Symbols: | INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF231, plant (InterPro:IPR004253); BEST Arabidopsis thaliana protein match is: YLS7 (TAIR:AT5G51640.1); Has 699 Blast hits to 688 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 699; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:12970187-12972404 FORWARDhighly similar to (754) loc_os01g68630 12001.m12965 protein expressed protein seq=cds; coord=8:162665398..162668419:-1; parent_gene=GRMZM2G096169'

'moderately similar to (480) AT2G19490 | Symbols: | recA family protein | chr2:8441732-8444006 FORWARDhighly similar to (627) loc_os01g67510 12001.m12855 protein DNA repair protein recA homolog 3, putative, expressed seq=cds; coord=8:163890807..163895364:1; parent_gene=GRMZM2G700757'

'very weakly similar to (81.6) AT3G16490 | Symbols: IQD26 | IQD26 (IQ-domain 26); calmodulin binding | chr3:5603962-5605489 REVERSEweakly similar to (197) loc_os01g53980 12001.m11562 protein calmodulin binding protein, putative, expressed seq=cds; coord=8:175150778..175151936:-1; parent_gene=AC203173.3_FG001'

'weakly similar to (191) AT1G24090 | Symbols: | RNase H domain-containing protein | chr1:8520834-8524690 FORWARDmoderately similar to (281) loc_os06g13010 12006.m06017 protein nucleic acid binding protein, putative, expressed seq=cds; coord=9:2485121..2487554:-1; parent_gene=GRMZM2G016275'

'weakly similar to (109) AT1G28210 | Symbols: ATJ1 | ATJ1; heat shock protein binding / nucleic acid binding / unfolded protein binding / zinc ion binding | chr1:9854598-9859977 FORWARDweakly similar to (149) loc_os06g11440 12006.m32015 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=9:6826102..6839564:-1; parent_gene=GRMZM2G097620'

'nearly identical (1504) AT5G65460 | Symbols: | kinesin motor protein-related | chr5:26161831-26169001 REVERSEweakly similar to (138) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiihighly similar to (894) loc_os06g11380 12006.m05855 protein ATP binding protein, putative, expressed seq=cds; coord=9:7186959..7210629:-1; parent_gene=GRMZM2G017257'

'moderately similar to (429) AT2G05940 | Symbols: | protein kinase, putative | chr2:2287514-2289270 REVERSEmoderately similar to (218) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (616) loc_os06g10160 12006.m05734 protein protein kinase APK1A, chloroplast precursor, putative, expressed seq=cds; coord=9:10125256..10127926:1; parent_gene=GRMZM2G055982'

'moderately similar to (233) AT5G16770 | Symbols: AtMYB9 | AtMYB9 (myb domain protein 9); DNA binding / transcription factor | chr5:5515209-5516734 FORWARDmoderately similar to (205) ODO1_PETHY ODORANT1 protein (MYB-like protein ODO1) - Petunia hybrida (Petunia)moderately similar to (296) loc_os06g02250 12006.m04959 protein transcription factor MYB102, putative seq=cds; coord=9:26630516..26631917:1; parent_gene=GRMZM2G044824'

'moderately similar to (233) AT5G16770 | Symbols: AtMYB9 | AtMYB9 (myb domain protein 9); DNA binding / transcription factor | chr5:5515209-5516734 FORWARDmoderately similar to (205) ODO1_PETHY ODORANT1 protein (MYB-like protein ODO1) - Petunia hybrida (Petunia)moderately similar to (296) loc_os06g02250 12006.m04959 protein transcription factor MYB102, putative seq=cds; coord=9:26630516..26631917:1; parent_gene=GRMZM2G044824'

'weakly similar to (127) AT5G34930 | Symbols: | arogenate dehydrogenase | chr5:13233391-13235522 FORWARDweakly similar to (181) loc_os06g35050 12006.m08042 protein arogenate dehydrogenase isoform 2, putative, expressed seq=cds; coord=9:61355950..61358310:-1; parent_gene=GRMZM2G324297'

'highly similar to (693) AT4G39800 | Symbols: MI-1-P SYNTHASE, MIPS1, ATMIPS1 | MIPS1 (MYO-INOSITOL-1 PHOSTPATE SYNTHASE 1); inositol-3-phosphate synthase | chr4:18469659-18471893 REVERSEhighly similar to (735) INO1_MAIZE Inositol-3-phosphate synthase (EC 5.5.1.4) (Myo-inositol-1-phosphate synthase) (MI-1-P synthase) (IPS) - Zea mays (Maize)highly similar to (732) loc_os03g09250 12003.m35064 protein inositol-3-phosphate synthase, putative, expressed seq=cds; coord=9:149240772..149244235:1; parent_gene=GRMZM2G004528'

'moderately similar to (417) AT2G25100 | Symbols: | ribonuclease HII family protein | chr2:10679767-10681654 REVERSEhighly similar to (537) loc_os11g05570 12011.m04754 protein ribonuclease HI large subunit, putative, expressed seq=cds; coord=10:5896223..5900069:1; parent_gene=GRMZM2G065804'

'weakly similar to (139) AT1G18480 | Symbols: | calcineurin-like phosphoesterase family protein | chr1:6361639-6362814 FORWARDmoderately similar to (205) loc_os11g15570 12011.m05691 protein expressed protein seq=cds; coord=10:53139082..53141917:1; parent_gene=GRMZM2G459370'

'moderately similar to (202) AT3G59550 | Symbols: SYN3, ATRAD21.2, ATSYN3 | SYN3 | chr3:21997262-22000496 FORWARDhighly similar to (589) loc_os08g16610 12008.m26637 protein sister chromatid cohesion 1 protein 3, putative, expressed seq=cds; coord=10:42878927..42884133:1; parent_gene=GRMZM2G074818'

'highly similar to (615) AT1G31830 | Symbols: | amino acid permease family protein | chr1:11418875-11420314 REVERSEhighly similar to (795) loc_os03g37984 12003.m35295 protein cationic amino acid transporter, putative, expressed seq=cds; coord=10:76224116..76227981:-1; parent_gene=GRMZM2G078292'

'highly similar to (543) AT1G07590 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:2336649-2338481 REVERSEhighly similar to (751) loc_os08g06500 12008.m04789 protein expressed protein seq=cds; coord=10:76508485..76510356:-1; parent_gene=GRMZM2G145130'

'moderately similar to (349) AT3G62260 | Symbols: | protein phosphatase 2C, putative / PP2C, putative | chr3:23038516-23040391 REVERSEhighly similar to (525) loc_os05g04360 12005.m04969 protein protein phosphatase 2C homolog 2, putative, expressed seq=cds; coord=10:85581746..85584681:1; parent_gene=GRMZM2G060798'

'moderately similar to (256) AT5G01670 | Symbols: | aldose reductase, putative | chr5:252000-253856 FORWARDmoderately similar to (339) ALDR_HORVU Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase) - Hordeum vulgare (Barley)moderately similar to (335) loc_os04g50790 12004.m35440 protein nucleic acid binding protein, putative, expressed seq=cds; coord=10:138493023..138500137:-1; parent_gene=AF466202.2_FG007' 'nearly identical (1069) AT5G64570 | Symbols: XYL4, ATBXL4 | XYL4; hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase | chr5:25810227-25813309 REVERSEmoderately similar to (468) XYNB_PRUPE Putative beta-D-xylosidase (EC 3.2.1.-) (PpAz152) (Fragment) - Prunus persica (Peach)nearly identical (1342) loc_os04g54810 12004.m10373 protein beta-D-xylosidase, putative, expressed seq=cds; coord=10:144683393..144689170:-1; parent_gene=GRMZM2G136895'

'weakly similar to (169) AT4G25540 | Symbols: MSH3, ATMSH3 | MSH3 (Arabidopsis homolog of DNA mismatch repair protein MSH3); damaged DNA binding / mismatched DNA binding / protein binding | chr4:13042700-13048115 REVERSEmoderately similar to (311) loc_os04g58630 12004.m101699 protein DNA mismatch repair protein MSH3, putative, expressed seq=cds; coord=10:148589707..148592889:-1; parent_gene=GRMZM2G093623'

'moderately similar to (484) AT2G27050 | Symbols: EIL1 | EIL1 (ETHYLENE-INSENSITIVE3-LIKE 1); transcription factor/ transcription regulator | chr2:11546314-11548068 FORWARDhighly similar to (991) loc_os03g20790 12003.m07486 protein ETHYLENE-INSENSITIVE3-like 1 protein, putative, expressed seq=cds; coord=1:52564282..52568326:-1; parent_gene=GRMZM2G033570'

'weakly similar to (159) AT5G55670 | Symbols: | RNA recognition motif (RRM)-containing protein | chr5:22544669-22546801 REVERSEmoderately similar to (216) loc_os08g38240 12008.m26723 protein cleavage and polyadenylation specificity factor 6, putative, expressed seq=cds; coord=1:182898704..182903336:-1; parent_gene=GRMZM2G107163'

'weakly similar to (159) AT5G55670 | Symbols: | RNA recognition motif (RRM)-containing protein | chr5:22544669-22546801 REVERSEmoderately similar to (216) loc_os08g38240 12008.m26723 protein cleavage and polyadenylation specificity factor 6, putative, expressed seq=cds; coord=1:182898704..182903336:-1; parent_gene=GRMZM2G107163'

'moderately similar to (478) AT4G39170 | Symbols: | SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative | chr4:18240887-18243621 FORWARDhighly similar to (889) loc_os08g38850 12008.m26728 protein phosphatidylinositol transporter/ transporter, putative, expressed seq=cds; coord=1:183807049..183811940:-1; parent_gene=GRMZM2G113840'

'highly similar to (835) AT1G28440 | Symbols: HSL1 | HSL1 (HAESA-Like 1); ATP binding / kinase/ protein serine/threonine kinase | chr1:9996914-10000171 FORWARDmoderately similar to (416) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1223) loc_os08g28870 12008.m06892 protein receptor-like protein kinase 5 precursor, putative, expressed seq=cds; coord=1:220056861..220060238:1; parent_gene=GRMZM2G136353'

'moderately similar to (332) AT5G33320 | Symbols: CUE1, PPT, ARAPPT | CUE1 (CAB UNDEREXPRESSED 1); antiporter/ triose-phosphate transmembrane transporter | chr5:12588950-12591408 FORWARDweakly similar to (177) TPT_SOLTU Triose phosphate/phosphate translocator, chloroplast precursor (cTPT) (E29) - Solanum tuberosum (Potato)moderately similar to (422) loc_os08g25624 12008.m26834 protein triose phosphate/phosphate translocator, non-green plastid,chloroplast precursor, putative, expressed seq=cds; coord=1:221486173..221490380:1; parent_gene=GRMZM2G174107'

'nearly identical (1679) AT4G38190 | Symbols: ATCSLD4, CSLD4 | ATCSLD4; cellulose synthase/ transferase, transferring glycosyl groups | chr4:17910096-17913641 REVERSEnearly identical (1967) loc_os08g25710 12008.m06587 protein CSLD3 - cellulose synthase-like family D, expressed seq=cds; coord=1:221785673..221789403:1; parent_gene=GRMZM2G044269' 'moderately similar to (206) AT3G01080 | Symbols: WRKY58, ATWRKY58 | WRKY58; transcription factor | chr3:25507-27449 FORWARDweakly similar to (184) loc_os03g55164 12003.m101731 protein OsWRKY4 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=1:278602439..278604715:1; parent_gene=GRMZM2G008029'

'moderately similar to (294) AT1G73110 | Symbols: | ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative | chr1:27494344-27496844 REVERSEmoderately similar to (202) RCA_MAIZE Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase) (RA) - Zea mays (Maize)moderately similar to (344) loc_os04g56320 12004.m10522 protein ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor, putative, expressed seq=cds; coord=2:4159971..4163217:1; parent_gene=GRMZM2G039345'

'moderately similar to (294) AT1G73110 | Symbols: | ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative | chr1:27494344-27496844 REVERSEmoderately similar to (202) RCA_MAIZE Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase) (RA) - Zea mays (Maize)moderately similar to (344) loc_os04g56320 12004.m10522 protein ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor, putative, expressed seq=cds; coord=2:4159971..4163217:1; parent_gene=GRMZM2G039345'

'very weakly similar to (96.7) AT5G25190 | Symbols: | ethylene-responsive element-binding protein, putative | chr5:8707007-8707655 REVERSEweakly similar to (121) loc_os04g56150 12004.m10506 protein ethylene-responsive transcription factor 4, putative seq=cds; coord=2:4347237..4347860:1; parent_gene=GRMZM2G067463'

'moderately similar to (295) AT2G37190 | Symbols: | 60S ribosomal protein L12 (RPL12A) | chr2:15619559-15620059 REVERSEmoderately similar to (246) RL12_CHLRE 60S ribosomal protein L12 (Fragment) - Chlamydomonas reinhardtiimoderately similar to (314) loc_os04g50990 12004.m09996 protein 60S ribosomal protein L12, putative, expressed seq=cds; coord=2:12677824..12680299:-1; parent_gene=GRMZM2G149649'

'moderately similar to (338) AT5G64440 | Symbols: AtFAAH | AtFAAH (Arabidopsis thaliana fatty acid amide hydrolase); N-(long-chain-acyl)ethanolamine deacylase/ amidase | chr5:25766229-25770260 FORWARDhighly similar to (616) loc_os11g06900 12011.m04887 protein N-acylethanolamine amidohydrolase, putative, expressed seq=cds; coord=2:136348649..136351410:-1; parent_gene=GRMZM2G053466'

'highly similar to (688) AT2G03890 | Symbols: | phosphatidylinositol 3- and 4-kinase family protein | chr2:1186199-1188151 FORWARDhighly similar to (948) loc_os09g29890 12009.m22000 protein phosphatidylinositol 3- and 4-kinase family protein, expressed seq=cds; coord=2:188414700..188417396:-1; parent_gene=GRMZM2G137558'

'weakly similar to (130) AT1G56170 | Symbols: HAP5B, ATHAP5B, NF-YC2 | NF-YC2 (NUCLEAR FACTOR Y, SUBUNIT C2); DNA binding / transcription activator/ transcription factor | chr1:21025118-21025717 FORWARDweakly similar to (141) loc_os09g30310 12009.m06182 protein nuclear transcription factor Y subunit C-2, putative, expressed seq=cds; coord=2:189204687..189208176:-1; parent_gene=GRMZM2G022162'

'moderately similar to (492) AT4G12570 | Symbols: UPL5 | UPL5 (UBIQUITIN PROTEIN LIGASE 5); acid-amino acid ligase/ binding / ubiquitin-protein ligase | chr4:7445585-7448819 FORWARDhighly similar to (917) loc_os09g31090 12009.m22004 protein HECT-domain, putative, expressed seq=cds; coord=2:189501893..189517266:-1; parent_gene=GRMZM2G080439' 'moderately similar to (492) AT4G12570 | Symbols: UPL5 | UPL5 (UBIQUITIN PROTEIN LIGASE 5); acid-amino acid ligase/ binding / ubiquitin-protein ligase | chr4:7445585-7448819 FORWARDhighly similar to (917) loc_os09g31090 12009.m22004 protein HECT-domain, putative, expressed seq=cds; coord=2:189501893..189517266:-1; parent_gene=GRMZM2G080439'

'moderately similar to (492) AT4G12570 | Symbols: UPL5 | UPL5 (UBIQUITIN PROTEIN LIGASE 5); acid-amino acid ligase/ binding / ubiquitin-protein ligase | chr4:7445585-7448819 FORWARDhighly similar to (917) loc_os09g31090 12009.m22004 protein HECT-domain, putative, expressed seq=cds; coord=2:189501893..189517266:-1; parent_gene=GRMZM2G080439'

'moderately similar to (492) AT4G12570 | Symbols: UPL5 | UPL5 (UBIQUITIN PROTEIN LIGASE 5); acid-amino acid ligase/ binding / ubiquitin-protein ligase | chr4:7445585-7448819 FORWARDhighly similar to (917) loc_os09g31090 12009.m22004 protein HECT-domain, putative, expressed seq=cds; coord=2:189501893..189517266:-1; parent_gene=GRMZM2G080439'

'weakly similar to (189) AT5G08565 | Symbols: | positive transcription elongation factor/ zinc ion binding | chr5:2775964-2777154 FORWARDmoderately similar to (223) loc_os07g43060 12007.m08534 protein transcription elongation factor SPT4 homolog 1, putative, expressed seq=cds; coord=2:212361624..212366846:-1; parent_gene=GRMZM2G086805'

'moderately similar to (201) AT4G16270 | Symbols: | peroxidase 40 (PER40) (P40) | chr4:9205038-9206483 FORWARDmoderately similar to (214) PERX_NICSY Lignin-forming anionic peroxidase precursor (EC 1.11.1.7) - Nicotiana sylvestris (Wood tobacco)moderately similar to (298) loc_os07g44460 12007.m08667 protein peroxidase 66 precursor, putative seq=cds; coord=2:213071989..213073476:-1; parent_gene=GRMZM2G156257'

'weakly similar to (156) AT2G03500 | Symbols: | myb family transcription factor | chr2:1059926-1062259 FORWARDmoderately similar to (367) loc_os07g02800 12007.m29048 protein myb-like DNA-binding domain, SHAQKYF class family protein, expressed seq=cds; coord=2:236187625..236189534:-1; parent_gene=GRMZM2G173882'

'weakly similar to (128) AT5G64810 | Symbols: WRKY51, ATWRKY51 | WRKY51; transcription factor | chr5:25908415-25909687 FORWARDweakly similar to (199) loc_os01g51690 12001.m11347 protein OsWRKY26 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=3:203083255..203084247:1; parent_gene=GRMZM2G101405'

'moderately similar to (329) AT2G34480 | Symbols: | 60S ribosomal protein L18A (RPL18aB) | chr2:14532916-14534161 REVERSEmoderately similar to (355) RL18A_ORYSA 60S ribosomal protein L18a - Oryza sativa (Rice)moderately similar to (363) loc_os05g49030 12005.m08974 protein 60S ribosomal protein L18a, putative, expressed seq=cds; coord=3:210714346..210715729:1; parent_gene=AC230013.2_FG007'

'weakly similar to (117) AT2G25355 | Symbols: | exonuclease-related | chr2:10801567-10803591 FORWARDweakly similar to (136) loc_os01g66730 12001.m150798 protein exosome complex exonuclease RRP40, putative, expressed seq=cds; coord=3:211858569..211859522:-1; parent_gene=GRMZM2G173989'

'moderately similar to (260) AT1G69640 | Symbols: SBH1 | SBH1 (SPHINGOID BASE HYDROXYLASE 1); catalytic/ sphingosine hydroxylase | chr1:26193933-26195466 REVERSEmoderately similar to (354) loc_os01g46940 12001.m10891 protein protein SUR2, putative, expressed seq=cds; coord=3:212266422..212268831:-1; parent_gene=GRMZM2G003526' 'moderately similar to (260) AT1G69640 | Symbols: SBH1 | SBH1 (SPHINGOID BASE HYDROXYLASE 1); catalytic/ sphingosine hydroxylase | chr1:26193933-26195466 REVERSEmoderately similar to (354) loc_os01g46940 12001.m10891 protein protein SUR2, putative, expressed seq=cds; coord=3:212266422..212268831:-1; parent_gene=GRMZM2G003526'

'very weakly similar to (100) AT4G11140 | Symbols: CRF1 | CRF1 (CYTOKININ RESPONSE FACTOR 1); DNA binding / transcription factor | chr4:6794930-6795793 REVERSEvery weakly similar to (86.3) ERF3_TOBAC Ethylene-responsive transcription factor 3 (Ethylene-responsive element-binding factor 3 homolog) (EREBP-5) (NtERF5) - Nicotiana tabacum (Common tobacco)moderately similar to (298) loc_os01g46870 12001.m10884 protein ap2 domain protein, putative, expressed seq=cds; coord=3:212501262..212503692:1; parent_gene=GRMZM2G160971'

'moderately similar to (259) AT5G41790 | Symbols: CIP1 | CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding | chr5:16727530-16732391 FORWARDweakly similar to (117) MFP1_TOBAC MAR-binding filament-like protein 1-1 - Nicotiana tabacum (Common tobacco)highly similar to (836) loc_os01g46810 12001.m10878 protein viral A-type inclusion protein repeat containing protein, expressed seq=cds; coord=3:212694107..212699938:1; parent_gene=GRMZM2G118403'

'highly similar to (868) AT3G58610 | Symbols: | ketol-acid reductoisomerase | chr3:21671561-21674639 FORWARDhighly similar to (858) ILV5_PEA Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) - Pisum sativum (Garden pea)highly similar to (920) loc_os01g46380 12001.m10836 protein ketol-acid reductoisomerase, chloroplast precursor, putative, expressed seq=cds; coord=3:213623450..213627174:-1; parent_gene=GRMZM2G004382'

'moderately similar to (410) AT4G18550 | Symbols: | lipase class 3 family protein | chr4:10225006-10226862 REVERSEhighly similar to (642) loc_os01g46240 12001.m10822 protein triacylglycerol lipase, putative, expressed seq=cds; coord=3:214200908..214203537:1; parent_gene=GRMZM2G153672'

'highly similar to (749) AT1G15500 | Symbols: ATNTT2 | ATNTT2; ATP:ADP antiporter | chr1:5326426-5328688 FORWARDhighly similar to (753) TLC1_SOLTU Plastidic ATP/ADP-transporter - Solanum tuberosum (Potato)highly similar to (887) loc_os01g45910 12001.m10791 protein plastidic ATP/ADP-transporter, putative, expressed seq=cds; coord=3:214471264..214476975:1; parent_gene=GRMZM2G064473'

'highly similar to (749) AT1G15500 | Symbols: ATNTT2 | ATNTT2; ATP:ADP antiporter | chr1:5326426-5328688 FORWARDhighly similar to (753) TLC1_SOLTU Plastidic ATP/ADP-transporter - Solanum tuberosum (Potato)highly similar to (887) loc_os01g45910 12001.m10791 protein plastidic ATP/ADP-transporter, putative, expressed seq=cds; coord=3:214471264..214476975:1; parent_gene=GRMZM2G064473'

'moderately similar to (260) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (338) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (331) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215425032..215437638:-1; parent_gene=GRMZM2G348512'

'weakly similar to (128) loc_os04g34984 12004.m08591 protein UBP27, putative, expressed seq=cds; coord=3:216795952..216802947:-1; parent_gene=GRMZM2G064283' 'moderately similar to (260) AT5G42050 | Symbols: | FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27090.1); Has 5084 Blast hits to 2870 proteins in 85 species: Archae - 0; Bacteria - 24; Metazoa - 270; Fungi - 58; Plants - 157; Viruses - 8; Other Eukaryotes - 4567 (source: NCBI BLink). | chr5:16815630-16816932 FORWARDmoderately similar to (262) B2_DAUCA B2 protein - Daucus carota (Carrot)moderately similar to (355) loc_os01g36950 12001.m150623 protein N-rich protein, putative, expressed seq=cds; coord=3:226769338..226771691:-1; parent_gene=GRMZM2G071154'

'highly similar to (539) AT2G26460 | Symbols: | RED family protein | chr2:11255049-11258913 REVERSEhighly similar to (744) loc_os11g04950 12011.m04693 protein expressed protein seq=cds; coord=3:229657774..229664681:-1; parent_gene=GRMZM2G015592'

'weakly similar to (147) AT5G18280 | Symbols: ATAPY2, APY2 | ATAPY2 (ARABIDOPSIS THALIANA APYRASE 2); ATPase/ nucleotide diphosphatase | chr5:6050799-6054875 REVERSEweakly similar to (120) NTPA_PEA Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate phosphohydrolase) (NTPase) (Apyrase) - Pisum sativum (Garden pea)weakly similar to (195) loc_os07g48430 12007.m29410 protein nucleoside-triphosphatase, putative, expressed seq=cds; coord=4:115030232..115033238:-1; parent_gene=GRMZM2G106618'

'highly similar to (520) AT1G10940 | Symbols: ASK1, SNRK2-4, SNRK2.4, SRK2A | SNRK2.4 (SNF1-RELATED PROTEIN KINASE 2.4); kinase | chr1:3656050-3658170 REVERSEhighly similar to (596) SAPK7_ORYSA Serine/threonine-protein kinase SAPK7 (EC 2.7.11.1) (Osmotic stress/abscisic acid-activated protein kinase 7) - Oryza sativa (Rice)highly similar to (596) loc_os04g35240 12004.m08614 protein serine/threonine-protein kinase SAPK7, putative, expressed seq=cds; coord=4:115154220..115165298:-1; parent_gene=GRMZM2G130018'

'moderately similar to (255) AT4G06634 | Symbols: | zinc finger (C2H2 type) family protein | chr4:3764499-3766177 REVERSEmoderately similar to (355) loc_os02g34680 12002.m08557 protein transcription repressor TRM protein, putative, expressed seq=cds; coord=4:115429773..115432652:1; parent_gene=GRMZM2G140016'

'moderately similar to (255) AT4G06634 | Symbols: | zinc finger (C2H2 type) family protein | chr4:3764499-3766177 REVERSEmoderately similar to (355) loc_os02g34680 12002.m08557 protein transcription repressor TRM protein, putative, expressed seq=cds; coord=4:115429773..115432652:1; parent_gene=GRMZM2G140016'

'nearly identical (1232) AT1G77760 | Symbols: NIA1, GNR1, NR1 | NIA1 (NITRATE REDUCTASE 1); nitrate reductase | chr1:29236005-29239367 REVERSEnearly identical (1540) NIA7_HORVU Nitrate reductase [NAD(P)H] (EC 1.7.1.2) - Hordeum vulgare (Barley)nearly identical (1573) loc_os02g53130 12002.m10342 protein nitrate reductase, putative, expressed seq=cds; coord=4:177655913..177659763:1; parent_gene=GRMZM2G428027'

'highly similar to (503) AT2G03220 | Symbols: FT1, ATFUT1, ATFT1, MUR2 | FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups | chr2:970401-972353 REVERSEhighly similar to (513) FUT1_PEA Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1) - Pisum sativum (Garden pea)highly similar to (697) loc_os02g52630 12002.m10293 protein fucosyltransferase 7, putative, expressed seq=cds; coord=4:178596383..178598254:-1; parent_gene=GRMZM2G471594' 'weakly similar to (177) AT4G09650 | Symbols: ATPD | ATPD (ATP SYNTHASE DELTA-SUBUNIT GENE); hydrogen ion transporting ATP synthase, rotational mechanism / proton-transporting ATPase, rotational mechanism | chr4:6100799-6101503 FORWARDmoderately similar to (273) ATPD_SORBI ATP synthase delta chain, chloroplast precursor (EC 3.6.3.14) - Sorghum bicolor (Sorghum) (Sorghum vulgare)moderately similar to (256) loc_os02g51470 12002.m33873 protein ATP synthase delta chain, chloroplast precursor, putative, expressed seq=cds; coord=4:181429409..181431608:-1; parent_gene=GRMZM2G025171'

'weakly similar to (177) AT4G09650 | Symbols: ATPD | ATPD (ATP SYNTHASE DELTA-SUBUNIT GENE); hydrogen ion transporting ATP synthase, rotational mechanism / proton-transporting ATPase, rotational mechanism | chr4:6100799-6101503 FORWARDmoderately similar to (273) ATPD_SORBI ATP synthase delta chain, chloroplast precursor (EC 3.6.3.14) - Sorghum bicolor (Sorghum) (Sorghum vulgare)moderately similar to (256) loc_os02g51470 12002.m33873 protein ATP synthase delta chain, chloroplast precursor, putative, expressed seq=cds; coord=4:181429409..181431608:-1; parent_gene=GRMZM2G025171'

'moderately similar to (433) AT5G59250 | Symbols: | sugar transporter family protein | chr5:23903958-23906853 FORWARDvery weakly similar to (94.4) HEX6_RICCO Hexose carrier protein HEX6 - Ricinus communis (Castor bean)highly similar to (506) loc_os03g60820 12003.m10970 protein sugar transporter family protein, putative, expressed seq=cds; coord=5:2181480..2183903:1; parent_gene=GRMZM2G085301'

'moderately similar to (433) AT5G59250 | Symbols: | sugar transporter family protein | chr5:23903958-23906853 FORWARDvery weakly similar to (94.4) HEX6_RICCO Hexose carrier protein HEX6 - Ricinus communis (Castor bean)highly similar to (506) loc_os03g60820 12003.m10970 protein sugar transporter family protein, putative, expressed seq=cds; coord=5:2181480..2183903:1; parent_gene=GRMZM2G085301'

'moderately similar to (459) AT3G51120 | Symbols: | DNA binding / nucleic acid binding / protein binding / zinc ion binding | chr3:18986026-18991886 REVERSEnearly identical (1229) loc_os10g36810 12010.m06486 protein plus-3 domain containing protein, expressed seq=cds; coord=5:22737810..22750836:-1; parent_gene=GRMZM2G078379'

'highly similar to (647) AT4G04950 | Symbols: | thioredoxin family protein | chr4:2517882-2519924 REVERSEhighly similar to (820) loc_os10g35720 12010.m22006 protein OsGrx_S17 - glutaredoxin subgroup II, expressed seq=cds; coord=5:24436192..24442540:-1; parent_gene=GRMZM2G090736'

'highly similar to (670) AT5G23190 | Symbols: CYP86B1 | CYP86B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr5:7803478-7805659 REVERSEweakly similar to (114) C97B2_SOYBN Cytochrome P450 97B2 (EC 1.14.-.-) - Glycine max (Soybean)highly similar to (830) loc_os10g34480 12010.m06272 protein cytochrome P450 86A2, putative, expressed seq=cds; coord=5:26443691..26446113:1; parent_gene=GRMZM2G013082'

'weakly similar to (108) AT1G77670 | Symbols: | aminotransferase class I and II family protein | chr1:29189043-29190901 REVERSEmoderately similar to (301) loc_os10g34350 12010.m06261 protein kynurenine--oxoglutarate transaminase 1, putative, expressed seq=cds; coord=5:27099256..27102677:1; parent_gene=GRMZM2G174145' 'highly similar to (629) AT1G59900 | Symbols: AT-E1 ALPHA | AT-E1 ALPHA; oxidoreductase, acting on the aldehyde or oxo group of donors, disulfide as acceptor / pyruvate dehydrogenase (acetyl-transferring) | chr1:22051368-22053660 FORWARDhighly similar to (631) ODPA_SOLTU Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) - Solanum tuberosum (Potato)highly similar to (712) loc_os02g50620 12002.m10096 protein pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor, putative, expressed seq=cds; coord=5:205777032..205781614:-1; parent_gene=GRMZM2G140150'

'weakly similar to (132) AT1G78080 | Symbols: RAP2.4 | RAP2.4 (related to AP2 4); DNA binding / transcription factor | chr1:29364790-29365794 FORWARDmoderately similar to (202) loc_os02g51670 12002.m10198 protein AP2 domain-containing protein, putative, expressed seq=cds; coord=5:208162767..208165707:1; parent_gene=GRMZM2G055204'

'weakly similar to (167) AT1G78260 | Symbols: | RNA recognition motif (RRM)-containing protein | chr1:29447317-29449246 FORWARDmoderately similar to (315) loc_os02g51890 12002.m10220 protein RNA-binding region-containing protein 1, putative, expressed seq=cds; coord=5:208556725..208565590:1; parent_gene=GRMZM2G303915'

'highly similar to (565) AT1G73400 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:27598412-27599812 FORWARDweakly similar to (137) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (868) loc_os02g52220 12002.m33882 protein ATP binding protein, putative, expressed seq=cds; coord=5:208957884..208961357:1; parent_gene=GRMZM2G161175'

'highly similar to (527) AT4G30340 | Symbols: ATDGK7 | ATDGK7 (Diacylglycerol kinase 7); diacylglycerol kinase chr4:14838465-14840941 REVERSEhighly similar to (728) loc_os02g54650 12002.m10494 protein diacylglycerol kinase, putative, expressed seq=cds; coord=5:212754787..212763972:-1; parent_gene=GRMZM2G128214'

'moderately similar to (420) AT1G12420 | Symbols: ACR8 | ACR8; amino acid binding | chr1:4226673-4228917 REVERSEhighly similar to (526) loc_os08g02500 12008.m04394 protein ACR8, putative seq=cds; coord=6:5641494..5643748:1; parent_gene=GRMZM2G034404'

'weakly similar to (118) AT4G33865 | Symbols: | 40S ribosomal protein S29 (RPS29C) | chr4:16233395-16234114 REVERSEweakly similar to (129) loc_os11g41610 12011.m08002 protein 40S ribosomal protein S29, putative, expressed seq=cds; coord=6:22305548..22307139:-1; parent_gene=GRMZM2G060373'

'very weakly similar to (93.2) AT3G54360 | Symbols: | protein binding / zinc ion binding | chr3:20128570-20131581 REVERSEweakly similar to (115) loc_os02g55200 12002.m33471 protein expressed protein seq=cds; coord=6:27809738..27811273:-1; parent_gene=GRMZM2G101662'

'moderately similar to (248) AT3G63460 | Symbols: | WD-40 repeat family protein | chr3:23431009-23437241 REVERSEmoderately similar to (410) loc_os07g46370 12007.m08854 protein EMB2221, putative, expressed seq=cds; coord=7:44760619..44768892:1; parent_gene=GRMZM2G435661'

'weakly similar to (146) loc_os12g37830 12012.m07569 protein transposon protein, putative, Ac/Ds sub-class seq=cds; coord=7:100267155..100284846:1; parent_gene=GRMZM2G436649' 'moderately similar to (382) AT4G34880 | Symbols: | amidase family protein | chr4:16615549-16617424 FORWARDhighly similar to (588) loc_os04g10460 12004.m06299 protein amidase, putative, expressed seq=cds; coord=7:148453586..148456184:-1; parent_gene=GRMZM2G111309'

'moderately similar to (362) AT2G41835 | Symbols: | zinc finger (C2H2 type, AN1-like) family protein | chr2:17458020-17459414 REVERSEhighly similar to (510) loc_os07g38240 12007.m08071 protein AN1-type zinc finger protein 2B, putative, expressed seq=cds; coord=7:158951176..158954111:1; parent_gene=GRMZM2G081782'

'moderately similar to (475) AT2G43750 | Symbols: OASB, ACS1, CPACS1, ATCS-B | OASB (O-ACETYLSERINE (THIOL) LYASE B); cysteine synthase | chr2:18129604-18132322 REVERSEmoderately similar to (486) CYSKP_SOLTU Cysteine synthase, chloroplast precursor (EC 2.5.1.47) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (CSase B) (CS-B) (OAS-TL B) - Solanum tuberosum (Potato)highly similar to (541) loc_os01g74650 12001.m42813 protein cysteine synthase, mitochondrial precursor, putative, expressed seq=cds; coord=8:6464565..6468039:1; parent_gene=GRMZM2G082185'

'moderately similar to (475) AT2G43750 | Symbols: OASB, ACS1, CPACS1, ATCS-B | OASB (O-ACETYLSERINE (THIOL) LYASE B); cysteine synthase | chr2:18129604-18132322 REVERSEmoderately similar to (486) CYSKP_SOLTU Cysteine synthase, chloroplast precursor (EC 2.5.1.47) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (CSase B) (CS-B) (OAS-TL B) - Solanum tuberosum (Potato)highly similar to (541) loc_os01g74650 12001.m42813 protein cysteine synthase, mitochondrial precursor, putative, expressed seq=cds; coord=8:6464565..6468039:1; parent_gene=GRMZM2G082185'

'moderately similar to (261) AT1G19600 | Symbols: | pfkB-type carbohydrate kinase family protein | chr1:6779085-6780898 FORWARDmoderately similar to (317) loc_os01g01620 12001.m06807 protein ribokinase, putative, expressed seq=cds; coord=8:7516007..7520374:-1; parent_gene=GRMZM2G051842'

'weakly similar to (153) loc_os05g35274 12005.m083726 protein RNA recognition motif-containing protein, putative, expressed seq=cds; coord=8:102262870..102264589:-1; parent_gene=GRMZM2G111596'

'weakly similar to (168) AT1G65620 | Symbols: AS2 | AS2 (ASYMMETRIC LEAVES 2); protein binding | chr1:24400146-24400745 FORWARDmoderately similar to (212) loc_os01g66590 12001.m97474 protein ASYMMETRIC LEAVES2, putative, expressed seq=cds; coord=8:104267219..104268277:1; parent_gene=GRMZM2G096064'

'moderately similar to (246) AT3G07880 | Symbols: | Rho GDP-dissociation inhibitor family protein | chr3:2514175-2515544 FORWARDmoderately similar to (345) loc_os01g68540 12001.m12957 protein rho GDP-dissociation inhibitor 1, putative, expressed seq=cds; coord=8:110142652..110144824:1; parent_gene=GRMZM2G150724'

'weakly similar to (166) AT5G53190 | Symbols: | nodulin MtN3 family protein | chr5:21572417-21574284 REVERSEmoderately similar to (253) loc_os05g12320 12005.m05698 protein mtN3 protein-like, putative, expressed seq=cds; coord=8:112530662..112532375:1; parent_gene=GRMZM2G179679' 'highly similar to (789) AT2G20370 | Symbols: KAM1, MUR3 | MUR3 (MURUS 3); catalytic/ transferase, transferring glycosyl groups | chr2:8792355-8794214 FORWARDhighly similar to (914) KATAM_ORYSA Xyloglucan galactosyltransferase KATAMARI1 homolog (EC 2.4.1.-) - Oryza sativa (Rice)highly similar to (938) loc_os03g05110 12003.m06035 protein xyloglucan galactosyltransferase KATAMARI 1, putative, expressed seq=cds; coord=9:152250791..152253278:1; parent_gene=GRMZM2G137779'

'moderately similar to (454) AT3G52780 | Symbols: ATPAP20, PAP20 | PAP20; acid phosphatase/ protein serine/threonine phosphatase | chr3:19561812-19564195 REVERSEmoderately similar to (230) PPAF_SOYBN Purple acid phosphatase precursor (EC 3.1.3.2) (Manganese(II) purple acid phosphatase) - Glycine max (Soybean)highly similar to (628) loc_os11g05410 12011.m079939 protein hydrolase/ protein serine/threonine phosphatase, putative, expressed seq=cds; coord=10:5222440..5225078:1; parent_gene=GRMZM2G434170'

'moderately similar to (454) AT3G52780 | Symbols: ATPAP20, PAP20 | PAP20; acid phosphatase/ protein serine/threonine phosphatase | chr3:19561812-19564195 REVERSEmoderately similar to (230) PPAF_SOYBN Purple acid phosphatase precursor (EC 3.1.3.2) (Manganese(II) purple acid phosphatase) - Glycine max (Soybean)highly similar to (628) loc_os11g05410 12011.m079939 protein hydrolase/ protein serine/threonine phosphatase, putative, expressed seq=cds; coord=10:5222440..5225078:1; parent_gene=GRMZM2G434170'

'weakly similar to (143) AT4G19810 | Symbols: | glycosyl hydrolase family 18 protein | chr4:10764151-10765753 REVERSEmoderately similar to (437) loc_os04g30770 12004.m08181 protein hydrolase, hydrolyzing O-glycosyl compounds, putative, expressed seq=cds; coord=10:107900408..107902133:1; parent_gene=GRMZM2G090441'

'very weakly similar to (81.3) AT5G42020 | Symbols: BIP | BIP2; ATP binding | chr5:16807697-16810480 REVERSEvery weakly similar to (84.7) BIP4_TOBAC Luminal-binding protein 4 precursor (BiP 4) (78 kDa glucose-regulated protein homolog 4) (GRP 78-4) - Nicotiana tabacum (Common tobacco)weakly similar to (172) loc_os06g10990 12006.m05816 protein luminal-binding protein precursor, putative, expressed seq=cds; coord=10:121369850..121371290:-1; parent_gene=GRMZM2G135608'

'weakly similar to (152) AT1G25682 | Symbols: | cell cycle control protein-related | chr1:9002532-9004550 REVERSEmoderately similar to (236) loc_os02g21880 12002.m33662 protein coiled-coil domain-containing protein 94, putative, expressed seq=cds; coord=10:144134861..144135949:1; parent_gene=GRMZM2G000650'

'weakly similar to (152) AT1G25682 | Symbols: | cell cycle control protein-related | chr1:9002532-9004550 REVERSEmoderately similar to (236) loc_os02g21880 12002.m33662 protein coiled-coil domain-containing protein 94, putative, expressed seq=cds; coord=10:144134861..144135949:1; parent_gene=GRMZM2G000650'

'moderately similar to (206) AT2G44050 | Symbols: COS1 | COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase | chr2:18224304-18225917 FORWARDweakly similar to (184) RISB_SPIOL 6,7-dimethyl-8-ribityllumazine synthase, chloroplast precursor (EC 2.5.1.9) (DMRL synthase) (Lumazine synthase) - Spinacia oleracea (Spinach)moderately similar to (262) loc_os04g42000 12004.m09174 protein 6,7-dimethyl-8-ribityllumazine synthase, chloroplast precursor, putative, expressed seq=cds; coord=10:145895417..145903773:1; parent_gene=GRMZM2G143480' 'moderately similar to (338) AT1G52520 | Symbols: FRS6 | FRS6 (FAR1-related sequence 6); zinc ion binding | chr1:19565933-19568248 FORWARDweakly similar to (136) NCPR_CATRO NADPH--cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)nearly identical (1222) loc_os07g31420 12007.m07411 protein transposon protein, putative, unclassified, expressed seq=cds; coord=10:146108256..146114652:1; parent_gene=GRMZM2G104268'

'weakly similar to (160) AT3G53160 | Symbols: UGT73C7 | UGT73C7 (UDP-glucosyl transferase 73C7); UDP-glycosyltransferase/ transferase, transferring glycosyl groups | chr3:19702485-19703957 REVERSEweakly similar to (126) ZOX_PHAVU Zeatin O-xylosyltransferase (EC 2.4.2.40) (Zeatin O-beta-D-xylosyltransferase) - Phaseolus vulgaris (Kidney bean) (French bean)moderately similar to (380) loc_os03g46400 12003.m09658 protein flavonol-3-O-glycoside-7-O-glucosyltransferase 1, putative, expressed seq=cds; coord=10:146643280..146645035:1; parent_gene=GRMZM2G067424'

'nearly identical (1680) AT5G65930 | Symbols: ZWI, PKCBP, KCBP | ZWI (ZWICHEL); calmodulin binding / microtubule motor | chr5:26370369-26376394 REVERSEmoderately similar to (217) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiinearly identical (2143) loc_os04g57140 12004.m10599 protein kinesin-like calmodulin binding protein, putative, expressed seq=cds; coord=10:147187794..147201486:-1; parent_gene=GRMZM2G423861'

'moderately similar to (257) AT3G10620 | Symbols: ATNUDX26 | ATNUDX26 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 26); bis(5'-adenosyl)-pentaphosphatase/ bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) | chr3:3320263-3321565 FORWARDmoderately similar to (315) loc_os04g58900 12004.m10770 protein expressed protein seq=cds; coord=10:148849233..148855901:1; parent_gene=GRMZM2G406074'

'highly similar to (580) AT2G02860 | Symbols: SUT2, ATSUC3, SUC3, ATSUT2 | SUT2 (SUCROSE TRANSPORTER 2); carbohydrate transmembrane transporter/ sucrose transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter | chr2:828546-832296 REVERSEmoderately similar to (424) SUT2_ORYSA Sucrose transport protein 2 (Sucrose permease 2) (Sucrose-proton symporter 2) (Sucrose transporter 2) (SUC4-like protein) - Oryza sativa (Rice)highly similar to (907) loc_os03g07480 12003.m35039 protein sucrose Transporter, putative, expressed seq=cds; coord=1:15069803..15075192:-1; parent_gene=GRMZM2G034302'

'moderately similar to (459) AT5G12040 | Symbols: | carbon-nitrogen hydrolase family protein | chr5:3885162-3887772 FORWARDhighly similar to (506) loc_os03g07910 12003.m06302 protein expressed protein seq=cds; coord=1:15990466..15997559:1; parent_gene=GRMZM2G156486'

'moderately similar to (459) AT5G12040 | Symbols: | carbon-nitrogen hydrolase family protein | chr5:3885162-3887772 FORWARDhighly similar to (506) loc_os03g07910 12003.m06302 protein expressed protein seq=cds; coord=1:15990466..15997559:1; parent_gene=GRMZM2G156486'

'moderately similar to (320) AT5G06060 | Symbols: | tropinone reductase, putative / tropine dehydrogenase, putative | chr5:1824066-1825833 REVERSEvery weakly similar to (96.7) GRDH_ORYSA Glucose and ribitol dehydrogenase homolog (EC 1.1.1.-) - Oryza sativa (Rice)moderately similar to (390) loc_os03g16220 12003.m101290 protein tropinone reductase, putative, expressed seq=cds; coord=1:39213217..39219522:-1; parent_gene=GRMZM2G141799'

'highly similar to (787) AT5G60020 | Symbols: LAC17, ATLAC17 | LAC17 (laccase 17); laccase | chr5:24168072-24170223 FORWARDmoderately similar to (205) ASO_CUCMA L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) (ASO) - Cucurbita maxima (Pumpkin) (Winter squash)highly similar to (934) loc_os03g16610 12003.m07094 protein L-ascorbate oxidase precursor, putative, expressed seq=cds; coord=1:39928338..39931744:-1; parent_gene=GRMZM2G305526'

'highly similar to (742) AT2G44900 | Symbols: | armadillo/beta-catenin repeat family protein / F-box family protein | chr2:18511719-18515762 REVERSEhighly similar to (532) loc_os10g41360 12010.m06900 protein ubiquitin-protein ligase, putative, expressed seq=cds; coord=1:93491345..93506165:1; parent_gene=GRMZM2G079031'

'moderately similar to (461) AT4G00460 | Symbols: ATROPGEF3, ROPGEF3 | Rho guanyl-nucleotide exchange factor | chr4:211146-213094 REVERSEhighly similar to (660) loc_os10g40270 12010.m06799 protein pollen-specific kinase partner protein, putative, expressed seq=cds; coord=1:88011829..88014372:-1; parent_gene=GRMZM2G071157'

'highly similar to (860) AT1G73080 | Symbols: PEPR1 | PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase | chr1:27484513-27488021 FORWARDhighly similar to (947) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1470) loc_os08g34640 12008.m07452 protein receptor-like protein kinase precursor, putative, expressed seq=cds; coord=1:210594694..210598577:-1; parent_gene=GRMZM2G428554'

'moderately similar to (284) AT5G25530 | Symbols: | DNAJ heat shock protein, putative | chr5:8889665-8890954 REVERSEvery weakly similar to (87.0) DNJH_CUCSA DnaJ protein homolog (DNAJ-1) - Cucumis sativus (Cucumber)moderately similar to (380) loc_os08g28700 12008.m06875 protein dnaJ homolog subfamily B member 1, putative, expressed seq=cds; coord=1:220116293..220118099:1; parent_gene=GRMZM2G047153'

'moderately similar to (284) AT5G25530 | Symbols: | DNAJ heat shock protein, putative | chr5:8889665-8890954 REVERSEvery weakly similar to (87.0) DNJH_CUCSA DnaJ protein homolog (DNAJ-1) - Cucumis sativus (Cucumber)moderately similar to (380) loc_os08g28700 12008.m06875 protein dnaJ homolog subfamily B member 1, putative, expressed seq=cds; coord=1:220116293..220118099:1; parent_gene=GRMZM2G047153'

'moderately similar to (409) loc_os10g37570 12010.m06544 protein F-box domain containing protein, expressed seq=cds; coord=1:222945692..222947391:-1; parent_gene=GRMZM2G067626'

'very weakly similar to (91.3) AT2G28710 | Symbols: | zinc finger (C2H2 type) family protein | chr2:12322974-12323444 FORWARDweakly similar to (134) loc_os03g60540 12003.m10943 protein zinc finger, C2H2 type family protein seq=cds; coord=1:293139250..293139702:-1; parent_gene=GRMZM2G061897' 'moderately similar to (402) AT4G28510 | Symbols: ATPHB1 | ATPHB1 (PROHIBITIN 1) | chr4:14084970-14086372 REVERSEmoderately similar to (436) loc_os03g62490 12003.m11125 protein mitochondrial prohibitin complex protein 2, putative, expressed seq=cds; coord=1:296891350..296893628:-1; parent_gene=AC217358.3_FG005'

'weakly similar to (135) AT3G48100 | Symbols: ARR5, ATRR2, IBC6 | ARR5 (ARABIDOPSIS RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator | chr3:17759112-17760740 REVERSEweakly similar to (189) loc_os04g57720 12004.m10657 protein OsRR6 - Rice type-A response regulator, expressed seq=cds; coord=2:2081848..2082630:-1; parent_gene=GRMZM2G040736'

'highly similar to (838) AT3G20290 | Symbols: ATEHD1 | ATEHD1 (EPS15 HOMOLOGY DOMAIN 1); GTP binding / GTPase/ calcium ion binding | chr3:7075057-7078655 REVERSEhighly similar to (971) loc_os04g57350 12004.m10620 protein EH-domain-containing protein 1, putative, expressed seq=cds; coord=2:2631218..2635350:-1; parent_gene=GRMZM2G065012'

'nearly identical (1518) AT4G30190 | Symbols: AHA2, PMA2 | AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism | chr4:14770820-14775920 REVERSEnearly identical (1675) PMA1_ORYSA Plasma membrane ATPase (EC 3.6.3.6) (Proton pump) - Oryza sativa (Rice)nearly identical (1675) loc_os04g56160 12004.m101441 protein plasma membrane ATPase, putative, expressed seq=cds; coord=2:4299718..4306692:-1; parent_gene=GRMZM2G019404'
'weakly similar to (177) loc_os04g55920 12004.m35599 protein ZIM motif family protein, expressed seq=cds; coord=2:4697104..4701070:-1; parent_gene=GRMZM2G086920'

'moderately similar to (204) AT3G16150 | Symbols: | L-asparaginase, putative / L-asparagine amidohydrolase, putative | chr3:5471794-5473033 FORWARDweakly similar to (155) ASPG_LUPLU L-asparaginase precursor (EC 3.5.1.1) (L-asparagine amidohydrolase) [Contains: L-asparaginase subunit alpha; L-asparaginase subunit beta] - Lupinus luteus (European yellow lupin)moderately similar to (242) loc_os04g55710 12004.m10462 protein transposon protein, putative, unclassified, expressed seq=cds; coord=2:5071039..5071551:-1; parent_gene=GRMZM2G531230'

'moderately similar to (204) AT3G16150 | Symbols: | L-asparaginase, putative / L-asparagine amidohydrolase, putative | chr3:5471794-5473033 FORWARDweakly similar to (155) ASPG_LUPLU L-asparaginase precursor (EC 3.5.1.1) (L-asparagine amidohydrolase) [Contains: L-asparaginase subunit alpha; L-asparaginase subunit beta] - Lupinus luteus (European yellow lupin)moderately similar to (242) loc_os04g55710 12004.m10462 protein transposon protein, putative, unclassified, expressed seq=cds; coord=2:5071039..5071551:-1; parent_gene=GRMZM2G531230'

'moderately similar to (268) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDweakly similar to (130) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (382) loc_os04g55560 12004.m35488 protein AP2 domain containing protein, expressed seq=cds; coord=2:5514479..5518846:-1; parent_gene=GRMZM2G174784'

'weakly similar to (148) AT4G24690 | Symbols: | ubiquitin-associated (UBA)/TS-N domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein | chr4:12741191-12744202 FORWARDmoderately similar to (422) loc_os04g40090 12004.m08993 protein zinc finger, ZZ type family protein, expressed seq=cds; coord=2:37844098..37854782:1; parent_gene=GRMZM2G139846'

'weakly similar to (154) loc_os12g06550 12012.m04645 protein expressed protein seq=cds; coord=2:52832595..52834639:-1; parent_gene=GRMZM2G541230'

'very weakly similar to (80.9) AT3G18610 | Symbols: ATRANGAP1, PARLL1 | ATRANGAP1 (RAN GTPASE-ACTIVATING PROTEIN 1); nucleic acid binding / nucleotide binding | chr3:6404270-6407822 REVERSEweakly similar to (131) loc_os08g09350 12008.m05069 protein protein gar2, putative, expressed seq=cds; coord=2:123918252..123940966:1; parent_gene=GRMZM2G435248'

'moderately similar to (284) AT1G76470 | Symbols: | 3-beta-hydroxy-delta5-steroid dehydrogenase/ binding / catalytic/ cinnamoyl-CoA reductase | chr1:28689955-28691405 REVERSEweakly similar to (157) DFRA_PETHY Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Petunia hybrida (Petunia)moderately similar to (422) loc_os09g31502 12009.m22008 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=2:190187087..190189448:-1; parent_gene=GRMZM2G078480'

'moderately similar to (221) AT4G18100 | Symbols: | 60S ribosomal protein L32 (RPL32A) | chr4:10035715-10036475 REVERSEmoderately similar to (259) loc_os08g41300 12008.m08108 protein 60S ribosomal protein L32, putative, expressed seq=cds; coord=2:191350704..191353166:1; parent_gene=GRMZM2G047971'

'highly similar to (653) AT2G31820 | Symbols: | ankyrin repeat family protein | chr2:13530350-13532562 FORWARDhighly similar to (940) loc_os09g34280 12009.m060043 protein protein binding protein, putative, expressed seq=cds; coord=2:193829792..193833616:1; parent_gene=GRMZM2G022032'

'highly similar to (653) AT2G31820 | Symbols: | ankyrin repeat family protein | chr2:13530350-13532562 FORWARDhighly similar to (940) loc_os09g34280 12009.m060043 protein protein binding protein, putative, expressed seq=cds; coord=2:193829792..193833616:1; parent_gene=GRMZM2G022032'

'very weakly similar to (87.0) AT1G72310 | Symbols: ATL3 | ATL3; protein binding / zinc ion binding | chr1:27226405-27227379 FORWARDvery weakly similar to (80.9) EL5_ORYSA E3 ubiquitin-protein ligase EL5 (EC 6.3.2.-) - Oryza sativa (Rice)weakly similar to (154) loc_os07g42610 12007.m08493 protein ring-H2 zinc finger protein, putative, expressed seq=cds; coord=2:211590201..211591615:-1; parent_gene=GRMZM2G358987'

'highly similar to (783) AT1G24190 | Symbols: SIN3, ATSIN3, SNL3 | SNL3 (SIN3-LIKE 3); transcription repressor | chr1:8563858-8569996 REVERSEnearly identical (1814) loc_os01g01960 12001.m06838 protein paired amphipathic helix repeat family protein, expressed seq=cds; coord=3:28819050..28829107:-1; parent_gene=GRMZM2G075320'

'moderately similar to (220) AT3G17840 | Symbols: RLK902 | RLK902; ATP binding / kinase/ protein serine/threonine kinase | chr3:6106092-6108430 FORWARDweakly similar to (152) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)moderately similar to (371) loc_os10g05400 12010.m03945 protein OsWAK102 - OsWAK receptor-like cytoplasmic kinase (OsWAK-RLCK) seq=cds; coord=3:114020698..114023620:-1; parent_gene=GRMZM2G026203' 'moderately similar to (222) AT2G19770 | Symbols: PRF5 | PRF5 (PROFILIN5); actin binding / actin monomer binding | chr2:8519885-8521119 REVERSEmoderately similar to (263) PROFA_ORYSA Profilin-A - Oryza sativa (Rice)moderately similar to (263) loc_os10g17680 12010.m04853 protein profilin A, putative, expressed seq=cds; coord=3:199620448..199621531:-1; parent_gene=GRMZM2G140455'

'weakly similar to (141) AT5G47210 | Symbols: | nuclear RNA-binding protein, putative | chr5:19169388-19171012 REVERSEmoderately similar to (265) loc_os01g52390 12001.m11413 protein plasminogen activator inhibitor 1 RNA-binding protein, putative, expressed seq=cds; coord=3:202432697..202435947:1; parent_gene=GRMZM2G055276'

'very weakly similar to (87.4) loc_os04g24530 12004.m101489 protein 4-coumarate--CoA ligase 2, putative, expressed seq=cds; coord=3:208890114..208890945:1; parent_gene=GRMZM2G012233'

'moderately similar to (452) AT2G33860 | Symbols: ETT, ARF3 | ETT (ETTIN); DNA binding / transcription factor | chr2:14325444-14328613 REVERSEhighly similar to (967) loc_os01g48060 12001.m43135 protein auxin response factor 3, putative, expressed seq=cds; coord=3:210265410..210273272:1; parent_gene=GRMZM2G437460'

'moderately similar to (452) AT2G33860 | Symbols: ETT, ARF3 | ETT (ETTIN); DNA binding / transcription factor | chr2:14325444-14328613 REVERSEhighly similar to (967) loc_os01g48060 12001.m43135 protein auxin response factor 3, putative, expressed seq=cds; coord=3:210265410..210273272:1; parent_gene=GRMZM2G437460'

'highly similar to (538) AT4G16745 | Symbols: | exostosin family protein | chr4:9412185-9414053 FORWARDhighly similar to (709) loc_os01g45350 12001.m10738 protein limonene cyclase like protein, putative, expressed seq=cds; coord=3:215380332..215382314:-1; parent_gene=GRMZM2G048010'

highly similar to (638) AT5G47560 | Symbols: ATTDT, ATSDAT, TDT | TDT (TONOPLAST DICARBOXYLATE TRANSPORTER); malate transmembrane transporter/ sodium:dicarboxylate symporter | chr5:19287895-19290347 REVERSEhighly similar to (820) loc_os08g39370 12008.m07918 protein tonoplast dicarboxylate transporter, putative, expressed seq=cds; coord=3:215902932..215905725:1; parent_gene=GRMZM2G099382'

'highly similar to (515) AT1G60590 | Symbols: | polygalacturonase, putative / pectinase, putative | chr1:22314426-22316867 REVERSEmoderately similar to (248) PGLR_ACTCH Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) - Actinidia chinensis (Kiwi) (Yangtao)highly similar to (734) loc_os01g44970 12001.m10703 protein polygalacturonase precursor, putative, expressed seq=cds; coord=3:215929238..215932695:-1; parent_gene=GRMZM2G037431'

'weakly similar to (189) loc_os01g42710 12001.m10535 protein LSD1 zinc finger family protein, expressed seq=cds; coord=3:225083458..225086011:1; parent_gene=GRMZM2G002646'

'moderately similar to (323) AT1G15950 | Symbols: CCR1, IRX4, ATCCR1 | CCR1 (CINNAMOYL COA REDUCTASE 1); cinnamoyl-CoA reductase | chr1:5478855-5481949 FORWARDweakly similar to (171) DFRA_MAIZE Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Zea mays (Maize)highly similar to (513) loc_os02g56460 12002.m10668 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=4:171783871..171785676:-1; parent_gene=GRMZM2G099420' 'highly similar to (694) AT5G60710 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24410953-24414849 REVERSEnearly identical (1189) loc_os02g56280 12002.m10651 protein protein binding protein, putative, expressed seq=cds; coord=4:172685051..172689834:1; parent_gene=GRMZM2G130002'

'moderately similar to (449) AT1G22170 | Symbols: | phosphoglycerate/bisphosphoglycerate mutase family protein | chr1:7826603-7828055 FORWARDhighly similar to (571) loc_os02g51590 12002.m33276 protein 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase, putative, expressed seq=cds; coord=4:181228946..181231966:-1; parent_gene=GRMZM2G021605'

'moderately similar to (352) AT5G58490 | Symbols: | cinnamoyl-CoA reductase family | chr5:23643068-23644455 FORWARDweakly similar to (154) DFRA_VITVI Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Vitis vinifera (Grape)moderately similar to (441) loc_os03g60380 12003.m10928 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=5:2705885..2708336:1; parent_gene=GRMZM2G107076'

'weakly similar to (174) AT4G18770 | Symbols: MYB98, AtMYB98 | MYB98 (myb domain protein 98); DNA binding / transcription factor | chr4:10311068-10312557 FORWARDvery weakly similar to (92.8) ODO1_PETHY ODORANT1 protein (MYB-like protein ODO1) - Petunia hybrida (Petunia)moderately similar to (227) loc_os12g07610 12012.m04750 protein myb family transcription factor, putative seq=cds; coord=5:4155876..4160856:1; parent_gene=GRMZM2G302549'

'weakly similar to (131) AT5G14570 | Symbols: ATNRT2.7 | ATNRT2.7 (Arabidopsis thaliana high affinity nitrate transporter 2.7); nitrate transmembrane transporter | chr5:4695331-4696890 REVERSEmoderately similar to (214) loc_os01g36720 12001.m09967 protein nitrate transporter, putative seq=cds; coord=5:5321650..5322849:-1; parent_gene=GRMZM2G377555'

'moderately similar to (272) AT1G17810 | Symbols: BETA-TIP | BETA-TIP (BETA-TONOPLAST INTRINSIC PROTEIN); water channel | chr1:6130209-6131442 FORWARDmoderately similar to (379) TIP31_ORYSA Probable aquaporin TIP3.1 (Tonoplast intrinsic protein 3.1) (OsTIP3.1) - Oryza sativa (Rice)moderately similar to (379) loc_os10g35050 12010.m06328 protein aquaporin TIP3.1, putative, expressed seq=cds; coord=5:25511080..25512421:1; parent_gene=GRMZM2G305446'

'moderately similar to (412) AT2G05940 | Symbols: | protein kinase, putative | chr2:2287514-2289270 REVERSEmoderately similar to (211) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (523) loc_os10g25550 12010.m05501 protein serine/threonine-protein kinase NAK, putative, expressed seq=cds; coord=5:36546532..36548678:1; parent_gene=GRMZM2G110968'

'moderately similar to (418) AT1G05840 | Symbols: | aspartyl protease family protein | chr1:1762843-1766150 REVERSEvery weakly similar to (98.2) ASP1_ORYSA Aspartic proteinase Asp1 precursor (EC 3.4.23.-) (OsAsp1) (OSAP1) (Nucellin-like protein) - Oryza sativa (Rice)highly similar to (591) loc_os02g27360 12002.m100207 protein pepsin A, putative, expressed seq=cds; coord=5:160161741..160166346:-1; parent_gene=GRMZM2G411333'

'weakly similar to (178) loc_os02g46220 12002.m09659 protein S-ribonuclease binding protein SBP1, putative, expressed seq=cds; coord=5:197784768..197786610:-1; parent_gene=GRMZM2G039725' 'weakly similar to (178) loc_os02g46220 12002.m09659 protein S-ribonuclease binding protein SBP1, putative, expressed seq=cds; coord=5:197784768..197786610:-1; parent_gene=GRMZM2G039725'

'weakly similar to (163) loc_os09g06740 12009.m03943 protein protein binding protein, putative, expressed seq=cds; coord=5:214077718..214078206:-1; parent_gene=GRMZM2G467756'

'moderately similar to (376) AT4G27100 | Symbols: | RAB GTPase activator | chr4:13595845-13598620 FORWARDhighly similar to (538) loc_os02g56570 12002.m10679 protein TBC domain containing protein, expressed seq=cds; coord=5:215006181..215011162:-1; parent_gene=GRMZM2G150876'

'moderately similar to (204) AT5G36210 | Symbols: | serine-type peptidase | chr5:14248202-14253272 REVERSEmoderately similar to (252) loc_os06g11180 12006.m05835 protein acyl-peptide hydrolase-like, putative, expressed seq=cds; coord=6:2047614..2057911:1; parent_gene=GRMZM2G313321'

'weakly similar to (182) AT3G07370 | Symbols: ATCHIP, CHIP | CHIP (CARBOXYL TERMINUS OF HSC70-INTERACTING PROTEIN); ubiquitin-protein ligase | chr3:2358323-2360301 REVERSEmoderately similar to (252) loc_os08g02140 12008.m080065 protein STIP1 homology and U box-containing protein 1, expressed seq=cds; coord=6:3643162..3647082:1; parent_gene=GRMZM2G104769'

'weakly similar to (107) AT3G14250 | Symbols: | protein binding / zinc ion binding | chr3:4745963-4746958 REVERSEweakly similar to (193) loc_os09g25190 12009.m05671 protein ubiquitin-protein ligase/ zinc ion binding protein, putative, expressed seq=cds; coord=6:6700670..6701561:1; parent_gene=GRMZM2G390009'

'moderately similar to (414) AT2G40010 | Symbols: | 60S acidic ribosomal protein P0 (RPP0A) | chr2:16708578-16710448 REVERSEhighly similar to (523) RLA0_MAIZE 60S acidic ribosomal protein P0 - Zea mays (Maize)moderately similar to (464) loc_os12g03880 12012.m04384 protein 60S acidic ribosomal protein P0, putative, expressed seq=cds; coord=6:9203729..9206286:-1; parent_gene=GRMZM2G066460'

'weakly similar to (170) AT5G52880 | Symbols: | F-box family protein | chr5:21432002-21433695 REVERSEmoderately similar to (424) loc_os05g45040 12005.m08629 protein F-box domain containing protein, expressed seq=cds; coord=6:160000083..160005049:-1; parent_gene=GRMZM2G004592'

'moderately similar to (413) AT2G19480 | Symbols: NFA02, NFA2 | NAP1;2 (NUCLEOSOME ASSEMBLY PROTEIN 1;2); DNA binding / binding | chr2:8438601-8441040 FORWARDhighly similar to (508) loc_os05g46230 12005.m083791 protein expressed protein seq=cds; coord=6:161659850..161663090:-1; parent_gene=GRMZM2G121186'

'moderately similar to (371) AT4G39150 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr4:18233651-18235740 REVERSEmoderately similar to (478) loc_os05g46620 12005.m08785 protein chaperone protein dnaJ 10, putative, expressed seq=cds; coord=6:162112265..162116068:-1; parent_gene=GRMZM2G175089'

'highly similar to (681) AT1G27440 | Symbols: GUT2, IRX10, ATGUT1 | GUT2; catalytic/ glucuronoxylan glucuronosyltransferase | chr1:9529265-9531213 REVERSEhighly similar to (738) loc_os01g70190 12001.m13067 protein secondary cell wall-related glycosyltransferase family 47, putative, expressed seq=cds; coord=6:162559883..162562784:1; parent_gene=GRMZM2G059845' 'moderately similar to (223) AT4G32590 | Symbols: | ferredoxin-related | chr4:15721417-15722781 FORWARDmoderately similar to (235) loc_os05g48160 12005.m27636 protein electron carrier/ electron transporter/ iron ion binding protein, putative, expressed seq=cds; coord=6:163178134..163181036:-1; parent_gene=GRMZM2G481261'

'highly similar to (733) AT4G11110 | Symbols: SPA2 | SPA2 (SPA1-RELATED 2); protein binding / signal transducer | chr4:6772163-6776675 FORWARDmoderately similar to (329) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)nearly identical (1523) loc_os05g49590 12005.m083816 protein SPA1, putative, expressed seq=cds; coord=6:165393177..165402270:-1; parent_gene=GRMZM2G145556'

'moderately similar to (442) AT2G30070 | Symbols: ATKT1, ATKT1P, ATKUP1, KUP1 | ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter | chr2:12835097-12838466 FORWARDnearly identical (1021) HAK17_ORYSA Probable potassium transporter 17 (OsHAK17) - Oryza sativa (Rice)nearly identical (1021) loc_os09g27580 12009.m22100 protein potassium transporter 17, putative, expressed seq=cds; coord=7:123669996..123673712:1; parent_gene=GRMZM2G088964'

'moderately similar to (204) AT3G01850 | Symbols: | ribulose-phosphate 3-epimerase, cytosolic, putative / pentose-5-phosphate 3-epimerase, putative | chr3:300428-301987 REVERSEmoderately similar to (231) RPE1_ORYSA Ribulose-phosphate 3-epimerase, cytoplasmic isoform (EC 5.1.3.1) (Ribulose-5-phosphate-epimerase) (Cyt-RPEase) (RPEcyt) (Pentose-5-phosphate 3-epimerase) (PPE) - Oryza sativa (Rice)moderately similar to (231) loc_os09g32810 12009.m22157 protein ribulose-phosphate 3-epimerase, putative, expressed seq=cds; coord=7:136742676..136746945:1; parent_gene=GRMZM2G083102'

'very weakly similar to (92.0) AT1G70150 | Symbols: | zinc ion binding | chr1:26416898-26419521 FORWARDweakly similar to (112) loc_os07g29770 12007.m079679 protein MYND finger family protein, expressed seq=cds; coord=7:148589249..148620557:1; parent_gene=GRMZM2G007190'

'moderately similar to (263) AT3G16520 | Symbols: UGT88A1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr3:5618847-5620833 REVERSEweakly similar to (135) ZOX_PHAVU Zeatin O-xylosyltransferase (EC 2.4.2.40) (Zeatin O-beta-D-xylosyltransferase) - Phaseolus vulgaris (Kidney bean) (French bean)highly similar to (627) loc_os07g32020 12007.m07468 protein anthocyanidin 3-O-glucosyltransferase, putative, expressed seq=cds; coord=7:151190045..151192101:1; parent_gene=GRMZM2G155911'

'highly similar to (620) AT4G21990 | Symbols: APR3, PRH-26, PRH26, ATAPR3 | APR3 (APS REDUCTASE 3); adenylyl-sulfate reductase | chr4:11657284-11658973 REVERSEhighly similar to (686) loc_os07g32570 12007.m07520 protein OsAPRL1 - Oryza sativa adenosine 5'-phosphosulfate reductase-like, expressed seq=cds; coord=7:152351854..152354543:-1; parent_gene=AC189750.4_FG004'

'weakly similar to (137) AT1G23100 | Symbols: | 10 kDa chaperonin, putative | chr1:8195867-8196336 FORWARDweakly similar to (133) CH10_BRANA 10 kDa chaperonin (Protein CPN10) (Protein groES) - Brassica napus (Rape)weakly similar to (177) loc_os07g44740 12007.m08695 protein chaperonin, putative, expressed seq=cds; coord=7:169267359..169269362:1; parent_gene=GRMZM2G013652' 'weakly similar to (120) AT5G18560 | Symbols: PUCHI | PUCHI; DNA binding / transcription factor | chr5:6164859-6165905 REVERSEvery weakly similar to (85.9) ERF4_TOBAC Ethylene-responsive transcription factor 4 (Ethylene-responsive element-binding factor 4 homolog) (EREBP-3) (NtERF3) - Nicotiana tabacum (Common tobacco)moderately similar to (264) loc_os07g47330 12007.m08950 protein branched silkless1, putative, expressed seq=cds; coord=7:172207717..172209213:-1; parent_gene=GRMZM2G307119'

'weakly similar to (120) AT5G18560 | Symbols: PUCHI | PUCHI; DNA binding / transcription factor | chr5:6164859-6165905 REVERSEvery weakly similar to (85.9) ERF4_TOBAC Ethylene-responsive transcription factor 4 (Ethylene-responsive element-binding factor 4 homolog) (EREBP-3) (NtERF3) - Nicotiana tabacum (Common tobacco)moderately similar to (264) loc_os07g47330 12007.m08950 protein branched silkless1, putative, expressed seq=cds; coord=7:172207717..172209213:-1; parent_gene=GRMZM2G307119'

'moderately similar to (312) AT5G05340 | Symbols: | peroxidase, putative | chr5:1579142-1580819 REVERSEmoderately similar to (340) PER2_ORYSA Peroxidase 2 precursor (EC 1.11.1.7) - Oryza sativa (Rice)moderately similar to (340) loc_os07g48030 12007.m09018 protein peroxidase 2 precursor, putative, expressed seq=cds; coord=7:172779032..172780863:1; parent_gene=GRMZM2G126261'

'moderately similar to (253) AT2G30360 | Symbols: CIPK11, PKS5, SIP4, SNRK3.22 | SIP4 (SOS3-INTERACTING PROTEIN 4); kinase/ protein kinase | chr2:12937265-12938572 REVERSEweakly similar to (193) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)moderately similar to (407) loc_os07g48090 12007.m09024 protein CBL-interacting serine/threonine-protein kinase 11, putative, expressed seq=cds; coord=7:172879486..172881907:1; parent_gene=GRMZM2G177050'

'moderately similar to (282) AT2G22230 | Symbols: | beta-hydroxyacyl-ACP dehydratase, putative | chr2:9450042-9451427 FORWARDmoderately similar to (344) loc_os05g36000 12005.m27841 protein beta-hydroxyacyl-ACP dehydratase, putative, expressed seq=cds; coord=8:101237177..101240478:-1; parent_gene=GRMZM2G055667'

'moderately similar to (246) AT3G07880 | Symbols: | Rho GDP-dissociation inhibitor family protein | chr3:2514175-2515544 FORWARDmoderately similar to (345) loc_os01g68540 12001.m12957 protein rho GDP-dissociation inhibitor 1, putative, expressed seq=cds; coord=8:110142652..110144824:1; parent_gene=GRMZM2G150724'

'weakly similar to (133) AT3G22780 | Symbols: TSO1, ATTSO1 | TSO1 (CHINESE FOR 'UGLY'); transcription factor | chr3:8048927-8052058 FORWARDmoderately similar to (500) loc_os05g43380 12005.m27907 protein CXC domain containing TSO1-like protein 1, putative, expressed seq=cds; coord=8:122238598..122240038:1; parent_gene=GRMZM2G173198'

'highly similar to (526) AT4G13260 | Symbols: YUC2 | YUC2 (YUCCA2); FAD binding / NADP or NADPH binding / flavin-containing monooxygenase/ oxidoreductase | chr4:7721840-7723616 REVERSEhighly similar to (720) loc_os01g53200 12001.m11489 protein disulfide oxidoreductase/ monooxygenase/ oxidoreductase, putative, expressed seq=cds; coord=8:156255731..156258807:1; parent_gene=GRMZM2G017193' 'weakly similar to (181) AT5G40950 | Symbols: RPL27 | RPL27 (RIBOSOMAL PROTEIN LARGE SUBUNIT 27); structural constituent of ribosome | chr5:16410866-16411845 FORWARDmoderately similar to (241) RK27_ORYSA 50S ribosomal protein L27, chloroplast precursor (CL27) - Oryza sativa (Rice)moderately similar to (241) loc_os01g69950 12001.m13044 protein 50S ribosomal protein L27, chloroplast precursor, putative, expressed seq=cds; coord=8:161078252..161080283:-1; parent_gene=GRMZM2G145496'

'moderately similar to (269) AT1G73030 | Symbols: VPS46.2 | VPS46.2 | chr1:27473938-27474848 FORWARDmoderately similar to (292) loc_os06g43590 12006.m091745 protein charged multivesicular body protein 1b, putative, expressed seq=cds; coord=9:94575435..94578265:-1; parent_gene=GRMZM2G117935'

'weakly similar to (174) AT4G27600 | Symbols: | pfkB-type carbohydrate kinase family protein | chr4:13782753-13785005 REVERSEmoderately similar to (224) loc_os10g42240 12010.m21983 protein carbohydrate kinase-like protein, putative, expressed seq=cds; coord=9:112819814..112820314:1; parent_gene=GRMZM2G144245'

'moderately similar to (418) AT4G14480 | Symbols: | protein kinase family protein | chr4:8330081-8331544 REVERSEweakly similar to (112) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)highly similar to (635) loc_os03g47470 12003.m09757 protein ATP binding protein, putative seq=cds; coord=10:1714434..1716242:-1; parent_gene=GRMZM2G430780'

'moderately similar to (397) AT4G10520 | Symbols: | subtilase family protein | chr4:6499794-6502866 FORWARDhighly similar to (617) loc_os04g03100 12004.m05621 protein xylem serine proteinase 1 precursor, putative, expressed seq=cds; coord=10:1891328..1894470:-1; parent_gene=GRMZM2G012062'

'nearly identical (1233) AT2G41560 | Symbols: ACA4 | ACA4 (AUTO-INHIBITED CA(2

'moderately similar to (388) AT3G04080 | Symbols: ATAPY1 | ATAPY1 (APYRASE 1); ATPase/ calmodulin binding / nucleotide diphosphatase | chr3:1068068-1070917 REVERSEmoderately similar to (386) APY_SOLTU Apyrase precursor (EC 3.6.1.5) (ATP-diphosphatase) (Adenosine diphosphatase) (ADPase) (ATP-diphosphohydrolase) - Solanum tuberosum (Potato)highly similar to (572) loc_os12g02980 12012.m26816 protein apyrase precursor, putative, expressed seq=cds; coord=10:2760826..2763337:-1; parent_gene=GRMZM2G431714'

'highly similar to (761) AT1G11680 | Symbols: CYP51G1, EMB1738, CYP51A2, CYP51 | CYP51G1 (CYTOCHROME P450 51G1); oxygen binding / sterol 14-demethylase | chr1:3938925-3940585 FORWARDhighly similar to (911) CP51_SORBI Cytochrome P450 51 (EC 1.14.13.70) (CYPLI) (P450-LIA1) (Obtusifoliol 14-alpha demethylase) - Sorghum bicolor (Sorghum) (Sorghum vulgare)highly similar to (862) loc_os11g32240 12011.m07126 protein cytochrome P450 51, putative, expressed seq=cds; coord=10:3062645..3066458:-1; parent_gene=GRMZM2G068465'

'moderately similar to (209) AT3G26085 | Symbols: | CAAX amino terminal protease family protein | chr3:9530842-9532397 FORWARDmoderately similar to (247) loc_os05g22930 12005.m06589 protein CAAX amino terminal protease family protein seq=cds; coord=10:4664889..4667695:-1; parent_gene=GRMZM2G003750' 'highly similar to (764) AT4G34200 | Symbols: EDA9 | EDA9 (embryo sac development arrest 9); ATP binding | chr4:16374041-16376561 REVERSEweakly similar to (102) DHGY_CUCSA Glycerate dehydrogenase (EC 1.1.1.29) (NADH-dependent hydroxypyruvate reductase) (HPR) (GDH) - Cucumis sativus (Cucumber)highly similar to (864) loc_os04g55720 12004.m35214 protein D-3-phosphoglycerate dehydrogenase, chloroplast precursor, putative, expressed seq=cds; coord=10:145794456..145798655:1; parent_gene=GRMZM2G009323'

'moderately similar to (204) AT2G44050 | Symbols: COS1 | COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase | chr2:18224304-18225917 FORWARDweakly similar to (181) RISB_SPIOL 6,7-dimethyl-8-ribityllumazine synthase, chloroplast precursor (EC 2.5.1.9) (DMRL synthase) (Lumazine synthase) - Spinacia oleracea (Spinach)moderately similar to (258) loc_os04g42000 12004.m09174 protein 6,7-dimethyl-8-ribityllumazine synthase, chloroplast precursor, putative, expressed seq=cds; coord=10:145895430..145900495:1; parent_gene=GRMZM2G143480'

'moderately similar to (338) AT1G52520 | Symbols: FRS6 | FRS6 (FAR1-related sequence 6); zinc ion binding | chr1:19565933-19568248 FORWARDweakly similar to (136) NCPR_CATRO NADPH--cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)nearly identical (1222) loc_os07g31420 12007.m07411 protein transposon protein, putative, unclassified, expressed seq=cds; coord=10:146108256..146114652:1; parent_gene=GRMZM2G104268'

'moderately similar to (261) AT4G32300 | Symbols: SD2-5 | SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase | chr4:15599970-15602435 FORWARDweakly similar to (176) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (570) loc_os04g56110 12004.m35493 protein ATP binding protein, putative, expressed seq=cds; coord=10:146170484..146172446:-1; parent_gene=GRMZM2G007477'

'highly similar to (663) AT1G01140 | Symbols: CIPK9, PKS6 | CIPK9 (CBL-INTERACTING PROTEIN KINASE 9); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr1:64398-67512 REVERSEhighly similar to (572) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)highly similar to (792) loc_os03g03510 12003.m34994 protein CIPK-like protein 1, putative, expressed seq=cds; coord=1:5538101..5542785:-1; parent_gene=GRMZM2G055575'

'moderately similar to (229) AT1G56500 | Symbols: | haloacid dehalogenase-like hydrolase family protein | chr1:21159775-21167092 FORWARDmoderately similar to (349) loc_os03g19760 12003.m35188 protein NHL repeat protein, putative, expressed seq=cds; coord=1:50700350..50712129:1; parent_gene=AC208571.4_FG001'

'highly similar to (505) AT2G47900 | Symbols: AtTLP3 | AtTLP3 (TUBBY LIKE PROTEIN 3); phosphoric diester hydrolase/ transcription factor | chr2:19611196-19612766 REVERSEhighly similar to (622) loc_os03g22800 12003.m78863 protein tubby protein, putative, expressed seq=cds; coord=1:60093104..60101657:-1; parent_gene=GRMZM2G378907'

'moderately similar to (221) AT1G05260 | Symbols: RCI3, RCI3A | RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase | chr1:1529827-1531271 FORWARDmoderately similar to (218) PER1_ARAHY Cationic peroxidase 1 precursor (EC 1.11.1.7) (PNPC1) - Arachis hypogaea (Peanut)moderately similar to (487) loc_os03g25330 12003.m07877 protein peroxidase 66 precursor, putative, expressed seq=cds; coord=1:63645310..63646802:1; parent_gene=GRMZM2G040638' 'moderately similar to (463) AT4G25000 | Symbols: ATAMY1, AMY1 | AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase | chr4:12852109-12853825 REVERSEhighly similar to (748) AMY3D_ORYSA Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) - Oryza sativa (Rice)highly similar to (748) loc_os08g36910 12008.m26515 protein alpha-amylase isozyme 3D precursor, putative, expressed seq=cds; coord=1:199630232..199632219:1; parent_gene=GRMZM2G070172'

'weakly similar to (111) AT2G40350 | Symbols: | DNA binding / transcription factor | chr2:16851595-16852068 REVERSEweakly similar to (144) loc_os08g45110 12008.m08481 protein dehydration-responsive element-binding protein 2D, putative, expressed seq=cds; coord=1:201957089..201958672:1; parent_gene=GRMZM2G028386'

'highly similar to (649) AT3G24660 | Symbols: TMKL1 | TMKL1 (transmembrane kinase-like 1); ATP binding / kinase/ protein serine/threonine kinase | chr3:9003641-9005751 FORWARDweakly similar to (173) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (740) loc_os08g45060 12008.m08476 protein protein Kinase-like protein TMKL1 precursor, putative, expressed seq=cds; coord=1:202158131..202160689:-1; parent_gene=GRMZM2G422373'

'moderately similar to (230) AT5G04410 | Symbols: NAC2, anac078 | NAC2; transcription factor | chr5:1243980-1246416 FORWARDweakly similar to (159) NAC74_ORYSA NAC domain-containing protein 74 (ONAC074) - Oryza sativa (Rice)highly similar to (845) loc_os08g44820 12008.m080239 protein no apical meristem protein, expressed seq=cds; coord=1:203087262..203092166:1; parent_gene=GRMZM2G340305'

'moderately similar to (485) AT5G21482 | Symbols: CKX7, ATCKX5 | CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase | chr5:7226842-7230052 FORWARDmoderately similar to (321) CKX1_MAIZE Cytokinin dehydrogenase 1 precursor (EC 1.5.99.12) (Cytokinin oxidase 1) (CKO 1) (COX 1) (ZmCKX1) - Zea mays (Maize)highly similar to (706) loc_os08g35860 12008.m07575 protein cytokinin dehydrogenase 7, putative, expressed seq=cds; coord=1:207708925..207713476:1; parent_gene=GRMZM2G348452'

'weakly similar to (101) AT5G20630 | Symbols: GLP3, GLP3A, GLP3B, ATGER3, GER3 | GER3 (GERMIN 3); oxalate oxidase | chr5:6975315-6975950 REVERSEweakly similar to (103) GLP1_SINAL Germin-like protein 1 precursor - Sinapis alba (White mustard) (Brassica hirta)weakly similar to (114) loc_os08g35750 12008.m07564 protein germin-like protein 1 precursor, putative, expressed seq=cds; coord=1:207865153..207865778:-1; parent_gene=GRMZM2G363004'

'weakly similar to (160) AT1G72610 | Symbols: GLP1, ATGER1, GER1 | GER1 (GERMIN-LIKE PROTEIN 1); oxalate oxidase | chr1:27339302-27339928 REVERSEweakly similar to (161) AB19B_PRUPE Auxin-binding protein ABP19b precursor - Prunus persica (Peach)moderately similar to (207) loc_os08g35750 12008.m07564 protein germin-like protein 1 precursor, putative, expressed seq=cds; coord=1:207891946..207892644:1; parent_gene=AC195794.3_FG002' 'moderately similar to (429) AT1G11190 | Symbols: BFN1, ENDO1 | BFN1 (BIFUNCTIONAL NUCLEASE I); T/G mismatch-specific endonuclease/ endoribonuclease, producing 5'-phosphomonoesters / nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease | chr1:3750338-3752696 REVERSEmoderately similar to (389) loc_os04g54390 12004.m10330 protein nuclease PA3, putative, expressed seq=cds; coord=1:224916793..224919064:-1; parent_gene=GRMZM2G168744'

'highly similar to (645) AT4G28600 | Symbols: NPGR2 | NPGR2 (no pollen germination related 2); calmodulin binding | chr4:14130046-14132599 FORWARDnearly identical (1135) loc_os10g33290 12010.m50421 protein NPGR2, putative, expressed seq=cds; coord=1:232995038..233002321:1; parent_gene=GRMZM2G117763'

'moderately similar to (469) AT5G60710 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24410953-24414849 REVERSEhighly similar to (660) loc_os10g32740 12010.m06110 protein protein binding protein, putative, expressed seq=cds; coord=1:233577053..233579470:-1; parent_gene=GRMZM2G343972'

'weakly similar to (143) AT4G18770 | Symbols: MYB98, AtMYB98 | MYB98 (myb domain protein 98); DNA binding / transcription factor | chr4:10311068-10312557 FORWARDweakly similar to (114) GAM1_ORYSA Transcription factor GAMYB (OsGAMyb) - Oryza sativa (Rice)moderately similar to (208) loc_os01g63680 12001.m12483 protein myb-like DNA-binding domain containing protein, expressed seq=cds; coord=1:252320123..252322173:1; parent_gene=GRMZM2G121570'

'highly similar to (568) AT4G33950 | Symbols: OST1, SNRK2-6, SRK2E, SNRK2.6, P44 | OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase | chr4:16272819-16274657 FORWARDhighly similar to (646) SAPKA_ORYSA Serine/threonine-protein kinase SAPK10 (EC 2.7.11.1) (Osmotic stress/abscisic acid-activated protein kinase 10) - Oryza sativa (Rice)highly similar to (646) loc_os03g41460 12003.m09212 protein serine/threonine-protein kinase SAPK10, putative, expressed seq=cds; coord=1:255084395..255087718:1; parent_gene=GRMZM2G081915'

'highly similar to (568) AT4G33950 | Symbols: OST1, SNRK2-6, SRK2E, SNRK2.6, P44 | OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase | chr4:16272819-16274657 FORWARDhighly similar to (646) SAPKA_ORYSA Serine/threonine-protein kinase SAPK10 (EC 2.7.11.1) (Osmotic stress/abscisic acid-activated protein kinase 10) - Oryza sativa (Rice)highly similar to (646) loc_os03g41460 12003.m09212 protein serine/threonine-protein kinase SAPK10, putative, expressed seq=cds; coord=1:255084395..255087718:1; parent_gene=GRMZM2G081915'

'weakly similar to (143) AT5G26751 | Symbols: ATSK11, SK 11 | ATSK11; protein kinase/ protein serine/threonine kinase | chr5:9399582-9401839 REVERSEweakly similar to (152) MSK1_TOBAC Shaggy-related protein kinase NtK-1 (EC 2.7.11.1) - Nicotiana tabacum (Common tobacco)weakly similar to (177) loc_os01g14860 12001.m43459 protein glycogen synthase kinase-3 homolog MsK-3, putative, expressed seq=cds; coord=1:257033199..257043603:1; parent_gene=GRMZM2G357081'

'weakly similar to (180) AT4G37740 | Symbols: AtGRF2 | AtGRF2 (GROWTHREGULATING FACTOR 2); transcription activator | chr4:17725533-17727609 REVERSEhighly similar to (517) loc_os03g47140 12003.m09727 protein atGRF2, putative, expressed seq=cds; coord=1:257186167..257188884:-1; parent_gene=GRMZM2G018414' 'weakly similar to (180) AT4G37740 | Symbols: AtGRF2 | AtGRF2 (GROWTHREGULATING FACTOR 2); transcription activator | chr4:17725533-17727609 REVERSEhighly similar to (517) loc_os03g47140 12003.m09727 protein atGRF2, putative, expressed seq=cds; coord=1:257186167..257188884:-1; parent_gene=GRMZM2G018414'

'moderately similar to (331) AT1G31260 | Symbols: ZIP10 | ZIP10 (ZINC TRANSPORTER 10 PRECURSOR); cation transmembrane transporter/ metal ion transmembrane transporter | chr1:11175559-11177362 REVERSEmoderately similar to (456) loc_os03g46470 12003.m09667 protein zinc transporter 10 precursor, putative, expressed seq=cds; coord=1:258353073..258355277:1; parent_gene=GRMZM2G118821'

'nearly identical (1030) AT1G61010 | Symbols: CPSF73-I | CPSF73-I (CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 73-I); protein binding | chr1:22474954-22477660 REVERSEweakly similar to (128) CPSF2_ORYSA Cleavage and polyadenylation specificity factor 100 kDa subunit (CPSF 100 kDa subunit) - Oryza sativa (Rice)nearly identical (1190) loc_os03g63590 12003.m11227 protein cleavage and polyadenylation specificity factor, 73 kDa subunit, putative, expressed seq=cds; coord=1:298965855..298969862:-1; parent_gene=GRMZM2G422649'

'moderately similar to (388) AT1G15820 | Symbols: LHCB6, CP24 | LHCB6 (LIGHT HARVESTING COMPLEX PSII SUBUNIT 6); chlorophyll binding | chr1:5446685-5447676 REVERSEmoderately similar to (388) CB4_SPIOL Chlorophyll a-b binding protein CP24, chloroplast precursor - Spinacia oleracea (Spinach)moderately similar to (405) loc_os04g38410 12004.m08831 protein chlorophyll a-b binding protein CP24, chloroplast precursor, putative, expressed seq=cds; coord=2:2018212..2019764:-1; parent_gene=GRMZM2G039996'

'weakly similar to (135) AT3G48100 | Symbols: ARR5, ATRR2, IBC6 | ARR5 (ARABIDOPSIS RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator | chr3:17759112-17760740 REVERSEweakly similar to (189) loc_os04g57720 12004.m10657 protein OsRR6 - Rice type-A response regulator, expressed seq=cds; coord=2:2081848..2082630:-1; parent_gene=GRMZM2G040736'

'moderately similar to (241) AT5G04490 | Symbols: VTE5 | VTE5 (vitamin E pathway gene5); phosphatidate cytidylyltransferase/ phytol kinase | chr5:1279867-1281587 FORWARDmoderately similar to (370) PHYK_MAIZE Probable phytol kinase, chloroplast precursor (EC 2.7.-.-) - Zea mays (Maize)weakly similar to (174) loc_os01g61560 12001.m43251 protein phytol kinase 2, chloroplast precursor, putative, expressed seq=cds; coord=2:2495821..2497668:-1; parent_gene=GRMZM2G104538'

'moderately similar to (424) AT1G16670 | Symbols: | protein kinase family protein | chr1:5697846-5699492 FORWARDmoderately similar to (205) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (542) loc_os04g52840 12004.m35461 protein serine/threonine-protein kinase receptor precursor, putative, expressed seq=cds; coord=2:9355771..9359630:1; parent_gene=GRMZM2G165060'

'very weakly similar to (97.4) AT1G62290 | Symbols: | aspartyl protease family protein | chr1:23010107-23012681 REVERSEweakly similar to (139) ASPRX_ORYSA Aspartic proteinase precursor (EC 3.4.23.-) - Oryza sativa (Rice)weakly similar to (139) loc_os05g04630 12005.m27692 protein retrotransposon protein, putative, SINE subclass, expressed seq=cds; coord=2:30497529..30524217:1; parent_gene=GRMZM2G333408' 'highly similar to (600) AT5G03860 | Symbols: MLS | MLS (MALATE SYNTHASE); malate synthase | chr5:1032276 1034527 REVERSEhighly similar to (762) MASY_MAIZE Malate synthase, glyoxysomal (EC 2.3.3.9) - Zea mays (Maize)highly similar to (689) loc_os04g40990 12004.m09079 protein malate synthase, glyoxysomal, putative, expressed seq=cds; coord=2:36317292..36319768:1; parent_gene=GRMZM2G102183'

'weakly similar to (129) AT5G14360 | Symbols: | ubiquitin family protein | chr5:4631038-4631641 FORWARDweakly similar to (167) loc_os02g38410 12002.m08929 protein BCL-2 binding anthanogene-1, putative, expressed seq=cds; coord=2:36824114..36825732:-1; parent_gene=GRMZM2G045117'

'moderately similar to (382) AT1G19150 | Symbols: LHCA6, LHCA2*1 | LHCA6; chlorophyll binding | chr1:6612806 6613799 FORWARDmoderately similar to (311) CB12_PETHY Chlorophyll a-b binding protein, chloroplast precursor (LHCI type II CAB) - Petunia hybrida (Petunia)moderately similar to (448) loc_os09g26810 12009.m05833 protein chlorophyll a-b binding protein, chloroplast precursor, putative, expressed seq=cds; coord=2:184011820..184014232:1; parent_gene=GRMZM2G117412'

'highly similar to (527) AT5G66960 | Symbols: | prolyl oligopeptidase family protein | chr5:26736209-26739493 REVERSEweakly similar to (108) loc_os09g29950 12009.m22244 protein protease 2, putative, expressed seq=cds; coord=2:185292654..185305292:1; parent_gene=GRMZM2G065665'

'moderately similar to (488) AT2G26560 | Symbols: PLP2, PLA IIA, PLA2A | PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir | chr2:11293912-11295708 REVERSEmoderately similar to (306) PAT3_SOLTU Patatin class 1 precursor (Patatin class I) (Potato tuber protein) - Solanum tuberosum (Potato)highly similar to (629) loc_os09g28770 12009.m06028 protein patatin class 1 precursor, putative, expressed seq=cds; coord=2:186851126..186853333:1; parent_gene=GRMZM2G123764'

'weakly similar to (139) loc_os12g32986 12012.m27011 protein heat shock protein 83, putative, expressed seq=cds; coord=2:189610974..189617149:1; parent_gene=GRMZM2G474367'

'moderately similar to (250) AT3G63170 | Symbols: | chalcone isomerase | chr3:23334675-23335993 FORWARDmoderately similar to (341) loc_os07g38390 12007.m08085 protein chalcone isomerase, putative, expressed seq=cds; coord=2:206127228..206130402:-1; parent_gene=GRMZM2G060011'

'moderately similar to (214) AT3G46730 | Symbols: | disease resistance protein (CC-NBS class), putative | chr3:17213069-17215612 REVERSEhighly similar to (946) loc_os11g13430 12011.m05485 protein RGH1A, putative seq=cds; coord=2:214204840..214207788:1; parent_gene=GRMZM2G379770'

'weakly similar to (137) AT1G03470 | Symbols: | kinase interacting family protein | chr1:866217-867493 REVERSEmoderately similar to (230) loc_os07g47090 12007.m079779 protein expressed protein seq=cds; coord=2:215519711..215522075:-1; parent_gene=GRMZM2G131554'

'moderately similar to (421) loc_os01g09020 12001.m07527 protein expressed protein seq=cds; coord=3:8271085..8273954:-1; parent_gene=GRMZM2G576002'

'moderately similar to (488) AT2G34930 | Symbols: | disease resistance family protein | chr2:14737169-14739886 REVERSEmoderately similar to (229) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (791) loc_os11g35450 12011.m07397 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed seq=cds; coord=3:8881267..8884385:1; parent_gene=GRMZM2G083797' 'moderately similar to (335) AT1G71710 | Symbols: | inositol polyphosphate 5-phosphatase, putative | chr1:26973796-26976774 REVERSEhighly similar to (567) loc_os01g08780 12001.m07503 protein type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2, putative, expressed seq=cds; coord=3:9112149..9120357:1; parent_gene=GRMZM2G355381'

'weakly similar to (136) AT5G50380 | Symbols: ATEXO70F1 | ATEXO70F1 (exocyst subunit EXO70 family protein F1); protein binding | chr5:20516382-20518433 REVERSEmoderately similar to (211) loc_os07g10910 12007.m079635 protein protein binding protein, putative, expressed seq=cds; coord=3:159726669..159743904:1; parent_gene=GRMZM2G436742'

'weakly similar to (134) AT3G27850 | Symbols: RPL12-C | RPL12-C (ribosomal protein l12-c); structural constituent of ribosome | chr3:10324905-10325468 FORWARDweakly similar to (199) RK12_ORYSA 50S ribosomal protein L12, chloroplast precursor (CL12) - Oryza sativa (Rice)weakly similar to (199) loc_os01g47330 12001.m10928 protein 50S ribosomal protein L12-1, chloroplast precursor, putative, expressed seq=cds; coord=3:211727508..211728617:-1; parent_gene=GRMZM2G360021'

'highly similar to (868) AT3G58610 | Symbols: | ketol-acid reductoisomerase | chr3:21671561-21674639 FORWARDhighly similar to (858) ILV5_PEA Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) - Pisum sativum (Garden pea)highly similar to (920) loc_os01g46380 12001.m10836 protein ketol-acid reductoisomerase, chloroplast precursor, putative, expressed seq=cds; coord=3:213623450..213627174:-1; parent_gene=GRMZM2G004382'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'highly similar to (538) AT4G16745 | Symbols: | exostosin family protein | chr4:9412185-9414053 FORWARDhighly similar to (709) loc_os01g45350 12001.m10738 protein limonene cyclase like protein, putative, expressed seq=cds; coord=3:215380332..215382314:-1; parent_gene=GRMZM2G048010'

'weakly similar to (111) AT1G14440 | Symbols: AtHB31 | AtHB31 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 31); DNA binding / transcription factor | chr1:4939076-4940014 REVERSEmoderately similar to (252) loc_os11g13930 12011.m05532 protein zinc finger homeodomain protein 1, putative, expressed seq=cds; coord=4:11264094..11266923:-1; parent_gene=GRMZM2G068330'

'weakly similar to (164) AT4G35160 | Symbols: | O-methyltransferase family 2 protein | chr4:16730989-16732808 REVERSEhighly similar to (647) ZRP4_MAIZE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT) - Zea mays (Maize)moderately similar to (410) loc_os05g43930 12005.m08519 protein O-methyltransferase ZRP4, putative, expressed seq=cds; coord=4:11916303..11917798:-1; parent_gene=GRMZM2G017557' 'moderately similar to (347) AT2G24765 | Symbols: ARF3, ARL1, ATARL1 | ARF3 (ADP-RIBOSYLATION FACTOR 3); protein binding | chr2:10562822-10564742 FORWARDmoderately similar to (237) ARF1_ORYSA ADP-ribosylation factor 1 (13 kDa cold-induced protein) - Oryza sativa (Rice)moderately similar to (358) loc_os08g15040 12008.m05627 protein ADP-ribosylation factor 3, putative, expressed seq=cds; coord=4:25788335..25797883:-1; parent_gene=GRMZM2G147726'

'moderately similar to (347) AT2G24765 | Symbols: ARF3, ARL1, ATARL1 | ARF3 (ADP-RIBOSYLATION FACTOR 3); protein binding | chr2:10562822-10564742 FORWARDmoderately similar to (237) ARF1_ORYSA ADP-ribosylation factor 1 (13 kDa cold-induced protein) - Oryza sativa (Rice)moderately similar to (358) loc_os08g15040 12008.m05627 protein ADP-ribosylation factor 3, putative, expressed seq=cds; coord=4:25788335..25797883:-1; parent_gene=GRMZM2G147726'

'moderately similar to (254) AT3G02450 | Symbols: | cell division protein ftsH, putative | chr3:502876-505030 REVERSEweakly similar to (190) FTSH_TOBAC Cell division protease ftsH homolog, chloroplast precursor (EC 3.4.24.-) (DS9) - Nicotiana tabacum (Common tobacco)moderately similar to (281) loc_os04g39190 12004.m08908 protein cell division protein ftsH homolog 4, putative, expressed seq=cds; coord=4:28322183..28324409:1; parent_gene=GRMZM2G125151'

'highly similar to (954) AT4G04890 | Symbols: PDF2 | PDF2 (PROTODERMAL FACTOR 2); DNA binding / transcription factor | chr4:2476970-2480090 REVERSEnearly identical (1140) loc_os08g08820 12008.m080098 protein homeobox protein GLABRA2, putative, expressed seq=cds; coord=4:28979897..28986080:-1; parent_gene=GRMZM2G130442'

'nearly identical (1254) AT5G07350 | Symbols: | tudor domain-containing protein / nuclease family protein | chr5:2319790-2324892 REVERSEnearly identical (1683) loc_os02g32350 12002.m33392 protein 4SNc-Tudor domain protein, putative, expressed seq=cds; coord=4:94432879..94438375:1; parent_gene=AC207890.3_FG002'

'weakly similar to (142) AT5G04840 | Symbols: | bZIP protein | chr5:1406005-1407648 FORWARDmoderately similar to (413) loc_os02g33560 12002.m08449 protein expressed protein seq=cds; coord=4:110523604..110529675:-1; parent_gene=GRMZM2G118870'

'moderately similar to (432) AT3G14090 | Symbols: ATEXO70D3 | ATEXO70D3 (exocyst subunit EXO70 family protein D3); protein binding | chr3:4669508-4671379 REVERSEmoderately similar to (444) HMDH_MAIZE 3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA reductase) - Zea mays (Maize)highly similar to (715) loc_os08g35470 12008.m07536 protein protein binding protein, putative, expressed seq=cds; coord=4:131371572..131383071:1; parent_gene=GRMZM2G390691'

'weakly similar to (157) AT1G76880 | Symbols: | trihelix DNA-binding protein, putative | chr1:28865594-28867931 FORWARDmoderately similar to (390) loc_os02g43300 12002.m09365 protein expressed protein seq=cds; coord=4:149896374..149900088:1; parent_gene=GRMZM2G063203'

'weakly similar to (181) AT3G20280 | Symbols: | PHD finger family protein | chr3:7072892-7074340 FORWARDhighly similar to (540) loc_os02g48810 12002.m09915 protein PHD-finger family protein, expressed seq=cds; coord=4:163892981..163897431:1; parent_gene=GRMZM2G411032' 'moderately similar to (329) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEhighly similar to (549) loc_os02g48860 12002.m09920 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=4:163962237..163964018:1; parent_gene=GRMZM2G141036'

'weakly similar to (130) AT2G03200 | Symbols: | aspartyl protease family protein | chr2:966506-967891 REVERSEweakly similar to (150) loc_os08g36530 12008.m07642 protein aspartic proteinase nepenthesin-2 precursor, putative seq=cds; coord=4:166481073..166482727:1; parent_gene=GRMZM2G444623'

'very weakly similar to (93.2) AT1G75580 | Symbols: | auxin-responsive protein, putative | chr1:28377530-28377856 FORWARDweakly similar to (129) loc_os06g04590 12006.m05189 protein OsSAUR24 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=4:167073486..167074934:-1; parent_gene=GRMZM2G015049'

'very weakly similar to (85.9) AT2G19690 | Symbols: PLA2-BETA | PLA2-BETA (PHOSPHOLIPASE A2-BETA); calcium ion binding / phospholipase A2 | chr2:8503326-8504549 FORWARDweakly similar to (106) loc_os02g58500 12002.m33321 protein phospholipase A2, putative, expressed seq=cds; coord=4:168739234..168740533:1; parent_gene=GRMZM2G045294'

'weakly similar to (167) loc_os02g57360 12002.m10758 protein metal ion binding protein, putative, expressed seq=cds; coord=4:171214402..171215201:-1; parent_gene=GRMZM2G120964'

'very weakly similar to (98.6) AT1G21910 | Symbols: | AP2 domain-containing transcription factor family protein | chr1:7696655-7697347 FORWARDweakly similar to (167) loc_os06g10780 12006.m05795 protein DNA binding protein, putative, expressed seq=cds; coord=4:178386285..178387653:1; parent_gene=GRMZM2G011110'

'weakly similar to (188) AT1G22400 | Symbols: UGT85A1, ATUGT85A1 | UGT85A1; UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucuronosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr1:7903851-7906607 REVERSEmoderately similar to (254) loc_os02g51900 12002.m10221 protein cytokinin-O-glucosyltransferase 2, putative, expressed seq=cds; coord=4:180437024..180437864:1; parent_gene=GRMZM2G383920'

'moderately similar to (420) AT1G79230 | Symbols: ST1, ATMST1, MST1, ATRDH1 | MST1 (MERCAPTOPYRUVATE SULFURTRANSFERASE 1); 3-mercaptopyruvate sulfurtransferase/ sulfurtransferase/ thiosulfate sulfurtransferase | chr1:29801358-29803679 FORWARDhighly similar to (516) loc_os02g07044 12002.m100460 protein thiosulfate transferase, putative, expressed seq=cds; coord=4:236383011..236388871:-1; parent_gene=GRMZM2G168888'

'weakly similar to (107) AT3G20570 | Symbols: | plastocyanin-like domain-containing protein | chr3:7186754-7187453 REVERSEweakly similar to (178) loc_os02g06690 12002.m06017 protein blue copper protein precursor, putative, expressed seq=cds; coord=4:236727165..236728151:-1; parent_gene=GRMZM2G101872' 'nearly identical (1162) AT5G46210 | Symbols: CUL4, ATCUL4 | CUL4 (CULLIN4); protein binding / ubiquitin-protein ligase | chr5:18731569-18736653 REVERSEnearly identical (1415) loc_os03g57290 12003.m10647 protein cullin-4B, putative, expressed seq=cds; coord=5:4777029..4786789:-1; parent_gene=AC155496.2_FG009'

'weakly similar to (107) AT1G30210 | Symbols: TCP24 | TCP24 (TEOSINTE BRANCHED1, CYCLOIDEA, AND PCF FAMILY 24); transcription factor | chr1:10628754-10629728 REVERSEmoderately similar to (248) loc_os03g57190 12003.m10638 protein TCP family transcription factor containing protein, expressed seq=cds; coord=5:4945066..4946626:-1; parent_gene=GRMZM2G089361'

'moderately similar to (375) AT3G22750 | Symbols: | protein kinase, putative | chr3:8037364-8039096 REVERSEhighly similar to (538) loc_os03g53410 12003.m10311 protein ATMRK1, putative, expressed seq=cds; coord=5:7587329..7589198:-1; parent_gene=GRMZM2G014618'

'moderately similar to (418) AT1G67480 | Symbols: | kelch repeat-containing F-box family protein | chr1:25277294-25278529 FORWARDhighly similar to (625) loc_os02g30210 12002.m100041 protein SKIP4, putative, expressed seq=cds; coord=5:163229123..163232017:-1; parent_gene=GRMZM2G011627'

'weakly similar to (137) AT3G52090 | Symbols: ATRPB13.6, NRPB11, NRPD11, NRPE11 | NRPB11; DNA binding / DNA-directed RNA polymerase | chr3:19318069-19318998 REVERSEweakly similar to (146) loc_os07g07610 12007.m05220 protein DNA-directed RNA polymerase II subunit J, putative, expressed seq=cds; coord=5:184738650..184741012:1; parent_gene=GRMZM2G043461'

'highly similar to (579) AT5G60710 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24410953-24414849 REVERSEnearly identical (1010) loc_os02g40664 12002.m09152 protein protein binding protein, putative, expressed seq=cds; coord=5:185572733..185577146:-1; parent_gene=GRMZM2G094602'

'moderately similar to (257) AT3G24800 | Symbols: PRT1 | PRT1 (PROTEOLYSIS 1); ubiquitin-protein ligase | chr3:9055653-9057795 FORWARDmoderately similar to (441) loc_os02g40810 12002.m09166 protein ubiquitin protein ligase PRT1, putative, expressed seq=cds; coord=5:185769439..185782378:-1; parent_gene=GRMZM2G362883'

'moderately similar to (257) AT3G24800 | Symbols: PRT1 | PRT1 (PROTEOLYSIS 1); ubiquitin-protein ligase | chr3:9055653-9057795 FORWARDmoderately similar to (441) loc_os02g40810 12002.m09166 protein ubiquitin protein ligase PRT1, putative, expressed seq=cds; coord=5:185769439..185782378:-1; parent_gene=GRMZM2G362883'

'moderately similar to (232) AT3G23250 | Symbols: MYB15, ATY19, ATMYB15 | MYB15 (MYB DOMAIN PROTEIN 15); DNA binding / transcription factor | chr3:8309742-8310624 FORWARDmoderately similar to (285) MYB4_ORYSA Myb-related protein Myb4 (OsMyb4) (Transcription factor RLTR1) - Oryza sativa (Rice)moderately similar to (322) loc_os02g41510 12002.m09187 protein myb-related protein Myb4, putative, expressed seq=cds; coord=5:186413823..186415077:-1; parent_gene=GRMZM2G095904'

'highly similar to (582) AT5G03300 | Symbols: ADK2 | ADK2 (ADENOSINE KINASE 2); adenosine kinase/ copper ion binding / kinase | chr5:796573-798997 FORWARDmoderately similar to (479) ADK_PHYPA Adenosine kinase (EC 2.7.1.20) (AK) (Adenosine 5'-phosphotransferase) - Physcomitrella patens (Moss)highly similar to (654) loc_os02g41590 12002.m09195 protein adenosine kinase 2, putative, expressed seq=cds; coord=5:186517098..186522957:-1; parent_gene=GRMZM2G540538' 'weakly similar to (124) loc_os02g43550 12002.m09390 protein nuc-1 negative regulatory protein preg, putative, expressed seq=cds; coord=5:195401851..195402389:1; parent_gene=GRMZM2G160563'

'weakly similar to (147) AT5G07450 | Symbols: CYCP4;3 | CYCP4;3 (cyclin p4;3); cyclin-dependent protein kinase | chr5:2358418-2359253 REVERSEmoderately similar to (227) loc_os02g43550 12002.m09390 protein nuc-1 negative regulatory protein preg, putative, expressed seq=cds; coord=5:195401851..195404340:1; parent_gene=GRMZM2G160563'

'weakly similar to (129) AT4G17500 | Symbols: ATERF-1 | ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor | chr4:9759405-9760211 FORWARDweakly similar to (131) ERF2_NICSY Ethylene-responsive transcription factor 2 (Ethylene-responsive element-binding factor 2) (EREBP-2) (NsERF2) - Nicotiana sylvestris (Wood tobacco)moderately similar to (241) loc_os02g43790 12002.m09413 protein ethylene responsive protein, putative, expressed seq=cds; coord=5:191217942..191219471:-1; parent_gene=GRMZM2G466044'

'very weakly similar to (97.1) AT1G35250 | Symbols: | thioesterase family protein | chr1:12933046-12934465 REVERSEweakly similar to (166) loc_os02g44200 12002.m09462 protein pollen thioesterase, putative seq=cds; coord=5:192252759..192253857:-1; parent_gene=GRMZM2G004752'

'moderately similar to (248) AT5G40250 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:16086056-16087186 FORWARDmoderately similar to (472) loc_os02g50930 12002.m10127 protein RING-H2 finger protein ATL5I, putative, expressed seq=cds; coord=5:206555179..206557068:1; parent_gene=GRMZM2G053303'

'highly similar to (790) AT1G73590 | Symbols: PIN1, ATPIN1 | PIN1 (PIN-FORMED 1); transporter | chr1:27659772-27662876 FORWARDnearly identical (1019) PIN1_ORYSA Auxin efflux carrier component 1 (OsPIN1) (Ethylene insensitive root 1 homolog) - Oryza sativa (Rice)nearly identical (1019) loc_os02g50960 12002.m33866 protein auxin efflux carrier component 1, putative, expressed seq=cds; coord=5:206727149..206730565:1; parent_gene=GRMZM2G074267'

'very weakly similar to (82.8) AMPD_ORYSA Probable AMP deaminase (EC 3.5.4.6) - Oryza sativa (Rice)very weakly similar to (82.8) loc_os07g49270 12007.m09136 protein AMP deaminase, putative, expressed seq=cds; coord=5:207021151..207021641:-1; parent_gene=GRMZM2G114362'

'weakly similar to (132) AT1G78080 | Symbols: RAP2.4 | RAP2.4 (related to AP2 4); DNA binding / transcription factor | chr1:29364790-29365794 FORWARDmoderately similar to (202) loc_os02g51670 12002.m10198 protein AP2 domain-containing protein, putative, expressed seq=cds; coord=5:208162767..208165707:1; parent_gene=GRMZM2G055204'

'very weakly similar to (84.0) AT2G30140 | Symbols: | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr2:12872200-12873691 FORWARDweakly similar to (135) loc_os10g12120 12010.m04526 protein UDP-glycosyltransferase/ transferase, transferring glycosyl groups, putative seq=cds; coord=5:208178465..208179815:1; parent_gene=GRMZM2G055124' 'moderately similar to (385) AT5G65020 | Symbols: ANNAT2 | ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding | chr5:25974366-25975554 FORWARDmoderately similar to (343) ANX4_FRAAN Annexin-like protein RJ4 - Fragaria ananassa (Strawberry)highly similar to (566) loc_os02g51750 12002.m10206 protein annexin-like protein RJ4, putative, expressed seq=cds; coord=5:208194750..208197747:1; parent_gene=GRMZM2G061950'

'moderately similar to (201) AT4G25780 | Symbols: | pathogenesis-related protein, putative | chr4:13121107-13121679 FORWARDweakly similar to (148) PR13_HORVU Pathogenesis-related protein PRB1-3 precursor (PR-1B) (HV-8) - Hordeum vulgare (Barley)moderately similar to (296) loc_os02g54560 12002.m10485 protein pathogenesis-related protein PR-1 precursor, putative, expressed seq=cds; coord=5:212617604..212618506:1; parent_gene=GRMZM2G008406'

'weakly similar to (104) AT2G23340 | Symbols: | AP2 domain-containing transcription factor, putative | chr2:9938186-9938716 FORWARDweakly similar to (151) loc_os06g07030 12006.m05428 protein dehydration responsive element binding protein, putative, expressed seq=cds; coord=6:79553937..79555390:1; parent_gene=GRMZM2G119865'

'moderately similar to (243) AT5G52660 | Symbols: | myb family transcription factor | chr5:21359423-21362037 REVERSEmoderately similar to (380) loc_os06g45840 12006.m71450 protein DNA binding protein, putative, expressed seq=cds; coord=6:93096804..93102645:-1; parent_gene=GRMZM2G057408'

'moderately similar to (291) AT1G04640 | Symbols: LIP2 | LIP2 (LIPOYLTRANSFERASE 2); lipoyltransferase | chr1:1292541-1293248 FORWARDmoderately similar to (371) loc_os03g20560 12003.m07463 protein lipoate-protein ligase, putative, expressed seq=cds; coord=6:163874844..163876139:-1; parent_gene=GRMZM2G085483'

'weakly similar to (155) AT4G39700 | Symbols: | heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related | chr4:18424265-18424906 FORWARDmoderately similar to (207) loc_os09g20000 12009.m05207 protein metal ion binding protein, putative, expressed seq=cds; coord=7:99384829..99386078:1; parent_gene=GRMZM2G086066'

'weakly similar to (105) AT3G48030 | Symbols: | hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein | chr3:17725410-17727954 REVERSEweakly similar to (157) loc_os09g20900 12009.m05297 protein RING-H2 finger protein ATL3I, putative, expressed seq=cds; coord=7:102395898..102397996:1; parent_gene=GRMZM2G030341'

'moderately similar to (211) AT3G48690 | Symbols: ATCXE12, CXE12 | CXE12; carboxylesterase | chr3:18037186-18038160 REVERSEvery weakly similar to (98.2) GID1_ORYSA Gibberellin receptor GID1 (EC 3.-.-.-) (Gibberellin-insensitive dwarf protein 1) (Protein GIBBERELLIN INSENSITIVE DWARF1) - Oryza sativa (Rice)moderately similar to (456) loc_os09g28740 12009.m06025 protein gibberellin receptor GID1L2, putative, expressed seq=cds; coord=7:126910131..126911577:1; parent_gene=GRMZM2G133836'

'very weakly similar to (89.7) AT3G46730 | Symbols: | disease resistance protein (CC-NBS class), putative | chr3:17213069-17215612 REVERSEmoderately similar to (232) loc_os07g31800 12007.m07447 protein NB-ARC domain containing protein, expressed seq=cds; coord=7:150887968..150889450:1; parent_gene=GRMZM2G163045' 'moderately similar to (413) AT4G03415 | Symbols: | catalytic/ protein serine/threonine phosphatase | chr4:1503789-1505510 REVERSEhighly similar to (585) loc_os07g37890 12007.m08038 protein catalytic/ protein phosphatase type 2C, putative, expressed seq=cds; coord=7:158156920..158160665:-1; parent_gene=GRMZM2G107565'

'highly similar to (506) AT4G32830 | Symbols: AtAUR1 | AtAUR1 (ATAURORA1); histone kinase(H3-S10 specific) / kinase/ protein serine/threonine kinase | chr4:15842557-15844354 FORWARDweakly similar to (164) CDPK_DAUCA Calcium-dependent protein kinase (EC 2.7.11.1) (CDPK) - Daucus carota (Carrot)highly similar to (552) loc_os01g09580 12001.m07583 protein serine/threonine-protein kinase Eg2-like, putative, expressed seq=cds; coord=8:20691284..20698300:1; parent_gene=GRMZM2G080588'

'moderately similar to (449) AT3G24503 | Symbols: ALDH2C4, ALDH1A, REF1 | ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase | chr3:8919732-8923029 REVERSEmoderately similar to (281) BADH_BETVU Betaine-aldehyde dehydrogenase, chloroplast precursor (EC 1.2.1.8) (BADH) - Beta vulgaris (Sugar beet)highly similar to (575) loc_os01g40870 12001.m10356 protein aldehyde dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=8:140688554..140691786:1; parent_gene=GRMZM2G407949'

'very weakly similar to (94.4) AT4G01200 | Symbols: | C2 domain-containing protein | chr4:506783-507535 REVERSEmoderately similar to (292) loc_os01g47040 12001.m10900 protein C2 domain containing protein, expressed seq=cds; coord=8:148351369..148357945:1; parent_gene=GRMZM2G114538'

'weakly similar to (174) AT3G18260 | Symbols: | reticulon family protein (RTNLB9) | chr3:6260328-6261504 REVERSEmoderately similar to (278) loc_os05g47690 12005.m08841 protein seed maturation protein, putative, expressed seq=cds; coord=8:152130316..152133931:1; parent_gene=GRMZM2G091973'

'weakly similar to (144) AT4G13850 | Symbols: ATGRP2 | GR-RBP2 (GLYCINE-RICH RNA-BINDING PROTEIN 2); ATP binding / RNA binding / double-stranded DNA binding / single-stranded DNA binding | chr4:8021314-8022065 FORWARDvery weakly similar to (99.8) ROC2_NICSY 29 kDa ribonucleoprotein B, chloroplast precursor (CP29B) - Nicotiana sylvestris (Wood tobacco)weakly similar to (179) loc_os01g68790 12001.m43348 protein glycine-rich RNA-binding protein 2, mitochondrial precursor, putative, expressed seq=cds; coord=8:162236975..162239554:-1; parent_gene=GRMZM2G042118'

'moderately similar to (276) AT4G14040 | Symbols: EDA38, SBP2 | SBP2 (SELENIUM-BINDING PROTEIN 2); selenium binding | chr4:8100691-8102828 REVERSEmoderately similar to (334) loc_os01g68770 12001.m12979 protein selenium-binding protein, putative, expressed seq=cds; coord=9:23290887..23295208:1; parent_gene=GRMZM2G171376'

'moderately similar to (276) AT4G14040 | Symbols: EDA38, SBP2 | SBP2 (SELENIUM-BINDING PROTEIN 2); selenium binding | chr4:8100691-8102828 REVERSEmoderately similar to (334) loc_os01g68770 12001.m12979 protein selenium-binding protein, putative, expressed seq=cds; coord=9:23290887..23295208:1; parent_gene=GRMZM2G171376'

'moderately similar to (263) AT1G50180 | Symbols: | disease resistance protein (CC-NBS-LRR class), putative | chr1:18584235-18587136 FORWARDhighly similar to (522) loc_os10g10360 12010.m065236 protein NBS-LRR disease resistance protein, putative, expressed seq=cds; coord=9:25062949..25065642:-1; parent_gene=GRMZM2G030051' 'moderately similar to (482) AT2G02180 | Symbols: TOM3 | TOM3; protein binding | chr2:560976-562961 FORWARDhighly similar to (532) loc_os10g39220 12010.m06692 protein tobamovirus multiplication 3, putative, expressed seq=cds; coord=9:125685665..125692703:1; parent_gene=GRMZM2G174286'

'highly similar to (951) AT2G44980 | Symbols: | transcription regulatory protein SNF2, putative | chr2:18552343-18556669 REVERSEmoderately similar to (321) ISW2_ORYSA Probable chromatin remodelling complex ATPase chain (EC 3.6.1.-) (ISW2-like) (Sucrose nonfermenting protein 2 homolog) - Oryza sativa (Rice)nearly identical (1258) loc_os03g01200 12003.m05671 protein SNF2P, putative, expressed seq=cds; coord=9:155457208..155470884:-1; parent_gene=GRMZM2G049168'

'moderately similar to (421) AT3G07270 | Symbols: | GTP cyclohydrolase I | chr3:2314005-2317059 FORWARDhighly similar to (572) loc_os04g56710 12004.m10558 protein GTP cyclohydrolase I 1, putative, expressed seq=cds; coord=10:146967602..146972055:-1; parent_gene=GRMZM2G106376'

'weakly similar to (119) AT2G17950 | Symbols: WUS, PGA6, WUS1 | WUS (WUSCHEL); DNA binding / protein binding / transcription factor/ transcription regulator | chr2:7809100-7810671 REVERSEweakly similar to (122) WUS_ANTMA Protein WUSCHEL (Protein ROSULATA) - Antirrhinum majus (Garden snapdragon)weakly similar to (168) loc_os04g56780 12004.m10565 protein protein WUSCHEL, putative, expressed seq=cds; coord=10:147059712..147061055:-1; parent_gene=GRMZM2G028622'

'nearly identical (1680) AT5G65930 | Symbols: ZWI, PKCBP, KCBP | ZWI (ZWICHEL); calmodulin binding / microtubule motor | chr5:26370369-26376394 REVERSEmoderately similar to (217) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiinearly identical (2143) loc_os04g57140 12004.m10599 protein kinesin-like calmodulin binding protein, putative, expressed seq=cds; coord=10:147187794..147201486:-1; parent_gene=GRMZM2G423861'

'moderately similar to (326) AT2G39270 | Symbols: | adenylate kinase family protein | chr2:16399983-16401408 FORWARDmoderately similar to (307) KADC_SOLTU Adenylate kinase, chloroplast precursor (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Solanum tuberosum (Potato)moderately similar to (390) loc_os04g57540 12004.m35511 protein adenylate kinase, chloroplast precursor, putative, expressed seq=cds; coord=10:147579294..147582200:-1; parent_gene=GRMZM2G150014'

'very weakly similar to (94.0) AT5G66940 | Symbols: | Dof-type zinc finger domain-containing protein | chr5:26727989-26728666 REVERSEvery weakly similar to (90.1) PBF_MAIZE Dof zinc finger protein PBF (Prolamin box-binding factor) - Zea mays (Maize)weakly similar to (158) loc_os04g58190 12004.m35517 protein expressed protein seq=cds; coord=10:148408926..148410383:-1; parent_gene=GRMZM2G142718'

'weakly similar to (177) AT1G21140 | Symbols: | nodulin, putative | chr1:7404464-7405066 FORWARDweakly similar to (123) NO21_SOYBN Nodulin 21 (N-21) - Glycine max (Soybean)moderately similar to (205) loc_os04g59020 12004.m10780 protein integral membrane protein, expressed seq=cds; coord=10:148991785..148992408:1; parent_gene=AC214046.4_FG005' 'moderately similar to (211) AT5G66760 | Symbols: SDH1-1 | SDH1-1; ATP binding / succinate dehydrogenase | chr5:26653776-26657224 FORWARDmoderately similar to (210) DHSA_ORYSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (EC 1.3.5.1) (FP) (Flavoprotein subunit of complex II) - Oryza sativa (Rice)moderately similar to (210) loc_os07g04240 12007.m04893 protein succinate dehydrogenase flavoprotein subunit,mitochondrial precursor, putative, expressed seq=cds; coord=1:64875250..64878499:-1; parent_gene=GRMZM2G306945'

'moderately similar to (211) AT5G66760 | Symbols: SDH1-1 | SDH1-1; ATP binding / succinate dehydrogenase | chr5:26653776-26657224 FORWARDmoderately similar to (210) DHSA_ORYSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (EC 1.3.5.1) (FP) (Flavoprotein subunit of complex II) - Oryza sativa (Rice)moderately similar to (210) loc_os07g04240 12007.m04893 protein succinate dehydrogenase flavoprotein subunit,mitochondrial precursor, putative, expressed seq=cds; coord=1:64875250..64878499:-1; parent_gene=GRMZM2G306945'

'highly similar to (651) AT2G26260 | Symbols: AT3BETAHSD/D2 | AT3BETAHSD/D2 (3BETA-HYDROXYSTEROID-DEHYDROGENASE/DECARBOXYLASE ISOFORM 2); 3-beta-hydroxy-delta5-steroid dehydrogenase/ sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) | chr2:11178586-11182872 FORWARDhighly similar to (942) loc_os03g29170 12003.m35269 protein sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating, putative, expressed seq=cds; coord=1:70155432..70163966:1; parent_gene=GRMZM2G149224'

'highly similar to (651) AT2G26260 | Symbols: AT3BETAHSD/D2 | AT3BETAHSD/D2 (3BETA-HYDROXYSTEROID-DEHYDROGENASE/DECARBOXYLASE ISOFORM 2); 3-beta-hydroxy-delta5-steroid dehydrogenase/ sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) | chr2:11178586-11182872 FORWARDhighly similar to (942) loc_os03g29170 12003.m35269 protein sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating, putative, expressed seq=cds; coord=1:70155432..70163966:1; parent_gene=GRMZM2G149224'

'moderately similar to (434) AT4G24220 | Symbols: VEP1, AWI31 | VEP1 (VEIN PATTERNING 1); binding / catalytic | chr4:12565219-12566474 FORWARDhighly similar to (581) loc_os03g32170 12003.m08461 protein progesterone 5-beta-reductase, putative, expressed seq=cds; coord=1:76154571..76156037:-1; parent_gene=GRMZM2G138710'

'moderately similar to (332) AT1G47510 | Symbols: AT5PTASE11, 5PTASE11 | 5PTASE11 (INOSITOL POLYPHOSPHATE 5-PHOSPHATASE 11); hydrolase/ phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase/ phosphatidylinositol-3,5-bisphosphate 5-phosphatase/ phosphatidylinositol-4,5-bisphosphate 5-phosphatase | chr1:17435991-17438296 REVERSEmoderately similar to (491) loc_os03g42810 12003.m09332 protein type II inositol-1,4,5-trisphosphate 5-phosphatase precursor, putative, expressed seq=cds; coord=1:253792928..253795422:-1; parent_gene=GRMZM2G043191'

'moderately similar to (202) AT3G60460 | Symbols: DUO1 | DUO1 (DUO POLLEN 1); DNA binding / transcription factor | chr3:22342429-22343491 REVERSEweakly similar to (133) GAM1_ORYSA Transcription factor GAMYB (OsGAMyb) - Oryza sativa (Rice)moderately similar to (323) loc_os04g46384 12004.m101864 protein DUO1, putative seq=cds; coord=2:20122023..20123440:-1; parent_gene=GRMZM2G105137' 'weakly similar to (106) loc_os09g29820 12009.m06133 protein BZIP family transcription factor, putative, expressed seq=cds; coord=2:188366213..188366707:-1; parent_gene=GRMZM2G137532'

'weakly similar to (103) AT5G54900 | Symbols: ATRBP45A | ATRBP45A (RNA-binding protein 45A); RNA binding | chr5:22295412-22298126 FORWARDweakly similar to (119) loc_os03g37270 12003.m08836 protein expressed protein seq=cds; coord=3:917514..921632:1; parent_gene=GRMZM2G461783'

'moderately similar to (472) AT5G24030 | Symbols: SLAH3 | SLAH3 (SLAC1 HOMOLOGUE 3); transporter | chr5:8118618-8120993 REVERSEhighly similar to (644) loc_os01g28840 12001.m09324 protein C4-dicarboxylate transporter/malic acid transport protein, expressed seq=cds; coord=3:131330167..131332146:1; parent_gene=GRMZM2G447657'

'moderately similar to (472) AT5G24030 | Symbols: SLAH3 | SLAH3 (SLAC1 HOMOLOGUE 3); transporter | chr5:8118618-8120993 REVERSEhighly similar to (644) loc_os01g28840 12001.m09324 protein C4-dicarboxylate transporter/malic acid transport protein, expressed seq=cds; coord=3:131330167..131332146:1; parent_gene=GRMZM2G447657'

'moderately similar to (448) AT1G72340 | Symbols: | eukaryotic translation initiation factor 2B family protein / eIF-2B family protein | chr1:27236898-27238482 FORWARDhighly similar to (531) loc_os12g31380 12012.m06947 protein translation initiation factor eIF-2B alpha subunit, putative, expressed seq=cds; coord=3:135445422..135448935:-1; parent_gene=GRMZM2G084647'

'highly similar to (588) AT2G39450 | Symbols: MTP11, ATMTP11 | MTP11; cation transmembrane transporter/ manganese ion transmembrane transporter/ manganese:hydrogen antiporter | chr2:16471744-16473735 REVERSEhighly similar to (716) loc_os01g62070 12001.m150770 protein metal tolerance protein C3, putative, expressed seq=cds; coord=3:181679706..181688287:1; parent_gene=GRMZM2G014454'

'weakly similar to (197) AT2G40830 | Symbols: RHC1A | RHC1A; protein binding / zinc ion binding | chr2:17043642-17044628 FORWARDmoderately similar to (393) loc_os01g58780 12001.m12020 protein RHC1A, putative, expressed seq=cds; coord=3:187930046..187931023:-1; parent_gene=AC213654.3_FG001'

'moderately similar to (421) AT1G79340 | Symbols: AtMC4 | AtMC4 (metacaspase 4); cysteine-type peptidase | chr1:29842849-29844368 FORWARDhighly similar to (642) loc_os01g58580 12001.m12000 protein latex-abundant protein, putative, expressed seq=cds; coord=3:188328660..188331609:-1; parent_gene=GRMZM2G047274'

'moderately similar to (386) AT5G54630 | Symbols: | zinc finger protein-related | chr5:22192607-22194260 REVERSEhighly similar to (570) loc_os01g57650 12001.m11914 protein nucleic acid binding protein, putative, expressed seq=cds; coord=3:190062951..190065367:1; parent_gene=GRMZM2G105224'

'highly similar to (537) AT5G47770 | Symbols: FPS1 | FPS1 (FARNESYL DIPHOSPHATE SYNTHASE 1); dimethylallyltranstransferase/ geranyltranstransferase | chr5:19345297-19347415 FORWARDhighly similar to (617) FPPS_MAIZE Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)] - Zea mays (Maize)highly similar to (657) loc_os01g50760 12001.m11257 protein farnesyl pyrophosphate synthetase, putative, expressed seq=cds; coord=3:205146239..205150759:-1; parent_gene=GRMZM2G098569' 'highly similar to (868) AT3G58610 | Symbols: | ketol-acid reductoisomerase | chr3:21671561-21674639 FORWARDhighly similar to (858) ILV5_PEA Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) - Pisum sativum (Garden pea)highly similar to (920) loc_os01g46380 12001.m10836 protein ketol-acid reductoisomerase, chloroplast precursor, putative, expressed seq=cds; coord=3:213623450..213627174:-1; parent_gene=GRMZM2G004382'

'highly similar to (868) AT3G58610 | Symbols: | ketol-acid reductoisomerase | chr3:21671561-21674639 FORWARDhighly similar to (858) ILV5_PEA Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) - Pisum sativum (Garden pea)highly similar to (920) loc_os01g46380 12001.m10836 protein ketol-acid reductoisomerase, chloroplast precursor, putative, expressed seq=cds; coord=3:213623450..213627174:-1; parent_gene=GRMZM2G004382'

'weakly similar to (174) AT1G68200 | Symbols: | zinc finger (CCCH-type) family protein | chr1:25562118-25563948 FORWARDmoderately similar to (234) loc_os01g45730 12001.m10773 protein nucleic acid binding protein, putative seq=cds; coord=3:214751394..214753488:1; parent_gene=GRMZM2G157927'

'highly similar to (606) AT3G01490 | Symbols: | protein kinase, putative | chr3:191095-193258 REVERSEvery weakly similar to (94.0) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (690) loc_os01g45380 12001.m10741 protein ATP binding protein, putative, expressed seq=cds; coord=3:215213789..215219139:-1; parent_gene=GRMZM2G088299'

'highly similar to (538) AT4G16745 | Symbols: | exostosin family protein | chr4:9412185-9414053 FORWARDhighly similar to (709) loc_os01g45350 12001.m10738 protein limonene cyclase like protein, putative, expressed seq=cds; coord=3:215380332..215382314:-1; parent_gene=GRMZM2G048010'

'weakly similar to (131) AT3G21330 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr3:7507720-7508841 FORWARDvery weakly similar to (80.9) LAX_ORYSA Transcription factor LAX PANICLE - Oryza sativa (Rice)moderately similar to (216) loc_os01g38610 12001.m10144 protein DNA binding protein, putative, expressed seq=cds; coord=3:219181998..219183697:-1; parent_gene=GRMZM2G081816'

'highly similar to (691) AT3G19760 | Symbols: | eukaryotic translation initiation factor 4A, putative / eIF-4A, putative / DEAD box RNA helicase, putative | chr3:6863790-6866242 FORWARDhighly similar to (699) IF4A3_NICPL Eukaryotic initiation factor 4A-3 (EC 3.6.1.-) (ATP-dependent RNA helicase eIF4A-3) (eIF-4A-3) - Nicotiana plumbaginifolia (Leadwort-leaved tobacco)highly similar to (760) loc_os01g45190 12001.m43108 protein eukaryotic initiation factor 4A-3, putative, expressed seq=cds; coord=4:168987228..168990822:1; parent_gene=GRMZM2G018947'

'moderately similar to (466) AT4G28860 | Symbols: ckl4 | ckl4 (Casein Kinase I-like 4); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr4:14246359-14248823 FORWARDhighly similar to (619) loc_os02g17910 12002.m33640 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=4:221511072..221528585:-1; parent_gene=GRMZM2G147026' 'moderately similar to (428) AT5G53140 | Symbols: | protein phosphatase 2C, putative / PP2C, putative | chr5:21549228-21552132 FORWARDhighly similar to (518) loc_os02g15594 12002.m06802 protein catalytic/ protein phosphatase type 2C/ protein serine/threonine phosphatase, putative, expressed seq=cds; coord=4:225064123..225073527:1; parent_gene=GRMZM2G073788'

'highly similar to (663) AT1G51680 | Symbols: 4CL1, 4CL.1, AT4CL1 | 4CL1 (4-COUMARATE:COA LIGASE 1); 4 coumarate-CoA ligase | chr1:19159080-19161464 REVERSEhighly similar to (691) 4CL1_PETCR 4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1) - Petroselinum crispum (Parsley) (Petroselinum hortense)highly similar to (896) loc_os02g08100 12002.m06156 protein 4-coumarate--CoA ligase 1, putative, expressed seq=cds; coord=5:89152269..89156855:-1; parent_gene=GRMZM2G075333'

'highly similar to (936) AT5G25060 | Symbols: | RNA recognition motif (RRM)-containing protein | chr5:8634219-8639984 REVERSEnearly identical (1183) loc_os02g08360 12002.m06182 protein RNA binding protein, putative, expressed seq=cds; coord=5:91582816..91615388:1; parent_gene=GRMZM2G174785'

'moderately similar to (417) AT2G28315 | Symbols: | LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: transporter-related (TAIR:AT1G06890.2); Has 1852 Blast hits to 1847 proteins in 207 species: Archae - 0; Bacteria - 58; Metazoa - 582; Fungi - 250; Plants - 685; Viruses - 0; Other Eukaryotes - 277 (source: NCBI BLink). | chr2:12088896-12090570 FORWARDhighly similar to (571) loc_os02g41780 12002.m09215 protein integral membrane protein like, putative, expressed seq=cds; coord=5:186828333..186832230:-1; parent_gene=GRMZM2G068714'

'weakly similar to (110) AT5G08410 | Symbols: FTRA2 | FTRA2 (ferredoxin/thioredoxin reductase subunit A (variable subunit) 2); catalytic/ ferredoxin reductase/ ferredoxin:thioredoxin reductase/ lipoate synthase | chr5:2709974-2710528 REVERSEweakly similar to (172) FTRV_MAIZE Ferredoxin-thioredoxin reductase, variable chain (FTR-V) (Ferredoxin-thioredoxin reductase subunit A) (FTR-A) - Zea mays (Maize)weakly similar to (153) loc_os02g42570 12002.m09292 protein ferredoxin-thioredoxin reductase, variable chain, putative, expressed seq=cds; coord=5:188659577..188660503:-1; parent_gene=GRMZM2G139803'

'weakly similar to (150) AT1G76800 | Symbols: | nodulin, putative | chr1:28829345-28829935 FORWARDweakly similar to (120) NO21_SOYBN Nodulin 21 (N-21) - Glycine max (Soybean)weakly similar to (174) loc_os02g43030 12002.m09338 protein conserved mebrane associated protein, DUF125, putative, expressed seq=cds; coord=5:189865490..189866191:-1; parent_gene=GRMZM2G409358'

'nearly identical (1013) AT4G12650 | Symbols: | LOCATED IN: integral to membrane, Golgi apparatus, plasma membrane, vacuole; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35160.1); Has 983 Blast hits to 980 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 434; Fungi - 144; Plants - 228; Viruses - 0; Other Eukaryotes - 177 (source: NCBI BLink). | chr4:7468207-7470165 REVERSEnearly identical (1152) loc_os02g49050 12002.m100343 protein transmembrane 9 superfamily protein member 4, putative, expressed seq=cds; coord=5:204006064..204008467:1; parent_gene=GRMZM2G018126' 'highly similar to (612) AT1G73660 | Symbols: | protein kinase family protein | chr1:27692247-27696718 REVERSEvery weakly similar to (97.8) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1146) loc_os02g50970 12002.m33450 protein protein kinase domain containing protein, expressed seq=cds; coord=5:206622614..206635150:-1; parent_gene=GRMZM2G127632'

'nearly identical (1182) AT1G26830 | Symbols: CUL3A, ATCUL3A, ATCUL3, CUL3 | ATCUL3 (ARABIDOPSIS THALIANA CULLIN 3); protein binding / ubiquitin-protein ligase | chr1:9296063-9298374 FORWARDnearly identical (1392) loc_os02g51180 12002.m10152 protein cullin-4B, putative, expressed seq=cds; coord=5:207060907..207063925:-1; parent_gene=GRMZM2G380184'

'weakly similar to (106) AT1G72230 | Symbols: | plastocyanin-like domain-containing protein | chr1:27188287-27189093 FORWARDweakly similar to (116) BCP_PEA Blue copper protein precursor - Pisum sativum (Garden pea)weakly similar to (150) loc_os02g52180 12002.m10249 protein uclacyanin-2 precursor, putative, expressed seq=cds; coord=5:208891470..208892610:-1; parent_gene=GRMZM2G045927'

'weakly similar to (144) AT1G12680 | Symbols: PEPKR2 | PEPKR2 (Phosphoenolpyruvate carboxylase-related kinase 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr1:4320123-4322269 REVERSEweakly similar to (181) loc_os09g29170 12009.m21997 protein calcium-dependent protein kinase, putative, expressed seq=cds; coord=6:32897930..32901697:-1; parent_gene=GRMZM2G395569'

'very weakly similar to (93.2) AT5G43320 | Symbols: ckl8 | ckl8 (Casein Kinase I-like 8); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr5:17386043-17388941 REVERSEvery weakly similar to (100) loc_os02g56560 12002.m77862 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=6:43344835..43349464:-1; parent_gene=GRMZM2G456423'

'weakly similar to (183) AT1G31490 | Symbols: | transferase family protein | chr1:11271744-11273078 REVERSEhighly similar to (577) loc_os06g05790 12006.m05305 protein transferase, putative, expressed seq=cds; coord=6:73908832..73911106:1; parent_gene=GRMZM2G362298'

'weakly similar to (183) AT1G31490 | Symbols: | transferase family protein | chr1:11271744-11273078 REVERSEhighly similar to (577) loc_os06g05790 12006.m05305 protein transferase, putative, expressed seq=cds; coord=6:73908832..73911106:1; parent_gene=GRMZM2G362298'

'weakly similar to (181) AT2G43190 | Symbols: | ribonuclease P family protein | chr2:17956220-17957833 FORWARDmoderately similar to (438) loc_os05g39530 12005.m083751 protein ribonuclease P/ ribonuclease, putative, expressed seq=cds; coord=6:74035080..74038340:-1; parent_gene=GRMZM2G047265'

'weakly similar to (181) AT4G38130 | Symbols: HD1, ATHD1, HDA1, RPD3A, HDA19 | HD1 (HISTONE DEACETYLASE 1); basal transcription repressor/ histone deacetylase/ protein binding | chr4:17896663-17899057 REVERSEweakly similar to (187) HDAC_MAIZE Probable histone deacetylase (RPD3 homolog) - Zea mays (Maize)moderately similar to (207) loc_os06g38470 12006.m32104 protein histone deacetylase, putative, expressed seq=cds; coord=6:168195273..168196277:-1; parent_gene=GRMZM2G367886'

'highly similar to (536) AT4G01100 | Symbols: ADNT1 | ADNT1 (ADENINE NUCLEOTIDE TRANSPORTER 1); ADP transmembrane transporter/ AMP transmembrane transporter/ ATP transmembrane transporter/ binding | chr4:477411-479590 FORWARDweakly similar to (153) BT1_MAIZE Protein brittle-1, chloroplast precursor - Zea mays (Maize)highly similar to (630) loc_os05g50840 12005.m083826 protein Grave disease carrier protein, putative, expressed seq=cds; coord=6:168175955..168188092:1; parent_gene=GRMZM2G067877'

'weakly similar to (160) loc_os07g05390 12007.m05003 protein expressed protein seq=cds; coord=7:5072345..5075429:-1; parent_gene=GRMZM2G093766'

'moderately similar to (354) AT5G24090 | Symbols: | acidic endochitinase (CHIB1) | chr5:8143805-8145153 REVERSEmoderately similar to (382) CHIA_TOBAC Acidic endochitinase precursor (EC 3.2.1.14) - Nicotiana tabacum (Common tobacco)moderately similar to (496) loc_os07g19040 12007.m06343 protein acidic endochitinase precursor, putative seq=cds; coord=7:31323387..31324388:-1; parent_gene=GRMZM2G160265'

'weakly similar to (200) AT3G02520 | Symbols: GRF7, GF14 NU | GRF7 (GENERAL REGULATORY FACTOR 7); protein binding / protein phosphorylated amino acid binding | chr3:526800-527915 REVERSEmoderately similar to (228) 14334_ORYSA 14-3-3-like protein GF14-D (G-box factor 14-3-3 homolog D) - Oryza sativa (Rice)moderately similar to (228) loc_os11g34450 12011.m07303 protein 14-3-3-like protein, putative, expressed seq=cds; coord=7:159919660..159920834:-1; parent_gene=GRMZM2G305211'

'weakly similar to (193) AT1G06260 | Symbols: | cysteine proteinase, putative | chr1:1916449-1917585 FORWARDweakly similar to (184) ORYA_ORYSA Oryzain alpha chain precursor (EC 3.4.22.-) - Oryza sativa (Rice)moderately similar to (260) loc_os09g21370 12009.m05344 protein cysteine proteinase EP-B 1 precursor, putative, expressed seq=cds; coord=7:162858798..162860272:-1; parent_gene=GRMZM2G049882'

'weakly similar to (125) AT1G18650 | Symbols: PDCB3 | PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding | chr1:6419036-6420413 REVERSEvery weakly similar to (90.9) E13B_WHEAT Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-endoglucanase) - Triticum aestivum (Wheat)weakly similar to (165) loc_os07g40940 12007.m08334 protein glucan endo-1,3-beta-glucosidase 3 precursor, putative, expressed seq=cds; coord=7:163670331..163673084:1; parent_gene=GRMZM2G131262'

'moderately similar to (251) AT2G18110 | Symbols: | elongation factor 1-beta, putative / EF-1-beta, putative | chr2:7872636-7873713 FORWARDmoderately similar to (288) EF1D1_ORYSA Elongation factor 1-delta 1 (EF-1-delta 1) (Elongation factor 1B-beta 1) (eEF-1B beta 1) - Oryza sativa (Rice)moderately similar to (290) loc_os07g42300 12007.m08465 protein elongation factor 1-delta 1, putative, expressed seq=cds; coord=7:165383929..165386707:-1; parent_gene=GRMZM2G031545'

'moderately similar to (352) AT3G06560 | Symbols: | polynucleotide adenylyltransferase/ protein binding | chr3:2044443-2047034 FORWARDhighly similar to (560) loc_os07g48890 12007.m09098 protein poly, putative, expressed seq=cds; coord=7:174102328..174107989:-1; parent_gene=GRMZM2G470461'

'highly similar to (693) AT3G28730 | Symbols: ATHMG, SSRP1, NFD | ATHMG (ARABIDOPSIS THALIANA HIGH MOBILITY GROUP); transcription factor | chr3:10784954-10788498 FORWARDnearly identical (1102) SSRP1_MAIZE FACT complex subunit SSRP1 (Facilitates chromatin transcription complex subunit SSRP1) (Recombination signal sequence recognition protein 1) (Zm-SSRP1) - Zea mays (Maize)highly similar to (997) loc_os01g08970 12001.m42895 protein structure-specific recognition protein 1, putative, expressed seq=cds; coord=8:21824201..21831003:-1; parent_gene=GRMZM2G032252'

'moderately similar to (248) AT3G07880 | Symbols: | Rho GDP-dissociation inhibitor family protein | chr3:2514175-2515544 FORWARDmoderately similar to (348) loc_os01g68540 12001.m12957 protein rho GDP-dissociation inhibitor 1, putative, expressed seq=cds; coord=8:110181330..110183162:-1; parent_gene=GRMZM2G072089' 'weakly similar to (151) AT5G59770 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein-tyrosine phosphatase-like, PTPLA (InterPro:IPR007482); BEST Arabidopsis thaliana protein match is: PAS2 (PASTICCINO 2); enoyl-CoA hydratase/ protein tyrosine phosphatase (TAIR:AT5G10480.2); Has 525 Blast hits to 525 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 286; Fungi - 120; Plants - 70; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink). | chr5:24079521-24081195 REVERSEmoderately similar to (230) loc_os05g38590 12005.m08038 protein protein tyrosine phosphatase-like protein PTPLB, putative, expressed seq=cds; coord=8:116854743..116858013:-1; parent_gene=GRMZM2G035202'

'highly similar to (803) AT2G13620 | Symbols: ATCHX15, CHX15 | ATCHX15; monovalent cation:proton antiporter/ sodium:hydrogen antiporter | chr2:5678006-5680621 FORWARDnearly identical (1224) loc_os05g40650 12005.m08241 protein ATCHX15, putative, expressed seq=cds; coord=8:119266312..119269960:-1; parent_gene=GRMZM2G138817'

'weakly similar to (191) AT1G56440 | Symbols: | serine/threonine protein phosphatase-related | chr1:21138765-21141482 REVERSEmoderately similar to (278) loc_os05g03910 12005.m04925 protein TPR Domain containing protein, expressed seq=cds; coord=8:130726762..130731051:1; parent_gene=GRMZM2G034043'

'very weakly similar to (82.4) AT1G75270 | Symbols: DHAR2 | DHAR2 (DEHYDROASCORBATE REDUCTASE 2) glutathione binding / glutathione dehydrogenase (ascorbate) | chr1:28250255-28251237 REVERSEvery weakly similar to (89.4) loc_os05g02530 12005.m04789 protein chloride intracellular channel 6, putative, expressed seq=cds; coord=8:133175515..133176352:1; parent_gene=GRMZM2G005710'

'moderately similar to (214) AT3G25220 | Symbols: FKBP15-1 | FKBP15-1; FK506 binding / peptidyl-prolyl cis-trans isomerase | chr3:9182691-9184463 FORWARDmoderately similar to (203) FKB15_VICFA FK506-binding protein 2 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (15 kDa FKBP) (FKBP-15) - Vicia faba (Broad bean)moderately similar to (248) loc_os01g68710 12001.m150820 protein FK506-binding protein 2-1 precursor, putative, expressed seq=cds; coord=8:162534879..162538967:1; parent_gene=GRMZM2G031204'

'highly similar to (559) AT2G41790 | Symbols: | peptidase M16 family protein / insulinase family protein | chr2:17429453-17436110 REVERSEhighly similar to (738) loc_os01g57073 12001.m11864 protein insulin-degrading enzyme, putative, expressed seq=cds; coord=8:172180747..172198680:-1; parent_gene=GRMZM2G133249'

'moderately similar to (370) AT4G18800 | Symbols: ATHSGBP, ATRAB11B, ATRABA1D | ATRABA1D (ARABIDOPSIS RAB GTPASE HOMOLOG A1D); GTP binding | chr4:10320156-10321339 REVERSEmoderately similar to (417) RIC2_ORYSA Ras-related protein RIC2 - Oryza sativa (Rice)moderately similar to (417) loc_os06g35814 12006.m08118 protein ras-related protein RIC2, putative, expressed seq=cds; coord=9:76755814..76760164:1; parent_gene=GRMZM2G018619'

'weakly similar to (103) AT5G56960 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr5:23038703-23041174 REVERSEmoderately similar to (221) loc_os06g37410 12006.m08276 protein helix-loop-helix DNA-binding domain containing protein seq=cds; coord=9:79118794..79123438:1; parent_gene=GRMZM2G340177' 'weakly similar to (140) AT1G69720 | Symbols: ho3 | ho3 (HEME OXYGENASE 3); heme oxygenase (decyclizing) | chr1:26227178-26228164 FORWARDweakly similar to (179) loc_os06g40080 12006.m08545 protein heme oxygenase 1, putative, expressed seq=cds; coord=9:88985396..88986632:-1; parent_gene=GRMZM2G157936'

'highly similar to (714) AT3G13770 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:4519647-4521533 FORWARDvery weakly similar to (86.7) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (939) loc_os06g41040 12006.m08639 protein pentatricopeptide repeat protein PPR1106-17, putative, expressed seq=cds; coord=9:101332438..101335090:1; parent_gene=GRMZM2G143377'

'moderately similar to (216) AT1G65680 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2) | chr1:24427266-24428399 FORWARDmoderately similar to (424) EXPB3_ORYSA Expansin-B3 precursor (OsEXPB3) (Beta-expansin-3) (OsaEXPb1.10) - Oryza sativa (Rice)moderately similar to (424) loc_os10g40720 12010.m06840 protein beta-expansin 1a precursor, putative, expressed seq=cds; coord=9:116268809..116270671:1; parent_gene=GRMZM2G013671'

'weakly similar to (191) AT3G11450 | Symbols: | DNAJ heat shock N-terminal domain-containing protein / cell division protein-related | chr3:3605459-3607477 REVERSE seq=cds; coord=9:116818179..116819389:-1; parent_gene=AC191253.3_FG004'

'moderately similar to (312) AT5G38710 | Symbols: | proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative | chr5:15501340-15503899 FORWARDhighly similar to (506) loc_os10g40360 12010.m06805 protein proline oxidase, mitochondrial precursor, putative, expressed seq=cds; coord=9:117306636..117309311:-1; parent_gene=GRMZM2G117956'

'moderately similar to (238) AT3G25780 | Symbols: AOC3 | AOC3 (ALLENE OXIDE CYCLASE 3); allene-oxide cyclase | chr3:9409362-9410409 FORWARDmoderately similar to (337) loc_os03g32314 12003.m08473 protein allene oxide cyclase 4, chloroplast precursor, putative, expressed seq=cds; coord=9:124917394..124918766:-1; parent_gene=GRMZM2G415793'

'highly similar to (525) AT4G38520 | Symbols: | protein phosphatase 2C family protein / PP2C family protein | chr4:18015999-18017514 REVERSEhighly similar to (685) loc_os10g39780 12010.m065325 protein protein phosphatase 2C, putative, expressed seq=cds; coord=9:126336491..126340954:1; parent_gene=GRMZM2G108309'

'moderately similar to (343) AT5G67500 | Symbols: VDAC2, ATVDAC2 | VDAC2 (VOLTAGE DEPENDENT ANION CHANNEL 2); voltage-gated anion channel | chr5:26935223-26937123 FORWARDmoderately similar to (267) VDAC2_SOLTU 36 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) (POM 36) - Solanum tuberosum (Potato)moderately similar to (480) loc_os03g10510 12003.m35080 protein outer mitochondrial membrane protein porin, putative, expressed seq=cds; coord=9:147891545..147896754:1; parent_gene=GRMZM2G137985'

'very weakly similar to (86.7) AT5G64080 | Symbols: | protease inhibitor/seed storage/lipid transfer protein (LTP) family protein | chr5:25645475-25646638 REVERSEweakly similar to (140) loc_os03g09230 12003.m35062 protein xylogen protein 1, putative, expressed seq=cds; coord=9:149245864..149247159:1; parent_gene=GRMZM2G004466' 'moderately similar to (448) AT1G77280 | Symbols: | protein kinase family protein | chr1:29031468-29035882 REVERSEweakly similar to (183) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (717) loc_os12g07990 12012.m04786 protein ATP binding protein, putative seq=cds; coord=10:10826331..10829269:-1; parent_gene=GRMZM2G418432'

'moderately similar to (268) AT1G74250 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr1:27920328-27922414 FORWARDhighly similar to (608) loc_os12g31840 12012.m06992 protein heat shock protein binding protein, putative, expressed seq=cds; coord=10:16655144..16659692:-1; parent_gene=GRMZM2G130127'

'moderately similar to (229) AT2G03690 | Symbols: | coenzyme Q biosynthesis Coq4 family protein / ubiquinone biosynthesis Coq4 family protein | chr2:1122122-1123011 REVERSEmoderately similar to (273) loc_os05g09650 12005.m05478 protein ubiquinone biosynthesis protein COQ4, putative, expressed seq=cds; coord=10:147886519..147887415:1; parent_gene=GRMZM2G092365'

'very weakly similar to (80.9) AT4G00630 | Symbols: KEA2, ATKEA2 | KEA2; potassium ion transmembrane transporter/ potassium:hydrogen antiporter | chr4:261655-267789 REVERSEvery weakly similar to (94.7) loc_os04g58620 12004.m10744 protein KEA1, putative, expressed seq=cds; coord=10:148570662..148572508:-1; parent_gene=GRMZM2G039797'

'weakly similar to (179) AT3G51320 | Symbols: | INVOLVED IN: biological_process unknown; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: binding (TAIR:AT3G62890.1); Has 12158 Blast hits to 4373 proteins in 95 species: Archae - 0; Bacteria - 0; Metazoa - 23; Fungi - 18; Plants - 12009; Viruses - 0; Other Eukaryotes - 108 (source: NCBI BLink). | chr3:19049853-19051445 REVERSEweakly similar to (133) loc_os06g40860 12006.m08621 protein EMB2261, putative, expressed seq=cds; coord=10:148782774..148783645:-1; parent_gene=GRMZM2G478807'

'moderately similar to (253) AT1G49180 | Symbols: | protein kinase family protein | chr1:18184840-18187444 REVERSEweakly similar to (128) CDPK_DAUCA Calcium-dependent protein kinase (EC 2.7.11.1) (CDPK) - Daucus carota (Carrot)moderately similar to (409) loc_os04g58990 12004.m10777 protein MAP/microtubule affinity-regulating kinase 4, putative, expressed seq=cds; coord=10:148972118..148974136:-1; parent_gene=GRMZM2G104658'

'moderately similar to (244) AT2G17040 | Symbols: anac036 | anac036 (Arabidopsis NAC domain containing protein 36); transcription factor | chr2:7407123-7408120 FORWARDweakly similar to (176) NAC68_ORYSA NAC domain-containing protein 68 (ONAC068) - Oryza sativa (Rice)moderately similar to (340) loc_os03g04070 12003.m05939 protein NAC domain-containing protein 68, putative, expressed seq=cds; coord=1:7488692..7490758:-1; parent_gene=GRMZM2G059428'

'moderately similar to (207) AT3G14205 | Symbols: | phosphoinositide phosphatase family protein | chr3:4716008-4720524 REVERSEmoderately similar to (449) loc_os03g08430 12003.m35047 protein SAC domain-containing protein 3, putative, expressed seq=cds; coord=1:17245821..17260824:1; parent_gene=GRMZM2G097434'

'highly similar to (512) AT1G74910 | Symbols: | ADP-glucose pyrophosphorylase family protein | chr1:28135770-28138456 REVERSEhighly similar to (603) loc_os03g11050 12003.m35086 protein mannose-1-phosphate guanyltransferase, putative, expressed seq=cds; coord=1:21196693..21221560:1; parent_gene=GRMZM2G064841'

'highly similar to (512) AT1G74910 | Symbols: | ADP-glucose pyrophosphorylase family protein | chr1:28135770-28138456 REVERSEhighly similar to (603) loc_os03g11050 12003.m35086 protein mannose-1-phosphate guanyltransferase, putative, expressed seq=cds; coord=1:21196693..21221560:1; parent_gene=GRMZM2G064841'

'highly similar to (570) AT2G37500 | Symbols: | arginine biosynthesis protein ArgJ family | chr2:15739904-15742430 REVERSEhighly similar to (729) loc_os03g17120 12003.m34841 protein arginine biosynthesis bifunctional protein argJ 1, putative, expressed seq=cds; coord=1:41956891..41966584:-1; parent_gene=GRMZM2G044237'

'highly similar to (787) AT3G47340 | Symbols: ASN1, DIN6, AT-ASN1 | ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing) | chr3:17438445-17441043 REVERSEhighly similar to (871) ASNS_MAIZE Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) (Glutamine-dependent asparagine synthetase) - Zea mays (Maize)highly similar to (971) loc_os03g18130 12003.m101311 protein asparagine synthetase, putative, expressed seq=cds; coord=1:45114258..45118291:-1; parent_gene=GRMZM2G053669'

'weakly similar to (198) AT2G38440 | Symbols: ITB1, SCAR2, DIS3, WAVE4, ATSCAR2 | SCAR2 (SCAR HOMOLOG 2) | chr2:16095550-16100851 FORWARDweakly similar to (192) SCRL1_ORYSA SCAR-like protein 1 - Oryza sativa (Rice)highly similar to (598) loc_os03g18710 12003.m07292 protein expressed protein seq=cds; coord=1:46576198..46582130:-1; parent_gene=GRMZM2G104534'

'moderately similar to (229) AT1G56500 | Symbols: | haloacid dehalogenase-like hydrolase family protein | chr1:21159775-21167092 FORWARDmoderately similar to (349) loc_os03g19760 12003.m35188 protein NHL repeat protein, putative, expressed seq=cds; coord=1:50700350..50712129:1; parent_gene=AC208571.4_FG001'

'moderately similar to (263) AT5G49620 | Symbols: AtMYB78 | AtMYB78 (myb domain protein 78); DNA binding / transcription factor | chr5:20137491-20139384 REVERSEweakly similar to (164) MYBA2_ORYSA Myb-related protein MYBAS2 - Oryza sativa (Rice)moderately similar to (343) loc_os03g20090 12003.m101325 protein MYB transcription factor, putative, expressed seq=cds; coord=1:51397954..51400225:-1; parent_gene=GRMZM2G070849'

'moderately similar to (262) AT1G08845 | Symbols: | structural constituent of ribosome | chr1:2838789-2840955 FORWARDmoderately similar to (334) loc_os10g41050 12010.m06870 protein expressed protein seq=cds; coord=1:90225656..90230346:-1; parent_gene=GRMZM2G154487'

'weakly similar to (150) AT2G45050 | Symbols: | zinc finger (GATA type) family protein | chr2:18582958-18583845 FORWARDmoderately similar to (362) loc_os10g40810 12010.m06851 protein GATA transcription factor 9, putative, expressed seq=cds; coord=1:90953352..90955047:1; parent_gene=GRMZM2G113098'

'weakly similar to (150) AT2G45050 | Symbols: | zinc finger (GATA type) family protein | chr2:18582958-18583845 FORWARDmoderately similar to (362) loc_os10g40810 12010.m06851 protein GATA transcription factor 9, putative, expressed seq=cds; coord=1:90953352..90955047:1; parent_gene=GRMZM2G113098'

'moderately similar to (399) AT1G30300 | Symbols: | unknown protein | chr1:10673084-10675061 FORWARDmoderately similar to (476) loc_os03g44140 12003.m09452 protein OsWAK26 - OsWAK receptor-like protein kinase, expressed seq=cds; coord=1:251155890..251159010:1; parent_gene=GRMZM2G103610'

'moderately similar to (236) AT2G42800 | Symbols: AtRLP29 | AtRLP29 (Receptor Like Protein 29); protein binding | chr2:17808157-17809545 REVERSEweakly similar to (122) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)moderately similar to (320) loc_os03g44270 12003.m09466 protein retrotransposon protein, putative, Ty1-copia subclass seq=cds; coord=1:251112471..251114311:1; parent_gene=GRMZM2G081099'

'highly similar to (516) AT2G28930 | Symbols: APK1B | APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr2:12424551-12426565 FORWARDmoderately similar to (233) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (647) loc_os03g60710 12003.m10960 protein protein kinase APK1B, chloroplast precursor, putative, expressed seq=cds; coord=1:293623063..293627778:1; parent_gene=GRMZM2G068117'

'moderately similar to (268) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDweakly similar to (130) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (382) loc_os04g55560 12004.m35488 protein AP2 domain containing protein, expressed seq=cds; coord=2:5514479..5518846:-1; parent_gene=GRMZM2G174784'

'moderately similar to (268) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDweakly similar to (130) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (382) loc_os04g55560 12004.m35488 protein AP2 domain containing protein, expressed seq=cds; coord=2:5514479..5518846:-1; parent_gene=GRMZM2G174784'

'moderately similar to (220) AT1G33260 | Symbols: | protein kinase family protein | chr1:12064796-12066114 FORWARDweakly similar to (144) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (433) loc_os04g45730 12004.m09524 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed seq=cds; coord=2:21820830..21822340:1; parent_gene=GRMZM2G168917'

'weakly similar to (170) AT4G00180 | Symbols: YAB3 | YAB3 (YABBY3); protein binding / transcription factor | chr4:72804-74888 REVERSEweakly similar to (109) YABDL_ORYSA Protein DROOPING LEAF - Oryza sativa (Rice)moderately similar to (262) loc_os04g45330 12004.m09486 protein yabby14 protein, putative, expressed seq=cds; coord=2:22756026..22758020:1; parent_gene=GRMZM2G054795'

'very weakly similar to (100) AT2G34730 | Symbols: | myosin heavy chain-related | chr2:14654611-14657443 FORWARDhighly similar to (625) loc_os04g44090 12004.m09367 protein expressed protein seq=cds; coord=2:27827322..27833556:-1; parent_gene=GRMZM2G387389'

'moderately similar to (395) AT1G04020 | Symbols: ATBARD1, BARD1 | BARD1 (BREAST CANCER ASSOCIATED RING 1); DNA binding / transcription coactivator | chr1:1036610-1040045 FORWARDhighly similar to (882) loc_os04g43300 12004.m09294 protein ATBRCA1, putative, expressed seq=cds; coord=2:28673566..28677785:-1; parent_gene=GRMZM2G052688'

'moderately similar to (395) AT1G04020 | Symbols: ATBARD1, BARD1 | BARD1 (BREAST CANCER ASSOCIATED RING 1); DNA binding / transcription coactivator | chr1:1036610-1040045 FORWARDhighly similar to (882) loc_os04g43300 12004.m09294 protein ATBRCA1, putative, expressed seq=cds; coord=2:28673566..28677785:-1; parent_gene=GRMZM2G052688'

'highly similar to (593) AT4G14340 | Symbols: CKI1, CKL11 | CKI1 (CASEIN KINASE I); kinase/ protein serine/threonine kinase | chr4:8248532-8251668 REVERSEhighly similar to (702) loc_os04g43490 12004.m101584 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=2:28936197..28940916:-1; parent_gene=GRMZM2G032694'

'highly similar to (593) AT4G14340 | Symbols: CKI1, CKL11 | CKI1 (CASEIN KINASE I); kinase/ protein serine/threonine kinase | chr4:8248532-8251668 REVERSEhighly similar to (702) loc_os04g43490 12004.m101584 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=2:28936197..28940916:-1; parent_gene=GRMZM2G032694'

'highly similar to (593) AT4G14340 | Symbols: CKI1, CKL11 | CKI1 (CASEIN KINASE I); kinase/ protein serine/threonine kinase | chr4:8248532-8251668 REVERSEhighly similar to (702) loc_os04g43490 12004.m101584 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=2:28936197..28940916:-1; parent_gene=GRMZM2G032694'

'very weakly similar to (84.7) AT4G13870 | Symbols: WRNEXO | WRNEXO (WERNER SYNDROME-LIKE EXONUCLEASE); 3'-5' exonuclease/ nucleic acid binding / protein binding | chr4:8023563-8025542 REVERSEweakly similar to (199) loc_os04g03990 12004.m05706 protein Werner syndrome ATP-dependent helicase, putative, expressed seq=cds; coord=2:110653506..110662313:-1; parent_gene=GRMZM2G053631'

'very weakly similar to (94.7) AT1G29450 | Symbols: | auxin-responsive protein, putative | chr1:10305981-10306406 REVERSEweakly similar to (187) loc_os09g37500 12009.m06697 protein OsSAUR55 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=2:197093510..197094134:-1; parent_gene=GRMZM2G156470'

'moderately similar to (462) AT4G23180 | Symbols: CRK10, RLK4 | CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr4:12138171-12140780 FORWARDweakly similar to (191) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (716) loc_os07g35370 12007.m07793 protein receptor-like protein kinase homolog RK20-1, putative, expressed seq=cds; coord=2:204080024..204082820:-1; parent_gene=GRMZM2G087625'

'moderately similar to (251) AT2G12190 | Symbols: | cytochrome P450, putative | chr2:4891807-4893345 REVERSEweakly similar to (171) C77A3_SOYBN Cytochrome P450 77A3 (EC 1.14.-.-) - Glycine max (Soybean)moderately similar to (472) loc_os10g37100 12010.m06510 protein cytochrome P450 89A2, putative seq=cds; coord=2:206538776..206540427:-1; parent_gene=GRMZM2G031909'

'moderately similar to (201) AT5G67590 | Symbols: FRO1 | FRO1 (FROSTBITE1); NADH dehydrogenase (ubiquinone) | chr5:26958073-26959356 FORWARDmoderately similar to (297) loc_os07g39710 12007.m08213 protein NADH-ubiquinone oxidoreductase 18 kDa subunit, mitochondrial precursor, putative, expressed seq=cds; coord=2:208123671..208129714:1; parent_gene=GRMZM2G105207' 'moderately similar to (201) AT5G67590 | Symbols: FRO1 | FRO1 (FROSTBITE1); NADH dehydrogenase (ubiquinone) | chr5:26958073-26959356 FORWARDmoderately similar to (297) loc_os07g39710 12007.m08213 protein NADH-ubiquinone oxidoreductase 18 kDa subunit, mitochondrial precursor, putative, expressed seq=cds; coord=2:208123671..208129714:1; parent_gene=GRMZM2G105207'

'very weakly similar to (95.1) loc_os07g48680 12007.m09079 protein RING-H2 finger protein ATL4L, putative, expressed seq=cds; coord=2:217695075..217695623:1; parent_gene=GRMZM2G402262'

'moderately similar to (254) AT2G37650 | Symbols: | scarecrow-like transcription factor 9 (SCL9) | chr2:15792623-15794779 FORWARDweakly similar to (112) CIGR2_ORYSA Chitin-inducible gibberellin-responsive protein 2 - Oryza sativa (Rice)moderately similar to (374) loc_os11g47910 12011.m08588 protein chitin-inducible gibberellin-responsive protein 2, putative seq=cds; coord=2:218855880..218857695:-1; parent_gene=GRMZM2G425366'

'moderately similar to (403) AT3G59010 | Symbols: | pectinesterase family protein | chr3:21803015-21805098 REVERSEmoderately similar to (367) PME2_CITSI Pectinesterase-2 precursor (EC 3.1.1.11) (Pectin methylesterase) (PE) - Citrus sinensis (Sweet orange)highly similar to (653) loc_os02g54190 12002.m10448 protein pectinesterase-2 precursor, putative, expressed seq=cds; coord=2:220142201..220144806:-1; parent_gene=GRMZM2G158240'

'moderately similar to (342) AT5G24400 | Symbols: emb2024 | emb2024 (embryo defective 2024); 6-phosphogluconolactonase/ catalytic | chr5:8330532-8331784 REVERSEmoderately similar to (464) loc_os09g35970 12009.m06548 protein 6-phosphogluconolactonase, putative, expressed seq=cds; coord=2:220832499..220836411:-1; parent_gene=GRMZM2G148769'

'weakly similar to (103) loc_os01g12090 12001.m07824 protein expressed protein seq=cds; coord=3:3027157..3028320:-1; parent_gene=GRMZM2G026868'

'highly similar to (622) AT2G34500 | Symbols: CYP710A1 | CYP710A1 (cytochrome P450, family 710, subfamily A, polypeptide 1); C-22 sterol desaturase/ oxygen binding | chr2:14539712-14541199 REVERSEvery weakly similar to (99.4) C88A1_MAIZE Cytochrome P450 88A1 (EC 1.14.-.-) (Dwarf3 protein) - Zea mays (Maize)highly similar to (881) loc_os01g11340 12001.m07753 protein CYP710A1, putative, expressed seq=cds; coord=3:3830545..3832095:1; parent_gene=AC233853.1_FG003'

'highly similar to (521) AT5G46240 | Symbols: KAT1 | KAT1 (POTASSIUM CHANNEL IN ARABIDOPSIS THALIANA 1); cyclic nucleotide binding / inward rectifier potassium channel | chr5:18743652-18746561 REVERSEmoderately similar to (447) AKT1_ORYSA Potassium channel AKT1 (OsAKT1) - Oryza sativa (Rice)highly similar to (691) loc_os01g11250 12001.m07744 protein potassium channel KAT1, putative, expressed seq=cds; coord=3:3843589..3847158:1; parent_gene=GRMZM2G093313'

'very weakly similar to (100) AT1G49950 | Symbols: TRB1, ATTRB1 | DNA-binding protein, putative | chr1:18494439-18496713 REVERSEweakly similar to (164) loc_os12g41920 12012.m26974 protein single myb histone 6, putative, expressed seq=cds; coord=3:14469142..14473799:-1; parent_gene=GRMZM2G163291' 'moderately similar to (280) AT5G02310 | Symbols: PRT6 | PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase | chr5:474279-482552 FORWARDhighly similar to (504) loc_os01g05500 12001.m42863 protein zinc finger in N-recognin family protein, putative, expressed seq=cds; coord=3:17607856..17610988:-1; parent_gene=GRMZM2G541193'

'moderately similar to (225) AT1G48000 | Symbols: MYB112, AtMYB112 | MYB112 (myb domain protein 112); DNA binding / transcription factor | chr1:17704269-17706377 REVERSEweakly similar to (154) MYBA2_ORYSA Myb-related protein MYBAS2 - Oryza sativa (Rice)moderately similar to (297) loc_os01g19330 12001.m08470 protein cpm7, putative, expressed seq=cds; coord=3:52308738..52309963:1; parent_gene=GRMZM2G158700'

'highly similar to (853) AT1G72180 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr1:27164074-27167204 FORWARDmoderately similar to (416) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1417) loc_os01g65650 12001.m12674 protein receptor-like protein kinase 5 precursor, putative, expressed seq=cds; coord=3:172374935..172378448:-1; parent_gene=GRMZM2G167253'

'weakly similar to (126) loc_os01g62584 12001.m12380 protein expressed protein seq=cds; coord=3:180570157..180570890:-1; parent_gene=GRMZM2G013463'

'highly similar to (726) AT4G37550 | Symbols: | formamidase, putative / formamide amidohydrolase, putative | chr4:17643684-17645249 FORWARDhighly similar to (837) loc_os01g55950 12001.m11751 protein acetamidase, putative, expressed seq=cds; coord=3:194348658..194355579:1; parent_gene=GRMZM2G089944'

'very weakly similar to (90.5) AT2G27035 | Symbols: | plastocyanin-like domain-containing protein | chr2:11535670-11536251 FORWARDweakly similar to (111) loc_os07g02200 12007.m04693 protein blue copper protein precursor, putative, expressed seq=cds; coord=3:194633422..194634335:1; parent_gene=GRMZM2G128531'

'very weakly similar to (90.5) AT2G27035 | Symbols: | plastocyanin-like domain-containing protein | chr2:11535670-11536251 FORWARDweakly similar to (111) loc_os07g02200 12007.m04693 protein blue copper protein precursor, putative, expressed seq=cds; coord=3:194633422..194634335:1; parent_gene=GRMZM2G128531'

'weakly similar to (128) AT1G52240 | Symbols: ATROPGEF11, ROPGEF11 | ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor | chr1:19458844-19459235 REVERSEweakly similar to (146) loc_os01g55510 12001.m11709 protein dynein light chain LC6, flagellar outer arm, putative, expressed seq=cds; coord=3:195397485..195398202:-1; parent_gene=GRMZM2G016435'

'weakly similar to (128) AT1G52240 | Symbols: ATROPGEF11, ROPGEF11 | ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor | chr1:19458844-19459235 REVERSEweakly similar to (146) loc_os01g55510 12001.m11709 protein dynein light chain LC6, flagellar outer arm, putative, expressed seq=cds; coord=3:195397485..195398202:-1; parent_gene=GRMZM2G016435' 'highly similar to (617) AT1G62430 | Symbols: ATCDS1 | ATCDS1; phosphatidate cytidylyltransferase | chr1:23106274-23108923 REVERSEhighly similar to (637) CDS1_SOLTU Phosphatidate cytidylyltransferase (EC 2.7.7.41) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDP-diacylglycerol synthase) (CDS) (CTP:phosphatidate cytidylyltransferase) (CDP-DAG synthase) (CDP-DG synthetase) - Solahighly similar to (761) loc_os01g55360 12001.m43197 protein phosphatidate cytidylyltransferase, putative, expressed seq=cds; coord=3:195881870..195897637:1; parent_gene=GRMZM2G452529'

'seq=cds; coord=4:24186613..24187104:-1; parent_gene=AC213666.3_FG003'

'highly similar to (512) loc_os08g09740 12008.m05108 protein F-box domain containing protein, expressed seq=cds; coord=4:27021370..27024643:1; parent_gene=GRMZM2G142043'

'moderately similar to (313) loc_os08g36450 12008.m07634 protein expressed protein seq=cds; coord=4:55755200..55757308:1; parent_gene=GRMZM2G423292'

'moderately similar to (264) AT1G26930 | Symbols: | kelch repeat-containing F-box family protein | chr1:9336211-9337476 REVERSEmoderately similar to (414) loc_os11g38980 12011.m080036 protein kelch motif family protein, expressed seq=cds; coord=4:117410977..117414545:-1; parent_gene=GRMZM2G423663'

'moderately similar to (317) AT3G16090 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr3:5456513-5458694 FORWARDmoderately similar to (449) loc_os06g19680 12006.m32051 protein protein binding protein, putative, expressed seq=cds; coord=4:189151150..189158507:-1; parent_gene=GRMZM2G055643'

'weakly similar to (102) loc_os11g05660 12011.m04763 protein F-box domain containing protein, expressed seq=cds; coord=4:189243822..189244974:-1; parent_gene=GRMZM2G302499'

'moderately similar to (407) AT1G79650 | Symbols: RAD23 | RAD23; damaged DNA binding | chr1:29972406-29975132 REVERSEmoderately similar to (300) RAD23_ORYSA Probable DNA repair protein RAD23 (OsRAD23) - Oryza sativa (Rice)highly similar to (522) loc_os02g08300 12002.m06176 protein DNA repair protein RAD23-1, putative, expressed seq=cds; coord=4:234901650..234908817:1; parent_gene=GRMZM2G143462'

'highly similar to (627) AT3G18040 | Symbols: MPK9 | MPK9 (MAP KINASE 9); MAP kinase | chr3:6175741-6178150 FORWARDhighly similar to (702) MPK13_ORYSA Mitogen-activated protein kinase 13 (EC 2.7.11.24) (MAP kinase 13) (Benzothiadiazole-induced MAP kinase 2) (OsBIMK2) (MAP kinase 2) (OsMAPK2) - Oryza sativa (Rice)highly similar to (702) loc_os02g04230 12002.m100091 protein OsMPK17-2 - putative MAPK based on amino acid sequence homology, expressed seq=cds; coord=4:239429006..239435447:-1; parent_gene=GRMZM2G374088'

'nearly identical (1055) AT5G42020 | Symbols: BIP | BIP2; ATP binding | chr5:16807697-16810480 REVERSEnearly identical (1158) BIP3_MAIZE Luminal-binding protein 3 precursor (BiP3) - Zea mays (Maize)nearly identical (1140) loc_os02g02410 12002.m05590 protein luminal-binding protein 3 precursor, putative, expressed seq=cds; coord=4:240050091..240053865:1; parent_gene=GRMZM2G415007' 'nearly identical (1055) AT5G42020 | Symbols: BIP | BIP2; ATP binding | chr5:16807697-16810480 REVERSEnearly identical (1158) BIP3_MAIZE Luminal-binding protein 3 precursor (BiP3) - Zea mays (Maize)nearly identical (1140) loc_os02g02410 12002.m05590 protein luminal-binding protein 3 precursor, putative, expressed seq=cds; coord=4:240050091..240053865:1; parent_gene=GRMZM2G415007'

'highly similar to (739) AT1G20630 | Symbols: CAT1 | CAT1 (CATALASE 1); catalase | chr1:7146812-7149609 FORWARDhighly similar to (964) CATA3_MAIZE Catalase isozyme 3 (EC 1.11.1.6) - Zea mays (Maize)highly similar to (859) loc_os02g02400 12002.m77750 protein catalase isozyme A, putative, expressed seq=cds; coord=4:240105016..240107173:1; parent_gene=GRMZM2G079348'

'highly similar to (507) AT1G12240 | Symbols: ATBETAFRUCT4, VAC-INV | ATBETAFRUCT4; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds | chr1:4153699-4157457 FORWARDhighly similar to (569) INV1_MAIZE Beta-fructofuranosidase 1 precursor (EC 3.2.1.26) (Sucrose 1) (Invertase 1) - Zea mays (Maize)highly similar to (739) loc_os02g01590 12002.m100068 protein beta-fructofuranosidase 1 precursor, putative, expressed seq=cds; coord=4:240446489..240449003:-1; parent_gene=GRMZM2G463871'

'moderately similar to (448) AT5G58420 | Symbols: | 40S ribosomal protein S4 (RPS4D) | chr5:23619599-23620896 FORWARDmoderately similar to (481) RS4_MAIZE 40S ribosomal protein S4 - Zea mays (Maize)moderately similar to (468) loc_os02g01560 12002.m05506 protein 40S ribosomal protein S4, putative, expressed seq=cds; coord=5:1488844..1491571:1; parent_gene=GRMZM2G125271'

'moderately similar to (448) AT5G58420 | Symbols: | 40S ribosomal protein S4 (RPS4D) | chr5:23619599-23620896 FORWARDmoderately similar to (481) RS4_MAIZE 40S ribosomal protein S4 - Zea mays (Maize)moderately similar to (468) loc_os02g01560 12002.m05506 protein 40S ribosomal protein S4, putative, expressed seq=cds; coord=5:1488844..1491571:1; parent_gene=GRMZM2G125271'

'moderately similar to (233) AT4G16070 | Symbols: | lipase class 3 family protein | chr4:9096808-9100596 REVERSEhighly similar to (515) loc_os03g61540 12003.m35500 protein triacylglycerol lipase, putative, expressed seq=cds; coord=5:1722294..1727548:1; parent_gene=GRMZM2G023049'

'highly similar to (557) AT2G47070 | Symbols: SPL1 | SPL1 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 1); DNA binding / transcription factor | chr2:19337144-19340552 FORWARDvery weakly similar to (97.8) LG1_MAIZE LIGULELESS1 protein - Zea mays (Maize)nearly identical (1281) loc_os03g61760 12003.m11057 protein squamosa promoter-binding-like protein 12, putative, expressed seq=cds; coord=5:1845813..1852802:-1; parent_gene=GRMZM2G138421'

'moderately similar to (248) loc_os12g24080 12012.m06242 protein UPL2, putative, expressed seq=cds; coord=5:20984676..20990310:1; parent_gene=GRMZM2G024054'

'moderately similar to (235) AT5G39790 | Symbols: | 5'-AMP-activated protein kinase beta-1 subunit-related | chr5:15932884-15935121 REVERSEmoderately similar to (387) loc_os02g04330 12002.m100032 protein expressed protein seq=cds; coord=5:76677057..76682688:1; parent_gene=GRMZM2G042245' 'moderately similar to (426) AT3G15890 | Symbols: | protein kinase family protein | chr3:5374389-5376114 FORWARDmoderately similar to (231) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (636) loc_os02g09359 12002.m06232 protein BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed seq=cds; coord=5:96751789..96755232:1; parent_gene=GRMZM2G118939'

'highly similar to (680) AT2G30980 | Symbols: ASKdZeta, ATSK23, BIL1, ATSK2-2 | ASKdZeta (Arabidopsis SHAGGY-related protein kinase dZeta); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr2:13182350-13185870 REVERSEhighly similar to (608) MSK1_TOBAC Shaggy-related protein kinase NtK-1 (EC 2.7.11.1) - Nicotiana tabacum (Common tobacco)highly similar to (721) loc_os02g14130 12002.m06659 protein shaggy-related protein kinase eta, putative, expressed seq=cds; coord=5:145863905..145869773:1; parent_gene=GRMZM2G151916'

'moderately similar to (299) AT3G10130 | Symbols: | SOUL heme-binding family protein | chr3:3131122-3133158 REVERSEmoderately similar to (405) loc_os02g33020 12002.m08395 protein SOUL heme-binding protein, putative, expressed seq=cds; coord=5:169224236..169226800:1; parent_gene=GRMZM2G074040'

'moderately similar to (437) AT1G35620 | Symbols: ATPDIL5-2, ATPDI8, PDI8 | ATPDIL5-2 (PDI-LIKE 5-2); protein disulfide isomerase | chr1:13156504-13158280 FORWARDweakly similar to (113) PDI_MEDSA Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) - Medicago sativa (Alfalfa)highly similar to (631) loc_os02g34530 12002.m08542 protein OsPDIL5-3 - Oryza sativa protein disulfide isomerase, expressed seq=cds; coord=5:171878652..171881421:-1; parent_gene=GRMZM2G007385'

'weakly similar to (108) AT1G47230 | Symbols: CYCA3;4 | cyclin, putative | chr1:17306752-17308587 FORWARDweakly similar to (101) CCNAL_DAUCA G2/mitotic-specific cyclin C13-1 (A-like cyclin) (Fragment) - Daucus carota (Carrot)weakly similar to (173) loc_os02g39420 12002.m09030 protein cyclin-A1, putative seq=cds; coord=5:174890976..174891830:-1; parent_gene=AC212449.4_FG004'

'moderately similar to (406) AT1G22400 | Symbols: UGT85A1, ATUGT85A1 | UGT85A1; UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucuronosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr1:7903851-7906607 REVERSEweakly similar to (164) UFO3_MAIZE Anthocyanidin 3-O-glucosyltransferase (EC 2.4.1.115) (Flavonol 3-O-glucosyltransferase) (UDP-glucose flavonoid 3-O-glucosyltransferase) (Bronze-1) (Bz-W22 allele) - Zea mays (Maize)moderately similar to (483) loc_os06g11720 12006.m05889 protein cytokinin-O-glucosyltransferase 2, putative, expressed seq=cds; coord=5:175587788..175589630:-1; parent_gene=GRMZM2G049798'

'moderately similar to (292) AT3G51390 | Symbols: | zinc finger (DHHC type) family protein | chr3:19075718-19077966 FORWARDmoderately similar to (484) loc_os12g29560 12012.m06770 protein metal ion binding protein, putative, expressed seq=cds; coord=5:193912373..193917165:1; parent_gene=GRMZM2G141503' 'weakly similar to (120) AT5G51990 | Symbols: CBF4, DREB1D | CBF4 (C- REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor | chr5:21117113-21117787 REVERSEmoderately similar to (233) loc_os02g45450 12002.m09582 protein dehydration-responsive element-binding protein 1A, putative, expressed seq=cds; coord=5:195834102..195835230:1; parent_gene=GRMZM2G137341'

'very weakly similar to (97.8) AT5G16000 | Symbols: NIK1 | NIK1 (NSP-INTERACTING KINASE 1); kinase | chr5:5224264-5227003 FORWARDweakly similar to (118) loc_os02g49600 12002.m09994 protein BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed seq=cds; coord=5:204589912..204594285:-1; parent_gene=GRMZM2G019317'

'highly similar to (580) AT2G01830 | Symbols: WOL, CRE1, WOL1, AHK4, ATCRE1 | WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase | chr2:363332-367429 REVERSEvery weakly similar to (92.4) ETR1_BRAOL Ethylene receptor (EC 2.7.13.3) - Brassica oleracea (Wild cabbage)highly similar to (800) loc_os02g50480 12002.m10082 protein histidine kinase 1, putative, expressed seq=cds; coord=5:205544166..205551400:1; parent_gene=GRMZM2G151223'

'moderately similar to (248) AT5G40250 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:16086056-16087186 FORWARDmoderately similar to (472) loc_os02g50930 12002.m10127 protein RING-H2 finger protein ATL5I, putative, expressed seq=cds; coord=5:206555179..206557068:1; parent_gene=GRMZM2G053303'

'weakly similar to (147) AT5G65220 | Symbols: | ribosomal protein L29 family protein | chr5:26061301-26062506 FORWARDmoderately similar to (228) RK29_MAIZE 50S ribosomal protein L29, chloroplast precursor (CL29) - Zea mays (Maize)weakly similar to (199) loc_os02g51790 12002.m10210 protein 50S ribosomal protein L29, chloroplast precursor, putative, expressed seq=cds; coord=5:208341565..208343539:1; parent_gene=GRMZM2G159554'

'moderately similar to (377) AT3G53620 | Symbols: AtPPa4 | AtPPa4 (Arabidopsis thaliana pyrophosphorylase 4); inorganic diphosphatase | chr3:19881491-19883308 FORWARDmoderately similar to (355) IPYR_ORYSA Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase) - Oryza sativa (Rice)moderately similar to (411) loc_os05g02310 12005.m04767 protein soluble inorganic pyrophosphatase, putative, expressed seq=cds; coord=6:35680626..35684863:1; parent_gene=GRMZM2G137930'

'highly similar to (669) AT1G70710 | Symbols: ATGH9B1, CEL1 | ATGH9B1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9B1); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds | chr1:26659356-26662962 REVERSEhighly similar to (804) GUN17_ORYSA Endoglucanase 17 precursor (EC 3.2.1.4) (Endo-1,4-beta glucanase 17) (OsGLU13) - Oryza sativa (Rice)highly similar to (804) loc_os06g14540 12006.m06169 protein endoglucanase 1 precursor, putative, expressed seq=cds; coord=6:118083995..118087966:1; parent_gene=GRMZM2G455642'

'weakly similar to (151) AT5G08120 | Symbols: MBP2C, ATMBP2C | MBP2C (MICROTUBULE BINDING PROTEIN 2C); protein binding | chr5:2600743-2602678 REVERSEmoderately similar to (392) loc_os06g17440 12006.m06456 protein TMV-MP30 binding protein 2C, putative, expressed seq=cds; coord=6:119162488..119165785:1; parent_gene=GRMZM2G018823'

'nearly identical (1219) AT2G41560 | Symbols: ACA4 | ACA4 (AUTO-INHIBITED CA(2 'very weakly similar to (86.7) AT1G75250 | Symbols: ATRL6 | ATRL6 (ARABIDOPSIS RAD-LIKE 6); transcription factor | chr1:28244463-28245453 REVERSEweakly similar to (126) loc_os05g50350 12005.m09104 protein DNA binding protein, putative seq=cds; coord=6:166238069..166238595:-1; parent_gene=GRMZM2G139174'

'moderately similar to (457) AT1G17050 | Symbols: SPS2 | SPS2 (Solanesyl diphosphate synthase 2); trans-octaprenyltranstransferase | chr1:5829289-5831215 FORWARDweakly similar to (118) GGPPS_CAPAN Geranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase) (GGPS) [Includes: Dimethylallyltranstransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10); Farnesyltranstransferase (EC 2.5.1.29)] - Capsicum anhighly similar to (562) loc_os05g50550 12005.m09124 protein prenyl transferase, putative, expressed seq=cds; coord=6:166823882..166829182:-1; parent_gene=GRMZM2G163809'

'moderately similar to (359) AT3G57490 | Symbols: | 40S ribosomal protein S2 (RPS2D) | chr3:21279824-21280887 REVERSEmoderately similar to (409) loc_os03g59310 12003.m10829 protein 40S ribosomal protein S2, putative, expressed seq=cds; coord=7:18473070..18475522:1; parent_gene=GRMZM2G168149'

'highly similar to (560) AT1G73100 | Symbols: SUVH3, SDG19 | SUVH3 (SU(VAR)3-9 HOMOLOG 3); histone methyltransferase | chr1:27491970-27493979 FORWARDnearly identical (1170) loc_os11g38900 12011.m07738 protein histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1, putative, expressed seq=cds; coord=7:20244021..20246591:1; parent_gene=AC233961.1_FG001'

'highly similar to (560) AT1G73100 | Symbols: SUVH3, SDG19 | SUVH3 (SU(VAR)3-9 HOMOLOG 3); histone methyltransferase | chr1:27491970-27493979 FORWARDnearly identical (1170) loc_os11g38900 12011.m07738 protein histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1, putative, expressed seq=cds; coord=7:20244021..20246591:1; parent_gene=AC233961.1_FG001'

'moderately similar to (355) AT3G11900 | Symbols: ANT1 | ANT1 (AROMATIC AND NEUTRAL TRANSPORTER 1); amino acid transmembrane transporter/ aromatic amino acid transmembrane transporter/ neutral amino acid transmembrane transporter | chr3:3758523-3760103 FORWARDhighly similar to (568) loc_os07g12770 12007.m05729 protein ANT1, putative, expressed seq=cds; coord=7:21546705..21550608:-1; parent_gene=GRMZM2G173967'

'moderately similar to (295) AT3G20830 | Symbols: | protein kinase family protein | chr3:7285024-7286250 REVERSEweakly similar to (128) G11A_ORYSA Protein kinase G11A (EC 2.7.11.1) - Oryza sativa (Rice)moderately similar to (491) loc_os08g39460 12008.m07927 protein protein kinase, putative, expressed seq=cds; coord=7:23598889..23600662:1; parent_gene=GRMZM2G050427'

'weakly similar to (182) AT1G72030 | Symbols: | GCN5-related N-acetyltransferase (GNAT) family protein | chr1:27110887-27111825 FORWARDmoderately similar to (317) loc_os07g16130 12007.m06056 protein histone acetyltransferase HPA2 and related acetyltransferases, putative, expressed seq=cds; coord=7:27679736..27681630:-1; parent_gene=GRMZM2G302778' 'moderately similar to (452) AT1G09795 | Symbols: ATATP-PRT2, HISN1B | ATATP-PRT2 (ATP PHOSPHORIBOSYL TRANSFERASE 2); ATP phosphoribosyltransferase | chr1:3173588-3176690 FORWARDhighly similar to (565) loc_os03g04169 12003.m05948 protein ATP phosphoribosyltransferase, putative, expressed seq=cds; coord=7:132157014..132162257:1; parent_gene=GRMZM2G068862'

'highly similar to (949) AT1G15690 | Symbols: AVP1, ATAVP3, AVP-3 | AVP1; ATPase/ hydrogen-translocating pyrophosphatase | chr1:5399115-5402185 FORWARDhighly similar to (949) AVP_PHAAU Pyrophosphate-energized vacuolar membrane proton pump (EC 3.6.1.1) (Pyrophosphate-energized inorganic pyrophosphatase) (H(

'moderately similar to (473) AT5G54270 | Symbols: LHCB3, LHCB3*1 | LHCB3 (LIGHT-HARVESTING CHLOROPHYLL B-BINDING PROTEIN 3); structural molecule | chr5:22038424-22039383 FORWARDhighly similar to (504) CB23_HORVU Chlorophyll a-b binding protein of LHCII type III, chloroplast precursor (CAB) - Hordeum vulgare (Barley)moderately similar to (494) loc_os07g37550 12007.m079717 protein chlorophyll a-b binding protein of LHCII type III, chloroplast precursor, putative, expressed seq=cds; coord=7:157568903..157570895:1; parent_gene=GRMZM2G057281'

'nearly identical (2229) AT3G43300 | Symbols: ATMIN7 | ATMIN7 (ARABIDOPSIS THALIANA HOPM INTERACTOR 7); guanyl-nucleotide exchange factor/ protein binding | chr3:15234235-15245034 REVERSEnearly identical (2746) loc_os07g37750 12007.m08025 protein guanyl-nucleotide exchange factor, putative, expressed seq=cds; coord=7:157907062..157937456:-1; parent_gene=GRMZM2G335287'

'moderately similar to (312) AT5G05340 | Symbols: | peroxidase, putative | chr5:1579142-1580819 REVERSEmoderately similar to (340) PER2_ORYSA Peroxidase 2 precursor (EC 1.11.1.7) - Oryza sativa (Rice)moderately similar to (340) loc_os07g48030 12007.m09018 protein peroxidase 2 precursor, putative, expressed seq=cds; coord=7:172779032..172780863:1; parent_gene=GRMZM2G126261'

'moderately similar to (290) AT2G45570 | Symbols: CYP76C2 | CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr2:18779935-18781922 REVERSEmoderately similar to (233) C76A2_SOLME Cytochrome P450 76A2 (EC 1.14.-.-) (CYPLXXVIA2) (P-450EG7) - Solanum melongena (Eggplant) (Aubergine)moderately similar to (349) loc_os09g27510 12009.m05902 protein cytochrome P450 76C4, putative, expressed seq=cds; coord=7:173961868..173963500:-1; parent_gene=GRMZM2G425127'

'moderately similar to (311) AT3G20770 | Symbols: EIN3 | EIN3 (ETHYLENE-INSENSITIVE3); transcription factor chr3:7260702-7262588 REVERSEmoderately similar to (433) loc_os07g48630 12007.m29024 protein ETHYLENE-INSENSITIVE3-like 1 protein, putative, expressed seq=cds; coord=7:173951359..173953387:-1; parent_gene=GRMZM2G151811'

'weakly similar to (171) AT4G35160 | Symbols: | O-methyltransferase family 2 protein | chr4:16730989-16732808 REVERSEmoderately similar to (452) ZRP4_MAIZE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT) - Zea mays (Maize)moderately similar to (416) loc_os12g25450 12012.m06370 protein O-methyltransferase ZRP4, putative, expressed seq=cds; coord=8:123041911..123044071:1; parent_gene=AC209819.3_FG005' 'moderately similar to (382) AT1G78680 | Symbols: ATGGH2 | ATGGH2 (gamma-glutamyl hydrolase 2); omega peptidase | chr1:29593933-29596037 FORWARDmoderately similar to (322) GGH_SOYBN Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-Glu-X carboxypeptidase) (Conjugase) (GH) - Glycine max (Soybean)highly similar to (513) loc_os05g44130 12005.m27626 protein gamma-glutamyl hydrolase precursor, putative, expressed seq=cds; coord=8:123149285..123153566:-1; parent_gene=GRMZM2G095955'

'moderately similar to (407) AT5G40850 | Symbols: UPM1 | UPM1 (UROPHORPHYRIN METHYLASE 1); uroporphyrin-III C-methyltransferase | chr5:16367205-16368724 FORWARDmoderately similar to (281) loc_os01g44050 12001.m10664 protein siroheme synthase, putative, expressed seq=cds; coord=8:145905785..145909658:1; parent_gene=GRMZM2G000739'

'weakly similar to (152) AT4G10040 | Symbols: CYTC-2 | CYTC-2 (cytochrome c-2); electron carrier/ heme binding / iron ion binding | chr4:6277083-6278281 FORWARDweakly similar to (157) CYC_PHAAU Cytochrome c - Phaseolus aureus (Mung bean) (Vigna radiata)weakly similar to (157) loc_os05g34770 12005.m27830 protein cytochrome c, putative, expressed seq=cds; coord=8:146114091..146116986:1; parent_gene=GRMZM2G013712'

'highly similar to (697) AT3G18040 | Symbols: MPK9 | MPK9 (MAP KINASE 9); MAP kinase | chr3:6175741-6178150 FORWARDhighly similar to (808) MPK16_ORYSA Mitogen-activated protein kinase 16 (EC 2.7.11.24) (MAP kinase 16) - Oryza sativa (Rice)highly similar to (808) loc_os01g45620 12001.m43112 protein OsMPK21-2 - putative MAPK based on amino acid sequence homology, expressed seq=cds; coord=8:146830973..146836666:-1; parent_gene=GRMZM2G375975'

'weakly similar to (152) AT3G12700 | Symbols: | aspartyl protease family protein | chr3:4037136-4038387 FORWARDmoderately similar to (280) loc_os01g48750 12001.m11064 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=8:150906867..150909121:1; parent_gene=GRMZM2G311680'

'highly similar to (770) AT3G18660 | Symbols: PGSIP1 | PGSIP1 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 1); transferase, transferring glycosyl groups | chr3:6419211-6421959 REVERSEnearly identical (1139) loc_os01g65780 12001.m150444 protein secondary cell wall-related glycosyltransferase family 8, putative, expressed seq=cds; coord=8:165234282..165239619:-1; parent_gene=GRMZM2G002023'

'moderately similar to (265) AT3G57030 | Symbols: | strictosidine synthase family protein | chr3:21101653-21103204 REVERSEweakly similar to (153) STSY_CATRO Strictosidine synthase precursor (EC 4.3.3.2) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)moderately similar to (497) loc_os08g07810 12008.m04918 protein strictosidine synthase 1 precursor, putative seq=cds; coord=8:165827475..165828933:-1; parent_gene=GRMZM2G338431'

'moderately similar to (265) AT3G57030 | Symbols: | strictosidine synthase family protein | chr3:21101653-21103204 REVERSEweakly similar to (153) STSY_CATRO Strictosidine synthase precursor (EC 4.3.3.2) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)moderately similar to (497) loc_os08g07810 12008.m04918 protein strictosidine synthase 1 precursor, putative seq=cds; coord=8:165827475..165828933:-1; parent_gene=GRMZM2G338431'

'moderately similar to (315) AT4G28190 | Symbols: ULT1, ULT | ULT1 (ULTRAPETALA1); DNA binding | chr4:13985753-13987050 FORWARDmoderately similar to (379) loc_os01g57240 12001.m11877 protein expressed protein seq=cds; coord=8:172005510..172009034:1; parent_gene=GRMZM2G004690'

'moderately similar to (386) AT4G11530 | Symbols: | kinase | chr4:6987093-6989599 FORWARDweakly similar to (181) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)moderately similar to (426) loc_os05g41370 12005.m08312 protein receptor-like protein kinase homolog RK20-1, putative, expressed seq=cds; coord=8:172251862..172254705:-1; parent_gene=GRMZM2G434363'

'moderately similar to (280) AT4G33460 | Symbols: ATNAP13, EMB2751 | ATNAP13; transporter | chr4:16098325-16100113 REVERSEvery weakly similar to (80.1) CYSA_MESVI Probable sulfate/thiosulfate import ATP-binding protein cysA (EC 3.6.3.25) (Sulfate-transporting ATPase) - Mesostigma viridemoderately similar to (377) loc_os01g56400 12001.m11796 protein cobalt import ATP-binding protein cbiO 2, putative, expressed seq=cds; coord=8:172455200..172464190:-1; parent_gene=GRMZM2G111511'

'moderately similar to (280) AT4G33460 | Symbols: ATNAP13, EMB2751 | ATNAP13; transporter | chr4:16098325-16100113 REVERSEvery weakly similar to (80.1) CYSA_MESVI Probable sulfate/thiosulfate import ATP-binding protein cysA (EC 3.6.3.25) (Sulfate-transporting ATPase) - Mesostigma viridemoderately similar to (377) loc_os01g56400 12001.m11796 protein cobalt import ATP-binding protein cbiO 2, putative, expressed seq=cds; coord=8:172455200..172464190:-1; parent_gene=GRMZM2G111511'

'weakly similar to (109) AT1G28210 | Symbols: ATJ1 | ATJ1; heat shock protein binding / nucleic acid binding / unfolded protein binding / zinc ion binding | chr1:9854598-9859977 FORWARDweakly similar to (149) loc_os06g11440 12006.m32015 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=9:6826102..6839564:-1; parent_gene=GRMZM2G097620'

'nearly identical (1504) AT5G65460 | Symbols: | kinesin motor protein-related | chr5:26161831-26169001 REVERSEweakly similar to (138) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiihighly similar to (894) loc_os06g11380 12006.m05855 protein ATP binding protein, putative, expressed seq=cds; coord=9:7186959..7210629:-1; parent_gene=GRMZM2G017257'

'nearly identical (1504) AT5G65460 | Symbols: | kinesin motor protein-related | chr5:26161831-26169001 REVERSEweakly similar to (138) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiihighly similar to (894) loc_os06g11380 12006.m05855 protein ATP binding protein, putative, expressed seq=cds; coord=9:7186959..7210629:-1; parent_gene=GRMZM2G017257'

'moderately similar to (367) AT2G36800 | Symbols: DOGT1, UGT73C5 | DOGT1 (DON-GLUCOSYLTRANSFERASE 1); UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transf | chr2:15423493-15424980 REVERSEweakly similar to (155) ZOX_PHAVU Zeatin O-xylosyltransferase (EC 2.4.2.40) (Zeatin O-beta-D-xylosyltransferase) - Phaseolus vulgaris (Kidney bean) (French bean)highly similar to (668) loc_os03g24430 12003.m07789 protein cytokinin-O-glucosyltransferase 3, putative seq=cds; coord=9:8354433..8356134:-1; parent_gene=GRMZM2G403740' 'nearly identical (1585) AT1G07670 | Symbols: ATECA4, ECA4 | calcium-transporting ATPase | chr1:2370305-2374196 REVERSEmoderately similar to (327) ACA5_ORYSA Probable calcium-transporting ATPase 5, plasma membrane-type (EC 3.6.3.8) (Ca(2

'nearly identical (1585) AT1G07670 | Symbols: ATECA4, ECA4 | calcium-transporting ATPase | chr1:2370305-2374196 REVERSEmoderately similar to (327) ACA5_ORYSA Probable calcium-transporting ATPase 5, plasma membrane-type (EC 3.6.3.8) (Ca(2

'moderately similar to (291) AT3G03470 | Symbols: CYP89A9 | CYP89A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr3:824692-826345 REVERSEmoderately similar to (224) C77A3_SOYBN Cytochrome P450 77A3 (EC 1.14.-.-) - Glycine max (Soybean)moderately similar to (412) loc_os10g05020 12010.m03909 protein transposon protein, putative, unclassified, expressed seq=cds; coord=10:717278..719105:-1; parent_gene=GRMZM2G179143'

'moderately similar to (323) AT5G04740 | Symbols: | ACT domain-containing protein | chr5:1368713-1371391 REVERSEmoderately similar to (415) loc_os12g05650 12012.m04558 protein ACT domain containing protein, expressed seq=cds; coord=10:5523751..5529199:-1; parent_gene=GRMZM2G066496'

'moderately similar to (456) AT5G65940 | Symbols: CHY1 | CHY1 (BETA-HYDROXYISOBUTYRYL-COA HYDROLASE 1); 3-hydroxyisobutyryl-CoA hydrolase | chr5:26376927-26379161 REVERSEhighly similar to (552) loc_os12g16350 12012.m073804 protein CHY1, putative, expressed seq=cds; coord=10:19475272..19481312:1; parent_gene=GRMZM2G181227'

'moderately similar to (233) AT5G57580 | Symbols: | calmodulin-binding protein | chr5:23314994-23317683 REVERSEhighly similar to (692) loc_os12g36110 12012.m07401 protein calmodulin binding protein, putative, expressed seq=cds; coord=10:23804445..23808523:-1; parent_gene=GRMZM2G176472'

'weakly similar to (117) AT1G54580 | Symbols: ACP2 | ACP2 (ACYL CARRIER PROTEIN 2); acyl carrier | chr1:20389572-20390770 FORWARDweakly similar to (186) ACP1_HORVU Acyl carrier protein 1, chloroplast precursor (Acyl carrier protein I) (ACP I) - Hordeum vulgare (Barley)weakly similar to (197) loc_os12g34890 12012.m07282 protein acyl carrier protein 1, chloroplast precursor, putative, expressed seq=cds; coord=10:25773815..25777130:1; parent_gene=GRMZM2G149580'

'moderately similar to (208) AT5G38280 | Symbols: PR5K | PR5K; kinase/ transmembrane receptor protein serine/threonine kinase | chr5:15293325-15295838 REVERSEweakly similar to (146) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (417) loc_os11g25510 12011.m06473 protein S-domain receptor-like protein kinase, putative, expressed seq=cds; coord=10:66956269..66957720:1; parent_gene=GRMZM2G481531'

'moderately similar to (408) AT3G27550 | Symbols: | group II intron splicing factor CRS1-related | chr3:10208010-10209899 REVERSEhighly similar to (602) loc_os05g05300 12005.m05057 protein CRS1 / YhbY domain containing protein, expressed seq=cds; coord=10:89435091..89438493:1; parent_gene=GRMZM2G039857'

'moderately similar to (430) AT1G20925 | Symbols: | auxin efflux carrier family protein | chr1:7290612-7292507 FORWARDhighly similar to (618) loc_os09g31478 12009.m06269 protein auxin hydrogen symporter, putative, expressed seq=cds; coord=10:128451470..128455073:1; parent_gene=GRMZM2G007481' 'weakly similar to (151) AT1G04790 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:1345469-1348143 FORWARDmoderately similar to (343) loc_os04g43220 12004.m35172 protein zinc finger, C3HC4 type family protein, expressed seq=cds; coord=10:130228571..130231882:-1; parent_gene=GRMZM2G016487'

'weakly similar to (137) AT5G10650 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:3365237-3367263 REVERSEmoderately similar to (459) loc_os04g51400 12004.m35451 protein zinc finger, C3HC4 type family protein, expressed seq=cds; coord=10:141076436..141079773:1; parent_gene=GRMZM2G140924'

'highly similar to (744) AT3G22200 | Symbols: POP2, GABA-T, HER1 | POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase/ 4-aminobutyrate:pyruvate transaminase | chr3:7835286-7838863 FORWARDvery weakly similar to (89.7) GSA_BRANA Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT) - Brassica napus (Rape)highly similar to (899) loc_os04g52450 12004.m101652 protein aminotransferase y4uB, putative, expressed seq=cds; coord=10:142279983..142291898:1; parent_gene=GRMZM2G108125'

'highly similar to (744) AT3G22200 | Symbols: POP2, GABA-T, HER1 | POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase/ 4-aminobutyrate:pyruvate transaminase | chr3:7835286-7838863 FORWARDvery weakly similar to (89.7) GSA_BRANA Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT) - Brassica napus (Rape)highly similar to (899) loc_os04g52450 12004.m101652 protein aminotransferase y4uB, putative, expressed seq=cds; coord=10:142279983..142291898:1; parent_gene=GRMZM2G108125'

'weakly similar to (169) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDvery weakly similar to (80.9) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (218) loc_os04g55560 12004.m35488 protein AP2 domain containing protein, expressed seq=cds; coord=10:145350317..145352828:1; parent_gene=GRMZM2G076602'

'moderately similar to (261) AT4G32300 | Symbols: SD2-5 | SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase | chr4:15599970-15602435 FORWARDweakly similar to (176) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (570) loc_os04g56110 12004.m35493 protein ATP binding protein, putative, expressed seq=cds; coord=10:146170484..146172446:-1; parent_gene=GRMZM2G007477'

'highly similar to (512) AT1G74910 | Symbols: | ADP-glucose pyrophosphorylase family protein | chr1:28135770-28138456 REVERSEhighly similar to (603) loc_os03g11050 12003.m35086 protein mannose-1-phosphate guanyltransferase, putative, expressed seq=cds; coord=1:21196693..21221560:1; parent_gene=GRMZM2G064841'

'highly similar to (512) AT1G74910 | Symbols: | ADP-glucose pyrophosphorylase family protein | chr1:28135770-28138456 REVERSEhighly similar to (603) loc_os03g11050 12003.m35086 protein mannose-1-phosphate guanyltransferase, putative, expressed seq=cds; coord=1:21196693..21221560:1; parent_gene=GRMZM2G064841'

'highly similar to (551) AT5G67385 | Symbols: | protein binding / signal transducer | chr5:26884754-26887083 FORWARDmoderately similar to (275) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)highly similar to (757) loc_os03g10880 12003.m101233 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=1:21471914..21474815:1; parent_gene=GRMZM2G004523'

'seq=cds; coord=1:21678945..21680766:-1; parent_gene=GRMZM2G415251'

'seq=cds; coord=1:21678945..21680766:-1; parent_gene=GRMZM2G415251'

'moderately similar to (253) AT3G51620 | Symbols: | unknown protein | chr3:19143859-19147944 FORWARDmoderately similar to (329) loc_os03g21850 12003.m35216 protein expressed protein seq=cds; coord=1:56283126..56286467:1; parent_gene=GRMZM2G063657'

'weakly similar to (194) AT1G19110 | Symbols: | inter-alpha-trypsin inhibitor heavy chain-related | chr1:6602270-6605766 FORWARDmoderately similar to (315) loc_os03g29350 12003.m34881 protein von Willebrand factor type A domain containing protein, expressed seq=cds; coord=1:70581525..70590132:-1; parent_gene=GRMZM2G524711'

'moderately similar to (249) AT2G15480 | Symbols: UGT73B5 | UGT73B5 (UDP-glucosyl transferase 73B5); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups | chr2:6758817-6760452 FORWARDweakly similar to (139) IAAG_MAIZE Indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) (IAA-Glu synthetase) ((Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase) - Zea mays (Maize)highly similar to (608) loc_os03g59350 12003.m10833 protein cytokinin-O-glucosyltransferase 3, putative, expressed seq=cds; coord=1:275582841..275584525:-1; parent_gene=GRMZM2G074395'

'weakly similar to (135) AT3G48100 | Symbols: ARR5, ATRR2, IBC6 | ARR5 (ARABIDOPSIS RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator | chr3:17759112-17760740 REVERSEweakly similar to (189) loc_os04g57720 12004.m10657 protein OsRR6 - Rice type-A response regulator, expressed seq=cds; coord=2:2081848..2082630:-1; parent_gene=GRMZM2G040736'

'moderately similar to (202) AT3G12130 | Symbols: | KH domain-containing protein / zinc finger (CCCH type) family protein | chr3:3864486-3866406 REVERSEmoderately similar to (430) loc_os04g57010 12004.m79001 protein zinc finger C-x8-C-x5-C-x3-H type family protein, expressed seq=cds; coord=2:3089969..3094480:-1; parent_gene=GRMZM2G071034'

'moderately similar to (490) AT4G23030 | Symbols: | MATE efflux protein-related | chr4:12072857-12074365 FORWARDhighly similar to (775) loc_os04g48290 12004.m09766 protein antiporter/ drug transporter/ transporter, putative, expressed seq=cds; coord=2:16638278..16640447:-1; parent_gene=GRMZM2G080992'

'highly similar to (764) AT1G62740 | Symbols: | stress-inducible protein, putative | chr1:23231026-23233380 FORWARDhighly similar to (620) STIP_SOYBN Heat shock protein STI (Stress-inducible protein) (GmSTI) - Glycine max (Soybean)highly similar to (858) loc_os04g45480 12004.m09501 protein heat shock protein STI, putative, expressed seq=cds; coord=2:22504092..22513426:-1; parent_gene=GRMZM2G070863' 'weakly similar to (164) AT5G43960 | Symbols: | nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein | chr5:17689154-17691653 REVERSEmoderately similar to (394) loc_os04g43150 12004.m09279 protein RNA-binding protein-like, putative, expressed seq=cds; coord=2:28564081..28569611:1; parent_gene=GRMZM2G002903'

'weakly similar to (164) AT5G43960 | Symbols: | nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein | chr5:17689154-17691653 REVERSEmoderately similar to (394) loc_os04g43150 12004.m09279 protein RNA-binding protein-like, putative, expressed seq=cds; coord=2:28564081..28569611:1; parent_gene=GRMZM2G002903'

'highly similar to (593) AT4G14340 | Symbols: CKI1, CKL11 | CKI1 (CASEIN KINASE I); kinase/ protein serine/threonine kinase | chr4:8248532-8251668 REVERSEhighly similar to (702) loc_os04g43490 12004.m101584 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=2:28936197..28940916:-1; parent_gene=GRMZM2G032694'

'weakly similar to (177) AT3G08710 | Symbols: ATH9 | ATH9 (thioredoxin H-type 9) | chr3:2645590-2646304 FORWARDweakly similar to (105) TRXH_WHEAT Thioredoxin H-type (TRX-H) (TrxTa) - Triticum aestivum (Wheat)moderately similar to (221) loc_os05g07690 12005.m27714 protein thioredoxin H-type, putative, expressed seq=cds; coord=3:13465241..13467448:1; parent_gene=GRMZM2G159145'

'moderately similar to (261) AT5G16450 | Symbols: | dimethylmenaquinone methyltransferase family protein | chr5:5374357-5375342 FORWARDmoderately similar to (306) loc_os01g52460 12001.m11420 protein regulator of ribonuclease activity A, putative, expressed seq=cds; coord=3:17033772..17034278:1; parent_gene=AC215260.3_FG004'

'moderately similar to (261) AT5G16450 | Symbols: | dimethylmenaquinone methyltransferase family protein | chr5:5374357-5375342 FORWARDmoderately similar to (306) loc_os01g52460 12001.m11420 protein regulator of ribonuclease activity A, putative, expressed seq=cds; coord=3:17033772..17034278:1; parent_gene=AC215260.3_FG004'

'moderately similar to (409) AT1G25390 | Symbols: | protein kinase family protein | chr1:8906640-8908800 REVERSEmoderately similar to (222) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (631) loc_os01g04409 12001.m07075 protein OsWAK1 - OsWAK receptor-like cytoplasmic kinase (OsWAK-RLCK), expressed seq=cds; coord=3:20399610..20409348:1; parent_gene=GRMZM2G013790'

'moderately similar to (253) AT3G14470 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4857940-4861104 FORWARDhighly similar to (985) loc_os01g35254 12001.m09827 protein transposon protein, putative, CACTA, En/Spm sub-class seq=cds; coord=3:113896010..113902317:-1; parent_gene=AC230011.2_FG002'

'highly similar to (630) AT3G44200 | Symbols: ATNEK6, NEK6, IBO1 | NEK6 ("NIMA (NEVER IN MITOSIS, GENE A)-RELATED 6"); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr3:15906788-15911365 FORWARDweakly similar to (130) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)nearly identical (1145) loc_os01g64490 12001.m12563 protein ATP binding protein, putative, expressed seq=cds; coord=3:176289472..176295491:1; parent_gene=GRMZM2G074262'

'very weakly similar to (85.1) loc_os01g41360 12001.m10403 protein expressed protein seq=cds; coord=3:222892155..222892812:-1; parent_gene=GRMZM2G368767' 'weakly similar to (164) AT4G35160 | Symbols: | O-methyltransferase family 2 protein | chr4:16730989-16732808 REVERSEhighly similar to (647) ZRP4_MAIZE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT) - Zea mays (Maize)moderately similar to (410) loc_os05g43930 12005.m08519 protein O-methyltransferase ZRP4, putative, expressed seq=cds; coord=4:11916303..11917798:-1; parent_gene=GRMZM2G017557'

'moderately similar to (376) AT3G03080 | Symbols: | NADP-dependent oxidoreductase, putative | chr3:698530-700278 REVERSEmoderately similar to (444) loc_os11g14910 12011.m05627 protein NADP-dependent oxidoreductase P1, putative, expressed seq=cds; coord=4:12220797..12222465:-1; parent_gene=GRMZM2G110965'

'weakly similar to (137) AT5G50570 | Symbols: | squamosa promoter-binding protein, putative | chr5:20582555-20583791 REVERSEweakly similar to (120) SBP1_ANTMA Squamosa promoter-binding protein 1 - Antirrhinum majus (Garden snapdragon)weakly similar to (155) loc_os08g41940 12008.m08172 protein teosinte glume architecture 1, putative, expressed seq=cds; coord=4:17489205..17501119:1; parent_gene=GRMZM2G106798'

'highly similar to (905) AT5G60790 | Symbols: ATGCN1, GCN1 | ATGCN1; transporter | chr5:24453760-24455767 REVERSEnearly identical (1004) loc_os08g45010 12008.m08472 protein ATP-binding cassette sub-family F member 2, putative, expressed seq=cds; coord=4:49443895..49447342:-1; parent_gene=GRMZM2G031954'

'weakly similar to (116) AT1G79460 | Symbols: GA2, KS, ATKS | GA2 (GA REQUIRING 2); ent-kaurene synthase | chr1:29890568-29894436 FORWARDweakly similar to (119) KSB_CUCMA Ent-kaurene synthase B, chloroplast precursor (EC 4.2.3.19) (KSB) - Cucurbita maxima (Pumpkin) (Winter squash)weakly similar to (175) loc_os04g52230 12004.m10118 protein ent-kaurene synthase B, chloroplast precursor, putative, expressed seq=cds; coord=4:53257241..53258494:-1; parent_gene=GRMZM2G391312'

'weakly similar to (113) AT3G18710 | Symbols: PUB29, ATPUB29 | PUB29 (PLANT U-BOX 29); ubiquitin-protein ligase | chr3:6434234-6435481 REVERSEmoderately similar to (438) loc_os02g33680 12002.m08459 protein U-box domain containing protein, expressed seq=cds; coord=4:111895429..111896985:1; parent_gene=GRMZM2G127690'

'seq=cds; coord=4:141593772..141594427:1; parent_gene=GRMZM2G118717'

'moderately similar to (221) AT4G13180 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr4:7657373-7658164 REVERSEmoderately similar to (206) SDR1_PICAB Short-chain type dehydrogenase/reductase (EC 1.-.-.-) - Picea abies (Norway spruce) (Picea excelsa)moderately similar to (344) loc_os06g08600 12006.m05579 protein versicolorin reductase, putative, expressed seq=cds; coord=4:174050248..174051484:1; parent_gene=GRMZM2G316789'

'moderately similar to (221) AT4G13180 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr4:7657373-7658164 REVERSEmoderately similar to (206) SDR1_PICAB Short-chain type dehydrogenase/reductase (EC 1.-.-.-) - Picea abies (Norway spruce) (Picea excelsa)moderately similar to (344) loc_os06g08600 12006.m05579 protein versicolorin reductase, putative, expressed seq=cds; coord=4:174050248..174051484:1; parent_gene=GRMZM2G316789'

'moderately similar to (221) AT4G13180 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr4:7657373-7658164 REVERSEmoderately similar to (206) SDR1_PICAB Short-chain type dehydrogenase/reductase (EC 1.-.-.-) - Picea abies (Norway spruce) (Picea excelsa)moderately similar to (344) loc_os06g08600 12006.m05579 protein versicolorin reductase, putative, expressed seq=cds; coord=4:174050248..174051484:1; parent_gene=GRMZM2G316789'

'moderately similar to (323) AT5G20720 | Symbols: CPN20, CPN10, CHCPN10, ATCPN21, CPN21 | CPN20 (CHAPERONIN 20); calmodulin binding | chr5:7015015-7016354 FORWARDmoderately similar to (298) CH10C_SPIOL 20 kDa chaperonin, chloroplast precursor (Protein Cpn21) (Chloroplast protein Cpn10) (Chloroplast chaperonin 10) (Ch-CPN10) - Spinacia oleracea (Spinach)moderately similar to (357) loc_os06g09679 12006.m31856 protein chaperonin, chloroplast precursor, putative, expressed seq=cds; coord=4:176500156..176502218:1; parent_gene=GRMZM2G091189'

'nearly identical (1585) AT2G31900 | Symbols: XIF, ATXIF, ATMYO5 | XIF; motor | chr2:13560760-13569623 REVERSEnearly identical (1782) loc_os03g53660 12003.m10336 protein XIF, putative, expressed seq=cds; coord=5:7359267..7367484:-1; parent_gene=GRMZM2G460396'

'moderately similar to (323) AT3G22845 | Symbols: | emp24/gp25L/p24 protein-related | chr3:8087373-8088550 FORWARDmoderately similar to (377) loc_os03g53310 12003.m10303 protein suppressor/enhancer of lin-12 protein 9 precursor, putative, expressed seq=cds; coord=5:7598126..7603275:1; parent_gene=GRMZM2G147046'

'moderately similar to (273) AT1G28590 | Symbols: | lipase, putative | chr1:10047509-10049300 REVERSEweakly similar to (146) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)highly similar to (553) loc_os06g47910 12006.m09317 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=5:53003394..53005408:-1; parent_gene=GRMZM2G048904'

'weakly similar to (183) AT5G52260 | Symbols: AtMYB19 | AtMYB19 (myb domain protein 19); DNA binding / transcription factor | chr5:21220165-21221223 FORWARDweakly similar to (172) MYB3_HORVU Myb-related protein Hv33 - Hordeum vulgare (Barley)moderately similar to (384) loc_os02g02370 12002.m05586 protein transcription factor MYB86, putative seq=cds; coord=5:69302388..69303967:-1; parent_gene=GRMZM2G088189'

'weakly similar to (183) AT5G52260 | Symbols: AtMYB19 | AtMYB19 (myb domain protein 19); DNA binding / transcription factor | chr5:21220165-21221223 FORWARDweakly similar to (172) MYB3_HORVU Myb-related protein Hv33 - Hordeum vulgare (Barley)moderately similar to (384) loc_os02g02370 12002.m05586 protein transcription factor MYB86, putative seq=cds; coord=5:69302388..69303967:-1; parent_gene=GRMZM2G088189'

'highly similar to (726) AT1G70570 | Symbols: | anthranilate phosphoribosyltransferase, putative | chr1:26608719-26612062 FORWARDhighly similar to (899) loc_os02g03850 12002.m05734 protein expressed protein seq=cds; coord=5:74621198..74625869:1; parent_gene=GRMZM2G168791' 'highly similar to (600) AT1G10930 | Symbols: ATSGS1, RECQ4A, ATRECQ4A | RECQ4A; ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding | chr1:3648032-3654997 REVERSEhighly similar to (664) loc_os04g35420 12004.m08631 protein ATSGS1, putative, expressed seq=cds; coord=5:77260588..77273432:-1; parent_gene=GRMZM2G319573'

'moderately similar to (459) AT4G29990 | Symbols: | light repressible receptor protein kinase | chr4:14665802-14669438 REVERSEmoderately similar to (224) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (924) loc_os02g05730 12002.m05921 protein protein kinase domain containing protein, expressed seq=cds; coord=5:80795990..80800856:-1; parent_gene=GRMZM2G093490'

'very weakly similar to (89.7) AT1G53820 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:20091491-20092423 FORWARDweakly similar to (146) EL5_ORYSA E3 ubiquitin-protein ligase EL5 (EC 6.3.2.-) - Oryza sativa (Rice)weakly similar to (146) loc_os02g35429 12002.m08631 protein zinc finger, C3HC4 type family protein seq=cds; coord=5:174017496..174018659:1; parent_gene=GRMZM2G460958'

'weakly similar to (137) AT3G52090 | Symbols: ATRPB13.6, NRPB11, NRPD11, NRPE11 | NRPB11; DNA binding / DNA-directed RNA polymerase | chr3:19318069-19318998 REVERSEweakly similar to (146) loc_os07g07610 12007.m05220 protein DNA-directed RNA polymerase II subunit J, putative, expressed seq=cds; coord=5:184738650..184741012:1; parent_gene=GRMZM2G043461'

'moderately similar to (477) AT5G19320 | Symbols: RANGAP2 | RANGAP2 (RAN GTPASE ACTIVATING PROTEIN 2); RAN GTPase activator | chr5:6505310-6506947 REVERSEhighly similar to (677) loc_os05g46560 12005.m27945 protein ran GTPase activating protein, putative, expressed seq=cds; coord=5:185399193..185401809:1; parent_gene=GRMZM2G148301'

'weakly similar to (161) AT1G70670 | Symbols: | caleosin-related family protein | chr1:26644830-26645970 FORWARDmoderately similar to (243) loc_os02g50174 12002.m10050 protein caleosin related protein, expressed seq=cds; coord=5:205154533..205156657:1; parent_gene=GRMZM2G090609'

'highly similar to (580) AT2G01830 | Symbols: WOL, CRE1, WOL1, AHK4, ATCRE1 | WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase | chr2:363332-367429 REVERSEvery weakly similar to (92.4) ETR1_BRAOL Ethylene receptor (EC 2.7.13.3) - Brassica oleracea (Wild cabbage)highly similar to (800) loc_os02g50480 12002.m10082 protein histidine kinase 1, putative, expressed seq=cds; coord=5:205544166..205551400:1; parent_gene=GRMZM2G151223'

'weakly similar to (137) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEmoderately similar to (312) loc_os06g20110 12006.m06668 protein chloroplast nucleoid DNA binding protein, putative seq=cds; coord=6:120607748..120609208:-1; parent_gene=GRMZM2G110168'

'moderately similar to (326) AT3G21770 | Symbols: | peroxidase 30 (PER30) (P30) (PRXR9) | chr3:7673345-7674661 FORWARDmoderately similar to (372) PER1_ORYSA Peroxidase 1 precursor (EC 1.11.1.7) - Oryza sativa (Rice)moderately similar to (484) loc_os06g29470 12006.m07491 protein peroxidase 1 precursor, putative, expressed seq=cds; coord=6:120912973..120914397:1; parent_gene=GRMZM2G104109' 'moderately similar to (283) AT1G05260 | Symbols: RCI3, RCI3A | RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase | chr1:1529827-1531271 FORWARDmoderately similar to (266) PER1_ORYSA Peroxidase 1 precursor (EC 1.11.1.7) - Oryza sativa (Rice)moderately similar to (459) loc_os05g06970 12005.m05223 protein peroxidase 1 precursor, putative, expressed seq=cds; coord=6:125154676..125157008:1; parent_gene=GRMZM2G450233'

'moderately similar to (228) AT1G22740 | Symbols: RAB7, ATRABG3B, RAB75, RABG3B | RABG3B; GTP binding | chr1:8049247-8050494 FORWARDmoderately similar to (244) RAB7_SOYBN Ras-related protein Rab7 - Glycine max (Soybean)moderately similar to (272) loc_os05g46000 12005.m08725 protein ras-related protein Rab7, putative, expressed seq=cds; coord=6:161464139..161465906:1; parent_gene=GRMZM2G090034'

'moderately similar to (209) AT1G09830 | Symbols: | phosphoribosylamine--glycine ligase (PUR2) | chr1:3192783-3194936 REVERSEweakly similar to (167) PUR2_VIGUN Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase) (Fragment) - Vigna unguiculata (Cowpea)moderately similar to (242) loc_os08g09210 12008.m080100 protein phosphoribosylamine--glycine ligase, putative, expressed seq=cds; coord=6:161796867..161797813:1; parent_gene=GRMZM2G088995'

'very weakly similar to (81.6) AT2G41900 | Symbols: | zinc finger (CCCH-type) family protein | chr2:17491352-17493502 FORWARDweakly similar to (166) loc_os12g33090 12012.m07107 protein nucleic acid binding protein, putative, expressed seq=cds; coord=7:2554871..2557423:-1; parent_gene=AC199624.4_FG007'

'weakly similar to (143) AT5G57625 | Symbols: | allergen V5/Tpx-1-related family protein | chr5:23337865-23338577 FORWARDweakly similar to (177) PR13_HORVU Pathogenesis-related protein PRB1-3 precursor (PR-1B) (HV-8) - Hordeum vulgare (Barley)weakly similar to (194) loc_os07g03710 12007.m04841 protein pathogenesis-related protein PRB1-3 precursor, putative, expressed seq=cds; coord=7:3483732..3484794:1; parent_gene=GRMZM2G465226'

'very weakly similar to (93.2) AT3G28917 | Symbols: MIF2 | MIF2 (MINI ZINC FINGER 2); DNA binding | chr3:10925014-10925316 FORWARDweakly similar to (139) loc_os09g24810 12009.m05635 protein mini zinc finger 3, putative, expressed seq=cds; coord=7:112630524..112633217:1; parent_gene=GRMZM2G071112'

'highly similar to (967) AT1G26850 | Symbols: | dehydration-responsive family protein | chr1:9301146-9303432 REVERSEnearly identical (1186) loc_os09g24900 12009.m22086 protein ankyrin protein kinase-like, putative, expressed seq=cds; coord=7:112980176..112983545:1; parent_gene=GRMZM2G114706'

'moderately similar to (329) AT3G02470 | Symbols: | SAMDC (S-ADENOSYLMETHIONINE DECARBOXYLASE); adenosylmethionine decarboxylase | chr3:510223-511323 FORWARDmoderately similar to (487) DCAM_ORYSA S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain] - Oryza sativa (Rice)highly similar to (592) loc_os09g25620 12009.m059977 protein S-adenosylmethionine decarboxylase proenzyme, putative, expressed seq=cds; coord=7:118016000..118018602:-1; parent_gene=GRMZM2G060369'

'very weakly similar to (81.3) AT2G41940 | Symbols: ZFP8 | ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding | chr2:17507556-17508329 FORWARDweakly similar to (182) loc_os09g27320 12009.m05884 protein zinc finger protein, putative seq=cds; coord=7:122716983..122718164:1; parent_gene=GRMZM2G128212' 'very weakly similar to (95.5) AT5G15350 | Symbols: | plastocyanin-like domain-containing protein | chr5:4985184-4986154 REVERSEmoderately similar to (222) loc_os09g38540 12009.m06795 protein blue copper protein precursor, putative, expressed seq=cds; coord=7:145769695..145771418:-1; parent_gene=GRMZM2G485559'

'moderately similar to (487) AT5G08030 | Symbols: | glycerophosphoryl diester phosphodiesterase family protein | chr5:2575152-2576770 REVERSEhighly similar to (584) loc_os07g41150 12007.m08351 protein glycerophosphoryl diester phosphodiesterase precursor, putative, expressed seq=cds; coord=7:163783254..163784893:-1; parent_gene=GRMZM2G017550'

'moderately similar to (319) AT4G35880 | Symbols: | aspartyl protease family protein | chr4:16993339-16995721 FORWARDvery weakly similar to (81.3) ASP1_ORYSA Aspartic proteinase Asp1 precursor (EC 3.4.23.-) (OsAsp1) (OSAP1) (Nucellin-like protein) - Oryza sativa (Rice)highly similar to (511) loc_os09g37012 12009.m06650 protein aspartic-type endopeptidase/ pepsin A, putative, expressed seq=cds; coord=7:175289779..175291198:1; parent_gene=GRMZM2G420910'

'weakly similar to (192) AT3G25480 | Symbols: | rhodanese-like domain-containing protein | chr3:9235591-9236598 REVERSEmoderately similar to (405) loc_os01g66600 12001.m12767 protein expressed protein seq=cds; coord=8:164616426..164619629:1; parent_gene=GRMZM2G080816'

'weakly similar to (171) AT3G08910 | Symbols: | DNAJ heat shock protein, putative | chr3:2710402-2711811 REVERSEmoderately similar to (434) loc_os01g65480 12001.m12659 protein dnaJ protein homolog 1, putative, expressed seq=cds; coord=8:165594730..165597234:-1; parent_gene=GRMZM2G128248'

'moderately similar to (434) AT4G06599 | Symbols: | ubiquitin family protein | chr4:3666079-3667495 REVERSEmoderately similar to (500) loc_os01g65450 12001.m150790 protein ubiquitin-like domain containing CTD phosphatase 1, putative, expressed seq=cds; coord=8:165678358..165682072:1; parent_gene=GRMZM2G114172'

'moderately similar to (434) AT4G06599 | Symbols: | ubiquitin family protein | chr4:3666079-3667495 REVERSEmoderately similar to (500) loc_os01g65450 12001.m150790 protein ubiquitin-like domain containing CTD phosphatase 1, putative, expressed seq=cds; coord=8:165678358..165682072:1; parent_gene=GRMZM2G114172'

'moderately similar to (434) AT4G06599 | Symbols: | ubiquitin family protein | chr4:3666079-3667495 REVERSEmoderately similar to (500) loc_os01g65450 12001.m150790 protein ubiquitin-like domain containing CTD phosphatase 1, putative, expressed seq=cds; coord=8:165678358..165682072:1; parent_gene=GRMZM2G114172'

'moderately similar to (233) AT1G07090 | Symbols: LSH6 | LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6) | chr1:2174202-2174792 REVERSEmoderately similar to (276) loc_os01g61310 12001.m12257 protein conserved hypothetical protein seq=cds; coord=8:169911769..169913354:1; parent_gene=GRMZM2G135332'

'highly similar to (520) AT5G08030 | Symbols: | glycerophosphoryl diester phosphodiesterase family protein | chr5:2575152-2576770 REVERSEhighly similar to (639) loc_os01g55780 12001.m11736 protein glycerophosphoryl diester phosphodiesterase precursor, putative, expressed seq=cds; coord=8:173244055..173251921:-1; parent_gene=GRMZM2G153274' 'highly similar to (520) AT5G08030 | Symbols: | glycerophosphoryl diester phosphodiesterase family protein | chr5:2575152-2576770 REVERSEhighly similar to (639) loc_os01g55780 12001.m11736 protein glycerophosphoryl diester phosphodiesterase precursor, putative, expressed seq=cds; coord=8:173244055..173251921:-1; parent_gene=GRMZM2G153274'

'highly similar to (523) AT5G55220 | Symbols: | trigger factor type chaperone family protein | chr5:22397677-22400678 FORWARDhighly similar to (772) loc_os06g20320 12006.m06689 protein trigger factor-like protein, putative, expressed seq=cds; coord=10:2654215..2662976:-1; parent_gene=GRMZM2G127393'

'very weakly similar to (87.4) AT3G14470 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4857940-4861104 FORWARDmoderately similar to (431) loc_os02g16270 12002.m100165 protein xa1-like protein, putative, expressed seq=cds; coord=10:3160819..3166305:1; parent_gene=GRMZM2G356817'

'moderately similar to (365) AT3G14460 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4851990-4856264 REVERSEnearly identical (1454) loc_os01g57340 12001.m11885 protein rp1-like protein, putative, expressed seq=cds; coord=10:3698044..3702576:-1; parent_gene=GRMZM2G443939'

'moderately similar to (302) AT1G32360 | Symbols: | zinc finger (CCCH-type) family protein | chr1:11673325-11675162 FORWARDmoderately similar to (438) loc_os08g06330 12008.m04772 protein zinc finger C-x8-C-x5-C-x3-H type family protein, expressed seq=cds; coord=10:77445844..77449872:1; parent_gene=GRMZM2G305582'

'weakly similar to (157) AT4G33420 | Symbols: | peroxidase, putative | chr4:16084856-16086105 FORWARDweakly similar to (138) PER1_ARAHY Cationic peroxidase 1 precursor (EC 1.11.1.7) (PNPC1) - Arachis hypogaea (Peanut)moderately similar to (436) loc_os05g04380 12005.m27687 protein peroxidase 1 precursor, putative, expressed seq=cds; coord=10:85644092..85645627:1; parent_gene=GRMZM2G394500'

'highly similar to (557) AT1G08250 | Symbols: ADT6 | ADT6 (arogenate dehydratase 6); arogenate dehydratase/ prephenate dehydratase | chr1:2588994-2590235 REVERSEhighly similar to (687) loc_os04g33390 12004.m08428 protein P-protein, putative, expressed seq=cds; coord=10:113515151..113516898:1; parent_gene=GRMZM2G125923'

'moderately similar to (484) AT2G27050 | Symbols: EIL1 | EIL1 (ETHYLENE-INSENSITIVE3-LIKE 1); transcription factor/ transcription regulator | chr2:11546314-11548068 FORWARDhighly similar to (991) loc_os03g20790 12003.m07486 protein ETHYLENE-INSENSITIVE3-like 1 protein, putative, expressed seq=cds; coord=1:52564282..52568326:-1; parent_gene=GRMZM2G033570'

'highly similar to (597) AT4G16600 | Symbols: | transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr4:9350039-9352707 FORWARDhighly similar to (822) loc_os10g40640 12010.m06834 protein transferase, transferring glycosyl groups, putative, expressed seq=cds; coord=1:92238858..92242166:1; parent_gene=GRMZM2G114772' 'moderately similar to (267) AT5G66880 | Symbols: SNRK2-3, SNRK2.3, SRK2I | SNRK2.3 (SUCROSE NONFERMENTING 1(SNF1)-RELATED PROTEIN KINASE 2.3); kinase/ protein kinase | chr5:26710697-26712732 FORWARDmoderately similar to (296) SAPK3_ORYSA Serine/threonine-protein kinase SAPK3 (EC 2.7.11.1) (Osmotic stress/abscisic acid-activated protein kinase 3) (Protein kinase REK) - Oryza sativa (Rice)moderately similar to (296) loc_os10g41490 12010.m065205 protein serine/threonine-protein kinase SAPK3, putative, expressed seq=cds; coord=1:94888584..94892171:-1; parent_gene=GRMZM2G180916'

'highly similar to (737) AT2G18900 | Symbols: | transducin family protein / WD-40 repeat family protein | chr2:8188491-8192409 REVERSEnearly identical (1244) loc_os12g41620 12012.m07942 protein nucleotide binding protein, putative, expressed seq=cds; coord=1:172815913..172822534:1; parent_gene=GRMZM2G049201'

'moderately similar to (445) AT1G16680 | Symbols: | DNAJ heat shock N-terminal domain-containing protein / S-locus protein, putative | chr1:5702813-5705537 FORWARDhighly similar to (924) loc_os12g41820 12012.m07963 protein S-locus protein 5, putative, expressed seq=cds; coord=1:173219421..173225579:-1; parent_gene=GRMZM2G003635'

'weakly similar to (109) loc_os09g01620 12009.m03537 protein RNA binding protein, putative, expressed seq=cds; coord=1:207183902..207184588:1; parent_gene=GRMZM2G037648'

'weakly similar to (172) AT1G26880 | Symbols: | 60S ribosomal protein L34 (RPL34A) | chr1:9315798-9316681 REVERSEweakly similar to (175) RL34_TOBAC 60S ribosomal protein L34 - Nicotiana tabacum (Common tobacco)weakly similar to (188) loc_os09g24690 12009.m05623 protein 60S ribosomal protein L34, putative, expressed seq=cds; coord=1:212949285..212951440:1; parent_gene=GRMZM2G152552'

'moderately similar to (253) AT3G15080 | Symbols: | exonuclease family protein | chr3:5074319-5076327 FORWARDmoderately similar to (375) loc_os08g28980 12008.m06902 protein RNA exonuclease 4, putative, expressed seq=cds; coord=1:219892621..219901471:1; parent_gene=GRMZM2G015925'

'nearly identical (1679) AT4G38190 | Symbols: ATCSLD4, CSLD4 | ATCSLD4; cellulose synthase/ transferase, transferring glycosyl groups | chr4:17910096-17913641 REVERSEnearly identical (1967) loc_os08g25710 12008.m06587 protein CSLD3 - cellulose synthase-like family D, expressed seq=cds; coord=1:221785673..221789403:1; parent_gene=GRMZM2G044269'

'weakly similar to (135) AT3G48100 | Symbols: ARR5, ATRR2, IBC6 | ARR5 (ARABIDOPSIS RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator | chr3:17759112-17760740 REVERSEweakly similar to (189) loc_os04g57720 12004.m10657 protein OsRR6 - Rice type-A response regulator, expressed seq=cds; coord=2:2081848..2082630:-1; parent_gene=GRMZM2G040736'

'weakly similar to (135) AT3G48100 | Symbols: ARR5, ATRR2, IBC6 | ARR5 (ARABIDOPSIS RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator | chr3:17759112-17760740 REVERSEweakly similar to (189) loc_os04g57720 12004.m10657 protein OsRR6 - Rice type-A response regulator, expressed seq=cds; coord=2:2081848..2082630:-1; parent_gene=GRMZM2G040736' 'very weakly similar to (96.7) AT5G25190 | Symbols: | ethylene-responsive element-binding protein, putative | chr5:8707007-8707655 REVERSEweakly similar to (121) loc_os04g56150 12004.m10506 protein ethylene-responsive transcription factor 4, putative seq=cds; coord=2:4347237..4347860:1; parent_gene=GRMZM2G067463'

'moderately similar to (285) AT1G18190 | Symbols: GC2 | GC2 (golgin candidate 2) | chr1:6257963-6261325 REVERSEvery weakly similar to (86.3) GOGA5_ORYSA Golgin-84 - Oryza sativa (Rice)moderately similar to (458) loc_os04g55810 12004.m10472 protein expressed protein seq=cds; coord=2:4876176..4880569:1; parent_gene=GRMZM2G095308'

'weakly similar to (171) loc_os05g41240 12005.m27895 protein MYB transcription factor, putative, expressed seq=cds; coord=2:36578346..36579034:1; parent_gene=GRMZM2G093832'

'weakly similar to (107) AT2G43670 | Symbols: | glycosyl hydrolase family protein 17 | chr2:18105145-18105874 FORWARDweakly similar to (148) loc_os01g14140 12001.m150537 protein glucan endo-1,3-beta-glucosidase 4 precursor, putative, expressed seq=cds; coord=2:38140570..38141696:-1; parent_gene=GRMZM2G447691'

'weakly similar to (196) loc_os10g20270 12010.m05048 protein conserved hypothetical protein seq=cds; coord=2:39033129..39046983:-1; parent_gene=GRMZM2G326631'

'highly similar to (537) AT5G23810 | Symbols: AAP7 | AAP7; amino acid transmembrane transporter | chr5:8028461-8030138 FORWARDhighly similar to (704) loc_os04g39489 12004.m35579 protein AAP7, putative, expressed seq=cds; coord=2:39327335..39330173:1; parent_gene=GRMZM2G155491'

'weakly similar to (105) AT1G22310 | Symbols: MBD8 | MBD8; methyl-CpG binding | chr1:7881714-7883644 REVERSEnearly identical (1142) loc_os09g29750 12009.m06126 protein expressed protein seq=cds; coord=2:188152279..188158014:-1; parent_gene=GRMZM2G048411'

'nearly identical (1037) AT4G26540 | Symbols: | kinase | chr4:13394673-13398028 REVERSEmoderately similar to (338) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1429) loc_os09g30190 12009.m06170 protein receptor-like protein kinase precursor, putative, expressed seq=cds; coord=2:189087675..189091198:1; parent_gene=AC233861.1_FG001'

'weakly similar to (130) AT1G56170 | Symbols: HAP5B, ATHAP5B, NF-YC2 | NF-YC2 (NUCLEAR FACTOR Y, SUBUNIT C2); DNA binding / transcription activator/ transcription factor | chr1:21025118-21025717 FORWARDweakly similar to (141) loc_os09g30310 12009.m06182 protein nuclear transcription factor Y subunit C-2, putative, expressed seq=cds; coord=2:189204687..189208176:-1; parent_gene=GRMZM2G022162'

'weakly similar to (139) loc_os12g32986 12012.m27011 protein heat shock protein 83, putative, expressed seq=cds; coord=2:189610974..189617149:1; parent_gene=GRMZM2G474367'

'seq=cds; coord=2:190503989..190505254:-1; parent_gene=GRMZM2G147955' 'moderately similar to (471) AT5G14780 | Symbols: FDH | FDH (FORMATE DEHYDROGENASE); NAD or NADH binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor | chr5:4777043-4779190 FORWARDhighly similar to (530) FDH1_ORYSA Formate dehydrogenase 1, mitochondrial precursor (EC 1.2.1.2) (NAD-dependent formate dehydrogenase 1) (FDH 1) - Oryza sativa (Rice)highly similar to (530) loc_os06g29180 12006.m07462 protein formate dehydrogenase 1, mitochondrial precursor, putative, expressed seq=cds; coord=2:211533717..211538264:-1; parent_gene=GRMZM2G124919'

'weakly similar to (104) AT5G58420 | Symbols: | 40S ribosomal protein S4 (RPS4D) | chr5:23619599-23620896 FORWARDweakly similar to (110) RS4_MAIZE 40S ribosomal protein S4 - Zea mays (Maize)weakly similar to (110) loc_os01g25610 12001.m09024 protein 40S ribosomal protein S4, putative, expressed seq=cds; coord=3:6744073..6746491:-1; parent_gene=GRMZM2G499197'

'highly similar to (560) AT1G80360 | Symbols: | aminotransferase class I and II family protein | chr1:30208736-30210643 REVERSEhighly similar to (711) loc_os01g08270 12001.m42887 protein transaminase/ transferase, transferring nitrogenous groups, putative, expressed seq=cds; coord=3:10175360..10222084:1; parent_gene=GRMZM2G029135'

'highly similar to (822) AT1G15460 | Symbols: ATBOR4, BOR4 | BOR4 (REQUIRES HIGH BORON 4); anion exchanger | chr1:5310196-5313376 REVERSEnearly identical (1013) loc_os01g08020 12001.m07427 protein boron transporter-like protein 2, putative, expressed seq=cds; coord=3:10934126..10940345:-1; parent_gene=GRMZM2G051753'

'moderately similar to (273) AT1G44575 | Symbols: NPQ4, PSBS | NPQ4 (NONPHOTOCHEMICAL QUENCHING); chlorophyll binding / xanthophyll binding | chr1:16871768-16872548 FORWARDmoderately similar to (286) PSBS_SPIOL Photosystem II 22 kDa protein, chloroplast precursor (CP22) - Spinacia oleracea (Spinach)moderately similar to (305) loc_os01g64960 12001.m150788 protein photosystem II 22 kDa protein, chloroplast precursor, putative, expressed seq=cds; coord=3:174825201..174827787:-1; parent_gene=GRMZM2G077333'

'moderately similar to (335) AT2G29680 | Symbols: CDC6, ATCDC6 | CDC6 (CELL DIVISION CONTROL 6) | chr2:12689586-12692854 FORWARDhighly similar to (549) loc_os01g63710 12001.m42760 protein cell division control protein 6, putative, expressed seq=cds; coord=3:178059283..178062665:-1; parent_gene=GRMZM2G007659'

'weakly similar to (125) loc_os01g63160 12001.m12433 protein MYB2, putative, expressed seq=cds; coord=3:179213283..179214280:1; parent_gene=GRMZM2G005112'

'moderately similar to (206) AT1G54290 | Symbols: | eukaryotic translation initiation factor SUI1, putative | chr1:20268710-20269390 REVERSEmoderately similar to (214) SUI1_ORYSA Protein translation factor SUI1 homolog (Protein GOS2) (Translational initiation factor 1) (Protein eIF1) - Oryza sativa (Rice)moderately similar to (228) loc_os01g58220 12001.m11966 protein protein translation factor SUI1 homolog 2, putative, expressed seq=cds; coord=3:189344756..189347802:1; parent_gene=GRMZM2G113414'

'weakly similar to (128) loc_os04g11450 12004.m35049 protein F-box domain containing protein, expressed seq=cds; coord=3:210065350..210067453:1; parent_gene=GRMZM2G059799' 'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'highly similar to (538) AT4G16745 | Symbols: | exostosin family protein | chr4:9412185-9414053 FORWARDhighly similar to (709) loc_os01g45350 12001.m10738 protein limonene cyclase like protein, putative, expressed seq=cds; coord=3:215380332..215382314:-1; parent_gene=GRMZM2G048010'

'moderately similar to (241) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (341) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215431519..215437533:-1; parent_gene=GRMZM2G348512'

'weakly similar to (119) AT1G52150 | Symbols: ATHB-15, ATHB15, CNA, ICU4 | ATHB-15; DNA binding / transcription factor | chr1:19410118-19413961 REVERSEmoderately similar to (210) loc_os03g01890 12003.m34764 protein rolled leaf1, putative, expressed seq=cds; coord=4:31771798..31787581:1; parent_gene=GRMZM2G048297'

'weakly similar to (105) AT5G22740 | Symbols: ATCSLA02, CSLA02, ATCSLA2 | ATCSLA02; mannan synthase/ transferase, transferring glycosyl groups | chr5:7555379-7559866 REVERSEweakly similar to (152) loc_os08g33740 12008.m07364 protein CSLA11 - cellulose synthase-like family A, expressed seq=cds; coord=4:83323033..83326629:-1; parent_gene=GRMZM2G093999'

'highly similar to (714) AT2G06510 | Symbols: ATRPA1A, RPA1A, RPA70A, ATRPA70A | RPA1A (REPLICATION PROTEIN A 1A); DNA binding / nucleic acid binding | chr2:2585215-2587601 FORWARDhighly similar to (938) loc_os02g53680 12002.m10397 protein replication protein A 70 kDa DNA-binding subunit, putative, expressed seq=cds; coord=4:177148507..177152445:1; parent_gene=GRMZM2G115013'

'highly similar to (917) AT2G32950 | Symbols: COP1, ATCOP1, DET340, FUS1, EMB168 | COP1 (CONSTITUTIVE PHOTOMORPHOGENIC 1); protein binding / ubiquitin-protein ligase | chr2:13978000-13983282 FORWARDhighly similar to (879) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)nearly identical (1137) loc_os02g53140 12002.m10343 protein ubiquitin ligase protein COP1, putative, expressed seq=cds; coord=4:177646925..177653783:1; parent_gene=GRMZM2G126795'

'nearly identical (1232) AT1G77760 | Symbols: NIA1, GNR1, NR1 | NIA1 (NITRATE REDUCTASE 1); nitrate reductase | chr1:29236005-29239367 REVERSEnearly identical (1540) NIA7_HORVU Nitrate reductase [NAD(P)H] (EC 1.7.1.2) - Hordeum vulgare (Barley)nearly identical (1573) loc_os02g53130 12002.m10342 protein nitrate reductase, putative, expressed seq=cds; coord=4:177655913..177659763:1; parent_gene=GRMZM2G428027' 'moderately similar to (343) AT4G08500 | Symbols: MEKK1, ATMEKK1, MAPKKK8, ARAKIN | MEKK1 (MAP KINASE KINASE KINASE 1); DNA binding / MAP kinase kinase kinase/ kinase/ kinase binding / protein binding | chr4:5404272-5407062 REVERSEweakly similar to (117) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)moderately similar to (393) loc_os03g15570 12003.m06994 protein mitogen-activated protein kinase 1, putative, expressed seq=cds; coord=4:178052009..178063510:-1; parent_gene=GRMZM2G158860'

'weakly similar to (124) loc_os10g24954 12010.m05448 protein ulp1 protease family, C-terminal catalytic domain containing protein seq=cds; coord=4:178285833..178288003:-1; parent_gene=GRMZM2G150153'

'nearly identical (1118) AT4G16130 | Symbols: ARA1, ISA1, ATISA1 | ARA1 (ARABINOSE KINASE); ATP binding / L-arabinokinase/ galactokinase | chr4:9120875-9127656 FORWARDnearly identical (1404) loc_os02g04840 12002.m05832 protein ARA1, putative, expressed seq=cds; coord=4:237704209..237711241:1; parent_gene=GRMZM2G165931'

'highly similar to (557) AT2G47070 | Symbols: SPL1 | SPL1 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 1); DNA binding / transcription factor | chr2:19337144-19340552 FORWARDvery weakly similar to (97.8) LG1_MAIZE LIGULELESS1 protein - Zea mays (Maize)nearly identical (1281) loc_os03g61760 12003.m11057 protein squamosa promoter-binding-like protein 12, putative, expressed seq=cds; coord=5:1845813..1852802:-1; parent_gene=GRMZM2G138421'

'highly similar to (525) AT4G30560 | Symbols: ATCNGC9, CNGC9 | ATCNGC9 (CYCLIC NUCLEOTIDE GATED CHANNEL 9); calmodulin binding / cyclic nucleotide binding / ion channel | chr4:14926974-14929681 REVERSEhighly similar to (652) loc_os03g44440 12003.m09483 protein cyclic nucleotide-gated ion channel 9, putative, expressed seq=cds; coord=5:16837450..16840121:-1; parent_gene=GRMZM2G077828'

'moderately similar to (209) AT1G13690 | Symbols: ATE1 | ATE1; nucleic acid binding / nucleotide binding | chr1:4693380-4694179 FORWARDmoderately similar to (256) loc_os03g40310 12003.m09113 protein peptidyl-prolyl cis-trans isomerase E, putative, expressed seq=cds; coord=5:18753627..18756558:1; parent_gene=GRMZM2G138572'

'moderately similar to (334) AT1G61250 | Symbols: SC3 | SC3 (SECRETORY CARRIER 3); transmembrane transporter | chr1:22586035-22588664 FORWARDmoderately similar to (493) loc_os03g38590 12003.m101386 protein SC3 protein, putative, expressed seq=cds; coord=5:19677495..19681425:-1; parent_gene=GRMZM2G124918'

'moderately similar to (270) AT1G55520 | Symbols: TBP2, ATTBP2 | TBP2 (TATA BINDING PROTEIN 2); DNA binding / RNA polymerase II transcription factor/ TATA-binding protein binding | chr1:20726150-20727483 REVERSEmoderately similar to (276) TBP_MESCR TATA-box-binding protein (TATA-box factor) (TATA-binding factor) (TATA sequence-binding protein) (TBP) (Transcription initiation factor TFIID TBP subunit) - Mesembryanthemum crystallinum (Common ice plant)moderately similar to (275) loc_os03g45410 12003.m09569 protein TATA-binding protein 2, putative, expressed seq=cds; coord=5:22291112..22293070:-1; parent_gene=GRMZM2G466938'

'moderately similar to (459) AT3G51120 | Symbols: | DNA binding / nucleic acid binding / protein binding / zinc ion binding | chr3:18986026-18991886 REVERSEnearly identical (1229) loc_os10g36810 12010.m06486 protein plus-3 domain containing protein, expressed seq=cds; coord=5:22737810..22750836:-1; parent_gene=GRMZM2G078379' 'highly similar to (576) AT4G21390 | Symbols: B120 | B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding | chr4:11394458-11397474 REVERSEmoderately similar to (271) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (927) loc_os08g08140 12008.m04949 protein receptor-like kinase, putative, expressed seq=cds; coord=5:23021471..23025066:1; parent_gene=GRMZM2G330751'

'highly similar to (670) AT5G23190 | Symbols: CYP86B1 | CYP86B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr5:7803478-7805659 REVERSEweakly similar to (114) C97B2_SOYBN Cytochrome P450 97B2 (EC 1.14.-.-) - Glycine max (Soybean)highly similar to (830) loc_os10g34480 12010.m06272 protein cytochrome P450 86A2, putative, expressed seq=cds; coord=5:26443691..26446113:1; parent_gene=GRMZM2G013082'

'highly similar to (664) AT4G30080 | Symbols: ARF16 | ARF16 (AUXIN RESPONSE FACTOR 16); miRNA binding / transcription factor | chr4:14703369-14705564 REVERSEhighly similar to (977) loc_os10g33940 12010.m06222 protein auxin response factor 16, putative, expressed seq=cds; coord=5:27944757..27949513:-1; parent_gene=GRMZM2G159399'

'highly similar to (790) AT1G73590 | Symbols: PIN1, ATPIN1 | PIN1 (PIN-FORMED 1); transporter | chr1:27659772-27662876 FORWARDnearly identical (1019) PIN1_ORYSA Auxin efflux carrier component 1 (OsPIN1) (Ethylene insensitive root 1 homolog) - Oryza sativa (Rice)nearly identical (1019) loc_os02g50960 12002.m33866 protein auxin efflux carrier component 1, putative, expressed seq=cds; coord=5:206727149..206730565:1; parent_gene=GRMZM2G074267'

'moderately similar to (213) AT5G37810 | Symbols: NIP4;1, NLM4 | NIP4;1 (NOD26-LIKE INTRINSIC PROTEIN 4;1); water channel | chr5:15045232-15047807 FORWARDmoderately similar to (473) LSI1_ORYSA Silicon transporter LSI1 (Low silicon protein 1) - Oryza sativa (Rice)moderately similar to (473) loc_os02g51110 12002.m10145 protein aquaporin NIP4.2, putative, expressed seq=cds; coord=5:206922588..206926444:1; parent_gene=GRMZM2G028325'

'very weakly similar to (100) AT1G26945 | Symbols: KDR | KDR (KIDARI); transcription regulator | chr1:9351571-9352474 FORWARDweakly similar to (155) loc_os02g51320 12002.m10166 protein DNA binding protein, putative, expressed seq=cds; coord=5:207504983..207506597:-1; parent_gene=GRMZM2G036092'

'highly similar to (908) AT1G78060 | Symbols: | glycosyl hydrolase family 3 protein | chr1:29349796-29352868 REVERSEmoderately similar to (376) XYNB_PRUPE Putative beta-D-xylosidase (EC 3.2.1.-) (PpAz152) (Fragment) - Prunus persica (Peach)nearly identical (1285) loc_os02g51620 12002.m10194 protein beta-D-xylosidase, putative, expressed seq=cds; coord=5:208090222..208094428:-1; parent_gene=GRMZM2G035503'

'weakly similar to (132) AT1G78080 | Symbols: RAP2.4 | RAP2.4 (related to AP2 4); DNA binding / transcription factor | chr1:29364790-29365794 FORWARDmoderately similar to (202) loc_os02g51670 12002.m10198 protein AP2 domain-containing protein, putative, expressed seq=cds; coord=5:208162767..208165707:1; parent_gene=GRMZM2G055204' 'weakly similar to (109) AT2G14210 | Symbols: ANR1, AGL44 | AGL44 (AGAMOUS-LIKE 44); DNA binding / transcription factor | chr2:6018841-6023585 FORWARDweakly similar to (112) MAD57_ORYSA MADS-box transcription factor 57 (OsMADS57) - Oryza sativa (Rice)weakly similar to (112) loc_os02g49840 12002.m33858 protein MADS-box transcription factor 57, putative, expressed seq=cds; coord=5:204742401..204743090:-1; parent_gene=GRMZM2G044408'

'weakly similar to (109) AT4G10170 | Symbols: | synaptobrevin-related family protein | chr4:6344587-6345351 FORWARDmoderately similar to (257) loc_os08g01880 12008.m04336 protein expressed protein seq=cds; coord=6:2721360..2722825:-1; parent_gene=GRMZM2G367941'

'moderately similar to (420) AT1G12420 | Symbols: ACR8 | ACR8; amino acid binding | chr1:4226673-4228917 REVERSEhighly similar to (526) loc_os08g02500 12008.m04394 protein ACR8, putative seq=cds; coord=6:5641494..5643748:1; parent_gene=GRMZM2G034404'

'weakly similar to (107) AT3G14250 | Symbols: | protein binding / zinc ion binding | chr3:4745963-4746958 REVERSEweakly similar to (193) loc_os09g25190 12009.m05671 protein ubiquitin-protein ligase/ zinc ion binding protein, putative, expressed seq=cds; coord=6:6700670..6701561:1; parent_gene=GRMZM2G390009'

'highly similar to (591) AT5G08560 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:2771104-2773827 REVERSEhighly similar to (850) loc_os02g19210 12002.m07164 protein WD-repeat protein 26, putative, expressed seq=cds; coord=6:8380046..8392601:1; parent_gene=GRMZM2G061186'

'moderately similar to (302) AT1G11330 | Symbols: | S-locus lectin protein kinase family protein | chr1:3810372-3813416 FORWARDweakly similar to (196) SLSG6_BRAOL S-locus-specific glycoprotein S6 precursor (SLSG-6) - Brassica oleracea (Wild cabbage)highly similar to (592) loc_os04g53994 12004.m10292 protein ATP binding protein, putative, expressed seq=cds; coord=6:24742749..24748211:1; parent_gene=GRMZM2G160853'

'weakly similar to (197) AT1G69010 | Symbols: BIM2 | BIM2 (BES1-interacting Myc-like protein 2); DNA binding / transcription factor | chr1:25941804-25943599 FORWARDhighly similar to (568) loc_os09g29930 12009.m060079 protein transcription factor BIM2, putative, expressed seq=cds; coord=7:130237175..130244865:1; parent_gene=GRMZM2G089501'

'weakly similar to (134) AT5G26330 | Symbols: | plastocyanin-like domain-containing protein / mavicyanin, putative | chr5:9241614-9242635 REVERSEvery weakly similar to (97.8) BCP_PEA Blue copper protein precursor - Pisum sativum (Garden pea)weakly similar to (157) loc_os07g38290 12007.m08076 protein copper ion binding protein, putative, expressed seq=cds; coord=7:159130478..159136959:-1; parent_gene=GRMZM2G107562'

'weakly similar to (199) AT5G67590 | Symbols: FRO1 | FRO1 (FROSTBITE1); NADH dehydrogenase (ubiquinone) | chr5:26958073-26959356 FORWARDmoderately similar to (299) loc_os07g39710 12007.m08213 protein NADH-ubiquinone oxidoreductase 18 kDa subunit, mitochondrial precursor, putative, expressed seq=cds; coord=7:161685025..161693219:-1; parent_gene=GRMZM2G396397' 'weakly similar to (149) AT5G50890 | Symbols: | LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: lipase class 3 family protein (TAIR:AT2G05260.1); Has 115 Blast hits to 115 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 115; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:20702684-20704235 FORWARDmoderately similar to (313) loc_os07g39810 12007.m08223 protein triacylglycerol lipase, putative, expressed seq=cds; coord=7:161804206..161805610:-1; parent_gene=GRMZM2G179777'

'moderately similar to (302) AT5G55600 | Symbols: | agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein | chr5:22522232-22524796 REVERSEhighly similar to (632) loc_os07g41640 12007.m29252 protein DNA binding protein, putative, expressed seq=cds; coord=7:164824657..164829482:1; parent_gene=GRMZM2G037444'

'very weakly similar to (83.2) loc_os08g23360 12008.m26659 protein signal recognition particle 68 kDa protein, putative, expressed seq=cds; coord=7:165096869..165097450:1; parent_gene=GRMZM2G121022'

'very weakly similar to (83.2) loc_os08g23360 12008.m26659 protein signal recognition particle 68 kDa protein, putative, expressed seq=cds; coord=7:165096869..165097450:1; parent_gene=GRMZM2G121022'

'moderately similar to (217) AT4G33160 | Symbols: | ubiquitin-protein ligase | chr4:15994160-15995533 FORWARDmoderately similar to (405) loc_os07g42590 12007.m08491 protein F-box protein, putative, expressed seq=cds; coord=7:165744759..165746434:1; parent_gene=GRMZM2G054032'

'nearly identical (1117) AT4G35790 | Symbols: ATPLDDELTA, PLDDELTA | ATPLDDELTA; phospholipase D | chr4:16955774-16959875 REVERSEhighly similar to (676) PLDA1_VIGUN Phospholipase D alpha 1 (EC 3.1.4.4) (PLD alpha 1) (Choline phosphatase 1) (Phosphatidylcholine-hydrolyzing phospholipase D 1) - Vigna unguiculata (Cowpea)nearly identical (1469) loc_os09g37100 12009.m06658 protein phospholipase D delta, putative, expressed seq=cds; coord=7:175180156..175187596:-1; parent_gene=GRMZM2G140811'

'weakly similar to (190) AT5G56340 | Symbols: ATCRT1 | zinc finger (C3HC4-type RING finger) family protein | chr5:22818254-22819444 FORWARDmoderately similar to (243) loc_os01g16950 12001.m08291 protein protein binding protein, putative, expressed seq=cds; coord=8:2079198..2081568:-1; parent_gene=GRMZM2G417125'

'weakly similar to (169) AT1G44970 | Symbols: | peroxidase, putative | chr1:17002237-17003563 FORWARDweakly similar to (131) PER1_ARAHY Cationic peroxidase 1 precursor (EC 1.11.1.7) (PNPC1) - Arachis hypogaea (Peanut)moderately similar to (205) loc_os01g15810 12001.m08179 protein peroxidase 9 precursor, putative, expressed seq=cds; coord=8:4359928..4360529:1; parent_gene=GRMZM2G037156'

'moderately similar to (306) AT5G46860 | Symbols: VAM3, ATVAM3, SYP22, ATSYP22, SGR3 | VAM3; SNAP receptor | chr5:19012342-19013795 REVERSEmoderately similar to (402) loc_os01g15110 12001.m08110 protein syntaxin 23, putative, expressed seq=cds; coord=8:5315352..5319733:1; parent_gene=GRMZM2G017329'

'highly similar to (555) AT1G24190 | Symbols: SIN3, ATSIN3, SNL3 | SNL3 (SIN3-LIKE 3); transcription repressor | chr1:8563858-8569996 REVERSEnearly identical (1498) loc_os01g01960 12001.m06838 protein paired amphipathic helix repeat family protein, expressed seq=cds; coord=8:8119203..8129694:-1; parent_gene=GRMZM2G334457' 'moderately similar to (249) AT1G70060 | Symbols: SNL4 | SNL4 (SIN3-LIKE 4) | chr1:26383789-26389568 FORWARDmoderately similar to (338) loc_os01g01960 12001.m06838 protein paired amphipathic helix repeat family protein, expressed seq=cds; coord=8:8136058..8139636:-1; parent_gene=AC234160.1_FG001'

'weakly similar to (168) AT1G65620 | Symbols: AS2 | AS2 (ASYMMETRIC LEAVES 2); protein binding | chr1:24400146-24400745 FORWARDmoderately similar to (212) loc_os01g66590 12001.m97474 protein ASYMMETRIC LEAVES2, putative, expressed seq=cds; coord=8:104267219..104268277:1; parent_gene=GRMZM2G096064'

'highly similar to (697) AT1G03380 | Symbols: ATATG18G | AtATG18g | chr1:836155-840362 FORWARDweakly similar to (160) ATPG_MAIZE ATP synthase subunit gamma, chloroplast precursor (EC 3.6.3.14) [Contains: Inceptin] - Zea mays (Maize)nearly identical (1384) loc_os05g33610 12005.m083719 protein expressed protein seq=cds; coord=8:106939155..106998860:-1; parent_gene=GRMZM2G078468'

'weakly similar to (117) AT4G23810 | Symbols: WRKY53, ATWRKY53 | WRKY53; DNA binding / protein binding / transcription activator/ transcription factor | chr4:12392666-12393739 REVERSEmoderately similar to (251) loc_os09g16510 12009.m04911 protein OsWRKY74 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=8:109566616..109568284:-1; parent_gene=GRMZM2G061408'

'moderately similar to (246) AT3G07880 | Symbols: | Rho GDP-dissociation inhibitor family protein | chr3:2514175-2515544 FORWARDmoderately similar to (345) loc_os01g68540 12001.m12957 protein rho GDP-dissociation inhibitor 1, putative, expressed seq=cds; coord=8:110142652..110144824:1; parent_gene=GRMZM2G150724'

'weakly similar to (166) AT5G53190 | Symbols: | nodulin MtN3 family protein | chr5:21572417-21574284 REVERSEmoderately similar to (253) loc_os05g12320 12005.m05698 protein mtN3 protein-like, putative, expressed seq=cds; coord=8:112530662..112532375:1; parent_gene=GRMZM2G179679'

'weakly similar to (140) AT1G65810 | Symbols: | tRNA-splicing endonuclease positive effector-related | chr1:24477043-24480728 REVERSEmoderately similar to (206) loc_os01g12530 12001.m150511 protein smr domain containing protein, expressed seq=cds; coord=8:118394306..118400023:1; parent_gene=GRMZM2G162112'

'highly similar to (803) AT2G13620 | Symbols: ATCHX15, CHX15 | ATCHX15; monovalent cation:proton antiporter/ sodium:hydrogen antiporter | chr2:5678006-5680621 FORWARDnearly identical (1224) loc_os05g40650 12005.m08241 protein ATCHX15, putative, expressed seq=cds; coord=8:119266312..119269960:-1; parent_gene=GRMZM2G138817'

'very weakly similar to (84.7) AT1G02900 | Symbols: RALFL1, RALF1, ATRALF1 | RALF1 (RAPID ALKALINIZATION FACTOR 1); signal transducer | chr1:653976-654338 REVERSEweakly similar to (103) loc_os01g70690 12001.m13115 protein RALFL33, putative seq=cds; coord=8:159709814..159710550:1; parent_gene=GRMZM2G423959'

'highly similar to (789) AT5G23670 | Symbols: LCB2 | LCB2; protein binding / serine C-palmitoyltransferase | chr5:7981889-7985037 FORWARDhighly similar to (915) loc_os01g70380 12001.m13086 protein serine palmitoyltransferase 2, putative, expressed seq=cds; coord=8:159979988..159983916:1; parent_gene=GRMZM2G010202'

'weakly similar to (124) loc_os11g15570 12011.m05691 protein expressed protein seq=cds; coord=8:161171663..161174060:-1; parent_gene=GRMZM2G364863'

'weakly similar to (124) loc_os11g15570 12011.m05691 protein expressed protein seq=cds; coord=8:161171663..161174060:-1; parent_gene=GRMZM2G364863'

'moderately similar to (356) AT1G05800 | Symbols: DGL | DGL (DONGLE); triacylglycerol lipase | chr1:1741204-1742619 FORWARDmoderately similar to (436) loc_os01g67430 12001.m12847 protein triacylglycerol lipase, putative, expressed seq=cds; coord=8:163911970..163913352:-1; parent_gene=AC233916.1_FG002'

'very weakly similar to (88.2) loc_os06g08564 12006.m91824 protein hydrophobic protein LTI6B, putative, expressed seq=cds; coord=9:12870907..12878495:-1; parent_gene=GRMZM2G079306'

'moderately similar to (362) AT5G61520 | Symbols: | hexose transporter, putative | chr5:24739358-24740833 REVERSEmoderately similar to (432) HEX6_RICCO Hexose carrier protein HEX6 - Ricinus communis (Castor bean)highly similar to (507) loc_os06g04900 12006.m05219 protein hexose carrier protein HEX6, putative, expressed seq=cds; coord=9:20747007..20749031:1; parent_gene=GRMZM2G404965'

'weakly similar to (152) AT2G44910 | Symbols: ATHB4, ATHB-4 | ATHB4 (ARABIDOPSIS THALIANA HOMEOBOX-LEUCINE ZIPPER PROTEIN 4); DNA binding / transcription factor | chr2:18517887-18519525 REVERSEmoderately similar to (243) loc_os06g04870 12006.m05216 protein homeobox-leucine zipper protein HAT1, putative, expressed seq=cds; coord=9:20827855..20829629:-1; parent_gene=GRMZM2G134260'

'moderately similar to (284) AT4G31300 | Symbols: PBA1 | PBA1; endopeptidase/ peptidase/ threonine-type endopeptidase | chr4:15188927-15190935 FORWARDmoderately similar to (274) PSB6_TOBAC Proteasome subunit beta type 6 precursor (EC 3.4.25.1) (Proteasome delta chain) (Tobacco cryptogein-induced protein 7) (tcI 7) - Nicotiana tabacum (Common tobacco)moderately similar to (335) loc_os06g04800 12006.m05209 protein proteasome subunit beta type 6 precursor, putative, expressed seq=cds; coord=9:20969486..20973151:1; parent_gene=GRMZM2G374881'

'highly similar to (679) AT5G35930 | Symbols: | AMP-dependent synthetase and ligase family protein | chr5:14067197-14074404 REVERSEnearly identical (1253) loc_os06g02160 12006.m091577 protein AMP-binding enzyme family protein, expressed seq=cds; coord=9:26478641..26484651:1; parent_gene=GRMZM2G393146'

'highly similar to (619) AT1G68940 | Symbols: | armadillo/beta-catenin repeat protein-related / U-box domain-containing protein | chr1:25921453-25925374 REVERSEnearly identical (1451) loc_os06g16410 12006.m06354 protein ubiquitin-protein ligase, putative, expressed seq=cds; coord=9:34703357..34723384:-1; parent_gene=GRMZM2G065612'

'weakly similar to (190) AT1G65680 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2) | chr1:24427266-24428399 FORWARDmoderately similar to (332) EXPB6_ORYSA Expansin-B6 precursor (OsEXPB6) (Beta-expansin-6) (OsaEXPb1.8) - Oryza sativa (Rice)moderately similar to (332) loc_os10g40700 12010.m06838 protein beta-expansin 1a precursor, putative, expressed seq=cds; coord=9:116443796..116445318:1; parent_gene=GRMZM2G059785' 'moderately similar to (299) AT3G47590 | Symbols: | esterase/lipase/thioesterase family protein | chr3:17536133-17537515 REVERSEmoderately similar to (311) loc_os01g39790 12001.m43070 protein esterase, putative, expressed seq=cds; coord=9:148668289..148672816:1; parent_gene=GRMZM2G017957'

'moderately similar to (308) AT5G55530 | Symbols: | C2 domain-containing protein | chr5:22494439-22495656 FORWARDmoderately similar to (489) loc_os03g09840 12003.m35067 protein C2 domain containing protein, expressed seq=cds; coord=9:149059296..149062459:1; parent_gene=GRMZM2G096355'

'highly similar to (973) AT1G80680 | Symbols: SAR3, MOS3, PRE, NUP96 | SAR3 (SUPPRESSOR OF AUXIN RESISTANCE 3); porin | chr1:30324219-30328489 FORWARDnearly identical (1486) loc_os03g07580 12003.m06270 protein PRE, putative, expressed seq=cds; coord=9:151118220..151121978:-1; parent_gene=AC149829.2_FG003'

'moderately similar to (296) AT3G08740 | Symbols: | elongation factor P (EF-P) family protein | chr3:2654788-2656154 REVERSEmoderately similar to (358) loc_os12g02380 12012.m04239 protein elongation factor P, putative, expressed seq=cds; coord=10:4071331..4073937:-1; parent_gene=GRMZM2G129804'

'weakly similar to (176) AT4G10250 | Symbols: ATHSP22.0 | ATHSP22.0 | chr4:6370537-6371124 FORWARDweakly similar to (185) HSP41_SOYBN 22.0 kDa class IV heat shock protein precursor - Glycine max (Soybean)moderately similar to (227) loc_os04g36750 12004.m08715 protein 22.0 kDa class IV heat shock protein precursor, putative, expressed seq=cds; coord=10:119759011..119760065:1; parent_gene=GRMZM2G346839'

'nearly identical (1382) AT1G48410 | Symbols: AGO1 | AGO1 (ARGONAUTE 1); endoribonuclease/ miRNA binding / protein binding / siRNA binding | chr1:17886285-17891892 REVERSEnearly identical (1631) loc_os04g47870 12004.m09728 protein PINHEAD protein, putative, expressed seq=cds; coord=10:137481424..137487962:1; parent_gene=AC209206.3_FG011'

'weakly similar to (132) AT3G13960 | Symbols: AtGRF5 | AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator | chr3:4608526-4610160 FORWARDmoderately similar to (404) loc_os04g51190 12004.m10015 protein growth-regulating factor, putative, expressed seq=cds; coord=10:140968794..140972587:-1; parent_gene=GRMZM2G129147'

'moderately similar to (449) AT2G05940 | Symbols: | protein kinase, putative | chr2:2287514-2289270 REVERSEmoderately similar to (213) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (564) loc_os03g08170 12003.m06326 protein protein kinase APK1B, chloroplast precursor, putative, expressed seq=cds; coord=1:16468414..16473940:1; parent_gene=GRMZM2G175164'

'weakly similar to (143) loc_os03g08330 12003.m06342 protein ZIM motif family protein, expressed seq=cds; coord=1:16792359..16793281:1; parent_gene=GRMZM2G445634' 'moderately similar to (382) AT1G72370 | Symbols: P40, AP40, RP40, RPSAA | P40; structural constituent of ribosome | chr1:27243148-27244842 REVERSEmoderately similar to (406) RSSA_SOYBN 40S ribosomal protein SA (p40) - Glycine max (Soybean)moderately similar to (477) loc_os03g08440 12003.m35048 protein 40S ribosomal protein SA, putative, expressed seq=cds; coord=1:17325366..17335709:-1; parent_gene=GRMZM2G145308'

'highly similar to (512) AT1G74910 | Symbols: | ADP-glucose pyrophosphorylase family protein | chr1:28135770-28138456 REVERSEhighly similar to (603) loc_os03g11050 12003.m35086 protein mannose-1-phosphate guanyltransferase, putative, expressed seq=cds; coord=1:21196693..21221560:1; parent_gene=GRMZM2G064841'

'seq=cds; coord=1:21678945..21680766:-1; parent_gene=GRMZM2G415251'

'moderately similar to (229) AT4G37580 | Symbols: HLS1, COP3, UNS2 | HLS1 (HOOKLESS 1); N-acetyltransferase | chr4:17658932-17660564 FORWARDmoderately similar to (366) loc_os03g10810 12003.m35083 protein HLS1, putative, expressed seq=cds; coord=1:21720856..21722289:1; parent_gene=GRMZM2G114184'

'highly similar to (743) AT4G29040 | Symbols: RPT2a | RPT2a (regulatory particle AAA-ATPase 2a); ATPase | chr4:14312369-14314386 FORWARDhighly similar to (783) PRS4_ORYSA 26S protease regulatory subunit 4 homolog (TAT-binding protein homolog 2) - Oryza sativa (Rice)highly similar to (794) loc_os03g18690 12003.m07290 protein 26S protease regulatory subunit 4, putative, expressed seq=cds; coord=1:46542947..46546531:1; parent_gene=GRMZM2G104373'

'weakly similar to (198) AT2G38440 | Symbols: ITB1, SCAR2, DIS3, WAVE4, ATSCAR2 | SCAR2 (SCAR HOMOLOG 2) | chr2:16095550-16100851 FORWARDweakly similar to (192) SCRL1_ORYSA SCAR-like protein 1 - Oryza sativa (Rice)highly similar to (598) loc_os03g18710 12003.m07292 protein expressed protein seq=cds; coord=1:46576198..46582130:-1; parent_gene=GRMZM2G104534'

'moderately similar to (346) AT4G02100 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr4:930228-932049 FORWARDhighly similar to (670) loc_os03g19200 12003.m07337 protein heat shock protein binding protein, putative, expressed seq=cds; coord=1:48553016..48556046:-1; parent_gene=GRMZM2G010000'

'very weakly similar to (80.1) AT4G01940 | Symbols: NFU1, AtCNFU1 | NFU1; structural molecule | chr4:842265-843388 REVERSEweakly similar to (127) loc_os03g20010 12003.m07414 protein NFU3, putative, expressed seq=cds; coord=1:51291271..51292601:1; parent_gene=GRMZM2G084783'

'highly similar to (691) AT1G56560 | Symbols: | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr1:21192593-21194948 FORWARDhighly similar to (795) loc_os03g20020 12003.m07415 protein beta-fructofuranosidase, putative, expressed seq=cds; coord=1:51318993..51329214:-1; parent_gene=GRMZM2G084940'

'moderately similar to (262) AT1G08845 | Symbols: | structural constituent of ribosome | chr1:2838789-2840955 FORWARDmoderately similar to (334) loc_os10g41050 12010.m06870 protein expressed protein seq=cds; coord=1:90225656..90230346:-1; parent_gene=GRMZM2G154487' 'weakly similar to (187) AT5G23370 | Symbols: | GRAM domain-containing protein / ABA-responsive protein-related | chr5:7863542-7864201 REVERSEmoderately similar to (335) loc_os10g34730 12010.m06300 protein FIP1, putative, expressed seq=cds; coord=1:229187112..229188270:1; parent_gene=GRMZM2G113167'

'moderately similar to (401) AT3G63440 | Symbols: ATCKX6, CKX6, ATCKX7 | CKX6 (CYTOKININ OXIDASE/DEHYDROGENASE 6); cytokinin dehydrogenase | chr3:23424291-23426265 FORWARDmoderately similar to (321) CKX1_MAIZE Cytokinin dehydrogenase 1 precursor (EC 1.5.99.12) (Cytokinin oxidase 1) (CKO 1) (COX 1) (ZmCKX1) - Zea mays (Maize)highly similar to (789) loc_os10g34230 12010.m06250 protein cytokinin dehydrogenase 5 precursor, putative, expressed seq=cds; coord=1:230012438..230016000:-1; parent_gene=GRMZM2G404443'

'moderately similar to (462) AT3G29090 | Symbols: PME31, ATPME31 | pectinesterase family protein | chr3:11073804-11075335 FORWARDweakly similar to (165) PME1_CITSI Pectinesterase-1 precursor (EC 3.1.1.11) (Pectin methylesterase) (PE) - Citrus sinensis (Sweet orange)highly similar to (558) loc_os10g26680 12010.m21883 protein pectinesterase-1 precursor, putative, expressed seq=cds; coord=1:242432528..242434998:1; parent_gene=GRMZM2G019411'

'highly similar to (659) AT4G13420 | Symbols: HAK5, ATHAK5 | HAK5 (HIGH AFFINITY K

'highly similar to (632) AT4G13420 | Symbols: HAK5, ATHAK5 | HAK5 (HIGH AFFINITY K

'moderately similar to (474) AT3G26590 | Symbols: | MATE efflux family protein | chr3:9761927-9765259 REVERSEhighly similar to (776) loc_os03g42830 12003.m09334 protein transparent testa 12 protein, putative, expressed seq=cds; coord=1:253715474..253720824:1; parent_gene=GRMZM2G021055'

'moderately similar to (341) AT4G34380 | Symbols: | transducin family protein / WD-40 repeat family protein | chr4:16438835-16440322 FORWARDmoderately similar to (479) loc_os03g42710 12003.m09323 protein nucleotide binding protein, putative seq=cds; coord=1:253911424..253913528:-1; parent_gene=GRMZM2G099023'

'highly similar to (673) AT4G15900 | Symbols: PRL1 | PRL1 (PLEIOTROPIC REGULATORY LOCUS 1); basal transcription repressor/ nucleotide binding / protein binding | chr4:9023775-9027443 FORWARDweakly similar to (120) PF20_CHLRE Flagellar WD repeat protein PF20 - Chlamydomonas reinhardtiihighly similar to (847) loc_os03g21990 12003.m07603 protein PP1/PP2A phosphatases pleiotropic regulator PRL1, putative, expressed seq=cds; coord=1:254094619..254104550:-1; parent_gene=GRMZM2G017089'

'moderately similar to (285) AT1G18190 | Symbols: GC2 | GC2 (golgin candidate 2) | chr1:6257963-6261325 REVERSEvery weakly similar to (86.3) GOGA5_ORYSA Golgin-84 - Oryza sativa (Rice)moderately similar to (458) loc_os04g55810 12004.m10472 protein expressed protein seq=cds; coord=2:4876176..4880569:1; parent_gene=GRMZM2G095308'

'moderately similar to (268) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDweakly similar to (130) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (382) loc_os04g55560 12004.m35488 protein AP2 domain containing protein, expressed seq=cds; coord=2:5514479..5518846:-1; parent_gene=GRMZM2G174784'

'moderately similar to (244) AT4G34040 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr4:16304638-16307503 REVERSEhighly similar to (936) loc_os04g55510 12004.m10442 protein zinc finger, C3HC4 type family protein, expressed seq=cds; coord=2:5566610..5573059:-1; parent_gene=GRMZM2G174926'

'very weakly similar to (84.0) AT4G15010 | Symbols: | mitochondrial substrate carrier family protein | chr4:8573125-8574864 REVERSEweakly similar to (160) loc_os04g44540 12004.m35174 protein mitochondrial carrier protein, expressed seq=cds; coord=2:26713018..26714723:1; parent_gene=GRMZM2G114149'

'weakly similar to (189) AT2G28350 | Symbols: ARF10 | ARF10 (AUXIN RESPONSE FACTOR 10); miRNA binding / transcription factor | chr2:12114331-12116665 FORWARDmoderately similar to (234) loc_os04g43910 12004.m09350 protein auxin response factor 16, putative, expressed seq=cds; coord=2:27979219..27980618:-1; parent_gene=GRMZM2G122614'

'highly similar to (593) AT4G14340 | Symbols: CKI1, CKL11 | CKI1 (CASEIN KINASE I); kinase/ protein serine/threonine kinase | chr4:8248532-8251668 REVERSEhighly similar to (702) loc_os04g43490 12004.m101584 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=2:28936197..28940916:-1; parent_gene=GRMZM2G032694'

'moderately similar to (300) AT3G54420 | Symbols: ATEP3, ATCHITIV, CHIV | ATEP3; chitinase | chr3:20145935-20147034 FORWARDmoderately similar to (370) CHIA_MAIZE Endochitinase A precursor (EC 3.2.1.14) (Seed chitinase A) - Zea mays (Maize)moderately similar to (343) loc_os04g41680 12004.m09144 protein endochitinase A precursor, putative, expressed seq=cds; coord=2:33507060..33508210:1; parent_gene=GRMZM2G051921'

'moderately similar to (332) AT1G69850 | Symbols: ATNRT1:2, NTL1 | ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter | chr1:26296945-26300407 REVERSEhighly similar to (771) loc_os04g41450 12004.m09123 protein TGF-beta receptor, type I/II extracellular region, putative, expressed seq=cds; coord=2:34431765..34434969:1; parent_gene=GRMZM2G138731'

'moderately similar to (218) AT2G43080 | Symbols: AT-P4H-1 | AT-P4H-1 (A. THALIANA P4H ISOFORM 1); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors / procollagen-proline 4-dioxygen | chr2:17915755-17918599 FORWARDmoderately similar to (256) loc_os04g27850 12004.m07907 protein prolyl 4-hydroxylase alpha-1 subunit, putative, expressed seq=cds; coord=2:81940047..81979763:-1; parent_gene=GRMZM2G028004'

'highly similar to (672) AT5G42240 | Symbols: scpl42 | scpl42 (serine carboxypeptidase-like 42); serine-type carboxypeptidase | chr5:16888717-16890931 FORWARDmoderately similar to (311) CBP23_HORVU Serine carboxypeptidase II-3 precursor (EC 3.4.16.6) (CP-MII.3) [Contains: Serine carboxypeptidase II-3 chain A; Serine carboxypeptidase II-3 chain B] - Hordeum vulgare (Barley)highly similar to (805) loc_os11g10750 12011.m05268 protein serine carboxypeptidase F13S12.6 precursor, putative, expressed seq=cds; coord=2:127442670..127445933:-1; parent_gene=GRMZM2G132154' 'highly similar to (672) AT5G42240 | Symbols: scpl42 | scpl42 (serine carboxypeptidase-like 42); serine-type carboxypeptidase | chr5:16888717-16890931 FORWARDmoderately similar to (311) CBP23_HORVU Serine carboxypeptidase II-3 precursor (EC 3.4.16.6) (CP-MII.3) [Contains: Serine carboxypeptidase II-3 chain A; Serine carboxypeptidase II-3 chain B] - Hordeum vulgare (Barley)highly similar to (805) loc_os11g10750 12011.m05268 protein serine carboxypeptidase F13S12.6 precursor, putative, expressed seq=cds; coord=2:127442670..127445933:-1; parent_gene=GRMZM2G132154'

'highly similar to (635) AT2G46370 | Symbols: JAR1, FIN219 | JAR1 (JASMONATE RESISTANT 1); ATP binding / adenylyltransferase/ catalytic/ jasmonate-amino synthetase | chr2:19034579-19036369 FORWARDhighly similar to (738) GH312_ORYSA Probable indole-3-acetic acid-amido synthetase GH3.12 (EC 6.3.2.-) (Auxin-responsive GH3-like protein 12) (OsGH3-12) - Oryza sativa (Rice)highly similar to (801) loc_os01g12160 12001.m07831 protein indole-3-acetic acid-amido synthetase GH3.3, putative, expressed seq=cds; coord=3:2946152..2948661:-1; parent_gene=GRMZM2G061005'

'highly similar to (903) AT4G27910 | Symbols: ATX4, SDG16 | SDG16 (SET DOMAIN PROTEIN 16); protein binding / zinc ion binding | chr4:13894694-13900256 FORWARDvery weakly similar to (92.4) EZ1_MAIZE Polycomb protein EZ1 (Enhancer of zeste protein 1) - Zea mays (Maize)nearly identical (1491) loc_os01g11952 12001.m07811 protein histone-lysine N-methyltransferase ATX5, putative, expressed seq=cds; coord=3:3200782..3209083:1; parent_gene=GRMZM2G085266'

'highly similar to (515) AT2G30050 | Symbols: | transducin family protein / WD-40 repeat family protein | chr2:12825540-12826448 FORWARDhighly similar to (616) loc_os02g04320 12002.m33334 protein SEC13-related protein, putative, expressed seq=cds; coord=3:3399286..3402872:-1; parent_gene=GRMZM2G102795'

'moderately similar to (385) AT2G36800 | Symbols: DOGT1, UGT73C5 | DOGT1 (DON-GLUCOSYLTRANSFERASE 1); UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transf | chr2:15423493-15424980 REVERSEweakly similar to (190) CZOG_SORBI Putative cis-zeatin O-glucosyltransferase (EC 2.4.1.215) - Sorghum bicolor (Sorghum) (Sorghum vulgare)highly similar to (681) loc_os10g09990 12010.m04338 protein cytokinin-O-glucosyltransferase 3, putative, expressed seq=cds; coord=3:10843334..10845067:1; parent_gene=GRMZM2G338465'

'highly similar to (822) AT1G15460 | Symbols: ATBOR4, BOR4 | BOR4 (REQUIRES HIGH BORON 4); anion exchanger | chr1:5310196-5313376 REVERSEnearly identical (1013) loc_os01g08020 12001.m07427 protein boron transporter-like protein 2, putative, expressed seq=cds; coord=3:10934126..10940345:-1; parent_gene=GRMZM2G051753'

'weakly similar to (177) AT3G08710 | Symbols: ATH9 | ATH9 (thioredoxin H-type 9) | chr3:2645590-2646304 FORWARDweakly similar to (105) TRXH_WHEAT Thioredoxin H-type (TRX-H) (TrxTa) - Triticum aestivum (Wheat)moderately similar to (221) loc_os05g07690 12005.m27714 protein thioredoxin H-type, putative, expressed seq=cds; coord=3:13465241..13467448:1; parent_gene=GRMZM2G159145'

'moderately similar to (410) loc_os02g43750 12002.m09409 protein transcription initiation factor, putative, expressed seq=cds; coord=3:13846717..13865900:-1; parent_gene=GRMZM2G102664'

'moderately similar to (410) loc_os02g43750 12002.m09409 protein transcription initiation factor, putative, expressed seq=cds; coord=3:13846717..13865900:-1; parent_gene=GRMZM2G102664'

'very weakly similar to (100) AT1G49950 | Symbols: TRB1, ATTRB1 | DNA-binding protein, putative | chr1:18494439-18496713 REVERSEweakly similar to (164) loc_os12g41920 12012.m26974 protein single myb histone 6, putative, expressed seq=cds; coord=3:14469142..14473799:-1; parent_gene=GRMZM2G163291'

'moderately similar to (280) AT5G02310 | Symbols: PRT6 | PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase | chr5:474279-482552 FORWARDhighly similar to (504) loc_os01g05500 12001.m42863 protein zinc finger in N-recognin family protein, putative, expressed seq=cds; coord=3:17607856..17610988:-1; parent_gene=GRMZM2G541193'

'moderately similar to (456) AT3G18270 | Symbols: CYP77A5P | CYP77A5P; catalytic | chr3:6262010-6264025 FORWARDhighly similar to (625) loc_os01g04630 12001.m07098 protein muconate cycloisomerase-like protein, putative, expressed seq=cds; coord=3:19939526..19944315:1; parent_gene=GRMZM2G169152'

'moderately similar to (358) AT5G38260 | Symbols: | serine/threonine protein kinase, putative | chr5:15283692-15285837 REVERSEweakly similar to (191) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (583) loc_os01g04490 12001.m07084 protein Ser/Thr protein kinase, putative, expressed seq=cds; coord=3:20059223..20068196:-1; parent_gene=GRMZM2G094028'

'moderately similar to (225) AT1G48000 | Symbols: MYB112, AtMYB112 | MYB112 (myb domain protein 112); DNA binding / transcription factor | chr1:17704269-17706377 REVERSEweakly similar to (154) MYBA2_ORYSA Myb-related protein MYBAS2 - Oryza sativa (Rice)moderately similar to (297) loc_os01g19330 12001.m08470 protein cpm7, putative, expressed seq=cds; coord=3:52308738..52309963:1; parent_gene=GRMZM2G158700'

'moderately similar to (293) AT2G03200 | Symbols: | aspartyl protease family protein | chr2:966506-967891 REVERSEmoderately similar to (321) loc_os04g37550 12004.m08744 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=3:54325528..54326895:-1; parent_gene=GRMZM2G102014'

'very weakly similar to (94.7) AT1G52950 | Symbols: | replication protein-related | chr1:19725483-19728007 FORWARDmoderately similar to (207) loc_os07g02230 12007.m04695 protein retrotransposon protein, putative, unclassified, expressed seq=cds; coord=3:88916116..88921100:1; parent_gene=GRMZM2G351307'

'moderately similar to (258) AT4G38620 | Symbols: ATMYB4, MYB4 | MYB4; DNA binding / transcription factor | chr4:18053866-18054876 FORWARDmoderately similar to (256) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (260) loc_os11g07890 12011.m04985 protein transposon protein, putative, CACTA, En/Spm sub-class seq=cds; coord=3:140124295..140125490:1; parent_gene=GRMZM2G041415'

'moderately similar to (402) AT4G09160 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr4:5839761-5842158 FORWARDhighly similar to (650) loc_os01g65380 12001.m12651 protein patellin-5, putative, expressed seq=cds; coord=3:173472565..173475730:-1; parent_gene=GRMZM2G081652'

'moderately similar to (209) AT4G38730 | Symbols: | unknown protein | chr4:18080484-18082305 REVERSEmoderately similar to (247) loc_os01g65310 12001.m12644 protein non-imprinted in Prader-Willi/Angelman syndrome region protein 1homolog, putative, expressed seq=cds; coord=3:173795427..173798467:1; parent_gene=GRMZM2G037229' 'moderately similar to (273) AT1G44575 | Symbols: NPQ4, PSBS | NPQ4 (NONPHOTOCHEMICAL QUENCHING); chlorophyll binding / xanthophyll binding | chr1:16871768-16872548 FORWARDmoderately similar to (286) PSBS_SPIOL Photosystem II 22 kDa protein, chloroplast precursor (CP22) - Spinacia oleracea (Spinach)moderately similar to (305) loc_os01g64960 12001.m150788 protein photosystem II 22 kDa protein, chloroplast precursor, putative, expressed seq=cds; coord=3:174825201..174827787:-1; parent_gene=GRMZM2G077333'

'very weakly similar to (85.1) AT1G23465 | Symbols: | signal peptidase-related | chr1:8330055-8330938 FORWARDweakly similar to (146) loc_os11g40500 12011.m080046 protein mitochondrial inner membrane protease subunit 1, putative, expressed seq=cds; coord=3:195670548..195673406:-1; parent_gene=GRMZM2G162274'

'weakly similar to (146) loc_os03g08400 12003.m06348 protein retrotransposon protein, putative, unclassified seq=cds; coord=3:200406586..200410117:-1; parent_gene=GRMZM2G330229'

'moderately similar to (340) AT2G37650 | Symbols: | scarecrow-like transcription factor 9 (SCL9) | chr2:15792623-15794779 FORWARDweakly similar to (144) CIGR2_ORYSA Chitin-inducible gibberellin-responsive protein 2 - Oryza sativa (Rice)moderately similar to (464) loc_os11g47870 12011.m08584 protein chitin-inducible gibberellin-responsive protein 2, putative, expressed seq=cds; coord=4:832522..834779:-1; parent_gene=GRMZM2G073805'

'highly similar to (675) AT1G11870 | Symbols: ATSRS, OVA7, SRS | SRS (SERYL-TRNA SYNTHETASE); serine-tRNA ligase | chr1:4003895-4006556 FORWARDmoderately similar to (237) SYS_HELAN Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS) - Helianthus annuus (Common sunflower)highly similar to (810) loc_os11g39670 12011.m28846 protein seryl-tRNA synthetase, putative, expressed seq=cds; coord=4:5666220..5677820:-1; parent_gene=GRMZM2G169160'

'highly similar to (570) AT2G27100 | Symbols: SE | SE (SERRATE); DNA binding / transcription factor | chr2:11572587-11576357 FORWARDhighly similar to (787) loc_os08g40560 12008.m26744 protein expressed protein seq=cds; coord=4:42144894..42148125:1; parent_gene=GRMZM2G377165'

'highly similar to (647) AT1G76270 | Symbols: | unknown protein | chr1:28613554-28616537 REVERSEhighly similar to (701) loc_os09g37590 12009.m06706 protein expressed protein seq=cds; coord=4:88514893..88534830:-1; parent_gene=GRMZM2G131699'

'very weakly similar to (82.8) AT4G24210 | Symbols: SLY1 | SLY1 (SLEEPY1) | chr4:12563658-12564113 FORWARDweakly similar to (148) GID2_ORYSA F-box protein GID2 (Gibberellin-insensitive dwarf protein 2) (Protein GIBBERELLIN INSENSITIVE DWARF2) - Oryza sativa (Rice)very weakly similar to (87.4) loc_os04g3887 12004.m35150 protein 14-3-3-like protein GF14-6, putative, expressed seq=cds; coord=4:126342399..126344503:1; parent_gene=GRMZM2G095397'

'moderately similar to (213) AT1G45230 | Symbols: | defective chloroplasts and leaves protein-related / DCL protein-related | chr1:17169874-17171381 REVERSEmoderately similar to (284) loc_os02g52744 12002.m10304 protein DCL protein, chloroplast precursor, putative, expressed seq=cds; coord=4:178575924..178580683:1; parent_gene=GRMZM2G079353' 'highly similar to (687) AT1G65430 | Symbols: | zinc finger protein-related | chr1:24301165-24306159 REVERSEhighly similar to (953) loc_os08g42740 12008.m26855 protein protein ariadne-1, putative, expressed seq=cds; coord=4:193995236..194011403:1; parent_gene=GRMZM2G100913'

'very weakly similar to (82.8) AT1G74320 | Symbols: | choline kinase, putative | chr1:27941192-27942903 FORWARDweakly similar to (154) loc_os01g08760 12001.m07501 protein choline/ethanolamine kinase, putative, expressed seq=cds; coord=4:236958349..236961455:1; parent_gene=GRMZM2G111319'

'moderately similar to (385) AT4G04860 | Symbols: DER2.2 | DER2.2 (DERLIN-2.2) | chr4:2460135-2461378 FORWARDmoderately similar to (478) DER21_MAIZE Derlin-2.1 (ZmDerlin2-1) - Zea mays (Maize)moderately similar to (473) loc_os03g63520 12003.m11220 protein derlin-2, putative, expressed seq=cds; coord=5:923899..928546:1; parent_gene=GRMZM2G082976'

'weakly similar to (144) AT5G27700 | Symbols: | structural constituent of ribosome | chr5:9807541-9808048 REVERSEweakly similar to (164) RS21_MAIZE 40S ribosomal protein S21 - Zea mays (Maize)weakly similar to (145) loc_os03g46490 12003.m09669 protein 40S ribosomal protein S21, putative seq=cds; coord=5:1565845..1568408:-1; parent_gene=GRMZM2G125300'

'weakly similar to (164) AT3G02875 | Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugate hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase | chr3:631993-633859 FORWARDmoderately similar to (204) loc_os03g62060 12003.m11084 protein IAA-amino acid hydrolase ILR1 precursor, putative, expressed seq=cds; coord=5:1571090..1572477:-1; parent_gene=GRMZM2G125552'

'moderately similar to (309) AT2G26740 | Symbols: ATSEH | ATSEH (Arabidopsis thaliana soluble epoxide hydrolase); epoxide hydrolase | chr2:11393148-11394257 REVERSEmoderately similar to (469) loc_os03g61360 12003.m11018 protein epoxide hydrolase 2, putative, expressed seq=cds; coord=5:1817218..1820652:-1; parent_gene=GRMZM2G133407'

'weakly similar to (160) AT5G02460 | Symbols: | Dof-type zinc finger domain-containing protein | chr5:539549-541058 REVERSEweakly similar to (115) PBF_MAIZE Dof zinc finger protein PBF (Prolamin box-binding factor) - Zea mays (Maize)moderately similar to (330) loc_os03g60630 12003.m10953 protein expressed protein seq=cds; coord=5:2336204..2338578:-1; parent_gene=GRMZM2G144172'

'nearly identical (1279) AT5G35840 | Symbols: PHYC | PHYC (phytochrome defective c); protein histidine kinase | chr5:14008049-14011619 FORWARDnearly identical (2006) PHYC_SORBI Phytochrome C - Sorghum bicolor (Sorghum) (Sorghum vulgare)nearly identical (1899) loc_os03g54084 12003.m101724 protein phytochrome C, putative, expressed seq=cds; coord=5:7121947..7126963:-1; parent_gene=GRMZM2G129889'

'highly similar to (747) AT3G12110 | Symbols: ACT11 | ACT11 (actin-11); structural constituent of cytoskeleton | chr3:3858116-3859609 FORWARDhighly similar to (758) ACT1_ORYSA Actin-1 - Oryza sativa (Rice)highly similar to (758) loc_os03g50890 12003.m10074 protein actin-1, putative, expressed seq=cds; coord=5:10223674..10226373:-1; parent_gene=GRMZM2G152328' 'highly similar to (670) AT5G23190 | Symbols: CYP86B1 | CYP86B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr5:7803478-7805659 REVERSEweakly similar to (114) C97B2_SOYBN Cytochrome P450 97B2 (EC 1.14.-.-) - Glycine max (Soybean)highly similar to (830) loc_os10g34480 12010.m06272 protein cytochrome P450 86A2, putative, expressed seq=cds; coord=5:26443691..26446113:1; parent_gene=GRMZM2G013082'

'very weakly similar to (95.1) AT3G03590 | Symbols: | SWIB complex BAF60b domain-containing protein | chr3:865341-866669 REVERSEweakly similar to (125) loc_os02g03730 12002.m05722 protein SWIb domain-containing protein, putative, expressed seq=cds; coord=5:74408556..74411160:-1; parent_gene=GRMZM2G524937'

'moderately similar to (237) AT3G59310 | Symbols: | unknown protein | chr3:21922316-21924313 REVERSEmoderately similar to (298) loc_os08g42720 12008.m26773 protein solute carrier family 35, member F1, putative, expressed seq=cds; coord=5:108648845..108650638:-1; parent_gene=GRMZM2G072407'

'very weakly similar to (89.0) loc_os02g14980 12002.m06741 protein sodium/calcium exchanger protein, expressed seq=cds; coord=5:143957640..143958195:-1; parent_gene=GRMZM2G030945'

'moderately similar to (413) AT3G02040 | Symbols: SRG3 | SRG3 (senescence-related gene 3); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase | chr3:348505-349909 REVERSEhighly similar to (585) loc_os02g31030 12002.m08246 protein glycerophosphodiester phosphodiesterase, putative, expressed seq=cds; coord=5:164727076..164730451:-1; parent_gene=GRMZM2G018820'

'weakly similar to (102) AT5G13910 | Symbols: LEP | LEP (LEAFY PETIOLE); DNA binding / transcription factor | chr5:4482450-4483085 REVERSEweakly similar to (195) loc_os02g32040 12002.m08297 protein AP2 domain containing protein seq=cds; coord=5:166514893..166515834:1; parent_gene=GRMZM2G047999'

'highly similar to (887) AT3G11670 | Symbols: DGD1 | DGD1 (DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1); UDP-galactosyltransferase/ galactolipid galactosyltransferase/ transferase, transferring glycosyl groups | chr3:3681679-3684495 REVERSEhighly similar to (901) DGDG1_SOYBN Digalactosyldiacylglycerol synthase 1, chloroplast precursor (EC 2.4.1.241) - Glycine max (Soybean)highly similar to (996) loc_os02g33580 12002.m33714 protein digalactosyldiacylglycerol synthase 1, putative, expressed seq=cds; coord=5:170070982..170073578:1; parent_gene=GRMZM2G092588'

'moderately similar to (322) AT1G12260 | Symbols: VND4, EMB2749, ANAC007 | ANAC007 (ARABIDOPSIS NAC 007); transcription factor | chr1:4163058-4164486 REVERSEmoderately similar to (229) NAC76_ORYSA NAC domain-containing protein 76 (ONAC076) - Oryza sativa (Rice)moderately similar to (478) loc_os02g42970 12002.m09332 protein NAC domain-containing protein 76, putative seq=cds; coord=5:189401545..189405925:-1; parent_gene=GRMZM2G315140'

'weakly similar to (105) loc_os04g47890 12004.m09729 protein myb-like DNA-binding domain, SHAQKYF class family protein, expressed seq=cds; coord=5:194250832..194253964:1; parent_gene=GRMZM2G106185' 'very weakly similar to (85.5) AT3G30390 | Symbols: | amino acid transporter family protein | chr3:11977112-11978827 REVERSEvery weakly similar to (95.5) loc_os02g49510 12002.m09985 protein amino acid transporter-like protein, putative, expressed seq=cds; coord=5:204528827..204529273:-1; parent_gene=GRMZM2G020738'

'nearly identical (1048) AT5G60930 | Symbols: | chromosome-associated kinesin, putative | chr5:24515398-24522511 REVERSEmoderately similar to (259) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiimoderately similar to (498) loc_os02g50910 12002.m10125 protein ATP binding protein, putative, expressed seq=cds; coord=5:206459893..206468689:-1; parent_gene=GRMZM2G026560'

'weakly similar to (147) AT5G65220 | Symbols: | ribosomal protein L29 family protein | chr5:26061301-26062506 FORWARDmoderately similar to (228) RK29_MAIZE 50S ribosomal protein L29, chloroplast precursor (CL29) - Zea mays (Maize)weakly similar to (199) loc_os02g51790 12002.m10210 protein 50S ribosomal protein L29, chloroplast precursor, putative, expressed seq=cds; coord=5:208341565..208343539:1; parent_gene=GRMZM2G159554'

'moderately similar to (299) ATCG00170 | Symbols: RPOC2 | RNA polymerase beta' subunit-2 | chrC:15938-20068 REVERSEnearly identical (1103) RPOC2_MAIZE DNA-directed RNA polymerase beta'' chain (EC 2.7.7.6) (PEP) (Plastid-encoded RNA polymerase beta'' subunit) (RNA polymerase beta'' subunit) - Zea mays (Maize)highly similar to (578) loc_osp1g00260 11562.m00015 protein RNA polymerase beta'' chain seq=cds; coord=5:210010750..210014897:1; parent_gene=GRMZM2G055859'

'weakly similar to (157) AT2G46620 | Symbols: | AAA-type ATPase family protein | chr2:19139071-19140546 REVERSEmoderately similar to (280) loc_os03g02330 12003.m05775 protein ATP binding protein, putative, expressed seq=cds; coord=5:210728409..210730929:-1; parent_gene=GRMZM2G403454'

'moderately similar to (285) AT1G13080 | Symbols: CYP71B2 | CYP71B2 (CYTOCHROME P450 71B2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr1:4459493-4460807 FORWARDmoderately similar to (464) C71C4_MAIZE Cytochrome P450 71C4 (EC 1.14.-.-) (Benzoxazineless 2) - Zea mays (Maize)moderately similar to (499) loc_os08g01510 12008.m04299 protein cytochrome P450 71C4, putative, expressed seq=cds; coord=6:792072..794081:1; parent_gene=GRMZM2G052825'

'moderately similar to (316) AT2G41900 | Symbols: | zinc finger (CCCH-type) family protein | chr2:17491352-17493502 FORWARDhighly similar to (654) loc_os07g38090 12007.m28994 protein nucleic acid binding protein, putative, expressed seq=cds; coord=6:1823029..1825102:-1; parent_gene=AC233871.1_FG008'

'weakly similar to (145) AT3G49050 | Symbols: | lipase class 3 family protein / calmodulin-binding heat-shock protein, putative | chr3:18181498-18183613 FORWARDmoderately similar to (257) loc_os06g14490 12006.m32040 protein calmodulin-binding heat-shock protein, putative, expressed seq=cds; coord=6:118603733..118605257:1; parent_gene=GRMZM2G174315'

'weakly similar to (104) AT4G30590 | Symbols: | plastocyanin-like domain-containing protein | chr4:14935760-14936469 REVERSEweakly similar to (180) loc_os06g17730 12006.m06485 protein blue copper protein precursor, putative, expressed seq=cds; coord=6:119641904..119642938:1; parent_gene=GRMZM2G148624' 'moderately similar to (326) AT3G21770 | Symbols: | peroxidase 30 (PER30) (P30) (PRXR9) | chr3:7673345-7674661 FORWARDmoderately similar to (372) PER1_ORYSA Peroxidase 1 precursor (EC 1.11.1.7) - Oryza sativa (Rice)moderately similar to (484) loc_os06g29470 12006.m07491 protein peroxidase 1 precursor, putative, expressed seq=cds; coord=6:120912973..120914397:1; parent_gene=GRMZM2G104109'

'highly similar to (733) AT4G11110 | Symbols: SPA2 | SPA2 (SPA1-RELATED 2); protein binding / signal transducer | chr4:6772163-6776675 FORWARDmoderately similar to (329) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)nearly identical (1523) loc_os05g49590 12005.m083816 protein SPA1, putative, expressed seq=cds; coord=6:165393177..165402270:-1; parent_gene=GRMZM2G145556'

'highly similar to (733) AT4G11110 | Symbols: SPA2 | SPA2 (SPA1-RELATED 2); protein binding / signal transducer | chr4:6772163-6776675 FORWARDmoderately similar to (329) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)nearly identical (1523) loc_os05g49590 12005.m083816 protein SPA1, putative, expressed seq=cds; coord=6:165393177..165402270:-1; parent_gene=GRMZM2G145556'

'highly similar to (733) AT4G11110 | Symbols: SPA2 | SPA2 (SPA1-RELATED 2); protein binding / signal transducer | chr4:6772163-6776675 FORWARDmoderately similar to (329) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)nearly identical (1523) loc_os05g49590 12005.m083816 protein SPA1, putative, expressed seq=cds; coord=6:165393177..165402270:-1; parent_gene=GRMZM2G145556'

'highly similar to (733) AT4G11110 | Symbols: SPA2 | SPA2 (SPA1-RELATED 2); protein binding / signal transducer | chr4:6772163-6776675 FORWARDmoderately similar to (329) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)nearly identical (1523) loc_os05g49590 12005.m083816 protein SPA1, putative, expressed seq=cds; coord=6:165393177..165402270:-1; parent_gene=GRMZM2G145556'

'weakly similar to (145) AT2G32060 | Symbols: | 40S ribosomal protein S12 (RPS12C) | chr2:13639228-13640104 REVERSEmoderately similar to (203) RS12_HORVU 40S ribosomal protein S12 - Hordeum vulgare (Barley)weakly similar to (197) loc_os07g12650 12007.m079809 protein 40S ribosomal protein S12, putative, expressed seq=cds; coord=6:165961344..165962988:-1; parent_gene=GRMZM2G132929'

'highly similar to (695) AT1G30220 | Symbols: ATINT2, INT2 | INT2 (INOSITOL TRANSPORTER 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter | chr1:10632957-10635439 REVERSEweakly similar to (124) STC_RICCO Sugar carrier protein C - Ricinus communis (Castor bean)highly similar to (787) loc_os07g05640 12007.m05028 protein proton myo-inositol cotransporter, putative, expressed seq=cds; coord=7:5335384..5337829:1; parent_gene=GRMZM2G142063' 'moderately similar to (260) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDweakly similar to (147) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (496) loc_os07g13170 12007.m29109 protein floral homeotic protein, putative, expressed seq=cds; coord=7:22004372..22015553:1; parent_gene=GRMZM2G176175'

'weakly similar to (150) AT5G28050 | Symbols: | cytidine/deoxycytidylate deaminase family protein | chr5:10044209-10045484 REVERSEweakly similar to (161) loc_os07g14150 12007.m079579 protein cytidine/deoxycytidylate deaminase family protein, putative, expressed seq=cds; coord=7:24368445..24370041:1; parent_gene=GRMZM2G173063'

'weakly similar to (150) AT5G28050 | Symbols: | cytidine/deoxycytidylate deaminase family protein | chr5:10044209-10045484 REVERSEweakly similar to (161) loc_os07g14150 12007.m079579 protein cytidine/deoxycytidylate deaminase family protein, putative, expressed seq=cds; coord=7:24368445..24370041:1; parent_gene=GRMZM2G173063'

'nearly identical (1554) AT4G39350 | Symbols: CESA2, ATH-A, ATCESA2 | CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups | chr4:18297078-18301890 FORWARDnearly identical (1955) loc_os07g14850 12007.m05929 protein CESA6 - cellulose synthase, expressed seq=cds; coord=7:26487882..26493965:1; parent_gene=GRMZM2G177631'

'very weakly similar to (100) loc_os09g29820 12009.m06133 protein BZIP family transcription factor, putative, expressed seq=cds; coord=7:129898415..129899290:-1; parent_gene=GRMZM2G358796'

'weakly similar to (149) AT5G50890 | Symbols: | LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: lipase class 3 family protein (TAIR:AT2G05260.1); Has 115 Blast hits to 115 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 115; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:20702684-20704235 FORWARDmoderately similar to (313) loc_os07g39810 12007.m08223 protein triacylglycerol lipase, putative, expressed seq=cds; coord=7:161804206..161805610:-1; parent_gene=GRMZM2G179777'

'very weakly similar to (95.1) AT5G04340 | Symbols: C2H2, CZF2, ZAT6 | ZAT6 (ZINC FINGER OF ARABIDOPSI THALIANA 6); nucleic acid binding / transcription factor/ zinc ion binding | chr5:1216321-1217037 REVERSEvery weakly similar to (82.8) ZFP1_WHEAT Zinc-finger protein 1 (WZF1) - Triticum aestivum (Wheat)weakly similar to (137) loc_os07g40080 12007.m08250 protein zinc-finger protein 1, putative, expressed seq=cds; coord=7:162313242..162313838:1; parent_gene=AC185108.3_FG011'

'nearly identical (1023) AT3G02050 | Symbols: KUP3, ATKUP3, ATKT4 | KUP3 (K

'highly similar to (580) AT5G58380 | Symbols: CIPK10, PKS2, SIP1, SNRK3.8 | SIP1 (SOS3-INTERACTING PROTEIN 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr5:23597092-23598531 REVERSEmoderately similar to (454) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)highly similar to (744) loc_os07g48100 12007.m09025 protein CBL-interacting serine/threonine-protein kinase 15, putative, expressed seq=cds; coord=7:172925400..172928378:-1; parent_gene=GRMZM2G166658' 'moderately similar to (308) AT1G55545 | Symbols: | unknown protein | chr1:20738987-20743049 REVERSEmoderately similar to (387) loc_os07g48602 12007.m66702 protein EMB1011, putative, expressed seq=cds; coord=7:173827304..173838463:-1; parent_gene=AC155434.2_FG004'

'moderately similar to (214) AT3G04030 | Symbols: | myb family transcription factor | chr3:1042920-1044574 REVERSEmoderately similar to (284) loc_os07g48596 12007.m09071 protein MYR1, putative, expressed seq=cds; coord=7:173817875..173820052:-1; parent_gene=AC155434.2_FG005'

'moderately similar to (224) AT2G01275 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:142610-143809 REVERSEmoderately similar to (413) loc_os01g03100 12001.m42845 protein protein binding protein, putative, expressed seq=cds; coord=8:10287956..10291623:-1; parent_gene=GRMZM2G003930'

'moderately similar to (205) AT5G05140 | Symbols: | transcription elongation factor-related | chr5:1520353-1522297 FORWARDhighly similar to (598) loc_os05g34210 12005.m07652 protein expressed protein seq=cds; coord=8:104616112..104619975:1; parent_gene=GRMZM2G087451'

'highly similar to (866) AT1G26370 | Symbols: | RNA helicase, putative | chr1:9122030-9125368 REVERSEnearly identical (1169) loc_os06g09280 12006.m05647 protein ATP-dependent RNA helicase DHX8, putative, expressed seq=cds; coord=8:160365905..160374292:1; parent_gene=GRMZM2G300375'

'moderately similar to (265) AT3G57170 | Symbols: | N-acetylglucosaminyl transferase component family protein / Gpi1 family protein | chr3:21159620-21162259 REVERSEweakly similar to (187) loc_os05g22370 12005.m27768 protein N-acetylglucosaminyl transferase component, putative, expressed seq=cds; coord=8:161880772..161882765:1; parent_gene=GRMZM2G070898'

'moderately similar to (265) AT3G57170 | Symbols: | N-acetylglucosaminyl transferase component family protein / Gpi1 family protein | chr3:21159620-21162259 REVERSEweakly similar to (187) loc_os05g22370 12005.m27768 protein N-acetylglucosaminyl transferase component, putative, expressed seq=cds; coord=8:161880772..161882765:1; parent_gene=GRMZM2G070898'

'moderately similar to (265) AT3G57030 | Symbols: | strictosidine synthase family protein | chr3:21101653-21103204 REVERSEweakly similar to (153) STSY_CATRO Strictosidine synthase precursor (EC 4.3.3.2) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)moderately similar to (497) loc_os08g07810 12008.m04918 protein strictosidine synthase 1 precursor, putative seq=cds; coord=8:165827475..165828933:-1; parent_gene=GRMZM2G338431'

'moderately similar to (335) AT5G54500 | Symbols: FQR1 | FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor | chr5:22124674-22126256 FORWARDmoderately similar to (385) loc_os01g57570 12001.m43222 protein minor allergen Alt a 7, putative, expressed seq=cds; coord=8:171852196..171855863:-1; parent_gene=GRMZM2G159643'

'moderately similar to (315) AT4G28190 | Symbols: ULT1, ULT | ULT1 (ULTRAPETALA1); DNA binding | chr4:13985753-13987050 FORWARDmoderately similar to (379) loc_os01g57240 12001.m11877 protein expressed protein seq=cds; coord=8:172005510..172009034:1; parent_gene=GRMZM2G004690' 'highly similar to (672) AT1G63640 | Symbols: | kinesin motor protein-related | chr1:23589234-23595139 REVERSEmoderately similar to (223) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiinearly identical (1002) loc_os01g54080 12001.m11572 protein ATP binding protein, putative, expressed seq=cds; coord=8:174956855..174961114:-1; parent_gene=GRMZM2G124883'

'moderately similar to (496) AT5G19730 | Symbols: | pectinesterase family protein | chr5:6670562-6673202 FORWARDweakly similar to (187) PME_PRUPE Pectinesterase PPE8B precursor (EC 3.1.1.11) (Pectin methylesterase) (PE) - Prunus persica (Peach)highly similar to (615) loc_os01g53990 12001.m42718 protein pectinesterase-2 precursor, putative, expressed seq=cds; coord=8:175092256..175093999:1; parent_gene=GRMZM2G120779'

'weakly similar to (191) AT1G24090 | Symbols: | RNase H domain-containing protein | chr1:8520834-8524690 FORWARDmoderately similar to (281) loc_os06g13010 12006.m06017 protein nucleic acid binding protein, putative, expressed seq=cds; coord=9:2485121..2487554:-1; parent_gene=GRMZM2G016275'

'highly similar to (791) AT1G73590 | Symbols: PIN1, ATPIN1 | PIN1 (PIN-FORMED 1); transporter | chr1:27659772-27662876 FORWARDhighly similar to (987) PIN1C_ORYSA Probable auxin efflux carrier component 1c (OsPIN1c) Oryza sativa (Rice)highly similar to (987) loc_os06g12610 12006.m05977 protein auxin efflux carrier component 1c, putative, expressed seq=cds; coord=9:3650766..3654174:1; parent_gene=GRMZM2G098643'

'nearly identical (1504) AT5G65460 | Symbols: | kinesin motor protein-related | chr5:26161831-26169001 REVERSEweakly similar to (138) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiihighly similar to (894) loc_os06g11380 12006.m05855 protein ATP binding protein, putative, expressed seq=cds; coord=9:7186959..7210629:-1; parent_gene=GRMZM2G017257'

'weakly similar to (174) AT4G27600 | Symbols: | pfkB-type carbohydrate kinase family protein | chr4:13782753-13785005 REVERSEmoderately similar to (224) loc_os10g42240 12010.m21983 protein carbohydrate kinase-like protein, putative, expressed seq=cds; coord=9:112819814..112820314:1; parent_gene=GRMZM2G144245'

'moderately similar to (352) loc_os08g37270 12008.m07713 protein AHM1, putative, expressed seq=cds; coord=9:113061120..113065160:1; parent_gene=AC225193.3_FG004'

'very weakly similar to (94.4) AT4G16580 | Symbols: | catalytic | chr4:9341152-9342555 REVERSEweakly similar to (184) loc_os02g42250 12002.m09261 protein T-cell activation protein phosphatase 2C-like protein, putative seq=cds; coord=9:122054370..122055332:1; parent_gene=AC217887.3_FG001'

'moderately similar to (379) AT3G59890 | Symbols: | dihydrodipicolinate reductase family protein | chr3:22124497-22126491 REVERSEmoderately similar to (488) loc_os03g14120 12003.m34820 protein dihydrodipicolinate reductase, putative, expressed seq=cds; coord=9:142950199..142960205:-1; parent_gene=GRMZM2G104575'

'moderately similar to (323) AT5G04740 | Symbols: | ACT domain-containing protein | chr5:1368713-1371391 REVERSEmoderately similar to (415) loc_os12g05650 12012.m04558 protein ACT domain containing protein, expressed seq=cds; coord=10:5523751..5529199:-1; parent_gene=GRMZM2G066496' 'moderately similar to (417) AT2G25100 | Symbols: | ribonuclease HII family protein | chr2:10679767-10681654 REVERSEhighly similar to (537) loc_os11g05570 12011.m04754 protein ribonuclease HI large subunit, putative, expressed seq=cds; coord=10:5896223..5900069:1; parent_gene=GRMZM2G065804'

'weakly similar to (110) AT1G67320 | Symbols: | DNA primase, large subunit family | chr1:25205520-25208966 REVERSEweakly similar to (136) loc_os07g22400 12007.m079652 protein DNA primase large subunit, putative, expressed seq=cds; coord=10:6593015..6594700:1; parent_gene=GRMZM2G044317'

'weakly similar to (104) AT5G66320 | Symbols: | zinc finger (GATA type) family protein | chr5:26496208-26497309 REVERSEweakly similar to (122) loc_os12g07120 12012.m04702 protein basic proline-rich protein, putative, expressed seq=cds; coord=10:9404998..9406937:1; parent_gene=GRMZM2G118214'

'nearly identical (1518) AT1G02730 | Symbols: ATCSLD5, CSLD5 | ATCSLD5; 1,4-beta-D-xylan synthase/ cellulose synthase | chr1:594697-598473 REVERSEnearly identical (1830) loc_os12g36890 12012.m07474 protein CSLD4 - cellulose synthase-like family D, expressed seq=cds; coord=10:22261833..22266237:1; parent_gene=GRMZM2G015886'

'moderately similar to (233) AT5G57580 | Symbols: | calmodulin-binding protein | chr5:23314994-23317683 REVERSEhighly similar to (692) loc_os12g36110 12012.m07401 protein calmodulin binding protein, putative, expressed seq=cds; coord=10:23804445..23808523:-1; parent_gene=GRMZM2G176472'

'nearly identical (2670) AT4G35800 | Symbols: NRPB1, RPB1, RNA_POL_II_LSRNA_POL_II_LS, RNA_POL_II_LS | NRPB1 (RNA POLYMERASE II LARGE SUBUNIT); DNA binding / DNA-directed RNA polymerase | chr4:16961115-16967892 REVERSEweakly similar to (145) RPOC1_MESVI DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (PEP) (Plastid-encoded RNA polymerase beta' subunit) (RNA polymerase beta' subunit) - Mesostigma viridenearly identical (2829) loc_os05g05860 12005.m05113 protein DNA-directed RNA polymerase II largest subunit, putative, expressed seq=cds; coord=10:79744869..79753713:1; parent_gene=GRMZM2G044306'

'moderately similar to (349) AT3G62260 | Symbols: | protein phosphatase 2C, putative / PP2C, putative | chr3:23038516-23040391 REVERSEhighly similar to (525) loc_os05g04360 12005.m04969 protein protein phosphatase 2C homolog 2, putative, expressed seq=cds; coord=10:85581746..85584681:1; parent_gene=GRMZM2G060798'

'moderately similar to (320) AT3G17510 | Symbols: CIPK1, SnRK3.16 | CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding | chr3:5989309-5992627 REVERSEmoderately similar to (277) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)moderately similar to (377) loc_os05g04550 12005.m04988 protein CBL-interacting serine/threonine-protein kinase 1, putative, expressed seq=cds; coord=10:86697591..86707160:-1; parent_gene=GRMZM2G099002'

'moderately similar to (328) AT1G47980 | Symbols: | unknown protein | chr1:17691985-17693818 REVERSEmoderately similar to (481) loc_os04g33150 12004.m08410 protein desiccation-related protein PCC13-62 precursor, putative, expressed seq=cds; coord=10:113302165..113304045:-1; parent_gene=GRMZM2G138937' 'weakly similar to (140) AT5G66320 | Symbols: | zinc finger (GATA type) family protein | chr5:26496208-26497309 REVERSEmoderately similar to (256) loc_os02g43150 12002.m100295 protein GATA zinc finger family protein, expressed seq=cds; coord=10:133367444..133369576:1; parent_gene=GRMZM2G054615'

'highly similar to (682) AT2G43020 | Symbols: ATPAO2 | ATPAO2 (Polyamine oxidase 2); amine oxidase/ electron carrier/ oxidoreductase | chr2:17891945-17894440 FORWARDweakly similar to (134) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)highly similar to (848) loc_os04g53190 12004.m35201 protein lysine-specific histone demethylase 1, putative, expressed seq=cds; coord=10:143058165..143063379:1; parent_gene=GRMZM2G396856'

'highly similar to (682) AT2G43020 | Symbols: ATPAO2 | ATPAO2 (Polyamine oxidase 2); amine oxidase/ electron carrier/ oxidoreductase | chr2:17891945-17894440 FORWARDweakly similar to (134) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)highly similar to (848) loc_os04g53190 12004.m35201 protein lysine-specific histone demethylase 1, putative, expressed seq=cds; coord=10:143058165..143063379:1; parent_gene=GRMZM2G396856'

'moderately similar to (216) AT1G62040 | Symbols: ATG8C | ATG8C (autophagy 8c); microtubule binding | chr1:22933216-22934253 FORWARDmoderately similar to (226) loc_os08g09240 12008.m26825 protein autophagy-related protein 8 precursor, putative, expressed seq=cds; coord=10:142965742..142968913:1; parent_gene=GRMZM2G419694'

'moderately similar to (394) AT4G23180 | Symbols: CRK10, RLK4 | CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr4:12138171-12140780 FORWARDmoderately similar to (203) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (523) loc_os04g53994 12004.m10292 protein ATP binding protein, putative, expressed seq=cds; coord=10:144138641..144143208:-1; parent_gene=GRMZM2G000633'

'nearly identical (1069) AT5G64570 | Symbols: XYL4, ATBXL4 | XYL4; hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase | chr5:25810227-25813309 REVERSEmoderately similar to (468) XYNB_PRUPE Putative beta-D-xylosidase (EC 3.2.1.-) (PpAz152) (Fragment) - Prunus persica (Peach)nearly identical (1342) loc_os04g54810 12004.m10373 protein beta-D-xylosidase, putative, expressed seq=cds; coord=10:144683393..144689170:-1; parent_gene=GRMZM2G136895'

'weakly similar to (125) AT3G19000 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr3:6554004-6554987 REVERSEweakly similar to (130) GAOX2_ORYSA Gibberellin 20 oxidase 2 (EC 1.14.11.-) (Gibberellin C-20 oxidase 2) (GA 20-oxidase 2) (Os20ox2) (Semidwarf-1 protein) - Oryza sativa (Rice)highly similar to (513) loc_os04g55070 12004.m10399 protein gibberellin 20 oxidase 2, putative seq=cds; coord=10:144978459..144980157:1; parent_gene=GRMZM2G127668'

First Predicted Gene to Right
Description
'moderately similar to (446) AT2G38110 | Symbols: ATGPAT6, GPAT6 | GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase | chr2:15952816-15955364 REVERSEhighly similar to (649) loc_os10g27330 12010.m05667 protein glycerol-3-phosphate acyltransferase 8, putative, expressed seq=cds; coord=1:14031387..14033776:-1; parent_gene=GRMZM2G124042'
'highly similar to (556) AT1G19250 | Symbols: FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase | chr1:6650656-6653053 REVERSEhighly similar to (833) loc_os03g08410 12003.m06349 protein monooxygenase/ oxidoreductase, putative, expressed seq=cds; coord=1:17015718..17018487:1; parent_gene=GRMZM2G000427'
'very weakly similar to (92.8) AT2G17880 | Symbols: | DNAJ heat shock protein, putative | chr2:7767176-7767658 REVERSEweakly similar to (110) loc_os08g43490 12008.m08323 protein chaperone protein dnaJ 11, chloroplast precursor, putative, expressed seq=cds; coord=1:33408583..33409730:-1; parent_gene=GRMZM2G448368'
'weakly similar to (195) AT3G18950 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:6536900-6538321 FORWARDmoderately similar to (253) loc_os12g40260 12012.m07810 protein nucleotide binding protein, putative, expressed seq=cds; coord=1:166060337..166065479:1; parent_gene=GRMZM2G088613'
'seq=cds; coord=1:177626745..177627125:-1; parent_gene=GRMZM2G422419'
'weakly similar to (104) loc_os08g38020 12008.m07787 protein bZIP protein, putative, expressed seq=cds; coord=1:182626670..182627576:-1; parent_gene=AC186606.4_FG003'
'weakly similar to (103) AT3G25070 | Symbols: RIN4 | RIN4 (RPM1 INTERACTING PROTEIN 4); protein binding | chr3:9132458-9133747 FORWARDmoderately similar to (235) loc_os08g41470 12008.m62027 protein expressed protein seq=cds; coord=1:192932651..192935281:-1; parent_gene=GRMZM2G703858'
'weakly similar to (157) AT3G11750 | Symbols: | dihydroneopterin aldolase, putative | chr3:3715071-3715904 REVERSEmoderately similar to (206) loc_os09g38759 12009.m50203 protein dihydroneopterin aldolase, putative, expressed seq=cds; coord=1:206197528..206201863:1; parent_gene=GRMZM2G095579'
'weakly similar to (184) AT2G17730 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:7704142-7705312 FORWARDmoderately similar to (257) loc_os08g43670 12008.m08341 protein RING-H2 finger protein ATL2B, putative, expressed seq=cds; coord=1:206463126..206464716:1; parent_gene=GRMZM2G112617'

'moderately similar to (205) AT5G21482 | Symbols: CKX7, ATCKX5 | CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase | chr5:7226842-7230052 FORWARDweakly similar to (159) CKX1_MAIZE Cytokinin dehydrogenase 1 precursor (EC 1.5.99.12) (Cytokinin oxidase 1) (CKO 1) (COX 1) (ZmCKX1) - Zea mays (Maize)moderately similar to (296) loc_os08g35860 12008.m07575 protein cytokinin dehydrogenase 7, putative, expressed seq=cds; coord=1:207710634..207712091:1; parent_gene=GRMZM2G348452'

'weakly similar to (101) AT5G20630 | Symbols: GLP3, GLP3A, GLP3B, ATGER3, GER3 | GER3 (GERMIN 3); oxalate oxidase | chr5:6975315-6975950 REVERSEweakly similar to (103) GLP1_SINAL Germin-like protein 1 precursor - Sinapis alba (White mustard) (Brassica hirta)weakly similar to (114) loc_os08g35750 12008.m07564 protein germin-like protein 1 precursor, putative, expressed seq=cds; coord=1:207865153..207865778:-1; parent_gene=GRMZM2G363004'

'weakly similar to (132) AT4G35160 | Symbols: | O-methyltransferase family 2 protein | chr4:16730989-16732808 REVERSEmoderately similar to (293) ZRP4_MAIZE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT) - Zea mays (Maize)moderately similar to (344) loc_os06g16960 12006.m06409 protein O-methyltransferase ZRP4, putative seq=cds; coord=1:209119391..209120903:1; parent_gene=GRMZM2G059465'

'weakly similar to (143) AT2G23810 | Symbols: TET8 | TET8 (TETRASPANIN8) | chr2:10135859-10137352 REVERSEweakly similar to (181) loc_os08g34460 12008.m07435 protein senescence-associated protein DH, putative, expressed seq=cds; coord=1:210740384..210741599:1; parent_gene=GRMZM2G059397'

'moderately similar to (274) AT1G74680 | Symbols: | exostosin family protein | chr1:28059528-28060984 FORWARDmoderately similar to (358) loc_os08g34020 12008.m080169 protein secondary cell wall-related glycosyltransferase family 47, putative, expressed seq=cds; coord=1:212502284..212503936:-1; parent_gene=GRMZM2G139355'

'very weakly similar to (86.7) AT1G09700 | Symbols: HYL1, DRB1 | HYL1 (HYPONASTIC LEAVES 1); double-stranded RNA binding / miRNA binding / protein binding | chr1:3137960-3140118 REVERSEweakly similar to (174) loc_os08g29530 12008.m26677 protein RBP2 protein, putative, expressed seq=cds; coord=1:219369608..219375936:1; parent_gene=GRMZM2G146111'

'weakly similar to (121) AT2G17950 | Symbols: WUS, PGA6, WUS1 | WUS (WUSCHEL); DNA binding / protein binding / transcription factor/ transcription regulator | chr2:7809100-7810671 REVERSEweakly similar to (122) WUS_ANTMA Protein WUSCHEL (Protein ROSULATA) - Antirrhinum majus (Garden snapdragon)weakly similar to (186) loc_os04g56780 12004.m10565 protein protein WUSCHEL, putative, expressed seq=cds; coord=2:3387696..3389171:1; parent_gene=GRMZM2G047448'

'moderately similar to (263) AT4G32300 | Symbols: SD2-5 | SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase | chr4:15599970-15602435 FORWARDweakly similar to (177) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (590) loc_os04g56110 12004.m35493 protein ATP binding protein, putative, expressed seq=cds; coord=2:4512059..4514096:-1; parent_gene=GRMZM2G059740'

'moderately similar to (268) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDweakly similar to (130) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (382) loc_os04g55560 12004.m35488 protein AP2 domain containing protein, expressed seq=cds; coord=2:5514479..5518846:-1; parent_gene=GRMZM2G174784'

'highly similar to (520) AT5G03250 | Symbols: | phototropic-responsive NPH3 family protein | chr5:774591-776855 FORWARDmoderately similar to (321) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)highly similar to (745) loc_os04g54400 12004.m10331 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=2:6853850..6856978:-1; parent_gene=GRMZM2G159161'

'highly similar to (513) AT4G24480 | Symbols: | serine/threonine protein kinase, putative | chr4:12650410-12654755 FORWARDvery weakly similar to (82.8) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (847) loc_os04g52140 12004.m10109 protein protein kinase domain containing protein, expressed seq=cds; coord=2:10652142..10657319:-1; parent_gene=GRMZM2G098187'

'nearly identical (1444) AT2G32730 | Symbols: | 26S proteasome regulatory subunit, putative | chr2:13880189-13885464 FORWARDnearly identical (1555) loc_os08g12820 12008.m26623 protein 26S proteasome non-ATPase regulatory subunit 1, putative, expressed seq=cds; coord=2:11209985..11217603:1; parent_gene=GRMZM2G102000'

'moderately similar to (251) AT1G32700 | Symbols: | zinc-binding family protein | chr1:11827986-11829444 FORWARDmoderately similar to (338) loc_os04g50120 12004.m09944 protein expressed protein seq=cds; coord=2:13545639..13547834:1; parent_gene=GRMZM2G131280'

'weakly similar to (120) AT4G17500 | Symbols: ATERF-1 | ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor | chr4:9759405-9760211 FORWARDweakly similar to (124) ERF2_TOBAC Ethylene-responsive transcription factor 2 (Ethylene-responsive element-binding factor 2) (EREBP-2) (NtERF2) - Nicotiana tabacum (Common tobacco)moderately similar to (272) loc_os04g46220 12004.m09573 protein ethylene-responsive transcription factor 2, putative, expressed seq=cds; coord=2:20723453..20724789:1; parent_gene=GRMZM2G055180'

'highly similar to (640) AT3G15130 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:5097153-5099222 REVERSEweakly similar to (104) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (998) loc_os04g58980 12004.m10776 protein EMB2261, putative, expressed seq=cds; coord=2:24360634..24363095:1; parent_gene=GRMZM2G447090'

'moderately similar to (473) AT4G24790 | Symbols: | ATP binding / DNA binding / DNA-directed DNA polymerase | chr4:12778222-12781345 FORWARDhighly similar to (870) loc_os12g19180 12012.m05871 protein nucleoside-triphosphatase/ nucleotide binding protein, putative, expressed seq=cds; coord=2:36838775..36842537:-1; parent_gene=GRMZM2G044989'

'weakly similar to (119) loc_os09g31300 12009.m22140 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=2:189701055..189703654:1; parent_gene=GRMZM2G417597'

'weakly similar to (154) AT2G42200 | Symbols: SPL9 | SPL9 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9); transcription factor | chr2:17587601-17589451 FORWARDweakly similar to (114) SBP2_ANTMA Squamosa promoter-binding protein 2 - Antirrhinum majus (Garden snapdragon)moderately similar to (281) loc_os09g31438 12009.m06260 protein squamosa promoter-binding-like protein 9, putative, expressed seq=cds; coord=2:189838793..189842695:-1; parent_gene=GRMZM2G126018'

'weakly similar to (190) AT5G64200 | Symbols: ATSC35, SC35 | ATSC35; RNA binding / nucleic acid binding / nucleotide binding | chr5:25681849-25683553 REVERSEmoderately similar to (208) loc_os07g43050 12007.m079757 protein splicing factor, arginine/serine-rich 2, putative, expressed seq=cds; coord=2:212349126..212354040:1; parent_gene=GRMZM2G077823'

'highly similar to (807) AT5G65700 | Symbols: BAM1 | BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase | chr5:26281826-26284945 FORWARDmoderately similar to (233) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (837) loc_os03g56270 12003.m35431 protein receptor protein kinase CLAVATA1 precursor, putative, expressed seq=cds; coord=2:219017513..219023443:1; parent_gene=GRMZM2G169681'

'moderately similar to (342) AT5G24400 | Symbols: emb2024 | emb2024 (embryo defective 2024); 6-phosphogluconolactonase/ catalytic | chr5:8330532-8331784 REVERSEmoderately similar to (464) loc_os09g35970 12009.m06548 protein 6-phosphogluconolactonase, putative, expressed seq=cds; coord=2:220832473..220835451:-1; parent_gene=GRMZM2G148769'

'very weakly similar to (94.0) AT2G35910 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:15073225-15073878 REVERSEweakly similar to (108) loc_os12g42540 12012.m08033 protein RING-H2 finger protein ATL2I, putative seq=cds; coord=3:88527498..88527953:1; parent_gene=AC206768.3_FG005'

'moderately similar to (258) AT4G38620 | Symbols: ATMYB4, MYB4 | MYB4; DNA binding / transcription factor | chr4:18053866-18054876 FORWARDmoderately similar to (256) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (260) loc_os11g07890 12011.m04985 protein transposon protein, putative, CACTA, En/Spm sub-class seq=cds; coord=3:140124295..140125490:1; parent_gene=GRMZM2G041415'

'moderately similar to (394) AT2G41370 | Symbols: BOP2 | BOP2 (BLADE ON PETIOLE2); protein binding | chr2:17238019-17240203 REVERSEhighly similar to (516) loc_os01g72020 12001.m43379 protein BOP2, putative, expressed seq=cds; coord=3:150049274..150052250:1; parent_gene=GRMZM2G039867'

'moderately similar to (207) AT1G33430 | Symbols: | galactosyltransferase family protein | chr1:12124438-12126052 REVERSEmoderately similar to (233) loc_os01g65590 12001.m12668 protein beta-1,3-galactosyltransferase sqv-2, putative, expressed seq=cds; coord=3:172444363..172446418:-1; parent_gene=GRMZM2G431006'

'moderately similar to (318) AT5G58060 | Symbols: YKT61, ATYKT61, ATGP1 | YKT61 | chr5:23498277-23500128 FORWARDmoderately similar to (353) loc_os01g64650 12001.m43292 protein VAMP-like protein YKT62, putative, expressed seq=cds; coord=3:175775929..175780870:-1; parent_gene=GRMZM2G178244'

'highly similar to (661) AT2G39940 | Symbols: COI1 | COI1 (CORONATINE INSENSITIVE 1); protein binding / ubiquitin-protein ligase | chr2:16672848-16675486 REVERSEhighly similar to (988) loc_os01g63420 12001.m43515 protein coronatine-insensitive protein 1, putative, expressed seq=cds; coord=3:178602863..178606881:-1; parent_gene=GRMZM2G125411' 'highly similar to (740) AT1G65930 | Symbols: | isocitrate dehydrogenase, putative / NADP

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'highly similar to (749) AT1G15500 | Symbols: ATNTT2 | ATNTT2; ATP:ADP antiporter | chr1:5326426-5328688 FORWARDhighly similar to (753) TLC1_SOLTU Plastidic ATP/ADP-transporter - Solanum tuberosum (Potato)highly similar to (887) loc_os01g45910 12001.m10791 protein plastidic ATP/ADP-transporter, putative, expressed seq=cds; coord=3:214471264..214476975:1; parent_gene=GRMZM2G064473'

'moderately similar to (434) AT5G40850 | Symbols: UPM1 | UPM1 (UROPHORPHYRIN METHYLASE 1); uroporphyrin-III C-methyltransferase | chr5:16367205-16368724 FORWARDmoderately similar to (279) loc_os01g44050 12001.m10664 protein siroheme synthase, putative, expressed seq=cds; coord=3:216593144..216597291:-1; parent_gene=GRMZM2G105604'

'highly similar to (692) AT3G23430 | Symbols: PHO1, ATPHO1 | PHO1 (phosphate 1) | chr3:8387818-8393242 REVERSEnearly identical (1109) loc_os02g56510 12002.m10672 protein phosphate transporter 1, putative, expressed seq=cds; coord=4:171917079..171922792:1; parent_gene=GRMZM2G466545'

'moderately similar to (400) AT5G65685 | Symbols: | soluble glycogen synthase-related | chr5:26273252-26275864 REVERSEweakly similar to (189) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Potato)highly similar to (907) loc_os02g56320 12002.m10655 protein glycogen synthase 2, putative, expressed seq=cds; coord=4:172606253..172677186:-1; parent_gene=GRMZM2G130043'

'moderately similar to (400) AT5G65685 | Symbols: | soluble glycogen synthase-related | chr5:26273252-26275864 REVERSEweakly similar to (189) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Potato)highly similar to (907) loc_os02g56320 12002.m10655 protein glycogen synthase 2, putative, expressed seq=cds; coord=4:172606253..172677186:-1; parent_gene=GRMZM2G130043'

'highly similar to (933) AT4G29380 | Symbols: | protein kinase family protein / WD-40 repeat family protein | chr4:14458822-14464692 FORWARDnearly identical (1718) loc_os02g55340 12002.m10560 protein HEAT repeat family protein, expressed seq=cds; coord=4:173805959..173816788:1; parent_gene=GRMZM2G111491' 'weakly similar to (162) AT3G07830 | Symbols: | polygalacturonase, putative / pectinase, putative | chr3:2499454-2500966 REVERSEmoderately similar to (207) PGLR3_MAIZE Exopolygalacturonase precursor (EC 3.2.1.67) (ExoPG) (Pectinase) (Galacturan 1,4-alpha-galacturonidase) - Zea mays (Maize)moderately similar to (208) loc_os06g35370 12006.m08074 protein exopolygalacturonase precursor, putative, expressed seq=cds; coord=4:233223024..233225418:1; parent_gene=GRMZM2G029566'

'moderately similar to (445) AT2G17220 | Symbols: | protein kinase, putative | chr2:7487866-7489768 REVERSEmoderately similar to (215) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (573) loc_os02g02600 12002.m05609 protein serine/threonine-protein kinase Cx32, chloroplast precursor, putative, expressed seq=cds; coord=4:239725555..239729685:1; parent_gene=GRMZM2G025127'

'highly similar to (856) AT5G46920 | Symbols: | intron maturase, type II family protein | chr5:19053668-19055875 FORWARDweakly similar to (147) YMF11_MARPO Hypothetical 83.1 kDa protein in COB-ATPA intergenic region (ORF 732) - Marchantia polymorpha (Liverwort)nearly identical (1159) loc_os10g41790 12010.m065344 protein type II intron maturase family protein, expressed seq=cds; coord=5:1579..3920:-1; parent_gene=GRMZM2G356204'

'very weakly similar to (100) AT3G25070 | Symbols: RIN4 | RIN4 (RPM1 INTERACTING PROTEIN 4); protein binding | chr3:9132458-9133747 FORWARDmoderately similar to (297) loc_os03g63140 12003.m35534 protein nitrate-induced NOI protein, expressed seq=cds; coord=5:1060917..1063511:-1; parent_gene=GRMZM2G012229'

'highly similar to (625) AT4G02510 | Symbols: TOC159, TOC86, PPI2, TOC160, ATTOC159 | TOC159 (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 159); transmembrane receptor chr4:1104766-1109360 FORWARDweakly similar to (103) TOC34_PEA Translocase of chloroplast 34 (EC 3.6.5.-) (34 kDa chloroplast outer envelope protein) (GTP-binding protein OEP34) (GTP-binding protein IAP34) - Pisum sativum (Garden pea)nearly identical (1082) loc_os03g61890 12003.m35506 protein chloroplast protein import component Toc159, putative, expressed seq=cds; coord=5:1621055..1624641:-1; parent_gene=GRMZM2G326272'

'weakly similar to (188) AT5G58490 | Symbols: | cinnamoyl-CoA reductase family | chr5:23643068-23644455 FORWARDweakly similar to (106) DFRA_DIACA Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Dianthus caryophyllus (Carnation) (Clove pink)moderately similar to (238) loc_os03g60380 12003.m10928 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=5:2600634..2603545:-1; parent_gene=GRMZM2G110881'

'moderately similar to (352) AT5G58490 | Symbols: | cinnamoyl-CoA reductase family | chr5:23643068-23644455 FORWARDweakly similar to (154) DFRA_VITVI Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Vitis vinifera (Grape)moderately similar to (441) loc_os03g60380 12003.m10928 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=5:2705885..2708336:1; parent_gene=GRMZM2G107076' 'highly similar to (998) AT1G17840 | Symbols: WBC11, ABCG11, DSO, COF1, ATWBC11 | WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter | chr1:6142870-6145894 FORWARDweakly similar to (186) PDR4_ORYSA Pleiotropic drug resistance protein 4 - Oryza sativa (Rice)nearly identical (1100) loc_os10g35180 12010.m06341 protein ATP-binding cassette sub-family G member 2, putative, expressed seq=cds; coord=5:25713468..25717083:1; parent_gene=GRMZM2G177314'

'weakly similar to (123) AT1G56120 | Symbols: | kinase | chr1:20987288-20993072 REVERSEmoderately similar to (243) loc_os11g28104 12011.m06728 protein protein kinase, putative, expressed seq=cds; coord=5:27198279..27204222:-1; parent_gene=GRMZM2G102862'

'moderately similar to (236) AT1G73230 | Symbols: | nascent polypeptide-associated complex (NAC) domain-containing protein | chr1:27540506-27541364 REVERSEmoderately similar to (262) loc_os10g34180 12010.m21923 protein transcription factor BTF3, putative, expressed seq=cds; coord=5:27393436..27396313:1; parent_gene=GRMZM2G001887'

'moderately similar to (283) AT1G36730 | Symbols: | eukaryotic translation initiation factor 5, putative / eIF-5, putative | chr1:13898706-13900025 REVERSEhighly similar to (572) IF5_MAIZE Eukaryotic translation initiation factor 5 (eIF-5) - Zea mays (Maize)highly similar to (536) loc_os06g48350 12006.m09361 protein eukaryotic translation initiation factor 5, putative, expressed seq=cds; coord=5:28208919..28211750:1; parent_gene=GRMZM2G369939'

'weakly similar to (177) AT1G25560 | Symbols: TEM1 | TEM1 (TEMPRANILLO 1); transcription factor | chr1:8981891-8982976 REVERSEmoderately similar to (265) loc_os01g49830 12001.m11168 protein DNA-binding protein RAV1, putative, expressed seq=cds; coord=5:28639860..28641213:-1; parent_gene=GRMZM2G018336'

'highly similar to (740) AT2G33340 | Symbols: | nucleotide binding / ubiquitin-protein ligase | chr2:14126703-14131000 REVERSEvery weakly similar to (95.5) PF20_CHLRE Flagellar WD repeat protein PF20 - Chlamydomonas reinhardtiihighly similar to (927) loc_os10g32880 12010.m21914 protein pre-mRNA-splicing factor 19, putative, expressed seq=cds; coord=5:30740679..30750954:1; parent_gene=GRMZM2G324540'

'moderately similar to (436) AT4G10200 | Symbols: | hAT dimerisation domain-containing protein / transposase-related | chr4:6353172-6355591 FORWARDnearly identical (1079) loc_os12g37830 12012.m07569 protein transposon protein, putative, Ac/Ds sub-class seq=cds; coord=5:31055094..31057648:-1; parent_gene=GRMZM2G132595'

'weakly similar to (195) AT3G60830 | Symbols: ATARP7, ARP7 | ATARP7 (ACTIN-RELATED PROTEIN 7); structural constituent of cytoskeleton | chr3:22474298-22476000 FORWARDvery weakly similar to (82.4) ACT13_SOLTU Actin-101 - Solanum tuberosum (Potato)weakly similar to (158) loc_os03g56970 12003.m10616 protein ATARP7, putative, expressed seq=cds; coord=5:31818815..31828131:1; parent_gene=GRMZM2G015861'

'moderately similar to (291) AT5G25120 | Symbols: CYP71B11 | CYP71B11; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr5:8662851-8664432 FORWARDmoderately similar to (356) C71DA_SOYBN Cytochrome P450 71D10 (EC 1.14.-.-) - Glycine max (Soybean)highly similar to (526) loc_os10g30390 12010.m05901 protein cytochrome P450 71D7, putative, expressed seq=cds; coord=5:31947869..31949808:-1; parent_gene=GRMZM2G122654' 'highly similar to (571) AT3G51370 | Symbols: | protein phosphatase 2C, putative / PP2C, putative | chr3:19070387-19071975 FORWARDhighly similar to (716) loc_os06g50380 12006.m31935 protein protein phosphatase 2C, putative, expressed seq=cds; coord=5:61837656..61842314:-1; parent_gene=GRMZM2G069970'

'highly similar to (721) AT5G57800 | Symbols: FLP1, YRE, CER3, WAX2 | CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase | chr5:23420589-23423832 FORWARDhighly similar to (982) loc_os02g08230 12002.m100034 protein gl1 protein, putative, expressed seq=cds; coord=5:90341589..90347811:1; parent_gene=GRMZM2G083526'

'moderately similar to (207) AT3G04530 | Symbols: PPCK2, PEPCK2 | PPCK2; kinase/ protein serine/threonine kinase | chr3:1221546-1222456 FORWARDweakly similar to (153) CDPK2_ORYSA Calcium-dependent protein kinase, isoform 2 (EC 2.7.11.1) (CDPK 2) - Oryza sativa (Rice)moderately similar to (419) loc_os02g41580 12002.m09194 protein calcium-dependent protein kinase 2, putative, expressed seq=cds; coord=5:186505821..186507490:1; parent_gene=GRMZM2G096753'

'moderately similar to (361) AT5G47450 | Symbols: ATTIP2;3, TIP2;3, DELTA-TIP3 | AtTIP2;3; ammonia transporter/ methylammonium transmembrane transporter/ water channel | chr5:19248509-19249466 REVERSEmoderately similar to (422) TIP21_ORYSA Probable aquaporin TIP2.1 (Tonoplast intrinsic protein 2.1) (OsTIP2.1) - Oryza sativa (Rice)moderately similar to (422) loc_os02g44080 12002.m09443 protein aquaporin TIP2.1, putative, expressed seq=cds; coord=5:191910165..191911369:-1; parent_gene=GRMZM2G056908'

'highly similar to (605) AT3G27740 | Symbols: CARA | CARA (CARBAMOYL PHOSPHATE SYNTHETASE A); carbamoyl-phosphate synthase (glutamine-hydrolyzing)/ carbamoyl-phosphate synthase/ catalytic | chr3:10281470-10283792 REVERSEhighly similar to (758) loc_os02g47850 12002.m33834 protein carbamoyl-phosphate synthase small chain, putative, expressed seq=cds; coord=5:201452200..201457279:1; parent_gene=GRMZM2G147450'

'highly similar to (914) AT5G35700 | Symbols: FIM2 | FIM2 (FIMBRIN-LIKE PROTEIN 2); actin binding | chr5:13872833-13876432 REVERSEnearly identical (1246) loc_os02g48740 12002.m09908 protein fimbrin 1, putative, expressed seq=cds; coord=5:203620982..203625743:1; parent_gene=GRMZM2G382341'

'weakly similar to (193) AT5G55050 | Symbols: | GDSL-motif lipase/hydrolase family protein | chr5:22337745-22339741 FORWARDweakly similar to (151) APG_BRANA Anter-specific proline-rich protein APG (Protein CEX) (Fragment) - Brassica napus (Rape)highly similar to (518) loc_os02g50690 12002.m10103 protein anther-specific proline-rich protein APG precursor, putative, expressed seq=cds; coord=5:205839220..205841246:-1; parent_gene=GRMZM2G335280'

'weakly similar to (172) AT5G39865 | Symbols: | glutaredoxin family protein | chr5:15965560-15966732 REVERSEmoderately similar to (362) loc_os02g51370 12002.m10171 protein glutaredoxin family protein, expressed seq=cds; coord=5:207655630..207657582:-1; parent_gene=GRMZM2G118366'

'highly similar to (738) AT1G62830 | Symbols: LDL1, SWP1, ATSWP1 | LDL1 (LSD1-LIKE1); amine oxidase/ electron carrier/ oxidoreductase | chr1:23264638-23267172 REVERSEweakly similar to (107) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)nearly identical (1155) loc_os02g51880 12002.m10219 protein amine oxidase/ oxidoreductase, putative, expressed seq=cds; coord=5:208426880..208429748:1; parent_gene=GRMZM2G059958' 'highly similar to (724) AT1G78240 | Symbols: TSD2, QUA2 | TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase | chr1:29433173-29435815 REVERSEnearly identical (1119) loc_os02g51860 12002.m10217 protein ATP binding protein, putative, expressed seq=cds; coord=5:208391972..208397053:-1; parent_gene=GRMZM2G140893'

'moderately similar to (393) AT5G35370 | Symbols: | ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding | chr5:13588564-13591182 REVERSEmoderately similar to (206) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (568) loc_os02g52850 12002.m10315 protein ATP binding protein, putative, expressed seq=cds; coord=5:210043564..210046543:-1; parent_gene=GRMZM2G058220'

'highly similar to (777) AT3G14067 | Symbols: | subtilase family protein | chr3:4658421-4660754 REVERSEnearly identical (1140) loc_os02g53860 12002.m10415 protein subtilisin-like protease precursor, putative, expressed seq=cds; coord=5:212027167..212030047:-1; parent_gene=GRMZM2G163749'

'highly similar to (777) AT3G14067 | Symbols: | subtilase family protein | chr3:4658421-4660754 REVERSEnearly identical (1140) loc_os02g53860 12002.m10415 protein subtilisin-like protease precursor, putative, expressed seq=cds; coord=5:212027167..212030047:-1; parent_gene=GRMZM2G163749'

'moderately similar to (477) AT1G02800 | Symbols: ATCEL2, CEL2 | ATCEL2; cellulase/ hydrolase, hydrolyzing O-glycosyl compounds | chr1:613386-616103 REVERSEhighly similar to (614) GUN19_ORYSA Endoglucanase 19 precursor (EC 3.2.1.4) (Endo-1,4-beta glucanase 19) - Oryza sativa (Rice)highly similar to (614) loc_os08g02220 12008.m04366 protein endoglucanase 1 precursor, putative, expressed seq=cds; coord=6:4015353..4017399:1; parent_gene=GRMZM2G009025'

'weakly similar to (192) AT3G04720 | Symbols: PR4, HEL, PR-4 | PR4 (PATHOGENESIS-RELATED 4); chitin binding | chr3:1285691-1286531 REVERSEweakly similar to (198) BARW_HORVU Barwin - Hordeum vulgare (Barley)moderately similar to (219) loc_os11g37970 12011.m07644 protein win1 precursor, putative, expressed seq=cds; coord=6:11555672..11556724:-1; parent_gene=GRMZM2G454556'

'weakly similar to (189) AT5G23960 | Symbols: ATTPS21, TPS21 | TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase | chr5:8092969-8095128 FORWARDmoderately similar to (233) DCS1_GOSHI (

'moderately similar to (392) AT3G22110 | Symbols: PAC1 | PAC1; endopeptidase/ peptidase/ threonine-type endopeptidase | chr3:7792819-7793571 REVERSEmoderately similar to (447) PSA4B_ORYSA Proteasome subunit alpha type 4-2 (EC 3.4.25.1) (20S proteasome alpha subunit C) (20S proteasome subunit alpha-3) - Oryza sativa (Rice)moderately similar to (447) loc_os06g07140 12006.m05438 protein proteasome subunit alpha type 4, putative, expressed seq=cds; coord=6:80974657..80975832:-1; parent_gene=GRMZM2G120047'

'highly similar to (629) AT4G22130 | Symbols: SRF8 | SRF8 (STRUBBELIG-RECEPTOR FAMILY 8); ATP binding / kinase/ protein binding / protein kinase | chr4:11724781-11727331 FORWARDmoderately similar to (202) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (792) loc_os02g09740 12002.m100127 protein receptor protein kinase TMK1 precursor, putative, expressed seq=cds; coord=6:97610091..97618916:1; parent_gene=GRMZM2G162531'

'nearly identical (1068) AT1G70300 | Symbols: KUP6 | KUP6; potassium ion transmembrane transporter | chr1:26477993-26481233 REVERSEnearly identical (1291) HAK10_ORYSA Potassium transporter 10 (OsHAK10) - Oryza sativa (Rice)nearly identical (1291) loc_os06g42030 12006.m08735 protein potassium transporter 10, putative, expressed seq=cds; coord=6:97941833..97946553:1; parent_gene=GRMZM2G146760'

'highly similar to (507) AT5G59810 | Symbols: ATSBT5.4, SBT5.4 | SBT5.4; identical protein binding / serine-type endopeptidase | chr5:24096895-24100387 REVERSEnearly identical (1123) loc_os06g41880 12006.m08720 protein subtilisin-like protease precursor, putative, expressed seq=cds; coord=6:98026824..98031029:-1; parent_gene=GRMZM2G073223'

'highly similar to (507) AT5G59810 | Symbols: ATSBT5.4, SBT5.4 | SBT5.4; identical protein binding / serine-type endopeptidase | chr5:24096895-24100387 REVERSEnearly identical (1123) loc_os06g41880 12006.m08720 protein subtilisin-like protease precursor, putative, expressed seq=cds; coord=6:98026824..98031029:-1; parent_gene=GRMZM2G073223'

'weakly similar to (117) loc_os09g29700 12009.m06121 protein retrotransposon protein, putative, unclassified seq=cds; coord=6:98260609..98290821:1; parent_gene=GRMZM2G082112'

'moderately similar to (293) AT4G17150 | Symbols: | unknown protein | chr4:9638591-9640983 FORWARDhighly similar to (522) loc_os06g40730 12006.m08608 protein expressed protein seq=cds; coord=6:99884497..99890846:1; parent_gene=GRMZM2G092895'

'very weakly similar to (81.3) AT3G58070 | Symbols: GIS | GIS (GLABROUS INFLORESCENCE STEMS); nucleic acid binding / transcription factor/ zinc ion binding | chr3:21506845-21507606 REVERSEweakly similar to (136) loc_os06g10470 12006.m05765 protein zinc finger protein, putative seq=cds; coord=6:108970623..108971435:1; parent_gene=GRMZM2G016744'

'weakly similar to (173) AT4G30930 | Symbols: NFD1 | NFD1 (NUCLEAR FUSION DEFECTIVE 1); RNA binding / structural constituent of ribosome | chr4:15050170-15051630 REVERSEvery weakly similar to (90.9) RK21_SPIOL 50S ribosomal protein L21, chloroplast precursor (CL21) (CS-L7) - Spinacia oleracea (Spinach)moderately similar to (264) loc_os05g48410 12005.m08912 protein 50S ribosomal protein L21, mitochondrial precursor, putative, expressed seq=cds; coord=6:163857872..163860907:-1; parent_gene=GRMZM2G085675'

'weakly similar to (117) AT5G05550 | Symbols: | transcription factor | chr5:1639529-1640550 REVERSEmoderately similar to (332) loc_os05g48690 12005.m83935 protein 6b-interacting protein 1, putative, expressed seq=cds; coord=6:164197747..164199562:1; parent_gene=GRMZM2G157219'

'very weakly similar to (92.8) AT4G22220 | Symbols: ISU1, ATISU1 | ISU1; structural molecule | chr4:11759444-11760881 REVERSEvery weakly similar to (97.4) loc_os01g47340 12001.m42683 protein nifU-like N-terminal domain-containing protein, mitochondrial precursor, putative, expressed seq=cds; coord=6:165206126..165207222:1; parent_gene=GRMZM2G141252'

'moderately similar to (451) AT1G32450 | Symbols: NRT1.5 | NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter | chr1:11715337-11719807 REVERSEmoderately similar to (434) loc_os02g46460 12002.m09683 protein peptide transporter PTR2, putative, expressed seq=cds; coord=7:25089776..25092351:-1; parent_gene=GRMZM2G156794'

'moderately similar to (464) AT3G02875 | Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugat hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase | chr3:631993-633859 FORWARDhighly similar to (640) loc_os07g14590 12007.m05904 protein IAA-amino acid hydrolase ILR1 precursor, putative, expressed seq=cds; coord=7:25903581..25911265:1; parent_gene=GRMZM2G016958'

'weakly similar to (163) loc_os07g14580 12007.m05903 protein dcp1-like decapping family protein, expressed seq=cds; coord=7:26227531..26234488:-1; parent_gene=GRMZM2G144618'

'weakly similar to (108) loc_os07g23450 12007.m06624 protein zinc finger, C2H2 type family protein seq=cds; coord=7:35363274..35363582:1; parent_gene=GRMZM2G443109'

'very weakly similar to (94.7) AT1G29660 | Symbols: | GDSL-motif lipase/hydrolase family protein | chr1:10371955-10373624 FORWARDweakly similar to (159) loc_os06g50940 12006.m09618 protein anther-specific proline-rich protein APG precursor, putative, expressed seq=cds; coord=7:79970165..79972088:1; parent_gene=GRMZM2G101117'

'highly similar to (778) AT1G07650 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr1:2359817-2366423 REVERSEmoderately similar to (227) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)nearly identical (1044) loc_os09g17630 12009.m05021 protein receptor-like protein kinase 2, putative, expressed seq=cds; coord=7:94201889..94238627:1; parent_gene=GRMZM2G011526'

'moderately similar to (263) AT2G28970 | Symbols: | leucine-rich repeat protein kinase, putative | chr2:12443919-12448163 FORWARDmoderately similar to (206) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)moderately similar to (427) loc_os09g17910 12009.m05049 protein protein kinase, putative, expressed seq=cds; coord=7:95428215..95431847:-1; parent_gene=GRMZM2G354621'

'moderately similar to (330) AT1G54320 | Symbols: | LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein | chr1:20275732-20277793 REVERSEmoderately similar to (421) loc_os09g38768 12009.m060069 protein cell division control protein 50, putative, expressed seq=cds; coord=7:145214640..145217247:-1; parent_gene=GRMZM2G114704'

'weakly similar to (188) AT1G01750 | Symbols: ADF11 | ADF11 (ACTIN DEPOLYMERIZING FACTOR 11); actin binding | chr1:275528-276126 FORWARDmoderately similar to (251) ADF1_MAIZE Actin-depolymerizing factor 1 (ADF 1) (ZmABP1) (ZmADF1) - Zea mays (Maize)moderately similar to (211) loc_os07g30090 12007.m29171 protein actin-depolymerizing factor 1, putative, expressed seq=cds; coord=7:148879558..148880837:1; parent_gene=GRMZM2G117603'

'highly similar to (709) AT3G03050 | Symbols: CSLD3, KJK, ATCSLD3 | CSLD3 (CELLULOSE SYNTHASE-LIKE D3); cellulose synthase/ transferase, transferring glycosyl groups | chr3:687873-691629 FORWARDnearly identical (1295) loc_os07g36750 12007.m07925 protein CSLF3 - cellulose synthase-like family F; beta1,3;1,4 glucan synthase, expressed seq=cds; coord=7:156285428..156288692:1; parent_gene=GRMZM2G339645' 'moderately similar to (241) AT5G07680 | Symbols: ANAC080 | ANAC080 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 80); transcription factor | chr5:2436134-2437322 FORWARDmoderately similar to (230) NAC77_ORYSA NAC domain-containing protein 77 (ONAC077) (ONAC300) - Oryza sativa (Rice)moderately similar to (298) loc_os07g48550 12007.m09066 protein NAC domain-containing protein 21/22, putative, expressed seq=cds; coord=7:173738865..173740690:1; parent_gene=GRMZM2G181605'

'moderately similar to (361) DCOR_CAPAN Ornithine decarboxylase (EC 4.1.1.17) (ODC) (CaODC1) (CapODC) - Capsicum annuum (Bell pepper)highly similar to (547) loc_os09g37120 12009.m06660 protein ornithine decarboxylase, putative, expressed seq=cds; coord=7:175174284..175176025:1; parent_gene=GRMZM2G140824'

'moderately similar to (205) AT5G05140 | Symbols: | transcription elongation factor-related | chr5:1520353-1522297 FORWARDhighly similar to (598) loc_os05g34210 12005.m07652 protein expressed protein seq=cds; coord=8:104616112..104619975:1; parent_gene=GRMZM2G087451'

'highly similar to (523) AT5G58430 | Symbols: ATEXO70B1 | ATEXO70B1 (exocyst subunit EXO70 family protein B1); protein binding | chr5:23621460-23623334 REVERSEhighly similar to (998) loc_os05g39610 12005.m083752 protein protein binding protein, putative, expressed seq=cds; coord=8:118678684..118681299:-1; parent_gene=GRMZM2G065566'

'very weakly similar to (87.0) HD2C_MAIZE Histone deacetylase 2c (HD2c) (Zm-HD2c) - Zea mays (Maize)very weakly similar to (87.4) loc_os05g51830 12005.m09245 protein histone deacetylase 2b, putative, expressed seq=cds; coord=8:163180384..163182820:1; parent_gene=AC183950.2_FG003'

'highly similar to (518) AT5G14420 | Symbols: RGLG2 | RGLG2 (RING domain Ligase2); ubiquitin-protein ligase | chr5:4648355-4650563 REVERSEhighly similar to (614) loc_os01g68060 12001.m12910 protein copine-6, putative, expressed seq=cds; coord=8:163281489..163285589:1; parent_gene=GRMZM2G065893'

'highly similar to (518) AT5G14420 | Symbols: RGLG2 | RGLG2 (RING domain Ligase2); ubiquitin-protein ligase | chr5:4648355-4650563 REVERSEhighly similar to (614) loc_os01g68060 12001.m12910 protein copine-6, putative, expressed seq=cds; coord=8:163281489..163285589:1; parent_gene=GRMZM2G065893'

'highly similar to (518) AT5G14420 | Symbols: RGLG2 | RGLG2 (RING domain Ligase2); ubiquitin-protein ligase | chr5:4648355-4650563 REVERSEhighly similar to (614) loc_os01g68060 12001.m12910 protein copine-6, putative, expressed seq=cds; coord=8:163281489..163285589:1; parent_gene=GRMZM2G065893'

'moderately similar to (412) AT3G51270 | Symbols: | ATP binding / catalytic/ protein serine/threonine kinase | chr3:19033851-19036772 FORWARDmoderately similar to (450) loc_os01g66520 12001.m12760 protein serine/threonine-protein kinase RIO2, putative, expressed seq=cds; coord=8:164737739..164742218:1; parent_gene=GRMZM2G472991'

'moderately similar to (322) AT5G54630 | Symbols: | zinc finger protein-related | chr5:22192607-22194260 REVERSEhighly similar to (574) loc_os01g57650 12001.m11914 protein nucleic acid binding protein, putative, expressed seq=cds; coord=8:171805293..171810996:1; parent_gene=GRMZM2G139160' 'moderately similar to (322) AT5G54630 | Symbols: | zinc finger protein-related | chr5:22192607-22194260 REVERSEhighly similar to (574) loc_os01g57650 12001.m11914 protein nucleic acid binding protein, putative, expressed seq=cds; coord=8:171805293..171810996:1; parent_gene=GRMZM2G139160'

'moderately similar to (322) AT5G54630 | Symbols: | zinc finger protein-related | chr5:22192607-22194260 REVERSEhighly similar to (574) loc_os01g57650 12001.m11914 protein nucleic acid binding protein, putative, expressed seq=cds; coord=8:171805293..171810996:1; parent_gene=GRMZM2G139160'

'weakly similar to (172) AT4G39870 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TLDc (InterPro:IPR006571); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G05590.2); Has 2018 Blast hits to 1865 proteins in 220 species: Archae - 0; Bacteria - 39; Metazoa - 1002; Fungi - 279; Plants - 129; Viruses - 34; Other Eukaryotes - 535 (source: NCBI BLink). | chr4:18502234-18504275 FORWARDmoderately similar to (400) loc_os06g11790 12006.m32019 protein oxidation resistance protein 1, putative, expressed seq=cds; coord=9:6051948..6065049:1; parent_gene=GRMZM2G019291'

'moderately similar to (290) AT3G21350 | Symbols: | RNA polymerase transcriptional regulation mediator-related | chr3:7517106-7518587 FORWARDmoderately similar to (407) loc_os06g11370 12006.m05854 protein RNA polymerase transcriptional regulation mediator, subunit 6, putative, expressed seq=cds; coord=9:7177254..7182212:-1; parent_gene=GRMZM2G017537'

'moderately similar to (483) AT1G76680 | Symbols: OPR1, ATOPR1 | OPR1; 12-oxophytodienoate reductase | chr1:28776982-28778271 FORWARDhighly similar to (601) loc_os06g11290 12006.m05846 protein 12-oxophytodienoate reductase 2, putative, expressed seq=cds; coord=9:7308153..7309906:1; parent_gene=GRMZM2G000236'

'moderately similar to (483) AT1G76680 | Symbols: OPR1, ATOPR1 | OPR1; 12-oxophytodienoate reductase | chr1:28776982-28778271 FORWARDhighly similar to (601) loc_os06g11290 12006.m05846 protein 12-oxophytodienoate reductase 2, putative, expressed seq=cds; coord=9:7308153..7309906:1; parent_gene=GRMZM2G000236'

'very weakly similar to (100) AT2G22490 | Symbols: CYCD2;1, ATCYCD2;1 | CYCD2;1 (Cyclin D2;1); cyclin-dependent protein kinase regulator/ protein binding | chr2:9554157-9555873 REVERSEweakly similar to (136) loc_os03g27420 12003.m08069 protein retrotransposon protein, putative, unclassified seq=cds; coord=9:9398191..9400228:1; parent_gene=AC213896.2_FG005'

'very weakly similar to (100) AT2G22490 | Symbols: CYCD2;1, ATCYCD2;1 | CYCD2;1 (Cyclin D2;1); cyclin-dependent protein kinase regulator/ protein binding | chr2:9554157-9555873 REVERSEweakly similar to (136) loc_os03g27420 12003.m08069 protein retrotransposon protein, putative, unclassified seq=cds; coord=9:9398191..9400228:1; parent_gene=AC213896.2_FG005' 'moderately similar to (419) AT4G25160 | Symbols: | protein kinase family protein | chr4:12903360-12906669 REVERSEweakly similar to (129) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (580) loc_os06g04880 12006.m31972 protein ATP binding protein, putative, expressed seq=cds; coord=9:20824694..20826403:1; parent_gene=GRMZM2G433433'

'moderately similar to (419) AT4G25160 | Symbols: | protein kinase family protein | chr4:12903360-12906669 REVERSEweakly similar to (129) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (580) loc_os06g04880 12006.m31972 protein ATP binding protein, putative, expressed seq=cds; coord=9:20824694..20826403:1; parent_gene=GRMZM2G433433'

'moderately similar to (419) AT4G25160 | Symbols: | protein kinase family protein | chr4:12903360-12906669 REVERSEweakly similar to (129) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (580) loc_os06g04880 12006.m31972 protein ATP binding protein, putative, expressed seq=cds; coord=9:20824694..20826403:1; parent_gene=GRMZM2G433433'

'moderately similar to (237) AT2G46770 | Symbols: NST1, EMB2301, ANAC043 | EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor | chr2:19220917-19222822 REVERSEmoderately similar to (213) NAC76_ORYSA NAC domain-containing protein 76 (ONAC076) - Oryza sativa (Rice)moderately similar to (300) loc_os06g04090 12006.m05140 protein NAM protein, putative, expressed seq=cds; coord=9:23279027..23283429:-1; parent_gene=GRMZM2G171395'

'very weakly similar to (83.2) ATCG00740 | Symbols: RPOA | RNA polymerase alpha subunit | chrC:77901-78890 REVERSEvery weakly similar to (100) RPOA_SACOF DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (PEP) (Plastid-encoded RNA polymerase subunit alpha) (RNA polymerase subunit alpha) - Saccharum officinarum (Sugarcane)very weakly similar to (97.4) loc_os01g57944 12001.m97470 protein DNA-directed RNA polymerase alpha chain, putative, expressed seq=cds; coord=9:89546232..89546523:1; parent_gene=GRMZM2G570791'

'moderately similar to (285) AT1G02170 | Symbols: LOL3, ATMCPB1, MCP1B, AMC1, ATMC1 | AMC1 (METACASPASE 1); cysteine-type endopeptidase | chr1:411883-413426 FORWARDmoderately similar to (416) loc_os03g27170 12003.m08047 protein LOL3, putative, expressed seq=cds; coord=9:120413925..120416480:-1; parent_gene=GRMZM2G320206'

'moderately similar to (285) AT1G02170 | Symbols: LOL3, ATMCPB1, MCP1B, AMC1, ATMC1 | AMC1 (METACASPASE 1); cysteine-type endopeptidase | chr1:411883-413426 FORWARDmoderately similar to (416) loc_os03g27170 12003.m08047 protein LOL3, putative, expressed seq=cds; coord=9:120413925..120416480:-1; parent_gene=GRMZM2G320206'

'moderately similar to (224) AT1G07140 | Symbols: SIRANBP | SIRANBP; Ran GTPase binding | chr1:2192360-2193688 REVERSEmoderately similar to (290) loc_os03g18180 12003.m07243 protein ran-binding protein 1 homolog c, putative, expressed seq=cds; coord=9:137487958..137491564:1; parent_gene=GRMZM2G078933' 'moderately similar to (330) AT5G02100 | Symbols: UNE18, ORP3A | UNE18 (UNFERTILIZED EMBRYO SAC 18); oxysterol binding / sterol binding | chr5:413639-416016 FORWARDmoderately similar to (377) loc_os03g16690 12003.m07102 protein oxysterol-binding protein homolog C2F12.05c, putative, expressed seq=cds; coord=9:139762641..139765741:-1; parent_gene=GRMZM2G114126'

'weakly similar to (165) AT1G75050 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to other organism; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Thaumatin, conserved site (InterPro:IPR017949), Thaumatin, pathogenesis-related (InterPro:IPR001938); BEST Arabidopsis thaliana protein match is: ATLP-3 (TAIR:AT1G75030.1); Has 1070 Blast hits to 1056 proteins in 144 species: Archae - 0; Bacteria - 18; Metazoa - 48; Fungi - 48; Plants - 944; Viruses - 4; Other Eukaryotes - 8 (source: NCBI BLink). | chr1:28180116-28181062 FORWARDweakly similar to (116) TP1A_MALDO Thaumatin-like protein 1a precursor (Allergen Mal d 2) (Mdtl1) (Pathogenesis-related protein 5a) (PR-5a) - Malus domestica (Apple) (Malus sylvestris)moderately similar to (231) loc_os03g13070 12003.m06753 protein pathogenesis-related protein 5 precursor, putative seq=cds; coord=9:145169449..145170513:-1; parent_gene=GRMZM2G393507'

'weakly similar to (116) AT5G21430 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:7222294-7223400 FORWARDweakly similar to (178) loc_os12g31460 12012.m06955 protein heat shock protein binding protein, putative, expressed seq=cds; coord=10:18671024..18674301:1; parent_gene=GRMZM2G068316'

'highly similar to (677) AT1G62340 | Symbols: ALE1, ALE | ALE1 (ABNORMAL LEAF-SHAPE 1); serine-type endopeptidase | chr1:23051123-23055656 REVERSEhighly similar to (547) loc_os06g48650 12006.m091776 protein SLP3, putative, expressed seq=cds; coord=10:99522491..99525216:1; parent_gene=GRMZM2G157313'

'weakly similar to (115) AT2G21045 | Symbols: | INVOLVED IN: aging; EXPRESSED IN: hypocotyl, root; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66170.2); Has 1919 Blast hits to 1917 proteins in 542 species: Archae - 34; Bacteria - 1258; Metazoa - 17; Fungi - 21; Plants - 115; Viruses - 0; Other Eukaryotes - 474 (source: NCBI BLink). | chr2:9027858-9028805 FORWARDweakly similar to (102) DIN1_RAPSA Senescence-associated protein DIN1 - Raphanus sativus (Radish)weakly similar to (173) loc_os04g17660 12004.m35123 protein senescence-associated protein DIN1, putative, expressed seq=cds; coord=10:102318701..102320375:-1; parent_gene=AC204711.3_FG003'

'moderately similar to (347) AT3G60800 | Symbols: | zinc finger (DHHC type) family protein | chr3:22467486-22469273 REVERSEmoderately similar to (416) loc_os03g58960 12003.m35468 protein palmitoyltransferase ZDHHC20, putative, expressed seq=cds; coord=10:103198521..103217029:1; parent_gene=GRMZM2G001265'

'moderately similar to (370) AT5G13430 | Symbols: | ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative | chr5:4305414-4307399 REVERSEmoderately similar to (490) UCRI_MAIZE Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor (EC 1.10.2.2) (Rieske iron-sulfur protein) (RISP) - Zea mays (Maize)moderately similar to (451) loc_os04g32660 12004.m08364 protein ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor, putative, expressed seq=cds; coord=10:111776610..111779617:1; parent_gene=GRMZM2G023194' 'moderately similar to (220) AT4G31550 | Symbols: WRKY11, ATWRKY11 | WRKY11; calmodulin binding / transcription factor | chr4:15290065-15291458 REVERSEmoderately similar to (355) loc_os04g51560 12004.m10052 protein OsWRKY68 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=10:141270670..141272273:1; parent_gene=GRMZM2G091331'

'very weakly similar to (87.0) AT5G43320 | Symbols: ckl8 | ckl8 (Casein Kinase I-like 8); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr5:17386043-17388941 REVERSEvery weakly similar to (93.2) loc_os02g56560 12002.m77862 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=10:143454604..143458499:-1; parent_gene=GRMZM2G148506'

'highly similar to (765) AT5G20990 | Symbols: B73, SIR4, CNX, CHL6, CNX1 | B73; molybdenum ion binding | chr5:7128737-7133397 REVERSEhighly similar to (696) loc_os04g56620 12004.m101683 protein molybdopterin biosynthesis CNX1 protein, putative, expressed seq=cds; coord=10:146668953..146673272:1; parent_gene=GRMZM2G067176'

'highly similar to (565) AT5G05780 | Symbols: RPN8A, AE3, ATHMOV34 | RPN8A (RP NON-ATPASE SUBUNIT 8A) | chr5:1735862-1738176 FORWARDmoderately similar to (260) loc_os04g56646 12004.m10553 protein expressed protein seq=cds; coord=10:146681843..146686842:1; parent_gene=GRMZM2G368908'

'highly similar to (508) AT3G48990 | Symbols: | AMP-dependent synthetase and ligase family protein | chr3:18159031-18161294 REVERSEweakly similar to (128) 4CL1_TOBAC 4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1) - Nicotiana tabacum (Common tobacco)highly similar to (606) loc_os04g58710 12004.m35525 protein peroxisomal-coenzyme A synthetase, putative, expressed seq=cds; coord=10:148627784..148629933:-1; parent_gene=GRMZM2G074759'

'weakly similar to (179) AT2G17700 | Symbols: | protein kinase family protein | chr2:7685778-7689278 REVERSEmoderately similar to (332) loc_os04g59000 12004.m10778 protein ATP binding protein, putative, expressed seq=cds; coord=10:148977449..148980886:-1; parent_gene=GRMZM2G104658'

'moderately similar to (297) AT1G76920 | Symbols: | F-box family protein (FBX3) | chr1:28892295-28893419 FORWARDweakly similar to (104) loc_os04g59010 12004.m10779 protein F-box domain containing protein, expressed seq=cds; coord=10:148984717..148986879:-1; parent_gene=GRMZM2G104882'

'moderately similar to (354) AT2G46950 | Symbols: CYP709B2 | CYP709B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr2:19289466-19291541 REVERSEmoderately similar to (296) C72A1_CATRO Cytochrome P450 72A1 (EC 1.3.3.9) (CYPLXXII) (Secologanin synthase) (SLS) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)moderately similar to (434) loc_os01g24780 12001.m08944 protein cytochrome P450 72A1, putative, expressed seq=cds; coord=1:64148065..64150545:1; parent_gene=GRMZM2G084407' 'weakly similar to (187) AT1G47290 | Symbols: AT3BETAHSD/D1 | AT3BETAHSD/D1 (3BETA-HYDROXYSTEROID-DEHYDROGENASE/DECARBOXYLASE ISOFORM 1); 3-beta-hydroxy-delta5-steroid dehydrogenase/ sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) | chr1:17336121-17339030 FORWARDmoderately similar to (389) loc_os07g27470 12007.m07022 protein transposon protein, putative, CACTA, En/Spm sub-class seq=cds; coord=1:70041332..70063271:1; parent_gene=GRMZM2G009435'

'weakly similar to (194) AT3G02550 | Symbols: LBD41 | LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41) | chr3:536747-537650 REVERSEmoderately similar to (226) loc_os01g32770 12001.m09596 protein seed specific protein Bn15D17A, putative, expressed seq=cds; coord=1:72351668..72352962:-1; parent_gene=GRMZM2G060544'

'highly similar to (653) AT1G18580 | Symbols: GAUT11 | GAUT11 (Galacturonosyltransferase 11); polygalacturonate 4-alpha-galacturonosyltransferase | chr1:6396144-6398005 FORWARDhighly similar to (881) loc_os03g30000 12003.m08261 protein transferase, transferring glycosyl groups, putative, expressed seq=cds; coord=1:72799953..72805415:-1; parent_gene=AC177908.3_FG002'

'moderately similar to (472) AT5G16120 | Symbols: | hydrolase, alpha/beta fold family protein | chr5:5265820-5267775 FORWARDhighly similar to (629) loc_os10g04620 12010.m21823 protein catalytic/ hydrolase, putative, expressed seq=cds; coord=1:115405246..115408968:1; parent_gene=GRMZM2G110198'

'moderately similar to (225) AT5G58420 | Symbols: | 40S ribosomal protein S4 (RPS4D) | chr5:23619599-23620896 FORWARDmoderately similar to (243) RS4_MAIZE 40S ribosomal protein S4 - Zea mays (Maize)moderately similar to (234) loc_os02g01560 12002.m05506 protein 40S ribosomal protein S4, putative, expressed seq=cds; coord=1:127558173..127560554:1; parent_gene=GRMZM2G159228'

'highly similar to (619) AT1G53730 | Symbols: SRF6 | SRF6 (STRUBBELIG-RECEPTOR FAMILY 6); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase | chr1:20061771-20065475 FORWARDweakly similar to (170) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (932) loc_os10g25090 12010.m05459 protein leucine-rich repeat transmembrane protein kinase 1, putative, expressed seq=cds; coord=1:141071460..141076910:-1; parent_gene=GRMZM2G004572'

'weakly similar to (189) AT1G10030 | Symbols: ERG28 | ERG28 (Arabidopsis homolog of yeast ergosterol28) | chr1:3273972-3275631 FORWARDmoderately similar to (222) loc_os12g43670 12012.m08141 protein erg28 like protein, expressed seq=cds; coord=1:179962460..179965637:1; parent_gene=GRMZM2G093828'

'moderately similar to (278) AT4G08150 | Symbols: KNAT1, BP, BP1 | KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor | chr4:5147969-5150610 REVERSEmoderately similar to (333) RSH1_MAIZE Homeobox protein rough sheath 1 - Zea mays (Maize)moderately similar to (332) loc_os07g03770 12007.m04847 protein homeobox protein rough sheath 1, putative, expressed seq=cds; coord=1:281820159..281827144:1; parent_gene=GRMZM2G135447' 'moderately similar to (298) AT2G17380 | Symbols: AP19 | AP19; protein binding / protein transporter | chr2:7553122-7554887 FORWARDweakly similar to (158) AP2S1_MAIZE AP-2 complex subunit sigma-1 (Clathrin coat assembly protein AP17) (Clathrin coat-associated protein AP17) (Plasma membrane adaptor AP-2 17 kDa protein) (Clathrin assembly protein 2 small chain) - Zea mays (Maize)moderately similar to (319) loc_os03g57040 12003.m78897 protein AP-1 complex subunit sigma-2, putative, expressed seq=cds; coord=1:285060087..285064322:-1; parent_gene=GRMZM2G361220'

'moderately similar to (298) AT2G17380 | Symbols: AP19 | AP19; protein binding / protein transporter | chr2:7553122-7554887 FORWARDweakly similar to (158) AP2S1_MAIZE AP-2 complex subunit sigma-1 (Clathrin coat assembly protein AP17) (Clathrin coat-associated protein AP17) (Plasma membrane adaptor AP-2 17 kDa protein) (Clathrin assembly protein 2 small chain) - Zea mays (Maize)moderately similar to (319) loc_os03g57040 12003.m78897 protein AP-1 complex subunit sigma-2, putative, expressed seq=cds; coord=1:285060087..285064322:-1; parent_gene=GRMZM2G361220'

'moderately similar to (298) AT2G17380 | Symbols: AP19 | AP19; protein binding / protein transporter | chr2:7553122-7554887 FORWARDweakly similar to (158) AP2S1_MAIZE AP-2 complex subunit sigma-1 (Clathrin coat assembly protein AP17) (Clathrin coat-associated protein AP17) (Plasma membrane adaptor AP-2 17 kDa protein) (Clathrin assembly protein 2 small chain) - Zea mays (Maize)moderately similar to (319) loc_os03g57040 12003.m78897 protein AP-1 complex subunit sigma-2, putative, expressed seq=cds; coord=1:285060087..285064322:-1; parent_gene=GRMZM2G361220'

'highly similar to (607) AT1G30510 | Symbols: ATRFNR2 | ATRFNR2 (ROOT FNR 2); FAD binding / NADP or NADPH binding / electron carrier/ ferredoxin-NADP

'moderately similar to (344) AT3G18620 | Symbols: | zinc finger (DHHC type) family protein | chr3:6408849-6410716 FORWARDhighly similar to (597) loc_os06g20400 12006.m31797 protein DHHC zinc finger domain containing protein, expressed seq=cds; coord=2:1971151..1974602:-1; parent_gene=GRMZM2G068177'

'moderately similar to (358) AT3G19850 | Symbols: | phototropic-responsive NPH3 family protein | chr3:6898383-6901157 REVERSEweakly similar to (109) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)highly similar to (691) loc_os04g57800 12004.m10665 protein photoreceptor-interacting protein-like, putative, expressed seq=cds; coord=2:2034098..2037473:1; parent_gene=GRMZM2G040115'

'highly similar to (687) AT5G37020 | Symbols: ARF8 | ARF8 (AUXIN RESPONSE FACTOR 8); transcription factor | chr5:14630151-14633916 FORWARDnearly identical (1283) loc_os04g57610 12004.m35224 protein auxin response factor 8, putative, expressed seq=cds; coord=2:2266715..2274671:1; parent_gene=GRMZM2G078274'

'highly similar to (504) AT5G55280 | Symbols: FTSZ1-1, ATFTSZ1-1, CPFTSZ | FTSZ1-1; protein binding / structural molecule | chr5:22420740-22422527 REVERSEhighly similar to (571) loc_os04g56970 12004.m35221 protein cell division protein ftsZ homolog, chloroplast precursor, putative, expressed seq=cds; coord=2:3176470..3180187:1; parent_gene=GRMZM2G119773'

'nearly identical (1071) AT1G76950 | Symbols: PRAF1 | PRAF1; Ran GTPase binding / chromatin binding / zinc ion binding | chr1:28906952-28911325 FORWARDnearly identical (1565) loc_os04g58960 12004.m10775 protein ran GTPase binding protein, putative, expressed seq=cds; coord=2:24030713..24037024:-1; parent_gene=GRMZM2G124371' 'nearly identical (1071) AT1G76950 | Symbols: PRAF1 | PRAF1; Ran GTPase binding / chromatin binding / zinc ion binding | chr1:28906952-28911325 FORWARDnearly identical (1565) loc_os04g58960 12004.m10775 protein ran GTPase binding protein, putative, expressed seq=cds; coord=2:24030713..24037024:-1; parent_gene=GRMZM2G124371'

'weakly similar to (181) AT1G21140 | Symbols: | nodulin, putative | chr1:7404464-7405066 FORWARDweakly similar to (125) NO21_SOYBN Nodulin 21 (N-21) - Glycine max (Soybean)moderately similar to (204) loc_os04g59020 12004.m10780 protein integral membrane protein, expressed seq=cds; coord=2:24387828..24389072:1; parent_gene=GRMZM2G434557'

'weakly similar to (133) AT3G44260 | Symbols: | CCR4-NOT transcription complex protein, putative | chr3:15952213-15953055 REVERSEmoderately similar to (209) loc_os10g03530 12010.m03770 protein CCR4-NOT transcription complex subunit 7, putative seq=cds; coord=2:24450176..24451317:-1; parent_gene=GRMZM2G064124'

'moderately similar to (261) AT1G71930 | Symbols: VND7, ANAC030 | VND7 (VASCULAR RELATED NAC-DOMAIN PROTEIN 7); transcription activator/ transcription factor/ transcription regulator | chr1:27076205-27077829 FORWARDmoderately similar to (212) NAC76_ORYSA NAC domain-containing protein 76 (ONAC076) - Oryza sativa (Rice)moderately similar to (304) loc_os08g01330 12008.m04282 protein ANAC030, putative, expressed seq=cds; coord=2:25745084..25746893:-1; parent_gene=AC212859.3_FG008'

'moderately similar to (261) AT1G71930 | Symbols: VND7, ANAC030 | VND7 (VASCULAR RELATED NAC-DOMAIN PROTEIN 7); transcription activator/ transcription factor/ transcription regulator | chr1:27076205-27077829 FORWARDmoderately similar to (212) NAC76_ORYSA NAC domain-containing protein 76 (ONAC076) - Oryza sativa (Rice)moderately similar to (304) loc_os08g01330 12008.m04282 protein ANAC030, putative, expressed seq=cds; coord=2:25745084..25746893:-1; parent_gene=AC212859.3_FG008'

'moderately similar to (376) AT3G52210 | Symbols: | mRNA capping enzyme family protein | chr3:19367035-19369293 FORWARDhighly similar to (541) MCES2_ORYSA mRNA cap guanine-N7 methyltransferase 2 (EC 2.1.1.56) (mRNA (guanine-N(7)-)-methyltransferase 2) (mRNA cap methyltransferase 2) - Oryza sativa (Rice)highly similar to (541) loc_os02g54000 12002.m10429 protein S-adenosylmethionine-dependent methyltransferase/ catalytic, putative, expressed seq=cds; coord=2:26771301..26774601:-1; parent_gene=GRMZM2G171410'

'moderately similar to (207) AT5G23230 | Symbols: NIC2 | NIC2 (NICOTINAMIDASE 2); catalytic/ nicotinamidase | chr5:7826005-7826601 REVERSEmoderately similar to (330) loc_os04g44420 12004.m09401 protein isochorismatase, putative, expressed seq=cds; coord=2:26875237..26876162:1; parent_gene=GRMZM2G362413'

'highly similar to (547) AT1G22360 | Symbols: AtUGT85A2 | AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups | chr1:7895068-7897527 REVERSEweakly similar to (200) IAAG_MAIZE Indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) (IAA-Glu synthetase) ((Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase) - Zea mays (Maize)highly similar to (806) loc_os04g37820 12004.m08771 protein cytokinin-O-glucosyltransferase 2, putative, expressed seq=cds; coord=2:43708019..43710470:-1; parent_gene=GRMZM2G009125' 'weakly similar to (145) AT1G77490 | Symbols: TAPX | TAPX (THYLAKOIDAL ASCORBATE PEROXIDASE); L-ascorbate peroxidase | chr1:29117688-29120046 FORWARDweakly similar to (161) APX6_ORYSA Probable L-ascorbate peroxidase 6, chloroplast precursor (EC 1.11.1.11) (OsAPx06) - Oryza sativa (Rice)weakly similar to (161) loc_os12g07820 12012.m04769 protein OsAPx6 - Stromal Ascorbate Peroxidase encoding gene, expressed seq=cds; coord=2:178407364..178411287:-1; parent_gene=GRMZM2G557799'

'moderately similar to (383) AT3G05840 | Symbols: ATSK12 | ATSK12; protein kinase/ protein serine/threonine kinase | chr3:1740793-1742927 FORWARDmoderately similar to (384) MSK3_MEDSA Glycogen synthase kinase-3 homolog MsK-3 (EC 2.7.11.1) - Medicago sativa (Alfalfa)moderately similar to (410) loc_os01g14860 12001.m43459 protein glycogen synthase kinase-3 homolog MsK-3, putative, expressed seq=cds; coord=3:13917982..13919834:-1; parent_gene=GRMZM2G129482'

'highly similar to (580) AT5G02310 | Symbols: PRT6 | PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase | chr5:474279-482552 FORWARDnearly identical (1182) loc_os01g05500 12001.m42863 protein zinc finger in N-recognin family protein, putative, expressed seq=cds; coord=3:17635017..17643029:-1; parent_gene=GRMZM2G438938'

'weakly similar to (152) AT1G53540 | Symbols: | 17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156) | chr1:19980510-19980983 FORWARDweakly similar to (179) HSP11_ORYSA 16.9 kDa class I heat shock protein 1 - Oryza sativa (Rice)weakly similar to (179) loc_os01g04370 12001.m07072 protein 16.9 kDa class I heat shock protein 1, putative, expressed seq=cds; coord=3:20425735..20426696:-1; parent_gene=GRMZM2G437100'

'moderately similar to (291) AT3G03440 | Symbols: | armadillo/beta-catenin repeat family protein | chr3:815709-818568 FORWARDmoderately similar to (412) loc_os01g02200 12001.m06862 protein ubiquitin-protein ligase, putative, expressed seq=cds; coord=3:28221287..28223015:1; parent_gene=AC183315.4_FG006'

'weakly similar to (115) AT2G34840 | Symbols: | coatomer protein epsilon subunit family protein / COPE family protein | chr2:14702932-14704165 FORWARDweakly similar to (135) loc_os04g52270 12004.m10122 protein coatomer subunit epsilon, putative, expressed seq=cds; coord=3:146776926..146781146:-1; parent_gene=GRMZM2G016368'

'highly similar to (684) AT2G38110 | Symbols: ATGPAT6, GPAT6 | GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase | chr2:15952816-15955364 REVERSEhighly similar to (835) loc_os01g63580 12001.m12474 protein glycerol-3-phosphate acyltransferase 8, putative, expressed seq=cds; coord=3:178181704..178185282:1; parent_gene=GRMZM2G083195'

'highly similar to (505) AT1G53240 | Symbols: | malate dehydrogenase (NAD), mitochondrial | chr1:19854966-19856802 REVERSEhighly similar to (508) MDHM_FRAAN Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Fragaria ananassa (Strawberry)highly similar to (587) loc_os01g46070 12001.m10806 protein malate dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=3:213896741..213905427:1; parent_gene=GRMZM2G466833'

'moderately similar to (245) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (340) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215466579..215473931:-1; parent_gene=GRMZM2G121878'

'moderately similar to (245) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (340) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215466579..215473931:-1; parent_gene=GRMZM2G121878'

'moderately similar to (357) AT5G14260 | Symbols: | SET domain-containing protein | chr5:4601139-4603873 FORWARDmoderately similar to (451) loc_os12g13460 12012.m05319 protein SET domain containing protein, expressed seq=cds; coord=3:215527347..215532128:-1; parent_gene=GRMZM2G047695'

'weakly similar to (183) AT3G27810 | Symbols: ATMYB21, ATMYB3, MYB21 | ATMYB21 (ARABIDOPSIS THALIANA MYB DOMAIN PROTEIN 21); DNA binding / transcription factor | chr3:10307596-10310093 FORWARDweakly similar to (148) MYBA2_ORYSA Myb-related protein MYBAS2 - Oryza sativa (Rice)moderately similar to (218) loc_os01g45090 12001.m10715 protein transcription factor MYB21, putative, expressed seq=cds; coord=3:215849697..215850742:-1; parent_gene=GRMZM2G143328'

'weakly similar to (183) AT3G27810 | Symbols: ATMYB21, ATMYB3, MYB21 | ATMYB21 (ARABIDOPSIS THALIANA MYB DOMAIN PROTEIN 21); DNA binding / transcription factor | chr3:10307596-10310093 FORWARDweakly similar to (148) MYBA2_ORYSA Myb-related protein MYBAS2 - Oryza sativa (Rice)moderately similar to (218) loc_os01g45090 12001.m10715 protein transcription factor MYB21, putative, expressed seq=cds; coord=3:215849697..215850742:-1; parent_gene=GRMZM2G143328'

'moderately similar to (494) AT3G14680 | Symbols: CYP72A14 | CYP72A14; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr3:4934478-4936462 FORWARDmoderately similar to (448) C72A1_CATRO Cytochrome P450 72A1 (EC 1.3.3.9) (CYPLXXII) (Secologanin synthase) (SLS) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)highly similar to (776) loc_os01g43844 12001.m97528 protein cytochrome P450 72A1, putative, expressed seq=cds; coord=3:216986019..216989235:-1; parent_gene=GRMZM2G370745'

'weakly similar to (178) AT3G24520 | Symbols: AT-HSFC1, HSFC1 | AT-HSFC1; DNA binding / transcription factor | chr3:8941455-8942531 FORWARDmoderately similar to (332) loc_os01g43590 12001.m42682 protein heat shock factor protein HSF8, putative, expressed seq=cds; coord=3:217357921..217359731:-1; parent_gene=GRMZM2G089525'

'very weakly similar to (100) AT3G06190 | Symbols: ATBPM2, BPM2 | BPM2 (BTB-POZ AND MATH DOMAIN 2); protein binding | chr3:1874577-1876575 REVERSEweakly similar to (144) loc_os08g13000 12008.m05427 protein speckle-type POZ protein, putative seq=cds; coord=4:25991768..25992949:-1; parent_gene=GRMZM2G026724'

'weakly similar to (146) AT1G74700 | Symbols: NUZ, TRZ1 | TRZ1 (TRNASE Z 1); 3'-tRNA processing endoribonuclease | chr1:28065345-28067130 FORWARDweakly similar to (192) RNZN_WHEAT Nuclear ribonuclease Z (EC 3.1.26.11) (RNase Z) (tRNase Z) (tRNA 3 endonuclease) (Zinc phosphodiesterase ELAC) (Fragment) - Triticum aestivum (Wheat)weakly similar to (181) loc_os02g12290 12002.m06477 protein nuclear ribonuclease Z, putative seq=cds; coord=4:33914057..33918460:-1; parent_gene=GRMZM2G394747' 'moderately similar to (473) AT3G20740 | Symbols: FIE, FIS3, FIE1 | FIE (FERTILIZATION-INDEPENDENT ENDOSPERM); nucleotide binding / transcription factor/ transcription regulator | chr3:7249064-7252254 REVERSEhighly similar to (847) FIE1_MAIZE Polycomb group protein FIE1 (FERTILIZATION-INDEPENDENT ENDOSPERM 1) - Zea mays (Maize)highly similar to (567) loc_os08g04270 12008.m26569 protein polycomb group protein FIE2, putative, expressed seq=cds; coord=4:35757180..35763186:-1; parent_gene=GRMZM2G118205'

'weakly similar to (118) loc_os08g03590 12008.m04503 protein expressed protein seq=cds; coord=4:36308276..36310775:1; parent_gene=GRMZM2G390489'

'moderately similar to (263) AT3G18430 | Symbols: | calcium-binding EF hand family protein | chr3:6326180-6327476 FORWARDmoderately similar to (317) loc_os02g55880 12002.m10612 protein calcineurin subunit B, putative, expressed seq=cds; coord=4:173371823..173374012:-1; parent_gene=GRMZM2G125838'

'moderately similar to (399) AT1G77800 | Symbols: | PHD finger family protein | chr1:29253800-29260190 FORWARDhighly similar to (842) loc_os02g52960 12002.m10326 protein PHD-finger family protein, expressed seq=cds; coord=4:178229465..178238103:1; parent_gene=GRMZM2G475583'

'weakly similar to (150) loc_os02g52990 12002.m10329 protein OsSAUR12 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=4:178244180..178245465:1; parent_gene=GRMZM2G475683'

'weakly similar to (190) AT2G22540 | Symbols: SVP, AGL22 | SVP (SHORT VEGETATIVE PHASE); transcription factor/ translation repressor, nucleic acid binding | chr2:9580417-9583603 FORWARDmoderately similar to (308) MAD22_ORYSA MADS-box transcription factor 22 (OsMADS22) - Oryza sativa (Rice)moderately similar to (308) loc_os02g52340 12002.m10265 protein MADS-box transcription factor 22, putative, expressed seq=cds; coord=4:178887359..178894404:-1; parent_gene=GRMZM2G370777'

'weakly similar to (140) AT5G38280 | Symbols: PR5K | PR5K; kinase/ transmembrane receptor protein serine/threonine kinase | chr5:15293325-15295838 REVERSEvery weakly similar to (94.4) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (270) loc_os01g02730 12001.m06913 protein TAK14, putative, expressed seq=cds; coord=5:167603689..167605451:-1; parent_gene=GRMZM2G496370'

'weakly similar to (105) AT4G39070 | Symbols: | zinc finger (B-box type) family protein | chr4:18205061-18206421 REVERSEweakly similar to (141) loc_os02g43170 12002.m09352 protein salt tolerance-like protein, putative, expressed seq=cds; coord=5:190052115..190053687:1; parent_gene=GRMZM2G110541'

'moderately similar to (329) AT1G69530 | Symbols: ATEXPA1, EXP1, AT-EXP1, ATEXP1, ATHEXP ALPHA 1.2 | ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1) | chr1:26142034-26143200 FORWARDmoderately similar to (395) EXPA5_ORYSA Expansin-A5 precursor (OsEXPA5) (Alpha-expansin-5) (OsEXP5) (OsaEXPa1.20) - Oryza sativa (Rice)moderately similar to (395) loc_os02g51040 12002.m10138 protein alpha-expansin 15 precursor, putative, expressed seq=cds; coord=5:206838596..206840547:1; parent_gene=GRMZM2G105844'

'moderately similar to (329) AT1G69530 | Symbols: ATEXPA1, EXP1, AT-EXP1, ATEXP1, ATHEXP ALPHA 1.2 | ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1) | chr1:26142034-26143200 FORWARDmoderately similar to (395) EXPA5_ORYSA Expansin-A5 precursor (OsEXPA5) (Alpha-expansin-5) (OsEXP5) (OsaEXPa1.20) - Oryza sativa (Rice)moderately similar to (395) loc_os02g51040 12002.m10138 protein alpha-expansin 15 precursor, putative, expressed seq=cds; coord=5:206838596..206840547:1; parent_gene=GRMZM2G105844'

'moderately similar to (330) AT1G26870 | Symbols: FEZ, ANAC009 | FEZ (FEZ); transcription factor | chr1:9312856-9314983 FORWARDweakly similar to (194) NAC68_ORYSA NAC domain-containing protein 68 (ONAC068) - Oryza sativa (Rice)moderately similar to (338) loc_os08g33910 12008.m07381 protein NAC domain-containing protein 9, putative, expressed seq=cds; coord=5:206975367..206978937:1; parent_gene=GRMZM2G100593'

'weakly similar to (140) AT5G27420 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:9684119-9685225 FORWARDvery weakly similar to (83.2) EL5_ORYSA E3 ubiquitin-protein ligase EL5 (EC 6.3.2.-) - Oryza sativa (Rice)moderately similar to (263) loc_os02g52210 12002.m10252 protein RING/C3HC4/PHD zinc finger-like protein, putative, expressed seq=cds; coord=5:208925097..208929323:1; parent_gene=GRMZM2G323013'

'weakly similar to (192) AT5G64350 | Symbols: FKBP12, ATFKBP12 | FKBP12 (FK506-BINDING PROTEIN); FK506 binding / peptidyl-prolyl cis-trans isomerase | chr5:25734810-25735990 REVERSEmoderately similar to (201) FKB12_VICFA Peptidyl-prolyl isomerase FKBP12 (EC 5.2.1.8) (12 kDa FK506-binding protein) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) - Vicia faba (Broad bean)moderately similar to (218) loc_os02g52290 12002.m10260 protein peptidyl-prolyl isomerase FKBP12, putative, expressed seq=cds; coord=5:209262549..209264524:-1; parent_gene=GRMZM2G015784'

'weakly similar to (196) AT2G24060 | Symbols: | translation initiation factor 3 (IF-3) family protein | chr2:10229453-10231390 FORWARDmoderately similar to (310) loc_os02g55120 12002.m10538 protein translation initiation factor IF-3, chloroplast precursor, putative, expressed seq=cds; coord=5:213363147..213366325:-1; parent_gene=GRMZM2G119691'

'moderately similar to (251) AT1G09390 | Symbols: | GDSL-motif lipase/hydrolase family protein | chr1:3031264-3033415 FORWARDweakly similar to (167) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)moderately similar to (341) loc_os01g22640 12001.m08743 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=6:125457786..125459555:1; parent_gene=GRMZM2G150187'

'moderately similar to (251) AT1G09390 | Symbols: | GDSL-motif lipase/hydrolase family protein | chr1:3031264-3033415 FORWARDweakly similar to (167) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)moderately similar to (341) loc_os01g22640 12001.m08743 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=6:125457786..125459555:1; parent_gene=GRMZM2G150187'

'weakly similar to (185) loc_os05g45460 12005.m08671 protein pistil-specific extensin-like protein precursor, putative, expressed seq=cds; coord=6:159464252..159465528:-1; parent_gene=GRMZM2G040517' 'weakly similar to (110) loc_os07g18990 12007.m06338 protein PVR3-like protein, putative, expressed seq=cds; coord=7:31086409..31087079:1; parent_gene=GRMZM2G000221'

'weakly similar to (119) AT5G63530 | Symbols: ATFP3, FP3 | ATFP3; metal ion binding / transition metal ion binding | chr5:25433423-25435614 FORWARDweakly similar to (198) loc_os07g20340 12007.m29133 protein ATFP3, putative, expressed seq=cds; coord=7:33007300..33009101:-1; parent_gene=GRMZM2G042692'

'weakly similar to (139) AT4G10200 | Symbols: | hAT dimerisation domain-containing protein / transposase-related | chr4:6353172-6355591 FORWARDmoderately similar to (288) loc_os02g14150 12002.m06661 protein transposon protein, putative, Ac/Ds sub-class seq=cds; coord=7:33279781..33282007:-1; parent_gene=GRMZM2G364697'

'very weakly similar to (99.0) AT5G41010 | Symbols: NRPB12, NRPD12, NRPE12 | NRPB12; DNA binding / DNA-directed RNA polymerase | chr5:16424050-16424921 FORWARDweakly similar to (115) loc_os01g34614 12001.m150942 protein DNA-directed RNA polymerases I, II, and III 7.3 kDa polypeptide, putative, expressed seq=cds; coord=7:40571562..40582802:-1; parent_gene=GRMZM2G146331'

'nearly identical (1088) AT5G56030 | Symbols: HSP81-2, ERD8, HSP90.2 | HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding | chr5:22686923-22689433 FORWARDnearly identical (1142) HSP81_ORYSA Heat shock protein 81-1 (HSP81-1) (Heat shock protein 82) - Oryza sativa (Rice)nearly identical (1142) loc_os08g39140 12008.m080203 protein heat shock protein 81-1, putative, expressed seq=cds; coord=7:131783728..131787563:1; parent_gene=GRMZM2G069651'

'highly similar to (567) AT5G15550 | Symbols: | transducin family protein / WD-40 repeat family protein | chr5:5059315-5062003 REVERSEhighly similar to (751) loc_os07g40930 12007.m08333 protein WD-repeat protein 12, putative, expressed seq=cds; coord=7:163610898..163623823:-1; parent_gene=GRMZM2G050501'

'highly similar to (668) AT3G18080 | Symbols: BGLU44 | BGLU44 (B-S GLUCOSIDASE 44); (R)-amygdalin beta-glucosidase/ 4-methylumbelliferyl-beta-D-glucopyranoside beta-glucosidase/ beta-gentiobiose beta-glucosidase/ cellobiose glucosidase/ esculin beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds | chr3:6191586-6194124 FORWARDmoderately similar to (350) BGLC_MAIZE Beta-glucosidase, chloroplast precursor (EC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucoside glucohydrolase) - Zea mays (Maize)highly similar to (773) loc_os01g32364 12001.m09560 protein non-cyanogenic beta-glucosidase precursor, putative, expressed seq=cds; coord=8:8302750..8305316:-1; parent_gene=AC234160.1_FG003'

'highly similar to (550) AT3G51160 | Symbols: MUR1, MUR_1, GMD2 | MUR1 (MURUS 1); GDP-mannose 4,6-dehydratase | chr3:19007232-19008353 REVERSEhighly similar to (639) loc_os06g04620 12006.m05192 protein GDP-mannose 4,6 dehydratase 2, putative, expressed seq=cds; coord=9:21726160..21727733:1; parent_gene=GRMZM2G115124'

'very weakly similar to (99.8) AT1G62290 | Symbols: | aspartyl protease family protein | chr1:23010107-23012681 REVERSEweakly similar to (141) ASPRX_ORYSA Aspartic proteinase precursor (EC 3.4.23.-) - Oryza sativa (Rice)weakly similar to (141) loc_os05g04630 12005.m27692 protein retrotransposon protein, putative, SINE subclass, expressed seq=cds; coord=9:21803822..21808911:1; parent_gene=GRMZM2G144440' 'moderately similar to (237) AT2G46770 | Symbols: NST1, EMB2301, ANAC043 | EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor | chr2:19220917-19222822 REVERSEmoderately similar to (213) NAC76_ORYSA NAC domain-containing protein 76 (ONAC076) - Oryza sativa (Rice)moderately similar to (300) loc_os06g04090 12006.m05140 protein NAM protein, putative, expressed seq=cds; coord=9:23279027..23283429:-1; parent_gene=GRMZM2G171395'

'weakly similar to (174) AT2G35540 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:14927158-14928930 FORWARDmoderately similar to (415) loc_os06g02170 12006.m091578 protein heat shock protein binding protein, putative, expressed seq=cds; coord=9:26548872..26550670:1; parent_gene=GRMZM2G152373'

'weakly similar to (160) AT1G25682 | Symbols: | cell cycle control protein-related | chr1:9002532-9004550 REVERSEweakly similar to (184) loc_os02g21880 12002.m33662 protein coiled-coil domain-containing protein 94, putative, expressed seq=cds; coord=10:144130489..144133047:1; parent_gene=GRMZM2G366270'

'weakly similar to (147) AT1G02065 | Symbols: SPL8 | SPL8 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 8); DNA binding | chr1:365625-367149 FORWARDhighly similar to (503) LG1_MAIZE LIGULELESS1 protein - Zea mays (Maize)moderately similar to (463) loc_os04g56170 12004.m10508 protein LIGULELESS1 protein, putative, expressed seq=cds; coord=10:146291533..146295099:-1; parent_gene=GRMZM2G058588'

'weakly similar to (172) AT5G22250 | Symbols: | CCR4-NOT transcription complex protein, putative | chr5:7365605-7366441 REVERSEmoderately similar to (209) loc_os04g58810 12004.m10761 protein CCR4-NOT transcription complex subunit 8, putative, expressed seq=cds; coord=10:148762274..148766456:1; parent_gene=GRMZM2G177340'

'highly similar to (598) AT1G80560 | Symbols: | 3-isopropylmalate dehydrogenase, chloroplast, putative | chr1:30287833-30290126 FORWARDhighly similar to (605) LEU3_BRANA 3-isopropylmalate dehydrogenase, chloroplast precursor (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH) - Brassica napus (Rape)highly similar to (683) loc_os03g45320 12003.m101427 protein 3-isopropylmalate dehydrogenase 2, chloroplast precursor, putative, expressed seq=cds; coord=10:148968847..148972562:1; parent_gene=GRMZM2G104613'

'moderately similar to (297) AT1G76920 | Symbols: | F-box family protein (FBX3) | chr1:28892295-28893419 FORWARDweakly similar to (104) loc_os04g59010 12004.m10779 protein F-box domain containing protein, expressed seq=cds; coord=10:148984717..148986879:-1; parent_gene=GRMZM2G104882'

'moderately similar to (297) AT1G76920 | Symbols: | F-box family protein (FBX3) | chr1:28892295-28893419 FORWARDweakly similar to (104) loc_os04g59010 12004.m10779 protein F-box domain containing protein, expressed seq=cds; coord=10:148984717..148986879:-1; parent_gene=GRMZM2G104882'

'moderately similar to (421) AT2G26890 | Symbols: GRV2, KAM2 | GRV2 (GRAVITROPISM DEFECTIVE 2); binding / heat shock protein binding | chr2:11462327-11472259 REVERSEhighly similar to (515) loc_os10g42439 12010.m06997 protein GRV2, putative, expressed seq=cds; coord=1:98318531..98326535:1; parent_gene=GRMZM2G367023' 'moderately similar to (278) AT4G18990 | Symbols: | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative | chr4:10401941-10404248 REVERSEweakly similar to (154) XTH_WHEAT Probable xyloglucan endotransglucosylase/hydrolase precursor (EC 2.4.1.207) - Triticum aestivum (Wheat)moderately similar to (381) loc_os10g42670 12010.m07020 protein xyloglucan endotransglucosylase/hydrolase protein 30 precursor, putative, expressed seq=cds; coord=1:103264053..103316049:-1; parent_gene=GRMZM2G070271'

'moderately similar to (408) AT4G15130 | Symbols: ATCCT2, CCT2 | catalytic/ choline-phosphate cytidylyltransferase/ nucleotidyltransferase | chr4:8637793-8639388 FORWARDhighly similar to (501) loc_os10g42790 12010.m07031 protein choline-phosphate cytidylyltransferase B, putative, expressed seq=cds; coord=1:105671918..105675900:-1; parent_gene=GRMZM2G132898'

'highly similar to (679) AT2G17980 | Symbols: ATSLY1 | ATSLY1; protein transporter | chr2:7824352-7826404 FORWARDhighly similar to (914) SLY1_ORYSA SEC1-family transport protein SLY1 - Oryza sativa (Rice)highly similar to (914) loc_os03g42320 12003.m09290 protein SEC1-family transport protein SLY1, putative, expressed seq=cds; coord=1:139596369..139599277:1; parent_gene=GRMZM2G014872'

'moderately similar to (260) AT3G13224 | Symbols: | RNA recognition motif (RRM)-containing protein | chr3:4254848-4256621 FORWARDmoderately similar to (382) loc_os08g23120 12008.m06333 protein heterogeneous nuclear ribonucleoprotein A3, putative, expressed seq=cds; coord=1:143622295..143626633:1; parent_gene=GRMZM2G152526'

'highly similar to (721) AT2G31400 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:13387201-13390550 REVERSEweakly similar to (180) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (758) loc_os12g37550 12012.m07539 protein expressed protein seq=cds; coord=1:147892201..147896066:1; parent_gene=GRMZM2G432850'

'moderately similar to (460) AT3G53580 | Symbols: | diaminopimelate epimerase family protein | chr3:19864784-19866907 FORWARDhighly similar to (547) loc_os12g37960 12012.m26936 protein diaminopimelate epimerase, putative, expressed seq=cds; coord=1:150669643..150682734:1; parent_gene=GRMZM2G130332'

'highly similar to (645) AT4G33300 | Symbols: ADR1-L1 | ADR1-L1 (ADR1-like 1); ATP binding / protein binding | chr4:16051162-16054005 REVERSEnearly identical (1217) loc_os12g39620 12012.m073872 protein disease resistance protein, putative, expressed seq=cds; coord=1:164086816..164092155:1; parent_gene=GRMZM2G443525'

'very weakly similar to (95.5) AT4G09040 | Symbols: | RNA recognition motif (RRM)-containing protein | chr4:5795075-5797193 REVERSEweakly similar to (145) loc_os08g37700 12008.m080189 protein ribonucleoprotein, chloroplast precursor, putative, expressed seq=cds; coord=1:182100190..182102107:-1; parent_gene=GRMZM2G023591'

'very weakly similar to (100) AT5G54490 | Symbols: PBP1 | PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding / protein binding | chr5:22121458-22121841 FORWARDweakly similar to (142) loc_os01g57470 12001.m11898 protein caltractin, putative, expressed seq=cds; coord=1:187344907..187345239:-1; parent_gene=AC213857.4_FG003' 'moderately similar to (281) AT2G37640 | Symbols: ATEXPA3, ATEXP3, ATHEXP ALPHA 1.9, EXP3 | EXP3 | chr2:15788077-15789812 REVERSEmoderately similar to (399) EXP32_ORYSA Expansin-A32 precursor (OsEXPA32) (Alpha-expansin-32) (OsEXP32) (OsaEXPa1.30) - Oryza sativa (Rice)moderately similar to (399) loc_os08g44790 12008.m08451 protein alpha-expansin 3 precursor, putative, expressed seq=cds; coord=1:203566426..203567543:1; parent_gene=GRMZM2G106899'

'weakly similar to (104) loc_os08g44190 12008.m08392 protein zinc finger protein 2, putative, expressed seq=cds; coord=1:205832080..205832623:1; parent_gene=GRMZM2G104516'

'nearly identical (1060) AT3G09920 | Symbols: PIP5K9 | PIP5K9 (PHOSPHATIDYL INOSITOL MONOPHOSPHATE 5 KINASE); 1-phosphatidylinositol-4-phosphate 5-kinase/ ATP binding / phosphatidylinositol phosphate kinase | chr3:3040426-3043676 REVERSEhighly similar to (723) PI5K1_ORYSA Phosphatidylinositol-4-phosphate 5-kinase 1 precursor (EC 2.7.1.68) (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) (Diphosphoinositide kinase) - Oryza sativa (Rice)nearly identical (1472) loc_os02g57660 12002.m10787 protein phosphatidylinositol-4-phosphate 5-kinase 9, putative, expressed seq=cds; coord=1:226316745..226321116:-1; parent_gene=GRMZM2G374973'

'moderately similar to (213) AT5G23290 | Symbols: PDF5 | PDF5 (PREFOLDIN 5); unfolded protein binding | chr5:7846144-7847428 FORWARDmoderately similar to (258) loc_os10g34670 12010.m22005 protein prefoldin subunit 5, putative, expressed seq=cds; coord=1:229567215..229571434:1; parent_gene=GRMZM2G014676'

'moderately similar to (442) AT1G05470 | Symbols: CVP2 | CVP2 (COTYLEDON VASCULAR PATTERN 2); hydrolase/ inositol trisphosphate phosphatase | chr1:1608558-1611291 REVERSEhighly similar to (717) loc_os03g57950 12003.m35640 protein inositol-1, 4, 5-trisphosphate 5-Phosphatase-like protein, putative seq=cds; coord=1:286983366..286991541:1; parent_gene=GRMZM2G371210'

'highly similar to (797) AT5G13520 | Symbols: | peptidase M1 family protein | chr5:4342117-4344571 REVERSEnearly identical (1127) loc_os03g60460 12003.m10935 protein leukotriene A-4 hydrolase, putative, expressed seq=cds; coord=1:292988864..292997657:1; parent_gene=GRMZM2G155580'

'moderately similar to (319) AT4G01950 | Symbols: ATGPAT3, GPAT3 | GPAT3 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 3); acyltransferase | chr4:844597-846710 REVERSEmoderately similar to (457) loc_os03g61720 12003.m11052 protein glycerol-3-phosphate acyltransferase 1, putative, expressed seq=cds; coord=1:295442987..295445179:-1; parent_gene=GRMZM2G156729'

'highly similar to (654) AT4G02510 | Symbols: TOC159, TOC86, PPI2, TOC160, ATTOC159 | TOC159 (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 159); transmembrane receptor chr4:1104766-1109360 FORWARDweakly similar to (115) TOC34_PEA Translocase of chloroplast 34 (EC 3.6.5.-) (34 kDa chloroplast outer envelope protein) (GTP-binding protein OEP34) (GTP-binding protein IAP34) - Pisum sativum (Garden pea)nearly identical (1167) loc_os03g61890 12003.m35506 protein chloroplast protein import component Toc159, putative, expressed seq=cds; coord=1:295982419..295987143:1; parent_gene=GRMZM2G448523' 'moderately similar to (207) AT1G33330 | Symbols: | peptide chain release factor, putative | chr1:12084968-12086238 FORWARDmoderately similar to (270) loc_os01g66379 12001.m12745 protein expressed protein seq=cds; coord=1:297169418..297180338:1; parent_gene=GRMZM2G304638'

'weakly similar to (136) AT2G14680 | Symbols: MEE13 | myosin heavy chain-related | chr2:6278256-6283766 FORWARDmoderately similar to (347) loc_os03g31730 12003.m08422 protein expressed protein seq=cds; coord=1:301252426..301259088:1; parent_gene=GRMZM2G160578'

'highly similar to (832) AT4G30560 | Symbols: ATCNGC9, CNGC9 | ATCNGC9 (CYCLIC NUCLEOTIDE GATED CHANNEL 9); calmodulin binding / cyclic nucleotide binding / ion channel | chr4:14926974-14929681 REVERSEnearly identical (1168) loc_os04g55080 12004.m10400 protein cyclic nucleotide-gated ion channel 9, putative, expressed seq=cds; coord=2:6019299..6030234:-1; parent_gene=GRMZM2G023037'

'weakly similar to (112) loc_os04g54900 12004.m10382 protein DNA binding protein, putative seq=cds; coord=2:6190524..6191628:1; parent_gene=GRMZM2G072820'

'highly similar to (669) AT3G01930 | Symbols: | nodulin family protein | chr3:319289-321488 REVERSEhighly similar to (747) loc_os04g31924 12004.m78931 protein nodulin-like protein, putative, expressed seq=cds; coord=2:69910297..69914524:-1; parent_gene=GRMZM2G179106'

'weakly similar to (121) loc_os05g14370 12005.m05848 protein WRKY transcription factor 70, putative, expressed seq=cds; coord=2:151685379..151686596:1; parent_gene=GRMZM2G400559'

'moderately similar to (288) AT1G79630 | Symbols: | protein phosphatase 2C family protein / PP2C family protein | chr1:29962931-29964920 REVERSEhighly similar to (555) loc_os11g01790 12011.m04380 protein catalytic/ protein phosphatase type 2C, putative, expressed seq=cds; coord=2:152500883..152503674:-1; parent_gene=GRMZM2G153675'

'weakly similar to (114) AT1G08170 | Symbols: | histone H2B family protein | chr1:2562941-2563672 REVERSEweakly similar to (105) H2B_GOSHI Histone H2B - Gossypium hirsutum (Upland cotton)weakly similar to (132) loc_os09g39730 12009.m06910 protein histone H2B, putative, expressed seq=cds; coord=2:164859248..164860288:1; parent_gene=GRMZM2G442555'

'moderately similar to (356) AT3G22250 | Symbols: | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr3:7867806-7870053 FORWARDweakly similar to (156) IAAG_MAIZE Indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) (IAA-Glu synthetase) ((Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase) - Zea mays (Maize)moderately similar to (492) loc_os02g42280 12002.m09263 protein UDP-glycosyltransferase/ transferase, transferring glycosyl groups, putative, expressed seq=cds; coord=2:175627952..175629743:1; parent_gene=GRMZM2G110816'

'highly similar to (721) AT5G47750 | Symbols: D6PKL2, PK5 | D6PKL2 (D6 PROTEIN KINASE LIKE 2); kinase | chr5:19339947-19341864 REVERSEhighly similar to (711) G11A_ORYSA Protein kinase G11A (EC 2.7.11.1) - Oryza sativa (Rice)highly similar to (900) loc_os09g30150 12009.m060006 protein protein kinase G11A, putative, expressed seq=cds; coord=2:188871530..188875337:1; parent_gene=GRMZM2G026065' 'weakly similar to (130) AT1G56170 | Symbols: HAP5B, ATHAP5B, NF-YC2 | NF-YC2 (NUCLEAR FACTOR Y, SUBUNIT C2); DNA binding / transcription activator/ transcription factor | chr1:21025118-21025717 FORWARDweakly similar to (141) loc_os09g30310 12009.m06182 protein nuclear transcription factor Y subunit C-2, putative, expressed seq=cds; coord=2:189204687..189208176:-1; parent_gene=GRMZM2G022162'

'nearly identical (1097) AT5G56030 | Symbols: HSP81-2, ERD8, HSP90.2 | HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding | chr5:22686923-22689433 FORWARDnearly identical (1135) HSP81_ORYSA Heat shock protein 81-1 (HSP81-1) (Heat shock protein 82) - Oryza sativa (Rice)nearly identical (1135) loc_os08g39140 12008.m080203 protein heat shock protein 81-1, putative, expressed seq=cds; coord=2:189443283..189447454:1; parent_gene=GRMZM2G112165'

'weakly similar to (101) AT2G16030 | Symbols: | methyltransferase | chr2:6974196-6974891 REVERSEweakly similar to (181) loc_os05g42140 12005.m08387 protein expressed protein seq=cds; coord=2:194045699..194046572:1; parent_gene=GRMZM2G530263'

'moderately similar to (363) AT2G21300 | Symbols: | kinesin motor family protein | chr2:9114396-9118292 REVERSEweakly similar to (122) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiihighly similar to (728) loc_os09g35890 12009.m060046 protein ATP binding protein, putative, expressed seq=cds; coord=2:195109765..195114177:-1; parent_gene=GRMZM2G015395'

'weakly similar to (161) AT4G37260 | Symbols: MYB73, ATMYB73 | MYB73 (MYB DOMAIN PROTEIN 73); DNA binding / transcription factor | chr4:17540602-17541564 FORWARDweakly similar to (102) MYBA2_ORYSA Myb-related protein MYBAS2 - Oryza sativa (Rice)weakly similar to (183) loc_os01g74590 12001.m13484 protein myb-like DNA-binding domain containing protein, expressed seq=cds; coord=3:143487289..143488936:1; parent_gene=GRMZM2G369799'

'nearly identical (1073) AT5G19420 | Symbols: | Ran GTPase binding / chromatin binding / zinc ion binding | chr5:6547945-6552866 REVERSEnearly identical (1410) loc_os01g72320 12001.m13267 protein ran GTPase binding protein, putative, expressed seq=cds; coord=3:148394779..148401859:-1; parent_gene=GRMZM2G125642'

'moderately similar to (377) AT1G50420 | Symbols: SCL3, SCL-3 | SCL3; transcription factor | chr1:18678177-18679625 REVERSEweakly similar to (185) CIGR1_ORYSA Chitin-inducible gibberellin-responsive protein 1 - Oryza sativa (Rice)highly similar to (655) loc_os01g71970 12001.m13235 protein GRAS family transcription factor containing protein, expressed seq=cds; coord=3:150830511..150832666:-1; parent_gene=GRMZM2G082387'

'highly similar to (747) AT2G41540 | Symbols: GPDHC1 | GPDHC1; NAD or NADH binding / glycerol-3-phosphate dehydrogenase (NAD+) | chr2:17326801-17328654 FORWARDhighly similar to (831) loc_os01g71280 12001.m13171 protein glycerol-3-phosphate dehydrogenase, putative, expressed seq=cds; coord=3:152493619..152499065:-1; parent_gene=GRMZM2G155348'

'highly similar to (749) AT1G15500 | Symbols: ATNTT2 | ATNTT2; ATP:ADP antiporter | chr1:5326426-5328688 FORWARDhighly similar to (753) TLC1_SOLTU Plastidic ATP/ADP-transporter - Solanum tuberosum (Potato)highly similar to (887) loc_os01g45910 12001.m10791 protein plastidic ATP/ADP-transporter, putative, expressed seq=cds; coord=3:214471264..214476975:1; parent_gene=GRMZM2G064473' 'highly similar to (707) AT4G01210 | Symbols: | transferase, transferring glycosyl groups | chr4:507738-512362 REVERSEhighly similar to (979) loc_os01g43380 12001.m10601 protein transferase, transferring glycosyl groups, putative, expressed seq=cds; coord=3:217820434..217831211:1; parent_gene=GRMZM2G053047'

'moderately similar to (486) AT1G33420 | Symbols: | PHD finger family protein | chr1:12121063-12123346 REVERSEhighly similar to (857) loc_os11g12650 12011.m05457 protein PHD-finger family protein, expressed seq=cds; coord=4:10228455..10233101:-1; parent_gene=GRMZM2G068331'

'moderately similar to (486) AT1G33420 | Symbols: | PHD finger family protein | chr1:12121063-12123346 REVERSEhighly similar to (857) loc_os11g12650 12011.m05457 protein PHD-finger family protein, expressed seq=cds; coord=4:10228455..10233101:-1; parent_gene=GRMZM2G068331'

'moderately similar to (204) AT2G02180 | Symbols: TOM3 | TOM3; protein binding | chr2:560976-562961 FORWARDmoderately similar to (229) loc_os10g39220 12010.m06692 protein tobamovirus multiplication 3, putative, expressed seq=cds; coord=4:10659805..10663175:1; parent_gene=GRMZM2G426306'

'moderately similar to (317) AT3G61060 | Symbols: AtPP2-A13 | AtPP2-A13 (Arabidopsis thaliana phloem protein 2-A13); carbohydrate binding | chr3:22603166-22604336 FORWARDmoderately similar to (469) loc_os02g45320 12002.m09569 protein ATPP2-A13, putative, expressed seq=cds; coord=4:155377261..155382600:1; parent_gene=GRMZM2G137029'

'moderately similar to (493) AT5G16880 | Symbols: | VHS domain-containing protein / GAT domain-containing protein | chr5:5549658-5551274 FORWARDhighly similar to (645) loc_os02g46962 12002.m100323 protein protein transporter, putative, expressed seq=cds; coord=4:158139356..158143482:1; parent_gene=GRMZM2G054354'

'moderately similar to (467) AT3G01580 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:223529-225454 REVERSEvery weakly similar to (83.6) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)moderately similar to (358) loc_os03g27880 12003.m08112 protein EMB2758, putative seq=cds; coord=4:160263671..160269260:1; parent_gene=GRMZM2G110483'

'very weakly similar to (100) AT1G79230 | Symbols: ST1, ATMST1, MST1, ATRDH1 | MST1 (MERCAPTOPYRUVATE SULFURTRANSFERASE 1); 3-mercaptopyruvate sulfurtransferase/ sulfurtransferase/ thiosulfate sulfurtransferase | chr1:29801358-29803679 FORWARDweakly similar to (105) loc_os02g07044 12002.m100460 protein thiosulfate transferase, putative, expressed seq=cds; coord=4:236385493..236388871:-1; parent_gene=GRMZM2G168888'

'highly similar to (735) AT4G05320 | Symbols: UBQ10 | UBQ10 (POLYUBIQUITIN 10); protein binding | chr4:2718559-2719932 FORWARDweakly similar to (150) UBIQ_WHEAT Ubiquitin - Triticum aestivum (Wheat)highly similar to (734) loc_os06g46770 12006.m091761 protein polyubiquitin containing 7 ubiquitin monomers, putative, expressed seq=cds; coord=4:236857988..236860949:1; parent_gene=GRMZM2G118637'

'weakly similar to (194) AT5G09920 | Symbols: RPB15.9, ATRPB15.9, RPB15.9.9, NRPB4 | NRPB4; DNA-directed RNA polymerase | chr5:3096276-3097370 FORWARDmoderately similar to (239) loc_os02g02510 12002.m33507 protein DNA-directed RNA polymerase II 16 kDa polypeptide, putative, expressed seq=cds; coord=4:239931798..239932992:1; parent_gene=GRMZM2G119393' 'highly similar to (724) AT1G05180 | Symbols: AXR1 | AXR1 (AUXIN RESISTANT 1); small protein activating enzyme | chr1:1498524-1501469 REVERSEhighly similar to (917) loc_os03g60550 12003.m35481 protein NEDD8-activating enzyme E1 regulatory subunit, putative, expressed seq=cds; coord=5:2386974..2400647:-1; parent_gene=GRMZM2G002765'

'very weakly similar to (83.6) AT1G27730 | Symbols: STZ, ZAT10 | STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding | chr1:9648302-9648985 REVERSEweakly similar to (145) ZFP1_WHEAT Zinc-finger protein 1 (WZF1) - Triticum aestivum (Wheat)weakly similar to (143) loc_os03g55540 12003.m10467 protein zinc-finger protein 1, putative, expressed seq=cds; coord=5:6315211..6316774:1; parent_gene=GRMZM2G035103'

'moderately similar to (391) AT1G05140 | Symbols: | membrane-associated zinc metalloprotease, putative | chr1:1482681-1484006 FORWARDhighly similar to (567) loc_os03g38230 12003.m08922 protein expressed protein seq=cds; coord=5:20133606..20135308:1; parent_gene=GRMZM2G062470'

'moderately similar to (448) AT1G02050 | Symbols: | chalcone and stilbene synthase family protein | chr1:359164-360441 REVERSEmoderately similar to (261) THS1_VITVI Stilbene synthase 1 (EC 2.3.1.95) (Resveratrol synthase 1) (Trihydroxystilbene synthase 1) (PSV25) - Vitis vinifera (Grape)highly similar to (619) loc_os10g34360 12010.m06262 protein chalcone synthase G, putative, expressed seq=cds; coord=5:26971466..26975726:1; parent_gene=GRMZM2G477683'

'highly similar to (643) AT4G33210 | Symbols: | F-box family protein (FBL15) | chr4:16015971-16020697 REVERSEhighly similar to (995) loc_os10g25680 12010.m05512 protein ubiquitin-protein ligase, putative, expressed seq=cds; coord=5:36058740..36071056:-1; parent_gene=GRMZM2G040182'

'weakly similar to (102) AT1G13920 | Symbols: | remorin family protein | chr1:4758188-4759754 FORWARDweakly similar to (196) loc_os10g17790 12010.m04863 protein remorin, C-terminal region family protein, expressed seq=cds; coord=5:46526520..46528270:-1; parent_gene=GRMZM2G148790'

'weakly similar to (172) AT1G68460 | Symbols: ATIPT1 | ATIPT1 (isopentenyltransferase 1); adenylate dimethylallyltransferase | chr1:25668976-25670049 REVERSEmoderately similar to (319) loc_os05g47840 12005.m08856 protein ATIPT1, putative, expressed seq=cds; coord=6:162742963..162744881:-1; parent_gene=GRMZM2G025429'

'weakly similar to (172) AT1G69310 | Symbols: WRKY57, ATWRKY57 | WRKY57; transcription factor | chr1:26056118-26057909 REVERSEweakly similar to (178) loc_os07g02060 12007.m04680 protein OsWRKY29 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=7:1920108..1921464:1; parent_gene=GRMZM2G018721'

'weakly similar to (144) AT1G69120 | Symbols: AP1, AGL7 | AP1 (APETALA1); DNA binding / protein binding / protein heterodimerization/ transcription activator/ transcription factor | chr1:25982576-25986102 REVERSEweakly similar to (169) MAD15_ORYSA MADS-box transcription factor 15 (OsMADS15) (Protein APETALA1-like A) (FDRMADS3) (RMADS215) - Oryza sativa (Rice)weakly similar to (171) loc_os07g01820 12007.m66706 protein MADS-box transcription factor 15, putative, expressed seq=cds; coord=7:2062067..2065923:1; parent_gene=GRMZM2G072582' 'moderately similar to (432) AT1G30540 | Symbols: | ATPase, BadF/BadG/BcrA/BcrD-type family | chr1:10816951-10819172 REVERSEhighly similar to (644) loc_os07g05380 12007.m05002 protein ATPase, putative, expressed seq=cds; coord=7:5069050..5071431:1; parent_gene=GRMZM2G093705'

'highly similar to (528) AT3G14420 | Symbols: | (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative | chr3:4821899-4823899 FORWARDhighly similar to (524) GOX_SPIOL Peroxisomal (S)-2-hydroxy-acid oxidase (EC 1.1.3.15) (Glycolate oxidase) (GOX) (Short chain alpha-hydroxy acid oxidase) - Spinacia oleracea (Spinach)highly similar to (556) loc_os07g05820 12007.m29070 protein hydroxyacid oxidase 1, putative, expressed seq=cds; coord=7:5523491..5527292:1; parent_gene=GRMZM2G129246'

'moderately similar to (204) AT5G16010 | Symbols: | 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein | chr5:5227982-5229012 FORWARDmoderately similar to (287) loc_os07g06800 12007.m05140 protein 3-oxo-5-alpha-steroid 4-dehydrogenase 2, putative, expressed seq=cds; coord=7:6854861..6856103:-1; parent_gene=GRMZM2G394968'

'moderately similar to (280) AT4G14770 | Symbols: TCX2, ATTCX2 | TCX2 (TESMIN/TSO1-LIKE CXC 2); transcription factor | chr4:8481522-8484825 REVERSEhighly similar to (861) loc_os07g07974 12007.m05257 protein TSO1, putative, expressed seq=cds; coord=7:9327103..9332339:1; parent_gene=GRMZM2G153754'

'moderately similar to (377) AT2G36870 | Symbols: | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative | chr2:15472869-15474630 REVERSEmoderately similar to (218) XTH_TOBAC Probable xyloglucan endotransglucosylase/hydrolase protein precursor (EC 2.4.1.207) - Nicotiana tabacum (Common tobacco)highly similar to (537) loc_os07g29750 12007.m07246 protein xyloglucan endotransglucosylase/hydrolase protein 32 precursor, putative, expressed seq=cds; coord=7:148463792..148465550:1; parent_gene=GRMZM2G413044'

'moderately similar to (329) AT4G05090 | Symbols: | inositol monophosphatase family protein | chr4:2609244-2611627 FORWARDweakly similar to (108) DPNP_ORYSA 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) (3'(2'),5-bisphosphonucleoside 3'(2')-phosphohydrolase) (DPNPase) - Oryza sativa (Rice)moderately similar to (486) loc_os07g37220 12007.m07972 protein PAP-specific phosphatase, mitochondrial precursor, putative, expressed seq=cds; coord=7:157202404..157207982:-1; parent_gene=GRMZM2G036007'
'very weakly similar to (97.4) loc_os03g38230 12003.m08922 protein expressed protein seq=cds; coord=7:158131754..158133567:-1; parent_gene=AC213455.3_FG008'

'highly similar to (788) AT2G14960 | Symbols: GH3.1 | GH3.1 | chr2:6451659-6453670 REVERSEhighly similar to (930) GH38_ORYSA Probable indole-3-acetic acid-amido synthetase GH3.8 (EC 6.3.2.-) (Auxin-responsive GH3-like protein 8) (OsGH3-8) - Oryza sativa (Rice)highly similar to (930) loc_os07g40290 12007.m08271 protein indole-3-acetic acid-amido synthetase GH3.8, putative, expressed seq=cds; coord=7:162669667..162672138:-1; parent_gene=GRMZM2G053338' 'weakly similar to (193) AT1G06260 | Symbols: | cysteine proteinase, putative | chr1:1916449-1917585 FORWARDweakly similar to (184) ORYA_ORYSA Oryzain alpha chain precursor (EC 3.4.22.-) - Oryza sativa (Rice)moderately similar to (260) loc_os09g21370 12009.m05344 protein cysteine proteinase EP-B 1 precursor, putative, expressed seq=cds; coord=7:162858798..162860272:-1; parent_gene=GRMZM2G049882'

'moderately similar to (271) AT3G04500 | Symbols: | RNA recognition motif (RRM)-containing protein | chr3:1212065-1213795 REVERSEmoderately similar to (320) loc_os08g45240 12008.m62038 protein expressed protein seq=cds; coord=7:163512342..163516768:1; parent_gene=GRMZM2G068255'

'nearly identical (1145) AT5G28740 | Symbols: | transcription-coupled DNA repair protein-related | chr5:10780774-10783772 FORWARDnearly identical (1513) loc_os07g44970 12007.m08717 protein XPA-binding protein 2, putative, expressed seq=cds; coord=7:170033313..170038657:-1; parent_gene=GRMZM2G356894'

'highly similar to (622) AT3G56310 | Symbols: | alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative | chr3:20882886-20885745 FORWARDmoderately similar to (474) AGAL_ORYSA Alpha-galactosidase precursor (EC 3.2.1.22) (Melibiase) (Alpha-D-galactoside galactohydrolase) - Oryza sativa (Rice)highly similar to (746) loc_os07g48160 12007.m09030 protein alpha-galactosidase precursor, putative, expressed seq=cds; coord=7:172979297..172984001:1; parent_gene=GRMZM2G053554'

'highly similar to (622) AT3G56310 | Symbols: | alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative | chr3:20882886-20885745 FORWARDmoderately similar to (474) AGAL_ORYSA Alpha-galactosidase precursor (EC 3.2.1.22) (Melibiase) (Alpha-D-galactoside galactohydrolase) - Oryza sativa (Rice)highly similar to (746) loc_os07g48160 12007.m09030 protein alpha-galactosidase precursor, putative, expressed seq=cds; coord=7:172979297..172984001:1; parent_gene=GRMZM2G053554'

'moderately similar to (274) AT1G09560 | Symbols: GLP5 | GLP5 (GERMIN-LIKE PROTEIN 5); manganese ion binding / nutrient reservoir | chr1:3093896-3094639 FORWARDmoderately similar to (264) RHRE_PEA Rhicadhesin receptor precursor (Germin-like protein) - Pisum sativum (Garden pea)moderately similar to (336) loc_os01g18170 12001.m08359 protein rhicadhesin receptor precursor, putative, expressed seq=cds; coord=8:1091537..1092833:-1; parent_gene=GRMZM2G103512'

'nearly identical (1376) AT4G31480 | Symbols: | coatomer beta subunit, putative / beta-coat protein, putative / beta-COP, putative | chr4:15264076-15267384 FORWARDnearly identical (1633) loc_os01g17430 12001.m08334 protein coatomer subunit beta, putative, expressed seq=cds; coord=8:1448424..1454503:1; parent_gene=GRMZM2G378906'

'moderately similar to (447) AT2G05920 | Symbols: | subtilase family protein | chr2:2269831-2272207 REVERSEhighly similar to (971) loc_os05g36010 12005.m07831 protein subtilisin-like protease precursor, putative, expressed seq=cds; coord=8:101208361..101210989:1; parent_gene=GRMZM2G055684'

'weakly similar to (151) AT1G17160 | Symbols: | pfkB-type carbohydrate kinase family protein | chr1:5867678-5869175 FORWARDweakly similar to (176) loc_os01g47550 12001.m10950 protein ribokinase, putative, expressed seq=cds; coord=8:149044077..149045102:1; parent_gene=GRMZM2G178346' 'weakly similar to (145) AT2G33880 | Symbols: WOX9, HB-3, STIP | HB-3; transcription factor | chr2:14341639-14343597 REVERSEmoderately similar to (292) loc_os01g47710 12001.m10964 protein homeobox domain containing protein, expressed seq=cds; coord=8:149301222..149304982:1; parent_gene=GRMZM2G133972'

'weakly similar to (145) AT2G33880 | Symbols: WOX9, HB-3, STIP | HB-3; transcription factor | chr2:14341639-14343597 REVERSEmoderately similar to (292) loc_os01g47710 12001.m10964 protein homeobox domain containing protein, expressed seq=cds; coord=8:149301222..149304982:1; parent_gene=GRMZM2G133972'

'moderately similar to (220) AT5G26660 | Symbols: ATMYB4, ATMYB86 | ATMYB86 (MYB DOMAIN PROTEIN 86); specific transcriptional repressor/ transcription repressor | chr5:9331775-9333044 REVERSEmoderately similar to (285) MYB3_HORVU Myb-related protein Hv33 - Hordeum vulgare (Barley)moderately similar to (405) loc_os01g50720 12001.m11253 protein myb-related protein Hv33, putative, expressed seq=cds; coord=8:153463293..153465006:-1; parent_gene=GRMZM2G003406'

'weakly similar to (131) loc_os01g06320 12001.m07262 protein myb-like DNA-binding domain, SHAQKYF class family protein, expressed seq=cds; coord=9:8775366..8777307:1; parent_gene=GRMZM2G371870'

'moderately similar to (328) AT1G21890 | Symbols: | nodulin MtN21 family protein | chr1:7682808-7685581 REVERSEmoderately similar to (478) loc_os06g10750 12006.m05792 protein nodulin protein, putative, expressed seq=cds; coord=9:8432717..8434846:-1; parent_gene=GRMZM2G088053'

'moderately similar to (237) AT2G46770 | Symbols: NST1, EMB2301, ANAC043 | EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor | chr2:19220917-19222822 REVERSEmoderately similar to (213) NAC76_ORYSA NAC domain-containing protein 76 (ONAC076) - Oryza sativa (Rice)moderately similar to (300) loc_os06g04090 12006.m05140 protein NAM protein, putative, expressed seq=cds; coord=9:23279027..23283429:-1; parent_gene=GRMZM2G171395'

'highly similar to (926) AT2G21480 | Symbols: | protein kinase family protein | chr2:9202753-9205368 REVERSEmoderately similar to (264) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)nearly identical (1276) loc_os06g03610 12006.m05093 protein protein kinase, putative, expressed seq=cds; coord=9:25086132..25089397:1; parent_gene=GRMZM2G335052'

'moderately similar to (296) AT1G33140 | Symbols: PGY2 | PGY2 (PIGGYBACK2); structural constituent of ribosome | chr1:12023360-12024502 FORWARDmoderately similar to (345) RL9_ORYSA 60S ribosomal protein L9 - Oryza sativa (Rice)moderately similar to (345) loc_os09g31180 12009.m060014 protein 60S ribosomal protein L9, putative, expressed seq=cds; coord=9:27092199..27094638:1; parent_gene=GRMZM2G084739'

'weakly similar to (131) AT2G37060 | Symbols: NF-YB8 | NF-YB8 (NUCLEAR FACTOR Y, SUBUNIT B8); transcription factor | chr2:15576336-15577660 FORWARDweakly similar to (160) NFYB4_ORYSA Nuclear transcription factor Y subunit B-4 (OsNF-YB-4) (Transcriptional activator HAP3C) - Oryza sativa (Rice)weakly similar to (160) loc_os05g49780 12005.m09048 protein nuclear transcription factor Y subunit B-4, putative, expressed seq=cds; coord=9:67719261..67720839:-1; parent_gene=GRMZM2G121897' 'highly similar to (572) AT4G39950 | Symbols: CYP79B2 | CYP79B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr4:18525311-18527284 FORWARDhighly similar to (753) C79A1_SORBI Cytochrome P450 79A1 (EC 1.14.13.41) (Tyrosine N-monooxygenase) (Cytochrome P450Tyr) - Sorghum bicolor (Sorghum) (Sorghum vulgare)highly similar to (543) loc_os03g37290 12003.m08838 protein cytochrome P450 79A1, putative, expressed seq=cds; coord=9:78205868..78207890:-1; parent_gene=GRMZM2G138248'

'moderately similar to (300) AT5G17000 | Symbols: | NADP-dependent oxidoreductase, putative | chr5:5584983-5586991 REVERSEhighly similar to (535) loc_os06g40070 12006.m08544 protein NADP-dependent oxidoreductase P2, putative, expressed seq=cds; coord=9:88874336..88876199:-1; parent_gene=GRMZM2G099642'

'moderately similar to (407) AT1G20650 | Symbols: | ATP binding / protein kinase/ protein serine/threonine kinase | chr1:7158422-7160022 REVERSEmoderately similar to (219) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (618) loc_os03g03880 12003.m05920 protein serine/threonine-protein kinase NAK, putative, expressed seq=cds; coord=9:151572087..151576489:1; parent_gene=GRMZM2G009869'

'moderately similar to (376) AT1G67440 | Symbols: emb1688 | emb1688 (embryo defective 1688); GTP binding / GTPase | chr1:25263905-25265551 REVERSEhighly similar to (512) loc_os04g31270 12004.m08230 protein EMB1688, putative, expressed seq=cds; coord=10:108218986..108230288:1; parent_gene=GRMZM2G097106'

'weakly similar to (118) AT2G22750 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr2:9672145-9673624 FORWARDmoderately similar to (202) loc_os03g46860 12003.m09702 protein DNA binding protein, putative, expressed seq=cds; coord=10:118369285..118370757:1; parent_gene=GRMZM2G355469'

'weakly similar to (138) AT3G58630 | Symbols: | transcription factor | chr3:21683928-21685771 REVERSEmoderately similar to (338) loc_os04g36790 12004.m08719 protein 6b-interacting protein 1, putative, expressed seq=cds; coord=10:119916059..119917843:-1; parent_gene=GRMZM2G392168'

'moderately similar to (215) AT5G20320 | Symbols: DCL4, ATDCL4 | DCL4 (DICER-LIKE 4); RNA binding / protein binding / ribonuclease III | chr5:6859571-6869068 REVERSEmoderately similar to (419) loc_os04g43050 12004.m78969 protein dicer-like protein 4, putative, expressed seq=cds; coord=10:129967983..129970444:-1; parent_gene=GRMZM2G160473'

'moderately similar to (363) AT1G13250 | Symbols: GATL3 | GATL3 (Galacturonosyltransferase-like 3); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr1:4528965-4530002 REVERSEhighly similar to (516) loc_os04g44850 12004.m09442 protein transferase, transferring glycosyl groups, putative, expressed seq=cds; coord=10:132525257..132527036:1; parent_gene=GRMZM2G468661'

'highly similar to (694) AT2G16950 | Symbols: TRN1, ATTRN1 | TRN1 (TRANSPORTIN 1); protein transporter | chr2:7353939-7360637 FORWARDhighly similar to (880) loc_os04g59494 12004.m35538 protein transportin-2, putative, expressed seq=cds; coord=10:149428267..149436396:1; parent_gene=GRMZM2G312026' 'moderately similar to (449) AT2G05940 | Symbols: | protein kinase, putative | chr2:2287514-2289270 REVERSEmoderately similar to (213) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (564) loc_os03g08170 12003.m06326 protein protein kinase APK1B, chloroplast precursor, putative, expressed seq=cds; coord=1:16468414..16473940:1; parent_gene=GRMZM2G175164'

'highly similar to (714) AT2G26250 | Symbols: FDH, KCS10 | KCS10 (3-KETOACYL-COA SYNTHASE 10); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups | chr2:11170799-11173059 REVERSEhighly similar to (929) loc_os03g08360 12003.m35563 protein fiddlehead-like protein, putative, expressed seq=cds; coord=1:16822675..16826498:1; parent_gene=GRMZM2G445602'

'highly similar to (556) AT1G19250 | Symbols: FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase | chr1:6650656-6653053 REVERSEhighly similar to (833) loc_os03g08410 12003.m06349 protein monooxygenase/ oxidoreductase, putative, expressed seq=cds; coord=1:17015718..17018487:1; parent_gene=GRMZM2G000427'

'very weakly similar to (98.6) loc_os03g08520 12003.m06360 protein expressed protein seq=cds; coord=1:17624743..17625481:-1; parent_gene=GRMZM2G496991'

'nearly identical (1672) AT1G80490 | Symbols: TPR1 | TPR1 (TOPLESS-RELATED 1) | chr1:30261094-30266446 REVERSEnearly identical (1944) loc_os03g14980 12003.m101111 protein lissencephaly type-1-like homology motif, putative, expressed seq=cds; coord=1:35240624..35250929:-1; parent_gene=GRMZM2G030422'

'weakly similar to (171) AT1G07960 | Symbols: ATPDIL5-1 | ATPDIL5-1 (PDI-like 5-1) | chr1:2467681-2468831 FORWARDweakly similar to (197) loc_os03g17860 12003.m101304 protein OsPDIL5-1 - Oryza sativa protein disulfide isomerase, expressed seq=cds; coord=1:44191574..44193212:-1; parent_gene=GRMZM2G073628'

'highly similar to (622) AT2G40116 | Symbols: | phosphoinositide-specific phospholipase C family protein | chr2:16751782-16754311 FORWARDhighly similar to (848) loc_os03g18010 12003.m07226 protein phosphoinositide-specific phospholipase C, putative, expressed seq=cds; coord=1:44996488..45002904:-1; parent_gene=GRMZM2G114354'

'weakly similar to (188) AT1G07150 | Symbols: MAPKKK13 | MAPKKK13; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr1:2194279-2195778 REVERSEvery weakly similar to (83.2) CDPK2_MAIZE Calcium-dependent protein kinase 2 (EC 2.7.11.1) (CDPK 2) - Zea mays (Maize)moderately similar to (427) loc_os03g18170 12003.m07242 protein mitogen-activated protein kinase kinase kinase 1, putative, expressed seq=cds; coord=1:45425093..45426565:1; parent_gene=GRMZM2G459824'

'moderately similar to (248) AT2G30260 | Symbols: U2B'' | U2B'' (U2 small nuclear ribonucleoprotein B); RNA binding / nucleic acid binding / nucleotide binding | chr2:12905557-12907434 REVERSEmoderately similar to (323) loc_os03g18720 12003.m35175 protein spliceosomal protein, putative, expressed seq=cds; coord=1:46622335..46627171:-1; parent_gene=GRMZM2G153450' 'moderately similar to (404) AT2G47590 | Symbols: PHR2 | PHR2 (photolyase/blue-light receptor 2); DNA photolyase | chr2:19521888-19523732 FORWARDmoderately similar to (206) CRYD_ORYSA Cryptochrome DASH, chloroplast/mitochondrial precursor - Oryza sativa (Rice)highly similar to (726) loc_os03g22330 12003.m07635 protein photolyase/blue-light receptor PHR2, putative, expressed seq=cds; coord=1:57479256..57483149:1; parent_gene=GRMZM2G158662'

'nearly identical (1066) AT5G27640 | Symbols: TIF3B1, EIF3B, ATEIF3B-1, EIF3B-1, ATTIF3B1 | TIF3B1 (TRANSLATION INITIATION FACTOR 3B1); nucleic acid binding / translation initiation factor | chr5:9781207-9784759 REVERSEnearly identical (1046) IF39_TOBAC Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p110) (eIF3b) - Nicotiana tabacum (Common tobacco)nearly identical (1300) loc_os10g41960 12010.m06952 protein eukaryotic translation initiation factor 3 subunit 9, putative, expressed seq=cds; coord=1:96834561..96839284:-1; parent_gene=GRMZM2G174757'

'weakly similar to (151) AT2G18040 | Symbols: PIN1AT | PIN1AT (PEPTIDYLPROLYL CIS/TRANS ISOMERASE, NIMA-INTERACTING 1); peptidyl-prolyl cis-trans isomerase | chr2:7842346-7843537 FORWARDweakly similar to (151) PIN1_MALDO Peptidyl-prolyl cis-trans isomerase 1 (EC 5.2.1.8) (Rotamase Pin1) (PPIase Pin1) (MdPin1) - Malus domestica (Apple) (Malus sylvestris)weakly similar to (195) loc_os04g56800 12004.m10567 protein peptidyl-prolyl cis-trans isomerase 1, putative, expressed seq=cds; coord=2:3366755..3373020:1; parent_gene=GRMZM2G047590'

'highly similar to (541) AT3G51240 | Symbols: F3H, TT6, F3'H | F3H (FLAVANONE 3-HYDROXYLASE); naringenin 3-dioxygenase | chr3:19025409-19026658 FORWARDhighly similar to (570) FL3H_HORVU Naringenin,2-oxoglutarate 3-dioxygenase (EC 1.14.11.9) (Flavonone-3-hydroxylase) (F3H) (FHT) - Hordeum vulgare (Barley)highly similar to (575) loc_os04g56700 12004.m10557 protein naringenin,2-oxoglutarate 3-dioxygenase, putative, expressed seq=cds; coord=2:3556786..3558729:1; parent_gene=GRMZM2G062396'

'highly similar to (541) AT3G51240 | Symbols: F3H, TT6, F3'H | F3H (FLAVANONE 3-HYDROXYLASE); naringenin 3-dioxygenase | chr3:19025409-19026658 FORWARDhighly similar to (570) FL3H_HORVU Naringenin,2-oxoglutarate 3-dioxygenase (EC 1.14.11.9) (Flavonone-3-hydroxylase) (F3H) (FHT) - Hordeum vulgare (Barley)highly similar to (575) loc_os04g56700 12004.m10557 protein naringenin,2-oxoglutarate 3-dioxygenase, putative, expressed seq=cds; coord=2:3556786..3558729:1; parent_gene=GRMZM2G062396'

'highly similar to (748) AT1G11390 | Symbols: | ABC1 family protein | chr1:3834762-3837305 REVERSEnearly identical (1090) loc_os04g56510 12004.m10540 protein protein kinase-like, putative, expressed seq=cds; coord=2:3859120..3863795:1; parent_gene=GRMZM2G087201'

'moderately similar to (294) AT1G73110 | Symbols: | ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative | chr1:27494344-27496844 REVERSEmoderately similar to (202) RCA_MAIZE Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase) (RA) - Zea mays (Maize)moderately similar to (344) loc_os04g56320 12004.m10522 protein ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor, putative, expressed seq=cds; coord=2:4159971..4163217:1; parent_gene=GRMZM2G039345'

'highly similar to (536) AT1G71230 | Symbols: CSN5B, CSN5, AJH2 | CSN5B (COP9-SIGNALOSOME 5B); protein binding | chr1:26852560-26854255 FORWARDhighly similar to (643) loc_os04g56070 12004.m101676 protein COP9 signalosome complex subunit 5b, putative, expressed seq=cds; coord=2:4687656..4692442:1; parent_gene=GRMZM2G086801'

'moderately similar to (255) AT3G54420 | Symbols: ATEP3, ATCHITIV, CHIV | ATEP3; chitinase | chr3:20145935-20147034 FORWARDmoderately similar to (295) CHIA_MAIZE Endochitinase A precursor (EC 3.2.1.14) (Seed chitinase A) - Zea mays (Maize)moderately similar to (303) loc_os04g41680 12004.m09144 protein endochitinase A precursor, putative, expressed seq=cds; coord=2:33537139..33539360:1; parent_gene=GRMZM2G052175'

'weakly similar to (146) AT1G68810 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr1:25861289-25862882 FORWARDmoderately similar to (253) loc_os09g24490 12009.m05603 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=2:180155096..180158005:-1; parent_gene=GRMZM2G176141'

'moderately similar to (437) AT5G10930 | Symbols: CIPK5, SnRK3.24 | CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr5:3445569-3446906 REVERSEmoderately similar to (337) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)highly similar to (634) loc_os09g25090 12009.m05662 protein CIPK-like protein 1, putative, expressed seq=cds; coord=2:180525710..180527829:1; parent_gene=GRMZM2G330049'

'moderately similar to (397) AT5G07990 | Symbols: TT7, CYP75B1, D501 | TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding | chr5:2560437-2562859 FORWARDmoderately similar to (405) F3PH_PETHY Flavonoid 3'-monooxygenase (EC 1.14.13.21) (Flavonoid 3'-hydroxylase) (Cytochrome P450 75B2) - Petunia hybrida (Petunia)highly similar to (893) loc_os09g26960 12009.m05848 protein flavonoid 3-monooxygenase, putative, expressed seq=cds; coord=2:184258075..184260458:1; parent_gene=GRMZM2G125482'

'moderately similar to (391) AT1G06240 | Symbols: | unknown protein | chr1:1911166-1912875 FORWARDhighly similar to (569) loc_os01g11590 12001.m42918 protein expressed protein seq=cds; coord=3:3448711..3456996:-1; parent_gene=GRMZM2G400907'

'moderately similar to (238) AT1G78440 | Symbols: ATGA2OX1 | ATGA2OX1 (gibberellin 2-oxidase 1); gibberellin 2-beta-dioxygenase | chr1:29511772-29512990 REVERSEmoderately similar to (262) G2OX1_PEA Gibberellin 2-beta-dioxygenase 1 (EC 1.14.11.13) (Gibberellin 2-beta-hydroxylase 1) (Gibberellin 2-oxidase 1) (GA 2-oxidase 1) (Protein SLENDER) - Pisum sativum (Garden pea)moderately similar to (365) loc_os01g11150 12001.m07735 protein gibberellin 2-beta-dioxygenase, putative, expressed seq=cds; coord=3:3994128..3996072:1; parent_gene=GRMZM2G031432'

'weakly similar to (173) AT5G26751 | Symbols: ATSK11, SK 11 | ATSK11; protein kinase/ protein serine/threonine kinase | chr5:9399582-9401839 REVERSEweakly similar to (173) MSK3_MEDSA Glycogen synthase kinase-3 homolog MsK-3 (EC 2.7.11.1) - Medicago sativa (Alfalfa)weakly similar to (175) loc_os05g04340 12005.m27537 protein glycogen synthase kinase-3 homolog MsK-1, putative, expressed seq=cds; coord=3:5009151..5011123:1; parent_gene=GRMZM2G477073' 'highly similar to (516) AT3G17510 | Symbols: CIPK1, SnRK3.16 | CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding | chr3:5989309-5992627 REVERSEmoderately similar to (389) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)highly similar to (749) loc_os01g18800 12001.m150556 protein CBL-interacting serine/threonine-protein kinase 1, putative, expressed seq=cds; coord=3:50604991..50610043:-1; parent_gene=GRMZM2G170120'

'highly similar to (706) AT1G36370 | Symbols: SHM7 | SHM7 (serine hydroxymethyltransferase 7); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding | chr1:13696240-13698576 REVERSEmoderately similar to (466) GLYM_SOLTU Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1) (Serine methylase) (Glycine hydroxymethyltransferase) (SHMT) - Solanum tuberosum (Potato)highly similar to (861) loc_os01g65410 12001.m12653 protein serine hydroxymethyltransferase, mitochondrial precursor, putative, expressed seq=cds; coord=3:173376685..173382485:-1; parent_gene=GRMZM2G452630'

'highly similar to (569) AT2G16570 | Symbols: ATASE, ATASE1 | ATASE1 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 1); amidophosphoribosyltransferase | chr2:7180424-7182124 REVERSEhighly similar to (562) PUR1_SOYBN Amidophosphoribosyltransferase, chloroplast precursor (EC 2.4.2.14) (Glutamine phosphoribosylpyrophosphate amidotransferase) (ATASE) (GPAT) - Glycine max (Soybean)highly similar to (800) loc_os01g65260 12001.m12639 protein amidophosphoribosyltransferase, chloroplast precursor, putative, expressed seq=cds; coord=3:173801386..173803474:1; parent_gene=GRMZM2G339699'

'highly similar to (505) AT1G10940 | Symbols: ASK1, SNRK2-4, SNRK2.4, SRK2A | SNRK2.4 (SNF1-RELATED PROTEIN KINASE 2.4); kinase | chr1:3656050-3658170 REVERSEhighly similar to (608) SAPK4_ORYSA Serine/threonine-protein kinase SAPK4 (EC 2.7.11.1) (Osmotic stress/abscisic acid-activated protein kinase 4) - Oryza sativa (Rice)highly similar to (608) loc_os01g64970 12001.m12610 protein serine/threonine-protein kinase SAPK4, putative, expressed seq=cds; coord=3:174770228..174775665:-1; parent_gene=GRMZM2G110922'

'very weakly similar to (94.4) loc_os01g24950 12001.m150578 protein exocyst complex subunit Sec15-like family protein, expressed seq=cds; coord=3:175323602..175324361:-1; parent_gene=GRMZM2G439532'

'moderately similar to (307) AT3G19510 | Symbols: HAT3.1 | HAT3.1; DNA binding / sequence-specific DNA binding / transcription activator/ transcription factor | chr3:6763205-6766049 REVERSEmoderately similar to (490) HOX1A_MAIZE Homeobox protein HOX1A - Zea mays (Maize)highly similar to (667) loc_os06g12400 12006.m05957 protein homeobox protein HOX1A, putative, expressed seq=cds; coord=3:197392618..197405889:-1; parent_gene=GRMZM2G314546'

'nearly identical (1195) AT1G06410 | Symbols: ATTPS7, TPS7, ATTPSA | ATTPS7; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase | chr1:1955413-1958153 FORWARDnearly identical (1543) loc_os01g54560 12001.m150713 protein trehalose synthase, putative, expressed seq=cds; coord=3:197947785..197952726:-1; parent_gene=GRMZM2G123277' 'moderately similar to (476) AT2G24370 | Symbols: | ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr2:10369979-10373063 REVERSEweakly similar to (165) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (608) loc_os01g39970 12001.m10270 protein serine threonine kinase 1, putative, expressed seq=cds; coord=3:220702531..220705512:1; parent_gene=GRMZM2G070961'

'moderately similar to (427) AT4G13340 | Symbols: | leucine-rich repeat family protein / extensin family protein | chr4:7758610-7760892 FORWARDweakly similar to (120) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (580) loc_os01g41120 12001.m10381 protein protein binding protein, putative, expressed seq=cds; coord=3:222594542..222596230:1; parent_gene=GRMZM2G333811'

'very weakly similar to (91.7) AT2G37740 | Symbols: ATZFP10, ZFP10 | ZFP10 (ZINC-FINGER PROTEIN 10); nucleic acid binding / transcription factor/ zinc ion binding | chr2:15827706-15828620 REVERSEweakly similar to (124) loc_os07g01180 12007.m04599 protein zinc finger, C2H2 type family protein seq=cds; coord=4:609416..610872:1; parent_gene=GRMZM2G058868'

'nearly identical (1254) AT5G07350 | Symbols: | tudor domain-containing protein / nuclease family protein | chr5:2319790-2324892 REVERSEnearly identical (1683) loc_os02g32350 12002.m33392 protein 4SNc-Tudor domain protein, putative, expressed seq=cds; coord=4:94432879..94438375:1; parent_gene=AC207890.3_FG002'

'very weakly similar to (95.1) AT4G27090 | Symbols: | 60S ribosomal protein L14 (RPL14B) | chr4:13594104-13595187 REVERSEvery weakly similar to (93.6) RL14_PEA Probable 60 ribosomal protein L14 (Hydroxyproline-rich glycoprotein HRGP1) - Pisum sativum (Garden pea)weakly similar to (117) loc_os04g43540 12004.m09314 protein 60 ribosomal protein L14, putative, expressed seq=cds; coord=4:111487916..111492785:1; parent_gene=GRMZM2G323971'

'moderately similar to (266) AT1G67590 | Symbols: | remorin family protein | chr1:25333255-25334472 REVERSEweakly similar to (166) loc_os03g02840 12003.m101163 protein DNA binding protein, putative, expressed seq=cds; coord=4:119470971..119472897:1; parent_gene=GRMZM2G009019'

'moderately similar to (353) AT1G47500 | Symbols: ATRBP47C' | ATRBP47C' (RNA-binding protein 47C'); RNA binding | chr1:17432682-17434805 FORWARDvery weakly similar to (86.3) ROC1_NICSY 29 kDa ribonucleoprotein A, chloroplast precursor (CP29A) - Nicotiana sylvestris (Wood tobacco)highly similar to (527) loc_os04g37690 12004.m35140 protein nucleic acid binding protein, putative, expressed seq=cds; coord=4:122869806..122879188:1; parent_gene=GRMZM2G069678'

'weakly similar to (108) AT4G33565 | Symbols: | protein binding / zinc ion binding | chr4:16136821-16137924 FORWARDweakly similar to (175) loc_os02g36330 12002.m08720 protein RING-H2 finger protein ATL1O, putative, expressed seq=cds; coord=4:123185031..123186547:-1; parent_gene=GRMZM2G041344'

'highly similar to (683) AT5G64300 | Symbols: ATGCH, GCH, ATRIBA1, RFD1 | ATGCH; 3,4-dihydroxy-2-butanone-4-phosphate synthase/ GTP cyclohydrolase II | chr5:25718459-25720790 FORWARDhighly similar to (876) loc_os02g36340 12002.m33397 protein riboflavin biosynthesis protein ribAB, chloroplast precursor, putative, expressed seq=cds; coord=4:123331634..123336680:-1; parent_gene=GRMZM2G156803' 'weakly similar to (139) AT1G23220 | Symbols: | dynein light chain type 1 family protein | chr1:8242614-8244136 FORWARDweakly similar to (190) loc_os02g36990 12002.m08787 protein microtubule motor, putative, expressed seq=cds; coord=4:126474274..126476909:-1; parent_gene=GRMZM2G145027'

'moderately similar to (301) AT5G61380 | Symbols: TOC1, APRR1, PRR1 | TOC1 (TIMING OF CAB EXPRESSION 1); transcription regulator/ two-component response regulator | chr5:24675540-24678176 FORWARDhighly similar to (734) PRR1_ORYSA Two-component response regulator-like PRR1 (Pseudo-response regulator 1) (OsPRR1) - Oryza sativa (Rice)highly similar to (734) loc_os02g40510 12002.m33775 protein two-component response regulator-like PRR1, putative, expressed seq=cds; coord=4:140699189..140702237:1; parent_gene=GRMZM2G020081'

'moderately similar to (495) AT5G22300 | Symbols: NIT4 | NIT4 (NITRILASE 4); 3-cyanoalanine hydratase/ cyanoalanine nitrilase/ indole-3-acetonitrile nitrilase/ nitrilase/ nitrile hydratase | chr5:7379401-7381764 FORWARDhighly similar to (530) NRL4_TOBAC Nitrilase 4 (EC 3.5.5.1) - Nicotiana tabacum (Common tobacco)highly similar to (644) loc_os02g42350 12002.m100293 protein nitrilase 4, putative, expressed seq=cds; coord=4:145562864..145569248:1; parent_gene=GRMZM2G111225'

'highly similar to (650) AT2G20300 | Symbols: ALE2 | ALE2 (Abnormal Leaf Shape 2); kinase | chr2:8756475-8759845 REVERSEmoderately similar to (228) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (922) loc_os02g57080 12002.m33474 protein ATP binding protein, putative, expressed seq=cds; coord=4:171665330..171672226:1; parent_gene=GRMZM2G102163'

'nearly identical (1070) AT1G60070 | Symbols: | binding / clathrin binding / protein binding / protein transporter | chr1:22142944-22149296 REVERSEnearly identical (1324) loc_os06g07090 12006.m091619 protein AP-1 complex subunit gamma-1, expressed seq=cds; coord=4:173209988..173224508:-1; parent_gene=GRMZM2G054210'

'moderately similar to (407) AT1G79650 | Symbols: RAD23 | RAD23; damaged DNA binding | chr1:29972406-29975132 REVERSEmoderately similar to (300) RAD23_ORYSA Probable DNA repair protein RAD23 (OsRAD23) - Oryza sativa (Rice)highly similar to (522) loc_os02g08300 12002.m06176 protein DNA repair protein RAD23-1, putative, expressed seq=cds; coord=4:234901650..234908817:1; parent_gene=GRMZM2G143462'

'moderately similar to (408) AT3G02875 | Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugat hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase | chr3:631993-633859 FORWARDhighly similar to (581) loc_os03g62060 12003.m11084 protein IAA-amino acid hydrolase ILR1 precursor, putative, expressed seq=cds; coord=5:1569535..1572475:-1; parent_gene=GRMZM2G125552'

'highly similar to (516) AT2G28930 | Symbols: APK1B | APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr2:12424551-12426565 FORWARDmoderately similar to (236) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (631) loc_os03g60710 12003.m10960 protein protein kinase APK1B, chloroplast precursor, putative, expressed seq=cds; coord=5:2283771..2290049:-1; parent_gene=GRMZM2G144042' 'moderately similar to (270) AT1G75560 | Symbols: | zinc knuckle (CCHC-type) family protein | chr1:28371420-28372717 REVERSEmoderately similar to (389) loc_os03g60600 12003.m10949 protein cellular nucleic acid-binding protein, putative, expressed seq=cds; coord=5:2358363..2361474:1; parent_gene=GRMZM2G003068'

'weakly similar to (119) loc_os03g60570 12003.m10946 protein zinc finger DNA-binding protein, putative, expressed seq=cds; coord=5:2365726..2366372:-1; parent_gene=GRMZM2G002815'

'weakly similar to (172) loc_os02g30810 12002.m08224 protein OsSAUR10 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=5:164364957..164366457:-1; parent_gene=GRMZM2G312274'

'moderately similar to (308) AT3G50700 | Symbols: AtIDD2 | AtIDD2 (Arabidopsis thaliana Indeterminate(ID)-Domain 2); nucleic acid binding / transcription factor/ zinc ion binding | chr3:18840945-18842829 FORWARDhighly similar to (734) loc_os02g31890 12002.m08282 protein zinc finger, C2H2-type, putative seq=cds; coord=5:166856814..166859192:1; parent_gene=GRMZM2G320287'

highly similar to (606) AT2G32990 | Symbols: AtGH9B8 | AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds | chr2:14003361-14005844 FORWARDhighly similar to (809) GUN7_ORYSA Endoglucanase 7 precursor (EC 3.2.1.4) (Endo-1,4-beta glucanase 7) (OsGLU10) - Oryza sativa (Rice)highly similar to (809) loc_os02g50490 12002.m10083 protein endoglucanase 1 precursor, putative, expressed seq=cds; coord=5:205562436..205565933:1; parent_gene=GRMZM2G151257'

'weakly similar to (118) loc_os02g51550 12002.m10188 protein expressed protein seq=cds; coord=5:208070590..208072068:1; parent_gene=GRMZM2G036286'

'moderately similar to (267) AT1G72650 | Symbols: TRFL6 | TRFL6 (TRF-LIKE 6); DNA binding / transcription factor | chr1:27350253-27353483 FORWARDhighly similar to (692) loc_os02g53670 12002.m100379 protein TRFL6, putative, expressed seq=cds; coord=5:211705203..211716883:1; parent_gene=GRMZM2G049194'

'weakly similar to (112) AT5G04260 | Symbols: WCRKC2 | WCRKC2 (WCRKC THIOREDOXIN 2) | chr5:1178901-1180022 REVERSEweakly similar to (136) loc_os02g57380 12002.m33948 protein thioredoxin-like 8, chloroplast precursor, putative, expressed seq=cds; coord=5:215924063..215926694:-1; parent_gene=GRMZM2G003028'

'highly similar to (848) AT3G51070 | Symbols: | dehydration-responsive protein-related | chr3:18969068-18972291 FORWARDnearly identical (1068) loc_os06g49860 12006.m09510 protein ankyrin-like protein, putative, expressed seq=cds; coord=6:84676115..84679470:-1; parent_gene=GRMZM2G387935'

'weakly similar to (184) AT1G56170 | Symbols: HAP5B, ATHAP5B, NF-YC2 | NF-YC2 (NUCLEAR FACTOR Y, SUBUNIT C2); DNA binding / transcription activator/ transcription factor | chr1:21025118-21025717 FORWARDmoderately similar to (241) loc_os02g07450 12002.m33577 protein nuclear transcription factor Y subunit C-2, putative, expressed seq=cds; coord=6:93496825..93502006:-1; parent_gene=GRMZM2G161680'

'moderately similar to (362) AT3G57670 | Symbols: NTT | NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding | chr3:21370936-21373121 FORWARDmoderately similar to (430) loc_os06g40960 12006.m08631 protein zinc finger protein, putative, expressed seq=cds; coord=6:117676121..117679658:1; parent_gene=GRMZM2G435357' 'very weakly similar to (93.6) AT2G04410 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Defence response, Rin4 (InterPro:IPR008700); BEST Arabidopsis thaliana protein match is: NOI (TAIR:AT5G55850.1); Has 141 Blast hits to 140 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 139; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:1534012-1535040 REVERSEweakly similar to (135) loc_os06g17870 12006.m06499 protein nitrate-induced NOI protein, putative, expressed seq=cds; coord=6:119855348..119858902:1; parent_gene=GRMZM2G162788'

'weakly similar to (189) AT1G10030 | Symbols: ERG28 | ERG28 (Arabidopsis homolog of yeast ergosterol28) | chr1:3273972-3275631 FORWARDmoderately similar to (219) loc_os12g43670 12012.m08141 protein erg28 like protein, expressed seq=cds; coord=6:124134969..124141392:1; parent_gene=GRMZM2G003064'

'moderately similar to (366) AT2G36770 | Symbols: | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr2:15415227-15416717 REVERSEweakly similar to (190) CZOG_SORBI Putative cis-zeatin O-glucosyltransferase (EC 2.4.1.215) - Sorghum bicolor (Sorghum) (Sorghum vulgare)highly similar to (630) loc_os05g08480 12005.m05364 protein cytokinin-O-glucosyltransferase 1, putative, expressed seq=cds; coord=6:128420261..128421880:1; parent_gene=GRMZM2G458776'

'moderately similar to (375) AT4G25730 | Symbols: | FtsJ-like methyltransferase family protein | chr4:13102906-13106718 REVERSEhighly similar to (537) loc_os05g49230 12005.m08993 protein adoMet-dependent rRNA methyltransferase spb1, putative, expressed seq=cds; coord=6:165089250..165094681:1; parent_gene=GRMZM2G128579'

'weakly similar to (127) AT2G30933 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: X8 (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: glucan endo-1,3-beta-glucosidase-related (TAIR:AT1G09460.1); Has 762 Blast hits to 726 proteins in 32 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 759; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:13165235-13166517 REVERSEvery weakly similar to (85.5) E13B_WHEAT Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-endoglucanase) - Triticum aestivum (Wheat)moderately similar to (205) loc_os05g50490 12005.m27988 protein expressed protein seq=cds; coord=6:166809944..166811348:-1; parent_gene=GRMZM2G163883'

'weakly similar to (127) AT2G30933 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: X8 (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: glucan endo-1,3-beta-glucosidase-related (TAIR:AT1G09460.1); Has 762 Blast hits to 726 proteins in 32 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 759; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr2:13165235-13166517 REVERSEvery weakly similar to (85.5) E13B_WHEAT Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-endoglucanase) - Triticum aestivum (Wheat)moderately similar to (205) loc_os05g50490 12005.m27988 protein expressed protein seq=cds; coord=6:166809944..166811348:-1; parent_gene=GRMZM2G163883'

'very weakly similar to (94.7) AT2G35910 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:15073225-15073878 REVERSEweakly similar to (152) loc_os07g06560 12007.m05116 protein RING-H2 finger protein ATL2I, putative seq=cds; coord=7:6139033..6139646:1; parent_gene=GRMZM2G029623'

'moderately similar to (201) AT3G22800 | Symbols: | leucine-rich repeat family protein / extensin family protein | chr3:8063063-8064475 REVERSEmoderately similar to (287) loc_os07g07990 12007.m05258 protein receptor protein kinase CLAVATA1 precursor, putative, expressed seq=cds; coord=7:9340555..9341531:-1; parent_gene=GRMZM2G153741'

'highly similar to (560) AT1G73100 | Symbols: SUVH3, SDG19 | SUVH3 (SU(VAR)3-9 HOMOLOG 3); histone methyltransferase | chr1:27491970-27493979 FORWARDnearly identical (1170) loc_os11g38900 12011.m07738 protein histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1, putative, expressed seq=cds; coord=7:20244021..20246591:1; parent_gene=AC233961.1_FG001'

'moderately similar to (207) AT4G19680 | Symbols: IRT2 | IRT2; iron ion transmembrane transporter/ zinc ion transmembrane transporter | chr4:10703385-10704621 FORWARDmoderately similar to (393) loc_os07g12890 12007.m28960 protein ZIP zinc/iron transport family protein, expressed seq=cds; coord=7:21798962..21800971:-1; parent_gene=GRMZM2G093276'

'weakly similar to (160) AT4G34960 | Symbols: | peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative | chr4:16648865-16650646 FORWARDweakly similar to (102) CYPH_MAIZE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) - Zea mays (Maize)weakly similar to (175) loc_os09g36670 12009.m06616 protein peptidyl-prolyl cis-trans isomerase CYP19-4 precursor, putative, expressed seq=cds; coord=7:30423336..30427964:1; parent_gene=GRMZM2G092072'

'very weakly similar to (100) AT3G45280 | Symbols: SYP72, ATSYP72 | SYP72 (SYNTAXIN OF PLANTS 72); protein transporter | chr3:16611445-16613304 REVERSEweakly similar to (136) loc_os09g19550 12009.m05163 protein syntaxin 72, putative seq=cds; coord=7:95533897..95534429:1; parent_gene=GRMZM2G360648'

'highly similar to (600) AT5G15080 | Symbols: | protein kinase, putative | chr5:4886414-4888555 FORWARDmoderately similar to (217) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (801) loc_os09g19700 12009.m05178 protein protein kinase APK1A, chloroplast precursor, putative, expressed seq=cds; coord=7:97336351..97341531:1; parent_gene=GRMZM2G132184'

'very weakly similar to (97.4) AT5G08690 | Symbols: | ATP synthase beta chain 2, mitochondrial | chr5:2825739-2828352 FORWARDweakly similar to (101) ATPBM_ORYSA ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Oryza sativa (Rice)weakly similar to (101) loc_os05g47980 12005.m08870 protein ATP synthase beta chain, mitochondrial precursor, putative, expressed seq=cds; coord=7:97688813..97735034:1; parent_gene=GRMZM2G405751'

'highly similar to (532) AT5G10190 | Symbols: | transporter-related | chr5:3199205-3201140 FORWARDhighly similar to (606) loc_os09g20490 12009.m05256 protein carbohydrate transporter/ sugar porter/ transporter, putative, expressed seq=cds; coord=7:100804201..100808837:-1; parent_gene=GRMZM2G176721'

'weakly similar to (171) loc_os04g02280 12004.m05541 protein F-box domain containing protein, expressed seq=cds; coord=7:114992560..114994386:1; parent_gene=GRMZM2G015349' 'moderately similar to (237) AT4G03140 | Symbols: | binding / catalytic/ oxidoreductase | chr4:1392191-1393662 FORWARDweakly similar to (192) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (368) loc_os07g40250 12007.m08266 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=7:162398192..162399451:1; parent_gene=GRMZM2G076981'

'weakly similar to (128) AT2G45100 | Symbols: | RNA polymerase II transcription factor/ protein binding / transcription activator/ transcription regulator/ translation initiation factor/ zinc ion binding | chr2:18595348-18598088 REVERSEweakly similar to (186) loc_os05g23940 12005.m06688 protein RNA polymerase II transcription factor/ transcription factor/ zinc ion binding protein, putative, expressed seq=cds; coord=9:2736110..2739733:-1; parent_gene=GRMZM2G180836'

'highly similar to (505) AT5G65090 | Symbols: MRH3, BST1, DER4 | BST1 (BRISTLED 1); hydrolase/ inositol or phosphatidylinositol phosphatase | chr5:26004837-26006656 FORWARDhighly similar to (706) loc_os06g11920 12006.m05909 protein hydrolase/ inositol or phosphatidylinositol phosphatase, putative, expressed seq=cds; coord=9:6006293..6008457:-1; parent_gene=GRMZM2G093772'

'weakly similar to (176) AT4G34990 | Symbols: AtMYB32 | AtMYB32 (myb domain protein 32); DNA binding / transcription factor | chr4:16661370-16662289 REVERSEmoderately similar to (426) MYBC_MAIZE Anthocyanin regulatory C1 protein - Zea mays (Maize)moderately similar to (276) loc_os06g10350 12006.m05753 protein anthocyanin regulatory C1 protein, putative, expressed seq=cds; coord=9:9740803..9741876:-1; parent_gene=GRMZM2G005066'

'moderately similar to (209) AT3G10610 | Symbols: | 40S ribosomal protein S17 (RPS17C) | chr3:3319459-3319881 FORWARDmoderately similar to (263) loc_os10g27190 12010.m05653 protein 40S ribosomal protein S17-4, putative, expressed seq=cds; coord=9:10319530..10320398:-1; parent_gene=GRMZM2G086906'

'highly similar to (765) AT2G36530 | Symbols: LOS2 | LOS2; copper ion binding / phosphopyruvate hydratase | chr2:15321081-15323786 REVERSEhighly similar to (882) ENO1_MAIZE Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1) - Zea mays (Maize)highly similar to (846) loc_os06g04510 12006.m05181 protein enolase 1, putative, expressed seq=cds; coord=9:22100864..22105552:1; parent_gene=GRMZM2G064302'

'nearly identical (1174) AT4G13780 | Symbols: | methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative | chr4:7993366-7998433 REVERSEnearly identical (1429) SYM_ORYSA Probable methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase) (MetRS) - Oryza sativa (Rice)nearly identical (1429) loc_os06g31210 12006.m07662 protein methionyl-tRNA synthetase, putative, expressed seq=cds; coord=9:146664972..146673514:1; parent_gene=GRMZM2G143450'

'moderately similar to (245) AT2G18540 | Symbols: | cupin family protein | chr2:8042382-8045008 REVERSEmoderately similar to (475) loc_os03g10110 12003.m06465 protein preproMP73, putative, expressed seq=cds; coord=9:148445803..148448625:-1; parent_gene=GRMZM2G078441'

'weakly similar to (113) AT5G65320 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr5:26107368-26108640 REVERSEmoderately similar to (253) loc_os03g08930 12003.m35054 protein helix-loop-helix-like protein, putative, expressed seq=cds; coord=9:149664143..149665651:-1; parent_gene=AC233899.1_FG002' 'nearly identical (1081) AT3G59420 | Symbols: ACR4 | ACR4 (ARABIDOPSIS CRINKLY4); kinase/ transmembrane receptor protein kinase | chr3:21959871-21962558 REVERSEnearly identical (1823) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1608) loc_os03g43670 12003.m09410 protein receptor protein kinase CRINKLY4 precursor, putative, expressed seq=cds; coord=10:5587952..5591862:1; parent_gene=GRMZM2G051637'

'highly similar to (706) AT3G14390 | Symbols: | diaminopimelate decarboxylase, putative / DAP carboxylase, putative | chr3:4806771-4808954 FORWARDhighly similar to (791) loc_os02g24354 12002.m07582 protein diaminopimelate decarboxylase, putative, expressed seq=cds; coord=10:5718777..5728532:-1; parent_gene=GRMZM2G020446'

'moderately similar to (331) AT5G04770 | Symbols: ATCAT6, CAT6 | CAT6 (CATIONIC AMINO ACID TRANSPORTER 6); amino acid transmembrane transporter/ basic amino acid transmembrane transporter/ cationic amino acid transmembrane transporter | chr5:1379118-1382304 FORWARDmoderately similar to (410) loc_os12g06060 12012.m04597 protein high-affinity cationic amino acid transporter 1, putative, expressed seq=cds; coord=10:6163655..6165665:-1; parent_gene=AC207755.3_FG005'

'moderately similar to (317) AT2G22240 | Symbols: ATMIPS2, MIPS2 | MIPS2 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase | chr2:9451901-9453375 REVERSEmoderately similar to (330) INO1_MAIZE Inositol-3-phosphate synthase (EC 5.5.1.4) (Myo-inositol-1-phosphate synthase) (MI-1-P synthase) (IPS) - Zea mays (Maize)moderately similar to (325) loc_os03g09250 12003.m35064 protein inositol-3-phosphate synthase, putative, expressed seq=cds; coord=10:11403432..11413687:-1; parent_gene=GRMZM2G392513'

'highly similar to (514) AT4G02500 | Symbols: ATXT2, XXT2, XT2 | XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase | chr4:1101638-1103345 FORWARDhighly similar to (543) loc_os03g18820 12003.m101316 protein glycosyltransferase 5, putative, expressed seq=cds; coord=10:135008283..135011071:1; parent_gene=GRMZM2G031453'

'very weakly similar to (87.4) AT1G28050 | Symbols: | zinc finger (B-box type) family protein | chr1:9775768-9777657 REVERSEmoderately similar to (486) loc_os08g42440 12008.m08222 protein CCT motif family protein, expressed seq=cds; coord=1:195557037..195561667:-1; parent_gene=GRMZM2G159996'

'highly similar to (563) AT1G52630 | Symbols: | unknown protein | chr1:19606470-19607848 REVERSEhighly similar to (709) loc_os08g42550 12008.m080223 protein AP2 domain containing protein, expressed seq=cds; coord=1:195775782..195780071:1; parent_gene=GRMZM2G080565'

'weakly similar to (135) AT2G47700 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:19552506-19554351 REVERSEhighly similar to (583) loc_os08g42640 12008.m08242 protein VIP2 protein, putative, expressed seq=cds; coord=1:196203304..196214408:1; parent_gene=GRMZM2G053027' 'highly similar to (884) AT1G09890 | Symbols: | lyase | chr1:3214237-3217386 REVERSEnearly identical (1221) loc_os08g44020 12008.m080048 protein lyase, putative, expressed seq=cds; coord=1:206155710..206160274:-1; parent_gene=GRMZM2G154124'

'weakly similar to (184) AT2G17730 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:7704142-7705312 FORWARDmoderately similar to (257) loc_os08g43670 12008.m08341 protein RING-H2 finger protein ATL2B, putative, expressed seq=cds; coord=1:206463126..206464716:1; parent_gene=GRMZM2G112617'

'moderately similar to (328) AT4G38660 | Symbols: | thaumatin, putative | chr4:18066448-18067792 REVERSEmoderately similar to (258) TLP1_PRUPE Thaumatin-like protein 1 precursor (PpAZ44) - Prunus persica (Peach)moderately similar to (438) loc_os08g43510 12008.m08325 protein thaumatin-like protein 1 precursor, putative, expressed seq=cds; coord=1:207035573..207037892:-1; parent_gene=GRMZM2G049057'

'weakly similar to (101) AT5G20630 | Symbols: GLP3, GLP3A, GLP3B, ATGER3, GER3 | GER3 (GERMIN 3); oxalate oxidase | chr5:6975315-6975950 REVERSEweakly similar to (103) GLP1_SINAL Germin-like protein 1 precursor - Sinapis alba (White mustard) (Brassica hirta)weakly similar to (114) loc_os08g35750 12008.m07564 protein germin-like protein 1 precursor, putative, expressed seq=cds; coord=1:207865153..207865778:-1; parent_gene=GRMZM2G363004'

'very weakly similar to (82.8) AT3G14200 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr3:4712881-4714361 REVERSEweakly similar to (136) loc_os08g35160 12008.m26703 protein chaperone protein dnaJ, putative, expressed seq=cds; coord=1:209125639..209127498:-1; parent_gene=GRMZM2G059502'

'weakly similar to (122) AT5G17520 | Symbols: RCP1, MEX1 | RCP1 (ROOT CAP 1); maltose transmembrane transporter | chr5:5772796-5775231 REVERSEweakly similar to (155) MEX1_ORYSA Maltose excess protein 1-like, chloroplast precursor - Oryza sativa (Rice)weakly similar to (155) loc_os04g51330 12004.m10029 protein maltose excess protein 1-like, chloroplast precursor, putative, expressed seq=cds; coord=1:209220135..209222754:1; parent_gene=GRMZM2G053037'

'weakly similar to (130) AT5G66590 | Symbols: | allergen V5/Tpx-1-related family protein | chr5:26574255-26574812 FORWARDweakly similar to (131) ST14_SOLTU STS14 protein precursor - Solanum tuberosum (Potato)weakly similar to (124) loc_os03g52300 12003.m10207 protein conserved hypothetical protein seq=cds; coord=1:273298297..273299437:-1; parent_gene=GRMZM2G481194'

'weakly similar to (130) AT5G66590 | Symbols: | allergen V5/Tpx-1-related family protein | chr5:26574255-26574812 FORWARDweakly similar to (131) ST14_SOLTU STS14 protein precursor - Solanum tuberosum (Potato)weakly similar to (124) loc_os03g52300 12003.m10207 protein conserved hypothetical protein seq=cds; coord=1:273298297..273299437:-1; parent_gene=GRMZM2G481194'

'highly similar to (816) AT5G15810 | Symbols: | N2,N2-dimethylguanosine tRNA methyltransferase family protein | chr5:5157798-5161121 FORWARDhighly similar to (897) loc_os03g57280 12003.m10646 protein N-dimethylguanosine tRNA methyltransferase, putative, expressed seq=cds; coord=1:290957733..290965627:-1; parent_gene=GRMZM2G077079' 'highly similar to (832) AT4G30560 | Symbols: ATCNGC9, CNGC9 | ATCNGC9 (CYCLIC NUCLEOTIDE GATED CHANNEL 9); calmodulin binding / cyclic nucleotide binding / ion channel | chr4:14926974-14929681 REVERSEnearly identical (1168) loc_os04g55080 12004.m10400 protein cyclic nucleotide-gated ion channel 9, putative, expressed seq=cds; coord=2:6019299..6030234:-1; parent_gene=GRMZM2G023037'

'moderately similar to (207) AT5G23230 | Symbols: NIC2 | NIC2 (NICOTINAMIDASE 2); catalytic/ nicotinamidase | chr5:7826005-7826601 REVERSEmoderately similar to (330) loc_os04g44420 12004.m09401 protein isochorismatase, putative, expressed seq=cds; coord=2:26875237..26876162:1; parent_gene=GRMZM2G362413'

'moderately similar to (204) AT3G59110 | Symbols: | protein kinase family protein | chr3:21855673-21857847 FORWARDweakly similar to (199) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (586) loc_os04g39180 12004.m08907 protein nodulation receptor kinase precursor, putative, expressed seq=cds; coord=2:40493826..40495596:1; parent_gene=GRMZM2G179268'

'moderately similar to (207) AT2G16250 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr2:7039682-7042933 REVERSEweakly similar to (106) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)moderately similar to (303) loc_os03g51440 12003.m10123 protein ATP binding protein, putative, expressed seq=cds; coord=2:104961688..104969752:1; parent_gene=GRMZM2G463227'

'moderately similar to (236) AT4G23900 | Symbols: | nucleoside diphosphate kinase 4 (NDK4) | chr4:12424505-12426318 FORWARDmoderately similar to (231) NDK4_SPIOL Nucleoside diphosphate kinase 4, chloroplast precursor (EC 2.7.4.6) (Nucleoside diphosphate kinase IV) (NDK IV) (NDP kinase IV) (NDPK IV) (Nucleoside diphosphate kinase III) - Spinacia oleracea (Spinach)moderately similar to (238) loc_os05g51700 12005.m083838 protein nucleoside diphosphate kinase 4, chloroplast precursor, putative, expressed seq=cds; coord=2:128936549..128937471:1; parent_gene=GRMZM2G001524'

'moderately similar to (211) AT1G21640 | Symbols: NADK2, ATNADK2 | NADK2; NAD

'weakly similar to (110) AT1G71860 | Symbols: PTP1, ATPTP1 | PTP1 (PROTEIN TYROSINE PHOSPHATASE 1); protein tyrosine phosphatase | chr1:27026866-27028675 FORWARDweakly similar to (172) loc_os12g07590 12012.m073780 protein receptor-type tyrosine-protein phosphatase S precursor, putative, expressed seq=cds; coord=2:132080689..132083859:1; parent_gene=GRMZM2G416491'

'weakly similar to (145) AT2G36090 | Symbols: | F-box family protein | chr2:15158631-15159584 FORWARDmoderately similar to (330) loc_os11g05660 12011.m04763 protein F-box domain containing protein, expressed seq=cds; coord=2:143043779..143045537:1; parent_gene=GRMZM2G348855'

'moderately similar to (382) AT1G35910 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr1:13363200-13364965 REVERSEmoderately similar to (413) loc_os07g43160 12007.m08544 protein expressed protein seq=cds; coord=2:212477947..212480732:1; parent_gene=GRMZM2G117564' 'moderately similar to (448) AT5G48910 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:19832969-19834909 REVERSEvery weakly similar to (80.5) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)moderately similar to (438) loc_os01g51790 12001.m11356 protein selenium-binding protein-like, putative seq=cds; coord=2:213162946..213164673:1; parent_gene=GRMZM2G703373'

'weakly similar to (124) AT5G37820 | Symbols: NIP4;2, NLM5 | NIP4;2 (NOD26-LIKE INTRINSIC PROTEIN 4;2); water channel | chr5:15050261-15051542 FORWARDweakly similar to (104) NO26_SOYBN Nodulin-26 (N-26) - Glycine max (Soybean)moderately similar to (286) loc_os01g02190 12001.m06861 protein aquaporin NIP1.1, putative, expressed seq=cds; coord=3:28230487..28232296:1; parent_gene=GRMZM2G103214'

'moderately similar to (490) AT1G53300 | Symbols: TTL1 | TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN LIKE 1); binding | chr1:19879726-19882375 FORWARDhighly similar to (828) loc_os01g42960 12001.m10559 protein electron transporter, putative, expressed seq=cds; coord=3:225545980..225550303:1; parent_gene=GRMZM2G093436'

'moderately similar to (490) AT1G53300 | Symbols: TTL1 | TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN LIKE 1); binding | chr1:19879726-19882375 FORWARDhighly similar to (828) loc_os01g42960 12001.m10559 protein electron transporter, putative, expressed seq=cds; coord=3:225545980..225550303:1; parent_gene=GRMZM2G093436'

'moderately similar to (266) AT5G53970 | Symbols: | aminotransferase, putative | chr5:21910676-21912594 FORWARDhighly similar to (597) loc_os11g42510 12011.m28857 protein tyrosine aminotransferase, putative, expressed seq=cds; coord=4:3888587..3891491:1; parent_gene=GRMZM2G006480'

'very weakly similar to (99.0) AT4G12600 | Symbols: | ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr4:7453296-7454208 FORWARDweakly similar to (102) loc_os03g13800 12003.m06824 protein NHP2-like protein 1, putative, expressed seq=cds; coord=4:4706034..4706834:-1; parent_gene=GRMZM2G089830'

'very weakly similar to (99.0) AT4G12600 | Symbols: | ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | chr4:7453296-7454208 FORWARDweakly similar to (102) loc_os03g13800 12003.m06824 protein NHP2-like protein 1, putative, expressed seq=cds; coord=4:4706034..4706834:-1; parent_gene=GRMZM2G089830'

'weakly similar to (170) AT2G45850 | Symbols: | DNA-binding family protein | chr2:18871901-18873457 REVERSEmoderately similar to (430) loc_os02g57820 12002.m10803 protein DNA binding protein, putative, expressed seq=cds; coord=4:169553785..169558577:1; parent_gene=GRMZM2G123887'

'moderately similar to (481) AT2G03220 | Symbols: FT1, ATFUT1, ATFT1, MUR2 | FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups | chr2:970401-972353 REVERSEmoderately similar to (473) FUT1_PEA Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1) - Pisum sativum (Garden pea)highly similar to (840) loc_os02g52560 12002.m10287 protein galactoside 2-alpha-L-fucosyltransferase, putative, expressed seq=cds; coord=4:178671950..178675419:1; parent_gene=GRMZM2G015983' 'moderately similar to (481) AT2G03220 | Symbols: FT1, ATFUT1, ATFT1, MUR2 | FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups | chr2:970401-972353 REVERSEmoderately similar to (473) FUT1_PEA Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1) - Pisum sativum (Garden pea)highly similar to (840) loc_os02g52560 12002.m10287 protein galactoside 2-alpha-L-fucosyltransferase, putative, expressed seq=cds; coord=4:178671950..178675419:1; parent_gene=GRMZM2G015983'

'moderately similar to (400) AT4G39770 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr4:18449138-18451218 REVERSEhighly similar to (531) loc_os02g51680 12002.m10199 protein expressed protein seq=cds; coord=4:180885525..180888567:-1; parent_gene=GRMZM2G151044'

'highly similar to (555) AT5G09360 | Symbols: LAC14 | LAC14 (laccase 14); laccase | chr5:2906426-2908658 REVERSEmoderately similar to (207) ASO_CUCMA L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) (ASO) - Cucurbita maxima (Pumpkin) (Winter squash)highly similar to (750) loc_os02g51440 12002.m10178 protein laccase, putative seq=cds; coord=4:181527348..181530838:1; parent_gene=GRMZM2G169033'

'nearly identical (1029) AT2G37050 | Symbols: | kinase | chr2:15569290-15573477 FORWARDmoderately similar to (377) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)nearly identical (1427) loc_os11g01200 12011.m079924 protein transposon protein, putative, unclassified, expressed seq=cds; coord=4:183207728..183213465:1; parent_gene=GRMZM2G091632'

'moderately similar to (283) AT2G40300 | Symbols: ATFER4 | ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding | chr2:16831501-16833214 REVERSEmoderately similar to (402) FRI1_MAIZE Ferritin-1, chloroplast precursor (EC 1.16.3.1) (ZmFer1) - Zea mays (Maize)moderately similar to (351) loc_os12g01530 12012.m26727 protein ferritin-1, chloroplast precursor, putative, expressed seq=cds; coord=4:183588190..183591209:-1; parent_gene=GRMZM2G325575'

'moderately similar to (400) AT5G05340 | Symbols: | peroxidase, putative | chr5:1579142-1580819 REVERSEmoderately similar to (385) PERP7_BRARA Peroxidase P7 (EC 1.11.1.7) (TP7) - Brassica rapa (Turnip)highly similar to (524) loc_os11g02130 12011.m04413 protein peroxidase 52 precursor, putative, expressed seq=cds; coord=4:183941776..183944103:1; parent_gene=AC197758.3_FG004'

'very weakly similar to (94.0) AT5G40190 | Symbols: | calmodulin-binding protein | chr5:16069298-16069849 REVERSEweakly similar to (174) loc_os09g20860 12009.m05293 protein calmodulin binding protein, putative, expressed seq=cds; coord=4:224779693..224780609:-1; parent_gene=GRMZM2G085022'

'moderately similar to (307) AT5G45775 | Symbols: | 60S ribosomal protein L11 (RPL11D) | chr5:18565281-18566496 REVERSEmoderately similar to (314) RL11_ORYSA 60S ribosomal protein L11 - Oryza sativa (Rice)moderately similar to (317) loc_os02g14059 12002.m77785 protein 60S ribosomal protein L11-1, putative, expressed seq=cds; coord=4:228642879..228646247:1; parent_gene=GRMZM2G018770' 'weakly similar to (192) AT1G32150 | Symbols: | bZIP transcription factor family protein | chr1:11566022-11568317 FORWARDmoderately similar to (351) HBP1A_WHEAT Transcription factor HBP-1a (Histone-specific transcription factor HBP1) - Triticum aestivum (Wheat)moderately similar to (369) loc_os02g03580 12002.m77766 protein transcription factor HBP-1a, putative, expressed seq=cds; coord=4:238990853..238994795:1; parent_gene=GRMZM2G019106'

'moderately similar to (298) AT3G02100 | Symbols: | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr3:368840-370484 REVERSEweakly similar to (155) IAAG_MAIZE Indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) (IAA-Glu synthetase) ((Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase) - Zea mays (Maize)highly similar to (532) loc_os03g55030 12003.m35419 protein glucosyl transferase, putative, expressed seq=cds; coord=5:6776441..6778115:1; parent_gene=GRMZM2G030821'

'highly similar to (855) AT5G39040 | Symbols: ATTAP2, TAP2 | ATTAP2; ATPase, coupled to transmembrane movement of substances / transporter | chr5:15625660-15629621 FORWARDmoderately similar to (316) MDR_ORYSA Putative multidrug resistance protein (P-glycoprotein) - Oryza sativa (Rice)nearly identical (1053) loc_os03g54790 12003.m10395 protein ATP-binding cassette sub-family B member 10, mitochondrial precursor, putative, expressed seq=cds; coord=5:6877441..6883253:-1; parent_gene=GRMZM2G072071'

'moderately similar to (375) AT3G22750 | Symbols: | protein kinase, putative | chr3:8037364-8039096 REVERSEhighly similar to (538) loc_os03g53410 12003.m10311 protein ATMRK1, putative, expressed seq=cds; coord=5:7587329..7589198:-1; parent_gene=GRMZM2G014618'

'highly similar to (677) AT1G58520 | Symbols: RXW8 | hydrolase, acting on ester bonds / lipase | chr1:21729913-21731344 FORWARDnearly identical (1130) loc_os03g51620 12003.m10140 protein RXW8, putative, expressed seq=cds; coord=5:9372046..9377144:1; parent_gene=GRMZM2G164470'

'moderately similar to (231) AT1G17950 | Symbols: ATMYB52, BW52, MYB52 | MYB52 (MYB DOMAIN PROTEIN 52); DNA binding / transcription factor | chr1:6177764-6179063 FORWARDweakly similar to (102) MYBC_MAIZE Anthocyanin regulatory C1 protein - Zea mays (Maize)moderately similar to (355) loc_os03g51110 12003.m10092 protein MYB52, putative, expressed seq=cds; coord=5:10172933..10174782:1; parent_gene=GRMZM2G455869'

'moderately similar to (231) AT1G17950 | Symbols: ATMYB52, BW52, MYB52 | MYB52 (MYB DOMAIN PROTEIN 52); DNA binding / transcription factor | chr1:6177764-6179063 FORWARDweakly similar to (102) MYBC_MAIZE Anthocyanin regulatory C1 protein - Zea mays (Maize)moderately similar to (355) loc_os03g51110 12003.m10092 protein MYB52, putative, expressed seq=cds; coord=5:10172933..10174782:1; parent_gene=GRMZM2G455869'

'moderately similar to (231) AT1G17950 | Symbols: ATMYB52, BW52, MYB52 | MYB52 (MYB DOMAIN PROTEIN 52); DNA binding / transcription factor | chr1:6177764-6179063 FORWARDweakly similar to (102) MYBC_MAIZE Anthocyanin regulatory C1 protein - Zea mays (Maize)moderately similar to (355) loc_os03g51110 12003.m10092 protein MYB52, putative, expressed seq=cds; coord=5:10172933..10174782:1; parent_gene=GRMZM2G455869'

'very weakly similar to (84.7) AT3G61610 | Symbols: | aldose 1-epimerase family protein | chr3:22799480-22801029 FORWARDweakly similar to (103) loc_os05g49430 12005.m09013 protein apospory-associated protein C, putative, expressed seq=cds; coord=6:165349659..165351490:1; parent_gene=GRMZM2G011662' 'moderately similar to (298) AT2G42990 | Symbols: | GDSL-motif lipase/hydrolase family protein | chr2:17879056-17880200 FORWARDweakly similar to (184) APG_BRANA Anter-specific proline-rich protein APG (Protein CEX) (Fragment) - Brassica napus (Rape)moderately similar to (480) loc_os09g04710 12009.m21966 protein anther-specific proline-rich protein APG precursor, putative, expressed seq=cds; coord=7:68344363..68349450:-1; parent_gene=GRMZM2G088919'

'weakly similar to (197) AT5G50850 | Symbols: MAB1 | MAB1 (MACCI-BOU); catalytic/ pyruvate dehydrogenase (acetyl-transferring) | chr5:20689671-20692976 FORWARDmoderately similar to (206) ODPB_PEA Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B) - Pisum sativum (Garden pea)moderately similar to (229) loc_os09g33500 12009.m22013 protein pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor, putative, expressed seq=cds; coord=7:135836369..135839558:-1; parent_gene=GRMZM2G128121'

'moderately similar to (304) AT2G05840 | Symbols: PAA2 | PAA2 (20S PROTEASOME SUBUNIT PAA2); endopeptidase/ peptidase/ threonine-type endopeptidase | chr2:2234226-2235973 FORWARDmoderately similar to (314) PSA6_TOBAC Proteasome subunit alpha type 6 (EC 3.4.25.1) (20S proteasome alpha subunit A) (20S proteasome subunit alpha-1) - Nicotiana tabacum (Common tobacco)moderately similar to (306) loc_os03g08280 12003.m101213 protein proteasome subunit alpha type 6, putative, expressed seq=cds; coord=7:165345022..165349965:-1; parent_gene=GRMZM2G080549'

'very weakly similar to (99.8) AT1G30210 | Symbols: TCP24 | TCP24 (TEOSINTE BRANCHED1, CYCLOIDEA, AND PCF FAMILY 24); transcription factor | chr1:10628754-10629728 REVERSEmoderately similar to (239) loc_os12g42190 12012.m07998 protein transposon protein, putative, unclassified, expressed seq=cds; coord=7:168217960..168219041:-1; parent_gene=GRMZM2G180568'

'very weakly similar to (99.8) AT1G30210 | Symbols: TCP24 | TCP24 (TEOSINTE BRANCHED1, CYCLOIDEA, AND PCF FAMILY 24); transcription factor | chr1:10628754-10629728 REVERSEmoderately similar to (239) loc_os12g42190 12012.m07998 protein transposon protein, putative, unclassified, expressed seq=cds; coord=7:168217960..168219041:-1; parent_gene=GRMZM2G180568'

'very weakly similar to (99.8) AT1G30210 | Symbols: TCP24 | TCP24 (TEOSINTE BRANCHED1, CYCLOIDEA, AND PCF FAMILY 24); transcription factor | chr1:10628754-10629728 REVERSEmoderately similar to (239) loc_os12g42190 12012.m07998 protein transposon protein, putative, unclassified, expressed seq=cds; coord=7:168217960..168219041:-1; parent_gene=GRMZM2G180568'

'highly similar to (528) AT5G66190 | Symbols: ATLFNR1 | FNR1 (FERREDOXIN-NADP(

'highly similar to (912) AT4G33650 | Symbols: ADL2, DRP3A | DRP3A (DYNAMIN-RELATED PROTEIN 3A); GTP binding / GTPase/ phosphoinositide binding | chr4:16161073-16166587 FORWARDnearly identical (1281) loc_os01g69130 12001.m150447 protein dynamin-related protein 3A, putative, expressed seq=cds; coord=8:161744495..161753951:1; parent_gene=GRMZM2G180335' 'weakly similar to (198) AT3G12600 | Symbols: atnudt16 | atnudt16 (Arabidopsis thaliana Nudix hydrolase homolog 16); hydrolase | chr3:4004676-4005995 FORWARDmoderately similar to (248) loc_os04g53380 12004.m10229 protein expressed protein seq=cds; coord=8:161926660..161930458:1; parent_gene=GRMZM2G013060'

'very weakly similar to (82.8) loc_os01g06320 12001.m07262 protein myb-like DNA-binding domain, SHAQKYF class family protein, expressed seq=cds; coord=8:162230463..162234568:-1; parent_gene=GRMZM2G107504'

'weakly similar to (130) loc_os05g05650 12005.m05092 protein SRC2, putative, expressed seq=cds; coord=10:90044647..90045538:1; parent_gene=GRMZM2G367330'

'moderately similar to (412) AT3G59950 | Symbols: | autophagy 4b (APG4b) | chr3:22145559-22146629 REVERSEhighly similar to (671) loc_os04g58560 12004.m79009 protein cysteine protease ATG4B, putative, expressed seq=cds; coord=10:148530254..148533742:-1; parent_gene=GRMZM2G173682'

'moderately similar to (412) AT3G59950 | Symbols: | autophagy 4b (APG4b) | chr3:22145559-22146629 REVERSEhighly similar to (671) loc_os04g58560 12004.m79009 protein cysteine protease ATG4B, putative, expressed seq=cds; coord=10:148530254..148533742:-1; parent_gene=GRMZM2G173682'

'moderately similar to (358) AT1G60600 | Symbols: ABC4 | ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4); 1,4-dihydroxy-2-naphthoate octaprenyltransferase/ prenyltransferase | chr1:22324807-22326759 REVERSEmoderately similar to (486) loc_os03g09060 12003.m06412 protein 1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative, expressed seq=cds; coord=1:19557389..19560305:1; parent_gene=GRMZM2G097283'

'moderately similar to (358) AT1G60600 | Symbols: ABC4 | ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4); 1,4-dihydroxy-2-naphthoate octaprenyltransferase/ prenyltransferase | chr1:22324807-22326759 REVERSEmoderately similar to (486) loc_os03g09060 12003.m06412 protein 1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative, expressed seq=cds; coord=1:19557389..19560305:1; parent_gene=GRMZM2G097283'

'moderately similar to (416) AT5G64970 | Symbols: | mitochondrial substrate carrier family protein | chr5:25958806-25960443 REVERSEweakly similar to (124) BT1_MAIZE Protein brittle-1, chloroplast precursor - Zea mays (Maize)moderately similar to (480) loc_os03g09110 12003.m06417 protein protein brittle-1, chloroplast precursor, putative, expressed seq=cds; coord=1:19817412..19820448:-1; parent_gene=GRMZM2G147481'

'moderately similar to (416) AT5G64970 | Symbols: | mitochondrial substrate carrier family protein | chr5:25958806-25960443 REVERSEweakly similar to (124) BT1_MAIZE Protein brittle-1, chloroplast precursor - Zea mays (Maize)moderately similar to (480) loc_os03g09110 12003.m06417 protein protein brittle-1, chloroplast precursor, putative, expressed seq=cds; coord=1:19817412..19820448:-1; parent_gene=GRMZM2G147481'

'moderately similar to (384) AT3G11180 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr3:3504249-3506688 FORWARDmoderately similar to (204) LDOX_MALDO Leucoanthocyanidin dioxygenase (EC 1.14.11.19) (LDOX) (Leucocyanidin oxygenase) (Leucoanthocyanidin hydroxylase) (Anthocyanidin synthase) - Malus domestica (Apple) (Malus sylvestris)highly similar to (520) loc_os03g18030 12003.m101308 protein leucoanthocyanidin dioxygenase, putative, expressed seq=cds; coord=1:44955003..44960551:-1; parent_gene=AC212219.3_FG005' 'weakly similar to (126) AT3G05870 | Symbols: APC11 | APC11; protein binding / ubiquitin-protein ligase/ zinc ion binding | chr3:1754463-1754802 FORWARDweakly similar to (197) loc_os03g19059 12003.m101651 protein anaphase-promoting complex subunit 11, putative, expressed seq=cds; coord=1:47900337..47901226:1; parent_gene=GRMZM2G162356'

'moderately similar to (202) AT5G52840 | Symbols: | NADH-ubiquinone oxidoreductase-related | chr5:21413718-21414794 FORWARDmoderately similar to (260) loc_os03g19890 12003.m07402 protein NADH-ubiquinone oxidoreductase 13 kDa-B subunit, putative, expressed seq=cds; coord=1:51013925..51015964:1; parent_gene=GRMZM2G018941'

'moderately similar to (219) AT2G40620 | Symbols: | bZIP transcription factor family protein | chr2:16954804-16956872 REVERSEmoderately similar to (323) RF2B_ORYSA Transcription factor RF2b - Oryza sativa (Rice)moderately similar to (324) loc_os03g21800 12003.m101333 protein transcription factor RF2b, putative, expressed seq=cds; coord=1:56215993..56221441:1; parent_gene=GRMZM2G062391'

'very weakly similar to (83.6) loc_os04g42580 12004.m09225 protein carboxyvinyl-carboxyphosphonate phosphorylmutase, putative, expressed seq=cds; coord=1:156159993..156161051:-1; parent_gene=AC210816.3_FG007'

'moderately similar to (201) AT4G15417 | Symbols: ATRTL1 | ATRTL1 (ARABIDOPSIS THALIANA RNASEIII-LIKE 1); RNA binding / ribonuclease III | chr4:8821759-8822991 FORWARDmoderately similar to (410) loc_os06g25250 12006.m07173 protein endoribonuclease Dicer, putative, expressed seq=cds; coord=1:220775956..220779312:1; parent_gene=GRMZM2G101105'

'moderately similar to (347) AT2G46620 | Symbols: | AAA-type ATPase family protein | chr2:19139071-19140546 REVERSEhighly similar to (650) loc_os10g37500 12010.m06538 protein ATP binding protein, putative, expressed seq=cds; coord=1:222980062..222981812:1; parent_gene=GRMZM2G170982'

'highly similar to (580) AT3G63240 | Symbols: | endonuclease/exonuclease/phosphatase family protein | chr3:23364411-23366876 REVERSEhighly similar to (866) loc_os10g28660 12010.m05745 protein type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2, putative, expressed seq=cds; coord=1:240379493..240383889:1; parent_gene=GRMZM2G017237'

'weakly similar to (179) loc_os04g56680 12004.m10555 protein OsSAUR22 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=2:3597793..3599010:1; parent_gene=GRMZM2G365162'

'weakly similar to (179) loc_os04g56680 12004.m10555 protein OsSAUR22 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=2:3597793..3599010:1; parent_gene=GRMZM2G365162'

'highly similar to (571) AT4G27650 | Symbols: PEL1 | PEL1 (PELOTA); translation release factor | chr4:13803459-13807556 REVERSEhighly similar to (660) loc_os04g56480 12004.m101682 protein protein pelota, putative, expressed seq=cds; coord=2:3923303..3934103:-1; parent_gene=GRMZM2G044011'

'moderately similar to (294) AT1G73110 | Symbols: | ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative | chr1:27494344-27496844 REVERSEmoderately similar to (202) RCA_MAIZE Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase) (RA) - Zea mays (Maize)moderately similar to (344) loc_os04g56320 12004.m10522 protein ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor, putative, expressed seq=cds; coord=2:4159971..4163217:1; parent_gene=GRMZM2G039345'

'weakly similar to (179) AT5G57330 | Symbols: | aldose 1-epimerase family protein | chr5:23218392-23220664 FORWARDmoderately similar to (216) loc_os04g56290 12004.m35496 protein apospory-associated protein C, putative, expressed seq=cds; coord=2:4174781..4178923:-1; parent_gene=GRMZM2G039588'

'moderately similar to (268) AT4G36920 | Symbols: AP2, FLO2, FL1 | AP2 (APETALA 2); transcription factor | chr4:17400998-17403140 FORWARDweakly similar to (130) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)moderately similar to (382) loc_os04g55560 12004.m35488 protein AP2 domain containing protein, expressed seq=cds; coord=2:5514479..5518846:-1; parent_gene=GRMZM2G174784'

'weakly similar to (113) AT2G46680 | Symbols: ATHB-7, ATHB7 | ATHB-7 (ARABIDOPSIS THALIANA HOMEOBOX 7); transcription activator/ transcription factor | chr2:19165777-19166773 REVERSEmoderately similar to (246) loc_os04g45810 12004.m09532 protein homeodomain-leucine zipper transcription factor TaHDZipI-1, putative, expressed seq=cds; coord=2:21596800..21598107:1; parent_gene=GRMZM2G351330'

'weakly similar to (140) AT5G66320 | Symbols: | zinc finger (GATA type) family protein | chr5:26496208-26497309 REVERSEweakly similar to (187) loc_os04g45650 12004.m35556 protein expressed protein seq=cds; coord=2:22069136..22071156:-1; parent_gene=GRMZM2G404973'

'moderately similar to (201) AT4G37925 | Symbols: NDH-M | NDH-M (subunit NDH-M of NAD(P)H:plastoquinone dehydrogenase complex) | chr4:17830748-17831485 REVERSEmoderately similar to (273) loc_os04g45600 12004.m09513 protein expressed protein seq=cds; coord=2:22192252..22193718:-1; parent_gene=GRMZM2G109244'

'moderately similar to (201) AT4G37925 | Symbols: NDH-M | NDH-M (subunit NDH-M of NAD(P)H:plastoquinone dehydrogenase complex) | chr4:17830748-17831485 REVERSEmoderately similar to (273) loc_os04g45600 12004.m09513 protein expressed protein seq=cds; coord=2:22192252..22193718:-1; parent_gene=GRMZM2G109244'

'moderately similar to (294) AT3G02070 | Symbols: | OTU-like cysteine protease family protein | chr3:361368-363132 FORWARDmoderately similar to (361) loc_os04g32970 12004.m08394 protein cysteine-type peptidase, putative, expressed seq=cds; coord=2:61323307..61328436:-1; parent_gene=GRMZM2G122239'

'moderately similar to (432) AT4G34220 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr4:16381653-16384054 REVERSEweakly similar to (112) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (897) loc_os09g02250 12009.m059931 protein transposon protein, putative, unclassified, expressed seq=cds; coord=2:163676823..163680091:1; parent_gene=GRMZM2G163724' 'moderately similar to (327) AT1G68090 | Symbols: ANNAT5, ANN5 | ANN5; calcium ion binding / calcium-dependent phospholipid binding | chr1:25519442-25520774 REVERSEmoderately similar to (209) ANX4_FRAAN Annexin-like protein RJ4 - Fragaria ananassa (Strawberry)highly similar to (572) loc_os09g23160 12009.m059972 protein annexin A4, putative, expressed seq=cds; coord=2:178875051..178880178:1; parent_gene=GRMZM2G009136'

'moderately similar to (434) AT3G20810 | Symbols: | transcription factor jumonji (jmjC) domain-containing protein | chr3:7275814-7278182 FORWARDhighly similar to (523) loc_os09g31380 12009.m06252 protein conserved hypothetical protein seq=cds; coord=2:189777176..189782078:1; parent_gene=GRMZM2G052908'

'weakly similar to (122) loc_os09g32430 12009.m06331 protein oxidoreductase, putative, expressed seq=cds; coord=2:191156336..191157580:-1; parent_gene=GRMZM2G087312'

'highly similar to (545) AT4G28880 | Symbols: ckl3 | ckl3 (Casein Kinase I-like 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr4:14251351-14254048 FORWARDhighly similar to (683) loc_os01g13060 12001.m150523 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=3:1885669..1901782:-1; parent_gene=GRMZM2G156035'

'highly similar to (545) AT4G28880 | Symbols: ckl3 | ckl3 (Casein Kinase I-like 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr4:14251351-14254048 FORWARDhighly similar to (683) loc_os01g13060 12001.m150523 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=3:1885669..1901782:-1; parent_gene=GRMZM2G156035'

'highly similar to (545) AT4G28880 | Symbols: ckl3 | ckl3 (Casein Kinase I-like 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr4:14251351-14254048 FORWARDhighly similar to (683) loc_os01g13060 12001.m150523 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=3:1885669..1901782:-1; parent_gene=GRMZM2G156035'

'weakly similar to (112) loc_os01g10470 12001.m07668 protein RALF precursor, putative, expressed seq=cds; coord=3:4752687..4753608:-1; parent_gene=GRMZM2G357124'

'very weakly similar to (84.3) AT2G16120 | Symbols: | mannitol transporter, putative | chr2:6996727-6998441 REVERSEweakly similar to (146) loc_os11g41840 12011.m08022 protein arabinose-proton symporter, putative seq=cds; coord=3:10319432..10322897:-1; parent_gene=GRMZM2G429964'

'highly similar to (822) AT1G15460 | Symbols: ATBOR4, BOR4 | BOR4 (REQUIRES HIGH BORON 4); anion exchanger | chr1:5310196-5313376 REVERSEnearly identical (1013) loc_os01g08020 12001.m07427 protein boron transporter-like protein 2, putative, expressed seq=cds; coord=3:10934126..10940345:-1; parent_gene=GRMZM2G051753'

'moderately similar to (468) AT1G06890 | Symbols: | transporter-related | chr1:2111728-2114038 REVERSEhighly similar to (557) loc_os01g07310 12001.m43446 protein integral membrane protein like, putative, expressed seq=cds; coord=3:13589786..13593160:1; parent_gene=GRMZM2G116053' 'moderately similar to (383) AT3G05840 | Symbols: ATSK12 | ATSK12; protein kinase/ protein serine/threonine kinase | chr3:1740793-1742927 FORWARDmoderately similar to (384) MSK3_MEDSA Glycogen synthase kinase-3 homolog MsK-3 (EC 2.7.11.1) - Medicago sativa (Alfalfa)moderately similar to (410) loc_os01g14860 12001.m43459 protein glycogen synthase kinase-3 homolog MsK-3, putative, expressed seq=cds; coord=3:13917982..13919834:-1; parent_gene=GRMZM2G129482'

'moderately similar to (261) AT5G16450 | Symbols: | dimethylmenaquinone methyltransferase family protein | chr5:5374357-5375342 FORWARDmoderately similar to (306) loc_os01g52460 12001.m11420 protein regulator of ribonuclease activity A, putative, expressed seq=cds; coord=3:17033772..17034278:1; parent_gene=AC215260.3_FG004'

'weakly similar to (182) AT3G49910 | Symbols: | 60S ribosomal protein L26 (RPL26A) | chr3:18504311-18504751 FORWARDweakly similar to (166) RL26_BRARA 60S ribosomal protein L26 - Brassica rapa (Turnip)moderately similar to (208) loc_os12g05430 12012.m04536 protein 60S ribosomal protein L26-1, putative, expressed seq=cds; coord=3:19669523..19670484:-1; parent_gene=GRMZM2G327564'

'highly similar to (516) AT3G17510 | Symbols: CIPK1, SnRK3.16 | CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding | chr3:5989309-5992627 REVERSEmoderately similar to (389) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)highly similar to (749) loc_os01g18800 12001.m150556 protein CBL-interacting serine/threonine-protein kinase 1, putative, expressed seq=cds; coord=3:50604991..50610043:-1; parent_gene=GRMZM2G170120'

'weakly similar to (116) AT3G21460 | Symbols: | electron carrier/ protein disulfide oxidoreductase | chr3:7557567-7557875 REVERSEweakly similar to (176) loc_os01g27140 12001.m09165 protein glutaredoxin, putative, expressed seq=cds; coord=3:68751791..68752302:-1; parent_gene=GRMZM2G110286'

'highly similar to (585) AT1G79460 | Symbols: GA2, KS, ATKS | GA2 (GA REQUIRING 2); ent-kaurene synthase | chr1:29890568-29894436 FORWARDhighly similar to (575) KSB_CUCMA Ent-kaurene synthase B, chloroplast precursor (EC 4.2.3.19) (KSB) - Cucurbita maxima (Pumpkin) (Winter squash)highly similar to (755) loc_os02g36220 12002.m100242 protein ent-kaurene synthase B, chloroplast precursor, putative, expressed seq=cds; coord=3:110185330..110189107:-1; parent_gene=AC214360.3_FG001'

'moderately similar to (319) AT1G27650 | Symbols: ATU2AF35A | ATU2AF35A; RNA binding / nucleic acid binding / nucleotide binding / zinc ion binding | chr1:9615302-9616042 FORWARDmoderately similar to (336) loc_os05g48960 12005.m27978 protein splicing factor U2af 38 kDa subunit, putative, expressed seq=cds; coord=3:130373684..130374882:1; parent_gene=GRMZM2G162119'

'highly similar to (527) AT1G34430 | Symbols: EMB3003 | EMB3003 (embryo defective 3003); acyltransferase/ dihydrolipoyllysine-residue acetyltransferase/ protein binding | chr1:12588027-12590084 REVERSEhighly similar to (592) loc_os12g08170 12012.m04804 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, mitochondrial precursor, putative, expressed seq=cds; coord=3:139285416..139291670:-1; parent_gene=GRMZM2G165176' 'highly similar to (600) AT2G01420 | Symbols: PIN4 | PIN4 (PIN-FORMED 4); auxin:hydrogen symporter/ transporter | chr2:180478-183199 REVERSEhighly similar to (747) PIN3A_ORYSA Probable auxin efflux carrier component 3a (OsPIN3a) - Oryza sativa (Rice)highly similar to (747) loc_os01g45550 12001.m150666 protein auxin efflux carrier component 3a, putative, expressed seq=cds; coord=3:214899506..214904595:-1; parent_gene=GRMZM2G126260'

'weakly similar to (116) AT3G12680 | Symbols: HUA1 | HUA1 (ENHANCER OF AG-4 1); RNA binding | chr3:4025276-4028999 REVERSEvery weakly similar to (89.4) ZFNL2_ORYSA Zinc finger CCCH domain-containing protein ZFN-like 2 - Oryza sativa (Rice)weakly similar to (140) loc_os01g42970 12001.m42678 protein zinc finger C-x8-C-x5-C-x3-H type family protein, expressed seq=cds; coord=3:225587126..225603442:-1; parent_gene=GRMZM2G422205'

'very weakly similar to (97.4) AT2G28660 | Symbols: | copper-binding family protein | chr2:12295419-12296944 FORWARDweakly similar to (172) loc_os08g31340 12008.m07132 protein heavy metal-associated domain containing protein, expressed seq=cds; coord=4:75504615..75508224:1; parent_gene=GRMZM2G166711'

'moderately similar to (213) AT5G65380 | Symbols: | ripening-responsive protein, putative | chr5:26123241-26126352 REVERSEmoderately similar to (300) loc_os08g37432 12008.m26847 protein transparent testa 12 protein, putative, expressed seq=cds; coord=4:86500374..86504689:1; parent_gene=GRMZM2G043075'

'very weakly similar to (99.0) AT1G03140 | Symbols: | splicing factor Prp18 family protein | chr1:754471-756223 REVERSEweakly similar to (122) loc_os07g38420 12007.m08088 protein prp18 domain containing protein, expressed seq=cds; coord=4:87875630..87877015:-1; parent_gene=GRMZM2G011034'

'very weakly similar to (99.0) AT2G41140 | Symbols: CRK1, ATCRK1, ATCBK3 | CRK1 (CDPK-RELATED KINASE 1); calcium ion binding / calcium-dependent protein serine/threonine phosphatase/ calmodulin-dependent protein kinase/ kinase | chr2:17150492-17153378 FORWARDvery weakly similar to (91.7) CRK_DAUCA CDPK-related protein kinase (EC 2.7.11.1) (PK421) - Daucus carota (Carrot)weakly similar to (109) loc_os10g36710 12010.m06477 protein CDPK-related protein kinase, putative, expressed seq=cds; coord=4:96426356..96430071:1; parent_gene=GRMZM2G378949'

'weakly similar to (113) AT3G18710 | Symbols: PUB29, ATPUB29 | PUB29 (PLANT U-BOX 29); ubiquitin-protein ligase | chr3:6434234-6435481 REVERSEmoderately similar to (438) loc_os02g33680 12002.m08459 protein U-box domain containing protein, expressed seq=cds; coord=4:111895429..111896985:1; parent_gene=GRMZM2G127690'

'highly similar to (729) AT3G10340 | Symbols: PAL4 | PAL4 (Phenylalanine ammonia-lyase 4); ammonia ligase/ ammonia-lyase/ catalytic | chr3:3204260-3207809 FORWARDhighly similar to (915) PAL1_ORYSA Phenylalanine ammonia-lyase (EC 4.3.1.5) - Oryza sativa (Rice)highly similar to (915) loc_os02g41630 12002.m33418 protein phenylalanine ammonia-lyase, putative, expressed seq=cds; coord=4:143376935..143381141:-1; parent_gene=GRMZM2G160541'

'moderately similar to (421) AT4G31750 | Symbols: WIN2 | WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase | chr4:15364657-15367207 REVERSEmoderately similar to (457) loc_os02g05630 12002.m33555 protein protein phosphatase 2C isoform epsilon, putative, expressed seq=cds; coord=4:237508371..237511930:-1; parent_gene=GRMZM2G166035'

'moderately similar to (421) AT4G31750 | Symbols: WIN2 | WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase | chr4:15364657-15367207 REVERSEmoderately similar to (457) loc_os02g05630 12002.m33555 protein protein phosphatase 2C isoform epsilon, putative, expressed seq=cds; coord=4:237508371..237511930:-1; parent_gene=GRMZM2G166035' 'moderately similar to (408) AT3G02875 | Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugat hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase | chr3:631993-633859 FORWARDhighly similar to (581) loc_os03g62060 12003.m11084 protein IAA-amino acid hydrolase ILR1 precursor, putative, expressed seq=cds; coord=5:1569535..1572475:-1; parent_gene=GRMZM2G125552'

'moderately similar to (270) AT1G75560 | Symbols: | zinc knuckle (CCHC-type) family protein | chr1:28371420-28372717 REVERSEmoderately similar to (389) loc_os03g60600 12003.m10949 protein cellular nucleic acid-binding protein, putative, expressed seq=cds; coord=5:2358363..2361474:1; parent_gene=GRMZM2G003068'

'moderately similar to (270) AT1G75560 | Symbols: | zinc knuckle (CCHC-type) family protein | chr1:28371420-28372717 REVERSEmoderately similar to (389) loc_os03g60600 12003.m10949 protein cellular nucleic acid-binding protein, putative, expressed seq=cds; coord=5:2358363..2361474:1; parent_gene=GRMZM2G003068'

'highly similar to (648) AT4G14680 | Symbols: APS3 | APS3; sulfate adenylyltransferase (ATP) | chr4:8413443-8415311 REVERSEhighly similar to (767) loc_os03g53230 12003.m10296 protein bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase, putative, expressed seq=cds; coord=5:7702248..7706223:1; parent_gene=GRMZM2G051270'

'weakly similar to (125) AT4G30820 | Symbols: | cyclin-dependent kinase-activating kinase assembly factor-related / CDK-activating kinase assembly factor-related | chr4:15007144-15008378 FORWARDmoderately similar to (251) loc_os11g28350 12011.m06753 protein CDK-activating kinase assembly factor MAT1 family protein, expressed seq=cds; coord=5:7856601..7858786:-1; parent_gene=GRMZM2G147814'

'moderately similar to (417) AT1G66170 | Symbols: MMD1 | MMD1 (MALE MEIOCYTE DEATH 1); DNA binding / protein binding / zinc ion binding | chr1:24638793-24641222 REVERSEhighly similar to (932) loc_os03g50780 12003.m10064 protein PHD-finger family protein, expressed seq=cds; coord=5:10436880..10440158:1; parent_gene=GRMZM2G408897'

'moderately similar to (268) AT1G73500 | Symbols: ATMKK9, MKK9 | MKK9 (MAP KINASE KINASE 9); MAP kinase kinase/ kinase/ protein kinase activator | chr1:27639419-27640351 REVERSEweakly similar to (162) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)moderately similar to (417) loc_os03g50550 12003.m10046 protein OsMKK10-3 - putative MAPKK based on amino acid sequence homology seq=cds; coord=5:10708282..10709572:-1; parent_gene=GRMZM2G163217'

'highly similar to (976) AT2G33730 | Symbols: | DEAD box RNA helicase, putative | chr2:14265679-14267880 REVERSEmoderately similar to (282) DB10_NICSY ATP-dependent RNA helicase-like protein DB10 (EC 3.6.1.-) - Nicotiana sylvestris (Wood tobacco)nearly identical (1077) loc_os03g50090 12003.m101465 protein ATP-dependent RNA helicase DDX23, putative, expressed seq=cds; coord=5:11603270..11605894:1; parent_gene=GRMZM2G123459'

'weakly similar to (112) AT5G47430 | Symbols: | zinc ion binding | chr5:19235819-19240147 REVERSEmoderately similar to (352) loc_os03g45730 12003.m09596 protein zinc knuckle family protein, expressed seq=cds; coord=5:15203912..15207473:1; parent_gene=GRMZM2G379428'

'moderately similar to (248) AT5G17860 | Symbols: CAX7 | CAX7 (calcium exchanger 7); calcium:sodium antiporter/ cation:cation antiporter | chr5:5902638-5904350 REVERSEmoderately similar to (434) loc_os03g45370 12003.m09566 protein K-exchanger-like protein, putative, expressed seq=cds; coord=5:15447458..15449344:-1; parent_gene=GRMZM2G340578' 'weakly similar to (140) AT4G01320 | Symbols: ATSTE24, STE24 | ATSTE24; endopeptidase/ metalloendopeptidase | chr4:545905-549002 FORWARDweakly similar to (169) loc_os02g45650 12002.m09602 protein CAAX prenyl protease 1, putative, expressed seq=cds; coord=5:23500810..23503479:1; parent_gene=GRMZM2G422539'

'moderately similar to (333) AT5G65270 | Symbols: AtRABA4a | AtRABA4a (Arabidopsis Rab GTPase homolog A4a); GTP binding | chr5:26083437-26084550 FORWARDmoderately similar to (347) RB11D_TOBAC Ras-related protein Rab11D - Nicotiana tabacum (Common tobacco)moderately similar to (413) loc_os10g23100 12010.m05315 protein ras-related protein Rab11D, putative, expressed seq=cds; coord=5:37836454..37846968:1; parent_gene=GRMZM2G122805'

'moderately similar to (333) AT5G65270 | Symbols: AtRABA4a | AtRABA4a (Arabidopsis Rab GTPase homolog A4a); GTP binding | chr5:26083437-26084550 FORWARDmoderately similar to (347) RB11D_TOBAC Ras-related protein Rab11D - Nicotiana tabacum (Common tobacco)moderately similar to (413) loc_os10g23100 12010.m05315 protein ras-related protein Rab11D, putative, expressed seq=cds; coord=5:37836454..37846968:1; parent_gene=GRMZM2G122805'

'moderately similar to (232) loc_os10g10180 12010.m065357 protein CMV 1a interacting protein 1, putative, expressed seq=cds; coord=5:38151595..38154162:1; parent_gene=GRMZM2G005260'

'weakly similar to (108) AT3G62770 | Symbols: AtATG18a | AtATG18a | chr3:23219091-23221110 REVERSEweakly similar to (133) loc_os01g70780 12001.m13123 protein WD-repeat domain phosphoinositide-interacting protein 3, putative, expressed seq=cds; coord=5:38858745..38859757:1; parent_gene=GRMZM2G436064'

'weakly similar to (133) AT1G02065 | Symbols: SPL8 | SPL8 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 8); DNA binding | chr1:365625-367149 FORWARDweakly similar to (127) LG1_MAIZE LIGULELESS1 protein - Zea mays (Maize)moderately similar to (228) loc_os02g08070 12002.m06153 protein SBP-domain protein 1, putative, expressed seq=cds; coord=5:88791487..88794405:1; parent_gene=GRMZM2G111136'

'highly similar to (567) AT2G25490 | Symbols: EBF1, FBL6 | EBF1 (EIN3-BINDING F BOX PROTEIN 1); protein binding / ubiquitin-protein ligase | chr2:10848018-10850275 REVERSEhighly similar to (974) loc_os02g10700 12002.m06368 protein EIN3-binding F-box protein 2, putative, expressed seq=cds; coord=5:115728940..115731973:1; parent_gene=GRMZM2G069649'

'moderately similar to (397) AT1G53490 | Symbols: | DNA binding | chr1:19965146-19966811 FORWARDhighly similar to (508) loc_os02g13810 12002.m33977 protein DNA binding protein, putative, expressed seq=cds; coord=5:150088686..150095175:1; parent_gene=GRMZM2G019971'

'weakly similar to (172) loc_os02g30810 12002.m08224 protein OsSAUR10 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=5:164364957..164366457:-1; parent_gene=GRMZM2G312274' 'weakly similar to (101) AT5G13330 | Symbols: Rap2.6L | Rap2.6L (related to AP2 6L); DNA binding / transcription factor | chr5:4272384-4274461 FORWARDvery weakly similar to (80.5) ERF1_TOBAC Ethylene-responsive transcription factor 1 (Ethylene-responsive element-binding factor 1) (EREBP-1) (NtERF1) - Nicotiana tabacum (Common tobacco)weakly similar to (151) loc_os02g32140 12002.m08307 protein AP2 domain transcription factor, putative, expressed seq=cds; coord=5:166319262..166321982:-1; parent_gene=GRMZM2G016434'

'nearly identical (1214) AT5G03650 | Symbols: SBE2.2 | SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme | chr5:931924-937470 FORWARDnearly identical (1638) GLGB_MAIZE 1,4-alpha-glucan branching enzyme IIB, chloroplast precursor (EC 2.4.1.18) (Starch branching enzyme IIB) (Q-enzyme) - Zea mays (Maize)nearly identical (1366) loc_os02g32660 12002.m33706 protein 1,4-alpha-glucan branching enzyme IIB, chloroplast precursor, putative, expressed seq=cds; coord=5:168451664..168468750:-1; parent_gene=GRMZM2G032628'

'highly similar to (891) AT5G22470 | Symbols: | NAD

'highly similar to (891) AT5G22470 | Symbols: | NAD

'moderately similar to (483) AT5G39350 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:15750929-15752962 FORWARDweakly similar to (110) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (803) loc_os02g44480 12002.m09488 protein vegetative storage protein, putative seq=cds; coord=5:193120609..193122819:-1; parent_gene=GRMZM2G014977'

'weakly similar to (123) AT4G34530 | Symbols: CIB1 | CIB1 (CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1); DNA binding / transcription factor | chr4:16498466-16499946 FORWARDmoderately similar to (310) loc_os02g47660 12002.m09800 protein BHLH transcription factor, putative, expressed seq=cds; coord=5:200937560..200939972:-1; parent_gene=GRMZM2G101350'

'highly similar to (605) AT3G27740 | Symbols: CARA | CARA (CARBAMOYL PHOSPHATE SYNTHETASE A); carbamoyl-phosphate synthase (glutamine-hydrolyzing)/ carbamoyl-phosphate synthase/ catalytic | chr3:10281470-10283792 REVERSEhighly similar to (758) loc_os02g47850 12002.m33834 protein carbamoyl-phosphate synthase small chain, putative, expressed seq=cds; coord=5:201452200..201457279:1; parent_gene=GRMZM2G147450'

'moderately similar to (285) AT3G03380 | Symbols: DegP7 | DegP7 (DegP protease 7); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase | chr3:799720-808319 FORWARDmoderately similar to (327) loc_os02g48180 12002.m09852 protein expressed protein seq=cds; coord=5:202209988..202211260:-1; parent_gene=GRMZM2G079352'

'weakly similar to (157) AT2G32950 | Symbols: COP1, ATCOP1, DET340, FUS1, EMB168 | COP1 (CONSTITUTIVE PHOTOMORPHOGENIC 1); protein binding / ubiquitin-protein ligase | chr2:13978000-13983282 FORWARDweakly similar to (155) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)moderately similar to (218) loc_os02g53140 12002.m10343 protein ubiquitin ligase protein COP1, putative, expressed seq=cds; coord=5:210747893..210749120:-1; parent_gene=GRMZM2G104920' 'weakly similar to (158) AT2G18650 | Symbols: MEE16 | MEE16 (maternal effect embryo arrest 16); protein binding / zinc ion binding | chr2:8086860-8088131 REVERSEvery weakly similar to (81.6) EL5_ORYSA E3 ubiquitin-protein ligase EL5 (EC 6.3.2.-) - Oryza sativa (Rice)moderately similar to (390) loc_os02g54830 12002.m10511 protein RING-H2 finger protein ATL2C, putative, expressed seq=cds; coord=5:213076220..213078683:-1; parent_gene=GRMZM2G122284'

'highly similar to (520) AT1G80480 | Symbols: PTAC17 | PTAC17 (PLASTID TRANSCRIPTIONALLY ACTIVE17) | chr1:30258272-30260570 REVERSEhighly similar to (599) loc_os02g55630 12002.m10588 protein nuclear WD protein, putative, expressed seq=cds; coord=5:214122497..214132628:1; parent_gene=GRMZM2G180418'

'moderately similar to (377) AT1G71980 | Symbols: | protease-associated zinc finger (C3HC4-type RING finger) family protein | chr1:27098250-27099881 FORWARDhighly similar to (561) loc_os03g07130 12003.m101101 protein RING finger protein 13, putative, expressed seq=cds; coord=6:1335084..1338778:1; parent_gene=GRMZM2G423956'

'weakly similar to (103) AT1G60950 | Symbols: FED A, ATFD2 | FED A; 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding | chr1:22444565-22445011 FORWARDweakly similar to (182) FER1_MAIZE Ferredoxin-1, chloroplast precursor (Ferredoxin I) (Fd I) - Zea mays (Maize)weakly similar to (130) loc_os08g01380 12008.m080056 protein ferredoxin-1, chloroplast precursor, putative, expressed seq=cds; coord=6:1340171..1341142:-1; parent_gene=GRMZM2G122337'

'moderately similar to (474) AT1G30520 | Symbols: AAE14 | AAE14 (Acyl-Activating Enzyme 14); AMP binding / o-succinylbenzoate-CoA ligase | chr1:10811039-10813546 FORWARDweakly similar to (141) 4CL1_ORYSA 4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1) - Oryza sativa (Rice)moderately similar to (379) loc_os08g03630 12008.m04507 protein AMP binding protein, putative, expressed seq=cds; coord=6:9200187..9203512:-1; parent_gene=GRMZM2G066426'

'weakly similar to (150) AT3G46920 | Symbols: | protein kinase family protein | chr3:17280430-17284857 REVERSEnearly identical (1098) loc_os06g08280 12006.m05549 protein protein kinase domain containing protein, expressed seq=cds; coord=6:50243540..50249018:1; parent_gene=GRMZM2G145360'

'weakly similar to (112) AT3G07490 | Symbols: AGD11 | AGD11 (ARF-GAP domain 11); calcium ion binding | chr3:2391189-2391650 FORWARDmoderately similar to (238) loc_os06g07560 12006.m05479 protein calcium ion binding protein, putative, expressed seq=cds; coord=6:122664101..122665496:1; parent_gene=GRMZM2G071100'

'nearly identical (1205) AT1G15690 | Symbols: AVP1, ATAVP3, AVP-3 | AVP1; ATPase/ hydrogen-translocating pyrophosphatase | chr1:5399115-5402185 FORWARDnearly identical (1279) AVP_HORVU Pyrophosphate-energized vacuolar membrane proton pump (EC 3.6.1.1) (Pyrophosphate-energized inorganic pyrophosphatase) (H(

'weakly similar to (106) loc_os06g45230 12006.m09050 protein pollen allergen Phl p 2 precursor, putative, expressed seq=cds; coord=6:157349767..157350512:1; parent_gene=GRMZM2G007708'

'weakly similar to (176) AT4G11060 | Symbols: MTSSB | MTSSB (mitochondrially targeted single-stranded DNA binding protein); single-stranded DNA binding | chr4:6754820-6756230 REVERSEmoderately similar to (241) loc_os05g43440 12005.m08472 protein single-stranded DNA-binding protein, putative, expressed seq=cds; coord=6:157863131..157865522:-1; parent_gene=GRMZM2G032847' 'moderately similar to (308) AT4G08150 | Symbols: KNAT1, BP, BP1 | KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor | chr4:5147969-5150610 REVERSEmoderately similar to (463) RSH1_MAIZE Homeobox protein rough sheath 1 - Zea mays (Maize)moderately similar to (427) loc_os07g03770 12007.m04847 protein homeobox protein rough sheath 1, putative, expressed seq=cds; coord=7:3664698..3670891:1; parent_gene=GRMZM2G028041'

'highly similar to (560) AT1G73100 | Symbols: SUVH3, SDG19 | SUVH3 (SU(VAR)3-9 HOMOLOG 3); histone methyltransferase | chr1:27491970-27493979 FORWARDnearly identical (1170) loc_os11g38900 12011.m07738 protein histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1, putative, expressed seq=cds; coord=7:20244021..20246591:1; parent_gene=AC233961.1_FG001'

'highly similar to (573) AT3G06920 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:2181717-2184449 FORWARDweakly similar to (186) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (697) loc_os07g14530 12007.m079646 protein expressed protein seq=cds; coord=7:25155947..25157555:1; parent_gene=GRMZM2G086757'

'weakly similar to (110) loc_os07g18990 12007.m06338 protein PVR3-like protein, putative, expressed seq=cds; coord=7:31086409..31087079:1; parent_gene=GRMZM2G000221'

'very weakly similar to (100) AT3G45280 | Symbols: SYP72, ATSYP72 | SYP72 (SYNTAXIN OF PLANTS 72); protein transporter | chr3:16611445-16613304 REVERSEweakly similar to (136) loc_os09g19550 12009.m05163 protein syntaxin 72, putative seq=cds; coord=7:95533897..95534429:1; parent_gene=GRMZM2G360648'

'moderately similar to (466) AT1G79360 | Symbols: ATOCT2 | ATOCT2 (ARABIDOPSIS THALIANA ORGANIC CATION/CARNITINE TRANSPORTER 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter | chr1:29854140-29855723 REVERSEhighly similar to (679) loc_os07g37510 12007.m08001 protein carbohydrate transporter/ sugar porter, putative seq=cds; coord=7:157503067..157505302:1; parent_gene=GRMZM2G019974'

'moderately similar to (466) AT1G79360 | Symbols: ATOCT2 | ATOCT2 (ARABIDOPSIS THALIANA ORGANIC CATION/CARNITINE TRANSPORTER 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter | chr1:29854140-29855723 REVERSEhighly similar to (679) loc_os07g37510 12007.m08001 protein carbohydrate transporter/ sugar porter, putative seq=cds; coord=7:157503067..157505302:1; parent_gene=GRMZM2G019974'

'moderately similar to (302) AT5G55600 | Symbols: | agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein | chr5:22522232-22524796 REVERSEhighly similar to (632) loc_os07g41640 12007.m29252 protein DNA binding protein, putative, expressed seq=cds; coord=7:164824657..164829482:1; parent_gene=GRMZM2G037444'

'moderately similar to (226) loc_os07g47400 12007.m08957 protein SRC2, putative, expressed seq=cds; coord=7:172433682..172434802:1; parent_gene=GRMZM2G364643' 'nearly identical (1079) AT2G40540 | Symbols: KT2, ATKT2, SHY3, KUP2, ATKUP2, TRK2 | KT2 (POTASSIUM TRANSPORTER 2); potassium ion transmembrane transporter | chr2:16931445-16934516 FORWARDnearly identical (1287) HAK9_ORYSA Probable potassium transporter 9 (OsHAK9) - Oryza sativa (Rice)nearly identical (1287) loc_os07g48130 12007.m079793 protein potassium transporter 9, putative, expressed seq=cds; coord=7:172935556..172939916:-1; parent_gene=GRMZM2G166738'

'weakly similar to (131) AT5G39660 | Symbols: CDF2 | CDF2 (CYCLING DOF FACTOR 2); DNA binding / protein binding / transcription factor | chr5:15878920-15880712 FORWARDvery weakly similar to (92.8) MNB1A_MAIZE Dof zinc finger protein MNB1A - Zea mays (Maize)moderately similar to (399) loc_os07g48570 12007.m09068 protein expressed protein seq=cds; coord=7:173806883..173808319:-1; parent_gene=AC155434.2_FG006'

'weakly similar to (131) AT5G39660 | Symbols: CDF2 | CDF2 (CYCLING DOF FACTOR 2); DNA binding / protein binding / transcription factor | chr5:15878920-15880712 FORWARDvery weakly similar to (92.8) MNB1A_MAIZE Dof zinc finger protein MNB1A - Zea mays (Maize)moderately similar to (399) loc_os07g48570 12007.m09068 protein expressed protein seq=cds; coord=7:173806883..173808319:-1; parent_gene=AC155434.2_FG006'

'moderately similar to (447) AT3G14067 | Symbols: | subtilase family protein | chr3:4658421-4660754 REVERSEhighly similar to (798) loc_os07g48650 12007.m09076 protein xylem serine proteinase 1 precursor, putative, expressed seq=cds; coord=7:174029436..174031718:1; parent_gene=GRMZM2G059165'

'moderately similar to (352) AT3G06560 | Symbols: | polynucleotide adenylyltransferase/ protein binding | chr3:2044443-2047034 FORWARDhighly similar to (560) loc_os07g48890 12007.m09098 protein poly, putative, expressed seq=cds; coord=7:174102328..174107989:-1; parent_gene=GRMZM2G470461'

'highly similar to (830) AT1G74850 | Symbols: PTAC2 | PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE2) | chr1:28119237-28122314 REVERSEweakly similar to (164) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)nearly identical (1404) loc_os03g60910 12003.m10978 protein ATP binding protein, putative, expressed seq=cds; coord=7:175277814..175287244:1; parent_gene=GRMZM2G122116'

'moderately similar to (228) AT5G58230 | Symbols: MSI1, MEE70, ATMSI1 | MSI1 (MULTICOPY SUPRESSOR OF IRA1); protein binding | chr5:23556112-23557994 FORWARDmoderately similar to (288) loc_os09g36900 12009.m06639 protein WD-40 repeat protein MSI1, putative, expressed seq=cds; coord=7:175560055..175567020:-1; parent_gene=GRMZM2G032711'

'moderately similar to (382) AT3G14440 | Symbols: NCED3, ATNCED3, STO1, SIS7 | NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase | chr3:4831678-4833477 REVERSEmoderately similar to (447) loc_os07g05940 12007.m05058 protein viviparous-14, putative, expressed seq=cds; coord=7:175861745..175863458:-1; parent_gene=GRMZM2G330848'

'moderately similar to (224) AT2G01275 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:142610-143809 REVERSEmoderately similar to (413) loc_os01g03100 12001.m42845 protein protein binding protein, putative, expressed seq=cds; coord=8:10287956..10291623:-1; parent_gene=GRMZM2G003930' 'highly similar to (870) AT3G18060 | Symbols: | transducin family protein / WD-40 repeat family protein | chr3:6183880-6186788 FORWARDnearly identical (1165) loc_os01g03510 12001.m06989 protein stress protein, putative, expressed seq=cds; coord=8:10870907..10877056:1; parent_gene=GRMZM2G030384'

'moderately similar to (223) AT1G66980 | Symbols: | protein kinase family protein / glycerophosphoryl diester phosphodiesterase family protein | chr1:24997491-25001961 REVERSEweakly similar to (111) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (433) loc_os01g04490 12001.m07084 protein Ser/Thr protein kinase, putative, expressed seq=cds; coord=8:13288169..13290813:1; parent_gene=GRMZM2G172368'

'highly similar to (825) AT5G54960 | Symbols: PDC2 | PDC2 (pyruvate decarboxylase-2); carboxy-lyase/ catalytic/ magnesium ion binding / pyruvate decarboxylase/ thiamin pyrophosphate binding | chr5:22310858-22312681 REVERSEhighly similar to (849) PDC1_MAIZE Pyruvate decarboxylase isozyme 1 (EC 4.1.1.1) (PDC) - Zea mays (Maize)highly similar to (943) loc_os01g06660 12001.m150484 protein pyruvate decarboxylase isozyme 1, putative, expressed seq=cds; coord=8:15548387..15551947:-1; parent_gene=GRMZM2G038821'

'weakly similar to (134) AT1G70550 | Symbols: | unknown protein | chr1:26597510-26599888 FORWARDweakly similar to (159) loc_os01g07570 12001.m07384 protein carboxyl-terminal proteinase, putative, expressed seq=cds; coord=8:17066051..17069207:-1; parent_gene=GRMZM2G162928'

'moderately similar to (300) AT4G15550 | Symbols: IAGLU | IAGLU (INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE); UDP-glycosyltransferase/ transferase, transferring glycosyl groups | chr4:8877877-8879301 REVERSEmoderately similar to (209) IAAG_MAIZE Indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) (IAA-Glu synthetase) ((Uridine 5'-diphosphate-glucose:indol-3-ylacetyl)-beta-D-glucosyl transferase) - Zea mays (Maize)highly similar to (521) loc_os01g08440 12001.m07469 protein indole-3-acetate beta-glucosyltransferase, putative, expressed seq=cds; coord=8:18822079..18824101:-1; parent_gene=GRMZM2G457929'

'highly similar to (563) AT5G45900 | Symbols: APG7, ATAPG7, ATG7, ATATG7 | APG7 (AUTOPHAGY 7); APG8 activating enzyme | chr5:18615304-18618436 FORWARDnearly identical (1514) loc_os01g42850 12001.m42676 protein autophagy-related protein 7, putative, expressed seq=cds; coord=8:143154536..143162905:-1; parent_gene=GRMZM2G005304'

'weakly similar to (198) AT3G12600 | Symbols: atnudt16 | atnudt16 (Arabidopsis thaliana Nudix hydrolase homolog 16); hydrolase | chr3:4004676-4005995 FORWARDmoderately similar to (248) loc_os04g53380 12004.m10229 protein expressed protein seq=cds; coord=8:161926660..161930458:1; parent_gene=GRMZM2G013060'

'weakly similar to (188) AT3G07340 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr3:2341188-2343288 REVERSEhighly similar to (584) loc_os01g68700 12001.m12972 protein BHLH transcription factor, putative, expressed seq=cds; coord=8:162557420..162560479:1; parent_gene=GRMZM2G030762'

'moderately similar to (287) AT1G05600 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:1672161-1673675 FORWARDweakly similar to (120) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)moderately similar to (454) loc_os01g68550 12001.m12958 protein expressed protein seq=cds; coord=8:162788741..162790666:-1; parent_gene=GRMZM2G170941' 'moderately similar to (360) AT5G16270 | Symbols: ATRAD21.3, SYN4 | SYN4 (SISTER CHROMATID COHESION 1 PROTEIN 4) | chr5:5316783-5322330 FORWARDnearly identical (1225) loc_os01g67250 12001.m42786 protein N terminus of Rad21 / Rec8 like protein, expressed seq=cds; coord=8:164083362..164092361:1; parent_gene=GRMZM2G421829'

'moderately similar to (354) AT5G25930 | Symbols: | leucine-rich repeat family protein / protein kinase family protein | chr5:9050880-9053978 FORWARDmoderately similar to (262) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (620) loc_os01g53920 12001.m42717 protein receptor-like protein kinase 5 precursor, putative, expressed seq=cds; coord=8:175185352..175188965:-1; parent_gene=AC203173.3_FG002'

'weakly similar to (128) AT2G45100 | Symbols: | RNA polymerase II transcription factor/ protein binding / transcription activator/ transcription regulator/ translation initiation factor/ zinc ion binding | chr2:18595348-18598088 REVERSEweakly similar to (186) loc_os05g23940 12005.m06688 protein RNA polymerase II transcription factor/ transcription factor/ zinc ion binding protein, putative, expressed seq=cds; coord=9:2736110..2739733:-1; parent_gene=GRMZM2G180836'

'moderately similar to (290) AT3G21350 | Symbols: | RNA polymerase transcriptional regulation mediator-related | chr3:7517106-7518587 FORWARDmoderately similar to (407) loc_os06g11370 12006.m05854 protein RNA polymerase transcriptional regulation mediator, subunit 6, putative, expressed seq=cds; coord=9:7177254..7182212:-1; parent_gene=GRMZM2G017537'

'moderately similar to (483) AT1G76680 | Symbols: OPR1, ATOPR1 | OPR1; 12-oxophytodienoate reductase | chr1:28776982-28778271 FORWARDhighly similar to (601) loc_os06g11290 12006.m05846 protein 12-oxophytodienoate reductase 2, putative, expressed seq=cds; coord=9:7308153..7309906:1; parent_gene=GRMZM2G000236'

'moderately similar to (209) AT3G10610 | Symbols: | 40S ribosomal protein S17 (RPS17C) | chr3:3319459-3319881 FORWARDmoderately similar to (263) loc_os10g27190 12010.m05653 protein 40S ribosomal protein S17-4, putative, expressed seq=cds; coord=9:10319530..10320398:-1; parent_gene=GRMZM2G086906'

'nearly identical (1092) AT1G18370 | Symbols: HIK, ATNACK1, NACK1 | HIK (HINKEL); ATP binding / microtubule motor | chr1:6319732-6323820 REVERSEmoderately similar to (228) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiinearly identical (1558) loc_os01g33040 12001.m09621 protein kinesin heavy chain, putative, expressed seq=cds; coord=9:26577949..26584519:1; parent_gene=GRMZM2G136838'

'nearly identical (1092) AT1G18370 | Symbols: HIK, ATNACK1, NACK1 | HIK (HINKEL); ATP binding / microtubule motor | chr1:6319732-6323820 REVERSEmoderately similar to (228) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiinearly identical (1558) loc_os01g33040 12001.m09621 protein kinesin heavy chain, putative, expressed seq=cds; coord=9:26577949..26584519:1; parent_gene=GRMZM2G136838'

'very weakly similar to (86.3) NLTP_HELAN Nonspecific lipid-transfer protein precursor (LTP) (NsLTP) (SDI-9) - Helianthus annuus (Common sunflower)very weakly similar to (97.1) loc_os06g34840 12006.m08021 protein nonspecific lipid-transfer protein 3 precursor, putative seq=cds; coord=9:61863515..61865024:1; parent_gene=GRMZM2G025026' 'moderately similar to (239) AT3G62240 | Symbols: | zinc finger (C2H2 type) family protein | chr3:23033592-23036653 REVERSEmoderately similar to (327) loc_os01g14840 12001.m08086 protein nucleic acid binding protein, putative, expressed seq=cds; coord=9:149278522..149280901:-1; parent_gene=GRMZM2G004157'

'very weakly similar to (84.3) AT1G19490 | Symbols: | bZIP transcription factor family protein | chr1:6751953-6753959 REVERSEvery weakly similar to (99.0) loc_os11g05640 12011.m04761 protein bZIP transcription factor family protein, expressed seq=cds; coord=10:5917109..5918148:1; parent_gene=GRMZM2G365754'

'highly similar to (551) AT5G57710 | Symbols: | heat shock protein-related | chr5:23384794-23388052 FORWARDnearly identical (1225) loc_os08g15230 12008.m05646 protein expressed protein seq=cds; coord=10:53478171..53482054:1; parent_gene=GRMZM2G117836'

'weakly similar to (131) AT3G61970 | Symbols: NGA2 | NGA2 (NGATHA2); transcription factor | chr3:22951829-22952728 FORWARDweakly similar to (142) loc_os11g05740 12011.m04770 protein B3 DNA binding domain containing protein, expressed seq=cds; coord=10:44121942..44122617:1; parent_gene=GRMZM2G405170'

'very weakly similar to (93.6) ACBP_RICCO Acyl-CoA-binding protein (ACBP) - Ricinus communis (Castor bean)very weakly similar to (99.0) loc_os08g06550 12008.m04794 protein acyl-CoA-binding protein, putative, expressed seq=cds; coord=10:76402555..76404935:1; parent_gene=GRMZM2G079908'

'weakly similar to (104) AT4G29930 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr4:14644108-14645168 FORWARDweakly similar to (127) loc_os04g23550 12004.m101486 protein DNA binding like, putative, expressed seq=cds; coord=10:76586652..76588863:1; parent_gene=GRMZM2G042895'

'weakly similar to (140) AT4G16270 | Symbols: | peroxidase 40 (PER40) (P40) | chr4:9205038-9206483 FORWARDweakly similar to (132) PERN_IPOBA Neutral peroxidase precursor (EC 1.11.1.7) (SwPN1) - Ipomoea batatas (Sweet potato) (Batate)moderately similar to (279) loc_os05g04410 12005.m04974 protein peroxidase 2 precursor, putative, expressed seq=cds; coord=10:85683513..85689992:1; parent_gene=GRMZM2G006727'

'very weakly similar to (88.6) loc_os04g58710 12004.m35525 protein peroxisomal-coenzyme A synthetase, putative, expressed seq=cds; coord=10:138676374..138677343:1; parent_gene=AF466202.2_FG012'

'nearly identical (1406) AT3G23780 | Symbols: NRPD2A, DRD2, NRPD2, DMS2, NRPE2 | NRPD2A; DNA binding / DNA-directed RNA polymerase | chr3:8567971-8573819 REVERSEweakly similar to (145) RPOB_CHAGL DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (PEP) (Plastid-encoded RNA polymerase subunit beta) (RNA polymerase subunit beta) - Chaetosphaeridium globosumnearly identical (2018) loc_os04g54840 12004.m10376 protein NRPD2a, putative, expressed seq=cds; coord=10:144716135..144739736:1; parent_gene=GRMZM2G427031'

'highly similar to (862) AT1G01790 | Symbols: KEA1, ATKEA1 | KEA1 (K EFFLUX ANTIPORTER 1); potassium ion transmembrane transporter/ potassium:hydrogen antiporter | chr1:284781-290869 FORWARDnearly identical (1261) loc_os04g58620 12004.m10744 protein KEA1, putative, expressed seq=cds; coord=10:148572678..148584114:-1; parent_gene=GRMZM2G093643' 'weakly similar to (101) loc_os03g20760 12003.m07483 protein lipid binding protein, putative, expressed seq=cds; coord=1:52625970..52627201:-1; parent_gene=GRMZM2G174680'

'highly similar to (909) AT4G26590 | Symbols: ATOPT5, OPT5 | OPT5 (OLIGOPEPTIDE TRANSPORTER 5); oligopeptide transporter | chr4:13414134-13416850 REVERSEnearly identical (1264) loc_os08g38400 12008.m26725 protein oligopeptide transporter 5, putative, expressed seq=cds; coord=1:183096381..183099093:1; parent_gene=GRMZM2G152555'

'very weakly similar to (97.4) AT3G13224 | Symbols: | RNA recognition motif (RRM)-containing protein | chr3:4254848-4256621 FORWARDweakly similar to (148) loc_os08g38410 12008.m07825 protein RNA recognition motif family protein, expressed seq=cds; coord=1:183150234..183151288:-1; parent_gene=AC233867.1_FG004'

'nearly identical (1025) AT4G12650 | Symbols: | LOCATED IN: integral to membrane, Golgi apparatus, plasma membrane, vacuole; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35160.1); Has 983 Blast hits to 980 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 434; Fungi - 144; Plants - 228; Viruses - 0; Other Eukaryotes - 177 (source: NCBI BLink). | chr4:7468207-7470165 REVERSEnearly identical (1158) loc_os08g38820 12008.m080200 protein transmembrane 9 superfamily protein member 2 precursor, putative, expressed seq=cds; coord=1:183841405..183844417:1; parent_gene=GRMZM2G113899'

'very weakly similar to (98.2) AT1G28960 | Symbols: ATNUDT15, ATNUDX15 | ATNUDX15 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 15); hydrolase | chr1:10110135-10111607 REVERSEweakly similar to (137) loc_os08g28840 12008.m06889 protein peroxisomal coenzyme A diphosphatase NUDT7, putative, expressed seq=cds; coord=1:220074365..220075536:-1; parent_gene=GRMZM2G136426'

'moderately similar to (209) AT3G24120 | Symbols: | myb family transcription factor | chr3:8705925-8708148 REVERSEmoderately similar to (307) loc_os08g25799 12008.m06596 protein myb family transcription factor-related protein, putative, expressed seq=cds; coord=1:221574382..221584578:-1; parent_gene=GRMZM2G113742'

'moderately similar to (384) AT1G61790 | Symbols: | OST3/OST6 family protein | chr1:22814390-22815430 FORWARDhighly similar to (535) loc_os03g36730 12003.m08792 protein oligosaccharide transporter, putative, expressed seq=cds; coord=1:222130457..222134768:1; parent_gene=GRMZM2G149946'

'weakly similar to (148) AT5G33320 | Symbols: CUE1, PPT, ARAPPT | CUE1 (CAB UNDEREXPRESSED 1); antiporter/ triose-phosphate transmembrane transporter | chr5:12588950-12591408 FORWARDweakly similar to (178) loc_os05g07870 12005.m05305 protein triose phosphate/phosphate translocator, non-green plastid,chloroplast precursor, putative, expressed seq=cds; coord=1:278628888..278632994:-1; parent_gene=GRMZM2G147589'

'weakly similar to (179) AT5G57330 | Symbols: | aldose 1-epimerase family protein | chr5:23218392-23220664 FORWARDmoderately similar to (216) loc_os04g56290 12004.m35496 protein apospory-associated protein C, putative, expressed seq=cds; coord=2:4174781..4178923:-1; parent_gene=GRMZM2G039588' 'weakly similar to (179) AT5G57330 | Symbols: | aldose 1-epimerase family protein | chr5:23218392-23220664 FORWARDmoderately similar to (216) loc_os04g56290 12004.m35496 protein apospory-associated protein C, putative, expressed seq=cds; coord=2:4174781..4178923:-1; parent_gene=GRMZM2G039588'

'nearly identical (1518) AT4G30190 | Symbols: AHA2, PMA2 | AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism | chr4:14770820-14775920 REVERSEnearly identical (1675) PMA1_ORYSA Plasma membrane ATPase (EC 3.6.3.6) (Proton pump) - Oryza sativa (Rice)nearly identical (1675) loc_os04g56160 12004.m101441 protein plasma membrane ATPase, putative, expressed seq=cds; coord=2:4299718..4306692:-1; parent_gene=GRMZM2G019404'

'moderately similar to (217) AT2G34830 | Symbols: WRKY35, MEE24, AtWRKY35 | WRKY35 (WRKY DNA-binding protein 35); transcription factor | chr2:14693839-14696378 REVERSEhighly similar to (550) loc_os04g50920 12004.m09989 protein WRKY DNA binding domain containing protein, expressed seq=cds; coord=2:12799342..12803684:-1; parent_gene=GRMZM2G024898'

'moderately similar to (224) AT2G41150 | Symbols: | unknown protein | chr2:17153851-17155633 FORWARDmoderately similar to (273) loc_os03g25110 12003.m07854 protein expressed protein seq=cds; coord=2:136416109..136419742:-1; parent_gene=GRMZM2G352947'

'weakly similar to (182) AT1G69010 | Symbols: BIM2 | BIM2 (BES1-interacting Myc-like protein 2); DNA binding / transcription factor | chr1:25941804-25943599 FORWARDhighly similar to (531) loc_os09g29930 12009.m060079 protein transcription factor BIM2, putative, expressed seq=cds; coord=2:188529569..188535342:-1; parent_gene=GRMZM2G009478'

'moderately similar to (485) AT4G39170 | Symbols: | SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative | chr4:18240887-18243621 FORWARDhighly similar to (822) loc_os09g30330 12009.m06184 protein phosphatidylinositol transporter/ transporter, putative, expressed seq=cds; coord=2:189219156..189224929:1; parent_gene=GRMZM2G031837'

'weakly similar to (194) AT2G04780 | Symbols: FLA7 | FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) | chr2:1677488-1678252 FORWARDmoderately similar to (267) loc_os09g30486 12009.m06208 protein fasciclin-like arabinogalactan protein 7 precursor, putative, expressed seq=cds; coord=2:189488589..189490512:-1; parent_gene=GRMZM2G081017'

'weakly similar to (194) AT2G04780 | Symbols: FLA7 | FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) | chr2:1677488-1678252 FORWARDmoderately similar to (267) loc_os09g30486 12009.m06208 protein fasciclin-like arabinogalactan protein 7 precursor, putative, expressed seq=cds; coord=2:189488589..189490512:-1; parent_gene=GRMZM2G081017'

'weakly similar to (194) AT2G04780 | Symbols: FLA7 | FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) | chr2:1677488-1678252 FORWARDmoderately similar to (267) loc_os09g30486 12009.m06208 protein fasciclin-like arabinogalactan protein 7 precursor, putative, expressed seq=cds; coord=2:189488589..189490512:-1; parent_gene=GRMZM2G081017'

'weakly similar to (194) AT2G04780 | Symbols: FLA7 | FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) | chr2:1677488-1678252 FORWARDmoderately similar to (267) loc_os09g30486 12009.m06208 protein fasciclin-like arabinogalactan protein 7 precursor, putative, expressed seq=cds; coord=2:189488589..189490512:-1; parent_gene=GRMZM2G081017'

'moderately similar to (382) AT1G35910 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr1:13363200-13364965 REVERSEmoderately similar to (413) loc_os07g43160 12007.m08544 protein expressed protein seq=cds; coord=2:212477947..212480732:1; parent_gene=GRMZM2G117564' 'moderately similar to (448) AT5G48910 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:19832969-19834909 REVERSEvery weakly similar to (80.5) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)moderately similar to (438) loc_os01g51790 12001.m11356 protein selenium-binding protein-like, putative seq=cds; coord=2:213162946..213164673:1; parent_gene=GRMZM2G703373'

'nearly identical (1081) AT5G66760 | Symbols: SDH1-1 | SDH1-1; ATP binding / succinate dehydrogenase | chr5:26653776-26657224 FORWARDnearly identical (1104) DHSA_ORYSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (EC 1.3.5.1) (FP) (Flavoprotein subunit of complex II) - Oryza sativa (Rice)nearly identical (1104) loc_os07g04240 12007.m04893 protein succinate dehydrogenase flavoprotein subunit,mitochondrial precursor, putative, expressed seq=cds; coord=2:236245150..236250456:-1; parent_gene=GRMZM2G079888'

'highly similar to (783) AT5G20490 | Symbols: XIK, ATXIK, XI-17 | XIK; motor/ protein binding | chr5:6927064-6936079 REVERSEhighly similar to (875) loc_os05g46030 12005.m08728 protein myosin head family protein, expressed seq=cds; coord=3:203473493..203479533:1; parent_gene=GRMZM2G113319'

'moderately similar to (247) AT4G18260 | Symbols: | cytochrome B561-related | chr4:10093524-10097337 REVERSEmoderately similar to (409) loc_os01g47620 12001.m10956 protein expressed protein seq=cds; coord=3:210755678..210758890:1; parent_gene=GRMZM2G024348'

'highly similar to (860) AT5G52920 | Symbols: PKP1, PKP-BETA1, PKP2 | PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate kinase | chr5:21463680-21466612 FORWARDhighly similar to (743) KPYG_TOBAC Pyruvate kinase isozyme G, chloroplast precursor (EC 2.7.1.40) - Nicotiana tabacum (Common tobacco)nearly identical (1006) loc_os01g47080 12001.m10904 protein pyruvate kinase isozyme G, chloroplast precursor, putative, expressed seq=cds; coord=3:211977378..211987454:1; parent_gene=GRMZM2G152686'

'very weakly similar to (100) AT4G11140 | Symbols: CRF1 | CRF1 (CYTOKININ RESPONSE FACTOR 1); DNA binding / transcription factor | chr4:6794930-6795793 REVERSEvery weakly similar to (86.3) ERF3_TOBAC Ethylene-responsive transcription factor 3 (Ethylene-responsive element-binding factor 3 homolog) (EREBP-5) (NtERF5) - Nicotiana tabacum (Common tobacco)moderately similar to (298) loc_os01g46870 12001.m10884 protein ap2 domain protein, putative, expressed seq=cds; coord=3:212501262..212503692:1; parent_gene=GRMZM2G160971'

'very weakly similar to (100) AT4G11140 | Symbols: CRF1 | CRF1 (CYTOKININ RESPONSE FACTOR 1); DNA binding / transcription factor | chr4:6794930-6795793 REVERSEvery weakly similar to (86.3) ERF3_TOBAC Ethylene-responsive transcription factor 3 (Ethylene-responsive element-binding factor 3 homolog) (EREBP-5) (NtERF5) - Nicotiana tabacum (Common tobacco)moderately similar to (298) loc_os01g46870 12001.m10884 protein ap2 domain protein, putative, expressed seq=cds; coord=3:212501262..212503692:1; parent_gene=GRMZM2G160971'

'moderately similar to (259) AT5G41790 | Symbols: CIP1 | CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding | chr5:16727530-16732391 FORWARDweakly similar to (117) MFP1_TOBAC MAR-binding filament-like protein 1-1 - Nicotiana tabacum (Common tobacco)highly similar to (836) loc_os01g46810 12001.m10878 protein viral A-type inclusion protein repeat containing protein, expressed seq=cds; coord=3:212694107..212699938:1; parent_gene=GRMZM2G118403' 'weakly similar to (107) AT4G23810 | Symbols: WRKY53, ATWRKY53 | WRKY53; DNA binding / protein binding / transcription activator/ transcription factor | chr4:12392666-12393739 REVERSEmoderately similar to (209) loc_os01g46800 12001.m10877 protein OsWRKY15 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=3:212739888..212741312:1; parent_gene=GRMZM2G408462'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'highly similar to (627) AT2G26650 | Symbols: AKT1, ATAKT1 | AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel | chr2:11331965-11336444 REVERSEhighly similar to (824) AKT1_ORYSA Potassium channel AKT1 (OsAKT1) - Oryza sativa (Rice)highly similar to (824) loc_os01g45990 12001.m10798 protein potassium channel AKT1, putative, expressed seq=cds; coord=3:214273957..214280038:1; parent_gene=GRMZM2G022915'

'very weakly similar to (97.4) loc_os02g49326 12002.m09967 protein ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I, putative, expressed seq=cds; coord=3:214717181..214719614:-1; parent_gene=AC212898.2_FG006'

'very weakly similar to (97.4) loc_os02g49326 12002.m09967 protein ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I, putative, expressed seq=cds; coord=3:214717181..214719614:-1; parent_gene=AC212898.2_FG006'

'moderately similar to (357) AT5G14260 | Symbols: | SET domain-containing protein | chr5:4601139-4603873 FORWARDmoderately similar to (451) loc_os12g13460 12012.m05319 protein SET domain containing protein, expressed seq=cds; coord=3:215527347..215532128:-1; parent_gene=GRMZM2G047695'

'moderately similar to (245) AT5G46410 | Symbols: | NLI interacting factor (NIF) family protein | chr5:18826007-18828156 FORWARDhighly similar to (522) loc_os01g43870 12001.m97456 protein CTD-phosphatase-like protein, putative, expressed seq=cds; coord=3:216839393..216845277:-1; parent_gene=GRMZM2G068690'

'weakly similar to (155) AT3G49290 | Symbols: ABIL2 | ABIL2 (ABL INTERACTOR-LIKE PROTEIN 2) | chr3:18273407-18275221 FORWARDmoderately similar to (213) ABIL2_ORYSA Putative protein ABIL2 (Abl interactor-like protein 2) - Oryza sativa (Rice)moderately similar to (213) loc_os01g37110 12001.m10006 protein protein ABIL1, putative, expressed seq=cds; coord=3:226872828..226873698:1; parent_gene=GRMZM2G001981'

'highly similar to (764) AT3G55200 | Symbols: | splicing factor, putative | chr3:20460533-20464361 FORWARDhighly similar to (842) loc_os02g04480 12002.m05797 protein splicing factor 3B subunit 3, putative, expressed seq=cds; coord=3:229845805..229849321:1; parent_gene=GRMZM2G078592' 'very weakly similar to (99.0) loc_os02g34630 12002.m100229 protein myb-like DNA-binding domain containing protein, expressed seq=cds; coord=4:115295668..115296003:-1; parent_gene=GRMZM2G059167'

'very weakly similar to (99.0) loc_os02g34630 12002.m100229 protein myb-like DNA-binding domain containing protein, expressed seq=cds; coord=4:115295668..115296003:-1; parent_gene=GRMZM2G059167'

'highly similar to (775) AT3G51460 | Symbols: RHD4 | RHD4 (ROOT HAIR DEFECTIVE4); phosphatidylinositol-4,5-bisphosphate 5-phosphatase/ phosphatidylinositol-4-phosphate phosphatase | chr3:19093007-19097142 FORWARDnearly identical (1032) loc_os02g34884 12002.m08576 protein recessive suppressor of secretory defect, putative, expressed seq=cds; coord=4:116432507..116450657:-1; parent_gene=GRMZM2G171080'

'highly similar to (775) AT3G51460 | Symbols: RHD4 | RHD4 (ROOT HAIR DEFECTIVE4); phosphatidylinositol-4,5-bisphosphate 5-phosphatase/ phosphatidylinositol-4-phosphate phosphatase | chr3:19093007-19097142 FORWARDnearly identical (1032) loc_os02g34884 12002.m08576 protein recessive suppressor of secretory defect, putative, expressed seq=cds; coord=4:116432507..116450657:-1; parent_gene=GRMZM2G171080'

'moderately similar to (251) AT5G64930 | Symbols: CPR5, HYS1 | CPR5 (CONSTITUTIVE EXPRESSION OF PR GENES 5) | chr5:25945885-25948321 REVERSEhighly similar to (576) loc_os02g53070 12002.m10337 protein HYS1, putative, expressed seq=cds; coord=4:178037799..178042552:1; parent_gene=GRMZM2G158811'

'moderately similar to (481) AT2G03220 | Symbols: FT1, ATFUT1, ATFT1, MUR2 | FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups | chr2:970401-972353 REVERSEmoderately similar to (473) FUT1_PEA Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1) - Pisum sativum (Garden pea)highly similar to (840) loc_os02g52560 12002.m10287 protein galactoside 2-alpha-L-fucosyltransferase, putative, expressed seq=cds; coord=4:178671950..178675419:1; parent_gene=GRMZM2G015983'

'highly similar to (555) AT5G09360 | Symbols: LAC14 | LAC14 (laccase 14); laccase | chr5:2906426-2908658 REVERSEmoderately similar to (207) ASO_CUCMA L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) (ASO) - Cucurbita maxima (Pumpkin) (Winter squash)highly similar to (750) loc_os02g51440 12002.m10178 protein laccase, putative seq=cds; coord=4:181527348..181530838:1; parent_gene=GRMZM2G169033'

'highly similar to (555) AT5G09360 | Symbols: LAC14 | LAC14 (laccase 14); laccase | chr5:2906426-2908658 REVERSEmoderately similar to (207) ASO_CUCMA L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) (ASO) - Cucurbita maxima (Pumpkin) (Winter squash)highly similar to (750) loc_os02g51440 12002.m10178 protein laccase, putative seq=cds; coord=4:181527348..181530838:1; parent_gene=GRMZM2G169033'

'weakly similar to (147) AT5G55140 | Symbols: | ribosomal protein L30 family protein | chr5:22381370-22381787 FORWARDweakly similar to (187) loc_os08g01859 12008.m80294 protein structural constituent of ribosome, putative, expressed seq=cds; coord=5:2186824..2188668:-1; parent_gene=GRMZM2G085336' 'weakly similar to (147) AT5G55140 | Symbols: | ribosomal protein L30 family protein | chr5:22381370-22381787 FORWARDweakly similar to (187) loc_os08g01859 12008.m80294 protein structural constituent of ribosome, putative, expressed seq=cds; coord=5:2186824..2188668:-1; parent_gene=GRMZM2G085336'

'highly similar to (600) AT4G36195 | Symbols: | serine carboxypeptidase S28 family protein | chr4:17127202-17129787 FORWARDhighly similar to (748) loc_os10g36780 12010.m06484 protein prolyl carboxypeptidase like protein, putative, expressed seq=cds; coord=5:22758895..22762980:-1; parent_gene=GRMZM2G082502'

'weakly similar to (197) AT3G51000 | Symbols: | epoxide hydrolase, putative | chr3:18945258-18946499 REVERSEmoderately similar to (457) loc_os10g35520 12010.m06376 protein epoxide hydrolase 2, putative, expressed seq=cds; coord=5:24616889..24618887:-1; parent_gene=GRMZM2G032910'

'moderately similar to (448) AT1G02050 | Symbols: | chalcone and stilbene synthase family protein | chr1:359164-360441 REVERSEmoderately similar to (261) THS1_VITVI Stilbene synthase 1 (EC 2.3.1.95) (Resveratrol synthase 1) (Trihydroxystilbene synthase 1) (PSV25) - Vitis vinifera (Grape)highly similar to (619) loc_os10g34360 12010.m06262 protein chalcone synthase G, putative, expressed seq=cds; coord=5:26971466..26975726:1; parent_gene=GRMZM2G477683'

'weakly similar to (123) AT1G56120 | Symbols: | kinase | chr1:20987288-20993072 REVERSEmoderately similar to (243) loc_os11g28104 12011.m06728 protein protein kinase, putative, expressed seq=cds; coord=5:27198279..27204222:-1; parent_gene=GRMZM2G102862'

'moderately similar to (419) AT1G70090 | Symbols: GATL9, LGT8 | LGT8 (GLUCOSYL TRANSFERASE FAMILY 8); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr1:26400927-26402099 FORWARDhighly similar to (596) loc_os02g50600 12002.m10094 protein transferase, transferring glycosyl groups, putative, expressed seq=cds; coord=5:205746626..205748479:-1; parent_gene=GRMZM2G142709'

'moderately similar to (407) AT4G39770 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr4:18449138-18451218 REVERSEhighly similar to (521) loc_os02g51680 12002.m10199 protein expressed protein seq=cds; coord=5:208172385..208174899:1; parent_gene=GRMZM2G055150'

'moderately similar to (288) AT4G08950 | Symbols: EXO | EXO (EXORDIUM) | chr4:5740378-5741322 FORWARDmoderately similar to (407) loc_os02g52000 12002.m10231 protein phi-1-like phosphate-induced protein, putative, expressed seq=cds; coord=5:208637277..208638686:-1; parent_gene=GRMZM2G081214'

'very weakly similar to (92.0) AT4G38100 | Symbols: | unknown protein | chr4:17887033-17888177 REVERSEmoderately similar to (219) loc_os02g52260 12002.m10257 protein threonine endopeptidase, putative, expressed seq=cds; coord=5:209141850..209147166:1; parent_gene=GRMZM2G371795'

'weakly similar to (190) AT4G30350 | Symbols: | heat shock protein-related | chr4:14848031-14850973 FORWARDhighly similar to (884) loc_os02g54720 12002.m10500 protein expressed protein seq=cds; coord=5:212817973..212821590:-1; parent_gene=GRMZM2G040890' 'weakly similar to (130) loc_os03g62379 12003.m11114 protein DNA binding protein, putative, expressed seq=cds; coord=6:6015317..6016569:1; parent_gene=GRMZM2G019257'

'moderately similar to (318) AT2G03340 | Symbols: WRKY3 | WRKY3; transcription factor | chr2:1014724-1016936 REVERSEhighly similar to (637) loc_os12g32250 12012.m07031 protein SPF1-like DNA-binding protein, putative, expressed seq=cds; coord=6:22907900..22912535:1; parent_gene=GRMZM2G143765'

'very weakly similar to (85.9) AT5G61330 | Symbols: | rRNA processing protein-related | chr5:24657287-24660103 REVERSEweakly similar to (115) loc_os01g34200 12001.m43037 protein protein AATF, putative, expressed seq=cds; coord=6:28075395..28081870:1; parent_gene=GRMZM2G465617'

'weakly similar to (149) AT4G35160 | Symbols: | O-methyltransferase family 2 protein | chr4:16730989-16732808 REVERSEmoderately similar to (225) ZRP4_MAIZE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT) - Zea mays (Maize)moderately similar to (311) loc_os07g28040 12007.m07076 protein O-methyltransferase ZRP4, putative, expressed seq=cds; coord=7:44803178..44815872:-1; parent_gene=GRMZM2G177424'

'weakly similar to (116) AT4G39740 | Symbols: | electron transport SCO1/SenC family protein | chr4:18435586-18437095 REVERSEweakly similar to (138) loc_os09g20430 12009.m22074 protein SCO1 protein homolog, mitochondrial precursor, putative, expressed seq=cds; coord=7:100475067..100477058:-1; parent_gene=GRMZM2G126408'

'highly similar to (631) AT2G19130 | Symbols: | S-locus lectin protein kinase family protein | chr2:8293789-8296275 FORWARDmoderately similar to (238) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1115) loc_os04g34370 12004.m08531 protein serine/threonine-protein kinase receptor precursor, putative, expressed seq=cds; coord=7:148487644..148490458:1; parent_gene=GRMZM2G413030'

'very weakly similar to (89.4) AT2G41790 | Symbols: | peptidase M16 family protein / insulinase family protein | chr2:17429453-17436110 REVERSEweakly similar to (119) loc_os07g38270 12007.m08074 protein insulin-degrading enzyme, putative, expressed seq=cds; coord=7:159033700..159034362:-1; parent_gene=AC197013.3_FG003'

'moderately similar to (337) AT2G37270 | Symbols: ATRPS5B | ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome | chr2:15647883-15649042 REVERSEmoderately similar to (336) RS5_CICAR 40S ribosomal protein S5 (Fragment) - Cicer arietinum (Chickpea) (Garbanzo)moderately similar to (358) loc_os11g29190 12011.m080000 protein 40S ribosomal protein S5, putative, expressed seq=cds; coord=8:6590983..6592937:1; parent_gene=GRMZM2G156673'

'moderately similar to (337) AT2G37270 | Symbols: ATRPS5B | ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome | chr2:15647883-15649042 REVERSEmoderately similar to (336) RS5_CICAR 40S ribosomal protein S5 (Fragment) - Cicer arietinum (Chickpea) (Garbanzo)moderately similar to (358) loc_os11g29190 12011.m080000 protein 40S ribosomal protein S5, putative, expressed seq=cds; coord=8:6590983..6592937:1; parent_gene=GRMZM2G156673'

'moderately similar to (248) AT4G39220 | Symbols: ATRER1A | ATRER1A | chr4:18264280-18265531 FORWARDmoderately similar to (307) loc_os01g01640 12001.m06808 protein RER1A protein, putative, expressed seq=cds; coord=8:7616848..7621407:1; parent_gene=GRMZM2G078941' 'moderately similar to (256) AT5G09330 | Symbols: | anac082 (Arabidopsis NAC domain containing protein 82); transcription factor | chr5:2892623-2894708 REVERSEweakly similar to (190) NAC74_ORYSA NAC domain-containing protein 74 (ONAC074) - Oryza sativa (Rice)moderately similar to (437) loc_os05g35170 12005.m27832 protein NAC domain-containing protein 78, putative, expressed seq=cds; coord=8:102534750..102538745:-1; parent_gene=GRMZM2G104400'

'moderately similar to (226) AT3G14470 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4857940-4861104 FORWARDhighly similar to (738) loc_os05g34230 12005.m07654 protein disease resistance protein RGA3, putative, expressed seq=cds; coord=8:104379532..104382273:1; parent_gene=GRMZM2G017603'

'moderately similar to (313) AT2G38470 | Symbols: WRKY33, ATWRKY33 | WRKY33; transcription factor | chr2:16108476-16110539 FORWARDmoderately similar to (484) loc_os05g27730 12005.m07061 protein OsWRKY53 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=8:110214059..110216431:-1; parent_gene=GRMZM2G449681'

'moderately similar to (295) AT1G21240 | Symbols: WAK3 | WAK3 (wall associated kinase 3); kinase/ protein serine/threonine kinase | chr1:7434303-7436702 FORWARDweakly similar to (177) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (484) loc_os08g39210 12008.m07902 protein OsWAK74 - OsWAK receptor-like protein kinase, expressed seq=cds; coord=8:112624757..112626912:1; parent_gene=GRMZM2G061718'

'weakly similar to (115) AT2G45050 | Symbols: | zinc finger (GATA type) family protein | chr2:18582958-18583845 FORWARDweakly similar to (153) loc_os03g05160 12003.m06040 protein GATA zinc finger family protein, expressed seq=cds; coord=9:152266750..152271833:1; parent_gene=GRMZM2G532534'

'weakly similar to (189) AT1G25550 | Symbols: | myb family transcription factor | chr1:8976644-8977942 FORWARDmoderately similar to (290) loc_os02g22020 12002.m07440 protein DNA binding protein, putative, expressed seq=cds; coord=10:5384582..5386647:1; parent_gene=GRMZM2G016370'

'moderately similar to (493) AT2G27690 | Symbols: CYP94C1 | CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding | chr2:11809373-11810860 FORWARDvery weakly similar to (92.4) C97B2_SOYBN Cytochrome P450 97B2 (EC 1.14.-.-) - Glycine max (Soybean)highly similar to (736) loc_os11g05380 12011.m04735 protein cytochrome P450 94A2, putative, expressed seq=cds; coord=10:5398299..5400462:1; parent_gene=GRMZM2G016264'

'moderately similar to (374) AT1G24360 | Symbols: | 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase | chr1:8640820-8643283 FORWARDmoderately similar to (397) FABG3_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 3, chloroplast precursor (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 3) - Brassica napus (Rape)moderately similar to (476) loc_os04g30760 12004.m08180 protein 3-oxoacyl-reductase, chloroplast precursor, putative, expressed seq=cds; coord=10:108122298..108130104:1; parent_gene=GRMZM2G099696' 'highly similar to (610) AT4G39910 | Symbols: ATUBP3, UBP3 | ATUBP3 (ARABIDOPSIS THALIANA UBIQUITIN-SPECIFIC PROTEASE 3); ubiquitin-specific protease | chr4:18511858-18514139 REVERSEhighly similar to (703) loc_os04g37950 12004.m08784 protein ubiquitin carboxyl-terminal hydrolase 4, putative, expressed seq=cds; coord=10:121505257..121515372:-1; parent_gene=GRMZM2G036186'

'moderately similar to (394) AT4G23180 | Symbols: CRK10, RLK4 | CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr4:12138171-12140780 FORWARDmoderately similar to (203) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (523) loc_os04g53994 12004.m10292 protein ATP binding protein, putative, expressed seq=cds; coord=10:144138641..144143208:-1; parent_gene=GRMZM2G000633'

'highly similar to (641) AT4G21380 | Symbols: ARK3 | ARK3 (A. THALIANA RECEPTOR KINASE 3); kinase/ transmembrane receptor protein serine/threonine kinase | chr4:11389219-11393090 REVERSEmoderately similar to (299) SLSG6_BRAOL S-locus-specific glycoprotein S6 precursor (SLSG-6) - Brassica oleracea (Wild cabbage)nearly identical (1018) loc_os04g54070 12004.m10299 protein receptor-like kinase, putative, expressed seq=cds; coord=10:144143811..144147098:1; parent_gene=GRMZM2G000620'

'very weakly similar to (92.0) AT5G20900 | Symbols: JAZ12, TIFY3B | JAZ12 (JASMONATE-ZIM-DOMAIN PROTEIN 12) | chr5:7090883-7092201 FORWARDweakly similar to (183) loc_os04g55920 12004.m35599 protein ZIM motif family protein, expressed seq=cds; coord=10:145933966..145937989:1; parent_gene=GRMZM2G143402'

'very weakly similar to (82.0) AT5G25190 | Symbols: | ethylene-responsive element-binding protein, putative | chr5:8707007-8707655 REVERSEweakly similar to (105) loc_os04g56150 12004.m10506 protein ethylene-responsive transcription factor 4, putative seq=cds; coord=10:146118823..146119727:1; parent_gene=GRMZM2G104260'

'highly similar to (765) AT5G20990 | Symbols: B73, SIR4, CNX, CHL6, CNX1 | B73; molybdenum ion binding | chr5:7128737-7133397 REVERSEhighly similar to (696) loc_os04g56620 12004.m101683 protein molybdopterin biosynthesis CNX1 protein, putative, expressed seq=cds; coord=10:146668953..146673272:1; parent_gene=GRMZM2G067176'

'weakly similar to (120) AT1G78690 | Symbols: | phospholipid/glycerol acyltransferase family protein | chr1:29597002-29598409 FORWARDweakly similar to (161) loc_os04g57150 12004.m35502 protein tafazzin, putative, expressed seq=cds; coord=10:147206883..147213776:-1; parent_gene=GRMZM2G125083'

'weakly similar to (139) AT3G10620 | Symbols: ATNUDX26 | ATNUDX26 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 26); bis(5'-adenosyl)-pentaphosphatase/ bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) | chr3:3320263-3321565 FORWARDweakly similar to (182) loc_os04g58900 12004.m10770 protein expressed protein seq=cds; coord=10:148870139..148873900:1; parent_gene=GRMZM2G001905'

'weakly similar to (105) AT1G26945 | Symbols: KDR | KDR (KIDARI); transcription regulator | chr1:9351571-9352474 FORWARDweakly similar to (122) loc_os10g26460 12010.m05586 protein DNA binding protein, putative seq=cds; coord=1:15133983..15136082:-1; parent_gene=GRMZM2G035156' 'very weakly similar to (91.7) AT5G10510 | Symbols: AIL6 | AIL6 (AINTEGUMENTA-LIKE 6); DNA binding / transcription factor | chr5:3315991-3320008 FORWARDvery weakly similar to (87.8) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)weakly similar to (194) loc_os03g07940 12003.m06305 protein AINTEGUMENTA-like protein, putative, expressed seq=cds; coord=1:16118862..16123188:-1; parent_gene=GRMZM2G399072'

'very weakly similar to (91.7) AT5G10510 | Symbols: AIL6 | AIL6 (AINTEGUMENTA-LIKE 6); DNA binding / transcription factor | chr5:3315991-3320008 FORWARDvery weakly similar to (87.8) BBM2_BRANA Protein BABY BOOM 2 (BnBBM2) - Brassica napus (Rape)weakly similar to (194) loc_os03g07940 12003.m06305 protein AINTEGUMENTA-like protein, putative, expressed seq=cds; coord=1:16118862..16123188:-1; parent_gene=GRMZM2G399072'

'weakly similar to (141) AT2G45430 | Symbols: | DNA-binding protein-related | chr2:18727848-18728801 FORWARDmoderately similar to (258) loc_os03g16350 12003.m07070 protein DNA-binding protein, putative, expressed seq=cds; coord=1:39332349..39333847:1; parent_gene=GRMZM2G119168'

'highly similar to (521) AT2G37650 | Symbols: | scarecrow-like transcription factor 9 (SCL9) | chr2:15792623-15794779 FORWARDmoderately similar to (218) CIGR2_ORYSA Chitin-inducible gibberellin-responsive protein 2 - Oryza sativa (Rice)nearly identical (1152) loc_os03g48450 12003.m101444 protein DELLA protein RGL1, putative, expressed seq=cds; coord=1:40139023..40143020:-1; parent_gene=GRMZM2G049159'

'highly similar to (524) AT2G44830 | Symbols: | protein kinase, putative | chr2:18490398-18492779 FORWARDhighly similar to (501) G11A_ORYSA Protein kinase G11A (EC 2.7.11.1) - Oryza sativa (Rice)highly similar to (769) loc_os10g41290 12010.m06893 protein protein kinase PVPK-1, putative, expressed seq=cds; coord=1:93908134..93911493:-1; parent_gene=GRMZM2G392477'

'moderately similar to (404) AT5G38710 | Symbols: | proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative | chr5:15501340-15503899 FORWARDhighly similar to (640) loc_os10g40360 12010.m06805 protein proline oxidase, mitochondrial precursor, putative, expressed seq=cds; coord=1:88340098..88342761:1; parent_gene=GRMZM2G053720'

'moderately similar to (347) AT3G53230 | Symbols: | cell division cycle protein 48, putative / CDC48, putative | chr3:19723416-19726489 FORWARDmoderately similar to (345) CDC48_SOYBN Cell division cycle protein 48 homolog (Valosin-containing protein homolog) (VCP) - Glycine max (Soybean)moderately similar to (351) loc_os10g30580 12010.m65393 protein cell division control protein 48 homolog E, putative, expressed seq=cds; coord=1:210639997..210645759:1; parent_gene=GRMZM2G128605'

'nearly identical (1109) AT5G58140 | Symbols: PHOT2, NPL1 | PHOT2 (PHOTOTROPIN 2); FMN binding / blue light photoreceptor/ kinase/ protein serine/threonine kinase | chr5:23524771-23529993 FORWARDmoderately similar to (335) KPK1_PHAVU Protein kinase PVPK-1 (EC 2.7.11.1) - Phaseolus vulgaris (Kidney bean) (French bean)nearly identical (1347) loc_os04g23890 12004.m35267 protein phototropin-1, putative, expressed seq=cds; coord=1:220307458..220339987:-1; parent_gene=GRMZM2G032351' 'nearly identical (1109) AT5G58140 | Symbols: PHOT2, NPL1 | PHOT2 (PHOTOTROPIN 2); FMN binding / blue light photoreceptor/ kinase/ protein serine/threonine kinase | chr5:23524771-23529993 FORWARDmoderately similar to (335) KPK1_PHAVU Protein kinase PVPK-1 (EC 2.7.11.1) - Phaseolus vulgaris (Kidney bean) (French bean)nearly identical (1347) loc_os04g23890 12004.m35267 protein phototropin-1, putative, expressed seq=cds; coord=1:220307458..220339987:-1; parent_gene=GRMZM2G032351'

'moderately similar to (347) AT2G46620 | Symbols: | AAA-type ATPase family protein | chr2:19139071-19140546 REVERSEhighly similar to (650) loc_os10g37500 12010.m06538 protein ATP binding protein, putative, expressed seq=cds; coord=1:222980062..222981812:1; parent_gene=GRMZM2G170982'

'weakly similar to (152) loc_os03g60560 12003.m10945 protein ZFP16-2, putative, expressed seq=cds; coord=1:293154769..293155800:1; parent_gene=GRMZM2G061626'

'moderately similar to (267) AT4G10020 | Symbols: AtHSD5 | AtHSD5 (hydroxysteroid dehydrogenase 5); binding / catalytic/ oxidoreductase | chr4:6268363-6270179 FORWARDmoderately similar to (306) loc_os03g62590 12003.m11136 protein expressed protein seq=cds; coord=1:296961161..296962159:-1; parent_gene=AC217358.3_FG007'

'highly similar to (934) AT2G02220 | Symbols: ATPSKR1, PSKR1 | PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase | chr2:584098-587124 REVERSEhighly similar to (910) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1459) loc_os04g57630 12004.m10648 protein phytosulfokine receptor precursor, putative, expressed seq=cds; coord=2:2222100..2225911:1; parent_gene=GRMZM2G452142'

'moderately similar to (377) AT4G22260 | Symbols: IM, IM1 | IM (IMMUTANS); alternative oxidase | chr4:11769967 11772350 REVERSEmoderately similar to (456) loc_os04g57320 12004.m79006 protein immutans protein, putative, expressed seq=cds; coord=2:2681445..2685261:1; parent_gene=GRMZM2G010555'

'weakly similar to (197) AT5G05450 | Symbols: | DEAD/DEAH box helicase, putative (RH18) | chr5:1612077-1615195 FORWARDvery weakly similar to (94.0) PMGI_MAIZE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (PGAM-I) - Zea mays (Maize)moderately similar to (254) loc_os01g07080 12001.m42877 protein ATP-dependent rRNA helicase spb4, putative, expressed seq=cds; coord=2:4320523..4326308:1; parent_gene=GRMZM2G314171'

'weakly similar to (187) AT1G68290 | Symbols: ENDO 2 | ENDO 2 (endonuclease 2); T/G mismatch-specific endonuclease/ endonuclease/ nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease | chr1:25596718-25598264 FORWARDmoderately similar to (300) loc_os04g55850 12004.m35489 protein nuclease PA3, putative, expressed seq=cds; coord=2:4847231..4848890:-1; parent_gene=GRMZM2G032977'

'moderately similar to (325) AT5G67240 | Symbols: SDN3 | SDN3 (SMALL RNA DEGRADING NUCLEASE 3); exonuclease/ nucleic acid binding | chr5:26824454-26828098 REVERSEhighly similar to (638) loc_os04g55700 12004.m10461 protein exonuclease, putative, expressed seq=cds; coord=2:5082653..5098185:1; parent_gene=GRMZM2G082097' 'moderately similar to (325) AT5G67240 | Symbols: SDN3 | SDN3 (SMALL RNA DEGRADING NUCLEASE 3); exonuclease/ nucleic acid binding | chr5:26824454-26828098 REVERSEhighly similar to (638) loc_os04g55700 12004.m10461 protein exonuclease, putative, expressed seq=cds; coord=2:5082653..5098185:1; parent_gene=GRMZM2G082097'

'moderately similar to (244) AT4G34040 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr4:16304638-16307503 REVERSEhighly similar to (936) loc_os04g55510 12004.m10442 protein zinc finger, C3HC4 type family protein, expressed seq=cds; coord=2:5566610..5573059:-1; parent_gene=GRMZM2G174926'

'nearly identical (1211) AT2G42490 | Symbols: | copper amine oxidase, putative | chr2:17691600-17695526 REVERSEmoderately similar to (231) AMO_PEA Amine oxidase [copper-containing] precursor (EC 1.4.3.6) - Pisum sativum (Garden pea)nearly identical (1355) loc_os04g40040 12004.m08988 protein copper methylamine oxidase precursor, putative, expressed seq=cds; coord=2:38132179..38142127:1; parent_gene=GRMZM2G147884'

'weakly similar to (146) loc_os12g06550 12012.m04645 protein expressed protein seq=cds; coord=2:53196865..53198964:-1; parent_gene=GRMZM2G014905'

'moderately similar to (462) AT4G32640 | Symbols: | protein binding / zinc ion binding | chr4:15742661-15750424 FORWARDhighly similar to (598) loc_os11g29200 12011.m06831 protein protein transport protein Sec24-like CEF, putative, expressed seq=cds; coord=2:124094006..124108029:-1; parent_gene=GRMZM2G075680'

'highly similar to (653) AT1G76490 | Symbols: HMG1, HMGR1 | HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase | chr1:28695801-28698206 FORWARDhighly similar to (746) HMDH_MAIZE 3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA reductase) - Zea mays (Maize)highly similar to (775) loc_os09g31970 12009.m06287 protein 3-hydroxy-3-methylglutaryl-coenzyme A reductase 3, putative, expressed seq=cds; coord=2:190414780..190419336:1; parent_gene=GRMZM2G058095'

'weakly similar to (159) AT1G68920 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr1:25915620-25917675 FORWARDmoderately similar to (244) loc_os09g32510 12009.m22151 protein BHLH transcription factor, putative, expressed seq=cds; coord=2:191378248..191380925:-1; parent_gene=GRMZM2G083504'

'very weakly similar to (81.3) AT1G32640 | Symbols: ATMYC2, RD22BP1, JAI1, JIN1, MYC2, ZBF1 | MYC2; DNA binding / transcription activator/ transcription factor | chr1:11799042-11800913 REVERSEmoderately similar to (204) loc_os09g34330 12009.m06482 protein transcription factor AtMYC2, putative seq=cds; coord=2:193882051..193882939:-1; parent_gene=GRMZM2G107560'

'very weakly similar to (81.3) AT1G32640 | Symbols: ATMYC2, RD22BP1, JAI1, JIN1, MYC2, ZBF1 | MYC2; DNA binding / transcription activator/ transcription factor | chr1:11799042-11800913 REVERSEmoderately similar to (204) loc_os09g34330 12009.m06482 protein transcription factor AtMYC2, putative seq=cds; coord=2:193882051..193882939:-1; parent_gene=GRMZM2G107560'

'weakly similar to (176) AT5G66840 | Symbols: | SAP domain-containing protein | chr5:26692922-26695296 REVERSEmoderately similar to (378) loc_os07g42760 12007.m08506 protein expressed protein seq=cds; coord=2:211726329..211731892:-1; parent_gene=GRMZM2G056564' 'highly similar to (506) AT5G38560 | Symbols: | protein kinase family protein | chr5:15439844-15443007 FORWARDmoderately similar to (252) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (707) loc_os01g02040 12001.m42834 protein ATP binding protein, putative, expressed seq=cds; coord=3:29009912..29013884:-1; parent_gene=GRMZM2G355636'

'moderately similar to (303) AT3G16520 | Symbols: UGT88A1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr3:5618847-5620833 REVERSEweakly similar to (153) UFO3_MAIZE Anthocyanidin 3-O-glucosyltransferase (EC 2.4.1.115) (Flavonol 3-O-glucosyltransferase) (UDP-glucose flavonoid 3-O-glucosyltransferase) (Bronze-1) (Bz-W22 allele) - Zea mays (Maize)moderately similar to (466) loc_os01g53330 12001.m11501 protein anthocyanidin 5,3-O-glucosyltransferase, putative, expressed seq=cds; coord=3:114351464..114353544:-1; parent_gene=GRMZM2G105991'

'moderately similar to (431) AT1G68690 | Symbols: | ATP binding / protein kinase/ protein serine/threonine kinase | chr1:25789192-25791886 FORWARDmoderately similar to (210) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (704) loc_os01g53640 12001.m11530 protein ATP binding protein, putative, expressed seq=cds; coord=3:199853295..199856980:-1; parent_gene=AC211175.3_FG005'

'weakly similar to (152) AT1G20980 | Symbols: SPL14, FBR6, SPL1R2, ATSPL14 | SPL14 (squamosa promoter binding protein-like 14); DNA binding / transcription activator/ transcription factor | chr1:7325042-7328933 FORWARDvery weakly similar to (81.6) VATB2_HORVU Vacuolar ATP synthase subunit B isoform 2 (EC 3.6.3.14) (V-ATPase B subunit 2) (Vacuolar proton pump B subunit 2) - Hordeum vulgare (Barley)moderately similar to (261) loc_os08g40260 12008.m08006 protein squamosa promoter-binding-like protein 16, putative, expressed seq=cds; coord=3:202509079..202513794:-1; parent_gene=GRMZM2G387993'

'moderately similar to (483) AT5G19580 | Symbols: | glyoxal oxidase-related | chr5:6607595-6609517 REVERSEhighly similar to (879) loc_os01g48540 12001.m11044 protein glyoxal oxidase, putative, expressed seq=cds; coord=3:209027465..209030003:-1; parent_gene=GRMZM2G164674'

'moderately similar to (345) AT1G34300 | Symbols: | lectin protein kinase family protein | chr1:12503450-12505939 FORWARDhighly similar to (633) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1279) loc_os01g47820 12001.m10975 protein S-locus-like receptor protein kinase, putative, expressed seq=cds; coord=3:210357435..210360168:1; parent_gene=GRMZM2G142207'

'moderately similar to (345) AT1G34300 | Symbols: | lectin protein kinase family protein | chr1:12503450-12505939 FORWARDhighly similar to (633) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1279) loc_os01g47820 12001.m10975 protein S-locus-like receptor protein kinase, putative, expressed seq=cds; coord=3:210357435..210360168:1; parent_gene=GRMZM2G142207'

'moderately similar to (245) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (340) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215466579..215473931:-1; parent_gene=GRMZM2G121878'

'highly similar to (515) AT1G60590 | Symbols: | polygalacturonase, putative / pectinase, putative | chr1:22314426-22316867 REVERSEmoderately similar to (248) PGLR_ACTCH Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) - Actinidia chinensis (Kiwi) (Yangtao)highly similar to (734) loc_os01g44970 12001.m10703 protein polygalacturonase precursor, putative, expressed seq=cds; coord=3:215929238..215932695:-1; parent_gene=GRMZM2G037431'

'weakly similar to (178) AT2G45620 | Symbols: | nucleotidyltransferase family protein | chr2:18792943-18795750 FORWARDmoderately similar to (226) loc_os02g02970 12002.m05647 protein poly, putative, expressed seq=cds; coord=3:215991469..215992380:-1; parent_gene=GRMZM2G132340'

'weakly similar to (111) AT5G45910 | Symbols: | GDSL-motif lipase/hydrolase family protein | chr5:18620420-18622264 REVERSEmoderately similar to (221) loc_os01g42730 12001.m10537 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=3:225122883..225124641:1; parent_gene=GRMZM2G022279'

'highly similar to (692) AT3G23430 | Symbols: PHO1, ATPHO1 | PHO1 (phosphate 1) | chr3:8387818-8393242 REVERSEnearly identical (1109) loc_os02g56510 12002.m10672 protein phosphate transporter 1, putative, expressed seq=cds; coord=4:171917079..171922792:1; parent_gene=GRMZM2G466545'

'moderately similar to (400) AT5G65685 | Symbols: | soluble glycogen synthase-related | chr5:26273252-26275864 REVERSEweakly similar to (189) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Potato)highly similar to (907) loc_os02g56320 12002.m10655 protein glycogen synthase 2, putative, expressed seq=cds; coord=4:172606253..172677186:-1; parent_gene=GRMZM2G130043'

'moderately similar to (444) AT5G10080 | Symbols: | aspartyl protease family protein | chr5:3150843-3153380 FORWARDvery weakly similar to (81.6) ASP1_ORYSA Aspartic proteinase Asp1 precursor (EC 3.4.23.-) (OsAsp1) (OSAP1) (Nucellin-like protein) - Oryza sativa (Rice)highly similar to (753) loc_os02g51540 12002.m10187 protein pepsin A, putative, expressed seq=cds; coord=4:181338045..181349423:-1; parent_gene=GRMZM2G098583'

'moderately similar to (310) AT3G14160 | Symbols: | oxidoreductase | chr3:4693495-4695198 FORWARDmoderately similar to (410) loc_os03g60190 12003.m10912 protein DNA repair protein, putative, expressed seq=cds; coord=5:2775245..2784967:-1; parent_gene=GRMZM2G165270'

'weakly similar to (139) AT1G04240 | Symbols: SHY2, IAA3 | SHY2 (SHORT HYPOCOTYL 2); transcription factor | chr1:1128564-1129319 REVERSEweakly similar to (196) IAA14_ORYSA Auxin-responsive protein IAA14 (Indoleacetic acid-induced protein 14) - Oryza sativa (Rice)weakly similar to (196) loc_os03g58350 12003.m10745 protein OsIAA14 - Auxin-responsive Aux/IAA gene family member, expressed seq=cds; coord=5:4200507..4201934:-1; parent_gene=GRMZM2G152796'

'moderately similar to (270) AT1G31330 | Symbols: PSAF | PSAF (photosystem I subunit F) | chr1:11215011-11215939 REVERSEmoderately similar to (305) PSAF_HORVU Photosystem I reaction center subunit III, chloroplast precursor (Light-harvesting complex I 17 kDa protein) (PSI-F) - Hordeum vulgare (Barley)moderately similar to (307) loc_os03g56670 12003.m34938 protein photosystem I reaction center subunit III, chloroplast precursor, putative, expressed seq=cds; coord=5:5286657..5288134:1; parent_gene=GRMZM2G085646' 'moderately similar to (224) AT5G01160 | Symbols: | e-cadherin binding protein-related | chr5:54280-55727 FORWARDhighly similar to (594) loc_os10g35190 12010.m06342 protein expressed protein seq=cds; coord=5:25791688..25795830:1; parent_gene=GRMZM2G120933'

'moderately similar to (274) AT1G28590 | Symbols: | lipase, putative | chr1:10047509-10049300 REVERSEweakly similar to (176) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)moderately similar to (471) loc_os10g25400 12010.m05487 protein esterase precursor, putative, expressed seq=cds; coord=5:36593492..36595356:1; parent_gene=GRMZM2G087827'

'moderately similar to (437) AT4G04950 | Symbols: | thioredoxin family protein | chr4:2517882-2519924 REVERSEhighly similar to (552) loc_os10g35720 12010.m22006 protein OsGrx_S17 - glutaredoxin subgroup II, expressed seq=cds; coord=5:160426855..160429034:-1; parent_gene=GRMZM2G052402'

'weakly similar to (162) AT3G62290 | Symbols: ATARFA1E | ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding | chr3:23052287-23053545 FORWARDweakly similar to (161) ARF1_CHLRE ADP-ribosylation factor 1 - Chlamydomonas reinhardtiiweakly similar to (162) loc_os07g12200 12007.m05673 protein ADP-ribosylation factor 1, putative, expressed seq=cds; coord=5:197869674..197870822:1; parent_gene=GRMZM2G075253'

'weakly similar to (162) AT3G62290 | Symbols: ATARFA1E | ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding | chr3:23052287-23053545 FORWARDweakly similar to (161) ARF1_CHLRE ADP-ribosylation factor 1 - Chlamydomonas reinhardtiiweakly similar to (162) loc_os07g12200 12007.m05673 protein ADP-ribosylation factor 1, putative, expressed seq=cds; coord=5:197869674..197870822:1; parent_gene=GRMZM2G075253'

'moderately similar to (348) AT2G25620 | Symbols: | protein phosphatase 2C, putative / PP2C, putative | chr2:10903154-10904978 REVERSEhighly similar to (590) loc_os02g55560 12002.m100396 protein DNA-binding protein phosphatase 2C, putative, expressed seq=cds; coord=5:214089781..214098932:1; parent_gene=GRMZM2G180430'

'highly similar to (595) AT3G23340 | Symbols: ckl10 | ckl10 (Casein Kinase I-like 10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr3:8351047-8353791 FORWARDhighly similar to (791) loc_os02g56560 12002.m77862 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=5:215017420..215021669:-1; parent_gene=GRMZM2G150932'

'weakly similar to (125) AT3G21260 | Symbols: | glycolipid transfer protein-related | chr3:7464132-7465785 REVERSEweakly similar to (194) loc_os08g01710 12008.m04319 protein expressed protein seq=cds; coord=6:2241302..2243599:-1; parent_gene=GRMZM2G118378'

'moderately similar to (282) AT2G02450 | Symbols: ANAC035 | ANAC035 (Arabidopsis NAC domain containing protein 35); transcription factor | chr2:648044-650649 FORWARDweakly similar to (172) NAC48_ORYSA NAC domain-containing protein 48 (ONAC048) - Oryza sativa (Rice)moderately similar to (355) loc_os08g02160 12008.m04362 protein NAC domain-containing protein 68, putative, expressed seq=cds; coord=6:3869561..3872846:1; parent_gene=GRMZM2G030325' 'moderately similar to (484) AT3G04120 | Symbols: GAPC, GAPC-1, GAPC1 | GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr3:1081077-1083131 FORWARDhighly similar to (557) G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 (EC 1.2.1.12) - Zea mays (Maize)highly similar to (519) loc_os08g03290 12008.m26460 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative, expressed seq=cds; coord=6:6898695..6903246:-1; parent_gene=GRMZM2G180625'

'highly similar to (720) AT1G30440 | Symbols: | phototropic-responsive NPH3 family protein | chr1:10759475-10762199 FORWARDmoderately similar to (409) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)nearly identical (1020) loc_os08g03650 12008.m04509 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=6:9497117..9501243:-1; parent_gene=GRMZM2G301803'

'weakly similar to (110) AT4G29190 | Symbols: | zinc finger (CCCH-type) family protein | chr4:14392233-14393303 REVERSEmoderately similar to (252) loc_os05g45020 12005.m08627 protein CCCH transcription factor, putative, expressed seq=cds; coord=6:160013893..160016282:1; parent_gene=GRMZM2G004795'

'highly similar to (585) AT5G26680 | Symbols: | endonuclease, putative | chr5:9311882-9315458 REVERSEhighly similar to (650) FEN1A_ORYSA Flap endonuclease 1a (EC 3.1.-.-) (OsFEN-1a) - Oryza sativa (Rice)highly similar to (617) loc_os05g46270 12005.m83948 protein flap endonuclease 1a, putative, expressed seq=cds; coord=6:161720046..161724633:-1; parent_gene=GRMZM2G121262'

'highly similar to (702) AT2G21520 | Symbols: | transporter | chr2:9215956-9218953 FORWARDhighly similar to (971) loc_os05g46720 12005.m27946 protein phosphatidylinositol transfer-like protein III, putative, expressed seq=cds; coord=6:162119858..162125056:1; parent_gene=GRMZM2G174990'

'weakly similar to (174) AT1G13260 | Symbols: RAV1 | RAV1; DNA binding / transcription factor/ transcription repressor | chr1:4542386-4543420 FORWARDmoderately similar to (261) loc_os05g47650 12005.m08837 protein DNA-binding protein RAV1, putative, expressed seq=cds; coord=6:162571228..162572866:1; parent_gene=GRMZM2G059939'

'nearly identical (3078) AT5G53460 | Symbols: GLT1 | GLT1; glutamate synthase (NADH) | chr5:21700518-21709629 FORWARDnearly identical (3057) GLSN_MEDSA Glutamate synthase [NADH], chloroplast precursor (EC 1.4.1.14) (NADH-GOGAT) - Medicago sativa (Alfalfa)nearly identical (3311) loc_os01g48960 12001.m11085 protein glutamate synthase, chloroplast precursor, putative, expressed seq=cds; coord=6:163217461..163229234:1; parent_gene=GRMZM2G375064'

'moderately similar to (368) AT4G18550 | Symbols: | lipase class 3 family protein | chr4:10225006-10226862 REVERSEhighly similar to (525) loc_os05g49830 12005.m09053 protein triacylglycerol lipase, putative, expressed seq=cds; coord=6:165625344..165626546:1; parent_gene=AC231411.1_FG011' 'moderately similar to (291) AT1G68130 | Symbols: AtIDD14 | AtIDD14 (Arabidopsis thaliana Indeterminate(ID)-Domain 14); nucleic acid binding / transcription factor/ zinc ion binding | chr1:25532843-25534317 FORWARDmoderately similar to (319) loc_os09g27650 12009.m05916 protein zinc finger, C2H2 type family protein, expressed seq=cds; coord=7:124146510..124150019:1; parent_gene=GRMZM2G141031'

'moderately similar to (469) AT3G25110 | Symbols: AtFaTA | AtFaTA (Arabidopsis FatA acyl-ACP thioesterase); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase | chr3:9146589-9148273 REVERSEmoderately similar to (239) FATB_GOSHI Myristoyl-acyl carrier protein thioesterase, chloroplast precursor (EC 3.1.2.-) (16:0-acyl-carrier protein thioesterase) (16:0-ACP thioesterase) (Acyl-[acyl-carrier-protein] hydrolase) (PATE) - Gossypium hirsutum (Upland cotton)highly similar to (599) loc_os09g32760 12009.m060080 protein oleoyl-acyl carrier protein thioesterase, chloroplast precursor, putative, expressed seq=cds; coord=7:136864624..136868251:-1; parent_gene=GRMZM2G143955'

'moderately similar to (281) AT3G14470 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4857940-4861104 FORWARDnearly identical (1321) loc_os07g29810 12007.m07252 protein plant disease resistant protein, putative seq=cds; coord=7:148700092..148704194:1; parent_gene=GRMZM2G397557'

'seq=cds; coord=7:151217709..151219397:-1; parent_gene=GRMZM2G067624'

'moderately similar to (280) AT1G76160 | Symbols: sks5 | sks5 (SKU5 Similar 5); copper ion binding / oxidoreductase | chr1:28578211-28581020 REVERSEmoderately similar to (215) NTP3_TOBAC Pollen-specific protein NTP303 precursor - Nicotiana tabacum (Common tobacco)moderately similar to (325) loc_os07g32660 12007.m07529 protein L-ascorbate oxidase homolog precursor, putative, expressed seq=cds; coord=7:152438526..152442219:1; parent_gene=GRMZM2G076225'

'very weakly similar to (94.7) AT2G29420 | Symbols: ATGSTU7, GST25 | ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase | chr2:12618111-12618871 REVERSEweakly similar to (120) GSTU6_ORYSA Probable glutathione S-transferase GSTU6 (EC 2.5.1.18) (28 kDa cold-induced protein) - Oryza sativa (Rice)weakly similar to (120) loc_os10g38740 12010.m06642 protein glutathione S-transferase GSTU6, putative, expressed seq=cds; coord=7:169378558..169379060:1; parent_gene=GRMZM2G109812'

'nearly identical (1023) AT3G02050 | Symbols: KUP3, ATKUP3, ATKT4 | KUP3 (K

'nearly identical (1023) AT3G02050 | Symbols: KUP3, ATKUP3, ATKT4 | KUP3 (K

'moderately similar to (253) AT2G30360 | Symbols: CIPK11, PKS5, SIP4, SNRK3.22 | SIP4 (SOS3-INTERACTING PROTEIN 4); kinase/ protein kinase | chr2:12937265-12938572 REVERSEweakly similar to (193) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)moderately similar to (407) loc_os07g48090 12007.m09024 protein CBL-interacting serine/threonine-protein kinase 11, putative, expressed seq=cds; coord=7:172879486..172881907:1; parent_gene=GRMZM2G177050' 'moderately similar to (298) AT5G05340 | Symbols: | peroxidase, putative | chr5:1579142-1580819 REVERSEmoderately similar to (325) PER1_ARAHY Cationic peroxidase 1 precursor (EC 1.11.1.7) (PNPC1) - Arachis hypogaea (Peanut)highly similar to (525) loc_os07g48060 12007.m09021 protein cationic peroxidase 1 precursor, putative, expressed seq=cds; coord=7:172823739..172825501:-1; parent_gene=GRMZM2G042347'

'highly similar to (580) AT2G22250 | Symbols: ATAAT, AAT, MEE17 | aminotransferase class I and II family protein | chr2:9458011-9460297 REVERSEhighly similar to (725) loc_os01g65090 12001.m42770 protein aspartate aminotransferase, putative, expressed seq=cds; coord=8:101408887..101413622:1; parent_gene=GRMZM2G033799'

'moderately similar to (313) AT2G38470 | Symbols: WRKY33, ATWRKY33 | WRKY33; transcription factor | chr2:16108476-16110539 FORWARDmoderately similar to (484) loc_os05g27730 12005.m07061 protein OsWRKY53 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=8:110214059..110216431:-1; parent_gene=GRMZM2G449681'

'very weakly similar to (82.4) AT1G04300 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TRAF-like (InterPro:IPR008974), MATH (InterPro:IPR002083); BEST Arabidopsis thaliana protein match is: meprin and TRAF homology domain-containing protein / MATH domain-containing protein (TAIR:AT5G43560.2); Has 15485 Blast hits to 9800 proteins in 673 species: Archae - 16; Bacteria - 1225; Metazoa - 5601; Fungi - 1994; Plants - 616; Viruses - 101; Other Eukaryotes - 5932 (source: NCBI BLink). | chr1:1148818-1153895 REVERSEhighly similar to (520) loc_os05g43280 12005.m08456 protein MATH domain containing protein, expressed seq=cds; coord=8:122408765..122413891:-1; parent_gene=GRMZM2G060213'

'moderately similar to (426) AT2G29390 | Symbols: ATSMO2 | SMO2-2 (STEROL 4-ALPHA-METHYL-OXIDASE 2-2); 4-alpha-methyl-delta7-sterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase | chr2:12610758-12611929 REVERSEhighly similar to (503) loc_os11g48020 12011.m08600 protein C-4 methylsterol oxidase, putative, expressed seq=cds; coord=8:156349765..156352110:-1; parent_gene=GRMZM2G176301'

'highly similar to (513) AT1G27340 | Symbols: | F-box family protein | chr1:9495741-9497857 FORWARDhighly similar to (804) loc_os01g69940 12001.m13043 protein F-box domain containing protein, expressed seq=cds; coord=8:161103602..161107787:1; parent_gene=GRMZM2G064954'

'moderately similar to (367) AT1G21720 | Symbols: PBC1 | PBC1 (PROTEASOME BETA SUBUNIT C1); peptidase/ threonine-type endopeptidase | chr1:7626394-7628070 FORWARDmoderately similar to (391) PSB3_ORYSA Proteasome subunit beta type 3 (EC 3.4.25.1) (20S proteasome alpha subunit C) (20S proteasome subunit beta-3) - Oryza sativa (Rice)moderately similar to (391) loc_os06g43570 12006.m08887 protein proteasome subunit beta type 3, putative, expressed seq=cds; coord=9:94789790..94794492:1; parent_gene=GRMZM2G092975'

'moderately similar to (216) AT2G33620 | Symbols: | DNA-binding family protein / AT-hook protein 1 (AHP1) | chr2:14234749-14236563 FORWARDmoderately similar to (385) loc_os10g42230 12010.m50380 protein AT-hook protein 1, putative, expressed seq=cds; coord=9:113056029..113059080:1; parent_gene=AC225193.3_FG003' 'highly similar to (752) AT1G74040 | Symbols: IMS1, MAML-3, IPMS2 | IMS1 (2-ISOPROPYLMALATE SYNTHASE 1); 2-isopropylmalate synthase | chr1:27842258-27845566 FORWARDhighly similar to (615) LEU1_SOYBN Probable 2-isopropylmalate synthase (EC 2.3.3.13) (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase) (Late nodulin 56) (N-56) - Glycine max (Soybean)highly similar to (962) loc_os12g04440 12012.m26829 protein 2-isopropylmalate synthase B, putative, expressed seq=cds; coord=10:1725712..1731899:-1; parent_gene=GRMZM2G130062'

'very weakly similar to (80.5) AT4G35160 | Symbols: | O-methyltransferase family 2 protein | chr4:16730989-16732808 REVERSEmoderately similar to (239) ZRP4_MAIZE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT) - Zea mays (Maize)moderately similar to (271) loc_os06g13280 12006.m06043 protein O-methyltransferase ZRP4, putative seq=cds; coord=10:1919386..1920869:-1; parent_gene=GRMZM2G104710'

'moderately similar to (359) AT5G25400 | Symbols: | phosphate translocator-related | chr5:8823283-8824332 FORWARDmoderately similar to (420) loc_os12g04170 12012.m04412 protein plastidic phosphate translocator-like protein1, putative, expressed seq=cds; coord=10:2005967..2007702:1; parent_gene=GRMZM2G178734'

'weakly similar to (176) AT1G53350 | Symbols: | ATP binding | chr1:19903899-19907515 FORWARDhighly similar to (519) loc_os11g37880 12011.m07634 protein stripe rust resistance protein Yr10, putative, expressed seq=cds; coord=10:2984369..2993434:1; parent_gene=GRMZM2G004412'

'moderately similar to (263) loc_os01g02280 12001.m06870 protein NB-ARC domain containing protein seq=cds; coord=10:3160480..3163283:1; parent_gene=GRMZM2G356817'

'moderately similar to (419) AT1G08960 | Symbols: CAX11, ATCAX11 | CAX11; calcium:sodium antiporter/ cation:cation antiporter | chr1:2879698-2881877 FORWARDweakly similar to (193) loc_os11g05070 12011.m04705 protein sodium/potassium/calcium exchanger 6 precursor, putative, expressed seq=cds; coord=10:4682046..4687554:-1; parent_gene=GRMZM2G004414'

'moderately similar to (206) AT2G44050 | Symbols: COS1 | COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase | chr2:18224304-18225917 FORWARDweakly similar to (184) RISB_SPIOL 6,7-dimethyl-8-ribityllumazine synthase, chloroplast precursor (EC 2.5.1.9) (DMRL synthase) (Lumazine synthase) - Spinacia oleracea (Spinach)moderately similar to (262) loc_os04g42000 12004.m09174 protein 6,7-dimethyl-8-ribityllumazine synthase, chloroplast precursor, putative, expressed seq=cds; coord=10:145895417..145903773:1; parent_gene=GRMZM2G143480'

'very weakly similar to (92.0) AT5G20900 | Symbols: JAZ12, TIFY3B | JAZ12 (JASMONATE-ZIM-DOMAIN PROTEIN 12) | chr5:7090883-7092201 FORWARDweakly similar to (183) loc_os04g55920 12004.m35599 protein ZIM motif family protein, expressed seq=cds; coord=10:145933966..145937989:1; parent_gene=GRMZM2G143402'

'very weakly similar to (82.0) AT5G25190 | Symbols: | ethylene-responsive element-binding protein, putative | chr5:8707007-8707655 REVERSEweakly similar to (105) loc_os04g56150 12004.m10506 protein ethylene-responsive transcription factor 4, putative seq=cds; coord=10:146118823..146119727:1; parent_gene=GRMZM2G104260' 'nearly identical (1538) AT4G30190 | Symbols: AHA2, PMA2 | AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism | chr4:14770820-14775920 REVERSEnearly identical (1693) PMA1_ORYSA Plasma membrane ATPase (EC 3.6.3.6) (Proton pump) - Oryza sativa (Rice)nearly identical (1693) loc_os04g56160 12004.m101441 protein plasma membrane ATPase, putative, expressed seq=cds; coord=10:146179462..146186581:1; parent_gene=GRMZM2G006894'

'moderately similar to (328) AT2G18060 | Symbols: VND1, ANAC037 | VND1 (VASCULAR RELATED NAC-DOMAIN PROTEIN 1); transcription factor | chr2:7848399-7850303 REVERSEmoderately similar to (232) NAC76_ORYSA NAC domain-containing protein 76 (ONAC076) - Oryza sativa (Rice)moderately similar to (439) loc_os03g03540 12003.m05887 protein ANAC037, putative, expressed seq=cds; coord=1:5635814..5642763:-1; parent_gene=GRMZM2G025642'

'moderately similar to (202) AT5G52840 | Symbols: | NADH-ubiquinone oxidoreductase-related | chr5:21413718-21414794 FORWARDmoderately similar to (260) loc_os03g19890 12003.m07402 protein NADH-ubiquinone oxidoreductase 13 kDa-B subunit, putative, expressed seq=cds; coord=1:51013925..51015964:1; parent_gene=GRMZM2G018941'

'moderately similar to (210) AT5G13850 | Symbols: NACA3 | NACA3 (NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX SUBUNIT ALPHA-LIKE PROTEIN 3) | chr5:4471361-4472676 FORWARDmoderately similar to (217) loc_os05g31000 12005.m07335 protein nascent polypeptide-associated complex alpha subunit-like protein, putative, expressed seq=cds; coord=1:60163114..60165406:1; parent_gene=GRMZM2G000923'

'weakly similar to (191) AT5G51890 | Symbols: | peroxidase | chr5:21091163-21092335 REVERSEweakly similar to (187) PER2_ORYSA Peroxidase 2 precursor (EC 1.11.1.7) - Oryza sativa (Rice)moderately similar to (394) loc_os03g25360 12003.m07880 protein peroxidase 66 precursor, putative, expressed seq=cds; coord=1:63676345..63677920:1; parent_gene=GRMZM2G004984'

'very weakly similar to (93.6) AT4G34410 | Symbols: RRTF1 | RRTF1 ({REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor | chr4:16451992-16452798 FORWARDmoderately similar to (204) loc_os08g36920 12008.m07680 protein AP2 domain containing protein, expressed seq=cds; coord=1:199639973..199641110:1; parent_gene=GRMZM2G369472'

'highly similar to (649) AT3G24660 | Symbols: TMKL1 | TMKL1 (transmembrane kinase-like 1); ATP binding / kinase/ protein serine/threonine kinase | chr3:9003641-9005751 FORWARDweakly similar to (173) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)highly similar to (740) loc_os08g45060 12008.m08476 protein protein Kinase-like protein TMKL1 precursor, putative, expressed seq=cds; coord=1:202158131..202160689:-1; parent_gene=GRMZM2G422373'

'very weakly similar to (93.2) AT2G36930 | Symbols: | zinc finger (C2H2 type) family protein | chr2:15510002-15511347 REVERSEweakly similar to (139) loc_os08g45040 12008.m080242 protein zinc finger protein 593, putative, expressed seq=cds; coord=1:202226326..202227433:1; parent_gene=GRMZM2G309269' 'moderately similar to (227) AT5G19910 | Symbols: | SOH1 family protein | chr5:6731484-6732821 REVERSEmoderately similar to (259) loc_os10g41450 12010.m06909 protein mediator complex subunit SOH1, putative, expressed seq=cds; coord=1:203330178..203337402:1; parent_gene=GRMZM2G139683'

'weakly similar to (160) AT1G72610 | Symbols: GLP1, ATGER1, GER1 | GER1 (GERMIN-LIKE PROTEIN 1); oxalate oxidase | chr1:27339302-27339928 REVERSEweakly similar to (161) AB19B_PRUPE Auxin-binding protein ABP19b precursor - Prunus persica (Peach)moderately similar to (207) loc_os08g35750 12008.m07564 protein germin-like protein 1 precursor, putative, expressed seq=cds; coord=1:207891946..207892644:1; parent_gene=AC195794.3_FG002'

'weakly similar to (160) AT1G72610 | Symbols: GLP1, ATGER1, GER1 | GER1 (GERMIN-LIKE PROTEIN 1); oxalate oxidase | chr1:27339302-27339928 REVERSEweakly similar to (161) AB19B_PRUPE Auxin-binding protein ABP19b precursor - Prunus persica (Peach)moderately similar to (207) loc_os08g35750 12008.m07564 protein germin-like protein 1 precursor, putative, expressed seq=cds; coord=1:207891946..207892644:1; parent_gene=AC195794.3_FG002'

'weakly similar to (164) AT2G06050 | Symbols: OPR3 | OPR3 (OPDA-REDUCTASE 3); 12-oxophytodienoate reductase | chr2:2359240-2361971 REVERSEmoderately similar to (213) loc_os08g35740 12008.m080177 protein 12-oxophytodienoate reductase 3, putative, expressed seq=cds; coord=1:207904053..207905956:-1; parent_gene=GRMZM2G148281'

'weakly similar to (183) AT4G00180 | Symbols: YAB3 | YAB3 (YABBY3); protein binding / transcription factor | chr4:72804-74888 REVERSEweakly similar to (106) YAB1_ORYSA Protein YABBY (OsYAB1) (Filamentous flower protein 1) - Oryza sativa (Rice)moderately similar to (230) loc_os10g36420 12010.m06452 protein axial regulator YABBY1, putative seq=cds; coord=1:225032510..225037728:1; parent_gene=GRMZM2G167824'

'nearly identical (1325) AT2G35920 | Symbols: | helicase domain-containing protein | chr2:15075674-15080506 FORWARDhighly similar to (738) loc_os03g53760 12003.m10345 protein helicase associated domain family protein, expressed seq=cds; coord=1:233184997..233210134:1; parent_gene=GRMZM2G399212'

'moderately similar to (350) AT2G38970 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:16274135-16276651 FORWARDhighly similar to (538) loc_os10g32760 12010.m06112 protein protein binding protein, putative, expressed seq=cds; coord=1:233813747..233815947:-1; parent_gene=GRMZM2G398198'

'weakly similar to (176) AT4G20380 | Symbols: | zinc finger protein (LSD1) | chr4:11005027-11006438 FORWARDmoderately similar to (243) loc_os03g43840 12003.m09425 protein zinc finger protein LSD2, putative, expressed seq=cds; coord=1:252257077..252261490:-1; parent_gene=GRMZM2G173425'

'weakly similar to (173) AT5G67420 | Symbols: LBD37 | LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37) | chr5:26904576-26905415 REVERSEmoderately similar to (262) loc_os03g41330 12003.m09201 protein seed specific protein Bn15D17A, putative, expressed seq=cds; coord=1:255323652..255325701:1; parent_gene=GRMZM2G017319' 'weakly similar to (173) AT5G67420 | Symbols: LBD37 | LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37) | chr5:26904576-26905415 REVERSEmoderately similar to (262) loc_os03g41330 12003.m09201 protein seed specific protein Bn15D17A, putative, expressed seq=cds; coord=1:255323652..255325701:1; parent_gene=GRMZM2G017319'

'weakly similar to (180) AT4G37740 | Symbols: AtGRF2 | AtGRF2 (GROWTHREGULATING FACTOR 2); transcription activator | chr4:17725533-17727609 REVERSEhighly similar to (517) loc_os03g47140 12003.m09727 protein atGRF2, putative, expressed seq=cds; coord=1:257186167..257188884:-1; parent_gene=GRMZM2G018414'

'highly similar to (775) AT1G58520 | Symbols: RXW8 | hydrolase, acting on ester bonds / lipase | chr1:21729913-21731344 FORWARDnearly identical (1125) loc_os12g43720 12012.m08145 protein RXW8, putative, expressed seq=cds; coord=1:257314578..257324941:1; parent_gene=GRMZM2G409093'

'highly similar to (775) AT1G58520 | Symbols: RXW8 | hydrolase, acting on ester bonds / lipase | chr1:21729913-21731344 FORWARDnearly identical (1125) loc_os12g43720 12012.m08145 protein RXW8, putative, expressed seq=cds; coord=1:257314578..257324941:1; parent_gene=GRMZM2G409093'

'moderately similar to (346) GLB1_MAIZE Globulin-1 S allele precursor (GLB1-S) (7S-like) - Zea mays (Maize)moderately similar to (264) loc_os03g46100 12003.m35340 protein globulin-1 S allele precursor, putative, expressed seq=cds; coord=1:258363413..258366718:1; parent_gene=GRMZM2G067919'

'highly similar to (675) AT4G28450 | Symbols: | nucleotide binding / protein binding | chr4:14061724-14064582 REVERSEhighly similar to (845) loc_os01g13730 12001.m07981 protein protein SOF1, putative, expressed seq=cds; coord=1:299113982..299122437:1; parent_gene=GRMZM2G590033'

'moderately similar to (367) AT5G03540 | Symbols: ATEXO70A1 | ATEXO70A1 (exocyst subunit EXO70 family protein A1); protein binding | chr5:890194-893916 FORWARDmoderately similar to (469) loc_os04g58880 12004.m10768 protein protein binding protein, putative, expressed seq=cds; coord=2:88161..90584:-1; parent_gene=GRMZM2G074530'

'nearly identical (1205) AT1G08190 | Symbols: | vacuolar assembly protein, putative (VPS41) | chr1:2567652-2573142 FORWARDnearly identical (1593) loc_os04g11880 12004.m35250 protein vacuolar assembly protein VPS41, putative, expressed seq=cds; coord=2:2040400..2047121:1; parent_gene=GRMZM2G040247'

'highly similar to (687) AT5G37020 | Symbols: ARF8 | ARF8 (AUXIN RESPONSE FACTOR 8); transcription factor | chr5:14630151-14633916 FORWARDnearly identical (1283) loc_os04g57610 12004.m35224 protein auxin response factor 8, putative, expressed seq=cds; coord=2:2266715..2274671:1; parent_gene=GRMZM2G078274'

'moderately similar to (310) AT5G67170 | Symbols: | SEC-C motif-containing protein / OTU-like cysteine protease family protein | chr5:26799851-26801763 FORWARDmoderately similar to (464) loc_os04g57480 12004.m101690 protein OTU domain-containing protein 3, putative, expressed seq=cds; coord=2:2533374..2536615:1; parent_gene=GRMZM2G107187' 'highly similar to (926) AT5G46330 | Symbols: FLS2 | FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase | chr5:18791802-18795407 FORWARDmoderately similar to (474) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1411) loc_os04g52780 12004.m10171 protein leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed seq=cds; coord=2:9441323..9445539:1; parent_gene=GRMZM2G080041'

'nearly identical (1261) AT2G33170 | Symbols: | leucine-rich repeat transmembrane protein kinase, putative | chr2:14056371-14059829 REVERSEmoderately similar to (440) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)nearly identical (1732) loc_os04g42700 12004.m09235 protein receptor-like protein kinase precursor, putative, expressed seq=cds; coord=2:30586576..30591920:1; parent_gene=GRMZM2G082191'

'moderately similar to (283) AT3G25980 | Symbols: | mitotic spindle checkpoint protein, putative (MAD2) | chr3:9503232-9504402 FORWARDmoderately similar to (330) MAD2_MAIZE Mitotic spindle checkpoint protein MAD2 - Zea mays (Maize)moderately similar to (312) loc_os04g40940 12004.m35349 protein mitotic spindle checkpoint protein MAD2, putative, expressed seq=cds; coord=2:36358387..36360987:1; parent_gene=GRMZM2G112072'

'moderately similar to (473) AT4G24790 | Symbols: | ATP binding / DNA binding / DNA-directed DNA polymerase | chr4:12778222-12781345 FORWARDhighly similar to (870) loc_os12g19180 12012.m05871 protein nucleoside-triphosphatase/ nucleotide binding protein, putative, expressed seq=cds; coord=2:36838775..36842537:-1; parent_gene=GRMZM2G044989'

'weakly similar to (134) loc_os09g26780 12009.m05830 protein pnFL-2, putative, expressed seq=cds; coord=2:183999694..184001704:-1; parent_gene=GRMZM2G005954'

'moderately similar to (301) AT2G03200 | Symbols: | aspartyl protease family protein | chr2:966506-967891 REVERSEhighly similar to (583) loc_os09g27910 12009.m05942 protein aspartic proteinase nepenthesin-1 precursor, putative, expressed seq=cds; coord=2:185438627..185440309:-1; parent_gene=GRMZM2G090603'

'moderately similar to (405) AT3G63470 | Symbols: scpl40 | scpl40 (serine carboxypeptidase-like 40); serine-type carboxypeptidase | chr3:23438561-23440862 FORWARDmoderately similar to (412) CBP23_HORVU Serine carboxypeptidase II-3 precursor (EC 3.4.16.6) (CP-MII.3) [Contains: Serine carboxypeptidase II-3 chain A; Serine carboxypeptidase II-3 chain B] - Hordeum vulgare (Barley)highly similar to (632) loc_os09g28840 12009.m06035 protein serine carboxypeptidase family protein, expressed seq=cds; coord=2:186899047..186901405:-1; parent_gene=GRMZM2G168196'

'weakly similar to (119) loc_os09g31300 12009.m22140 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=2:189701055..189703654:1; parent_gene=GRMZM2G417597'

'highly similar to (648) AT1G31690 | Symbols: | amine oxidase/ copper ion binding / quinone binding | chr1:11343980-11347767 FORWARDhighly similar to (628) AMO_PEA Amine oxidase [copper-containing] precursor (EC 1.4.3.6) - Pisum sativum (Garden pea)highly similar to (917) loc_os06g23114 12006.m06963 protein amine oxidase precursor, putative, expressed seq=cds; coord=2:206256271..206260005:1; parent_gene=GRMZM2G042660'

'very weakly similar to (89.4) loc_os10g42830 12010.m07035 protein D-xylose-proton symporter, putative, expressed seq=cds; coord=2:214300285..214302406:1; parent_gene=GRMZM2G452930'

'weakly similar to (129) AT5G65980 | Symbols: | auxin efflux carrier family protein | chr5:26392444-26394232 FORWARDmoderately similar to (266) loc_os09g38130 12009.m060062 protein auxin Efflux Carrier family protein, expressed seq=cds; coord=2:215629822..215632213:-1; parent_gene=GRMZM2G070563'

'weakly similar to (127) AT5G46860 | Symbols: VAM3, ATVAM3, SYP22, ATSYP22, SGR3 | VAM3; SNAP receptor | chr5:19012342-19013795 REVERSEweakly similar to (164) loc_os01g15110 12001.m08110 protein syntaxin 23, putative, expressed seq=cds; coord=3:8304153..8306580:1; parent_gene=GRMZM2G015509'

'weakly similar to (150) AT5G12020 | Symbols: HSP17.6II | HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN) | chr5:3882409-3882876 REVERSEmoderately similar to (231) HSP21_MAIZE 17.5 kDa class II heat shock protein - Zea mays (Maize)weakly similar to (197) loc_os01g08860 12001.m150501 protein 17.5 kDa class II heat shock protein, putative, expressed seq=cds; coord=3:8884623..8885815:-1; parent_gene=GRMZM2G083810'

'weakly similar to (156) AT4G39410 | Symbols: WRKY13, ATWRKY13 | WRKY13; transcription factor | chr4:18332937-18334789 REVERSEweakly similar to (166) loc_os01g08710 12001.m07496 protein OsWRKY79 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=3:9234113..9242047:1; parent_gene=GRMZM2G151444'

'weakly similar to (126) loc_os01g69270 12001.m13027 protein MYND finger family protein, expressed seq=cds; coord=3:159817015..159819103:1; parent_gene=GRMZM2G133428'

'moderately similar to (327) AT4G32175 | Symbols: | RNA binding | chr4:15535555-15537537 FORWARDmoderately similar to (424) loc_os01g66730 12001.m150798 protein exosome complex exonuclease RRP40, putative, expressed seq=cds; coord=3:211858569..211866122:-1; parent_gene=GRMZM2G173989'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'moderately similar to (252) AT1G31550 | Symbols: | GDSL-motif lipase, putative | chr1:11295635-11297284 REVERSEweakly similar to (145) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)moderately similar to (292) loc_os01g42730 12001.m10537 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=3:213800453..213804523:-1; parent_gene=GRMZM2G047129' 'weakly similar to (178) AT1G28600 | Symbols: | lipase, putative | chr1:10051604-10053073 REVERSEvery weakly similar to (86.7) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)weakly similar to (194) loc_os01g42730 12001.m10537 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=3:213800866..213804340:-1; parent_gene=GRMZM2G047129'

'highly similar to (505) AT1G53240 | Symbols: | malate dehydrogenase (NAD), mitochondrial | chr1:19854966-19856802 REVERSEhighly similar to (508) MDHM_FRAAN Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Fragaria ananassa (Strawberry)highly similar to (587) loc_os01g46070 12001.m10806 protein malate dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=3:213896741..213905427:1; parent_gene=GRMZM2G466833'

'moderately similar to (245) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (340) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215466579..215473931:-1; parent_gene=GRMZM2G121878'

'moderately similar to (205) AT1G14510 | Symbols: AL7 | AL7 (ALFIN-LIKE 7); DNA binding / methylated histone residue binding | chr1:4962171-4964154 REVERSEmoderately similar to (268) loc_os11g14010 12011.m28769 protein PHD finger protein, putative, expressed seq=cds; coord=4:11389157..11413875:-1; parent_gene=GRMZM2G008259'

'weakly similar to (135) AT3G25470 | Symbols: | bacterial hemolysin-related | chr3:9233039-9235022 FORWARDweakly similar to (166) loc_os11g14230 12011.m05560 protein hemolysin A, putative, expressed seq=cds; coord=4:12043149..12045067:-1; parent_gene=GRMZM2G010056'

'very weakly similar to (100) AT3G06190 | Symbols: ATBPM2, BPM2 | BPM2 (BTB-POZ AND MATH DOMAIN 2); protein binding | chr3:1874577-1876575 REVERSEweakly similar to (144) loc_os08g13000 12008.m05427 protein speckle-type POZ protein, putative seq=cds; coord=4:25991768..25992949:-1; parent_gene=GRMZM2G026724'

'very weakly similar to (100) AT3G06190 | Symbols: ATBPM2, BPM2 | BPM2 (BTB-POZ AND MATH DOMAIN 2); protein binding | chr3:1874577-1876575 REVERSEweakly similar to (144) loc_os08g13000 12008.m05427 protein speckle-type POZ protein, putative seq=cds; coord=4:25991768..25992949:-1; parent_gene=GRMZM2G026724'

'moderately similar to (400) AT1G11650 | Symbols: ATRBP45B, RBP45B | RNA-binding protein 45 (RBP45), putative | chr1:3914895-3917301 FORWARDhighly similar to (518) loc_os08g09100 12008.m05045 protein expressed protein seq=cds; coord=4:28340661..28347586:1; parent_gene=GRMZM2G426591'

'moderately similar to (276) AT1G75660 | Symbols: XRN3 | XRN3; 5'-3' exoribonuclease | chr1:28408289-28414825 FORWARDweakly similar to (143) CR2_HORVU Cold-regulated protein 2 (Fragment) - Hordeum vulgare (Barley)highly similar to (501) loc_os01g65220 12001.m12635 protein XRN3, putative, expressed seq=cds; coord=4:29116247..29129683:1; parent_gene=GRMZM2G064868' 'moderately similar to (370) AT3G26670 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF803 (InterPro:IPR008521); BEST Arabidopsis thaliana protein match is: permease-related (TAIR:AT3G23870.1); Has 715 Blast hits to 711 proteins in 119 species: Archae - 0; Bacteria - 0; Metazoa - 298; Fungi - 244; Plants - 119; Viruses - 2; Other Eukaryotes - 52 (source: NCBI BLink). | chr3:9798236-9800562 REVERSEhighly similar to (508) loc_os02g31874 12002.m08280 protein expressed protein seq=cds; coord=4:94742292..94746687:-1; parent_gene=GRMZM2G144254'

'very weakly similar to (95.1) AT4G27090 | Symbols: | 60S ribosomal protein L14 (RPL14B) | chr4:13594104-13595187 REVERSEvery weakly similar to (93.6) RL14_PEA Probable 60 ribosomal protein L14 (Hydroxyproline-rich glycoprotein HRGP1) - Pisum sativum (Garden pea)weakly similar to (117) loc_os04g43540 12004.m09314 protein 60 ribosomal protein L14, putative, expressed seq=cds; coord=4:111487916..111492785:1; parent_gene=GRMZM2G323971'

'moderately similar to (208) loc_os07g23900 12007.m06668 protein F-box domain containing protein, expressed seq=cds; coord=4:131648815..131650074:-1; parent_gene=GRMZM2G139670'

'moderately similar to (491) AT3G50790 | Symbols: | late embryogenesis abundant protein, putative / LEA protein, putative | chr3:18880074-18881940 REVERSEhighly similar to (627) loc_os02g43340 12002.m33800 protein embryogenesis-associated protein EMB8, putative, expressed seq=cds; coord=4:150464178..150469660:-1; parent_gene=GRMZM2G100716'

'moderately similar to (230) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEmoderately similar to (429) loc_os02g48870 12002.m09921 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=4:163993868..163995643:-1; parent_gene=GRMZM2G168431'

'moderately similar to (230) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEmoderately similar to (429) loc_os02g48870 12002.m09921 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=4:163993868..163995643:-1; parent_gene=GRMZM2G168431'

'weakly similar to (161) AT4G01150 | Symbols: | unknown protein | chr4:493692-494379 FORWARDweakly similar to (187) loc_os02g49870 12002.m10021 protein expressed protein seq=cds; coord=4:166773457..166774717:1; parent_gene=GRMZM2G380457'

'moderately similar to (243) AT2G01680 | Symbols: | ankyrin repeat family protein | chr2:306597-308427 FORWARDmoderately similar to (378) loc_os02g50270 12002.m10061 protein protein binding protein, putative, expressed seq=cds; coord=4:167169708..167183709:1; parent_gene=GRMZM2G136996'

'nearly identical (1001) AT1G73370 | Symbols: SUS6, ATSUS6 | SUS6 (SUCROSE SYNTHASE 6); UDP-glycosyltransferase/ sucrose synthase | chr1:27584533-27588326 REVERSEhighly similar to (816) SUS2_PEA Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2) - Pisum sativum (Garden pea)nearly identical (1244) loc_os02g58480 12002.m10869 protein sucrose synthase 2, putative, expressed seq=cds; coord=4:168743488..168746616:-1; parent_gene=GRMZM2G045171' 'weakly similar to (148) AT2G33310 | Symbols: IAA13 | IAA13; transcription factor | chr2:14114569-14115757 REVERSEmoderately similar to (288) IAA10_ORYSA Auxin-responsive protein IAA10 (Indoleacetic acid-induced protein 10) - Oryza sativa (Rice)moderately similar to (292) loc_os02g57250 12002.m33477 protein OsIAA10 - Auxin-responsive Aux/IAA gene family member, expressed seq=cds; coord=4:171373109..171375531:1; parent_gene=GRMZM2G142768'

'moderately similar to (207) AT1G44835 | Symbols: | YbaK/prolyl-tRNA synthetase family protein | chr1:16939909-16942337 FORWARDmoderately similar to (273) loc_os02g52880 12002.m10318 protein ybaK/prolyl-tRNA synthetase associated region, putative, expressed seq=cds; coord=4:178455228..178463927:1; parent_gene=GRMZM2G170313'

'highly similar to (709) AT1G78240 | Symbols: TSD2, QUA2 | TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase | chr1:29433173-29435815 REVERSEnearly identical (1086) loc_os02g51860 12002.m10217 protein ATP binding protein, putative, expressed seq=cds; coord=4:180498698..180504090:1; parent_gene=GRMZM2G000764'

'moderately similar to (410) AT1G16670 | Symbols: | protein kinase family protein | chr1:5697846-5699492 FORWARDmoderately similar to (216) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (596) loc_os02g06930 12002.m100111 protein serine/threonine-protein kinase receptor precursor, putative, expressed seq=cds; coord=4:236412858..236415822:-1; parent_gene=GRMZM2G169020'

'weakly similar to (161) loc_os02g06660 12002.m06014 protein desiccation-associated protein, putative seq=cds; coord=4:236733466..236735600:-1; parent_gene=GRMZM2G101920'

'weakly similar to (107) AT1G30210 | Symbols: TCP24 | TCP24 (TEOSINTE BRANCHED1, CYCLOIDEA, AND PCF FAMILY 24); transcription factor | chr1:10628754-10629728 REVERSEmoderately similar to (248) loc_os03g57190 12003.m10638 protein TCP family transcription factor containing protein, expressed seq=cds; coord=5:4945066..4946626:-1; parent_gene=GRMZM2G089361'

'weakly similar to (102) loc_os03g57240 12003.m10643 protein expressed protein seq=cds; coord=5:4917795..4919451:1; parent_gene=GRMZM2G089448'

'weakly similar to (149) AT5G63370 | Symbols: | protein kinase family protein | chr5:25384954-25386390 REVERSEweakly similar to (115) CDC2_VIGUN Cell division control protein 2 homolog (EC 2.7.11.22) (EC 2.7.11.23) (p34cdc2) - Vigna unguiculata (Cowpea)moderately similar to (218) loc_os12g23930 12012.m06228 protein protein kinase domain containing protein, expressed seq=cds; coord=5:7719942..7721101:1; parent_gene=GRMZM2G350844'

'moderately similar to (458) AT3G01750 | Symbols: | ankyrin repeat family protein | chr3:270615-272691 FORWARDhighly similar to (729) loc_os05g23320 12005.m06627 protein expressed protein seq=cds; coord=5:163409583..163412899:1; parent_gene=GRMZM2G474531'

'weakly similar to (107) AT3G01490 | Symbols: | protein kinase, putative | chr3:191095-193258 REVERSEweakly similar to (114) loc_os01g45380 12001.m10741 protein ATP binding protein, putative, expressed seq=cds; coord=5:185221807..185225537:1; parent_gene=GRMZM2G463711'

'highly similar to (606) AT1G64780 | Symbols: ATAMT1;2, AMT1;2 | ATAMT1;2 (AMMONIUM TRANSPORTER 1;2); ammonium transmembrane transporter | chr1:24061021-24062565 REVERSEhighly similar to (730) loc_os02g40730 12002.m09159 protein ammonium transporter 1, member 2, putative, expressed seq=cds; coord=5:185655742..185657715:1; parent_gene=GRMZM2G028736' 'highly similar to (638) AT2G20420 | Symbols: | succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative | chr2:8805574-8807858 FORWARDhighly similar to (696) SUCB_ORYSA Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, beta chain) (SCS-beta) - Oryza sativa (Rice)highly similar to (696) loc_os02g40830 12002.m100283 protein succinyl-CoA ligase beta-chain, mitochondrial precursor, putative, expressed seq=cds; coord=5:186081955..186094328:1; parent_gene=GRMZM2G064695'

'highly similar to (638) AT2G20420 | Symbols: | succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative | chr2:8805574-8807858 FORWARDhighly similar to (696) SUCB_ORYSA Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, beta chain) (SCS-beta) - Oryza sativa (Rice)highly similar to (696) loc_os02g40830 12002.m100283 protein succinyl-CoA ligase beta-chain, mitochondrial precursor, putative, expressed seq=cds; coord=5:186081955..186094328:1; parent_gene=GRMZM2G064695'

'highly similar to (582) AT5G03300 | Symbols: ADK2 | ADK2 (ADENOSINE KINASE 2); adenosine kinase/ copper ion binding / kinase | chr5:796573-798997 FORWARDmoderately similar to (479) ADK_PHYPA Adenosine kinase (EC 2.7.1.20) (AK) (Adenosine 5'-phosphotransferase) - Physcomitrella patens (Moss)highly similar to (654) loc_os02g41590 12002.m09195 protein adenosine kinase 2, putative, expressed seq=cds; coord=5:186517098..186522957:-1; parent_gene=GRMZM2G540538'

'weakly similar to (139) AT2G37040 | Symbols: pal1, ATPAL1 | pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase | chr2:15557602-15560237 REVERSEmoderately similar to (221) PAL1_ORYSA Phenylalanine ammonia-lyase (EC 4.3.1.5) - Oryza sativa (Rice)moderately similar to (221) loc_os02g41630 12002.m33418 protein phenylalanine ammonia-lyase, putative, expressed seq=cds; coord=5:186679860..186680704:-1; parent_gene=GRMZM2G074604'

'moderately similar to (224) AT5G47180 | Symbols: | vesicle-associated membrane family protein / VAMP family protein | chr5:19161384-19163265 REVERSEmoderately similar to (362) loc_os10g40140 12010.m06786 protein structural molecule, putative, expressed seq=cds; coord=5:190745409..190748730:-1; parent_gene=GRMZM2G171406'

'moderately similar to (224) AT5G47180 | Symbols: | vesicle-associated membrane family protein / VAMP family protein | chr5:19161384-19163265 REVERSEmoderately similar to (362) loc_os10g40140 12010.m06786 protein structural molecule, putative, expressed seq=cds; coord=5:190745409..190748730:-1; parent_gene=GRMZM2G171406'

'moderately similar to (243) AT5G47310 | Symbols: | unknown protein | chr5:19201325-19202674 FORWARDmoderately similar to (338) loc_os02g43840 12002.m09418 protein EREBP-4 like protein, putative, expressed seq=cds; coord=5:191360703..191363562:-1; parent_gene=GRMZM2G071844'

'weakly similar to (105) AT1G68280 | Symbols: | thioesterase-related | chr1:25592467-25593595 REVERSEweakly similar to (146) loc_os02g44136 12002.m09455 protein retrotransposon protein, putative, Ty1-copia subclass seq=cds; coord=5:192258201..192258960:-1; parent_gene=GRMZM2G306566' 'highly similar to (838) AT1G68930 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:25918314-25920545 FORWARDweakly similar to (103) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)nearly identical (1197) loc_os02g01610 12002.m33989 protein tetratricopeptide-like helical, putative, expressed seq=cds; coord=5:206572964..206575640:-1; parent_gene=GRMZM2G053396'

'moderately similar to (329) AT1G69530 | Symbols: ATEXPA1, EXP1, AT-EXP1, ATEXP1, ATHEXP ALPHA 1.2 | ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1) | chr1:26142034-26143200 FORWARDmoderately similar to (395) EXPA5_ORYSA Expansin-A5 precursor (OsEXPA5) (Alpha-expansin-5) (OsEXP5) (OsaEXPa1.20) - Oryza sativa (Rice)moderately similar to (395) loc_os02g51040 12002.m10138 protein alpha-expansin 15 precursor, putative, expressed seq=cds; coord=5:206838596..206840547:1; parent_gene=GRMZM2G105844'

'highly similar to (503) AT2G02910 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF616 (InterPro:IPR006852); BEST Arabidopsis thaliana protein match is: EMB2756 (EMBRYO DEFECTIVE 2756) (TAIR:AT1G34550.1); Has 191 Blast hits to 191 proteins in 22 species: Archae - 6; Bacteria - 21; Metazoa - 0; Fungi - 0; Plants - 106; Viruses - 0; Other Eukaryotes - 58 (source: NCBI BLink). | chr2:847335-849371 REVERSEmoderately similar to (498) loc_os11g09170 12011.m05114 protein EMB2756, putative, expressed seq=cds; coord=5:207056026..207062515:1; parent_gene=GRMZM2G380177'

'moderately similar to (407) AT4G39770 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr4:18449138-18451218 REVERSEhighly similar to (521) loc_os02g51680 12002.m10199 protein expressed protein seq=cds; coord=5:208172385..208174899:1; parent_gene=GRMZM2G055150'

'weakly similar to (175) AT1G25440 | Symbols: | zinc finger (B-box type) family protein | chr1:8933939-8935284 REVERSEmoderately similar to (419) loc_os02g49880 12002.m10022 protein zinc finger protein CONSTANS-LIKE 16, putative, expressed seq=cds; coord=5:204604955..204606998:1; parent_gene=GRMZM2G041991'

'highly similar to (738) AT1G62830 | Symbols: LDL1, SWP1, ATSWP1 | LDL1 (LSD1-LIKE1); amine oxidase/ electron carrier/ oxidoreductase | chr1:23264638-23267172 REVERSEweakly similar to (107) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)nearly identical (1155) loc_os02g51880 12002.m10219 protein amine oxidase/ oxidoreductase, putative, expressed seq=cds; coord=5:208426880..208429748:1; parent_gene=GRMZM2G059958'

'moderately similar to (406) AT4G32600 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr4:15724010-15725737 FORWARDhighly similar to (666) loc_os02g54624 12002.m10491 protein protein binding protein, putative, expressed seq=cds; coord=5:212679128..212684059:1; parent_gene=GRMZM2G089466' 'very weakly similar to (94.0) AT5G43700 | Symbols: ATAUX2-11, IAA4 | ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor | chr5:17550465-17551206 FORWARDweakly similar to (164) IAA20_ORYSA Auxin-responsive protein IAA20 (Indoleacetic acid-induced protein 20) - Oryza sativa (Rice)weakly similar to (164) loc_os06g07040 12006.m05429 protein OsIAA20 - Auxin-responsive Aux/IAA gene family member, expressed seq=cds; coord=6:79914748..79916501:-1; parent_gene=GRMZM2G000158'

'highly similar to (675) AT1G16540 | Symbols: SIR3, LOS5, ABA3, ATABA3 | ABA3 (ABA DEFICIENT 3); Mo-molybdopterin cofactor sulfurase/ selenocysteine lyase | chr1:5659465-5665201 FORWARDhighly similar to (769) MOCOS_ORYSA Molybdenum cofactor sulfurase (EC 4.4.-.-) (MoCo sulfurase) (MOS) - Oryza sativa (Rice)highly similar to (769) loc_os06g45860 12006.m09114 protein molybdenum cofactor sulfurase, putative, expressed seq=cds; coord=6:93182154..93194374:1; parent_gene=GRMZM2G061821'

'weakly similar to (127) AT3G16140 | Symbols: PSAH-1 | PSAH-1 (photosystem I subunit H-1) | chr3:5468670-5469415 REVERSEweakly similar to (166) PSAH_MAIZE Photosystem I reaction center subunit VI, chloroplast precursor (PSI-H) (Light-harvesting complex I 11 kDa protein) - Zea mays (Maize)weakly similar to (145) loc_os05g48630 12005.m08934 protein expressed protein seq=cds; coord=6:163973641..163974980:-1; parent_gene=GRMZM2G451224'

'highly similar to (694) AT4G39830 | Symbols: | L-ascorbate oxidase, putative | chr4:18479103-18481184 FORWARDhighly similar to (581) ASO_CUCSA L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) (ASO) - Cucumis sativus (Cucumber)highly similar to (907) loc_os09g20090 12009.m05216 protein L-ascorbate oxidase precursor, putative, expressed seq=cds; coord=7:99535861..99539292:-1; parent_gene=GRMZM2G064106'

'very weakly similar to (82.0) loc_os05g02120 12005.m04748 protein carboxylic ester hydrolase, putative, expressed seq=cds; coord=7:102656684..102659068:1; parent_gene=GRMZM2G113750'

'weakly similar to (165) AT1G19190 | Symbols: | hydrolase | chr1:6623876-6624832 FORWARDmoderately similar to (241) loc_os09g28760 12009.m06027 protein 2-hydroxyisoflavanone dehydratase, putative, expressed seq=cds; coord=7:126977721..126979734:1; parent_gene=GRMZM2G420786'

'highly similar to (751) AT1G28340 | Symbols: AtRLP4 | AtRLP4 (Receptor Like Protein 4); protein binding | chr1:9940175-9943252 FORWARDweakly similar to (115) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)nearly identical (1021) loc_os07g31840 12007.m07450 protein protein binding protein, putative, expressed seq=cds; coord=7:150897734..150908003:-1; parent_gene=GRMZM2G163138'

'weakly similar to (189) AT3G15510 | Symbols: ATNAC2, ANAC056, NARS1 | ATNAC2 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 2); transcription factor | chr3:5243696-5245037 FORWARDweakly similar to (163) NAC71_ORYSA NAC domain-containing protein 71 (ONAC071) - Oryza sativa (Rice)moderately similar to (323) loc_os07g37920 12007.m08041 protein NAM-like protein, putative, expressed seq=cds; coord=7:158236773..158238970:-1; parent_gene=GRMZM2G179885'

'moderately similar to (393) AT4G29230 | Symbols: anac075 | anac075 (Arabidopsis NAC domain containing protein 75); transcription factor | chr4:14410338-14414956 FORWARDhighly similar to (612) loc_os01g09550 12001.m42902 protein ANAC075, putative, expressed seq=cds; coord=8:20827673..20834211:1; parent_gene=GRMZM2G112681' 'moderately similar to (312) AT4G23620 | Symbols: | 50S ribosomal protein-related | chr4:12315016-12316659 REVERSEmoderately similar to (421) loc_os01g41030 12001.m10372 protein 5S rRNA binding protein, putative, expressed seq=cds; coord=8:140749438..140752609:-1; parent_gene=GRMZM2G423169'

'moderately similar to (230) AT4G22220 | Symbols: ISU1, ATISU1 | ISU1; structural molecule | chr4:11759444-11760881 REVERSEmoderately similar to (253) loc_os01g47340 12001.m42683 protein nifU-like N-terminal domain-containing protein, mitochondrial precursor, putative, expressed seq=cds; coord=8:148514901..148519447:-1; parent_gene=GRMZM2G064336'

'weakly similar to (167) AT3G19980 | Symbols: ATFYPP3, EMB2736, STPP | ATFYPP3 (FLOWER-SPECIFIC, PHYTOCHROME-ASSOCIATED PROTEIN PHOSPHATASE 3); protein binding / protein serine/threonine kinase/ protein serine/threonine phosphatase | chr3:6962008-6964761 FORWARDweakly similar to (127) PP2A3_ORYSA Serine/threonine-protein phosphatase PP2A-3 catalytic subunit (EC 3.1.3.16) - Oryza sativa (Rice)weakly similar to (174) loc_os01g49690 12001.m11156 protein serine/threonine-protein phosphatase 6, putative, expressed seq=cds; coord=8:152248696..152251518:1; parent_gene=GRMZM2G518717'

'moderately similar to (418) AT1G31730 | Symbols: | epsilon-adaptin, putative | chr1:11359907-11363916 FORWARDmoderately similar to (486) loc_os01g68750 12001.m12977 protein clathrin binding protein, putative, expressed seq=cds; coord=8:162507000..162511297:1; parent_gene=GRMZM2G031352'

'highly similar to (766) AT4G34710 | Symbols: ADC2, SPE2, ATADC2 | ADC2 (ARGININE DECARBOXYLASE 2); arginine decarboxylase | chr4:16560315-16562450 REVERSEnearly identical (1060) SPE1_ORYSA Arginine decarboxylase (EC 4.1.1.19) (ARGDC) (ADC) - Oryza sativa (Rice)nearly identical (1060) loc_os06g04070 12006.m05138 protein arginine decarboxylase, putative, expressed seq=cds; coord=9:23526334..23529702:1; parent_gene=GRMZM2G396553'

'highly similar to (766) AT4G34710 | Symbols: ADC2, SPE2, ATADC2 | ADC2 (ARGININE DECARBOXYLASE 2); arginine decarboxylase | chr4:16560315-16562450 REVERSEnearly identical (1060) SPE1_ORYSA Arginine decarboxylase (EC 4.1.1.19) (ARGDC) (ADC) - Oryza sativa (Rice)nearly identical (1060) loc_os06g04070 12006.m05138 protein arginine decarboxylase, putative, expressed seq=cds; coord=9:23526334..23529702:1; parent_gene=GRMZM2G396553'

'highly similar to (926) AT2G21480 | Symbols: | protein kinase family protein | chr2:9202753-9205368 REVERSEmoderately similar to (264) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)nearly identical (1276) loc_os06g03610 12006.m05093 protein protein kinase, putative, expressed seq=cds; coord=9:25086132..25089397:1; parent_gene=GRMZM2G335052'

'very weakly similar to (87.8) AT1G51405 | Symbols: | myosin-related | chr1:19057780-19059582 FORWARDmoderately similar to (261) loc_os03g11770 12003.m06629 protein expressed protein seq=cds; coord=9:125860814..125864356:1; parent_gene=GRMZM2G343856' 'moderately similar to (250) AT1G17020 | Symbols: SRG1, ATSRG1 | SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc | chr1:5820258-5821741 FORWARDweakly similar to (149) FLS_SOLTU Flavonol synthase/flavanone 3-hydroxylase (EC 1.14.11.23) (EC 1.14.11.9) (FLS) - Solanum tuberosum (Potato)moderately similar to (375) loc_os01g24980 12001.m43008 protein naringenin,2-oxoglutarate 3-dioxygenase, putative, expressed seq=cds; coord=9:155437067..155438681:-1; parent_gene=GRMZM2G168355'

'weakly similar to (113) AT1G19840 | Symbols: | auxin-responsive family protein | chr1:6872794-6873255 REVERSEweakly similar to (194) loc_os04g56680 12004.m10555 protein OsSAUR22 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=10:146941492..146942867:-1; parent_gene=GRMZM2G442000'

'highly similar to (552) AT1G19850 | Symbols: MP, ARF5, IAA24 | MP (MONOPTEROS); transcription factor | chr1:6887353-6891182 FORWARDnearly identical (1387) loc_os04g56850 12004.m78925 protein auxin response factor family protein, expressed seq=cds; coord=10:147118003..147123097:-1; parent_gene=GRMZM2G086949'

'weakly similar to (120) AT1G78690 | Symbols: | phospholipid/glycerol acyltransferase family protein | chr1:29597002-29598409 FORWARDweakly similar to (161) loc_os04g57150 12004.m35502 protein tafazzin, putative, expressed seq=cds; coord=10:147206883..147213776:-1; parent_gene=GRMZM2G125083'

'moderately similar to (207) AT1G65840 | Symbols: ATPAO4, PAO4 | ATPAO4 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 4); amine oxidase/ polyamine oxidase | chr1:24490173-24492728 FORWARDmoderately similar to (274) loc_os04g57560 12004.m10641 protein lysine-specific histone demethylase 1, putative, expressed seq=cds; coord=10:147594420..147597270:-1; parent_gene=GRMZM2G150248'

'highly similar to (648) AT4G04955 | Symbols: ATALN | ATALN (Arabidopsis allantoinase); allantoinase/ hydrolase | chr4:2522301-2525259 REVERSEmoderately similar to (342) loc_os04g58390 12004.m10721 protein allantoinase, putative, expressed seq=cds; coord=10:148502046..148506482:1; parent_gene=GRMZM2G173413'

'highly similar to (809) AT1G63660 | Symbols: | GMP synthase (glutamine-hydrolyzing), putative / glutamine amidotransferase, putative | chr1:23604874-23607080 REVERSEhighly similar to (972) loc_os08g23730 12008.m06393 protein GMP synthase, putative, expressed seq=cds; coord=10:149089396..149092794:1; parent_gene=GRMZM2G136283'

'moderately similar to (419) AT3G13620 | Symbols: | amino acid permease family protein | chr3:4450904-4452556 REVERSEhighly similar to (600) loc_os03g25920 12003.m07936 protein cationic amino acid transporter, putative seq=cds; coord=1:64964613..64967070:-1; parent_gene=GRMZM2G127138'

'moderately similar to (419) AT3G13620 | Symbols: | amino acid permease family protein | chr3:4450904-4452556 REVERSEhighly similar to (600) loc_os03g25920 12003.m07936 protein cationic amino acid transporter, putative seq=cds; coord=1:64964613..64967070:-1; parent_gene=GRMZM2G127138'

'very weakly similar to (89.0) loc_os06g47340 12006.m09260 protein glycosyltransferase, putative, expressed seq=cds; coord=1:70503212..70503722:1; parent_gene=GRMZM2G123872' 'very weakly similar to (89.0) loc_os06g47340 12006.m09260 protein glycosyltransferase, putative, expressed seq=cds; coord=1:70503212..70503722:1; parent_gene=GRMZM2G123872'

'moderately similar to (431) AT4G24220 | Symbols: VEP1, AWI31 | VEP1 (VEIN PATTERNING 1); binding / catalytic | chr4:12565219-12566474 FORWARDhighly similar to (581) loc_os03g32170 12003.m08461 protein progesterone 5-beta-reductase, putative, expressed seq=cds; coord=1:76234318..76235779:-1; parent_gene=GRMZM2G075892'

'moderately similar to (341) AT4G34380 | Symbols: | transducin family protein / WD-40 repeat family protein | chr4:16438835-16440322 FORWARDmoderately similar to (479) loc_os03g42710 12003.m09323 protein nucleotide binding protein, putative seq=cds; coord=1:253911424..253913528:-1; parent_gene=GRMZM2G099023'

'moderately similar to (495) AT5G61540 | Symbols: | L-asparaginase, putative / L-asparagine amidohydrolase, putative | chr5:24745887-24747142 FORWARDhighly similar to (624) loc_os04g46370 12004.m101606 protein L-asparaginase 3 precursor, putative, expressed seq=cds; coord=2:20195602..20205929:1; parent_gene=GRMZM2G139463'

'moderately similar to (219) AT1G68920 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr1:25915620-25917675 FORWARDmoderately similar to (482) loc_os09g29830 12009.m06134 protein DNA binding protein, putative, expressed seq=cds; coord=2:188403767..188407063:1; parent_gene=GRMZM2G137541'

'very weakly similar to (94.4) AT2G35270 | Symbols: | DNA-binding protein-related | chr2:14857021-14857878 FORWARDweakly similar to (150) loc_os01g14430 12001.m08048 protein DNA binding protein, putative, expressed seq=cds; coord=3:1289442..1290365:1; parent_gene=AC233880.1_FG005'

'very weakly similar to (92.0) AT3G17510 | Symbols: CIPK1, SnRK3.16 | CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding | chr3:5989309-5992627 REVERSEvery weakly similar to (97.1) loc_os05g04550 12005.m04988 protein CBL-interacting serine/threonine-protein kinase 1, putative, expressed seq=cds; coord=3:131847059..131848547:1; parent_gene=AC206425.3_FG004'

'very weakly similar to (92.0) AT3G17510 | Symbols: CIPK1, SnRK3.16 | CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding | chr3:5989309-5992627 REVERSEvery weakly similar to (97.1) loc_os05g04550 12005.m04988 protein CBL-interacting serine/threonine-protein kinase 1, putative, expressed seq=cds; coord=3:131847059..131848547:1; parent_gene=AC206425.3_FG004'

'moderately similar to (327) AT5G39850 | Symbols: | 40S ribosomal protein S9 (RPS9C) | chr5:15950053-15951171 FORWARDweakly similar to (110) RS9_TOBAC 40S ribosomal protein S9 (S4) (Fragment) - Nicotiana tabacum (Common tobacco)moderately similar to (354) loc_os11g38959 12011.m80083 protein 40S ribosomal protein S9, putative, expressed seq=cds; coord=3:135594596..135597030:-1; parent_gene=GRMZM2G108348'

'weakly similar to (144) AT5G22330 | Symbols: ATTIP49A, RIN1 | RIN1 (RESISTANCE TO PSEUDOMONAS SYRINGAE PV MACULICOLA INTERACTOR 1); protein binding | chr5:7391026-7394071 REVERSEweakly similar to (171) loc_os07g08170 12007.m05274 protein ruvB-like 1, putative, expressed seq=cds; coord=3:181698730..181700453:-1; parent_gene=GRMZM2G359230' 'weakly similar to (101) AT1G67750 | Symbols: | pectate lyase family protein | chr1:25401660-25403165 FORWARDweakly similar to (111) loc_os04g05050 12004.m35243 protein pectate lyase 8 precursor, putative, expressed seq=cds; coord=3:188017138..188020110:-1; parent_gene=AC213654.3_FG006'

'very weakly similar to (90.1) AT4G26090 | Symbols: RPS2 | RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding | chr4:13224596-13227325 FORWARDmoderately similar to (332) loc_os01g58530 12001.m11995 protein Leucine Rich Repeat family protein, expressed seq=cds; coord=3:188374974..188376493:-1; parent_gene=GRMZM2G047652'

'moderately similar to (306) AT5G54500 | Symbols: FQR1 | FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor | chr5:22124674-22126256 FORWARDmoderately similar to (362) loc_os01g57570 12001.m43222 protein minor allergen Alt a 7, putative, expressed seq=cds; coord=3:190321122..190324751:-1; parent_gene=GRMZM2G138800'

'weakly similar to (174) AT1G29520 | Symbols: | AWPM-19-like membrane family protein | chr1:10323735-10324525 FORWARDmoderately similar to (229) loc_os01g50440 12001.m11226 protein plasma membrane associated protein, putative, expressed seq=cds; coord=3:205294776..205296372:-1; parent_gene=GRMZM2G057283'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'weakly similar to (163) AT5G55340 | Symbols: | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein | chr5:22439985-22440986 REVERSEmoderately similar to (475) loc_os01g46270 12001.m10825 protein wax synthase isoform 3, putative, expressed seq=cds; coord=3:213797343..213799289:-1; parent_gene=GRMZM2G349407'

'weakly similar to (178) AT2G01430 | Symbols: ATHB17, ATHB-17 | ATHB17 (ARABIDOPSIS THALIANA HOMEOBOX-LEUCINE ZIPPER PROTEIN 17); transcription factor | chr2:187798-190369 REVERSEmoderately similar to (291) loc_os01g45570 12001.m10759 protein homeobox-leucine zipper protein ATHB-4, putative, expressed seq=cds; coord=3:214857327..214861719:1; parent_gene=GRMZM2G126239'

'highly similar to (538) AT4G16745 | Symbols: | exostosin family protein | chr4:9412185-9414053 FORWARDhighly similar to (709) loc_os01g45350 12001.m10738 protein limonene cyclase like protein, putative, expressed seq=cds; coord=3:215380332..215382314:-1; parent_gene=GRMZM2G048010'

'moderately similar to (245) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (340) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215466579..215473931:-1; parent_gene=GRMZM2G121878'

'moderately similar to (454) AT2G25910 | Symbols: | 3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein | chr2:11049379-11051997 REVERSEhighly similar to (542) loc_os01g38620 12001.m43061 protein 3-5 exonuclease/ nucleic acid binding protein, putative, expressed seq=cds; coord=3:219191471..219198169:-1; parent_gene=GRMZM2G081924' 'highly similar to (874) AT4G26590 | Symbols: ATOPT5, OPT5 | OPT5 (OLIGOPEPTIDE TRANSPORTER 5); oligopeptide transporter | chr4:13414134-13416850 REVERSEnearly identical (1185) loc_os08g23130 12008.m080127 protein oligopeptide transporter 5, putative, expressed seq=cds; coord=4:169011560..169014163:1; parent_gene=GRMZM2G019209'

'highly similar to (673) AT2G37710 | Symbols: RLK | RLK (receptor lectin kinase); kinase | chr2:15814934-15816961 REVERSEmoderately similar to (208) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (815) loc_os07g03830 12007.m04853 protein lectin-like receptor kinase 7, putative seq=cds; coord=4:221759308..221761618:-1; parent_gene=GRMZM2G142037'

'highly similar to (809) AT5G53130 | Symbols: CNGC1, ATCNGC1 | CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1); calmodulin binding / cation channel/ cyclic nucleotide binding / intracellular cyclic nucleotide activated cation channel/ inward rectifier potassium channel | chr5:21537830-21540490 REVERSEhighly similar to (959) loc_os06g33570 12006.m07894 protein cyclic nucleotide-gated ion channel 1, putative, expressed seq=cds; coord=4:225259158..225269632:1; parent_gene=GRMZM2G148118'

'weakly similar to (162) AT4G30220 | Symbols: RUXF | RUXF (SMALL NUCLEAR RIBONUCLEOPROTEIN F) | chr4:14803100-14804259 REVERSEweakly similar to (176) loc_os11g43620 12011.m28864 protein small nuclear ribonucleoprotein F, putative, expressed seq=cds; coord=5:89314594..89320408:-1; parent_gene=GRMZM2G058252'

'highly similar to (518) AT4G31860 | Symbols: | protein phosphatase 2C, putative / PP2C, putative | chr4:15406685-15408589 REVERSEhighly similar to (598) loc_os02g08364 12002.m100028 protein protein phosphatase 2C isoform gamma, putative, expressed seq=cds; coord=5:91798187..91814550:1; parent_gene=GRMZM2G360455'

'highly similar to (799) AT2G28260 | Symbols: ATCNGC15, CNGC15 | ATCNGC15; calmodulin binding / cation channel/ cyclic nucleotide binding | chr2:12049989-12052453 FORWARDnearly identical (1106) loc_os02g41710 12002.m09208 protein cyclic nucleotide-gated ion channel 15, putative, expressed seq=cds; coord=5:186838856..186841594:-1; parent_gene=GRMZM2G068904'

'weakly similar to (152) AT2G20880 | Symbols: | AP2 domain-containing transcription factor, putative | chr2:8986053-8987063 FORWARDvery weakly similar to (87.4) ERF1_ORYSA Ethylene-responsive transcription factor 1 (Ethylene-responsive element-binding factor 1) (EREBP-1) (OsEREBP1) - Oryza sativa (Rice)moderately similar to (266) loc_os04g44670 12004.m09426 protein AP2 domain containing protein, expressed seq=cds; coord=5:188666370..188668441:-1; parent_gene=GRMZM2G139765'

'weakly similar to (148) loc_os02g43120 12002.m09347 protein RING-H2 finger protein ATL1I, putative, expressed seq=cds; coord=5:189906521..189907598:-1; parent_gene=GRMZM2G409372'

'moderately similar to (494) AT5G23810 | Symbols: AAP7 | AAP7; amino acid transmembrane transporter | chr5:8028461-8030138 FORWARDhighly similar to (677) loc_os02g49060 12002.m09940 protein AAP7, putative, expressed seq=cds; coord=5:204062211..204065565:1; parent_gene=GRMZM2G161641'

'moderately similar to (329) AT1G69530 | Symbols: ATEXPA1, EXP1, AT-EXP1, ATEXP1, ATHEXP ALPHA 1.2 | ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1) | chr1:26142034-26143200 FORWARDmoderately similar to (395) EXPA5_ORYSA Expansin-A5 precursor (OsEXPA5) (Alpha-expansin-5) (OsEXP5) (OsaEXPa1.20) - Oryza sativa (Rice)moderately similar to (395) loc_os02g51040 12002.m10138 protein alpha-expansin 15 precursor, putative, expressed seq=cds; coord=5:206838596..206840547:1; parent_gene=GRMZM2G105844'

'weakly similar to (150) AT1G69690 | Symbols: | TCP family transcription factor, putative | chr1:26216449-26217426 FORWARDmoderately similar to (317) loc_os02g51280 12002.m10162 protein TCP-domain protein, putative, expressed seq=cds; coord=5:207135266..207137587:1; parent_gene=GRMZM2G077755'

'weakly similar to (140) AT5G27420 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:9684119-9685225 FORWARDvery weakly similar to (83.2) EL5_ORYSA E3 ubiquitin-protein ligase EL5 (EC 6.3.2.-) - Oryza sativa (Rice)moderately similar to (263) loc_os02g52210 12002.m10252 protein RING/C3HC4/PHD zinc finger-like protein, putative, expressed seq=cds; coord=5:208925097..208929323:1; parent_gene=GRMZM2G323013'

'weakly similar to (169) AT2G19130 | Symbols: | S-locus lectin protein kinase family protein | chr2:8293789-8296275 FORWARDweakly similar to (130) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (202) loc_os07g08860 12007.m05342 protein S-domain receptor-like protein kinase, putative seq=cds; coord=6:33477184..33478109:-1; parent_gene=GRMZM2G179270'

'moderately similar to (244) AT3G01410 | Symbols: | RNase H domain-containing protein | chr3:153650-155439 REVERSEmoderately similar to (380) loc_os08g08050 12008.m04940 protein retrotransposon protein, putative, Ty3-gypsy subclass seq=cds; coord=6:43497340..43503135:1; parent_gene=GRMZM2G124509'

'weakly similar to (181) AT2G43190 | Symbols: | ribonuclease P family protein | chr2:17956220-17957833 FORWARDmoderately similar to (438) loc_os05g39530 12005.m083751 protein ribonuclease P/ ribonuclease, putative, expressed seq=cds; coord=6:74035080..74038340:-1; parent_gene=GRMZM2G047265'

'weakly similar to (136) AT4G31410 | Symbols: | unknown protein | chr4:15244259-15245474 FORWARDmoderately similar to (288) loc_os06g47860 12006.m31919 protein expressed protein seq=cds; coord=6:74144320..74146448:-1; parent_gene=GRMZM2G430152'

'weakly similar to (136) AT4G31410 | Symbols: | unknown protein | chr4:15244259-15245474 FORWARDmoderately similar to (288) loc_os06g47860 12006.m31919 protein expressed protein seq=cds; coord=6:74144320..74146448:-1; parent_gene=GRMZM2G430152'

'moderately similar to (480) AT4G01030 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr4:448336-449838 REVERSEweakly similar to (116) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)nearly identical (1134) loc_os05g50950 12005.m09162 protein pentatricopeptide repeat protein PPR986-12, putative, expressed seq=cds; coord=6:168066381..168069793:-1; parent_gene=GRMZM2G440349' 'moderately similar to (480) AT4G01030 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr4:448336-449838 REVERSEweakly similar to (116) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)nearly identical (1134) loc_os05g50950 12005.m09162 protein pentatricopeptide repeat protein PPR986-12, putative, expressed seq=cds; coord=6:168066381..168069793:-1; parent_gene=GRMZM2G440349'

'highly similar to (593) AT1G30510 | Symbols: ATRFNR2 | ATRFNR2 (ROOT FNR 2); FAD binding / NADP or NADPH binding / electron carrier/ ferredoxin-NADP

'moderately similar to (358) AT5G24090 | Symbols: | acidic endochitinase (CHIB1) | chr5:8143805-8145153 REVERSEmoderately similar to (379) CHIA_TOBAC Acidic endochitinase precursor (EC 3.2.1.14) - Nicotiana tabacum (Common tobacco)moderately similar to (495) loc_os07g19040 12007.m06343 protein acidic endochitinase precursor, putative seq=cds; coord=7:31446367..31447379:1; parent_gene=GRMZM2G080547'

'moderately similar to (239) AT4G35335 | Symbols: | nucleotide-sugar transmembrane transporter/ sugar:hydrogen symporter | chr4:16807286-16810015 FORWARDmoderately similar to (254) loc_os07g38610 12007.m08106 protein UDP-galactose translocator, putative, expressed seq=cds; coord=7:159863258..159865012:-1; parent_gene=GRMZM2G007909'

'highly similar to (649) AT1G18670 | Symbols: IBS1 | IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr1:6427242-6430696 REVERSEmoderately similar to (220) CDC2_VIGUN Cell division control protein 2 homolog (EC 2.7.11.22) (EC 2.7.11.23) (p34cdc2) - Vigna unguiculata (Cowpea)highly similar to (956) loc_os07g40550 12007.m29001 protein transposon protein, putative, unclassified, expressed seq=cds; coord=7:162983903..162989308:-1; parent_gene=GRMZM2G432796'

'highly similar to (980) AT3G02130 | Symbols: RPK2, TOAD2 | RPK2 (RECEPTOR-LIKE PROTEIN KINASE 2); ATP binding / kinase/ protein serine/threonine kinase | chr3:381224-384181 FORWARDmoderately similar to (391) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1607) loc_os07g41140 12007.m08350 protein receptor-like protein kinase precursor, putative, expressed seq=cds; coord=7:163778995..163782507:1; parent_gene=GRMZM2G017409'

'moderately similar to (379) AT4G38180 | Symbols: FRS5 | FRS5 (FAR1-related sequence 5); zinc ion binding | chr4:17906702-17909404 REVERSEnearly identical (1313) loc_os07g42400 12007.m29004 protein transposon protein, putative, unclassified, expressed seq=cds; coord=7:165466726..165470875:1; parent_gene=GRMZM2G114461'

'moderately similar to (390) AT2G47180 | Symbols: AtGolS1 | AtGolS1 (Arabidopsis thaliana galactinol synthase 1); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr2:19369049-19370372 REVERSEmoderately similar to (411) loc_os07g48830 12007.m09092 protein galactinol synthase 3, putative, expressed seq=cds; coord=7:174158639..174179366:1; parent_gene=GRMZM2G361984'

'moderately similar to (239) AT5G11900 | Symbols: | eukaryotic translation initiation factor SUI1 family protein | chr5:3834154-3836023 FORWARDmoderately similar to (287) loc_os01g09890 12001.m07613 protein density-regulated protein, putative, expressed seq=cds; coord=8:21874081..21876830:1; parent_gene=GRMZM2G033283' 'highly similar to (537) AT3G61790 | Symbols: | seven in absentia (SINA) family protein | chr3:22871974-22873543 REVERSEweakly similar to (149) SINAL_DROME Probable E3 ubiquitin-protein ligase sina-like CG13030 (EC 6.3.2.-) - Drosophila melanogaster (Fruit fly)highly similar to (607) loc_os05g14860 12005.m05897 protein ubiquitin ligase SINAT3, putative, expressed seq=cds; coord=8:110374175..110378712:-1; parent_gene=GRMZM2G101852'

'moderately similar to (376) AT3G07070 | Symbols: | protein kinase family protein | chr3:2238455-2240074 FORWARDmoderately similar to (207) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (534) loc_os05g38770 12005.m08056 protein protein kinase APK1B, chloroplast precursor, putative, expressed seq=cds; coord=8:117194313..117197273:-1; parent_gene=GRMZM2G090732'

moderately similar to (207) AT3G53020 | Symbols: STV1, RPL24B, RPL24 | STV1 (SHORT VALVE1); structural constituent of ribosome | chr3:19660749-19661912 REVERSEmoderately similar to (218) RL24_HORVU 60S ribosomal protein L24 - Hordeum vulgare (Barley)moderately similar to (224) loc_os05g40820 12005.m083765 protein 60S ribosomal protein L24, putative, expressed seq=cds; coord=8:119372356..119376074:-1; parent_gene=GRMZM2G142640'

'moderately similar to (243) AT1G23380 | Symbols: KNAT6, KNAT6L, KNAT6S | KNAT6; DNA binding / transcription activator/ transcription factor | chr1:8297499-8302492 REVERSEmoderately similar to (226) RSH1_MAIZE Homeobox protein rough sheath 1 - Zea mays (Maize)moderately similar to (384) loc_os05g03884 12005.m04922 protein homeotic protein knotted-1, putative, expressed seq=cds; coord=8:130850435..130856001:1; parent_gene=GRMZM2G094241'

'highly similar to (583) AT3G55270 | Symbols: MKP1, ATMKP1 | MKP1 (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 1); MAP kinase tyrosine/serine/threonine phosphatase | chr3:20496775-20499408 FORWARDvery weakly similar to (85.5) PTP3_CHLEU Dual specificity protein phosphatase (EC 3.1.3.48) (EC 3.1.3.16) - Chlamydomonas eugametoshighly similar to (685) loc_os05g02500 12005.m64196 protein MAP kinase phosphatase, putative, expressed seq=cds; coord=8:133181699..133186955:1; parent_gene=GRMZM2G005350'

'weakly similar to (188) AT3G07340 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr3:2341188-2343288 REVERSEhighly similar to (584) loc_os01g68700 12001.m12972 protein BHLH transcription factor, putative, expressed seq=cds; coord=8:162557420..162560479:1; parent_gene=GRMZM2G030762'

'moderately similar to (477) AT5G22850 | Symbols: | aspartyl protease family protein | chr5:7633717-7636298 REVERSEweakly similar to (111) ASP1_ORYSA Aspartic proteinase Asp1 precursor (EC 3.4.23.-) (OsAsp1) (OSAP1) (Nucellin-like protein) - Oryza sativa (Rice)highly similar to (702) loc_os01g56930 12001.m150738 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=8:172223115..172227824:-1; parent_gene=GRMZM2G133029'

'moderately similar to (310) AT5G45775 | Symbols: | 60S ribosomal protein L11 (RPL11D) | chr5:18565281-18566496 REVERSEmoderately similar to (321) RL11_ORYSA 60S ribosomal protein L11 - Oryza sativa (Rice)moderately similar to (322) loc_os02g14059 12002.m77785 protein 60S ribosomal protein L11-1, putative, expressed seq=cds; coord=9:77021422..77026624:1; parent_gene=GRMZM2G001816' 'moderately similar to (491) AT5G26040 | Symbols: HDA2 | HDA2; histone deacetylase | chr5:9099321-9101598 REVERSEvery weakly similar to (93.2) HDAC_MAIZE Probable histone deacetylase (RPD3 homolog) - Zea mays (Maize)highly similar to (582) loc_os06g37420 12006.m091722 protein histone deacetylase 11, putative, expressed seq=cds; coord=9:79411227..79415471:-1; parent_gene=GRMZM2G008425'

'weakly similar to (154) AT5G23710 | Symbols: | DNA binding / DNA-directed RNA polymerase | chr5:7996528-7997220 REVERSEmoderately similar to (261) loc_os06g40110 12006.m08547 protein RNA polymerase Rpc34 subunit family protein, expressed seq=cds; coord=9:89198117..89199404:-1; parent_gene=GRMZM2G058336'

'moderately similar to (362) AT3G57670 | Symbols: NTT | NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding | chr3:21370936-21373121 FORWARDmoderately similar to (430) loc_os06g40960 12006.m08631 protein zinc finger protein, putative, expressed seq=cds; coord=9:101771087..101774624:-1; parent_gene=GRMZM2G436344'

'weakly similar to (190) AT1G65680 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2) | chr1:24427266-24428399 FORWARDmoderately similar to (332) EXPB6_ORYSA Expansin-B6 precursor (OsEXPB6) (Beta-expansin-6) (OsaEXPb1.8) - Oryza sativa (Rice)moderately similar to (332) loc_os10g40700 12010.m06838 protein beta-expansin 1a precursor, putative, expressed seq=cds; coord=9:116443796..116445318:1; parent_gene=GRMZM2G059785'

'very weakly similar to (99.4) AT2G45120 | Symbols: | zinc finger (C2H2 type) family protein | chr2:18603680-18604624 FORWARDweakly similar to (197) loc_os10g40660 12010.m06836 protein cys2/His2 zinc-finger transcription factor, putative, expressed seq=cds; coord=9:116896122..116897766:1; parent_gene=GRMZM2G152214'

'moderately similar to (479) AT5G23870 | Symbols: | pectinacetylesterase family protein | chr5:8046309-8049999 REVERSEmoderately similar to (422) loc_os07g44070 12007.m29010 protein carboxylic ester hydrolase, putative, expressed seq=cds; coord=9:117322363..117325885:1; parent_gene=GRMZM2G117999'

'weakly similar to (188) AT3G51850 | Symbols: CPK13 | CPK13; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr3:19232667-19235526 FORWARDweakly similar to (129) CDPK2_MAIZE Calcium-dependent protein kinase 2 (EC 2.7.11.1) (CDPK 2) - Zea mays (Maize)moderately similar to (210) loc_os01g61590 12001.m12285 protein calcium-dependent protein kinase, isoform AK1, putative, expressed seq=cds; coord=9:125057730..125059364:-1; parent_gene=GRMZM2G047546'

'moderately similar to (298) AT1G75560 | Symbols: | zinc knuckle (CCHC-type) family protein | chr1:28371420-28372717 REVERSEmoderately similar to (481) loc_os10g39820 12010.m06753 protein DNA-binding protein HEXBP, putative, expressed seq=cds; coord=9:126504746..126511455:-1; parent_gene=GRMZM2G127340'

'moderately similar to (436) AT4G33860 | Symbols: | glycosyl hydrolase family 10 protein | chr4:16230142-16232309 REVERSEhighly similar to (684) loc_os03g10440 12003.m06497 protein 1,4-beta-xylanase, putative, expressed seq=cds; coord=9:147979786..147981553:-1; parent_gene=GRMZM2G048375' 'moderately similar to (239) AT3G62240 | Symbols: | zinc finger (C2H2 type) family protein | chr3:23033592-23036653 REVERSEmoderately similar to (327) loc_os01g14840 12001.m08086 protein nucleic acid binding protein, putative, expressed seq=cds; coord=9:149278522..149280901:-1; parent_gene=GRMZM2G004157'

'highly similar to (636) AT1G77380 | Symbols: AAP3, ATAAP3 | AAP3; amino acid transmembrane transporter | chr1:29075201-29077252 REVERSEhighly similar to (796) loc_os12g08090 12012.m04796 protein amino acid transporter, putative, expressed seq=cds; coord=10:11081436..11083714:1; parent_gene=GRMZM2G076593'

'moderately similar to (310) AT1G74250 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr1:27920328-27922414 FORWARDmoderately similar to (447) loc_os12g31840 12012.m06992 protein heat shock protein binding protein, putative, expressed seq=cds; coord=10:16928881..16930864:-1; parent_gene=GRMZM2G170027'

'moderately similar to (279) AT1G15820 | Symbols: LHCB6, CP24 | LHCB6 (LIGHT HARVESTING COMPLEX PSII SUBUNIT 6); chlorophyll binding | chr1:5446685-5447676 REVERSEmoderately similar to (282) CB4_SPIOL Chlorophyll a-b binding protein CP24, chloroplast precursor - Spinacia oleracea (Spinach)moderately similar to (289) loc_os04g38410 12004.m08831 protein chlorophyll a-b binding protein CP24, chloroplast precursor, putative, expressed seq=cds; coord=10:147890562..147891878:1; parent_gene=GRMZM2G092427'

'weakly similar to (172) AT5G22250 | Symbols: | CCR4-NOT transcription complex protein, putative | chr5:7365605-7366441 REVERSEmoderately similar to (209) loc_os04g58810 12004.m10761 protein CCR4-NOT transcription complex subunit 8, putative, expressed seq=cds; coord=10:148762274..148766456:1; parent_gene=GRMZM2G177340'

'weakly similar to (157) AT3G44220 | Symbols: | harpin-induced family protein / HIN1 family protein / harpin-responsive family protein | chr3:15928216-15929645 FORWARDmoderately similar to (282) loc_os04g58860 12004.m10766 protein VAMP protein SEC22, putative, expressed seq=cds; coord=10:148832965..148833998:-1; parent_gene=GRMZM2G406119'

'moderately similar to (297) AT1G76920 | Symbols: | F-box family protein (FBX3) | chr1:28892295-28893419 FORWARDweakly similar to (104) loc_os04g59010 12004.m10779 protein F-box domain containing protein, expressed seq=cds; coord=10:148984717..148986879:-1; parent_gene=GRMZM2G104882'

'weakly similar to (135) AT2G17120 | Symbols: LYM2 | LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR) | chr2:7459156-7460648 FORWARDmoderately similar to (219) loc_os03g04110 12003.m101179 protein receptor-like GPI-anchored protein 2, putative, expressed seq=cds; coord=1:7566218..7567090:1; parent_gene=GRMZM2G410991'

'moderately similar to (455) AT1G15170 | Symbols: | MATE efflux family protein | chr1:5220690-5222756 FORWARDhighly similar to (719) loc_os01g31980 12001.m150603 protein transparent testa 12 protein, putative, expressed seq=cds; coord=1:17383726..17395138:1; parent_gene=GRMZM2G115105'

'weakly similar to (152) AT3G59650 | Symbols: | mitochondrial ribosomal protein L51/S25/CI-B8 family protein | chr3:22033216-22033928 FORWARDweakly similar to (182) loc_os03g10930 12003.m06545 protein mitochondrial ribosomal protein L43, putative, expressed seq=cds; coord=1:21456899..21461749:1; parent_gene=GRMZM2G004259'

'weakly similar to (152) AT3G59650 | Symbols: | mitochondrial ribosomal protein L51/S25/CI-B8 family protein | chr3:22033216-22033928 FORWARDweakly similar to (182) loc_os03g10930 12003.m06545 protein mitochondrial ribosomal protein L43, putative, expressed seq=cds; coord=1:21456899..21461749:1; parent_gene=GRMZM2G004259' 'weakly similar to (109) AT2G28710 | Symbols: | zinc finger (C2H2 type) family protein | chr2:12322974-12323444 FORWARDmoderately similar to (208) loc_os03g17150 12003.m07146 protein ZFP16-1, putative, expressed seq=cds; coord=1:42121563..42122262:-1; parent_gene=GRMZM2G048154'

'moderately similar to (484) AT5G01340 | Symbols: | mitochondrial substrate carrier family protein | chr5:143240-144561 REVERSEhighly similar to (553) loc_os03g18160 12003.m07241 protein tricarboxylate transport protein, mitochondrial precursor, putative, expressed seq=cds; coord=1:45400061..45402643:1; parent_gene=AC208201.3_FG001'

'moderately similar to (248) AT2G30260 | Symbols: U2B" | U2B" (U2 small nuclear ribonucleoprotein B); RNA binding / nucleic acid binding / nucleotide binding | chr2:12905557-12907434 REVERSEmoderately similar to (323) loc_os03g18720 12003.m35175 protein spliceosomal protein, putative, expressed seq=cds; coord=1:46622335..46627171:-1; parent_gene=GRMZM2G153450'

'moderately similar to (202) AT5G52840 | Symbols: | NADH-ubiquinone oxidoreductase-related | chr5:21413718-21414794 FORWARDmoderately similar to (260) loc_os03g19890 12003.m07402 protein NADH-ubiquinone oxidoreductase 13 kDa-B subunit, putative, expressed seq=cds; coord=1:51013925..51015964:1; parent_gene=GRMZM2G018941'

'highly similar to (506) AT2G47180 | Symbols: AtGolS1 | AtGolS1 (Arabidopsis thaliana galactinol synthase 1); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups | chr2:19369049-19370372 REVERSEhighly similar to (588) loc_os03g20120 12003.m07424 protein galactinol synthase 3, putative, expressed seq=cds; coord=1:51534145..51536353:1; parent_gene=GRMZM2G165919'

'moderately similar to (286) AT4G16640 | Symbols: | matrix metalloproteinase, putative | chr4:9367396-9368490 REVERSEmoderately similar to (209) MEP1_SOYBN Metalloendoproteinase 1 precursor (EC 3.4.24.-) (SMEP1) - Glycine max (Soybean)moderately similar to (441) loc_os10g40830 12010.m06853 protein metalloendoproteinase 1 precursor, putative, expressed seq=cds; coord=1:90788877..90790064:1; parent_gene=GRMZM2G317386'

'moderately similar to (201) AT1G65680 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2) | chr1:24427266-24428399 FORWARDhighly similar to (505) EXPB4_ORYSA Expansin-B4 precursor (OsEXPB4) (Beta-expansin-4) (OsaEXPb1.7) - Oryza sativa (Rice)highly similar to (505) loc_os10g40730 12010.m06841 protein beta-expansin 1a precursor, putative, expressed seq=cds; coord=1:91247118..91249938:-1; parent_gene=GRMZM2G021621'

'moderately similar to (201) AT1G65680 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2) | chr1:24427266-24428399 FORWARDhighly similar to (505) EXPB4_ORYSA Expansin-B4 precursor (OsEXPB4) (Beta-expansin-4) (OsaEXPb1.7) - Oryza sativa (Rice)highly similar to (505) loc_os10g40730 12010.m06841 protein beta-expansin 1a precursor, putative, expressed seq=cds; coord=1:91247118..91249938:-1; parent_gene=GRMZM2G021621'

'moderately similar to (236) AT2G42800 | Symbols: AtRLP29 | AtRLP29 (Receptor Like Protein 29); protein binding | chr2:17808157-17809545 REVERSEweakly similar to (122) RPK1_IPONI Receptor-like protein kinase precursor (EC 2.7.11.1) - Ipomoea nil (Japanese morning glory) (Pharbitis nil)moderately similar to (320) loc_os03g44270 12003.m09466 protein retrotransposon protein, putative, Ty1-copia subclass seq=cds; coord=1:251112471..251114311:1; parent_gene=GRMZM2G081099'

'highly similar to (621) AT5G46180 | Symbols: DELTA-OAT | delta-OAT; ornithine-oxo-acid transaminase | chr5:18718766-18721271 REVERSEweakly similar to (115) GSA_HORVU Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT) - Hordeum vulgare (Barley)highly similar to (742) loc_os03g44150 12003.m09454 protein ornithine aminotransferase, putative, expressed seq=cds; coord=1:251088454..251096714:-1; parent_gene=GRMZM2G080828'

'moderately similar to (413) AT2G37640 | Symbols: ATEXPA3, ATEXP3, ATHEXP ALPHA 1.9, EXP3 | EXP3 | chr2:15788077-15789812 REVERSEmoderately similar to (462) EXPA7_ORYSA Expansin-A7 precursor (OsEXPA7) (Alpha-expansin-7) (OsEXP7) (OsaEXPa1.26) - Oryza sativa (Rice)moderately similar to (462) loc_os03g60720 12003.m10961 protein alpha-expansin 6 precursor, putative, expressed seq=cds; coord=1:293628223..293631846:-1; parent_gene=GRMZM2G368886'

'weakly similar to (101) AT5G67190 | Symbols: | AP2 domain-containing transcription factor, putative | chr5:26809135-26809689 REVERSEweakly similar to (168) loc_os04g55520 12004.m10443 protein dehydration responsive element binding protein, putative, expressed seq=cds; coord=2:5562976..5564647:1; parent_gene=GRMZM2G174917'

'weakly similar to (101) AT5G67190 | Symbols: | AP2 domain-containing transcription factor, putative | chr5:26809135-26809689 REVERSEweakly similar to (168) loc_os04g55520 12004.m10443 protein dehydration responsive element binding protein, putative, expressed seq=cds; coord=2:5562976..5564647:1; parent_gene=GRMZM2G174917'

'very weakly similar to (93.2) loc_os04g45690 12004.m09520 protein salt tolerance-like protein, putative, expressed seq=cds; coord=2:21903375..21906486:-1; parent_gene=GRMZM2G131982'

'moderately similar to (361) AT4G16563 | Symbols: | aspartyl protease family protein | chr4:9329933-9331432 REVERSEhighly similar to (550) loc_os04g45270 12004.m09480 protein pepsin A, putative, expressed seq=cds; coord=2:22946935..22949075:1; parent_gene=GRMZM2G003784'

'weakly similar to (189) AT2G28350 | Symbols: ARF10 | ARF10 (AUXIN RESPONSE FACTOR 10); miRNA binding / transcription factor | chr2:12114331-12116665 FORWARDmoderately similar to (234) loc_os04g43910 12004.m09350 protein auxin response factor 16, putative, expressed seq=cds; coord=2:27979219..27980618:-1; parent_gene=GRMZM2G122614' 'moderately similar to (351) AT4G26090 | Symbols: RPS2 | RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding | chr4:13224596-13227325 FORWARDnearly identical (1111) loc_os04g43440 12004.m09307 protein NB-ARC domain containing protein, expressed seq=cds; coord=2:28929571..28933965:-1; parent_gene=GRMZM2G032602'

'moderately similar to (351) AT4G26090 | Symbols: RPS2 | RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding | chr4:13224596-13227325 FORWARDnearly identical (1111) loc_os04g43440 12004.m09307 protein NB-ARC domain containing protein, expressed seq=cds; coord=2:28929571..28933965:-1; parent_gene=GRMZM2G032602'

'weakly similar to (171) ATMG01275 | Symbols: NAD1A, NAD1, ND1 | Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C. | chrM:318004-318390 REVERSEweakly similar to (181) NU1M_OENBE NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3) (NADH dehydrogenase subunit 1) - Oenothera bertiana (Bertero's evening primrose) seq=cds; coord=9:68016311..68020591:1; parent_gene=GRMZM2G141605'

'weakly similar to (171) ATMG01275 | Symbols: NAD1A, NAD1, ND1 | Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C. | chrM:318004-318390 REVERSEweakly similar to (181) NU1M_OENBE NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3) (NADH dehydrogenase subunit 1) - Oenothera bertiana (Bertero's evening primrose) seq=cds; coord=9:68016311..68020591:1; parent_gene=GRMZM2G141605'

'weakly similar to (171) ATMG01275 | Symbols: NAD1A, NAD1, ND1 | Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C. | chrM:318004-318390 REVERSEweakly similar to (181) NU1M_OENBE NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3) (NADH dehydrogenase subunit 1) - Oenothera bertiana (Bertero's evening primrose) seq=cds; coord=9:68016311..68020591:1; parent_gene=GRMZM2G141605'

'highly similar to (624) AT1G01090 | Symbols: PDH-E1 ALPHA | PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring) | chr1:47705-49166 REVERSEmoderately similar to (240) ODPA_SOLTU Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) - Solanum tuberosum (Potato)highly similar to (725) loc_os04g02900 12004.m101452 protein pyruvate dehydrogenase E1 component alpha subunit, putative, expressed seq=cds; coord=2:110896551..110900469:-1; parent_gene=GRMZM2G033894'

'very weakly similar to (89.7) AT1G29450 | Symbols: | auxin-responsive protein, putative | chr1:10305981-10306406 REVERSEweakly similar to (179) loc_os09g37470 12009.m06694 protein OsSAUR52 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=2:197145274..197145964:1; parent_gene=GRMZM2G151656'

'very weakly similar to (86.7) AT4G31460 | Symbols: | ribosomal protein L28 family protein | chr4:15259773-15260847 REVERSEweakly similar to (124) loc_os07g36090 12007.m079708 protein 60S ribosomal protein L24, mitochondrial precursor, putative, expressed seq=cds; coord=2:204272930..204286337:1; parent_gene=GRMZM2G319634' 'very weakly similar to (81.3) AT3G52120 | Symbols: | SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein | chr3:19329243-19331466 FORWARDvery weakly similar to (95.1) loc_os09g10930 12009.m059950 protein gamma response I protein, putative, expressed seq=cds; coord=2:206621294..206623116:1; parent_gene=GRMZM2G099105'

'moderately similar to (232) AT2G21470 | Symbols: SAE2, ATSAE2, EMB2764 | SAE2 (SUMO-ACTIVATING ENZYME 2); SUMO activating enzyme | chr2:9198752-9202136 FORWARDmoderately similar to (357) loc_os07g39780 12007.m08220 protein ubiquitin-like 1-activating enzyme E1B, putative, expressed seq=cds; coord=2:208223142..208227514:1; parent_gene=GRMZM2G129575'

'moderately similar to (232) AT2G21470 | Symbols: SAE2, ATSAE2, EMB2764 | SAE2 (SUMO-ACTIVATING ENZYME 2); SUMO activating enzyme | chr2:9198752-9202136 FORWARDmoderately similar to (357) loc_os07g39780 12007.m08220 protein ubiquitin-like 1-activating enzyme E1B, putative, expressed seq=cds; coord=2:208223142..208227514:1; parent_gene=GRMZM2G129575'

'highly similar to (881) AT5G26860 | Symbols: LON_ARA_ARA, LON1 | LON1 (LON PROTEASE 1); ATP binding / ATP-dependent peptidase/ serine-type peptidase | chr5:9451048-9456631 FORWARDnearly identical (1009) LONH2_MAIZE Lon protease homolog 2, mitochondrial precursor (EC 3.4.21.-) - Zea mays (Maize)highly similar to (988) loc_os07g48960 12007.m09105 protein lon protease homolog 2, mitochondrial precursor, putative, expressed seq=cds; coord=2:217836574..217843754:1; parent_gene=GRMZM2G387383'

'highly similar to (572) AT5G50300 | Symbols: | xanthine/uracil/vitamin C permease family protein | chr5:20466492-20468084 REVERSEhighly similar to (792) loc_os11g24060 12011.m06332 protein transmembrane transport protein-like, putative, expressed seq=cds; coord=2:218937924..218939954:1; parent_gene=GRMZM2G068220'

'moderately similar to (326) AT3G07550 | Symbols: | F-box family protein (FBL12) | chr3:2409946-2411133 FORWARDhighly similar to (562) loc_os11g16280 12011.m05713 protein F-box-like protein, putative, expressed seq=cds; coord=2:220223475..220230281:1; parent_gene=GRMZM2G048661'

'weakly similar to (114) AT1G76940 | Symbols: | RNA recognition motif (RRM)-containing protein | chr1:28902707-28904085 REVERSEweakly similar to (139) loc_os08g43360 12008.m080227 protein nucleic acid binding protein, putative, expressed seq=cds; coord=2:220923627..220927138:-1; parent_gene=GRMZM2G124809'

'highly similar to (903) AT4G27910 | Symbols: ATX4, SDG16 | SDG16 (SET DOMAIN PROTEIN 16); protein binding / zinc ion binding | chr4:13894694-13900256 FORWARDvery weakly similar to (92.4) EZ1_MAIZE Polycomb protein EZ1 (Enhancer of zeste protein 1) - Zea mays (Maize)nearly identical (1491) loc_os01g11952 12001.m07811 protein histone-lysine N-methyltransferase ATX5, putative, expressed seq=cds; coord=3:3200782..3209083:1; parent_gene=GRMZM2G085266'

'moderately similar to (231) AT4G18270 | Symbols: ATTRANS11, TRANS11 | ATTRANS11; P-P-bond-hydrolysis-driven protein transmembrane transporter/ catalytic | chr4:10099364-10101897 REVERSEmoderately similar to (384) loc_os01g11260 12001.m07745 protein phospho-N-acetylmuramoyl-pentapeptide-transferase, putative, expressed seq=cds; coord=3:3835088..3839366:-1; parent_gene=GRMZM2G093278' 'highly similar to (695) AT2G34960 | Symbols: CAT5 | CAT5 (CATIONIC AMINO ACID TRANSPORTER 5); L-glutamate transmembrane transporter/ L-lysine transmembrane transporter/ arginine transmembrane transporter/ cationic amino acid transmembrane transporter | chr2:14744175-14745884 REVERSEhighly similar to (887) loc_os01g11160 12001.m07736 protein cationic amino acid transporter 4, putative, expressed seq=cds; coord=3:3923176..3925460:1; parent_gene=GRMZM2G146161'

'moderately similar to (388) AT1G45616 | Symbols: AtRLP6 | AtRLP6 (Receptor Like Protein 6); protein binding | chr1:17183550-17186534 REVERSEmoderately similar to (207) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1443) loc_os04g28210 12004.m07938 protein verticillium wilt disease resistance protein, putative, expressed seq=cds; coord=3:14685361..14688745:1; parent_gene=GRMZM2G062576'

'highly similar to (564) loc_os01g05660 12001.m150482 protein expressed protein seq=cds; coord=3:17580074..17584970:1; parent_gene=GRMZM2G166064'

'moderately similar to (297) AT1G17020 | Symbols: SRG1, ATSRG1 | SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc | chr1:5820258-5821741 FORWARDweakly similar to (195) FLS_PETHY Flavonol synthase/flavanone 3-hydroxylase (EC 1.14.11.23) (EC 1.14.11.9) (FLS) - Petunia hybrida (Petunia)moderately similar to (468) loc_os10g40880 12010.m06856 protein flavonol synthase/flavanone 3-hydroxylase, putative, expressed seq=cds; coord=3:52450288..52452458:-1; parent_gene=GRMZM2G363893'

'moderately similar to (207) AT1G33430 | Symbols: | galactosyltransferase family protein | chr1:12124438-12126052 REVERSEmoderately similar to (233) loc_os01g65590 12001.m12668 protein beta-1,3-galactosyltransferase sqv-2, putative, expressed seq=cds; coord=3:172444363..172446418:-1; parent_gene=GRMZM2G431006'

'weakly similar to (127) loc_os01g62514 12001.m150967 protein hypothetical protein seq=cds; coord=3:180598307..180598998:1; parent_gene=GRMZM2G178671'

'very weakly similar to (86.3) AT1G26640 | Symbols: | aspartate/glutamate/uridylate kinase family protein | chr1:9207620-9209766 REVERSEweakly similar to (112) loc_os01g55890 12001.m150726 protein archaeal kinase, putative, expressed seq=cds; coord=3:194512254..194513303:1; parent_gene=GRMZM2G052816'

'weakly similar to (134) AT1G18650 | Symbols: PDCB3 | PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding | chr1:6419036-6420413 REVERSEvery weakly similar to (84.3) E13B_WHEAT Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-endoglucanase) - Triticum aestivum (Wheat)weakly similar to (181) loc_os01g55820 12001.m11738 protein glucan endo-1,3-beta-glucosidase 1 precursor, putative, expressed seq=cds; coord=3:194739182..194740582:1; parent_gene=GRMZM2G162768' 'weakly similar to (134) AT1G18650 | Symbols: PDCB3 | PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding | chr1:6419036-6420413 REVERSEvery weakly similar to (84.3) E13B_WHEAT Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-endoglucanase) - Triticum aestivum (Wheat)weakly similar to (181) loc_os01g55820 12001.m11738 protein glucan endo-1,3-beta-glucosidase 1 precursor, putative, expressed seq=cds; coord=3:194739182..194740582:1; parent_gene=GRMZM2G162768'

'weakly similar to (155) AT1G29220 | Symbols: | transcriptional regulator family protein | chr1:10210678-10212571 REVERSEmoderately similar to (389) loc_os01g55490 12001.m42726 protein transcription regulator, putative, expressed seq=cds; coord=3:195416508..195423273:-1; parent_gene=GRMZM2G015881'

'weakly similar to (155) AT1G29220 | Symbols: | transcriptional regulator family protein | chr1:10210678-10212571 REVERSEmoderately similar to (389) loc_os01g55490 12001.m42726 protein transcription regulator, putative, expressed seq=cds; coord=3:195416508..195423273:-1; parent_gene=GRMZM2G015881'

'weakly similar to (102) AT2G34140 | Symbols: | Dof-type zinc finger domain-containing protein | chr2:14414188-14414700 REVERSEvery weakly similar to (83.6) MNB1A_MAIZE Dof zinc finger protein MNB1A - Zea mays (Maize)weakly similar to (106) loc_os01g55340 12001.m11693 protein expressed protein seq=cds; coord=3:195926190..195927293:1; parent_gene=GRMZM2G394973'

'moderately similar to (239) AT3G58680 | Symbols: MBF1B, ATMBF1B | MBF1B (MULTIPROTEIN BRIDGING FACTOR 1B); DNA binding / transcription coactivator | chr3:21707367-21708625 FORWARDmoderately similar to (268) loc_os08g27850 12008.m080145 protein endothelial differentiation-related factor 1, putative, expressed seq=cds; coord=4:24613100..24615973:-1; parent_gene=GRMZM2G101480'

'weakly similar to (140) AT1G79040 | Symbols: PSBR | PSBR (photosystem II subunit R) | chr1:29736085-29736781 FORWARDweakly similar to (154) PSBR_SOLTU Photosystem II 10 kDa polypeptide, chloroplast precursor (Light-inducible tissue-specific ST-LS1 protein) - Solanum tuberosum (Potato)weakly similar to (174) loc_os08g10020 12008.m26609 protein photosystem II 10 kDa polypeptide, chloroplast precursor, putative, expressed seq=cds; coord=4:27094767..27097143:-1; parent_gene=GRMZM2G174984'

'very weakly similar to (97.4) loc_os08g33530 12008.m07343 protein teosinte branched1 protein, putative seq=cds; coord=4:55919615..55920304:-1; parent_gene=GRMZM2G062711'

'weakly similar to (131) AT1G59940 | Symbols: ARR3 | ARR3 (RESPONSE REGULATOR 3); transcription regulator/ two-component response regulator | chr1:22065894-22066895 REVERSEmoderately similar to (282) loc_os02g35180 12002.m08606 protein OsRR2 - Rice type-A response regulator, expressed seq=cds; coord=4:118065448..118068066:1; parent_gene=GRMZM2G096171'

'nearly identical (1095) AT1G30450 | Symbols: CCC1, ATCCC1, HAP5 | CCC1 (CATION-CHLORIDE CO-TRANSPORTER 1); cation:chloride symporter/ sodium:potassium:chloride symporter | chr1:10762905-10769061 FORWARDnearly identical (1221) loc_os08g23440 12008.m06365 protein CCC1, putative, expressed seq=cds; coord=4:189189209..189199161:1; parent_gene=GRMZM2G401874' 'moderately similar to (275) AT3G07040 | Symbols: RPM1, RPS3 | RPM1 (RESISTANCE TO P. SYRINGAE PV MACULICOLA 1); nucleotide binding / protein binding | chr3:2226244-2229024 REVERSEhighly similar to (776) loc_os11g11960 12011.m05388 protein NBS-LRR type disease resistance protein, putative, expressed seq=cds; coord=4:189294131..189297207:-1; parent_gene=GRMZM2G050959'

'moderately similar to (410) AT2G21270 | Symbols: | ubiquitin fusion degradation UFD1 family protein | chr2:9107841-9110012 FORWARDhighly similar to (521) loc_os02g08480 12002.m06194 protein ubiquitin fusion degradation protein 1, putative, expressed seq=cds; coord=4:235163242..235166429:1; parent_gene=GRMZM2G037185'

'moderately similar to (303) AT3G54170 | Symbols: ATFIP37, FIP37 | ATFIP37 (ARABIDOPSIS THALIANA FKBP12 INTERACTING PROTEIN 37); protein binding | chr3:20056848-20059396 FORWARDmoderately similar to (416) loc_os06g27970 12006.m07342 protein FKBP12-interacting protein of 37 kDa, putative, expressed seq=cds; coord=4:239482617..239492011:1; parent_gene=GRMZM2G169871'

'highly similar to (739) AT1G20630 | Symbols: CAT1 | CAT1 (CATALASE 1); catalase | chr1:7146812-7149609 FORWARDhighly similar to (962) CATA3_MAIZE Catalase isozyme 3 (EC 1.11.1.6) - Zea mays (Maize)highly similar to (857) loc_os02g02400 12002.m77750 protein catalase isozyme A, putative, expressed seq=cds; coord=4:240105137..240108983:1; parent_gene=GRMZM2G079348'

'highly similar to (739) AT1G20630 | Symbols: CAT1 | CAT1 (CATALASE 1); catalase | chr1:7146812-7149609 FORWARDhighly similar to (962) CATA3_MAIZE Catalase isozyme 3 (EC 1.11.1.6) - Zea mays (Maize)highly similar to (857) loc_os02g02400 12002.m77750 protein catalase isozyme A, putative, expressed seq=cds; coord=4:240105137..240108983:1; parent_gene=GRMZM2G079348'

'moderately similar to (438) AT1G75500 | Symbols: | nodulin MtN21 family protein | chr1:28338282-28340091 REVERSEmoderately similar to (477) loc_os02g02310 12002.m05580 protein nodulin-like protein 5NG4, putative, expressed seq=cds; coord=4:240225659..240227771:1; parent_gene=GRMZM2G010372'

'weakly similar to (145) AT1G76890 | Symbols: GT2, AT-GT2 | GT2; transcription factor | chr1:28873211-28875203 REVERSEmoderately similar to (307) loc_os02g01380 12002.m77761 protein expressed protein seq=cds; coord=4:240522539..240525539:1; parent_gene=GRMZM2G037128'

'moderately similar to (371) AT1G77280 | Symbols: | protein kinase family protein | chr1:29031468-29035882 REVERSEweakly similar to (172) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1138) loc_os03g62340 12003.m11110 protein ATP binding protein, putative, expressed seq=cds; coord=5:1533338..1538690:1; parent_gene=GRMZM2G148962'

'moderately similar to (371) AT1G77280 | Symbols: | protein kinase family protein | chr1:29031468-29035882 REVERSEweakly similar to (172) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1138) loc_os03g62340 12003.m11110 protein ATP binding protein, putative, expressed seq=cds; coord=5:1533338..1538690:1; parent_gene=GRMZM2G148962' 'very weakly similar to (84.7) AT5G06470 | Symbols: | glutaredoxin family protein | chr5:1974659-1975378 REVERSEweakly similar to (129) loc_os07g06600 12007.m05120 protein electron transporter/ thiol-disulfide exchange intermediate, putative, expressed seq=cds; coord=5:1756402..1757081:-1; parent_gene=GRMZM2G053378'

'moderately similar to (394) AT5G26680 | Symbols: | endonuclease, putative | chr5:9311882-9315458 REVERSEmoderately similar to (474) FEN1B_ORYSA Flap endonuclease 1b (EC 3.1.-.-) (OsFEN-1b) - Oryza sativa (Rice)moderately similar to (474) loc_os03g61820 12003.m11063 protein flap endonuclease 1b, putative, expressed seq=cds; coord=5:1879148..1895175:1; parent_gene=GRMZM2G398668'

'weakly similar to (166) loc_os05g15890 12005.m27751 protein ATP binding protein, putative, expressed seq=cds; coord=5:21044389..21046589:1; parent_gene=GRMZM2G146041'

'moderately similar to (228) AT4G22130 | Symbols: SRF8 | SRF8 (STRUBBELIG-RECEPTOR FAMILY 8); ATP binding / kinase/ protein binding / protein kinase | chr4:11724781-11727331 FORWARDweakly similar to (118) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)moderately similar to (384) loc_os02g04430 12002.m05792 protein protein kinase, putative, expressed seq=cds; coord=5:76726269..76729394:1; parent_gene=GRMZM2G398559'

'weakly similar to (115) AT1G21150 | Symbols: | mitochondrial transcription termination factor family protein / mTERF family protein | chr1:7406406-7407578 REVERSEmoderately similar to (333) loc_os06g12060 12006.m05923 protein mTERF family protein, expressed seq=cds; coord=5:97174141..97175862:1; parent_gene=GRMZM2G119921'

'weakly similar to (131) AT1G79990 | Symbols: | protein binding / structural molecule | chr1:30085910-30091949 FORWARDweakly similar to (136) loc_os11g10710 12011.m05264 protein protein kinase domain containing protein, expressed seq=cds; coord=5:146430831..146434116:-1; parent_gene=GRMZM2G372812'

'weakly similar to (177) AT5G06130 | Symbols: | chaperone protein dnaJ-related | chr5:1853754-1855763 REVERSEmoderately similar to (229) loc_os02g33149 12002.m100716 protein expressed protein seq=cds; coord=5:169576839..169579921:-1; parent_gene=GRMZM2G039089'

'moderately similar to (353) AT1G21710 | Symbols: OGG1, ATOGG1 | OGG1 (8-OXOGUANINE-DNA GLYCOSYLASE 1); oxidized purine base lesion DNA N-glycosylase | chr1:7624439-7625869 FORWARDhighly similar to (554) loc_os02g34750 12002.m100230 protein receptor-like protein kinase 5 precursor, putative, expressed seq=cds; coord=5:172291156..172294857:-1; parent_gene=GRMZM2G139031'

'moderately similar to (224) AT5G60580 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:24354298-24356706 FORWARDmoderately similar to (334) loc_os06g23274 12006.m06979 protein zinc finger, C3HC4 type family protein, expressed seq=cds; coord=5:174988527..174990580:1; parent_gene=GRMZM2G331253'

'moderately similar to (417) AT5G64330 | Symbols: NPH3, RPT3, JK218 | NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3); protein binding / signal transducer | chr5:25727568-25729510 FORWARDhighly similar to (922) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)highly similar to (922) loc_os02g35970 12002.m08685 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=5:175597610..175602037:-1; parent_gene=GRMZM2G105400' 'very weakly similar to (80.9) HMGL_VICFA HMG1/2-like protein - Vicia faba (Broad bean)weakly similar to (133) loc_os02g44930 12002.m09533 protein HMG1/2-like protein, putative, expressed seq=cds; coord=5:194043178..194045076:1; parent_gene=GRMZM2G013821'

'moderately similar to (488) AT1G63000 | Symbols: NRS/ER, UER1 | NRS/ER (NUCLEOTIDE-RHAMNOSE SYNTHASE/EPIMERASE-REDUCTASE); UDP-4-keto-6-deoxy-glucose-3,5-epimerase/ UDP-4-keto-rhamnose-4-keto-reductase/ dTDP-4-dehydrorhamnose 3,5-epimerase/ dTDP-4-dehydrorhamnose reductase | chr1:23342510-23343859 FORWARDhighly similar to (532) loc_os02g45540 12002.m09591 protein dTDP-4-dehydrorhamnose reductase, putative, expressed seq=cds; coord=5:196103861..196107190:1; parent_gene=GRMZM2G072911'

'moderately similar to (308) AT5G37680 | Symbols: ATARLA1A | ATARLA1A (ADP-ribosylation factor-like A1A); GTP binding | chr5:14969797-14971098 REVERSEweakly similar to (105) ARF1_SOLTU ADP-ribosylation factor 1 - Solanum tuberosum (Potato)moderately similar to (317) loc_os02g49980 12002.m100351 protein ADP-ribosylation factor-like protein 8A, putative, expressed seq=cds; coord=5:204908277..204911697:-1; parent_gene=GRMZM2G089454'

'highly similar to (606) AT2G32990 | Symbols: AtGH9B8 | AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds | chr2:14003361-14005844 FORWARDhighly similar to (809) GUN7_ORYSA Endoglucanase 7 precursor (EC 3.2.1.4) (Endo-1,4-beta glucanase 7) (OsGLU10) - Oryza sativa (Rice)highly similar to (809) loc_os02g50490 12002.m10083 protein endoglucanase 1 precursor, putative, expressed seq=cds; coord=5:205562436..205565933:1; parent_gene=GRMZM2G151257'

'highly similar to (838) AT1G68930 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:25918314-25920545 FORWARDweakly similar to (103) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)nearly identical (1197) loc_os02g01610 12002.m33989 protein tetratricopeptide-like helical, putative, expressed seq=cds; coord=5:206572964..206575640:-1; parent_gene=GRMZM2G053396'

'weakly similar to (171) AT1G78260 | Symbols: | RNA recognition motif (RRM)-containing protein | chr1:29447317-29449246 FORWARDmoderately similar to (299) loc_os02g51890 12002.m10220 protein RNA-binding region-containing protein 1, putative, expressed seq=cds; coord=5:208556677..208562996:1; parent_gene=GRMZM2G303915'

'weakly similar to (151) AT5G02560 | Symbols: HTA12 | HTA12; DNA binding | chr5:575437-576456 FORWARDweakly similar to (159) H2A6_ORYSA Probable histone H2A.6 - Oryza sativa (Rice)weakly similar to (159) loc_os05g02300 12005.m04766 protein histone H2A, putative, expressed seq=cds; coord=6:35731319..35732475:-1; parent_gene=GRMZM2G448458'

'moderately similar to (248) AT1G70670 | Symbols: | caleosin-related family protein | chr1:26644830-26645970 FORWARDmoderately similar to (315) loc_os06g14370 12006.m32034 protein ABA-induced protein, putative, expressed seq=cds; coord=6:118130928..118144112:1; parent_gene=GRMZM2G164308'

'highly similar to (526) AT5G55830 | Symbols: | lectin protein kinase, putative | chr5:22594655-22596700 FORWARDweakly similar to (189) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (858) loc_os06g17490 12006.m06461 protein protein kinase, putative, expressed seq=cds; coord=6:119395032..119397840:1; parent_gene=GRMZM2G159953' 'moderately similar to (241) AT3G57260 | Symbols: BGL2, PR2, BG2, PR-2 | BGL2 (BETA-1,3-GLUCANASE 2); cellulase/ glucan 1,3-beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds | chr3:21188709-21189822 REVERSEmoderately similar to (369) E13F_HORVU Putative glucan endo-1,3-beta-glucosidase GVI precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase GVI) ((1->3)-beta-glucanase isoenzyme GVI) (Beta-1,3-endoglucanase GVI) (Fragment) - Hordeum vulgare (Barley)moderately similar to (434) loc_os05g41610 12005.m08335 protein glucan endo-1,3-beta-glucosidase GVI precursor, putative, expressed seq=cds; coord=6:156249134..156253222:1; parent_gene=GRMZM2G088951'

'moderately similar to (235) AT4G36520 | Symbols: | heat shock protein binding | chr4:17230589-17235435 REVERSEhighly similar to (692) loc_os05g50370 12005.m09106 protein AUL1, putative, expressed seq=cds; coord=6:166249166..166256866:1; parent_gene=GRMZM2G438895'

'moderately similar to (419) AT1G15000 | Symbols: scpl50 | scpl50 (serine carboxypeptidase-like 50); serine-type carboxypeptidase | chr1:5168613-5169947 FORWARDweakly similar to (199) CBPX_ORYSA Serine carboxypeptidase-like precursor (EC 3.4.16.-) - Oryza sativa (Rice)highly similar to (621) loc_os05g50600 12005.m09129 protein serine carboxypeptidase CPVL precursor, putative, expressed seq=cds; coord=6:166885737..166887580:1; parent_gene=GRMZM2G159016'

'nearly identical (1679) AT5G05170 | Symbols: CESA3, IXR1, ATCESA3, ATH-B, CEV1 | CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups | chr5:1530401-1535090 REVERSEnearly identical (2085) loc_os07g10770 12007.m05532 protein CESA8 - cellulose synthase, expressed seq=cds; coord=7:18609337..18615348:-1; parent_gene=GRMZM2G424832'

'moderately similar to (394) AT2G47990 | Symbols: SWA1, EDA13, EDA19 | SWA1 (SLOW WALKER1); nucleotide binding | chr2:19637010-19638602 REVERSEhighly similar to (726) loc_os07g12320 12007.m05685 protein small nucleolar ribonucleoprotein complex subunit, putative, expressed seq=cds; coord=7:20619448..20621061:1; parent_gene=AC212570.3_FG006'

'moderately similar to (394) AT2G47990 | Symbols: SWA1, EDA13, EDA19 | SWA1 (SLOW WALKER1); nucleotide binding | chr2:19637010-19638602 REVERSEhighly similar to (726) loc_os07g12320 12007.m05685 protein small nucleolar ribonucleoprotein complex subunit, putative, expressed seq=cds; coord=7:20619448..20621061:1; parent_gene=AC212570.3_FG006'

'moderately similar to (207) AT4G19680 | Symbols: IRT2 | IRT2; iron ion transmembrane transporter/ zinc ion transmembrane transporter | chr4:10703385-10704621 FORWARDmoderately similar to (393) loc_os07g12890 12007.m28960 protein ZIP zinc/iron transport family protein, expressed seq=cds; coord=7:21798962..21800971:-1; parent_gene=GRMZM2G093276'

'highly similar to (640) AT1G27680 | Symbols: APL2 | APL2 (ADPGLC-PPASE LARGE SUBUNIT); glucose-1-phosphate adenylyltransferase | chr1:9631630-9634450 FORWARDhighly similar to (617) GLGL1_BETVU Glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase S) (Alpha-D-glucose-1-phosphate adenyl transferase) - Beta vulgaris (Sugar beet)highly similar to (791) loc_os07g13980 12007.m05843 protein glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor, putative, expressed seq=cds; coord=7:23756173..23767134:-1; parent_gene=GRMZM2G144002' 'moderately similar to (386) AT2G44060 | Symbols: | late embryogenesis abundant family protein / LEA family protein | chr2:18226922-18227988 FORWARDvery weakly similar to (92.8) LEA14_SOYBN Desiccation protectant protein Lea14 homolog - Glycine max (Soybean)moderately similar to (441) loc_os03g62620 12003.m101565 protein salt tolerance protein, putative, expressed seq=cds; coord=7:27804756..27806317:1; parent_gene=GRMZM2G053637'

'highly similar to (503) AT4G12570 | Symbols: UPL5 | UPL5 (UBIQUITIN PROTEIN LIGASE 5); acid-amino acid ligase/ binding / ubiquitin-protein ligase | chr4:7445585-7448819 FORWARDhighly similar to (915) loc_os09g31090 12009.m22004 protein HECT-domain, putative, expressed seq=cds; coord=7:132186216..132203350:-1; parent_gene=GRMZM2G181378'

'moderately similar to (266) AT4G21440 | Symbols: ATMYB102, ATM4 | ATMYB102 (ARABIDOPSIS MYB-LIKE 102); DNA binding / transcription factor | chr4:11418425-11419652 REVERSEmoderately similar to (215) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (355) loc_os07g37210 12007.m07971 protein MYB transcription factor, putative, expressed seq=cds; coord=7:157167150..157168689:-1; parent_gene=GRMZM2G031323'

'weakly similar to (154) AT4G21540 | Symbols: SPHK1 | SPHK1 (SPHINGOSINE KINASE 1); D-erythro-sphingosine kinase/ diacylglycerol kinase/ sphinganine kinase | chr4:11460703-11462356 FORWARDmoderately similar to (249) loc_os07g37580 12007.m29228 protein D-erythro-sphingosine kinase/ diacylglycerol kinase, putative, expressed seq=cds; coord=7:157593622..157598024:1; parent_gene=GRMZM2G057475'

'very weakly similar to (87.4) AT1G61215 | Symbols: BRD4 | BRD4 (BROMODOMAIN 4); DNA binding | chr1:22573173-22575374 FORWARDmoderately similar to (262) loc_os07g37800 12007.m29230 protein DNA binding protein, putative, expressed seq=cds; coord=7:158037365..158041856:-1; parent_gene=GRMZM2G434301'

'moderately similar to (253) AT2G30360 | Symbols: CIPK11, PKS5, SIP4, SNRK3.22 | SIP4 (SOS3-INTERACTING PROTEIN 4); kinase/ protein kinase | chr2:12937265-12938572 REVERSEweakly similar to (193) CIPK1_ORYSA CIPK-like protein 1 (EC 2.7.11.1) (OsCK1) - Oryza sativa (Rice)moderately similar to (407) loc_os07g48090 12007.m09024 protein CBL-interacting serine/threonine-protein kinase 11, putative, expressed seq=cds; coord=7:172879486..172881907:1; parent_gene=GRMZM2G177050'

'moderately similar to (311) AT3G20770 | Symbols: EIN3 | EIN3 (ETHYLENE-INSENSITIVE3); transcription factor chr3:7260702-7262588 REVERSEmoderately similar to (433) loc_os07g48630 12007.m29024 protein ETHYLENE-INSENSITIVE3-like 1 protein, putative, expressed seq=cds; coord=7:173951359..173953387:-1; parent_gene=GRMZM2G151811'

'moderately similar to (447) AT3G14067 | Symbols: | subtilase family protein | chr3:4658421-4660754 REVERSEhighly similar to (798) loc_os07g48650 12007.m09076 protein xylem serine proteinase 1 precursor, putative, expressed seq=cds; coord=7:174029436..174031718:1; parent_gene=GRMZM2G059165'

'weakly similar to (108) AT2G34140 | Symbols: | Dof-type zinc finger domain-containing protein | chr2:14414188-14414700 REVERSEvery weakly similar to (100) MNB1A_MAIZE Dof zinc finger protein MNB1A - Zea mays (Maize)weakly similar to (120) loc_os01g55340 12001.m11693 protein expressed protein seq=cds; coord=8:123061033..123061653:-1; parent_gene=AC209819.3_FG009' 'weakly similar to (167) AT3G02550 | Symbols: LBD41 | LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41) | chr3:536747-537650 REVERSEmoderately similar to (201) loc_os01g32770 12001.m09596 protein seed specific protein Bn15D17A, putative, expressed seq=cds; coord=8:123322670..123323521:-1; parent_gene=AC234149.1_FG002'

'highly similar to (538) AT2G42960 | Symbols: | protein kinase family protein | chr2:17868597-17870630 REVERSEmoderately similar to (211) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (823) loc_os01g44110 12001.m10669 protein BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed seq=cds; coord=8:146029595..146033938:1; parent_gene=GRMZM2G017386'

'weakly similar to (133) AT1G10640 | Symbols: | polygalacturonase | chr1:3515478-3517807 REVERSEmoderately similar to (229) loc_os01g44970 12001.m10703 protein polygalacturonase precursor, putative, expressed seq=cds; coord=8:146183315..146186058:1; parent_gene=GRMZM2G179696'

'highly similar to (746) AT1G80300 | Symbols: NTT1, ATNTT1 | NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter | chr1:30191954-30194280 FORWARDhighly similar to (754) TLC1_SOLTU Plastidic ATP/ADP-transporter - Solanum tuberosum (Potato)highly similar to (919) loc_os01g45910 12001.m10791 protein plastidic ATP/ADP-transporter, putative, expressed seq=cds; coord=8:146989849..146994732:1; parent_gene=GRMZM2G050003'

'very weakly similar to (91.7) AT1G65780 | Symbols: | tRNA-splicing endonuclease positive effector-related | chr1:24462958-24466888 REVERSEweakly similar to (110) loc_os04g49270 12004.m09862 protein expressed protein seq=cds; coord=8:150897458..150899203:1; parent_gene=GRMZM2G052296'

'moderately similar to (203) AT3G56570 | Symbols: | SET domain-containing protein | chr3:20958660-20961137 FORWARDmoderately similar to (308) loc_os01g65730 12001.m12682 protein SET domain containing protein, expressed seq=cds; coord=8:165266558..165269212:1; parent_gene=GRMZM2G092759'

'moderately similar to (266) AT4G38620 | Symbols: ATMYB4, MYB4 | MYB4; DNA binding / transcription factor | chr4:18053866-18054876 FORWARDmoderately similar to (273) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (325) loc_os01g65370 12001.m12650 protein transcription repressor MYB4, putative seq=cds; coord=8:165875616..165876842:-1; parent_gene=GRMZM2G405094'

'moderately similar to (266) AT4G38620 | Symbols: ATMYB4, MYB4 | MYB4; DNA binding / transcription factor | chr4:18053866-18054876 FORWARDmoderately similar to (273) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (325) loc_os01g65370 12001.m12650 protein transcription repressor MYB4, putative seq=cds; coord=8:165875616..165876842:-1; parent_gene=GRMZM2G405094'

'highly similar to (559) AT2G41790 | Symbols: | peptidase M16 family protein / insulinase family protein | chr2:17429453-17436110 REVERSEhighly similar to (738) loc_os01g57073 12001.m11864 protein insulin-degrading enzyme, putative, expressed seq=cds; coord=8:172180747..172198680:-1; parent_gene=GRMZM2G133249' 'highly similar to (600) AT1G75450 | Symbols: CKX5, ATCKX5, ATCKX6 | CKX5 (CYTOKININ OXIDASE 5); cytokinin dehydrogenase | chr1:28315248-28318064 REVERSEmoderately similar to (418) CKX1_MAIZE Cytokinin dehydrogenase 1 precursor (EC 1.5.99.12) (Cytokinin oxidase 1) (CKO 1) (COX 1) (ZmCKX1) - Zea mays (Maize)highly similar to (822) loc_os01g56810 12001.m11838 protein cytokinin dehydrogenase 5 precursor, putative, expressed seq=cds; coord=8:172364590..172368643:1; parent_gene=GRMZM2G024476'

'moderately similar to (283) AT4G17650 | Symbols: | aromatic-rich family protein | chr4:9827749-9829443 FORWARDmoderately similar to (368) loc_os01g56560 12001.m11813 protein protein COQ10 A, mitochondrial precursor, putative, expressed seq=cds; coord=8:172486699..172489943:1; parent_gene=GRMZM2G111472'

'moderately similar to (240) AT5G39990 | Symbols: | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein | chr5:16004494-16006428 FORWARDmoderately similar to (445) loc_os01g56570 12001.m11814 protein xylosyltransferase 2, putative, expressed seq=cds; coord=8:172491525..172493375:1; parent_gene=GRMZM2G111428'

'moderately similar to (290) AT3G21350 | Symbols: | RNA polymerase transcriptional regulation mediator-related | chr3:7517106-7518587 FORWARDmoderately similar to (407) loc_os06g11370 12006.m05854 protein RNA polymerase transcriptional regulation mediator, subunit 6, putative, expressed seq=cds; coord=9:7177254..7182212:-1; parent_gene=GRMZM2G017537'

'moderately similar to (483) AT1G76680 | Symbols: OPR1, ATOPR1 | OPR1; 12-oxophytodienoate reductase | chr1:28776982-28778271 FORWARDhighly similar to (601) loc_os06g11290 12006.m05846 protein 12-oxophytodienoate reductase 2, putative, expressed seq=cds; coord=9:7308153..7309906:1; parent_gene=GRMZM2G000236'

'moderately similar to (483) AT1G76680 | Symbols: OPR1, ATOPR1 | OPR1; 12-oxophytodienoate reductase | chr1:28776982-28778271 FORWARDhighly similar to (601) loc_os06g11290 12006.m05846 protein 12-oxophytodienoate reductase 2, putative, expressed seq=cds; coord=9:7308153..7309906:1; parent_gene=GRMZM2G000236'

'moderately similar to (454) AT1G73360 | Symbols: HDG11, EDT1, ATHDG11 | HDG11 (HOMEODOMAIN GLABROUS 11); DNA binding / transcription factor | chr1:27578893-27581820 REVERSEhighly similar to (659) loc_os06g10600 12006.m05778 protein DNA binding protein, putative, expressed seq=cds; coord=9:8971612..8975297:1; parent_gene=GRMZM2G062318'

'moderately similar to (408) AT3G62830 | Symbols: UXS2, ATUXS2 | AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase | chr3:23232539-23235353 FORWARDmoderately similar to (465) loc_os03g17230 12003.m07153 protein UDP-glucuronic acid decarboxylase 1, putative, expressed seq=cds; coord=9:138880653..138883538:1; parent_gene=GRMZM2G347717'

'moderately similar to (408) AT3G62830 | Symbols: UXS2, ATUXS2 | AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase | chr3:23232539-23235353 FORWARDmoderately similar to (465) loc_os03g17230 12003.m07153 protein UDP-glucuronic acid decarboxylase 1, putative, expressed seq=cds; coord=9:138880653..138883538:1; parent_gene=GRMZM2G347717'

'moderately similar to (330) AT1G64900 | Symbols: CYP89A2, CYP89 | CYP89A2 (CYTOCHROME P450 89A2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr1:24113283-24114803 FORWARDmoderately similar to (258) C77A3_SOYBN Cytochrome P450 77A3 (EC 1.14.-.-) - Glycine max (Soybean)moderately similar to (460) loc_os10g05020 12010.m03909 protein transposon protein, putative, unclassified, expressed seq=cds; coord=10:893976..895713:-1; parent_gene=GRMZM2G135536'

'nearly identical (1081) AT3G59420 | Symbols: ACR4 | ACR4 (ARABIDOPSIS CRINKLY4); kinase/ transmembrane receptor protein kinase | chr3:21959871-21962558 REVERSEnearly identical (1823) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1608) loc_os03g43670 12003.m09410 protein receptor protein kinase CRINKLY4 precursor, putative, expressed seq=cds; coord=10:5587952..5591862:1; parent_gene=GRMZM2G051637'

'weakly similar to (102) loc_os08g40620 12008.m26746 protein microtubule-associated protein, putative, expressed seq=cds; coord=10:19538082..19540456:1; parent_gene=GRMZM2G006206'

'weakly similar to (175) AT3G03860 | Symbols: ATAPRL5 | ATAPRL5 (APR-like 5) | chr3:992465-994315 FORWARDmoderately similar to (325) loc_os12g35640 12012.m07357 protein OsAPRL6 - Oryza sativa adenosine 5'-phosphosulfate reductase-like, expressed seq=cds; coord=10:24443942..24448936:-1; parent_gene=GRMZM2G141848'

'highly similar to (563) AT3G06350 | Symbols: EMB3004, MEE32 | MEE32 (MATERNAL EFFECT EMBRYO ARREST 32); 3-dehydroquinate dehydratase/ NADP or NADPH binding / binding / catalytic/ shikimate 5-dehydrogenase | chr3:1924536-1927701 REVERSEhighly similar to (792) loc_os12g34874 12012.m73984 protein shikimate dehydrogenase, putative, expressed seq=cds; coord=10:25975417..25980229:-1; parent_gene=GRMZM2G014376'

'weakly similar to (125) AT2G46870 | Symbols: NGA1 | NGA1 (NGATHA1); transcription factor | chr2:19261313-19262245 FORWARDweakly similar to (119) loc_os04g49230 12004.m09858 protein RAV transcription factor, putative, expressed seq=cds; coord=10:67362570..67363460:1; parent_gene=GRMZM2G423393'

'moderately similar to (253) AT3G24440 | Symbols: VRN5, VIL1 | VRN5 (VERNALIZATION 5) | chr3:8876207-8878171 REVERSEhighly similar to (569) loc_os05g05310 12005.m27699 protein fibronectin type III domain containing protein, expressed seq=cds; coord=10:89495479..89498597:-1; parent_gene=GRMZM2G339820'

'highly similar to (620) AT2G24240 | Symbols: | potassium channel tetramerisation domain-containing protein | chr2:10310838-10312163 FORWARDhighly similar to (833) loc_os04g42310 12004.m09202 protein K

'weakly similar to (103) AT1G61820 | Symbols: BGLU46 | BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds | chr1:22836707-22838444 FORWARDweakly similar to (152) loc_os04g43410 12004.m09304 protein beta-glucosidase homolog precursor, putative, expressed seq=cds; coord=10:130299046..130299754:-1; parent_gene=GRMZM2G031628' 'moderately similar to (313) AT4G30270 | Symbols: MERI5B, MERI-5, SEN4 | MERI5B (meristem-5); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase | chr4:14819445-14820448 REVERSEmoderately similar to (300) BRU1_SOYBN Brassinosteroid-regulated protein BRU1 precursor - Glycine max (Soybean)moderately similar to (436) loc_os04g51460 12004.m10042 protein xyloglucan endotransglucosylase/hydrolase protein 15 precursor, putative, expressed seq=cds; coord=10:141234026..141235309:1; parent_gene=GRMZM2G142857'

'weakly similar to (114) loc_os04g52530 12004.m10146 protein metal ion binding protein, putative, expressed seq=cds; coord=10:142368728..142370473:1; parent_gene=GRMZM2G354855'

'weakly similar to (114) loc_os04g52530 12004.m10146 protein metal ion binding protein, putative, expressed seq=cds; coord=10:142368728..142370473:1; parent_gene=GRMZM2G354855'

'weakly similar to (136) AT5G65420 | Symbols: CYCD4;1 | CYCD4;1 (CYCLIN D4;1); cyclin-dependent protein kinase regulator | chr5:26141592-26143750 REVERSEweakly similar to (197) loc_os09g29100 12009.m06061 protein cyclin delta-2, putative, expressed seq=cds; coord=10:145376015..145380746:1; parent_gene=GRMZM2G546369'

'weakly similar to (147) AT1G02065 | Symbols: SPL8 | SPL8 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 8); DNA binding | chr1:365625-367149 FORWARDhighly similar to (503) LG1_MAIZE LIGULELESS1 protein - Zea mays (Maize)moderately similar to (463) loc_os04g56170 12004.m10508 protein LIGULELESS1 protein, putative, expressed seq=cds; coord=10:146291533..146295099:-1; parent_gene=GRMZM2G058588'

'weakly similar to (152) AT3G59650 | Symbols: | mitochondrial ribosomal protein L51/S25/CI-B8 family protein | chr3:22033216-22033928 FORWARDweakly similar to (182) loc_os03g10930 12003.m06545 protein mitochondrial ribosomal protein L43, putative, expressed seq=cds; coord=1:21456899..21461749:1; parent_gene=GRMZM2G004259'

'very weakly similar to (96.3) AT1G49850 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:18455326-18456444 REVERSEmoderately similar to (368) loc_os03g10890 12003.m06541 protein RING-H2 finger protein, putative, expressed seq=cds; coord=1:21469310..21471441:-1; parent_gene=GRMZM2G004422'

'seq=cds; coord=1:21603261..21604413:-1; parent_gene=AC200038.4_FG011'

'moderately similar to (229) AT4G37580 | Symbols: HLS1, COP3, UNS2 | HLS1 (HOOKLESS 1); N-acetyltransferase | chr4:17658932-17660564 FORWARDmoderately similar to (366) loc_os03g10810 12003.m35083 protein HLS1, putative, expressed seq=cds; coord=1:21720856..21722289:1; parent_gene=GRMZM2G114184'

'moderately similar to (229) AT4G37580 | Symbols: HLS1, COP3, UNS2 | HLS1 (HOOKLESS 1); N-acetyltransferase | chr4:17658932-17660564 FORWARDmoderately similar to (366) loc_os03g10810 12003.m35083 protein HLS1, putative, expressed seq=cds; coord=1:21720856..21722289:1; parent_gene=GRMZM2G114184'

'highly similar to (581) AT2G40490 | Symbols: HEME2 | HEME2; uroporphyrinogen decarboxylase | chr2:16912961-16914988 FORWARDhighly similar to (677) DCUP_MAIZE Uroporphyrinogen decarboxylase, chloroplast precursor (EC 4.1.1.37) (URO-D) (UPD) - Zea mays (Maize)highly similar to (696) loc_os03g21900 12003.m07594 protein uroporphyrinogen decarboxylase, putative, expressed seq=cds; coord=1:56558221..56561693:1; parent_gene=GRMZM2G044074'

'moderately similar to (446) AT2G05940 | Symbols: | protein kinase, putative | chr2:2287514-2289270 REVERSEmoderately similar to (215) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (603) loc_os03g29410 12003.m08215 protein protein kinase APK1B, chloroplast precursor, putative, expressed seq=cds; coord=1:70768373..70772393:-1; parent_gene=GRMZM2G142390'

'moderately similar to (432) AT3G22750 | Symbols: | protein kinase, putative | chr3:8037364-8039096 REVERSEvery weakly similar to (99.4) NORK_MEDTR Nodulation receptor kinase precursor (EC 2.7.11.1) (Does not make infections protein 2) (Symbiosis receptor-like kinase) (MtSYMRK) - Medicago truncatula (Barrel medic)highly similar to (603) loc_os03g53410 12003.m10311 protein ATMRK1, putative, expressed seq=cds; coord=1:275646520..275650740:1; parent_gene=GRMZM2G131629'

'highly similar to (934) AT2G02220 | Symbols: ATPSKR1, PSKR1 | PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase | chr2:584098-587124 REVERSEhighly similar to (910) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1459) loc_os04g57630 12004.m10648 protein phytosulfokine receptor precursor, putative, expressed seq=cds; coord=2:2222100..2225911:1; parent_gene=GRMZM2G452142'

'nearly identical (1456) AT1G09620 | Symbols: | ATP binding / aminoacyl-tRNA ligase/ leucine-tRNA ligase/ nucleotide binding | chr1:3113077-3116455 REVERSEnearly identical (1784) loc_os09g32650 12009.m06352 protein leucyl-tRNA synthetase, cytoplasmic, putative, expressed seq=cds; coord=2:3098932..3104990:1; parent_gene=GRMZM2G071333'

'moderately similar to (318) AT3G61060 | Symbols: AtPP2-A13 | AtPP2-A13 (Arabidopsis thaliana phloem protein 2-A13); carbohydrate binding | chr3:22603166-22604336 FORWARDmoderately similar to (485) loc_os04g48270 12004.m35429 protein ATPP2-A13, putative, expressed seq=cds; coord=2:16654256..16656867:-1; parent_gene=GRMZM2G081032'

'weakly similar to (171) AT3G60720 | Symbols: PDLP8 | PDLP8 (PLASMODESMATA-LOCATED PROTEIN 8) | chr3:22442035-22443608 FORWARDmoderately similar to (305) loc_os04g45460 12004.m09499 protein secretory protein-like, putative, expressed seq=cds; coord=2:22574071..22577248:-1; parent_gene=GRMZM2G062471'

'moderately similar to (395) AT1G04020 | Symbols: ATBARD1, BARD1 | BARD1 (BREAST CANCER ASSOCIATED RING 1); DNA binding / transcription coactivator | chr1:1036610-1040045 FORWARDhighly similar to (882) loc_os04g43300 12004.m09294 protein ATBRCA1, putative, expressed seq=cds; coord=2:28673566..28677785:-1; parent_gene=GRMZM2G052688'

'moderately similar to (395) AT1G04020 | Symbols: ATBARD1, BARD1 | BARD1 (BREAST CANCER ASSOCIATED RING 1); DNA binding / transcription coactivator | chr1:1036610-1040045 FORWARDhighly similar to (882) loc_os04g43300 12004.m09294 protein ATBRCA1, putative, expressed seq=cds; coord=2:28673566..28677785:-1; parent_gene=GRMZM2G052688'

'weakly similar to (171) ATMG01275 | Symbols: NAD1A, NAD1, ND1 | Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C. | chrM:318004-318390 REVERSEweakly similar to (181) NU1M_OENBE NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3) (NADH dehydrogenase subunit 1) - Oenothera bertiana (Bertero's evening primrose) seq=cds; coord=9:68016311..68020591:1; parent_gene=GRMZM2G141605'

'moderately similar to (228) AT2G25810 | Symbols: TIP4;1 | TIP4;1 (tonoplast intrinsic protein 4;1); water channel | chr2:11012658-11013906 FORWARDmoderately similar to (287) TIP42_ORYSA Probable aquaporin TIP4.2 (Tonoplast intrinsic protein 4.2) (OsTIP4.2) - Oryza sativa (Rice)moderately similar to (287) loc_os01g13130 12001.m07923 protein aquaporin TIP4.1, putative, expressed seq=cds; coord=3:13529209..13532077:1; parent_gene=GRMZM2G146627'

'very weakly similar to (91.3) AT1G65870 | Symbols: | disease resistance-responsive family protein | chr1:24503624-24504193 FORWARDweakly similar to (169) loc_os07g42520 12007.m08484 protein dirigent-like protein pDIR12, putative, expressed seq=cds; coord=3:17116070..17116597:1; parent_gene=AC215260.3_FG001'

'very weakly similar to (91.3) AT1G65870 | Symbols: | disease resistance-responsive family protein | chr1:24503624-24504193 FORWARDweakly similar to (169) loc_os07g42520 12007.m08484 protein dirigent-like protein pDIR12, putative, expressed seq=cds; coord=3:17116070..17116597:1; parent_gene=AC215260.3_FG001'

'weakly similar to (152) AT1G53540 | Symbols: | 17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156) | chr1:19980510-19980983 FORWARDweakly similar to (179) HSP11_ORYSA 16.9 kDa class I heat shock protein 1 - Oryza sativa (Rice)weakly similar to (179) loc_os01g04370 12001.m07072 protein 16.9 kDa class I heat shock protein 1, putative, expressed seq=cds; coord=3:20425735..20426696:-1; parent_gene=GRMZM2G437100'

'moderately similar to (275) AT1G19660 | Symbols: | wound-responsive family protein | chr1:6800361-6802240 REVERSEmoderately similar to (422) loc_os01g50622 12001.m150696 protein wound inducive gene, putative, expressed seq=cds; coord=3:114083665..114087490:-1; parent_gene=GRMZM2G028665'

'weakly similar to (159) AT2G38090 | Symbols: | myb family transcription factor | chr2:15945278-15946775 FORWARDmoderately similar to (232) loc_os01g64360 12001.m12550 protein DNA binding protein, putative, expressed seq=cds; coord=3:176433983..176435494:-1; parent_gene=GRMZM2G027914'

'weakly similar to (182) AT5G15240 | Symbols: | amino acid transporter family protein | chr5:4947762-4950211 FORWARDmoderately similar to (288) loc_os01g41400 12001.m10407 protein amino acid permease, putative, expressed seq=cds; coord=3:222933071..222933984:-1; parent_gene=GRMZM2G476954'

'weakly similar to (135) AT3G25470 | Symbols: | bacterial hemolysin-related | chr3:9233039-9235022 FORWARDweakly similar to (166) loc_os11g14230 12011.m05560 protein hemolysin A, putative, expressed seq=cds; coord=4:12043149..12045067:-1; parent_gene=GRMZM2G010056'

'highly similar to (756) AT3G09100 | Symbols: | mRNA capping enzyme family protein | chr3:2788435-2792913 REVERSEnearly identical (1124) loc_os11g11070 12011.m80137 protein mRNA capping enzyme, putative, expressed seq=cds; coord=4:12580010..12609706:1; parent_gene=GRMZM2G030463' 'moderately similar to (358) AT5G44400 | Symbols: | FAD-binding domain-containing protein | chr5:17886365-17888071 REVERSEhighly similar to (615) loc_os11g30310 12011.m06940 protein reticuline oxidase precursor, putative seq=cds; coord=4:17740852..17742683:-1; parent_gene=GRMZM2G173105'

'weakly similar to (197) AT4G14465 | Symbols: | DNA-binding protein-related | chr4:8320972-8321817 FORWARDmoderately similar to (239) loc_os08g44910 12008.m08462 protein DNA-binding protein, putative, expressed seq=cds; coord=4:49728248..49730155:1; parent_gene=GRMZM2G173479'

'nearly identical (1048) AT3G44600 | Symbols: CYP71 | CYP71 (CYCLOPHILIN71); chromatin binding / histone binding / peptidyl-prolyl cis-trans isomerase | chr3:16165368-16169201 REVERSEweakly similar to (143) CYPB_VICFA Peptidyl-prolyl cis-trans isomerase, chloroplast precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) (CYP B) - Vicia faba (Broad bean)nearly identical (1172) loc_os08g44330 12008.m26789 protein peptidyl-prolyl cis-trans isomerase, putative, expressed seq=cds; coord=4:53440616..53446854:-1; parent_gene=GRMZM2G049525'

'weakly similar to (119) loc_os02g33710 12002.m08462 protein histidine decarboxylase, putative, expressed seq=cds; coord=4:112611130..112612458:1; parent_gene=AC217811.3_FG002'

'moderately similar to (452) AT4G14340 | Symbols: CKI1, CKL11 | CKI1 (CASEIN KINASE I); kinase/ protein serine/threonine kinase | chr4:8248532-8251668 REVERSEhighly similar to (595) loc_os02g40860 12002.m09171 protein casein kinase I isoform delta-like, putative, expressed seq=cds; coord=4:142153473..142160815:1; parent_gene=GRMZM2G162637'

'highly similar to (687) AT1G79640 | Symbols: | ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr1:29966913-29971387 REVERSEweakly similar to (152) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)highly similar to (865) loc_os02g54900 12002.m10518 protein STE20/SPS1-related proline-alanine-rich protein kinase, putative, expressed seq=cds; coord=4:174766200..174772539:-1; parent_gene=GRMZM2G135073'

'highly similar to (687) AT1G79640 | Symbols: | ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr1:29966913-29971387 REVERSEweakly similar to (152) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)highly similar to (865) loc_os02g54900 12002.m10518 protein STE20/SPS1-related proline-alanine-rich protein kinase, putative, expressed seq=cds; coord=4:174766200..174772539:-1; parent_gene=GRMZM2G135073'

'highly similar to (687) AT1G79640 | Symbols: | ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr1:29966913-29971387 REVERSEweakly similar to (152) M2K1_ORYSA Mitogen-activated protein kinase kinase 1 (EC 2.7.12.2) (MAP kinase kinase 1) (MAPKK1) (OsMEK1) - Oryza sativa (Rice)highly similar to (865) loc_os02g54900 12002.m10518 protein STE20/SPS1-related proline-alanine-rich protein kinase, putative, expressed seq=cds; coord=4:174766200..174772539:-1; parent_gene=GRMZM2G135073' 'highly similar to (658) AT1G19170 | Symbols: | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein | chr1:6616777-6618875 FORWARDweakly similar to (112) PGLR_ACTCH Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) - Actinidia chinensis (Kiwi) (Yangtao)highly similar to (592) loc_os09g26800 12009.m05832 protein polygalacturonase, putative, expressed seq=cds; coord=4:176647392..176650969:1; parent_gene=GRMZM2G047414'

'highly similar to (520) AT1G05380 | Symbols: | DNA binding | chr1:1577231-1582190 FORWARDhighly similar to (945) loc_os03g53630 12003.m10334 protein DNA binding protein, putative, expressed seq=cds; coord=5:7443884..7459423:-1; parent_gene=GRMZM2G087482'

'highly similar to (648) AT4G14680 | Symbols: APS3 | APS3; sulfate adenylyltransferase (ATP) | chr4:8413443-8415311 REVERSEhighly similar to (767) loc_os03g53230 12003.m10296 protein bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase, putative, expressed seq=cds; coord=5:7702248..7706223:1; parent_gene=GRMZM2G051270'

'moderately similar to (263) AT2G18980 | Symbols: | peroxidase, putative | chr2:8233419-8235294 REVERSEweakly similar to (182) PERP7_BRARA Peroxidase P7 (EC 1.11.1.7) (TP7) - Brassica rapa (Turnip)moderately similar to (396) loc_os06g48010 12006.m09327 protein peroxidase 16 precursor, putative, expressed seq=cds; coord=5:53198317..53200020:-1; parent_gene=GRMZM2G142011'

'moderately similar to (280) AT5G23730 | Symbols: | nucleotide binding | chr5:8005286-8006392 FORWARDweakly similar to (116) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)moderately similar to (453) loc_os02g02380 12002.m05587 protein SPA4, putative seq=cds; coord=5:69307253..69308503:-1; parent_gene=GRMZM2G389155'

'moderately similar to (280) AT5G23730 | Symbols: | nucleotide binding | chr5:8005286-8006392 FORWARDweakly similar to (116) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)moderately similar to (453) loc_os02g02380 12002.m05587 protein SPA4, putative seq=cds; coord=5:69307253..69308503:-1; parent_gene=GRMZM2G389155'

'moderately similar to (343) AT1G50440 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:18686099-18687646 FORWARDmoderately similar to (466) loc_os02g03950 12002.m33537 protein zinc finger, C3HC4 type family protein, expressed seq=cds; coord=5:74902955..74910523:1; parent_gene=GRMZM2G072142'

'weakly similar to (189) AT5G38020 | Symbols: | S-adenosyl-L-methionine:carboxyl methyltransferase family protein | chr5:15165953-15167612 REVERSEweakly similar to (186) BAMT_ANTMA Benzoate carboxyl methyltransferase (EC 2.1.1.-) (S-adenosyl-L-methionine:benzoic acid carboxyl methyltransferase) - Antirrhinum majus (Garden snapdragon)moderately similar to (322) loc_os06g13310 12006.m06046 protein benzoate carboxyl methyltransferase, putative seq=cds; coord=5:77571906..77574552:1; parent_gene=GRMZM2G303419'

'moderately similar to (438) AT4G30200 | Symbols: VEL1 | Encodes a protein with similarity to VRN5 and VIN3.Contains both a fibronectin III and PHD finger domain. VEL1 is a part of a polycomb repressive complex (PRC2) that is involved in epigenetic silencing of the FLC flowering locus. | chr4:14786852-14790070 REVERSEnearly identical (1080) loc_os02g05840 12002.m05932 protein expressed protein seq=cds; coord=5:80828457..80835734:-1; parent_gene=GRMZM2G425774' 'very weakly similar to (82.8) AT1G71450 | Symbols: | AP2 domain-containing transcription factor, putative | chr1:26927088-26927639 FORWARDweakly similar to (166) loc_os02g35240 12002.m08612 protein dehydration-responsive element-binding protein 1A, putative seq=cds; coord=5:174160362..174160921:1; parent_gene=GRMZM2G087040'

'weakly similar to (107) AT3G01490 | Symbols: | protein kinase, putative | chr3:191095-193258 REVERSEweakly similar to (114) loc_os01g45380 12001.m10741 protein ATP binding protein, putative, expressed seq=cds; coord=5:185221807..185225537:1; parent_gene=GRMZM2G463711'

'weakly similar to (149) AT5G40370 | Symbols: | glutaredoxin, putative | chr5:16147826-16148900 REVERSEweakly similar to (155) GLRX_ORYSA Glutaredoxin - Oryza sativa (Rice)weakly similar to (166) loc_os02g40500 12002.m09136 protein OsGrx_C2.1 - glutaredoxin subgroup I, expressed seq=cds; coord=5:185405145..185408787:1; parent_gene=GRMZM2G148387'

'moderately similar to (392) AT5G51740 | Symbols: | peptidase M48 family protein | chr5:21017110-21018987 FORWARDhighly similar to (577) loc_os02g50230 12002.m10057 protein peptidase family M48 containing protein, expressed seq=cds; coord=5:205230215..205235779:1; parent_gene=GRMZM2G090981'

'highly similar to (629) AT1G59900 | Symbols: AT-E1 ALPHA | AT-E1 ALPHA; oxidoreductase, acting on the aldehyde or oxo group of donors, disulfide as acceptor / pyruvate dehydrogenase (acetyl-transferring) | chr1:22051368-22053660 FORWARDhighly similar to (631) ODPA_SOLTU Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) - Solanum tuberosum (Potato)highly similar to (712) loc_os02g50620 12002.m10096 protein pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor, putative, expressed seq=cds; coord=5:205777032..205781614:-1; parent_gene=GRMZM2G140150'

'moderately similar to (273) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEhighly similar to (542) loc_os06g20190 12006.m06676 protein aspartic proteinase nepenthesin-2 precursor, putative seq=cds; coord=6:120847595..120849186:1; parent_gene=GRMZM2G174129'

'very weakly similar to (81.3) AT2G35040 | Symbols: | AICARFT/IMPCHase bienzyme family protein | chr2:14765347-14768269 REVERSEvery weakly similar to (82.4) loc_os08g10570 12008.m26473 protein bifunctional purine biosynthesis protein purH, putative, expressed seq=cds; coord=6:121022185..121024287:1; parent_gene=GRMZM2G164665'

'very weakly similar to (83.6) loc_os05g06890 12005.m05216 protein relA-SpoT like protein RSH4, putative, expressed seq=cds; coord=6:125189402..125190276:-1; parent_gene=GRMZM2G152040'

'moderately similar to (426) AT5G20490 | Symbols: XIK, ATXIK, XI-17 | XIK; motor/ protein binding | chr5:6927064 6936079 REVERSEmoderately similar to (498) loc_os05g46030 12005.m08728 protein myosin head family protein, expressed seq=cds; coord=6:161483674..161486706:1; parent_gene=GRMZM2G445423'

'weakly similar to (102) AT3G21330 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr3:7507720-7508841 FORWARDweakly similar to (130) loc_os05g46370 12005.m08762 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=6:161863300..161865047:1; parent_gene=GRMZM2G094892' 'highly similar to (932) AT1G24510 | Symbols: | T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative | chr1:8685504-8687660 REVERSEhighly similar to (941) TCPE2_AVESA T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon) (TCP-K36) - Avena sativa (Oat)highly similar to (985) loc_os06g36700 12006.m08205 protein T-complex protein 1 subunit epsilon, putative, expressed seq=cds; coord=7:2584958..2590700:-1; parent_gene=GRMZM2G043383'

'moderately similar to (308) AT4G08150 | Symbols: KNAT1, BP, BP1 | KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor | chr4:5147969-5150610 REVERSEmoderately similar to (463) RSH1_MAIZE Homeobox protein rough sheath 1 - Zea mays (Maize)moderately similar to (427) loc_os07g03770 12007.m04847 protein homeobox protein rough sheath 1, putative, expressed seq=cds; coord=7:3664698..3670891:1; parent_gene=GRMZM2G028041'

'weakly similar to (111) AT3G28920 | Symbols: AtHB34 | AtHB34 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 34); DNA binding / transcription factor | chr3:10940598-10941536 REVERSEmoderately similar to (258) loc_os09g24820 12009.m05636 protein ZF-HD homeobox protein, putative, expressed seq=cds; coord=7:112875599..112877310:1; parent_gene=GRMZM2G161315'

'highly similar to (682) AT4G02050 | Symbols: | sugar transporter, putative | chr4:898387-900095 REVERSEhighly similar to (651) STA_RICCO Sugar carrier protein A - Ricinus communis (Castor bean)highly similar to (743) loc_os09g24924 12009.m05646 protein sugar carrier protein A, putative, expressed seq=cds; coord=7:113163366..113166072:1; parent_gene=GRMZM2G029153'

'moderately similar to (302) AT2G23810 | Symbols: TET8 | TET8 (TETRASPANIN8) | chr2:10135859-10137352 REVERSEmoderately similar to (396) loc_os09g25760 12009.m05728 protein senescence-associated protein DH, putative, expressed seq=cds; coord=7:118310662..118312830:1; parent_gene=GRMZM2G041175'

'weakly similar to (133) AT5G63370 | Symbols: | protein kinase family protein | chr5:25384954-25386390 REVERSEweakly similar to (107) MPK16_ORYSA Mitogen-activated protein kinase 16 (EC 2.7.11.24) (MAP kinase 16) - Oryza sativa (Rice)moderately similar to (265) loc_os09g27350 12009.m05887 protein protein kinase domain containing protein seq=cds; coord=7:122987242..122988347:1; parent_gene=GRMZM2G396350'

'nearly identical (1006) AT5G54830 | Symbols: | DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein | chr5:22273394-22276117 FORWARDnearly identical (1452) loc_os09g38520 12009.m06793 protein DOMON domain containing protein, expressed seq=cds; coord=7:145913776..145916844:1; parent_gene=GRMZM2G041394'

'moderately similar to (398) AT3G29770 | Symbols: ATMES11, MES11 | MES11 (METHYL ESTERASE 11); hydrolase | chr3:11648471-11650565 FORWARDweakly similar to (154) PIR7A_ORYSA Probable esterase PIR7A (EC 3.1.-.-) - Oryza sativa (Rice)highly similar to (550) loc_os07g41230 12007.m08359 protein esterase PIR7B, putative, expressed seq=cds; coord=7:163964195..163968081:1; parent_gene=GRMZM2G151801' 'very weakly similar to (93.6) AT5G58420 | Symbols: | 40S ribosomal protein S4 (RPS4D) | chr5:23619599-23620896 FORWARDvery weakly similar to (100) RS4_ORYSA 40S ribosomal protein S4 (SCAR protein SS620) - Oryza sativa (Rice)very weakly similar to (100) loc_os02g01560 12002.m05506 protein 40S ribosomal protein S4, putative, expressed seq=cds; coord=7:175395356..175396189:1; parent_gene=GRMZM2G086656'

'highly similar to (550) AT5G53350 | Symbols: CLPX | CLPX; ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding | chr5:21644060-21647503 FORWARDhighly similar to (840) loc_os01g66330 12001.m12741 protein ATP-dependent Clp protease ATP-binding subunit clpX, putative, expressed seq=cds; coord=8:164810797..164816886:1; parent_gene=GRMZM2G172829'

'moderately similar to (434) AT4G06599 | Symbols: | ubiquitin family protein | chr4:3666079-3667495 REVERSEmoderately similar to (500) loc_os01g65450 12001.m150790 protein ubiquitin-like domain containing CTD phosphatase 1, putative, expressed seq=cds; coord=8:165678358..165682072:1; parent_gene=GRMZM2G114172'

'moderately similar to (286) AT1G36370 | Symbols: SHM7 | SHM7 (serine hydroxymethyltransferase 7); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding | chr1:13696240-13698576 REVERSEweakly similar to (158) GLYM_SOLTU Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1) (Serine methylase) (Glycine hydroxymethyltransferase) (SHMT) - Solanum tuberosum (Potato)moderately similar to (334) loc_os01g65410 12001.m12653 protein serine hydroxymethyltransferase, mitochondrial precursor, putative, expressed seq=cds; coord=8:165728910..165730561:-1; parent_gene=GRMZM2G113959'

'moderately similar to (286) AT1G36370 | Symbols: SHM7 | SHM7 (serine hydroxymethyltransferase 7); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding | chr1:13696240-13698576 REVERSEweakly similar to (158) GLYM_SOLTU Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1) (Serine methylase) (Glycine hydroxymethyltransferase) (SHMT) - Solanum tuberosum (Potato)moderately similar to (334) loc_os01g65410 12001.m12653 protein serine hydroxymethyltransferase, mitochondrial precursor, putative, expressed seq=cds; coord=8:165728910..165730561:-1; parent_gene=GRMZM2G113959'

'moderately similar to (286) AT1G36370 | Symbols: SHM7 | SHM7 (serine hydroxymethyltransferase 7); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding | chr1:13696240-13698576 REVERSEweakly similar to (158) GLYM_SOLTU Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1) (Serine methylase) (Glycine hydroxymethyltransferase) (SHMT) - Solanum tuberosum (Potato)moderately similar to (334) loc_os01g65410 12001.m12653 protein serine hydroxymethyltransferase, mitochondrial precursor, putative, expressed seq=cds; coord=8:165728910..165730561:-1; parent_gene=GRMZM2G113959'

'weakly similar to (181) AT2G40330 | Symbols: | Bet v I allergen family protein | chr2:16845177-16845824 REVERSEmoderately similar to (208) loc_os05g39580 12005.m08136 protein AT-rich element binding factor 3, putative, expressed seq=cds; coord=8:169996084..170002291:-1; parent_gene=GRMZM2G169695' 'moderately similar to (279) AT2G20110 | Symbols: | tesmin/TSO1-like CXC domain-containing protein | chr2:8684496-8686870 FORWARDmoderately similar to (485) loc_os01g55580 12001.m43204 protein tesmin/TSO1-like CXC domain containing protein, expressed seq=cds; coord=8:173389290..173393839:1; parent_gene=GRMZM2G104246'

'moderately similar to (279) AT2G20110 | Symbols: | tesmin/TSO1-like CXC domain-containing protein | chr2:8684496-8686870 FORWARDmoderately similar to (485) loc_os01g55580 12001.m43204 protein tesmin/TSO1-like CXC domain containing protein, expressed seq=cds; coord=8:173389290..173393839:1; parent_gene=GRMZM2G104246'

'weakly similar to (157) AT5G66190 | Symbols: ATLFNR1 | FNR1 (FERREDOXIN-NADP(

'weakly similar to (186) AT3G08570 | Symbols: | protein binding / signal transducer | chr3:2602258-2604412 REVERSEweakly similar to (135) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)moderately similar to (277) loc_os12g02540 12012.m04255 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=10:3184922..3188148:1; parent_gene=GRMZM2G058531'

'weakly similar to (120) AT3G14470 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4857940-4861104 FORWARDhighly similar to (719) loc_os01g57340 12001.m11885 protein rp1-like protein, putative, expressed seq=cds; coord=10:3764373..3766967:-1; parent_gene=GRMZM2G349565'

'moderately similar to (286) AT4G20860 | Symbols: | FAD-binding domain-containing protein | chr4:11172726-11174318 FORWARDhighly similar to (630) loc_os08g06190 12008.m04758 protein reticuline oxidase precursor, putative, expressed seq=cds; coord=10:78060284..78062034:1; parent_gene=GRMZM2G078906'

'weakly similar to (140) AT4G16270 | Symbols: | peroxidase 40 (PER40) (P40) | chr4:9205038-9206483 FORWARDweakly similar to (132) PERN_IPOBA Neutral peroxidase precursor (EC 1.11.1.7) (SwPN1) - Ipomoea batatas (Sweet potato) (Batate)moderately similar to (279) loc_os05g04410 12005.m04974 protein peroxidase 2 precursor, putative, expressed seq=cds; coord=10:85683513..85689992:1; parent_gene=GRMZM2G006727'

'weakly similar to (157) AT3G09980 | Symbols: | unknown protein | chr3:3069358-3071145 FORWARDmoderately similar to (218) loc_os04g33450 12004.m35299 protein expressed protein seq=cds; coord=10:113709280..113710910:-1; parent_gene=GRMZM2G147390'

'weakly similar to (101) loc_os03g20760 12003.m07483 protein lipid binding protein, putative, expressed seq=cds; coord=1:52625970..52627201:-1; parent_gene=GRMZM2G174680' 'weakly similar to (199) AT1G12140 | Symbols: FMO GS-OX5 | FMO GS-OX5 (FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5); 8-methylthiopropyl glucosinolate S-oxygenase/ flavin-containing monooxygenase/ monooxygenase | chr1:4121386-4123366 FORWARDmoderately similar to (263) loc_os10g40610 12010.m06829 protein disulfide oxidoreductase/ monooxygenase, putative, expressed seq=cds; coord=1:92342987..92345452:1; parent_gene=GRMZM2G425719'

'moderately similar to (351) AT5G47100 | Symbols: CBL9 | CBL9; calcium ion binding | chr5:19129896-19131727 REVERSEmoderately similar to (402) loc_os10g41510 12010.m06915 protein calcineurin B-like protein 9, putative, expressed seq=cds; coord=1:94985068..94989733:1; parent_gene=GRMZM2G107575'

'highly similar to (562) AT3G22330 | Symbols: PMH2 | PMH2 (putative mitochondrial RNA helicase 2); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding | chr3:7892641-7895145 FORWARDmoderately similar to (291) RH7_SPIOL DEAD-box ATP-dependent RNA helicase 7 (EC 3.6.1.-) - Spinacia oleracea (Spinach)highly similar to (588) loc_os07g05050 12007.m04971 protein nucleolar RNA helicase 2, putative, expressed seq=cds; coord=1:172936435..172940871:-1; parent_gene=GRMZM2G107984'

'weakly similar to (131) AT1G30500 | Symbols: NF-YA7 | NF-YA7 (NUCLEAR FACTOR Y, SUBUNIT A7); specific transcriptional repressor/ transcription factor | chr1:10804736-10805896 REVERSEmoderately similar to (290) loc_os12g41880 12012.m26973 protein nuclear transcription factor Y subunit A-7, putative, expressed seq=cds; coord=1:173316803..173321819:-1; parent_gene=GRMZM2G361842'

'weakly similar to (171) AT4G36260 | Symbols: STY2, SRS2 | STY2 (STYLISH 2); transcription factor | chr4:17155705-17157006 REVERSEmoderately similar to (244) loc_os08g43410 12008.m08315 protein SHI, putative, expressed seq=cds; coord=1:207389667..207391680:1; parent_gene=GRMZM2G042407'

'moderately similar to (335) AT1G14270 | Symbols: | CAAX amino terminal protease family protein | chr1:4875099-4876443 REVERSEmoderately similar to (419) loc_os09g24670 12009.m60228 protein CAAX amino terminal protease family protein, putative, expressed seq=cds; coord=1:212977758..212982384:-1; parent_gene=GRMZM2G152485'

'moderately similar to (446) AT2G35160 | Symbols: SUVH5, SGD9 | SUVH5 (SU(VAR)3-9 HOMOLOG 5); histone methyltransferase | chr2:14823562-14825946 FORWARDhighly similar to (683) loc_os08g30910 12008.m07091 protein YDG/SRA domain containing protein, expressed seq=cds; coord=1:220005584..220009243:-1; parent_gene=GRMZM2G074094'

'moderately similar to (384) AT1G61790 | Symbols: | OST3/OST6 family protein | chr1:22814390-22815430 FORWARDhighly similar to (535) loc_os03g36730 12003.m08792 protein oligosaccharide transporter, putative, expressed seq=cds; coord=1:222130457..222134768:1; parent_gene=GRMZM2G149946'

'highly similar to (687) AT5G37020 | Symbols: ARF8 | ARF8 (AUXIN RESPONSE FACTOR 8); transcription factor | chr5:14630151-14633916 FORWARDnearly identical (1283) loc_os04g57610 12004.m35224 protein auxin response factor 8, putative, expressed seq=cds; coord=2:2266715..2274671:1; parent_gene=GRMZM2G078274'

'highly similar to (687) AT5G37020 | Symbols: ARF8 | ARF8 (AUXIN RESPONSE FACTOR 8); transcription factor | chr5:14630151-14633916 FORWARDnearly identical (1283) loc_os04g57610 12004.m35224 protein auxin response factor 8, putative, expressed seq=cds; coord=2:2266715..2274671:1; parent_gene=GRMZM2G078274' 'nearly identical (1518) AT4G30190 | Symbols: AHA2, PMA2 | AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism | chr4:14770820-14775920 REVERSEnearly identical (1675) PMA1_ORYSA Plasma membrane ATPase (EC 3.6.3.6) (Proton pump) - Oryza sativa (Rice)nearly identical (1675) loc_os04g56160 12004.m101441 protein plasma membrane ATPase, putative, expressed seq=cds; coord=2:4299718..4306692:-1; parent_gene=GRMZM2G019404'

'highly similar to (883) AT1G23090 | Symbols: AST91, SULTR3;3 | AST91 (SULFATE TRANSPORTER 91); sulfate transmembrane transporter | chr1:8185238-8188954 REVERSEmoderately similar to (348) NO70_SOYBN Early nodulin 70 - Glycine max (Soybean)nearly identical (1099) loc_os04g55800 12004.m10471 protein sulfate transporter 3.3, putative, expressed seq=cds; coord=2:4890135..4895146:1; parent_gene=GRMZM2G395114'

'moderately similar to (489) loc_os04g40720 12004.m09052 protein expressed protein seq=cds; coord=2:36767527..36778587:-1; parent_gene=GRMZM2G063163'

'weakly similar to (155) loc_os04g39980 12004.m08982 protein gibberellin 20 oxidase 2, putative, expressed seq=cds; coord=2:38192410..38193491:1; parent_gene=GRMZM2G121700'

'weakly similar to (147) AT4G02840 | Symbols: | small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative | chr4:1264726-1266253 FORWARDweakly similar to (151) loc_os04g39444 12004.m101729 protein small nuclear ribonucleoprotein Sm D1, putative, expressed seq=cds; coord=2:39420411..39422539:1; parent_gene=GRMZM2G027571'

'weakly similar to (147) AT4G02840 | Symbols: | small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative | chr4:1264726-1266253 FORWARDweakly similar to (151) loc_os04g39444 12004.m101729 protein small nuclear ribonucleoprotein Sm D1, putative, expressed seq=cds; coord=2:39420411..39422539:1; parent_gene=GRMZM2G027571'

'weakly similar to (106) loc_os09g29820 12009.m06133 protein BZIP family transcription factor, putative, expressed seq=cds; coord=2:188366213..188366707:-1; parent_gene=GRMZM2G137532'

'weakly similar to (130) AT1G56170 | Symbols: HAP5B, ATHAP5B, NF-YC2 | NF-YC2 (NUCLEAR FACTOR Y, SUBUNIT C2); DNA binding / transcription activator/ transcription factor | chr1:21025118-21025717 FORWARDweakly similar to (141) loc_os09g30310 12009.m06182 protein nuclear transcription factor Y subunit C-2, putative, expressed seq=cds; coord=2:189204687..189208176:-1; parent_gene=GRMZM2G022162'

'moderately similar to (485) AT4G39170 | Symbols: | SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative | chr4:18240887-18243621 FORWARDhighly similar to (822) loc_os09g30330 12009.m06184 protein phosphatidylinositol transporter/ transporter, putative, expressed seq=cds; coord=2:189219156..189224929:1; parent_gene=GRMZM2G031837'

'moderately similar to (434) AT3G20810 | Symbols: | transcription factor jumonji (jmjC) domain-containing protein | chr3:7275814-7278182 FORWARDhighly similar to (523) loc_os09g31380 12009.m06252 protein conserved hypothetical protein seq=cds; coord=2:189777176..189782078:1; parent_gene=GRMZM2G052908' 'moderately similar to (231) AT5G35330 | Symbols: MBD02, MBD2 | MBD02 (METHYL-CPG-BINDING DOMAIN PROTEIN 02); DNA binding / DNA demethylase | chr5:13523725-13525270 REVERSEmoderately similar to (386) loc_os09g32090 12009.m50206 protein methyl-binding domain protein MBD111, putative, expressed seq=cds; coord=2:190664560..190686734:-1; parent_gene=GRMZM2G025095'

'very weakly similar to (87.0) AT1G72310 | Symbols: ATL3 | ATL3; protein binding / zinc ion binding | chr1:27226405-27227379 FORWARDvery weakly similar to (80.9) EL5_ORYSA E3 ubiquitin-protein ligase EL5 (EC 6.3.2.-) - Oryza sativa (Rice)weakly similar to (154) loc_os07g42610 12007.m08493 protein ring-H2 zinc finger protein, putative, expressed seq=cds; coord=2:211590201..211591615:-1; parent_gene=GRMZM2G358987'

'highly similar to (734) AT4G26270 | Symbols: PFK3 | PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase | chr4:13301094-13304030 REVERSEhighly similar to (939) loc_os01g09570 12001.m07582 protein 6-phosphofructokinase 2, putative, expressed seq=cds; coord=3:6801004..6804943:-1; parent_gene=GRMZM2G132069'

'nearly identical (1256) AT2G26910 | Symbols: PDR4, ATPDR4 | PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances | chr2:11481623-11487874 FORWARDnearly identical (1686) PDR6_ORYSA Pleiotropic drug resistance protein 6 - Oryza sativa (Rice)nearly identical (1060) loc_os02g11760 12002.m06425 protein PDR5-like ABC transporter, putative, expressed seq=cds; coord=3:10273100..10283228:1; parent_gene=GRMZM2G118243'

'highly similar to (659) AT2G26710 | Symbols: BAS1, CYP734A1, CYP72B1 | BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase | chr2:11380700-11383413 FORWARDmoderately similar to (372) C72A1_CATRO Cytochrome P450 72A1 (EC 1.3.3.9) (CYPLXXII) (Secologanin synthase) (SLS) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)highly similar to (836) loc_os01g29150 12001.m09352 protein cytochrome P450 72A1, putative, expressed seq=cds; coord=3:11212000..11215671:1; parent_gene=GRMZM2G138750'

'very weakly similar to (94.4) loc_os01g24950 12001.m150578 protein exocyst complex subunit Sec15-like family protein, expressed seq=cds; coord=3:175323602..175324361:-1; parent_gene=GRMZM2G439532'

'highly similar to (684) AT2G38110 | Symbols: ATGPAT6, GPAT6 | GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase | chr2:15952816-15955364 REVERSEhighly similar to (835) loc_os01g63580 12001.m12474 protein glycerol-3-phosphate acyltransferase 8, putative, expressed seq=cds; coord=3:178181704..178185282:1; parent_gene=GRMZM2G083195'

'weakly similar to (139) AT5G05960 | Symbols: | protease inhibitor/seed storage/lipid transfer protein (LTP) family protein | chr5:1790256-1790694 FORWARDmoderately similar to (201) loc_os01g62980 12001.m43276 protein lipid binding protein, putative, expressed seq=cds; coord=3:179414637..179416401:1; parent_gene=GRMZM2G065557'

'moderately similar to (290) AT1G30350 | Symbols: | pectate lyase family protein | chr1:10710194-10711664 REVERSEmoderately similar to (259) PEL_LILLO Pectate lyase precursor (EC 4.2.2.2) - Lilium longiflorum (Trumpet lily)moderately similar to (474) loc_os08g18970 12008.m05967 protein major pollen allergen Jun a 1 precursor, putative seq=cds; coord=3:189464384..189466218:1; parent_gene=AC233851.1_FG011' 'weakly similar to (176) AT1G28420 | Symbols: HB-1 | HB-1 (homeobox-1); transcription factor | chr1:9979936-9987460 FORWARDhighly similar to (577) loc_os01g48180 12001.m11010 protein DDT domain containing protein, expressed seq=cds; coord=3:210103369..210107016:-1; parent_gene=GRMZM2G002548'

'weakly similar to (178) AT1G28600 | Symbols: | lipase, putative | chr1:10051604-10053073 REVERSEvery weakly similar to (86.7) EST_HEVBR Esterase precursor (EC 3.1.1.-) (Early nodule-specific protein homolog) (Latex allergen Hev b 13) - Hevea brasiliensis (Para rubber tree)weakly similar to (194) loc_os01g42730 12001.m10537 protein alpha-L-fucosidase 2 precursor, putative, expressed seq=cds; coord=3:213800866..213804340:-1; parent_gene=GRMZM2G047129'

'highly similar to (505) AT1G53240 | Symbols: | malate dehydrogenase (NAD), mitochondrial | chr1:19854966-19856802 REVERSEhighly similar to (508) MDHM_FRAAN Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Fragaria ananassa (Strawberry)highly similar to (587) loc_os01g46070 12001.m10806 protein malate dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=3:213896741..213905427:1; parent_gene=GRMZM2G466833'

'moderately similar to (241) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (341) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215431519..215437533:-1; parent_gene=GRMZM2G348512'

'moderately similar to (245) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (340) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215466579..215473931:-1; parent_gene=GRMZM2G121878'

'weakly similar to (159) AT5G44340 | Symbols: TUB4 | TUB4; structural constituent of cytoskeleton | chr5:17859442-17860994 REVERSEweakly similar to (171) TBB7_MAIZE Tubulin beta-7 chain (Beta-7 tubulin) - Zea mays (Maize)weakly similar to (169) loc_os02g07060 12002.m06053 protein tubulin beta-5 chain, putative, expressed seq=cds; coord=4:32162277..32162762:1; parent_gene=AC203909.3_FG006'

'highly similar to (528) AT3G47520 | Symbols: MDH | MDH (MALATE DEHYDROGENASE); L-malate dehydrogenase/ binding / catalytic/ malate dehydrogenase/ oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor | chr3:17513657-17514868 FORWARDmoderately similar to (390) MDHG_ORYSA Malate dehydrogenase, glyoxysomal precursor (EC 1.1.1.37) - Oryza sativa (Rice)highly similar to (650) loc_os08g33720 12008.m07362 protein malate dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=4:83505768..83508091:1; parent_gene=GRMZM2G068455'

'very weakly similar to (94.4) AT2G41940 | Symbols: ZFP8 | ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding | chr2:17507556-17508329 FORWARDweakly similar to (187) loc_os02g53530 12002.m10382 protein zinc finger protein, putative, expressed seq=cds; coord=4:177327886..177329473:1; parent_gene=GRMZM2G121151' 'moderately similar to (251) AT5G64930 | Symbols: CPR5, HYS1 | CPR5 (CONSTITUTIVE EXPRESSION OF PR GENES 5) | chr5:25945885-25948321 REVERSEhighly similar to (576) loc_os02g53070 12002.m10337 protein HYS1, putative, expressed seq=cds; coord=4:178037799..178042552:1; parent_gene=GRMZM2G158811'

'moderately similar to (251) AT5G64930 | Symbols: CPR5, HYS1 | CPR5 (CONSTITUTIVE EXPRESSION OF PR GENES 5) | chr5:25945885-25948321 REVERSEhighly similar to (576) loc_os02g53070 12002.m10337 protein HYS1, putative, expressed seq=cds; coord=4:178037799..178042552:1; parent_gene=GRMZM2G158811'

'moderately similar to (399) AT1G77800 | Symbols: | PHD finger family protein | chr1:29253800-29260190 FORWARDhighly similar to (842) loc_os02g52960 12002.m10326 protein PHD-finger family protein, expressed seq=cds; coord=4:178229465..178238103:1; parent_gene=GRMZM2G475583'

'very weakly similar to (98.6) AT1G21910 | Symbols: | AP2 domain-containing transcription factor family protein | chr1:7696655-7697347 FORWARDweakly similar to (167) loc_os06g10780 12006.m05795 protein DNA binding protein, putative, expressed seq=cds; coord=4:178386285..178387653:1; parent_gene=GRMZM2G011110'

'nearly identical (1220) AT2G07050 | Symbols: CAS1 | CAS1 (cycloartenol synthase 1); cycloartenol synthase | chr2:2924629-2930295 FORWARDnearly identical (1393) loc_os02g04710 12002.m33547 protein cycloartenol synthase, putative, expressed seq=cds; coord=4:237767177..237775740:1; parent_gene=GRMZM2G065494'

'moderately similar to (394) AT5G26680 | Symbols: | endonuclease, putative | chr5:9311882-9315458 REVERSEmoderately similar to (474) FEN1B_ORYSA Flap endonuclease 1b (EC 3.1.-.-) (OsFEN-1b) - Oryza sativa (Rice)moderately similar to (474) loc_os03g61820 12003.m11063 protein flap endonuclease 1b, putative, expressed seq=cds; coord=5:1879148..1895175:1; parent_gene=GRMZM2G398668'

'highly similar to (618) AT5G38640 | Symbols: | eukaryotic translation initiation factor 2B family protein / eIF-2B family protein | chr5:15468020-15470674 REVERSEhighly similar to (832) loc_os03g44310 12003.m09470 protein translation initiation factor eIF-2B delta subunit, putative, expressed seq=cds; coord=5:17058108..17064678:1; parent_gene=GRMZM2G018943'

'highly similar to (655) AT5G15650 | Symbols: RGP2, ATRGP2 | RGP2 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 2); transferase, transferring hexosyl groups | chr5:5092203-5094093 FORWARDhighly similar to (739) UPTG_MAIZE Alpha-1,4-glucan-protein synthase [UDP-forming] (EC 2.4.1.112) (UDP-glucose:protein transglucosylase) (UPTG) (Amylogenin) (Golgi-associated protein se-wap41) - Zea mays (Maize)highly similar to (714) loc_os03g40270 12003.m35306 protein alpha-1,4-glucan-protein synthase, putative, expressed seq=cds; coord=5:18767810..18770458:1; parent_gene=GRMZM2G087326'

'moderately similar to (411) AT1G52870 | Symbols: | peroxisomal membrane protein-related | chr1:19685856-19687678 FORWARDhighly similar to (536) loc_os03g38730 12003.m35298 protein mpv17 / PMP22 family protein, expressed seq=cds; coord=5:19890055..19894035:1; parent_gene=GRMZM2G001724' 'moderately similar to (253) AT1G33260 | Symbols: | protein kinase family protein | chr1:12064796-12066114 FORWARDweakly similar to (166) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (478) loc_os10g37190 12010.m06516 protein protein kinase domain containing protein, expressed seq=cds; coord=5:22355892..22357850:1; parent_gene=GRMZM2G166719'

'highly similar to (600) AT4G36195 | Symbols: | serine carboxypeptidase S28 family protein | chr4:17127202-17129787 FORWARDhighly similar to (748) loc_os10g36780 12010.m06484 protein prolyl carboxypeptidase like protein, putative, expressed seq=cds; coord=5:22758895..22762980:-1; parent_gene=GRMZM2G082502'

'weakly similar to (188) AT2G46910 | Symbols: | plastid-lipid associated protein PAP / fibrillin family protein | chr2:19272427-19273856 FORWARD seq=cds; coord=5:23255313..23259490:-1; parent_gene=GRMZM2G026800'

'moderately similar to (448) AT1G02050 | Symbols: | chalcone and stilbene synthase family protein | chr1:359164-360441 REVERSEmoderately similar to (261) THS1_VITVI Stilbene synthase 1 (EC 2.3.1.95) (Resveratrol synthase 1) (Trihydroxystilbene synthase 1) (PSV25) - Vitis vinifera (Grape)highly similar to (619) loc_os10g34360 12010.m06262 protein chalcone synthase G, putative, expressed seq=cds; coord=5:26971466..26975726:1; parent_gene=GRMZM2G477683'

'weakly similar to (122) AT1G06890 | Symbols: | transporter-related | chr1:2111728-2114038 REVERSEweakly similar to (158) loc_os10g33920 12010.m065290 protein integral membrane protein like, putative, expressed seq=cds; coord=5:28086355..28088103:-1; parent_gene=GRMZM2G462081'

'moderately similar to (329) AT1G69530 | Symbols: ATEXPA1, EXP1, AT-EXP1, ATEXP1, ATHEXP ALPHA 1.2 | ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1) | chr1:26142034-26143200 FORWARDmoderately similar to (395) EXPA5_ORYSA Expansin-A5 precursor (OsEXPA5) (Alpha-expansin-5) (OsEXP5) (OsaEXPa1.20) - Oryza sativa (Rice)moderately similar to (395) loc_os02g51040 12002.m10138 protein alpha-expansin 15 precursor, putative, expressed seq=cds; coord=5:206838596..206840547:1; parent_gene=GRMZM2G105844'

'moderately similar to (330) AT1G26870 | Symbols: FEZ, ANAC009 | FEZ (FEZ); transcription factor | chr1:9312856-9314983 FORWARDweakly similar to (194) NAC68_ORYSA NAC domain-containing protein 68 (ONAC068) - Oryza sativa (Rice)moderately similar to (338) loc_os08g33910 12008.m07381 protein NAC domain-containing protein 9, putative, expressed seq=cds; coord=5:206975367..206978937:1; parent_gene=GRMZM2G100593'

'weakly similar to (172) AT5G39865 | Symbols: | glutaredoxin family protein | chr5:15965560-15966732 REVERSEmoderately similar to (362) loc_os02g51370 12002.m10171 protein glutaredoxin family protein, expressed seq=cds; coord=5:207655630..207657582:-1; parent_gene=GRMZM2G118366'

'moderately similar to (407) AT4G39770 | Symbols: | trehalose-6-phosphate phosphatase, putative | chr4:18449138-18451218 REVERSEhighly similar to (521) loc_os02g51680 12002.m10199 protein expressed protein seq=cds; coord=5:208172385..208174899:1; parent_gene=GRMZM2G055150' 'very weakly similar to (84.0) AT2G30140 | Symbols: | UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr2:12872200-12873691 FORWARDweakly similar to (135) loc_os10g12120 12010.m04526 protein UDP-glycosyltransferase/ transferase, transferring glycosyl groups, putative seq=cds; coord=5:208178465..208179815:1; parent_gene=GRMZM2G055124'

'highly similar to (993) AT5G14880 | Symbols: | potassium transporter, putative | chr5:4814244-4817667 FORWARDnearly identical (1028) HAK10_ORYSA Potassium transporter 10 (OsHAK10) - Oryza sativa (Rice)nearly identical (1248) loc_os02g49760 12002.m33855 protein potassium transporter 8, putative, expressed seq=cds; coord=5:204821695..204826748:-1; parent_gene=GRMZM2G375116'

'highly similar to (854) AT1G31480 | Symbols: SGR2 | SGR2 (SHOOT GRAVITROPISM 2); phospholipase A1 | chr1:11266225-11271527 FORWARDnearly identical (1211) loc_os08g01920 12008.m04340 protein SGR2, putative, expressed seq=cds; coord=6:2895769..2912016:-1; parent_gene=GRMZM2G023335'

'weakly similar to (130) loc_os03g62379 12003.m11114 protein DNA binding protein, putative, expressed seq=cds; coord=6:6015317..6016569:1; parent_gene=GRMZM2G019257'

'moderately similar to (484) AT3G04120 | Symbols: GAPC, GAPC-1, GAPC1 | GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr3:1081077-1083131 FORWARDhighly similar to (557) G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 (EC 1.2.1.12) - Zea mays (Maize)highly similar to (519) loc_os08g03290 12008.m26460 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative, expressed seq=cds; coord=6:6898695..6903246:-1; parent_gene=GRMZM2G180625'

'weakly similar to (132) AT4G20380 | Symbols: | zinc finger protein (LSD1) | chr4:11005027-11006438 FORWARDmoderately similar to (220) loc_os08g03610 12008.m04505 protein LSD1, putative, expressed seq=cds; coord=6:8679614..8681295:-1; parent_gene=GRMZM2G060057'

'weakly similar to (103) AT5G01380 | Symbols: | transcription factor | chr5:155784-157451 REVERSEweakly similar to (197) loc_os05g03740 12005.m04908 protein transcription factor GT-3b, putative seq=cds; coord=6:25704008..25705812:-1; parent_gene=GRMZM2G016637'

'highly similar to (667) AT5G15740 | Symbols: | unknown protein | chr5:5134788-5136956 REVERSEhighly similar to (758) loc_os09g29940 12009.m06145 protein auxin-independent growth promoter, putative, expressed seq=cds; coord=7:130246697..130249893:-1; parent_gene=GRMZM2G089854'

'weakly similar to (122) AT4G00180 | Symbols: YAB3 | YAB3 (YABBY3); protein binding / transcription factor | chr4:72804-74888 REVERSEweakly similar to (103) YAB1_ORYSA Protein YABBY (OsYAB1) (Filamentous flower protein 1) - Oryza sativa (Rice)weakly similar to (115) loc_os02g42950 12002.m33795 protein yabby15 protein, putative, expressed seq=cds; coord=7:159462826..159464816:1; parent_gene=GRMZM2G046829'

'highly similar to (560) AT5G44240 | Symbols: | haloacid dehalogenase-like hydrolase family protein | chr5:17817619-17823598 FORWARDhighly similar to (662) loc_os11g25980 12011.m06519 protein phospholipid-transporting ATPase 2, putative, expressed seq=cds; coord=7:161813482..161823445:-1; parent_gene=GRMZM2G479163'

'highly similar to (610) AT5G44240 | Symbols: | haloacid dehalogenase-like hydrolase family protein | chr5:17817619
17823598 FORWARDhighly similar to (603) loc_os11g25980 12011.m06519 protein phospholipid-transporting ATPase 2, putative, expressed seq=cds; coord=7:161834088..161851386:-1; parent_gene=GRMZM2G411916'

'moderately similar to (317) AT3G53870 | Symbols: | 40S ribosomal protein S3 (RPS3B) | chr3:19951547-19952782 FORWARDmoderately similar to (339) loc_os07g41750 12007.m29256 protein 40S ribosomal protein S3-A, putative, expressed seq=cds; coord=7:165012263..165014081:-1; parent_gene=GRMZM2G093902'

'moderately similar to (255) AT1G70600 | Symbols: | structural constituent of ribosome | chr1:26621168-26621608 REVERSEmoderately similar to (280) loc_os03g29460 12003.m08219 protein 60S ribosomal protein L27a-3, putative, expressed seq=cds; coord=7:165243551..165244574:-1; parent_gene=GRMZM2G030731'

'moderately similar to (255) AT1G70600 | Symbols: | structural constituent of ribosome | chr1:26621168-26621608 REVERSEmoderately similar to (280) loc_os03g29460 12003.m08219 protein 60S ribosomal protein L27a-3, putative, expressed seq=cds; coord=7:165243551..165244574:-1; parent_gene=GRMZM2G030731'

'very weakly similar to (85.9) AT5G13910 | Symbols: LEP | LEP (LEAFY PETIOLE); DNA binding / transcription factor | chr5:4482450-4483085 REVERSEvery weakly similar to (91.3) loc_os04g32790 12004.m08376 protein AP2 domain containing protein, expressed seq=cds; coord=7:165809813..165810646:-1; parent_gene=GRMZM2G060876'

'weakly similar to (187) AT2G17730 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:7704142-7705312 FORWARDmoderately similar to (202) loc_os06g50370 12006.m09561 protein RING-H2 finger protein ATL2B, putative, expressed seq=cds; coord=7:175204235..175205552:1; parent_gene=GRMZM2G440866'

'moderately similar to (334) AT1G31860 | Symbols: AT-IE, HISN2 | AT-IE; phosphoribosyl-AMP cyclohydrolase/ phosphoribosyl-ATP diphosphatase | chr1:11434250-11436530 REVERSEmoderately similar to (437) loc_os01g16940 12001.m08290 protein histidine biosynthesis bifunctional protein hisIE, chloroplast precursor, putative, expressed seq=cds; coord=8:2110920..2115595:1; parent_gene=GRMZM2G082214'

'weakly similar to (144) loc_os07g07680 12007.m29080 protein hydroxyproline-rich glycoprotein, putative, expressed seq=cds; coord=8:4449649..4453055:-1; parent_gene=GRMZM2G006734'

'moderately similar to (398) AT2G18700 | Symbols: ATTPS11, TPS11, ATTPSB | ATTPS11; transferase, transferring glycosyl groups | chr2:8109043-8111799 FORWARDhighly similar to (546) loc_os02g54820 12002.m33906 protein trehalose-6-phosphate synthase, putative, expressed seq=cds; coord=8:5487619..5499781:1; parent_gene=GRMZM2G416836' 'highly similar to (668) AT3G18080 | Symbols: BGLU44 | BGLU44 (B-S GLUCOSIDASE 44); (R)-amygdalin beta-glucosidase/ 4-methylumbelliferyl-beta-D-glucopyranoside beta-glucosidase/ beta-gentiobiose beta-glucosidase/ cellobiose glucosidase/ esculin beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds | chr3:6191586-6194124 FORWARDmoderately similar to (350) BGLC_MAIZE Beta-glucosidase, chloroplast precursor (EC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucoside glucohydrolase) - Zea mays (Maize)highly similar to (773) loc_os01g32364 12001.m09560 protein non-cyanogenic beta-glucosidase precursor, putative, expressed seq=cds; coord=8:8302750..8305316:-1; parent_gene=AC234160.1_FG003'

'highly similar to (668) AT3G18080 | Symbols: BGLU44 | BGLU44 (B-S GLUCOSIDASE 44); (R)-amygdalin beta-glucosidase/ 4-methylumbelliferyl-beta-D-glucopyranoside beta-glucosidase/ beta-gentiobiose beta-glucosidase/ cellobiose glucosidase/ esculin beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds | chr3:6191586-6194124 FORWARDmoderately similar to (350) BGLC_MAIZE Beta-glucosidase, chloroplast precursor (EC 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucoside glucohydrolase) - Zea mays (Maize)highly similar to (773) loc_os01g32364 12001.m09560 protein non-cyanogenic beta-glucosidase precursor, putative, expressed seq=cds; coord=8:8302750..8305316:-1; parent_gene=AC234160.1_FG003'

'moderately similar to (226) AT3G14470 | Symbols: | disease resistance protein (NBS-LRR class), putative | chr3:4857940-4861104 FORWARDhighly similar to (738) loc_os05g34230 12005.m07654 protein disease resistance protein RGA3, putative, expressed seq=cds; coord=8:104379532..104382273:1; parent_gene=GRMZM2G017603'

'moderately similar to (369) AT4G15530 | Symbols: PPDK | PPDK (pyruvate orthophosphate dikinase); kinase/ pyruvate, phosphate dikinase | chr4:8864828-8870748 REVERSEmoderately similar to (416) PPDK_MAIZE Pyruvate, phosphate dikinase, chloroplast precursor (EC 2.7.9.1) (Pyruvate, orthophosphate dikinase) - Zea mays (Maize)moderately similar to (417) loc_os05g33570 12005.m083718 protein pyruvate, phosphate dikinase, chloroplast precursor, putative, expressed seq=cds; coord=8:107012660..107014828:1; parent_gene=GRMZM2G097457'

'moderately similar to (263) AT2G21520 | Symbols: | transporter | chr2:9215956-9218953 FORWARDmoderately similar to (446) loc_os08g38850 12008.m26728 protein phosphatidylinositol transporter/ transporter, putative, expressed seq=cds; coord=8:109946142..109950400:-1; parent_gene=GRMZM2G312198'

'moderately similar to (313) AT2G38470 | Symbols: WRKY33, ATWRKY33 | WRKY33; transcription factor | chr2:16108476-16110539 FORWARDmoderately similar to (484) loc_os05g27730 12005.m07061 protein OsWRKY53 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed seq=cds; coord=8:110214059..110216431:-1; parent_gene=GRMZM2G449681'

'moderately similar to (295) AT1G21240 | Symbols: WAK3 | WAK3 (wall associated kinase 3); kinase/ protein serine/threonine kinase | chr1:7434303-7436702 FORWARDweakly similar to (177) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (484) loc_os08g39210 12008.m07902 protein OsWAK74 - OsWAK receptor-like protein kinase, expressed seq=cds; coord=8:112624757..112626912:1; parent_gene=GRMZM2G061718'

'moderately similar to (310) AT2G40280 | Symbols: | dehydration-responsive family protein | chr2:16825707-16828300 REVERSEmoderately similar to (459) loc_os05g39520 12005.m08130 protein ankyrin-like protein, putative, expressed seq=cds; coord=8:118529129..118653539:-1; parent_gene=AC204277.3_FG006' 'highly similar to (684) AT3G13390 | Symbols: sks11 | sks11 (SKU5 Similar 11); copper ion binding / oxidoreductase | chr3:4351401-4353289 REVERSEhighly similar to (686) NTP3_TOBAC Pollen-specific protein NTP303 precursor - Nicotiana tabacum (Common tobacco)highly similar to (927) loc_os05g40740 12005.m083761 protein pollen-specific protein NTP303 precursor, putative, expressed seq=cds; coord=8:119369178..119371841:-1; parent_gene=GRMZM2G142584'

'moderately similar to (417) AT3G05510 | Symbols: | phospholipid/glycerol acyltransferase family protein | chr3:1596133-1598074 FORWARDhighly similar to (706) loc_os01g70570 12001.m150833 protein acyltransferase, putative, expressed seq=cds; coord=8:159882828..159886413:1; parent_gene=GRMZM2G002135'

'highly similar to (617) AT5G62000 | Symbols: ARF2, ARF1-BP, HSS | ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor | chr5:24910859-24914680 FORWARDnearly identical (1014) loc_os01g70270 12001.m43358 protein auxin response factor 2, putative, expressed seq=cds; coord=8:160100153..160104047:-1; parent_gene=GRMZM2G116557'

'moderately similar to (280) AT1G23280 | Symbols: | MAK16 protein-related | chr1:8260865-8262650 REVERSEmoderately similar to (362) loc_os07g16950 12007.m079650 protein MAK16-like protein RBM13, putative, expressed seq=cds; coord=8:161187376..161192709:-1; parent_gene=GRMZM2G461793'

'highly similar to (616) AT1G27320 | Symbols: AHK3 | AHK3 (ARABIDOPSIS HISTIDINE KINASE 3); cytokinin receptor/ osmosensor/ protein histidine kinase | chr1:9487780-9492027 FORWARDweakly similar to (113) ETR1_PRUPE Ethylene receptor (EC 2.7.13.3) - Prunus persica (Peach)highly similar to (945) loc_os01g69920 12001.m42798 protein histidine kinase 2, putative, expressed seq=cds; coord=8:161390595..161396494:1; parent_gene=GRMZM2G423456'

'moderately similar to (360) AT5G16270 | Symbols: ATRAD21.3, SYN4 | SYN4 (SISTER CHROMATID COHESION 1 PROTEIN 4) | chr5:5316783-5322330 FORWARDnearly identical (1225) loc_os01g67250 12001.m42786 protein N terminus of Rad21 / Rec8 like protein, expressed seq=cds; coord=8:164083362..164092361:1; parent_gene=GRMZM2G421829'

'highly similar to (506) AT4G31820 | Symbols: ENP, NPY1, MAB4 | ENP (ENHANCER OF PINOID); protein binding / signal transducer | chr4:15390788-15393627 REVERSEmoderately similar to (317) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)highly similar to (843) loc_os06g08550 12006.m05574 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=9:12791598..12796435:-1; parent_gene=GRMZM2G067053'

'moderately similar to (419) AT4G25160 | Symbols: | protein kinase family protein | chr4:12903360-12906669 REVERSEweakly similar to (129) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (580) loc_os06g04880 12006.m31972 protein ATP binding protein, putative, expressed seq=cds; coord=9:20824694..20826403:1; parent_gene=GRMZM2G433433'

'weakly similar to (146) AT5G06710 | Symbols: HAT14 | HAT14 (HOMEOBOX FROM ARABIDOPSIS THALIANA); DNA binding / transcription factor | chr5:2069093-2070284 REVERSEweakly similar to (175) loc_os06g04850 12006.m05214 protein homeobox-leucine zipper protein ATHB-4, putative, expressed seq=cds; coord=9:20869132..20870463:-1; parent_gene=GRMZM2G106276' 'moderately similar to (395) AT4G36090 | Symbols: | oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr4:17078376-17080670 REVERSEhighly similar to (731) loc_os06g04660 12006.m091594 protein oxidoreductase, 2OG-Fe oxygenase family protein, expressed seq=cds; coord=9:21580594..21585837:-1; parent_gene=GRMZM2G114098'

'weakly similar to (174) AT2G35540 | Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr2:14927158-14928930 FORWARDmoderately similar to (415) loc_os06g02170 12006.m091578 protein heat shock protein binding protein, putative, expressed seq=cds; coord=9:26548872..26550670:1; parent_gene=GRMZM2G152373'

'moderately similar to (482) AT3G30390 | Symbols: | amino acid transporter family protein | chr3:11977112-11978827 REVERSEhighly similar to (628) loc_os06g16420 12006.m32253 protein amino acid transporter-like protein, putative, expressed seq=cds; coord=9:34842506..34845871:1; parent_gene=GRMZM2G150406'

'moderately similar to (205) AT1G65680 | Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 | ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2) | chr1:24427266-24428399 FORWARDmoderately similar to (373) EXPB3_ORYSA Expansin-B3 precursor (OsEXPB3) (Beta-expansin-3) (OsaEXPb1.10) - Oryza sativa (Rice)moderately similar to (373) loc_os10g40720 12010.m06840 protein beta-expansin 1a precursor, putative, expressed seq=cds; coord=9:116749793..116751376:1; parent_gene=GRMZM2G094990'

'highly similar to (859) AT1G78000 | Symbols: SULTR1;2, SEL1 | SULTR1;2 (SULFATE TRANSPORTER 1;2); sulfate transmembrane transporter | chr1:29329889-29332877 FORWARDmoderately similar to (370) NO70_SOYBN Early nodulin 70 - Glycine max (Soybean)nearly identical (1032) loc_os03g09970 12003.m101107 protein sulfate transporter 1.2, putative, expressed seq=cds; coord=9:148914087..148917604:-1; parent_gene=GRMZM2G342907'

'highly similar to (512) AT5G48150 | Symbols: PAT1 | PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor | chr5:19522497-19524053 REVERSEhighly similar to (537) CIGR2_ORYSA Chitin-inducible gibberellin-responsive protein 2 - Oryza sativa (Rice)highly similar to (796) loc_os03g09280 12003.m101225 protein chitin-inducible gibberellin-responsive protein 2, putative, expressed seq=cds; coord=9:149164041..149170542:-1; parent_gene=GRMZM2G028039'

'very weakly similar to (84.0) AT3G28857 | Symbols: | transcription regulator | chr3:10855781-10856313 REVERSEweakly similar to (117) loc_os03g07540 12003.m06267 protein DNA binding protein, putative, expressed seq=cds; coord=9:151129408..151129907:-1; parent_gene=AC149829.2_FG004'

'very weakly similar to (100) AT5G01880 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr5:339017-339496 FORWARDvery weakly similar to (87.8) EL5_ORYSA E3 ubiquitin-protein ligase EL5 (EC 6.3.2.-) - Oryza sativa (Rice)weakly similar to (102) loc_os12g02350 12012.m04236 protein RING-H2 finger protein ATL5A, putative, expressed seq=cds; coord=10:4098565..4099212:-1; parent_gene=GRMZM2G467576'

'weakly similar to (138) AT3G58630 | Symbols: | transcription factor | chr3:21683928-21685771 REVERSEmoderately similar to (338) loc_os04g36790 12004.m08719 protein 6b-interacting protein 1, putative, expressed seq=cds; coord=10:119916059..119917843:-1; parent_gene=GRMZM2G392168' 'moderately similar to (251) AT3G52390 | Symbols: | tatD-related deoxyribonuclease family protein | chr3:19423105-19425183 REVERSEmoderately similar to (280) loc_os07g06440 12007.m05105 protein deoxyribonuclease tatD, putative, expressed seq=cds; coord=10:137622400..137640740:-1; parent_gene=GRMZM2G455171'

'weakly similar to (129) AT2G38250 | Symbols: | DNA-binding protein-related | chr2:16018384-16019500 FORWARDmoderately similar to (325) loc_os04g51320 12004.m10028 protein transcription factor GT-3b, putative, expressed seq=cds; coord=10:141020599..141023637:-1; parent_gene=GRMZM2G415229'

'moderately similar to (218) AT2G26280 | Symbols: CID7 | CID7; ATP binding / damaged DNA binding / protein binding | chr2:11188143-11190579 REVERSEhighly similar to (762) loc_os03g08270 12003.m101105 protein ataxin-2 C-terminal region family protein, expressed seq=cds; coord=1:16595443..16603430:1; parent_gene=GRMZM2G017254'

'highly similar to (556) AT1G19250 | Symbols: FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase | chr1:6650656-6653053 REVERSEhighly similar to (833) loc_os03g08410 12003.m06349 protein monooxygenase/ oxidoreductase, putative, expressed seq=cds; coord=1:17015718..17018487:1; parent_gene=GRMZM2G000427'

'moderately similar to (206) AT4G33250 | Symbols: EIF3K, TIF3K1, ATTIF3K1 | EIF3K (EUKARYOTIC TRANSLATION INITIATION FACTOR 3K); translation initiation factor | chr4:16039066-16040617 REVERSEmoderately similar to (241) IF3C_ORYSA Eukaryotic translation initiation factor 3 subunit 12 (eIF-3 p25) (eIF3k) - Oryza sativa (Rice)moderately similar to (241) loc_os03g08450 12003.m06353 protein eukaryotic translation initiation factor 3 subunit 12, putative, expressed seq=cds; coord=1:17408930..17412458:-1; parent_gene=GRMZM2G115182'

'weakly similar to (152) AT3G59650 | Symbols: | mitochondrial ribosomal protein L51/S25/CI-B8 family protein | chr3:22033216-22033928 FORWARDweakly similar to (182) loc_os03g10930 12003.m06545 protein mitochondrial ribosomal protein L43, putative, expressed seq=cds; coord=1:21456899..21461749:1; parent_gene=GRMZM2G004259'

'moderately similar to (229) AT4G37580 | Symbols: HLS1, COP3, UNS2 | HLS1 (HOOKLESS 1); N-acetyltransferase | chr4:17658932-17660564 FORWARDmoderately similar to (366) loc_os03g10810 12003.m35083 protein HLS1, putative, expressed seq=cds; coord=1:21720856..21722289:1; parent_gene=GRMZM2G114184'

'highly similar to (545) AT2G14820 | Symbols: NPY2 | NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer | chr2:6358864-6361300 FORWARDmoderately similar to (320) NPH3_ORYSA Coleoptile phototropism protein 1 (Non-phototropic hypocotyl 3-like protein) (NPH3-like protein) - Oryza sativa (Rice)highly similar to (942) loc_os03g10800 12003.m34805 protein transposon protein, putative, Mutator sub-class, expressed seq=cds; coord=1:21757362..21776523:-1; parent_gene=GRMZM2G114055'

'moderately similar to (248) AT2G30260 | Symbols: U2B" | U2B" (U2 small nuclear ribonucleoprotein B); RNA binding / nucleic acid binding / nucleotide binding | chr2:12905557-12907434 REVERSEmoderately similar to (323) loc_os03g18720 12003.m35175 protein spliceosomal protein, putative, expressed seq=cds; coord=1:46622335..46627171:-1; parent_gene=GRMZM2G153450' 'moderately similar to (248) AT2G30260 | Symbols: U2B'' | U2B'' (U2 small nuclear ribonucleoprotein B); RNA binding / nucleic acid binding / nucleotide binding | chr2:12905557-12907434 REVERSEmoderately similar to (323) loc_os03g18720 12003.m35175 protein spliceosomal protein, putative, expressed seq=cds; coord=1:46622335..46627171:-1; parent_gene=GRMZM2G153450'

'highly similar to (853) AT3G16910 | Symbols: AAE7, ACN1 | AAE7 (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase | chr3:5773231-5775411 REVERSEweakly similar to (139) 4CL1_SOLTU 4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1) - Solanum tuberosum (Potato)nearly identical (1050) loc_os03g19240 12003.m07341 protein AMP-binding protein, putative, expressed seq=cds; coord=1:48684987..48690042:-1; parent_gene=GRMZM2G013783'

'highly similar to (691) AT1G56560 | Symbols: | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr1:21192593-21194948 FORWARDhighly similar to (795) loc_os03g20020 12003.m07415 protein beta-fructofuranosidase, putative, expressed seq=cds; coord=1:51318993..51329214:-1; parent_gene=GRMZM2G084940'

'moderately similar to (263) AT5G49620 | Symbols: AtMYB78 | AtMYB78 (myb domain protein 78); DNA binding / transcription factor | chr5:20137491-20139384 REVERSEweakly similar to (164) MYBA2_ORYSA Myb-related protein MYBAS2 - Oryza sativa (Rice)moderately similar to (343) loc_os03g20090 12003.m101325 protein MYB transcription factor, putative, expressed seq=cds; coord=1:51397954..51400225:-1; parent_gene=GRMZM2G070849'

'moderately similar to (286) AT4G16640 | Symbols: | matrix metalloproteinase, putative | chr4:9367396-9368490 REVERSEmoderately similar to (209) MEP1_SOYBN Metalloendoproteinase 1 precursor (EC 3.4.24.-) (SMEP1) - Glycine max (Soybean)moderately similar to (441) loc_os10g40830 12010.m06853 protein metalloendoproteinase 1 precursor, putative, expressed seq=cds; coord=1:90788877..90790064:1; parent_gene=GRMZM2G317386'

'moderately similar to (213) AT5G23290 | Symbols: PDF5 | PDF5 (PREFOLDIN 5); unfolded protein binding | chr5:7846144-7847428 FORWARDmoderately similar to (258) loc_os10g34670 12010.m22005 protein prefoldin subunit 5, putative, expressed seq=cds; coord=1:229567215..229571434:1; parent_gene=GRMZM2G014676'

'moderately similar to (214) AT1G73230 | Symbols: | nascent polypeptide-associated complex (NAC) domain-containing protein | chr1:27540506-27541364 REVERSEmoderately similar to (235) loc_os10g34180 12010.m21923 protein transcription factor BTF3, putative, expressed seq=cds; coord=1:230179502..230183279:1; parent_gene=GRMZM2G131577'

'highly similar to (608) AT5G03760 | Symbols: ATCSLA09, CSLA09, ATCSLA9, CSLA9, RAT4 | ATCSLA09; mannan synthase/ transferase, transferring glycosyl groups | chr5:985910-990087 REVERSEhighly similar to (780) loc_os10g26630 12010.m65488 protein CSLA2 - cellulose synthase-like family A; mannan synthase, expressed seq=cds; coord=1:242575182..242581195:-1; parent_gene=GRMZM2G115772'

'moderately similar to (212) AT2G32460 | Symbols: MYB101, ATMYB101, ATM1 | MYB101; DNA binding / transcription factor | chr2:13782419-13784359 REVERSEmoderately similar to (207) GAM1_ORYSA Transcription factor GAMYB (OsGAMyb) - Oryza sativa (Rice)moderately similar to (341) loc_os03g38210 12003.m08921 protein myb-like DNA-binding domain containing protein, expressed seq=cds; coord=1:246031095..246033561:1; parent_gene=AC217264.3_FG005' 'moderately similar to (212) AT2G32460 | Symbols: MYB101, ATMYB101, ATM1 | MYB101; DNA binding / transcription factor | chr2:13782419-13784359 REVERSEmoderately similar to (207) GAM1_ORYSA Transcription factor GAMYB (OsGAMyb) - Oryza sativa (Rice)moderately similar to (341) loc_os03g38210 12003.m08921 protein myb-like DNA-binding domain containing protein, expressed seq=cds; coord=1:246031095..246033561:1; parent_gene=AC217264.3_FG005'

'moderately similar to (341) AT4G34380 | Symbols: | transducin family protein / WD-40 repeat family protein | chr4:16438835-16440322 FORWARDmoderately similar to (479) loc_os03g42710 12003.m09323 protein nucleotide binding protein, putative seq=cds; coord=1:253911424..253913528:-1; parent_gene=GRMZM2G099023'

'moderately similar to (272) AT3G18400 | Symbols: anac058 | anac058 (Arabidopsis NAC domain containing protein 58); transcription factor | chr3:6318745-6320593 REVERSEmoderately similar to (209) NAC77_ORYSA NAC domain-containing protein 77 (ONAC077) (ONAC300) - Oryza sativa (Rice)moderately similar to (349) loc_os03g42630 12003.m09316 protein GRAB2 protein, putative, expressed seq=cds; coord=1:254075089..254076572:1; parent_gene=GRMZM2G031120'

'moderately similar to (229) loc_os03g42370 12003.m09294 protein B3 DNA binding domain containing protein seq=cds; coord=1:254400478..254402593:1; parent_gene=GRMZM2G098063'

'highly similar to (883) AT1G23090 | Symbols: AST91, SULTR3;3 | AST91 (SULFATE TRANSPORTER 91); sulfate transmembrane transporter | chr1:8185238-8188954 REVERSEmoderately similar to (348) NO70_SOYBN Early nodulin 70 - Glycine max (Soybean)nearly identical (1099) loc_os04g55800 12004.m10471 protein sulfate transporter 3.3, putative, expressed seq=cds; coord=2:4890135..4895146:1; parent_gene=GRMZM2G395114'

'weakly similar to (101) AT5G67190 | Symbols: | AP2 domain-containing transcription factor, putative | chr5:26809135-26809689 REVERSEweakly similar to (168) loc_os04g55520 12004.m10443 protein dehydration responsive element binding protein, putative, expressed seq=cds; coord=2:5562976..5564647:1; parent_gene=GRMZM2G174917'

'very weakly similar to (81.6) AT2G42160 | Symbols: | zinc finger (ubiquitin-hydrolase) domain-containing protein | chr2:17574843-17577397 REVERSEweakly similar to (134) loc_os04g55480 12004.m35484 protein BRCA1-associated protein, putative, expressed seq=cds; coord=2:5765904..5767125:1; parent_gene=GRMZM2G066169'

'weakly similar to (159) AT5G23350 | Symbols: | GRAM domain-containing protein / ABA-responsive protein-related | chr5:7858545-7859387 REVERSEmoderately similar to (290) loc_os04g44510 12004.m09410 protein FIP1, putative, expressed seq=cds; coord=2:26726276..26727564:1; parent_gene=GRMZM2G114153'

'moderately similar to (285) AT2G28305 | Symbols: | unknown protein | chr2:12081186-12084307 FORWARDmoderately similar to (317) loc_os04g43840 12004.m09343 protein carboxy-lyase, putative, expressed seq=cds; coord=2:28002262..28006292:-1; parent_gene=GRMZM2G471931' 'weakly similar to (171) ATMG01275 | Symbols: NAD1A, NAD1, ND1 | Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C. | chrM:318004-318390 REVERSEweakly similar to (181) NU1M_OENBE NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3) (NADH dehydrogenase subunit 1) - Oenothera bertiana (Bertero's evening primrose) seq=cds; coord=9:68016311..68020591:1; parent_gene=GRMZM2G141605'

'moderately similar to (255) AT3G54420 | Symbols: ATEP3, ATCHITIV, CHIV | ATEP3; chitinase | chr3:20145935-20147034 FORWARDmoderately similar to (295) CHIA_MAIZE Endochitinase A precursor (EC 3.2.1.14) (Seed chitinase A) - Zea mays (Maize)moderately similar to (303) loc_os04g41680 12004.m09144 protein endochitinase A precursor, putative, expressed seq=cds; coord=2:33537139..33539360:1; parent_gene=GRMZM2G052175'

'moderately similar to (343) AT3G59350 | Symbols: | serine/threonine protein kinase, putative | chr3:21932930-21934883 FORWARDweakly similar to (183) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (545) loc_os04g41310 12004.m09110 protein expressed protein seq=cds; coord=2:34537876..34541534:-1; parent_gene=GRMZM2G051984'

'moderately similar to (312) AT1G08110 | Symbols: | lactoylglutathione lyase, putative / glyoxalase I, putative | chr1:2535463-2537630 FORWARDmoderately similar to (314) LGUL_CICAR Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) - Cicer arietinum (Chickpea) (Garbanzo)moderately similar to (363) loc_os05g22970 12005.m06592 protein lactoylglutathione lyase, putative, expressed seq=cds; coord=2:82246568..82258715:1; parent_gene=GRMZM2G125310'

'moderately similar to (238) AT5G47850 | Symbols: CCR4 | CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase | chr5:19378803-19381058 REVERSEweakly similar to (194) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (852) loc_os11g11490 12011.m05341 protein protein kinase, putative, expressed seq=cds; coord=2:127824056..127827013:1; parent_gene=GRMZM2G301355'

'moderately similar to (238) AT5G47850 | Symbols: CCR4 | CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase | chr5:19378803-19381058 REVERSEweakly similar to (194) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (852) loc_os11g11490 12011.m05341 protein protein kinase, putative, expressed seq=cds; coord=2:127824056..127827013:1; parent_gene=GRMZM2G301355'

'moderately similar to (244) AT5G53190 | Symbols: | nodulin MtN3 family protein | chr5:21572417-21574284 REVERSEmoderately similar to (321) loc_os01g12130 12001.m07828 protein mtN3 protein-like, putative, expressed seq=cds; coord=3:2956021..2957784:1; parent_gene=GRMZM2G060974'

'weakly similar to (127) AT1G15860 | Symbols: | INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Defective in cullin neddylation (InterPro:IPR014764), Protein of unknown function DUF298 (InterPro:IPR005176); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12760.1). | chr1:5455055-5456741 FORWARDweakly similar to (154) loc_os08g34070 12008.m07396 protein DCN1-like protein 4, putative, expressed seq=cds; coord=3:3234584..3239066:-1; parent_gene=GRMZM2G001566' 'moderately similar to (391) AT1G06240 | Symbols: | unknown protein | chr1:1911166-1912875 FORWARDhighly similar to (569) loc_os01g11590 12001.m42918 protein expressed protein seq=cds; coord=3:3448711..3456996:-1; parent_gene=GRMZM2G400907'

'highly similar to (822) AT1G15460 | Symbols: ATBOR4, BOR4 | BOR4 (REQUIRES HIGH BORON 4); anion exchanger | chr1:5310196-5313376 REVERSEnearly identical (1013) loc_os01g08020 12001.m07427 protein boron transporter-like protein 2, putative, expressed seq=cds; coord=3:10934126..10940345:-1; parent_gene=GRMZM2G051753'

'highly similar to (659) AT2G26710 | Symbols: BAS1, CYP734A1, CYP72B1 | BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase | chr2:11380700-11383413 FORWARDmoderately similar to (372) C72A1_CATRO Cytochrome P450 72A1 (EC 1.3.3.9) (CYPLXXII) (Secologanin synthase) (SLS) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)highly similar to (836) loc_os01g29150 12001.m09352 protein cytochrome P450 72A1, putative, expressed seq=cds; coord=3:11212000..11215671:1; parent_gene=GRMZM2G138750'

'moderately similar to (468) AT1G06890 | Symbols: | transporter-related | chr1:2111728-2114038 REVERSEhighly similar to (557) loc_os01g07310 12001.m43446 protein integral membrane protein like, putative, expressed seq=cds; coord=3:13589786..13593160:1; parent_gene=GRMZM2G116053'

'moderately similar to (383) AT3G05840 | Symbols: ATSK12 | ATSK12; protein kinase/ protein serine/threonine kinase | chr3:1740793-1742927 FORWARDmoderately similar to (384) MSK3_MEDSA Glycogen synthase kinase-3 homolog MsK-3 (EC 2.7.11.1) - Medicago sativa (Alfalfa)moderately similar to (410) loc_os01g14860 12001.m43459 protein glycogen synthase kinase-3 homolog MsK-3, putative, expressed seq=cds; coord=3:13917982..13919834:-1; parent_gene=GRMZM2G129482'

'moderately similar to (383) AT3G05840 | Symbols: ATSK12 | ATSK12; protein kinase/ protein serine/threonine kinase | chr3:1740793-1742927 FORWARDmoderately similar to (384) MSK3_MEDSA Glycogen synthase kinase-3 homolog MsK-3 (EC 2.7.11.1) - Medicago sativa (Alfalfa)moderately similar to (410) loc_os01g14860 12001.m43459 protein glycogen synthase kinase-3 homolog MsK-3, putative, expressed seq=cds; coord=3:13917982..13919834:-1; parent_gene=GRMZM2G129482'

'moderately similar to (388) AT1G45616 | Symbols: AtRLP6 | AtRLP6 (Receptor Like Protein 6); protein binding | chr1:17183550-17186534 REVERSEmoderately similar to (207) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)nearly identical (1443) loc_os04g28210 12004.m07938 protein verticillium wilt disease resistance protein, putative, expressed seq=cds; coord=3:14685361..14688745:1; parent_gene=GRMZM2G062576'

'highly similar to (564) loc_os01g05660 12001.m150482 protein expressed protein seq=cds; coord=3:17580074..17584970:1; parent_gene=GRMZM2G166064'

'moderately similar to (339) AT1G67000 | Symbols: | ATP binding / kinase/ protein kinase/ protein serine/threonine kinase | chr1:25004217-25007604 REVERSEweakly similar to (183) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (800) loc_os01g04580 12001.m07093 protein Ser/Thr protein kinase, putative, expressed seq=cds; coord=3:19965649..19969019:-1; parent_gene=GRMZM2G467671' 'moderately similar to (343) AT1G66910 | Symbols: | protein kinase, putative | chr1:24961634-24963941 REVERSEweakly similar to (196) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (572) loc_os01g04570 12001.m42597 protein Ser/Thr protein kinase, putative, expressed seq=cds; coord=3:20173885..20177370:-1; parent_gene=GRMZM2G412760'

'moderately similar to (297) AT1G17020 | Symbols: SRG1, ATSRG1 | SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc | chr1:5820258-5821741 FORWARDweakly similar to (195) FLS_PETHY Flavonol synthase/flavanone 3-hydroxylase (EC 1.14.11.23) (EC 1.14.11.9) (FLS) - Petunia hybrida (Petunia)moderately similar to (468) loc_os10g40880 12010.m06856 protein flavonol synthase/flavanone 3-hydroxylase, putative, expressed seq=cds; coord=3:52450288..52452458:-1; parent_gene=GRMZM2G363893'

'moderately similar to (219) AT2G47460 | Symbols: MYB12, ATMYB12, PFG1 | MYB12 (MYB DOMAIN PROTEIN 12); DNA binding / transcription activator/ transcription factor | chr2:19476438-19479242 FORWARDmoderately similar to (232) MYBP_MAIZE Myb-related protein P - Zea mays (Maize)moderately similar to (258) loc_os01g19970 12001.m08532 protein myb-like transcription factor, putative, expressed seq=cds; coord=3:54469147..54472943:1; parent_gene=GRMZM2G051256'

'very weakly similar to (94.0) AT2G35910 | Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr2:15073225-15073878 REVERSEweakly similar to (108) loc_os12g42540 12012.m08033 protein RING-H2 finger protein ATL2I, putative seq=cds; coord=3:88527498..88527953:1; parent_gene=AC206768.3_FG005'

'moderately similar to (292) AT3G56310 | Symbols: | alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative | chr3:20882886-20885745 FORWARDmoderately similar to (231) AGAL_ORYSA Alpha-galactosidase precursor (EC 3.2.1.22) (Melibiase) (Alpha-D-galactoside galactohydrolase) - Oryza sativa (Rice)moderately similar to (359) loc_os07g48160 12007.m09030 protein alpha-galactosidase precursor, putative, expressed seq=cds; coord=3:140682835..140687208:-1; parent_gene=GRMZM2G402368'

'moderately similar to (255) AT4G38620 | Symbols: ATMYB4, MYB4 | MYB4; DNA binding / transcription factor | chr4:18053866-18054876 FORWARDmoderately similar to (263) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (356) loc_os01g65370 12001.m12650 protein transcription repressor MYB4, putative seq=cds; coord=3:173520271..173521619:-1; parent_gene=GRMZM2G160838'

'highly similar to (569) AT2G16570 | Symbols: ATASE, ATASE1 | ATASE1 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 1); amidophosphoribosyltransferase | chr2:7180424-7182124 REVERSEhighly similar to (562) PUR1_SOYBN Amidophosphoribosyltransferase, chloroplast precursor (EC 2.4.2.14) (Glutamine phosphoribosylpyrophosphate amidotransferase) (ATASE) (GPAT) - Glycine max (Soybean)highly similar to (800) loc_os01g65260 12001.m12639 protein amidophosphoribosyltransferase, chloroplast precursor, putative, expressed seq=cds; coord=3:173801386..173803474:1; parent_gene=GRMZM2G339699'

'very weakly similar to (94.4) loc_os01g24950 12001.m150578 protein exocyst complex subunit Sec15-like family protein, expressed seq=cds; coord=3:175323602..175324361:-1; parent_gene=GRMZM2G439532' 'highly similar to (617) AT1G62430 | Symbols: ATCDS1 | ATCDS1; phosphatidate cytidylyltransferase | chr1:23106274-23108923 REVERSEhighly similar to (637) CDS1_SOLTU Phosphatidate cytidylyltransferase (EC 2.7.7.41) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDP-diacylglycerol synthase) (CDS) (CTP:phosphatidate cytidylyltransferase) (CDP-DAG synthase) (CDP-DG synthetase) - Solahighly similar to (761) loc_os01g55360 12001.m43197 protein phosphatidate cytidylyltransferase, putative, expressed seq=cds; coord=3:195881870..195897637:1; parent_gene=GRMZM2G452529'

'weakly similar to (193) AT5G11480 | Symbols: | GTP binding | chr5:3669350-3671471 REVERSEmoderately similar to (255) loc_os01g53150 12001.m43175 protein GTP-binding protein, putative, expressed seq=cds; coord=3:200701564..200707398:-1; parent_gene=GRMZM2G022625'

'moderately similar to (439) AT2G37650 | Symbols: | scarecrow-like transcription factor 9 (SCL9) | chr2:15792623-15794779 FORWARDweakly similar to (199) CIGR2_ORYSA Chitin-inducible gibberellin-responsive protein 2 - Oryza sativa (Rice)highly similar to (771) loc_os11g47870 12011.m08584 protein chitin-inducible gibberellin-responsive protein 2, putative, expressed seq=cds; coord=4:843149..845669:-1; parent_gene=GRMZM2G163427'

'nearly identical (1818) AT1G15520 | Symbols: PDR12, ATPDR12 | PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances | chr1:5331993-5338175 REVERSEnearly identical (2339) PDR7_ORYSA Putative pleiotropic drug resistance protein 7 - Oryza sativa (Rice)nearly identical (2339) loc_os02g11760 12002.m06425 protein PDR5-like ABC transporter, putative, expressed seq=cds; coord=4:5786645..5793503:1; parent_gene=GRMZM2G421495'

'weakly similar to (128) AT3G07040 | Symbols: RPM1, RPS3 | RPM1 (RESISTANCE TO P. SYRINGAE PV MACULICOLA 1); nucleotide binding / protein binding | chr3:2226244-2229024 REVERSEmoderately similar to (339) loc_os02g19890 12002.m100181 protein stripe rust resistance protein Yr10, putative, expressed seq=cds; coord=4:42260480..42262502:-1; parent_gene=GRMZM2G304049'

'moderately similar to (261) AT1G47480 | Symbols: | hydrolase | chr1:17417623-17419296 FORWARDweakly similar to (126) GID1_ORYSA Gibberellin receptor GID1 (EC 3.-.-.-) (Gibberellin-insensitive dwarf protein 1) (Protein GIBBERELLIN INSENSITIVE DWARF1) - Oryza sativa (Rice)highly similar to (550) loc_os08g37060 12008.m07693 protein gibberellin receptor GID1L2, putative, expressed seq=cds; coord=4:89515292..89516903:-1; parent_gene=GRMZM2G064193'

'weakly similar to (139) AT1G23220 | Symbols: | dynein light chain type 1 family protein | chr1:8242614-8244136 FORWARDweakly similar to (190) loc_os02g36990 12002.m08787 protein microtubule motor, putative, expressed seq=cds; coord=4:126474274..126476909:-1; parent_gene=GRMZM2G145027'

'moderately similar to (498) AT2G15620 | Symbols: NIR1, NIR, ATHNIR | NIR1 (NITRITE REDUCTASE 1); ferredoxin-nitrate reductase/ nitrite reductase (NO-forming) | chr2:6810552-6812666 FORWARDhighly similar to (641) NIR_MAIZE Ferredoxin--nitrite reductase, chloroplast precursor (EC 1.7.7.1) (Fragment) - Zea mays (Maize)highly similar to (566) loc_os01g25484 12001.m43466 protein ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed seq=cds; coord=4:178582502..178585778:1; parent_gene=GRMZM2G079381' 'highly similar to (570) AT3G51850 | Symbols: CPK13 | CPK13; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase | chr3:19232667-19235526 FORWARDmoderately similar to (452) CDPK_SOYBN Calcium-dependent protein kinase SK5 (EC 2.7.11.1) (CDPK) - Glycine max (Soybean)highly similar to (830) loc_os08g42750 12008.m08253 protein calcium-dependent protein kinase, isoform AK1, putative, expressed seq=cds; coord=4:194112157..194114320:-1; parent_gene=GRMZM2G332660'

'moderately similar to (416) AT1G17240 | Symbols: AtRLP2 | AtRLP2 (Receptor Like Protein 2); protein binding / protein kinase | chr1:5896528-5898717 REVERSEmoderately similar to (353) PSKR_DAUCA Phytosulfokine receptor precursor (EC 2.7.11.1) (Phytosulfokine LRR receptor kinase) - Daucus carota (Carrot)highly similar to (738) loc_os02g06070 12002.m05955 protein phytosulfokine receptor precursor, putative seq=cds; coord=4:236965967..236968129:1; parent_gene=GRMZM2G410963'

'weakly similar to (145) AT5G02560 | Symbols: HTA12 | HTA12; DNA binding | chr5:575437-576456 FORWARDweakly similar to (156) H2A1_MEDTR Probable histone H2A.1 - Medicago truncatula (Barrel medic)weakly similar to (154) loc_os03g17100 12003.m07141 protein histone H2A, putative, expressed seq=cds; coord=5:937749..938605:1; parent_gene=GRMZM2G028955'

'moderately similar to (408) AT3G02875 | Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugat hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase | chr3:631993-633859 FORWARDhighly similar to (581) loc_os03g62060 12003.m11084 protein IAA-amino acid hydrolase ILR1 precursor, putative, expressed seq=cds; coord=5:1569977..1573584:-1; parent_gene=GRMZM2G125552'

'weakly similar to (126) AT5G40080 | Symbols: | 60S ribosomal protein-related | chr5:16040190-16041529 REVERSEweakly similar to (160) loc_os02g40490 12002.m09135 protein conserved hypothetical protein seq=cds; coord=5:1578552..1582765:-1; parent_gene=GRMZM2G125784'

'highly similar to (557) AT2G47070 | Symbols: SPL1 | SPL1 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 1); DNA binding / transcription factor | chr2:19337144-19340552 FORWARDvery weakly similar to (97.8) LG1_MAIZE LIGULELESS1 protein - Zea mays (Maize)nearly identical (1281) loc_os03g61760 12003.m11057 protein squamosa promoter-binding-like protein 12, putative, expressed seq=cds; coord=5:1845813..1852802:-1; parent_gene=GRMZM2G138421'

'moderately similar to (366) AT3G46450 | Symbols: | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein | chr3:17093297-17095319 REVERSEhighly similar to (694) loc_os03g60610 12003.m101547 protein CRAL/TRIO domain containing protein, expressed seq=cds; coord=5:2350263..2356801:1; parent_gene=GRMZM2G003108'

'moderately similar to (253) AT4G16420 | Symbols: ADA2B, PRZ1 | ADA2B (HOMOLOG OF YEAST ADA2 2B); DNA binding / transcription coactivator/ transcription factor | chr4:9262805-9265775 REVERSEmoderately similar to (436) loc_os03g53960 12003.m10361 protein transcriptional adaptor, putative, expressed seq=cds; coord=5:7144610..7149251:-1; parent_gene=GRMZM2G129817'

'moderately similar to (417) AT1G66170 | Symbols: MMD1 | MMD1 (MALE MEIOCYTE DEATH 1); DNA binding / protein binding / zinc ion binding | chr1:24638793-24641222 REVERSEhighly similar to (932) loc_os03g50780 12003.m10064 protein PHD-finger family protein, expressed seq=cds; coord=5:10436880..10440158:1; parent_gene=GRMZM2G408897' 'moderately similar to (448) AT1G02050 | Symbols: | chalcone and stilbene synthase family protein | chr1:359164-360441 REVERSEmoderately similar to (261) THS1_VITVI Stilbene synthase 1 (EC 2.3.1.95) (Resveratrol synthase 1) (Trihydroxystilbene synthase 1) (PSV25) - Vitis vinifera (Grape)highly similar to (619) loc_os10g34360 12010.m06262 protein chalcone synthase G, putative, expressed seq=cds; coord=5:26971466..26975726:1; parent_gene=GRMZM2G477683'

'moderately similar to (349) AT1G80830 | Symbols: NRAMP1, PMIT1, ATNRAMP1 | NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter | chr1:30373066-30375644 REVERSEhighly similar to (516) loc_os02g03900 12002.m05739 protein metal transporter Nramp6, putative, expressed seq=cds; coord=5:74612262..74615918:1; parent_gene=GRMZM2G168747'

'highly similar to (588) AT2G26710 | Symbols: BAS1, CYP734A1, CYP72B1 | BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase | chr2:11380700-11383413 FORWARDmoderately similar to (328) C72A1_CATRO Cytochrome P450 72A1 (EC 1.3.3.9) (CYPLXXII) (Secologanin synthase) (SLS) - Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)highly similar to (860) loc_os02g11020 12002.m06400 protein cytochrome P450 72A1, putative, expressed seq=cds; coord=5:110010532..110013072:1; parent_gene=GRMZM2G045319'

'nearly identical (1221) AT3G14570 | Symbols: ATGSL04, gsl04, atgsl4 | ATGSL04 (glucan synthase-like 4); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups | chr3:4892643-4902628 FORWARDnearly identical (1493) loc_os02g14900 12002.m06734 protein 1,3-beta-glucan synthase component family protein, expressed seq=cds; coord=5:144098266..144117111:-1; parent_gene=GRMZM2G111529'

'highly similar to (617) AT5G13160 | Symbols: PBS1 | PBS1 (avrPphB susceptible 1); kinase/ protein serine/threonine kinase | chr5:4176854-4179682 FORWARDmoderately similar to (247) NORK_PEA Nodulation receptor kinase precursor (EC 2.7.11.1) - Pisum sativum (Garden pea)highly similar to (846) loc_os02g30900 12002.m08233 protein protein kinase APK1A, chloroplast precursor, putative, expressed seq=cds; coord=5:164881570..164887792:-1; parent_gene=GRMZM2G137468'

'moderately similar to (308) AT3G50700 | Symbols: AtIDD2 | AtIDD2 (Arabidopsis thaliana Indeterminate(ID)-Domain 2); nucleic acid binding / transcription factor/ zinc ion binding | chr3:18840945-18842829 FORWARDhighly similar to (734) loc_os02g31890 12002.m08282 protein zinc finger, C2H2-type, putative seq=cds; coord=5:166856814..166859192:1; parent_gene=GRMZM2G320287'

'moderately similar to (302) AT2G35930 | Symbols: PUB23 | PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase | chr2:15083101-15084336 REVERSEvery weakly similar to (95.5) SPL11_ORYSA Spotted leaf protein 11 (Spotted leaf11) (Cell death-related protein SPL11) - Oryza sativa (Rice)highly similar to (515) loc_os02g33590 12002.m08452 protein ubiquitin-protein ligase, putative, expressed seq=cds; coord=5:170163954..170165367:-1; parent_gene=GRMZM2G071484'

'very weakly similar to (87.8) AT2G45210 | Symbols: | auxin-responsive protein-related | chr2:18641884-18642372 FORWARDweakly similar to (181) loc_os02g42990 12002.m100801 protein OsSAUR11 - Auxin-responsive SAUR gene family member, expressed seq=cds; coord=5:189620994..189622113:-1; parent_gene=GRMZM2G391596' 'moderately similar to (223) AT2G27230 | Symbols: LHW | LHW (LONESOME HIGHWAY); protein homodimerization/ transcription activator/ transcription factor | chr2:11650895-11653840 FORWARDhighly similar to (880) loc_os02g45170 12002.m09556 protein expressed protein seq=cds; coord=5:194705173..194710444:1; parent_gene=GRMZM2G144097'

'weakly similar to (108) AT5G08130 | Symbols: | BIM1; DNA binding / protein binding / transcription factor | chr5:2606655-2608652 REVERSEmoderately similar to (290) loc_os02g49480 12002.m09982 protein transcription factor BIM1, putative, expressed seq=cds; coord=5:204517824..204522813:-1; parent_gene=GRMZM2G317450'

'highly similar to (838) AT1G68930 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:25918314-25920545 FORWARDweakly similar to (103) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)nearly identical (1197) loc_os02g01610 12002.m33989 protein tetratricopeptide-like helical, putative, expressed seq=cds; coord=5:206572964..206575640:-1; parent_gene=GRMZM2G053396'

'moderately similar to (288) AT4G08950 | Symbols: EXO | EXO (EXORDIUM) | chr4:5740378-5741322 FORWARDmoderately similar to (407) loc_os02g52000 12002.m10231 protein phi-1-like phosphate-induced protein, putative, expressed seq=cds; coord=5:208637277..208638686:-1; parent_gene=GRMZM2G081214'

'moderately similar to (393) AT5G35370 | Symbols: | ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding | chr5:13588564-13591182 REVERSEmoderately similar to (206) KPRO_MAIZE Putative receptor protein kinase ZmPK1 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (568) loc_os02g52850 12002.m10315 protein ATP binding protein, putative, expressed seq=cds; coord=5:210043564..210046543:-1; parent_gene=GRMZM2G058220'

'weakly similar to (157) AT2G32950 | Symbols: COP1, ATCOP1, DET340, FUS1, EMB168 | COP1 (CONSTITUTIVE PHOTOMORPHOGENIC 1); protein binding / ubiquitin-protein ligase | chr2:13978000-13983282 FORWARDweakly similar to (155) COP1_PEA E3 ubiquitin ligase protein COP1 (EC 6.3.2.-) (Constitutive photomorphogenesis protein 1) - Pisum sativum (Garden pea)moderately similar to (218) loc_os02g53140 12002.m10343 protein ubiquitin ligase protein COP1, putative, expressed seq=cds; coord=5:210747893..210749120:-1; parent_gene=GRMZM2G104920'

'moderately similar to (243) AT4G33440 | Symbols: | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein | chr4:16092020-16094732 FORWARDmoderately similar to (298) loc_os08g01600 12008.m04308 protein polygalacturonase, putative, expressed seq=cds; coord=6:1239602..1242853:-1; parent_gene=GRMZM2G004435'

'weakly similar to (137) loc_os08g01670 12008.m04315 protein c/VIF2, putative, expressed seq=cds; coord=6:1996014..1996736:-1; parent_gene=AC186577.3_FG006'

'weakly similar to (148) AT5G37710 | Symbols: | lipase class 3 family protein / calmodulin-binding heat-shock protein, putative | chr5:14979159-14981400 FORWARDmoderately similar to (204) loc_os06g14490 12006.m32040 protein calmodulin-binding heat-shock protein, putative, expressed seq=cds; coord=6:118601060..118602117:1; parent_gene=GRMZM2G174315' 'very weakly similar to (93.6) AT2G04410 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Defence response, Rin4 (InterPro:IPR008700); BEST Arabidopsis thaliana protein match is: NOI (TAIR:AT5G55850.1); Has 141 Blast hits to 140 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 139; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink). | chr2:1534012-1535040 REVERSEweakly similar to (135) loc_os06g17870 12006.m06499 protein nitrate-induced NOI protein, putative, expressed seq=cds; coord=6:119855348..119858902:1; parent_gene=GRMZM2G162788'

'very weakly similar to (81.3) AT2G35040 | Symbols: | AICARFT/IMPCHase bienzyme family protein | chr2:14765347-14768269 REVERSEvery weakly similar to (82.4) loc_os08g10570 12008.m26473 protein bifunctional purine biosynthesis protein purH, putative, expressed seq=cds; coord=6:121022185..121024287:1; parent_gene=GRMZM2G164665'

'moderately similar to (368) AT4G18550 | Symbols: | lipase class 3 family protein | chr4:10225006-10226862 REVERSEhighly similar to (525) loc_os05g49830 12005.m09053 protein triacylglycerol lipase, putative, expressed seq=cds; coord=6:165625344..165626546:1; parent_gene=AC231411.1_FG011'

'moderately similar to (368) AT4G18550 | Symbols: | lipase class 3 family protein | chr4:10225006-10226862 REVERSEhighly similar to (525) loc_os05g49830 12005.m09053 protein triacylglycerol lipase, putative, expressed seq=cds; coord=6:165625344..165626546:1; parent_gene=AC231411.1_FG011'

'moderately similar to (368) AT4G18550 | Symbols: | lipase class 3 family protein | chr4:10225006-10226862 REVERSEhighly similar to (525) loc_os05g49830 12005.m09053 protein triacylglycerol lipase, putative, expressed seq=cds; coord=6:165625344..165626546:1; parent_gene=AC231411.1_FG011'

'moderately similar to (368) AT4G18550 | Symbols: | lipase class 3 family protein | chr4:10225006-10226862 REVERSEhighly similar to (525) loc_os05g49830 12005.m09053 protein triacylglycerol lipase, putative, expressed seq=cds; coord=6:165625344..165626546:1; parent_gene=AC231411.1_FG011'

'weakly similar to (116) loc_os05g50270 12005.m09096 protein GATA transcription factor 19, putative, expressed seq=cds; coord=6:166077055..166078403:-1; parent_gene=GRMZM2G325850'

'highly similar to (528) AT3G14420 | Symbols: | (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative | chr3:4821899-4823899 FORWARDhighly similar to (524) GOX_SPIOL Peroxisomal (S)-2-hydroxy-acid oxidase (EC 1.1.3.15) (Glycolate oxidase) (GOX) (Short chain alpha-hydroxy acid oxidase) - Spinacia oleracea (Spinach)highly similar to (556) loc_os07g05820 12007.m29070 protein hydroxyacid oxidase 1, putative, expressed seq=cds; coord=7:5523491..5527292:1; parent_gene=GRMZM2G129246'

'moderately similar to (319) AT2G06530 | Symbols: VPS2.1 | VPS2.1 | chr2:2588740-2590285 REVERSEmoderately similar to (342) loc_os07g13270 12007.m29110 protein charged multivesicular body protein 2a, putative, expressed seq=cds; coord=7:22154867..22161180:1; parent_gene=GRMZM2G431900'

'moderately similar to (451) AT1G32450 | Symbols: NRT1.5 | NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter | chr1:11715337-11719807 REVERSEmoderately similar to (434) loc_os02g46460 12002.m09683 protein peptide transporter PTR2, putative, expressed seq=cds; coord=7:25089776..25092351:-1; parent_gene=GRMZM2G156794'

'highly similar to (573) AT3G06920 | Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:2181717-2184449 FORWARDweakly similar to (186) RF1_ORYSA Rf1 protein, mitochondrial precursor (PPR protein) (Fertility restorer) (Restorer for CMS) - Oryza sativa (Rice)highly similar to (697) loc_os07g14530 12007.m079646 protein expressed protein seq=cds; coord=7:25155947..25157555:1; parent_gene=GRMZM2G086757'

'moderately similar to (434) AT1G80830 | Symbols: NRAMP1, PMIT1, ATNRAMP1 | NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter | chr1:30373066-30375644 REVERSEhighly similar to (632) loc_os07g15370 12007.m05981 protein metal transporter Nramp6, putative, expressed seq=cds; coord=7:26964762..26967940:-1; parent_gene=GRMZM2G147560'

'moderately similar to (236) AT2G03890 | Symbols: | phosphatidylinositol 3- and 4-kinase family protein | chr2:1186199-1188151 FORWARDmoderately similar to (404) loc_os09g29890 12009.m22000 protein phosphatidylinositol 3- and 4-kinase family protein, expressed seq=cds; coord=7:130092349..130094061:-1; parent_gene=AC225205.3_FG003'

'highly similar to (610) AT5G44240 | Symbols: | haloacid dehalogenase-like hydrolase family protein | chr5:17817619-17823598 FORWARDhighly similar to (603) loc_os11g25980 12011.m06519 protein phospholipid-transporting ATPase 2, putative, expressed seq=cds; coord=7:161834088..161851386:-1; parent_gene=GRMZM2G411916'

'moderately similar to (237) AT4G03140 | Symbols: | binding / catalytic/ oxidoreductase | chr4:1392191-1393662 FORWARDweakly similar to (192) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (368) loc_os07g40250 12007.m08266 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=7:162398192..162399451:1; parent_gene=GRMZM2G076981'

'moderately similar to (226) loc_os07g47400 12007.m08957 protein SRC2, putative, expressed seq=cds; coord=7:172433682..172434802:1; parent_gene=GRMZM2G364643'

'nearly identical (1079) AT2G40540 | Symbols: KT2, ATKT2, SHY3, KUP2, ATKUP2, TRK2 | KT2 (POTASSIUM TRANSPORTER 2); potassium ion transmembrane transporter | chr2:16931445-16934516 FORWARDnearly identical (1287) HAK9_ORYSA Probable potassium transporter 9 (OsHAK9) - Oryza sativa (Rice)nearly identical (1287) loc_os07g48130 12007.m079793 protein potassium transporter 9, putative, expressed seq=cds; coord=7:172935556..172939916:-1; parent_gene=GRMZM2G166738'

'weakly similar to (131) AT5G39660 | Symbols: CDF2 | CDF2 (CYCLING DOF FACTOR 2); DNA binding / protein binding / transcription factor | chr5:15878920-15880712 FORWARDvery weakly similar to (92.8) MNB1A_MAIZE Dof zinc finger protein MNB1A - Zea mays (Maize)moderately similar to (399) loc_os07g48570 12007.m09068 protein expressed protein seq=cds; coord=7:173806883..173808319:-1; parent_gene=AC155434.2_FG006' 'moderately similar to (290) AT2G45570 | Symbols: CYP76C2 | CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding | chr2:18779935-18781922 REVERSEmoderately similar to (233) C76A2_SOLME Cytochrome P450 76A2 (EC 1.14.-.-) (CYPLXXVIA2) (P-450EG7) - Solanum melongena (Eggplant) (Aubergine)moderately similar to (349) loc_os09g27510 12009.m05902 protein cytochrome P450 76C4, putative, expressed seq=cds; coord=7:173961868..173963500:-1; parent_gene=GRMZM2G425127'

'highly similar to (929) AT2G01320 | Symbols: | ABC transporter family protein | chr2:154669-158063 REVERSEmoderately similar to (243) PDR15_ORYSA Pleiotropic drug resistance protein 15 - Oryza sativa (Rice)nearly identical (1115) loc_os01g03144 12001.m06953 protein ABC-2 type transporter family protein, expressed seq=cds; coord=8:10755838..10761776:-1; parent_gene=GRMZM2G119345'

'moderately similar to (414) AT5G16440 | Symbols: IPP1 | IPP1 (ISOPENTENYL DIPHOSPHATE ISOMERASE 1); isopentenyl-diphosphate delta-isomerase | chr5:5371765-5373575 FORWARDmoderately similar to (434) loc_os05g34180 12005.m07649 protein isopentenyl-diphosphate delta-isomerase I, putative, expressed seq=cds; coord=8:104659886..104663941:-1; parent_gene=GRMZM2G145029'

'highly similar to (657) AT5G61840 | Symbols: GUT1 | GUT1; catalytic/ glucuronoxylan glucuronosyltransferase | chr5:24839365-24841703 REVERSEhighly similar to (707) loc_os01g70180 12001.m150448 protein secondary cell wall-related glycosyltransferase family 47, putative, expressed seq=cds; coord=8:160385132..160388604:1; parent_gene=GRMZM2G134308'

'weakly similar to (198) AT3G12600 | Symbols: atnudt16 | atnudt16 (Arabidopsis thaliana Nudix hydrolase homolog 16); hydrolase | chr3:4004676-4005995 FORWARDmoderately similar to (248) loc_os04g53380 12004.m10229 protein expressed protein seq=cds; coord=8:161926660..161930458:1; parent_gene=GRMZM2G013060'

'weakly similar to (198) AT3G12600 | Symbols: atnudt16 | atnudt16 (Arabidopsis thaliana Nudix hydrolase homolog 16); hydrolase | chr3:4004676-4005995 FORWARDmoderately similar to (248) loc_os04g53380 12004.m10229 protein expressed protein seq=cds; coord=8:161926660..161930458:1; parent_gene=GRMZM2G013060'

'moderately similar to (266) AT4G38620 | Symbols: ATMYB4, MYB4 | MYB4; DNA binding / transcription factor | chr4:18053866-18054876 FORWARDmoderately similar to (273) MYB38_MAIZE Myb-related protein Zm38 - Zea mays (Maize)moderately similar to (325) loc_os01g65370 12001.m12650 protein transcription repressor MYB4, putative seq=cds; coord=8:165875616..165876842:-1; parent_gene=GRMZM2G405094'

'moderately similar to (225) AT1G11360 | Symbols: | universal stress protein (USP) family protein | chr1:3822171-3822899 REVERSEmoderately similar to (330) loc_os01g57450 12001.m11896 protein USP family protein, putative, expressed seq=cds; coord=8:171885210..171889098:1; parent_gene=GRMZM2G106690'

'highly similar to (559) AT2G41790 | Symbols: | peptidase M16 family protein / insulinase family protein | chr2:17429453-17436110 REVERSEhighly similar to (738) loc_os01g57073 12001.m11864 protein insulin-degrading enzyme, putative, expressed seq=cds; coord=8:172180747..172198680:-1; parent_gene=GRMZM2G133249' 'highly similar to (719) AT5G19740 | Symbols: | peptidase M28 family protein | chr5:6673986-6676767 FORWARDnearly identical (1075) loc_os01g54010 12001.m11565 protein glutamate carboxypeptidase 2, putative, expressed seq=cds; coord=8:175065667..175070741:-1; parent_gene=GRMZM2G118806'

'very weakly similar to (81.6) AT3G16490 | Symbols: IQD26 | IQD26 (IQ-domain 26); calmodulin binding | chr3:5603962-5605489 REVERSEweakly similar to (197) loc_os01g53980 12001.m11562 protein calmodulin binding protein, putative, expressed seq=cds; coord=8:175150778..175151936:-1; parent_gene=AC203173.3_FG001'

'weakly similar to (128) AT2G45100 | Symbols: | RNA polymerase II transcription factor/ protein binding / transcription activator/ transcription regulator/ translation initiation factor/ zinc ion binding | chr2:18595348-18598088 REVERSEweakly similar to (186) loc_os05g23940 12005.m06688 protein RNA polymerase II transcription factor/ transcription factor/ zinc ion binding protein, putative, expressed seq=cds; coord=9:2736110..2739733:-1; parent_gene=GRMZM2G180836'

'moderately similar to (421) AT1G66430 | Symbols: | pfkB-type carbohydrate kinase family protein | chr1:24778400-24780393 FORWARDmoderately similar to (337) SCRK2_MAIZE Fructokinase-2 (EC 2.7.1.4) (ZmFRK2) - Zea mays (Maize)highly similar to (530) loc_os06g12600 12006.m05976 protein fructokinase-2, putative, expressed seq=cds; coord=9:3856795..3860954:-1; parent_gene=GRMZM2G072091'

'moderately similar to (483) AT1G76680 | Symbols: OPR1, ATOPR1 | OPR1; 12-oxophytodienoate reductase | chr1:28776982-28778271 FORWARDhighly similar to (601) loc_os06g11290 12006.m05846 protein 12-oxophytodienoate reductase 2, putative, expressed seq=cds; coord=9:7308153..7309906:1; parent_gene=GRMZM2G000236'

'moderately similar to (216) AT2G33620 | Symbols: | DNA-binding family protein / AT-hook protein 1 (AHP1) | chr2:14234749-14236563 FORWARDmoderately similar to (385) loc_os10g42230 12010.m50380 protein AT-hook protein 1, putative, expressed seq=cds; coord=9:113056029..113059080:1; parent_gene=AC225193.3_FG003'

'weakly similar to (180) AT5G50400 | Symbols: ATPAP27, PAP27 | PAP27 (PURPLE ACID PHOSPHATASE 27); acid phosphatase/ protein serine/threonine phosphatase | chr5:20523575-20526231 REVERSEweakly similar to (159) NPP_HORVU Nucleotide pyrophosphatase/phosphodiesterase (EC 3.-.-.-) (Fragments) - Hordeum vulgare (Barley)moderately similar to (397) loc_os01g58640 12001.m12006 protein nucleotide pyrophosphatase/phosphodiesterase, putative, expressed seq=cds; coord=9:113231980..113237852:-1; parent_gene=GRMZM2G007754'

'moderately similar to (367) AT2G26450 | Symbols: | pectinesterase family protein | chr2:11251279-11253446 FORWARDmoderately similar to (298) PME3_CITSI Pectinesterase-3 precursor (EC 3.1.1.11) (Pectin methylesterase 3) (PE 3) - Citrus sinensis (Sweet orange)highly similar to (716) loc_os03g28090 12003.m08133 protein pectinesterase-2 precursor, putative, expressed seq=cds; coord=9:122123285..122129038:1; parent_gene=GRMZM2G314663'

'moderately similar to (285) AT1G20030 | Symbols: | pathogenesis-related thaumatin family protein | chr1:6945850-6947017 FORWARDmoderately similar to (210) TLP1_PRUPE Thaumatin-like protein 1 precursor (PpAZ44) - Prunus persica (Peach)moderately similar to (374) loc_os03g14050 12003.m34813 protein thaumatin-like protein 1 precursor, putative, expressed seq=cds; coord=9:143036859..143040005:-1; parent_gene=GRMZM2G149809' 'nearly identical (1081) AT3G59420 | Symbols: ACR4 | ACR4 (ARABIDOPSIS CRINKLY4); kinase/ transmembrane receptor protein kinase | chr3:21959871-21962558 REVERSEnearly identical (1823) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)nearly identical (1608) loc_os03g43670 12003.m09410 protein receptor protein kinase CRINKLY4 precursor, putative, expressed seq=cds; coord=10:5587952..5591862:1; parent_gene=GRMZM2G051637'

'very weakly similar to (84.3) AT1G19490 | Symbols: | bZIP transcription factor family protein | chr1:6751953-6753959 REVERSEvery weakly similar to (99.0) loc_os11g05640 12011.m04761 protein bZIP transcription factor family protein, expressed seq=cds; coord=10:5917109..5918148:1; parent_gene=GRMZM2G365754'

'weakly similar to (132) AT4G08150 | Symbols: KNAT1, BP, BP1 | KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor | chr4:5147969-5150610 REVERSEmoderately similar to (216) KN1_MAIZE Homeotic protein knotted-1 - Zea mays (Maize)weakly similar to (192) loc_os03g51690 12003.m35624 protein homeobox protein OSH1, putative, expressed seq=cds; coord=10:6748624..6749646:-1; parent_gene=GRMZM2G060050'

'weakly similar to (103) AT5G25830 | Symbols: | zinc finger (GATA type) family protein | chr5:9004398-9005502 REVERSEweakly similar to (105) loc_os01g54210 12001.m11585 protein GATA transcription factor 13, putative, expressed seq=cds; coord=10:9530641..9532659:1; parent_gene=GRMZM2G324131'

'highly similar to (525) AT3G16850 | Symbols: | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein | chr3:5748692-5750981 FORWARDhighly similar to (698) loc_os12g36810 12012.m07466 protein polygalacturonase, putative, expressed seq=cds; coord=10:22363483..22367295:-1; parent_gene=GRMZM2G113815'

'weakly similar to (175) AT3G03860 | Symbols: ATAPRL5 | ATAPRL5 (APR-like 5) | chr3:992465-994315 FORWARDmoderately similar to (325) loc_os12g35640 12012.m07357 protein OsAPRL6 - Oryza sativa adenosine 5'-phosphosulfate reductase-like, expressed seq=cds; coord=10:24443942..24448936:-1; parent_gene=GRMZM2G141848'

'highly similar to (590) AT1G12110 | Symbols: NRT1.1, CHL1-1, NRT1, B-1, ATNRT1, CHL1 | NRT1.1; nitrate transmembrane transporter/ transporter | chr1:4105341-4109290 FORWARDhighly similar to (811) loc_os08g05910 12008.m26584 protein peptide transporter PTR2, putative, expressed seq=cds; coord=10:80042433..80048640:1; parent_gene=GRMZM2G086496'

'weakly similar to (140) AT4G16270 | Symbols: | peroxidase 40 (PER40) (P40) | chr4:9205038-9206483 FORWARDweakly similar to (132) PERN_IPOBA Neutral peroxidase precursor (EC 1.11.1.7) (SwPN1) - Ipomoea batatas (Sweet potato) (Batate)moderately similar to (279) loc_os05g04410 12005.m04974 protein peroxidase 2 precursor, putative, expressed seq=cds; coord=10:85683513..85689992:1; parent_gene=GRMZM2G006727'

'weakly similar to (160) AT4G05490 | Symbols: | F-box family protein (FBL22) | chr4:2771044-2772252 REVERSEmoderately similar to (315) loc_os02g21240 12002.m07364 protein ubiquitin-protein ligase, putative, expressed seq=cds; coord=10:87007644..87011667:1; parent_gene=GRMZM2G028014' 'highly similar to (557) AT1G08250 | Symbols: ADT6 | ADT6 (arogenate dehydratase 6); arogenate dehydratase/ prephenate dehydratase | chr1:2588994-2590235 REVERSEhighly similar to (687) loc_os04g33390 12004.m08428 protein P-protein, putative, expressed seq=cds; coord=10:113515151..113516898:1; parent_gene=GRMZM2G125923'

'weakly similar to (143) AT1G75540 | Symbols: STH2 | STH2 (SALT TOLERANCE HOMOLOG2); transcription factor/ zinc ion binding | chr1:28366059-28367398 FORWARDmoderately similar to (280) loc_os04g45690 12004.m09520 protein salt tolerance-like protein, putative, expressed seq=cds; coord=10:133502022..133503566:1; parent_gene=GRMZM2G098442'

'moderately similar to (216) AT1G62040 | Symbols: ATG8C | ATG8C (autophagy 8c); microtubule binding | chr1:22933216-22934253 FORWARDmoderately similar to (226) loc_os08g09240 12008.m26825 protein autophagy-related protein 8 precursor, putative, expressed seq=cds; coord=10:142965742..142968913:1; parent_gene=GRMZM2G419694'

'moderately similar to (216) AT1G62040 | Symbols: ATG8C | ATG8C (autophagy 8c); microtubule binding | chr1:22933216-22934253 FORWARDmoderately similar to (226) loc_os08g09240 12008.m26825 protein autophagy-related protein 8 precursor, putative, expressed seq=cds; coord=10:142965742..142968913:1; parent_gene=GRMZM2G419694'

'nearly identical (1130) AT1G11720 | Symbols: ATSS3 | ATSS3 (starch synthase 3); starch synthase/ transferase, transferring glycosyl groups | chr1:3952511-3956840 FORWARDnearly identical (1201) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Potato)nearly identical (1712) loc_os04g53310 12004.m10222 protein soluble starch synthase 3, chloroplast precursor, putative, expressed seq=cds; coord=10:142920487..142929525:1; parent_gene=GRMZM2G121612'

'very weakly similar to (99.4) AT1G78390 | Symbols: NCED9, ATNCED9 | NCED9 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 9); 9-cis-epoxycarotenoid dioxygenase | chr1:29490895-29492868 REVERSEweakly similar to (121) loc_os07g05940 12007.m05058 protein viviparous-14, putative, expressed seq=cds; coord=10:144189184..144189881:-1; parent_gene=AC188128.3_FG002'

'nearly identical (1406) AT3G23780 | Symbols: NRPD2A, DRD2, NRPD2, DMS2, NRPE2 | NRPD2A; DNA binding / DNA-directed RNA polymerase | chr3:8567971-8573819 REVERSEweakly similar to (145) RPOB_CHAGL DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (PEP) (Plastid-encoded RNA polymerase subunit beta) (RNA polymerase subunit beta) - Chaetosphaeridium globosumnearly identical (2018) loc_os04g54840 12004.m10376 protein NRPD2a, putative, expressed seq=cds; coord=10:144716135..144739736:1; parent_gene=GRMZM2G427031' 'moderately similar to (289) AT1G62640 | Symbols: KAS III | KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-oxoacyl-[acyl-carrier-protein] synthase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups | chr1:23192502-23194737 FORWARDmoderately similar to (275) FABH_SPIOL 3-oxoacyl-[acyl-carrier-protein] synthase III, chloroplast precursor (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase III) (KAS III) - Spinacia oleracea (Spinach)moderately similar to (400) loc_os04g55060 12004.m10398 protein 3-oxoacyl-synthase III, chloroplast precursor, putative, expressed seq=cds; coord=10:144982082..144986585:-1; parent_gene=GRMZM2G003190'