Table S7. Differentially regulated genes (up and down regulated) in the control compared with THyPRP silenced plants in FAZ at 20 h along with their expression values, fold changes, annotations, GO ids and terms.

Worksheet 2 & 3

Set6					
Line	Array	Details	Time	Treated vs. Con	Set
Control – New Yorker	254331010027_1_3	20h_11_AZ	20h	Control	Set 6
Control – New Yorker	254331010027_1_4	20h_12_AZ	20h		
TAPG + TPRP	254331010036_1_3	20h_47_AZ	20h	Treated	
TAPG + TPRP	254331010036_1_4	20h_48_AZ	20h		

Note:

Fold change expression values are provided as logbase 2

Flagging Criteria:

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

Detected: If the gProcessedSignal value is above background intensity

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

Cut off used to filter up and down regulated genes

Upregulated

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

Downregulated

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

Differentially Regulated Probes

Sample	Up	Down
20h_TPRP_ AZ vs. 20h_Control_AZ_Sense	1663	1160
20h_TPRP_ AZ vs. 20h_Control_AZ_Antisense	1029	807

Worksheet 4 & 5

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

GO ID

Gene Ontology ID

GO ACCESSION

Gene Ontology Function name

p-value :

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

Significant pvalue<0.05

Count in Selection :

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

%Count in Selection :

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

Count in Total :

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

%Count in Total :

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

		20h_AZ_Control					20h_AZ_TAPG + TPRP vs. 20h_AZ_Control					
ProbeNar	Orientatic	Fold 20h	Flag 20h	Fold 20h	Flag 20h	Geomean	Fold 20h	Flag 20h	Fold 20h	Flag 20h	Geomean	P-value
A 96 P00	Sense	0.305	Detected	-0.305	Detected	0.000	1.159	Detected	1.751	Detected	1.455	0.076
A 96 P01	Sense	-0.615	Detected	0.615	Detected	0.000	1.856	Detected	2.337	Detected	2.097	0.087
A 96 P01	Sense	-0.262	Detected	0.262	Detected	0.000	1.181	Detected	1.499	Detected	1.340	0.049
A 96 P01	Sense	-0.487	Detected	0.487	Detected	0.000	2.952	Detected	1.262	Detected	2.107	0.163
A 96 P01	Sense	0.249	Comprom	-0.249	Comprom	0.000	3.566	Detected	3.208	Detected	3.387	0.008
A 96 P04	Sense	0.205	Detected	-0.205	Detected	0.000	1.372	Detected	0.843	Detected	1.108	0.080
A 96 P05	Sense	0.053	Detected	-0.053	Detected	0.000	2.165	Detected	1.518	Detected	1.841	0.030
A 96 P05	Sense	0.549	Detected	-0.549	Detected	0.000	1.830	Detected	1.577	Detected	1.704	0.094
A 96 P05	Sense	-0.284	Detected	0.284	Detected	0.000	1.608	Detected	1.338	Detected	1.473	0.043
A 96 P07	Sense	0.214	Detected	-0.214	Detected	0.000	1.236	Detected	1.679	Detected	1.457	0.042
A 96 P07	Sense	0.365	Detected	-0.365	Detected	0.000	1.707	Detected	1.778	Detected	1.742	0.042
A 96 P07	Sense	-0.903	Detected	0.903	Detected	0.000	1.011	Detected	1.422	Detected	1.217	0.319
A 96 P07	Sense	-0.606	Detected	0.606	Detected	0.000	4.154	Detected	1.461	Detected	2.807	0.198
A 96 P07	Sense	0.403	Detected	-0.403	Detected	0.000	1.406	Detected	1.444	Detected	1.425	0.072
A 96 P08	Sense	-0.057	Detected	0.057	Detected	0.000	1.080	Detected	1.838	Detected	1.459	0.063
A 96 P08	Sense	-0.010	Detected	0.010	Detected	0.000	1.098	Detected	1.008	Detected	1.053	0.002
A 96 P08	Sense	0.437	Detected	-0.437	Detected	0.000	1.288	Detected	1.361	Detected	1.324	0.094
A 96 P08	Sense	0.176	Detected	-0.176	Detected	0.000	1.162	Detected	1.554	Detected	1.358	0.036
A 96 P08	Sense	-0.180	Detected	0.180	Detected	0.000	2.960	Detected	0.858	Detected	1.909	0.215
A 96 P08	Sense	-0.727	Detected	0.727	Detected	0.000	4.100	Detected	1.368	Detected	2.734	0.219
A 96 P08	Sense	-0.688	Detected	0.688	Detected	0.000	4.236	Detected	1.569	Detected	2.903	0.193
A 96 P09	Sense	-0.048	Detected	0.048	Detected	0.000	1.725	Detected	1.109	Detected	1.417	0.045
A 96 P09	Sense	0.220	Detected	-0.220	Detected	0.000	2.134	Detected	1.197	Detected	1.665	0.084
A 96 P10	Sense	0.012	Detected	-0.012	Detected	0.000	2.073	Detected	1.262	Detected	1.668	0.054
A 96 P11	Sense	0.234	Detected	-0.234	Detected	0.000	1.731	Detected	1.675	Detected	1.703	0.019
A 96 P12	Sense	-0.246	Detected	0.246	Detected	0.000	1.728	Detected	1.880	Detected	1.804	0.020
A 96 P12	Sense	-0.273	Comprom	0.273	Detected	0.000	1.297	Detected	1.366	Detected	1.332	0.040
A 96 P12	Sense	-0.314	Detected	0.314	Detected	0.000	1.165	Detected	0.929	Detected	1.047	0.089
A 96 P12	Sense	-0.110	Detected	0.110	Detected	0.000	2.276	Detected	1.785	Detected	2.030	0.017
A 96 P12	Sense	-0.488	Comprom	0.488	Detected	0.000	3.568	Detected	0.855	Detected	2.211	0.265
A 96 P12	Sense	-0.615	Comprom	0.615	Detected	0.000	1.186	Detected	1.999	Detected	1.592	0.163
A 96 P13	Sense	0.391	Detected	-0.391	Detected	0.000	1.351	Detected	1.661	Detected	1.506	0.070
A 96 P14	Sense	-0.667	Detected	0.667	Detected	0.000	4.247	Detected	1.708	Detected	2.978	0.174
A 96 P15	Sense	-1.029	Comprom	1.029	Detected	0.000	3.543	Detected	1.466	Detected	2.505	0.229
A 96 P15	Sense	0.153	Detected	-0.153	Detected	0.000	2.135	Detected	1.311	Detected	1.723	0.059
A 96 P15	Sense	-0.076	Detected	0.076	Detected	0.000	1.495	Detected	1.458	Detected	1.477	0.003
A 96 P16	Sense	0.823	Detected	-0.823	Comprom	0.000	2.506	Detected	1.858	Detected	2.182	0.132
A 96 P17	Sense	0.656	Detected	-0.656	Detected	0.000	1.907	Detected	0.801	Detected	1.354	0.255
A 96 P18	Sense	0.305	Detected	-0.305	Detected	0.000	1.411	Detected	1.311	Detected	1.361	0.048
A 96 P19	Sense	0.155	Detected	-0.155	Detected	0.000	1.408	Detected	1.199	Detected	1.304	0.020
A 96 P19	Sense	0.022	Detected	-0.022	Detected	0.000	1.299	Detected	1.178	Detected	1.238	0.003
A 96 P19	Sense	0.053	Detected	-0.053	Detected	0.000	1.480	Detected	1.426	Detected	1.453	0.002
A 96 P19	Sense	-0.038	Detected	0.038	Detected	0.000	1.662	Detected	2.221	Detected	1.942	0.020
A 96 P19	Sense	0.290	Detected	-0.290	Detected	0.000	1.265	Detected	1.886	Detected	1.576	0.066
A 96 P21	Sense	0.424	Comprom	-0.424	Comprom	0.000	1.364	Detected	2.604	Detected	1.984	0.118
A 96 P22	Sense	0.353	Detected	-0.353	Detected	0.000	1.178	Detected	1.069	Detected	1.123	0.088
A 96 P23	Sense	0.174	Comprom	-0.174	Comprom	0.000	3.082	Detected	1.336	Detected	2.209	0.131
A 96 P24	Sense	-0.322	Detected	0.322	Detected	0.000	1.156	Detected	1.303	Detected	1.230	0.065
A 96 P25	Sense	-0.072	Detected	0.072	Detected	0.000	1.338	Detected	1.721	Detected	1.530	0.017
A 96 P25	Sense	-0.515	Detected	0.515	Detected	0.000	3.745	Detected	0.985	Detected	2.365	0.250
A 96 P26	Sense	-1.026	Detected	1.026	Detected	0.000	1.016	Detected	1.491	Detected	1.253	0.356
GT Sense	Sense	-0.632	Detected	0.632	Detected	0.000	1.443	Detected	1.638	Detected	1.541	0.138
GT Sense	Sense	-0.369	Comprom	0.369	Comprom	0.000	1.200	Detected	1.558	Detected	1.379	0.078
GT Sense	Sense	-0.393	Comprom	0.393	Comprom	0.000	1.458	Detected	2.722	Detected	2.090	0.107
GT Sense	Sense	0.124	Comprom	-0.124	Comprom	0.000	1.446	Detected	1.755	Detected	1.600	0.015
GT Sense	Sense	0.633	Detected	-0.633	Detected	0.000	1.926	Detected	1.731	Detected	1.829	0.104
GT Sense	Sense	-0.026	Comprom	0.026	Comprom	0.000	1.811	Detected	2.836	Detected	2.323	0.045
GT Sense	Sense	0.357	Detected	-0.357	Detected	0.000	0.974	Detected	1.517	Detected	1.246	0.109
GT Sense	Sense	0.435	Detected	-0.435	Detected	0.000	1.741	Detected	1.750	Detected	1.745	0.057
GT Sense	Sense	1.100	Detected	-1.100	Detected	0.000	1.637	Detected	2.195	Detected	1.916	0.233
GT Sense	Sense	-0.266	Detected	0.266	Detected	0.000	1.173	Detected	0.830	Detected	1.002	0.087
GT Sense	Sense	-0.592	Comprom	0.592	Comprom	0.000	2.977	Detected	1.889	Detected	2.433	0.094
GT Sense	Sense	0.819	Detected	-0.819	Detected	0.000	1.491	Detected	1.403	Detected	1.447	0.220
GT Sense	Sense	0.151	Detected	-0.151	Detected	0.000	1.227	Detected	1.209	Detected	1.218	0.015
GT Sense	Sense	0.451	Comprom	-0.451	Comprom	0.000	1.072	Detected	2.047	Detected	1.560	0.144
GT Sense	Sense	0.691	Detected	-0.691	Comprom	0.000	5.037	Detected	2.153	Detected	3.595	0.154
GT Sense	Sense	-0.174	Detected	0.174	Detected	0.000	1.360	Detected	1.708	Detected	1.534	0.025
GT Sense	Sense	-1.051	Comprom	1.051	Detected	0.000	4.033	Detected	3.036	Detected	3.534	0.093
GT Sense	Sense	0.115	Comprom	-0.115	Comprom	0.000	1.132	Detected	2.564	Detected	1.848	0.126
GT Sense	Sense	-0.197	Detected	0.197	Detected	0.000	1.367	Detected	1.525	Detected	1.446	0.021
GT Sense	Sense	-0.292	Comprom	0.292	Comprom	0.000	1.929	Detected	3.230	Detected	2.579	0.069
GT Sense	Sense	0.080	Comprom	-0.080	Comprom	0.000	1.527	Detected	2.562	Detected	2.045	0.060
GT Sense	Sense	0.922	Detected	-0.922	Detected	0.000	0.877	Detected	1.483	Detected	1.180	0.348
GT Sense	Sense	0.163	Comprom	-0.163	Comprom	0.000	4.128	Detected	2.860	Detected	3.494	0.033
GT Sense	Sense	-0.293	Comprom	0.293	Comprom	0.000	0.854	Detected	3.211	Detected	2.032	0.236
GT Sense	Sense	1.298	Detected	-1.298	Detected	0.000	0.891	Detected	1.666	Detected	1.279	0.445
GT Sense	Sense	0.082	Comprom	-0.082	Comprom	0.000	2.826	Detected	3.016	Detected	2.921	0.002
GT Sense	Sense	0.099	Detected	-0.099	Detected	0.000	2.356	Detected	1.612	Detected	1.984	0.036
GT Sense	Sense	0.229	Comprom	-0.229	Comprom	0.000	0.973	Detected	1.743	Detected	1.358	0.094
GT Sense	Sense	1.244	Detected	-1.244	Comprom	0.000	0.829	Detected	1.829	Detected	1.329	0.426
GT Sense	Sense	0.170	Detected	-0.170	Detected	0.000	1.220	Detected	0.951	Detected	1.086	0.038
GT Sense	Sense	-0.952	Comprom	0.952	Detected	0.000	1.860	Detected	2.434	Detected	2.147	0.163
GT Sense	Sense	0.509	Detected	-0.509	Detected	0.000	1.035	Detected	1.012	Detected	1.023	0.182
GT Sense	Sense	-0.449	Comprom	0.449	Comprom	0.000	2.539	Detected	2.645	Detected	2.592	0.029
GT Sense	Sense	0.272	Detected	-0.272	Detected	0.000	1.458	Detected	1.723	Detected	1.591	0.034
GT Sense	Sense	0.807	Comprom	-0.807	Comprom	0.000	0.807	Detected	1.405	Detected	1.106	0.328
GT Sense	Sense	0.228	Detected	-0.228	Detected	0.000	0.912	Detected	1.664	Detected	1.288	0.099
GT Sense	Sense	0.325	Comprom	-0.325	Comprom	0.000	3.426	Detected	1.870	Detected	2.648	0.088
GT Sense	Sense	-0.152	Detected	0.152	Detected	0.000	1.151	Detected	1.134	Detected	1.142	0.017
GT Sense	Sense	0.211	Detected	-0.211	Detected	0.000	2.260	Detected	2.334	Detected	2.297	0.009
GT Sense	Sense	-0.132	Comprom	0.132	Comprom	0.000	0.990	Detected	2.885	Detected	1.938	0.180
GT Sense	Sense	-0.258	Detected	0.258	Detected	0.000	1.361	Detected	1.180	Detected	1.270	0.043
GT Sense	Sense	0.117	Detected	-0.117	Detected	0.000	2.538	Detected	2.802	Detected	2.670	0.004
GT Sense	Sense	0.156	Detected	-0.156	Detected	0.000	1.818	Detected	1.672	Detected	1.745	0.010
GT Sense	Sense	0.002	Comprom	-0.002	Comprom	0.000	1.890	Detected	2.547	Detected	2.219	0.021
GT Sense	Sense	-0.441	Detected	0.441	Detected	0.000	2.036	Detected	1.319	Detected	1.678	0.098
GT Sense	Sense	0.098	Detected	-0.098	Detected	0.000	1.078	Detected	0.949	Detected	1.013	0.013
GT Sense	Sense	0.237	Comprom	-0.237	Comprom	0.000	1.570	Detected	3.051	Detected	2.311	0.097
GT Sense	Sense	0.178	Detected	-0.178	Detected	0.000	1.182	Detected	1.845	Detected	1.514	0.057
GT Sense	Sense	0.186	Detected	-0.186	Detected	0.000	1.807	Detected	1.521	Detected	1.664	0.019
GT Sense	Sense	0.004	Detected	-0.004	Detected	0.000	0.989	Detected	1.130	Detected	1.060	0.004
GT Sense	Sense	0.777	Comprom	-0.777	Comprom	0.000	1.345	Detected	2.562	Detected	1.953	0.186
GT Sense	Sense	-0.785	Comprom	0.785	Detected	0.000	1.610	Detected	1.430	Detected	1.520	0.194
GT Sense	Sense	-0.231	Comprom	0.231	Comprom	0.000	2.235	Detected	1.791	Detected	2.013	0.024
GT Sense	Sense	-0.134	Detected	0.134	Detected	0.000	0.956	Detected	1.199	Detected	1.077	0.027
GT Sense	Sense	-0.185	Detected	0.185	Detected	0.000	0.977	Detected	1.060	Detected	1.019	0.033
GT Sense	Sense	-0.475	Detected	0.475	Detected	0.000	2.822	Detected	1.647	Detected	2.235	0.098
GT Sense	Sense	-0.309	Comprom	0.309	Comprom	0.000	2.109	Detected	1.670	Detected	1.889	0.038
GT Sense	Sense	-0.583	Comprom	0.583	Detected	0.000	1.295	Detected	1.595	Detected	1.445	0.138
GT Sense	Sense	0.178	Detected	-0.178	Detected	0.000	2.345	Detected	0.996	Detected	1.671	0.139
GT Sense	Sense	0.054	Detected	-0.054	Detected	0.000	1.961	Detected	1.393	Detected	1.677	0.028
GT Sense	Sense	-0.570	Comprom	0.570	Comprom	0.000	2.039	Detected	2.269	Detected	2.154	0.066
GT Sense	Sense	0.095	Detected	-0.095	Detected	0.000	1.533	Detected	1.590	Detected	1.562	0.004
GT Sense	Sense	-0.020	Detected	0.020	Detected	0.000	1.268	Detected	0.849	Detected	1.058	0.037
GT Sense	Sense	0.100	Comprom	-0.100	Comprom	0.000	2.265	Detected	2.357	Detected	2.311	0.002
GT Sense	Sense	1.104	Comprom	-1.104	Comprom	0.000	2.686	Detected	3.666	Detected	3.176	0.119
GT Sense	Sense	-0.008	Comprom	0.008	Detected	0.000	2.765	Detected	2.686	Detected	2.725	0.000
GT Sense	Sense	-0.073	Comprom	0.073	Comprom	0.000	0.841	Detected	1.811	Detected	1.326	0.114
GT Sense	Sense	0.774	Detected	-0.774	Comprom	0.000	1.286	Detected	1.053	Detected	1.169	0.274
GT Sense	Sense	-0.071	Detected	0.071	Detected	0.000	2.092	Detected	2.180	Detected	2.136	0.002
GT Sense	Sense	-0.468	Detected	0.468	Detected	0.000	0.900	Detected	1.105	Detected	1.002	0.172
GT Sense	Sense	0.473	Detected	-0.473	Detected	0.000	1.194	Detected	1.189	Detected	1.192	0.128
GT Sense	Sense	0.286	Detected	-0.286	Detected	0.000	1.053	Detected	1.138	Detected	1.095	0.063
GT Sense	Sense	-0.938	Comprom	0.938	Detected	0.000	1.898	Detected	1.092	Detected	1.495	0.281
GT Sense	Sense	-0.169	Comprom	0.169	Comprom	0.000	4.488	Detected	3.701	Detected	4.094	0.011
GT Sense	Sense	-0.365	Detected	0.365	Detected	0.000	1.677	Detected	1.312	Detected	1.494	0.067
GT Sense	Sense	0.838	Detected	-0.838	Detected	0.000	2.466	Detected	1.182	Detected	1.824	0.226
GT Sense	Sense	-0.090	Comprom	0.090	Comprom	0.000	1.360	Detected	2.280	Detected	1.820	0.060
GT Sense	Sense	0.893	Detected	-0.893	Detected	0.000	1.775	Detected	1.791	Detected	1.783	0.184
GT Sense	Sense	-0.067	Detected	0.067	Detected	0.000	4.452	Detected	1.829	Detected	3.140	0.139
GT Sense	Sense	-0.090	Detected	0.090	Detected	0.000	2.045	Detected	1.872	Detected	1.959	0.004
GT Sense	Sense	0.281	Detected	-0.281	Detected	0.000	1.128	Detected	1.336	Detected	1.232	0.054
GT Sense	Sense	-0.003	Comprom	0.003	Comprom	0.000	1.011	Detected	1.392	Detected	1.201	0.024
GT Sense	Sense	0.176	Detected	-0.176	Detected	0.000	1.346	Detected	1.650	Detected	1.498	0.023
GT Sense	Sense	0.640	Detected	-0.640	Detected	0.000	1.109	Detected	1.531	Detected	1.320	0.189
GT Sense	Sense	0.125	Detected	-0.125	Detected	0.000	2.210	Detected	2.176	Detected	2.193	0.003
GT Sense	Sense	0.348	Detected	-0.348	Detected	0.000	2.153	Detected	0.946	Detected	1.550	0.156
GT Sense	Sense	-0.322	Detected	0.322	Detected	0.000	3.432	Detected	2.657	Detected	3.045	0.026
GT Sense	Sense	0.374	Comprom	-0.374	Comprom	0.000	1.399	Detected	1.406	Detected	1.403	0.064
GT Sense	Sense	0.027	Comprom	-0.027	Comprom	0.000	1.529	Detected	1.443	Detected	1.486	0.001
GT Sense	Sense	0.001	Detected	-0.001	Detected	0.000	1.411	Detected	1.621	Detected	1.516	0.005
GT Sense	Sense	-0.015	Comprom	0.015	Comprom	0.000	2.092	Detected	2.785	Detected	2.439	0.020
GT Sense	Sense	-0.448	Comprom	0.448	Comprom	0.000	1.155	Detected	1.847	Detected	1.501	0.118
GT Sense	Sense	-0.096	Detected	0.096	Detected	0.000	2.056	Detected	2.451	Detected	2.254	0.009
GT Sense	Sense	-0.457	Detected	0.457	Detected	0.000	2.446	Detected	1.562	Detected	2.004	0.088
GT Sense	Sense	0.324	Detected	-0.324	Detected	0.000	2.258	Detected	1.702	Detected	1.980	0.043
GT Sense	Sense	-0.753	Comprom	0.753	Detected	0.000	1.242	Detected	1.264	Detected	1.253	0.238
GT Sense	Sense	-0.137	Comprom	0.137	Detected	0.000	1.061	Detected	1.089	Detected	1.075	0.016
GT Sense	Sense	0.670	Comprom	-0.670	Comprom	0.000	1.505	Detected	2.157	Detected	1.831	0.133
GT Sense	Sense	-0.497	Comprom	0.497	Detected	0.000	1.403	Detected	1.547	Detected	1.475	0.099
GT Sense	Sense	-0.260	Comprom	0.260	Detected	0.000	1.893	Detected	2.077	Detected	1.985	0.019
GT Sense	Sense	0.330	Detected	-0.330	Detected	0.000	1.287	Detected	1.150	Detected	1.219	0.069
GT Sense	Sense	0.170	Detected	-0.170	Detected	0.000	1.489	Detected	0.909	Detected	1.199	0.070
GT Sense	Sense	0.160	Comprom	-0.160	Comprom	0.000	2.284	Detected	2.660	Detected	2.472	0.010
GT Sense	Sense	-0.652	Detected	0.652	Detected	0.000	2.806	Detected	1.290	Detected	2.048	0.177
GT Sense	Sense	0.905	Detected	-0.905	Detected	0.000	1.171	Detected	1.572	Detected	1.371	0.277
GT Sense	Sense	0.031	Detected	-0.031	Detected	0.000	0.849	Detected	1.180	Detected	1.014	0.026
GT Sense	Sense	0.132	Detected	-0.132	Detected	0.000	1.189	Detected	1.452	Detected	1.321	0.019
GT Sense	Sense	0.427	Detected	-0.427	Detected	0.000	1.257	Detected	1.746	Detected	1.502	0.093
GT Sense	Sense	0.687	Detected	-0.687	Detected	0.000	1.295	Detected	1.220	Detected	1.257	0.209
GT Sense	Sense	0.223	Comprom	-0.223	Comprom	0.000	1.333	Detected	1.087	Detected	1.210	0.042
GT Sense	Sense	-0.997	Comprom	0.997	Detected	0.000	2.636	Detected	1.555	Detected	2.096	0.206
GT Sense	Sense	0.152	Detected	-0.152	Detected	0.000	2.470	Detected	2.342	Detected	2.406	0.005
GT Sense	Sense	0.093	Detected	-0.093	Detected	0.000	1.810	Detected	2.248	Detected	2.029	0.013
GT Sense	Sense	0.149	Comprom	-0.149	Comprom	0.000	1.689	Detected	2.058	Detected	1.874	0.016
GT Sense	Sense	0.057	Detected	-0.057	Detected	0.000	1.055	Detected	1.249	Detected	1.152	0.009
GT Sense	Sense	0.049	Detected	-0.049	Detected	0.000	1.045	Detected	1.660	Detected	1.352	0.049
GT Sense	Sense	-1.525	Comprom	1.525	Detected	0.000	2.836	Detected	1.637	Detected	2.237	0.306
GT Sense	Sense	0.280	Comprom	-0.280	Comprom	0.000	1.854	Detected	2.873	Detected	2.364	0.056
GT Sense	Sense	-0.133	Detected	0.133	Detected	0.000	1.576	Detected	1.465	Detected	1.521	0.009
GT Sense	Sense	-0.538	Comprom	0.538	Comprom	0.000	2.637	Detected	2.139	Detected	2.388	0.056
GT Sense	Sense	-0.317	Comprom	0.317	Comprom	0.000	1.085	Detected	1.728	Detected	1.406	0.089
GT Sense	Sense	-0.165	Detected	0.165	Detected	0.000	1.086	Detected	1.942	Detected	1.514	0.081
GT Sense	Sense	0.307	Detected	-0.307	Comprom	0.000	3.955	Detected	4.757	Detected	4.356	0.013
GT Sense	Sense	0.408	Comprom	-0.408	Comprom	0.000	0.970	Detected	1.133	Detected	1.052	0.127
GT Sense	Sense	-0.100	Detected	0.100	Detected	0.000	1.336	Detected	1.190	Detected	1.263	0.009
GT Sense	Sense	0.110	Detected	-0.110	Detected	0.000	0.801	Detected	1.412	Detected	1.107	0.076
GT Sense	Sense	0.266	Comprom	-0.266	Comprom	0.000	1.125	Detected	1.952	Detected	1.539	0.089
GT Sense	Sense	0.112	Detected	-0.112	Detected	0.000	2.603	Detected	3.207	Detected	2.905	0.012
GT Sense	Sense	0.472	Detected	-0.472	Detected	0.000	3.338	Detected	2.997	Detected	3.167	0.024
GT Sense	Sense	0.242	Detected	-0.242	Detected	0.000	1.409	Detected	0.931	Detected	1.170	0.075
GT Sense	Sense	0.392	Comprom	-0.392	Comprom	0.000	1.422	Detected	1.476	Detected	1.449	0.066
GT Sense	Sense	-0.058	Comprom	0.058	Comprom	0.000	2.105	Detected	1.671	Detected	1.888	0.014
GT Sense	Sense	0.588	Detected	-0.588	Comprom	0.000	2.246	Detected	1.035	Detected	1.640	0.191
GT Sense	Sense	2.212	Detected	-2.212	Detected	0.000	1.586	Detected	1.492	Detected	1.539	0.559
GT Sense	Sense	-0.094	Detected	0.094	Detected	0.000	1.074	Detected	1.231	Detected	1.152	0.011
GT Sense	Sense	0.165	Detected	-0.165	Detected	0.000	2.140	Detected	1.819	Detected	1.980	0.013
GT Sense	Sense	0.494	Comprom	-0.494	Comprom	0.000	1.588	Detected	2.147	Detected	1.867	0.081
GT Sense	Sense	-0.193	Detected	0.193	Detected	0.000	3.456	Detected	1.102	Detected	2.279	0.196
GT Sense	Sense	-0.701	Detected	0.701	Detected	0.000	3.494	Detected	4.385	Detected	3.939	0.042
GT Sense	Sense	0.251	Detected	-0.251	Detected	0.000	1.989	Detected	2.810	Detected	2.400	0.038
GT Sense	Sense	0.543	Detected	-0.543	Detected	0.000	1.131	Detected	1.483	Detected	1.307	0.149
GT Sense	Sense	-0.127	Detected	0.127	Detected	0.000	1.583	Detected	1.649	Detected	1.616	0.007
GT Sense	Sense	0.673	Comprom	-0.673	Comprom	0.000	3.493	Detected	2.742	Detected	3.118	0.056
GT Sense	Sense	0.082	Comprom	-0.082	Comprom	0.000	1.133	Detected	2.915	Detected	2.024	0.152
GT Sense	Sense	-0.229	Comprom	0.229	Comprom	0.000	4.264	Detected	2.240	Detected	3.252	0.088
GT Sense	Sense	0.414	Comprom	-0.414	Comprom	0.000	1.609	Detected	2.446	Detected	2.028	0.075
GT Sense	Sense	-0.410	Detected	0.410	Detected	0.000	1.331	Detected	0.976	Detected	1.153	0.123
GT Sense	Sense	-0.013	Detected	0.013	Detected	0.000	2.024	Detected	2.120	Detected	2.072	0.001
GT Sense	Sense	0.199	Detected	-0.199	Detected	0.000	1.255	Detected	1.772	Detected	1.514	0.043
GT Sense	Sense	-0.014	Detected	0.014	Detected	0.000	1.860	Detected	2.289	Detected	2.074	0.011
GT Sense	Sense	0.306	Detected	-0.306	Detected	0.000	1.853	Detected	1.986	Detected	1.920	0.026
GT Sense	Sense	0.481	Detected	-0.481	Detected	0.000	1.890	Detected	1.722	Detected	1.806	0.066
GT Sense	Sense	1.074	Detected	-1.074	Detected	0.000	1.111	Detected	1.312	Detected	1.211	0.378
GT Sense	Sense	0.286	Comprom	-0.286	Comprom	0.000	3.244	Detected	4.346	Detected	3.795	0.026
GT Sense	Sense	-0.447	Detected	0.447	Detected	0.000	2.274	Detected	2.000	Detected	2.137	0.045
GT Sense	Sense	1.026	Detected	-1.026	Comprom	0.000	1.076	Detected	1.906	Detected	1.491	0.310
GT Sense	Sense	-0.198	Comprom	0.198	Comprom	0.000	1.175	Detected	1.482	Detected	1.329	0.034
GT Sense	Sense	0.973	Comprom	-0.973	Comprom	0.000	1.098	Detected	2.158	Detected	1.628	0.279
GT Sense	Sense	-0.522	Comprom	0.522	Comprom	0.000	1.335	Detected	1.955	Detected	1.645	0.114
GT Sense	Sense	0.048	Detected	-0.048	Detected	0.000	1.454	Detected	0.929	Detected	1.191	0.047
GT Sense	Sense	-0.267	Comprom	0.267	Detected	0.000	1.014	Detected	1.334	Detected	1.174	0.064
GT Sense	Sense	0.102	Detected	-0.102	Detected	0.000	1.241	Detected	0.945	Detected	1.093	0.026
GT Sense	Sense	-0.035	Detected	0.035	Detected	0.000	1.766	Detected	3.074	Detected	2.420	0.066
GT Sense	Sense	0.376	Detected	-0.376	Detected	0.000	2.383	Detected	0.830	Detected	1.607	0.204
GT Sense	Sense	-0.216	Detected	0.216	Detected	0.000	1.110	Detected	1.305	Detected	1.207	0.036
GT Sense	Sense	0.191	Comprom	-0.191	Comprom	0.000	2.014	Detected	2.558	Detected	2.286	0.021
GT Sense	Sense	0.094	Detected	-0.094	Detected	0.000	2.218	Detected	2.521	Detected	2.370	0.006
GT Sense	Sense	-0.146	Comprom	0.146	Comprom	0.000	1.856	Detected	3.534	Detected	2.695	0.087
GT Sense	Sense	-1.224	Comprom	1.224	Detected	0.000	1.372	Detected	2.406	Detected	1.889	0.291
GT Sense	Sense	-0.964	Comprom	0.964	Detected	0.000	0.895	Detected	2.254	Detected	1.574	0.314
GT Sense	Sense	0.437	Detected	-0.437	Detected	0.000	1.756	Detected	2.059	Detected	1.907	0.054
GT Sense	Sense	0.083	Comprom	-0.083	Comprom	0.000	2.605	Detected	2.704	Detected	2.655	0.001
GT Sense	Sense	-0.148	Comprom	0.148	Comprom	0.000	2.157	Detected	2.619	Detected	2.388	0.013
GT Sense	Sense	-0.107	Detected	0.107	Detected	0.000	1.121	Detected	1.054	Detected	1.087	0.010
GT Sense	Sense	-0.367	Comprom	0.367	Comprom	0.000	0.917	Detected	2.341	Detected	1.629	0.179
GT Sense	Sense	0.446	Detected	-0.446	Detected	0.000	1.549	Detected	0.893	Detected	1.221	0.158
GT Sense	Sense	0.576	Comprom	-0.576	Comprom	0.000	0.949	Detected	1.459	Detected	1.204	0.196
GT Sense	Sense	0.026	Detected	-0.026	Detected	0.000	1.693	Detected	1.358	Detected	1.525	0.012
GT Sense	Sense	-0.766	Comprom	0.766	Detected	0.000	1.815	Detected	1.206	Detected	1.511	0.208
GT Sense	Sense	0.478	Detected	-0.478	Detected	0.000	1.339	Detected	1.028	Detected	1.184	0.143
GT Sense	Sense	0.557	Comprom	-0.557	Comprom	0.000	2.328	Detected	2.371	Detected	2.350	0.052
GT Sense	Sense	-0.316	Detected	0.316	Detected	0.000	4.646	Detected	2.761	Detected	3.704	0.065
GT Sense	Sense	0.116	Comprom	-0.116	Comprom	0.000	7.145	Detected	2.605	Detected	4.875	0.165
GT Sense	Sense	-0.556	Detected	0.556	Detected	0.000	2.714	Detected	2.812	Detected	2.763	0.038
GT Sense	Sense	0.291	Detected	-0.291	Detected	0.000	1.658	Detected	1.280	Detected	1.469	0.052
GT Sense	Sense	0.174	Detected	-0.174	Detected	0.000	1.568	Detected	1.375	Detected	1.472	0.018
GT Sense	Sense	0.161	Comprom	-0.161	Comprom	0.000	2.055	Detected	2.668	Detected	2.361	0.021
GT Sense	Sense	0.619	Detected	-0.619	Detected	0.000	1.244	Detected	1.079	Detected	1.162	0.204
GT Sense	Sense	0.472	Detected	-0.472	Detected	0.000	1.269	Detected	1.163	Detected	1.216	0.124
GT Sense	Sense	0.159	Detected	-0.159	Detected	0.000	0.899	Detected	1.273	Detected	1.086	0.047
GT Sense	Sense	0.004	Detected	-0.004	Detected	0.000	1.826	Detected	1.711	Detected	1.769	0.001

GT	Sense	Sense	-0.172	Comprom	0.172	Comprom	0.000	0.838	Detected	1.841	Detected	1.340	0.127	GT	Sens	contig168	contig168	Cytokinin	CCCAGC	contig168	Solyc11g	Solyc11g	Cytokinin riboside 5%26apos%			contig168	Solyc11g	Cytokinin riboside 5		SL2.40ch	AT2G28305.1		unknown	chr2:120	6.07042	9.16733	10.4773	12.0576	15.0239	25.2698
GT	Sense	Sense	0.031	Comprom	-0.031	Comprom	0.000	1.401	Detected	1.605	Detected	1.503	0.005	GT	Sens	contig168	contig168	Unknown	CATTAG	contig168	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)%:			contig168	Solyc01g	Unknown Protein (A		SL2.40ch	AT1G58070.1		unknown	chr1:215	4.7419	5.41019	11.4076	5.6772	15.0666	14.573
GT	Sense	Sense	-0.467	Comprom	0.467	Comprom	0.000	1.926	Detected	2.635	Detected	2.281	0.060	GT	Sens	contig168	contig168	Multidrug	GAACAC	contig168	Solyc06g	Solyc06g	Multidrug	GO:0015	GO:0015	contig168	Solyc06g	Multidrug	GO:0015	SL2.40ch	AT1G23710.1		unknown	chr1:838	2.51208	5.7138	3.4656	2.14405	16.2134	22.2589
GT	Sense	Sense	-0.274	Detected	0.274	Detected	0.000	3.031	Detected	2.637	Detected	2.834	0.014	GT	Sens	contig169	contig169	40S ribos	TGATGT	contig169	Solyc05g	Solyc05g	40S ribos	GO:0003	GO:0003	contig169	Solyc03g	40S ribos	GO:0032	SL2.40ch	AT3G02560.2		40S ribos	chr3:542	43.6674	76.0073	154.082	243.112	530.555	338.81
GT	Sense	Sense	-0.254	Detected	0.254	Detected	0.000	1.297	Detected	1.878	Detected	1.588	0.054	GT	Sens	contig169	contig169	Unknown	TCTTTT	contig169	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig169	Solyc03g	Unknown Protein (A		SL2.40ch	AT2G35155.1		catalytic	chr2:148	15.5586	26.3377	62.0396	60.4507	56.0343	70.358
GT	Sense	Sense	0.170	Detected	-0.170	Detected	0.000	1.129	Detected	1.049	Detected	1.089	0.025	GT	Sens	contig170	contig170	Prolyl 4-h	CAGCAG	contig170	Solyc02g	Solyc02g	Prolyl 4-h	GO:0016	GO:0016	contig170	Solyc02g	Prolyl 4-h	GO:0004	SL2.40ch	AT4G33910.1		oxidored	chr4:162	1556.06	1463.91	2419.94	2160.22	3717.49	2952.24
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	1.084	Detected	1.479	Detected	1.282	0.042	GT	Sens	contig171	contig171	Protein L	GAGCAT	contig171	Solyc03g	Solyc03g	Protein LSM14 homolog A-B (A			contig171	Solyc03g	Protein LSM14 hom		SL2.40ch	AT5G238	EMB1265	CPSF100	chr5:805	17.3973	15.9744	18.7426	17.0487	39.8123	43.9436
GT	Sense	Sense	0.731	Comprom	-0.731	Comprom	0.000	0.878	Detected	1.710	Detected	1.294	0.264	GT	Sens	contig171	contig171	Heavy me	ATTTGT	contig171	Solyc07g	Solyc07g	Heavy me	GO:0030	GO:0030	contig171	Solyc07g	Heavy me	GO:0030	SL2.40ch	AT5G08415.1		lipoic aci	chr5:271	8.23315	3.55949	7.94752	7.07406	11.2084	16.7469
GT	Sense	Sense	0.434	Detected	-0.434	Detected	0.000	1.372	Detected	1.877	Detected	1.624	0.084	GT	Sens	contig171	contig171	Myb-relat	TTGGAC	contig171	Solyc12g	Solyc12g	Myb-relat	GO:0045449		contig171	Solyc12g	Myb-relat	GO:0003	SL2.40ch	AT5G542	MYB49. A	MYB49 (	chr5:220	66.7738	43.5738	124.509	73.1359	157.308	187.272
GT	Sense	Sense	-0.730	Detected	0.730	Detected	0.000	1.282	Detected	0.921	Detected	1.101	0.280	GT	Sens	contig172	contig172	Transmem	AGTAAG	contig172	Solyc07g	Solyc07g	Transmem	GO:0016	GO:0016	contig172	Solyc07g	Transmem	GO:0016	SL2.40ch	AT5G569	emb1789	emb1789	chr5:230	290.883	952.034	2081.87	1766.6	1441.41	941.841
GT	Sense	Sense	0.336	Comprom	-0.336	Comprom	0.000	2.328	Detected	2.452	Detected	2.390	0.020	GT	Sens	contig172	contig172	GTP bind	AATTTT	contig172	Solyc08g	Solyc08g	GTP binding protein (AHRD V1			contig172	Solyc08g	GTP binding protein		SL2.40ch	AT4G01895.1		systemic	chr4:819	7.45906	5.57718	37.8021	26.3949	36.4938	33.3658
GT	Sense	Sense	0.315	Detected	-0.315	Detected	0.000	1.260	Detected	1.415	Detected	1.337	0.054	GT	Sens	contig173	contig173	Zinc finge	ATAGAT	contig173	Solyc09g	Solyc09g	Zinc finge	GO:0005	GO:0005	contig173	Solyc09g	Zinc finge	GO:0005	SL2.40ch	AT2G36320.1		zinc fing	chr2:152	2888.19	2222.59	6688.32	5892.6	6836.04	6387.22
GT	Sense	Sense	0.287	Comprom	-0.287	Comprom	0.000	1.695	Detected	1.491	Detected	1.593	0.035	GT	Sens	contig173	contig173	Transpos	GTCAGA	contig173	Solyc02g	Solyc02g	Transposase (Fragment) (AHR			contig173	Solyc02g	Transposase (Fragm		SL2.40ch	AT4G055	ATEHD2	ATEHD2	chr4:280	7.75716	6.20136	21.8189	31.5294	25.2971	18.433
GT	Sense	Sense	-0.116	Detected	0.116	Detected	0.000	1.586	Detected	1.462	Detected	1.524	0.007	GT	Sens	contig173	contig173	Unknown	AATTTCT	contig173	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig173	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G26540.1		kinase	chr4:133	1543.55	2159.53	2983.02	2909.58	6176.04	4755.16
GT	Sense	Sense	0.197	Detected	-0.197	Detected	0.000	0.998	Detected	1.173	Detected	1.085	0.037	GT	Sens	contig174	contig174	LINE-type	TTGTTT	contig174	Solyc04g	Solyc04g	LINE-type retrotransposon LIb			contig174	Solyc10g	Linalool s	GO:0034	SL2.40ch	AT1G181	ATMPK8	ATMPK8	chr1:624	372.173	336.994	574.308	605.087	796.583	755.205
GT	Sense	Sense	-0.388	Detected	0.388	Detected	0.000	4.327	Detected	2.158	Detected	3.242	0.106	GT	Sens	contig174	contig174	Ferredox	CTCGTG	contig174	Solyc11g	Solyc11g	Ferredox	GO:0051	GO:0051	contig174	Solyc11g	Ferredox	GO:0051	SL2.40ch	AT1G07620.1		FUNCTIO	chr1:234	22.7332	46.3307	157.829	84.1344	733.758	136.915
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	1.006	Detected	1.226	Detected	1.116	0.013	GT	Sens	contig174	contig174	Unknown	TTTAAT	contig174	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig174	Solyc02g	Unknown Protein (A		SL2.40ch	AT1G692	RPK1	RPK1 (RE	chr1:260	15.1433	19.6987	50.3928	63.5641	39.0687	38.2094
GT	Sense	Sense	-0.227	Detected	0.227	Detected	0.000	2.334	Detected	1.945	Detected	2.140	0.019	GT	Sens	contig175	contig175	ATP-bind	GTGATT	contig175	Solyc11g	Solyc11g	ATP-bind	GO:0016	GO:0016	contig175	Solyc05g	ATP-bind	GO:0042	SL2.40ch	AT2G363	PDR6. AT	PDR6: AT	chr2:152	311.217	507.613	833.319	1294.45	2258.2	1446.84
GT	Sense	Sense	0.799	Detected	-0.799	Detected	0.000	1.425	Detected	1.240	Detected	1.332	0.239	GT	Sens	contig175	contig175	Pollen all	GGCAGA	contig175	Solyc06g	Solyc06g	Pollen allergen (AHRD V1 *-*- O			contig175	Solyc06g	Pollen allergen (AHR		SL2.40ch	AT2G30370.1		allergen-	chr2:129	556.153	218.709	777.379	456.163	1055	778.772
GT	Sense	Sense	0.279	Detected	-0.279	Detected	0.000	0.993	Detected	1.380	Detected	1.187	0.073	GT	Sens	contig175	contig175	Unknown	TCTGGT	contig175	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig175	Solyc04g	Unknown Protein (A		SL2.40ch	AT2G30730.1		serine/th	chr2:130	25.7977	20.8751	93.985	59.4032	52.0381	57.1053
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	1.464	Detected	1.380	Detected	1.422	0.004	GT	Sens	contig175	contig175	Magnesiu	TGGTAT	contig175	Solyc03g	Solyc03g	Magnesiu	GO:0005	GO:0005	contig175	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	103.84	110.453	252.107	228.04	332.742	263.494
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	1.169	Detected	1.791	Detected	1.480	0.048	GT	Sens	contig176	contig176	Genomic	TGAACA	contig176	Solyc10g	Solyc10g	Genomic DNA chromosome 5			contig176	Solyc03g	Jp18 (AHRD V1 ***- (		SL2.40ch	AT1G283	AtRLP4	AtRLP4 (	chr1:994	20.8235	20.7519	32.3836	32.2881	52.6576	68.0349
GT	Sense	Sense	0.232	Detected	-0.232	Detected	0.000	1.241	Detected	1.003	Detected	1.122	0.050	GT	Sens	contig177	contig177	Abscisic	AATTACA	contig177	Solyc03g	Solyc03g	Abscisic	GO:0004	GO:0004	contig177	Solyc03g	Abscisic	GO:0004	SL2.40ch	AT2G38310.1		unknown	chr2:160	292.679	252.697	581.471	514.301	724.157	515.204
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	1.601	Detected	1.090	Detected	1.345	0.040	GT	Sens	contig177	contig177	L-tyrosin	GGTATT	contig177	Solyc12g	Solyc12g	L-tyrosine transporter (AHRD V			contig177	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G51160.1				3589.93	3698.03	8874.41	7825.57	12447.1	7332
GT	Sense	Sense	-0.192	Detected	0.192	Detected	0.000	1.093	Detected	0.941	Detected	1.017	0.039	GT	Sens	contig178	contig178	Unknown	CAATTG	contig178	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig178	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G33820.1		glycosyl	chr4:162	3831.45	5951.9	13117.5	7042.74	11474.3	8666.04
GT	Sense	Sense	0.527	Detected	-0.527	Detected	0.000	1.273	Detected	1.884	Detected	1.579	0.122	GT	Sens	contig178	contig178	Glutathio	ATACAT	contig178	Solyc10g	Solyc10g	Glutathio	GO:0004	GO:0004	contig178	Solyc10g	Glutathio	GO:0004	SL2.40ch	AT3G43800.1				48.4684	27.7809	71.6975	58.7188	99.8799	128.088
GT	Sense	Sense	-0.581	Detected	0.581	Detected	0.000	4.337	Detected	1.005	Detected	2.671	0.269	GT	Sens	contig179	contig179	Cytochro	TTCGAC	contig179	Solyc06g	Solyc06g	Cytochro	GO:0019	GO:0019	contig179	Solyc06g	Cytochro	GO:0019	SL2.40ch	AT3G566	CYP94D2	CYP94D2	chr3:209	19.0742	50.8229	102.154	82.128	709.038	59.0934
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	2.009	Detected	1.131	Detected	1.570	0.073	GT	Sens	contig179	contig179	Cc-nbs-lr	GGTCCC	contig179	Solyc10g	Solyc10g	Cc-nbs-lr	GO:0006	GO:0006	contig179	Solyc10g	Cc-nbs-lr	GO:0005	SL2.40ch	AT2G46780.1				88.1323	92.0511	234.969	199.303	408.275	186.578
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	1.497	Detected	1.792	Detected	1.644	0.015	GT	Sens	contig179	contig179	Protein ki	GGGTAA	contig179	Solyc07g	Solyc07g	Protein ki	GO:0005	GO:0005	contig179	Solyc07g	Protein ki	GO:0005	SL2.40ch	AT3G458	RUS1	RUS1 (RO	chr3:168	99.352	97.8215	105.358	171.663	313.405	322.697
GT	Sense	Sense	-0.030	Comprom	0.030	Comprom	0.000	1.301	Detected	2.177	Detected	1.739	0.058	GT	Sens	contig179	contig179	Cytochro	CGGTTC	contig179	Solyc04g	Solyc04g	Cytochro	GO:0019	GO:0019	contig179	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT1G130	CYP71B2	CYP71B2	chr1:445	3.48301	4.32432	11.7585	12.6171	10.771	16.5963
GT	Sense	Sense	-0.249	Detected	0.249	Detected	0.000	1.994	Detected	1.793	Detected	1.894	0.020	GT	Sens	contig179	contig179	Serine ca	CAACTA	contig179	Solyc02g	Solyc02g	Serine ca	GO:0004	GO:0004	contig179	Solyc02g	Serine ca	GO:0042	SL2.40ch	AT1G110	scpl31	scpl31 (s	chr1:369	15.7623	26.4891	62.5173	47.7846	91.7198	66.9372
GT	Sense	Sense	-0.811	Comprom	0.811	Detected	0.000	1.905	Detected	1.681	Detected	1.793	0.160	GT	Sens	contig179	contig179	LRR rece	AGTATC	contig179	Solyc07g	Solyc07g	LRR rece	GO:0005	GO:0005	contig179	Solyc07g	LRR rece	GO:0004	SL2.40ch	#N/A	#N/A	#N/A	#N/A	3.33817	12.2334	5.17295	8.26336	26.9664	19.3691
GT	Sense	Sense	-0.540	Detected	0.540	Detected	0.000	3.075	Detected	0.973	Detected	2.024	0.229	GT	Sens	contig179	contig179	Metal ion	ACTACT	contig179	Solyc06g	Solyc06g	Metal ion	GO:0030	GO:0030	contig179	Solyc06g	Metal ion	GO:0046	SL2.40ch	AT5G50740.3		metal ion	chr5:206	52.7922	132.886	145.89	223.278	795.159	155.48
GT	Sense	Sense	-1.927	Comprom	1.927	Detected	0.000	1.740	Detected	1.601	Detected	1.670	0.478	GT	Sens	contig180	contig180	Early nod	CAAAAAT	contig180	Solyc08g	Solyc08g	Early nod	GO:0009	GO:0009	contig180	Solyc08g	Early nod	GO:0009	SL2.40ch	AT4G32490.1		plastocy	chr4:156	2.78544	47.964	28.3455	20.7292	43.4829	33.1524
GT	Sense	Sense	0.260	Comprom	-0.260	Comprom	0.000	1.895	Detected	1.815	Detected	1.855	0.020	GT	Sens	contig180	contig180	Uncharac	TCTAAT	contig180	Solyc06g	Solyc06g	Uncharacterized GPI-anchored			contig180	Solyc06g	Uncharacterized GP		SL2.40ch	AT3G27810.1				4.90636	4.07107	3.00978	4.52535	18.7192	14.8682
GT	Sense	Sense	-0.133	Detected	0.133	Detected	0.000	3.400	Detected	0.928	Detected	2.164	0.224	GT	Sens	contig180	contig180	Histidine	CCAAGA	contig180	Solyc05g	Solyc05g	Histidine	GO:0015	GO:0015	contig180	Solyc05g	Histidine	GO:0015	SL2.40ch	AT1G25530.1		lysine an	chr1:896	67.3934	96.4958	190.858	212.137	958.743	145.066
GT	Sense	Sense	0.194	Comprom	-0.194	Comprom	0.000	5.503	Detected	2.529	Detected	4.016	0.116	GT	Sens	contig181	contig181	Unknown	GTTGAT	contig181	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig181	Solyc04g	Unknown Protein (A		SL2.40ch	AT4G141	MET2. DM	DMT2 (D	chr4:814	2.58609	2.35206	2.61962	2.08223	125.974	13.4581
GT	Sense	Sense	0.095	Comprom	-0.095	Comprom	0.000	0.948	Detected	2.956	Detected	1.952	0.193	GT	Sens	contig181	contig181	Ethylene	GGACAA	contig181	Solyc12g	Solyc12g	Ethylene	GO:0006	GO:0006	contig181	Solyc04g	Ethylene-	GO:0003	SL2.40ch	AT4G28140.1		AP2 dom	chr4:139	5.72143	5.97141	3.97335	6.25482	12.7003	42.899
GT	Sense	Sense	0.304	Detected	-0.304	Detected	0.000	1.169	Detected	2.441	Detected	1.805	0.125	GT	Sens	contig181	contig181	Myb fami	CTAACG	contig181	Solyc01g	Solyc01g	Myb fami	GO:0003	GO:0003	contig181	Solyc09g	Cytochro	GO:0005	SL2.40ch	AT5G016	BRCA2B.	BRCA2B	chr5:235	100.068	78.1621	164.967	159.554	224.058	454.031
GT	Sense	Sense	-0.237	Detected	0.237	Detected	0.000	0.964	Detected	1.207	Detected	1.085	0.055	GT	Sens	contig182	contig182	EPF-type	AATTAT	contig182	Solyc03g	Solyc03g	EPF-type	GO:0003	GO:0003	contig182	Solyc03g	EPF-type	GO:0003	SL2.40ch	AT3G580	GIS	GIS (GLA	chr3:215	45.8906	75.8485	87.1983	98.4609	129.638	128.763
GT	Sense	Sense	-0.422	Comprom	0.422	Comprom	0.000	3.471	Detected	3.414	Detected	3.442	0.015	GT	Sens	contig182	contig182	Unknown	GTGTAT	contig182	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig182	Solyc09g	Unknown Protein (A		SL2.40ch	AT3G52700.1		unknown	chr3:195	3.43595	7.34253	19.6555	29.7923	62.7279	50.6212
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	0.924	Detected	1.436	Detected	1.180	0.044	GT	Sens	contig182	contig182	Unknown	ACTGGT	contig182	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig182	Solyc04g	Unknown Protein (A		SL2.40ch	AT4G34360.1		protease	chr4:164	397.278	463.466	676.704	741.876	917.116	1097.81
GT	Sense	Sense	-0.292	Comprom	0.292	Comprom	0.000	1.249	Detected	2.832	Detected	2.041	0.137	GT	Sens	contig182	contig182	LEA-like	TTACAA	contig182	Solyc02g	Solyc02g	LEA-like protein (AHRD V1 *-*- (			contig182	Solyc02g	LEA-like protein (AH		SL2.40ch	AT1G072	UGT71C4	UGT71C4	chr1:222	4.12086	7.35311	10.3071	6.27124	14.7347	37.0708
GT	Sense	Sense	-0.805	Comprom	0.805	Detected	0.000	1.861	Detected	1.580	Detected	1.721	0.170	GT	Sens	contig183	contig183	Unknown	GCTCTA	contig183	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig183	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G454	ZPR1	ZPR1 (LIT	chr2:187	7.70076	27.9673	34.9315	21.3305	60.0602	41.4822
GT	Sense	Sense	-0.258	Comprom	0.258	Comprom	0.000	1.538	Detected	1.815	Detected	1.677	0.029	GT	Sens	contig183	contig183	Swap (Su	ATCTTC	contig183	Solyc10g	Solyc10g	Swap (Suppressor-of-White-AP			contig183	Solyc10g	Swap (Suppressor-o		SL2.40ch	AT5G41550.1		disease r	chr5:166	5.19755	8.84975	6.83413	7.26997	22.1891	22.5659
GT	Sense	Sense	0.164	Comprom	-0.164	Comprom	0.000	1.056	Detected	2.222	Detected	1.639	0.114	GT	Sens	contig184	contig184	Ethylene-	TCACCA	contig184	Solyc05g	Solyc05g	Ethylene-	GO:0006	GO:0006	contig184	Solyc05g	Ethylene-	GO:0003	SL2.40ch	AT2G312	ATERF15	ATERF15	chr2:133	4.51774	4.28335	2.62222	3.80402	10.3009	19.4101
GT	Sense	Sense	0.685	Comprom	-0.685	Comprom	0.000	2.699	Detected	2.589	Detected	2.644	0.061	GT	Sens	contig184	contig184	Sucrose s	GTGCTC	contig184	Solyc12g	Solyc12g	Sucrose s	GO:0016	GO:0016	contig184	Solyc12g	Sucrose s	GO:0016	SL2.40ch	AT3G431	SUS4. AT	SUS4: UD	chr3:151	9.46581	4.35964	13.2109	13.5488	46.9954	36.5383
GT	Sense	Sense	-0.116	Detected	0.116	Detected	0.000	1.683	Detected	1.648	Detected	1.666	0.005	GT	Sens	contig184	contig184	Heat shoc	AAGGAG	contig184	Solyc07g	Solyc07g	Heat shock protein Hsp20 (AHR			contig184	Solyc07g	Heat shock protein		SL2.40ch	AT5G64690.1		neurofila	chr5:258	44.9398	62.8668	76.1302	90.4241	192.288	157.513
GT	Sense	Sense	0.171	Comprom	-0.171	Comprom	0.000	2.854	Detected	2.653	Detected	2.754	0.005	GT	Sens	contig184	contig184	Glycogen	GATGAA	contig184	Solyc01g	Solyc01g	Glycogen	GO:0016	GO:0016	contig184	Solyc01g	Glycogen	GO:0016	SL2.40ch	AT3G186	PGSIP1	PGSIP1 (	chr3:641	2.40471	2.25822	11.0968	13.6569	18.9831	13.8569
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	1.897	Detected	0.863	Detected	1.380	0.131	GT	Sens	contig185	contig185	Serine/thr	GATGCT	contig185	Solyc05g	Solyc05g	Serine/thr	GO:0019	GO:0019	contig185	Solyc05g	Serine/thr	GO:0019	SL2.40ch	AT4G03230.1		ATP bind	chr4:141	41.5352	37.3147	68.5043	50.9896	165.13	67.6823
GT	Sense	Sense	0.375	Detected	-0.375	Detected	0.000	1.540	Detected	1.839	Detected	1.689	0.053	GT	Sens	contig185	contig185	Unknown	TTCTTT	contig185	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig185	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G229	ATCHX9.	ATCHX9:	chr5:766	92.0275	65.1351	149.338	150.409	253.61	261.856
GT	Sense	Sense	-0.666	Comprom	0.666	Comprom	0.000	6.452	Detected	4.350	Detected	5.401	0.049	GT	Sens	contig185	contig185	Non-syml	CTTTGA	contig185	Solyc07g	Solyc07g	Non-syml	GO:0019	GO:0019	contig185	Solyc07g	Non-syml	GO:0005	SL2.40ch	AT2G160	GLB1. AH	AHB1 (AR	chr2:698	2.40583	7.20743	19.6508	36.1206	410.64	80.2898
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	1.634	Detected	1.088	Detected	1.361	0.039	GT	Sens	contig186	contig186	Gibberell	GTTTTG	contig186	Solyc02g	Solyc02g	Gibberell	GO:0045	GO:0045	contig186	Solyc02g	Gibberell	GO:0045	SL2.40ch	AT4G212	ATGA2OX	GA2OX8	chr4:113	35.3942	39.1572	55.777	38.8574	130.163	74.8154
GT	Sense	Sense	0.342	Detected	-0.342	Detected	0.000	0.905	Detected	2.031	Detected	1.468	0.156	GT	Sens	contig186	contig186	1-aminoc	GTCCTG	contig186	Solyc09g	Solyc09g	1-aminoc	GO:0010	|GO:0016	contig186	Solyc09g	1-aminoc	GO:0010	SL2.40ch	AT2G30840.1		2-oxoglu	chr2:131	112.053	83.0838	355.768	604.485	203.574	372.959
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	0.877	Detected	1.292	Detected	1.085	0.040	GT	Sens	contig187	contig187	Protein p	GAAAAG	contig187	Solyc01g	Solyc01g	Protein phosphatase-2C (AHRD			contig187	Solyc01g067980.1.1				AT1G32670.1		unknown	chr1:118	55.0204	58.1159	153.841	141.571	117.022	130.952
GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	1.831	Detected	2.525	Detected	2.178	0.027	GT	Sens	contig187	contig187	Unknown	GGCGCG	contig187	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)%:			contig187	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G390	AtGH9B18	AtGH9B1	chr4:181	65.1075	89.6999	503.389	198.956	306.214	415.883
GT	Sense	Sense	-0.046	Comprom	0.046	Comprom	0.000	2.952	Detected	1.179	Detected	2.065	0.146	GT	Sens	contig188	contig188	Glutathio	AAATTT	contig188	Solyc09g	Solyc09g	Glutathio	GO:0004	GO:0004	contig188	Solyc09g	Glutathio	GO:0004	SL2.40ch	AT1G55080.1		unknown	chr1:205	5.94825	7.55163	15.8551	17.8004	58.4143	14.3437
GT	Sense	Sense	-0.552	Comprom	0.552	Detected	0.000	1.291	Detected	1.525	Detected	1.408	0.130	GT	Sens	contig188	contig188	Unknown	AGAGAA	contig188	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig188	Solyc08g	Unknown Protein (A		SL2.40ch	AT3G05470.1		formin h	chr3:157	6.10909	15.6366	20.2955	23.7958	26.9333	26.5918
GT	Sense	Sense	-0.089	Comprom	0.089	Comprom	0.000	1.031	Detected	1.092	Detected	1.061	0.008	GT	Sens	contig188	contig188	cDNA clo	TGAGTT	contig188	Solyc06g	Solyc06g	cDNA clone J023134O11 full in			contig188	Solyc10g	40S ribos	GO:0003	SL2.40ch	AT5G651	ACX2. AT	ACX2 (AC	chr5:260	6.23947	8.40748	18.4589	11.9063	16.6701	14.5978
GT	Sense	Sense	0.269	Detected	-0.269	Detected	0.000	1.424	Detected	1.460	Detected	1.442	0.033	GT	Sens	contig189	contig189	Ethylene-	TCAAGA	contig189	Solyc03g	Solyc03g	Ethylene-	GO:0005	GO:0005	contig189	Solyc03g	Ethylene-	GO:0005	SL2.40ch	AT5G472	ERF5. AT	ERF5 (ET	chr5:191	266.2	218.227	792.777	596.365	728.579	626.769
GT	Sense	Sense	0.229	Detected	-0.229	Detected	0.000	1.117	Detected	1.784	Detected	1.451	0.070	GT	Sens	contig190	contig190	Aspartic	TCGGAG	contig190	Solyc08g	Solyc08g	Aspartic	GO:0006	GO:0006	contig190	Solyc01g	ORF91 (AHRD V1 *--		SL2.40ch	AT1G663	ATMYB90	MYB90 (I	chr1:247	97.8227	84.7672	207.966	166.082	222.435	296.589
GT	Sense	Sense	0.731	Comprom	-0.731	Comprom	0.000	1.255	Detected	1.152	Detected	1.203	0.242	GT	Sens	contig190	contig190	F-box fam	ACTGCA	contig190	Solyc08g	Solyc08g	F-box fam	GO:0004	GO:0004	contig190	Solyc08g	F-box fam	GO:0004	SL2.40ch	AT5G53670.1		unknown	chr5:217	11.2363	4.855	20.9497	13.1764	19.8597	15.5158
GT	Sense	Sense	-0.361	Detected	0.361	Detected	0.000	0.882	Detected	1.273	Detected	1.078	0.119	GT	Sens	contig191	contig191	Kunitz-ty	TATTTG	contig191	Solyc03g	Solyc03g	Kunitz-ty	GO:0004	GO:0004	contig191	Solyc03g	Kunitz-ty	GO:0004	SL2.40ch	AT5G04070.1		short-cha	chr5:110	912.2	1790.58	2648.87	1094.35	2654.11	2920.96
GT	Sense	Sense	0.609	Detected	-0.609	Detected	0.000	1.196	Detected	1.333	Detected	1.265	0.175	GT	Sens	contig191	contig191	C2 domai	GAGAGT	contig191	Solyc12g	Solyc12g	C2 domain-containing protein			contig191	Solyc12g	C2 domain-containi		SL2.40ch	AT3G17980.1		C2 doma	chr3:615	774.854	396.363	2618.78	1532.54	1430.14	1320.52
GT	Sense	Sense	0.621	Comprom	-0.621	Comprom	0.000	1.567	Detected	2.259	Detected	1.913	0.115	GT	Sens	contig192	contig192	2-oxoglut	ACTACA	contig192	Solyc06g	Solyc06g	2-oxoglut	GO:0016	GO:0016	contig192	Solyc06g	2-oxoglut	GO:0016	SL2.40ch	AT1G52820.1		2-oxoglu	chr1:196	4.57523	2.30232	6.91961	14.2204	10.8344	14.6843
GT	Sense	Sense	0.179	Detected	-0.179	Detected	0.000	1.022	Detected	1.350	Detected	1.186	0.040	GT	Sens	contig192	contig192	Genomic	ATGTTT	contig192	Solyc11g	Solyc11g	Genomic DNA chromosome 5			contig192	Solyc11g	Genomic DNA chror		SL2.40ch	AT5G04830.2		unknown	chr5:140	117.839	109.388	170.1	161.36	259.711	273.712
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	0.808	Detected	1.773	Detected	1.291	0.120	GT	Sens	contig192	contig192	Endochit	AAGCAA	contig192	Solyc10g	Solyc10g	Endochiti	GO:0008	GO:0008	contig192	Solyc10g	Endochiti	GO:0008	SL2.40ch	AT3G125	ATHCHIB	ATHCHIB	chr3:396	133.439	138.715	198.216	216.5	268.384	439.652
GT	Sense	Sense	-0.514	Comprom	0.514	Comprom	0.000	4.631	Detected	3.441	Detected	4.036	0.036	GT	Sens	contig192	contig192	Homeobo	CATGTT	contig192	Solyc07g	Solyc07g	Homeobo	GO:0006	GO:0006	contig192	Solyc07g	Homeobo	GO:0005	SL2.40ch	AT5G63640.1		VHS dom	chr5:254	2.29465	5.57375	32.9004	50.4363	99.7955	36.7185
GT	Sense	Sense	0.708	Detected	-0.708	Detected	0.000	1.062	Detected	1.247	Detected	1.155	0.247	GT	Sens	contig193	contig193	Pectinest	AATTGC	contig193	Solyc07g	Solyc07g	Pectinest	GO:0030	GO:0030	contig193	Solyc07g	Pectinest	GO:0030	SL2.40ch	AT1G05310.1		pectinest	chr1:155	12421.5	5542.09	14777.9	12078.5	19518.5	18626.2
GT	Sense	Sense	-0.957	Comprom	0.957	Detected	0.000	1.044	Detected	1.877	Detected	1.461	0.297	GT	Sens	contig193	contig193	Unknown	TCCCAA	contig193	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig193	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G61470.1		zinc fing	chr5:247	2.67737	12.0118	4.51584	8.31315	13.1761	19.6948
GT	Sense	Sense	0.722	Detected	-0.722	Detected	0.000	1.358	Detected	1.490	Detected	1.424	0.188	GT	Sens	contig193	contig193	Flotillin d	CTTCTAT	contig193	Solyc01g	Solyc01g	Flotillin domain protein (AHRD			contig193	Solyc01g	Flotillin domain prot		SL2.40ch	AT5G25250.1		FUNCTIO	chr5:874	289.343	126.579	398.708	293.88	552.735	508.43
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	2.033	Detected	1.547	Detected	1.790	0.019	GT	Sens	contig193	contig193	Unknown	GCTACA	contig193	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig193	Solyc09g	Unknown Protein (A		SL2.40ch	AT2G23142.1		FUNCTIO	chr2:985	163.458	207.221	351.48	800.271	848.566	508.453
GT	Sense	Sense	0.397	Detected	-0.397	Detected	0.000	1.353	Detected	1.660	Detected	1.506	0.071	GT	Sens	contig193	contig193	Unknown	GCGATA	contig193	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig193	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G03980.1		GDSL-m	chr2:126	35.9056	24.6478	66.3325	59.6528	85.5904	88.8769
GT	Sense	Sense	0.074	Comprom	-0.074	Comprom	0.000	1.275	Detected	1.397	Detected	1.336	0.005	GT	Sens	contig194	contig194	Movemen	CCATCA	contig194	Solyc08g	Solyc08g	Movemen	GO:0006	GO:0006	contig194	Solyc08g	Movemen	GO:0006	SL2.40ch	AT3G44440.1				9.55692	10.2668	26.9016	19.2583	26.9952	24.6622
GT	Sense	Sense	-0.351	Detected	0.351	Detected	0.000	1.263	Detected	0.888	Detected	1.076	0.114	GT	Sens	contig194	contig194	AAA-ATP	CGAGGG	contig194	Solyc10g	Solyc10g	AAA-ATP	GO:0017	GO:0017	contig194	Solyc10g	AAA-ATP	GO:0016	SL2.40ch	AT2G18190.1		AAA-type	chr2:791	233.82	452.815	752.695	688.01	879.821	569.297
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	1.215	Detected	0.928	Detected	1.072	0.025	GT	Sens	contig194	contig194	Mitochon	AGGTGG	contig194	Solyc05g	Solyc05g	Mitochon	GO:0015	GO:0015	contig194	Solyc05g	Mitochon	GO:0015	SL2.40ch	AT2G225	UCP5. AT	UCP5 (UN	chr2:956	121.191	164.504	392.445	270.563	369.206	254.058
GT	Sense	Sense	0.265	Detected	-0.265	Detected	0.000	1.248	Detected	1.046	Detected	1.147	0.056	GT	Sens	contig194	contig194	BHLH trai	GCAAAT	contig194	Solyc08g	Solyc08g	BHLH trai	GO:0003	GO:0003	contig194	Solyc08g	BHLH trai	GO:0003	SL2.40ch	AT1G128	SCRM2. I	SCRM2 (	chr1:438	20.3094	16.7408	30.7365	21.9301	49.3425	36.0002
GT	Sense	Sense	0.363	Detected	-0.363	Detected	0.000	1.116	Detected	0.970	Detected	1.043	0.106	GT	Sens	contig194	contig194	Glycopro	TTTCTG	contig194	Solyc01g	Solyc01g	Glycopro	GO:0016	GO:0016	contig194	Solyc12g	Unknown	GO:0016	SL2.40ch	AT3G24580.1				594.347	427.852	1385.3	1100.29	1231.53	934.241
GT	Sense	Sense	-0.301	Detected	0.301	Detected	0.000	1.454	Detected	0.822	Detected	1.138	0.121	GT	Sens	contig194	contig194	B12D-like	TGCAGC	contig194	Solyc02g	Solyc02g	B12D-like protein (AHRD V1 ***			contig194	Solyc02g	B12D-like protein (A		SL2.40ch	AT5G181	ATAPRL7	ATAPRL7	chr5:599	923.276	1668.98	2063.15	1898.57	3830.59	2075.61
GT	Sense	Sense	0.258	Detected	-0.258	Detected	0.000	3.574	Detected	1.882	Detected	2.728	0.091	GT	Sens	contig196	contig196	Receptor	TTGTTC	contig196	Solyc02g	Solyc02g	Receptor	GO:0005	GO:0005	contig196	Solyc02g	Receptor	GO:0005	SL2.40ch	AT1G29730.1		ATP bind	chr1:104	54.1541	45.1118	213.268	124.778	663.297	172.227
GT	Sense	Sense	-0.236	Comprom	0.236	Comprom	0.000	2.818	Detected	2.309	Detected	2.564	0.018	GT	Sens	contig196	contig196	Unknown	TATGTG	contig196	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig196	Solyc10g	Unknown Protein (A		SL2.40ch	AT3G27770.2		unknown	chr3:102	2.42481	4.00428	2.45678	2.09707	24.7592	14.6019
GT	Sense	Sense	-0.147	Detected	0.147	Detected	0.000	1.002	Detected	1.002	Detected	1.002	0.021	GT	Sens	contig197	contig197	Unknown	TGAGAA	contig197	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig197	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G14440.2		FUNCTIO	chr5:465	57.7402	84.3078	115.744	136.795	157.376	132.15
GT	Sense	Sense	0.502	Comprom	-0.502	Comprom	0.000	1.754	Detected	3.300	Detected	2.527	0.111	GT	Sens	contig197	contig197	Heat stre	ATGGTA	contig197	Solyc09g	Solyc09g	Heat stres	GO:0005	GO:0005	contig197	Solyc09g	Heat stres	GO:0003	SL2.40ch	AT5G457	AT-HSFA	RHA1 (RO	chr5:185	3.89261	2.31086	2.29621	2.33715	11.396	27.9247
GT	Sense	Sense	0.380	Detected	-0.380	Detected	0.000	2.061	Detected	1.657	Detected	1.859	0.050	GT	Sens	contig197	contig197	Sister chi	ACTGCA	contig197	Solyc01g	Solyc01g	Sister chi	GO:0005	GO:0005	contig197	Solyc01g	Sister chi	GO:0005	SL2.40ch	AT3G19630.1		radical S	chr3:681	1738.78	1222	2693.46	2529.51	6851.48	4345.25
GT	Sense	Sense	-0.556	Comprom	0.556	Detected	0.000	4.456	Detected	0.924	Detected	2.690	0.283	GT	Sens	contig197	contig197	Unknown	CTTGTA	contig197	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig197	Solyc05g	Vernalization insens		SL2.40ch	AT5G57380.1				6.55203	16.8626	12.7827	8.10519	259.96	18.8605
GT	Sense	Sense	-0.116	Comprom	0.116	Comprom	0.000	1.255	Detected	1.556	Detected	1.405	0.018	GT	Sens	contig197	contig197	NAC dom	TAAAAA	contig197	Solyc07g	Solyc07g	NAC dom	GO:0045449		contig197	Solyc07g	60S acidi	GO:0005	SL2.40ch	AT5G615	ATATG3.	ATG3	chr5:247	4.52972	6.33153	9.89154	19.5542	14.3947	14.8869
GT	Sense	Sense	-0.464	Detected	0.464	Detected	0.000	1.326	Detected	1.320	Detected	1.323	0.104	GT	Sens	contig198	contig198	TMV resp	GATATG	contig198	Solyc01g	Solyc01g	TMV response-related protein			contig198	Solyc01g	TMV resp	GO:0005	SL2.40ch	AT1G54575.1		unknown	chr1:203	196.919	445.987	317.53	417.188	836.69	699.623
GT	Sense	Sense	-0.097	Comprom	0.097	Comprom	0.000	2.190	Detected	1.905	Detected	2.047	0.007	GT	Sens	contig198	contig198	Cyclin B	AAACACT	contig198	Solyc12g	Solyc12g	Cyclin B (	GO:0005	GO:0005	contig198	Solyc12g	Cyclin B (	GO:0004	SL2.40ch	AT1G763	CYCB2:4	CYCB2:4	chr1:286	5.1194	6.97549	14.0576	12.716	30.7095	21.1541
GT	Sense	Sense	0.122	Comprom	-0.122	Comprom	0.000	1.466	Detected	2.821	Detected	2.143	0.090	GT	Sens	contig198	contig198	Non-LTR	CAAAGG	contig198	Solyc11g	Solyc11g	Non-LTR retroelement reverse			contig198	Solyc06g	Protein-O-fucosyltra		SL2.40ch	AT5G10740.1		protein p	chr5:339	3.62567	3.64566	11.5944	5.49049	11.3114	24.2894
GT	Sense	Sense	-0.042	Comprom	0.042	Detected	0.000	2.361	Detected	2.398	Detected	2.379	0.000	GT	Sens	contig198	contig198	D5-type c	AAATTG	contig198	Solyc04g	Solyc04g	D5-type cyclin (AHRD V1 *-*- A8			contig198	Solyc02g076900.2.1				AT3G52700.1		unknown	chr3:195	11.3695	14.3377	37.7695	34.2005	73.8735	63.6134
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	1.045	Detected	1.184	Detected	1.114	0.007	GT	Sens	contig199	contig199	Receptor	CTAAAC	contig199	Solyc10g	Solyc10g	Receptor	GO:0006	GO:0006	contig199	Solyc10g	Receptor	GO:0006	SL2.40ch	AT3G09010.1		protein k	chr3:275	75.9256	98.5391	126.429	113.729	200.998	185.778
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	2.771	Detected	2.101	Detected	2.436	0.019	GT	Sens	contig199	contig199	Respirato	GACAAG	contig199	Solyc05g	Solyc05g	Respirato	GO:0055	GO:0055	contig199	Solyc05g	Respirato	GO:0016	SL2.40ch	AT1G19230.1		respirato	chr1:664	24.567	27.7951	90.3657	52.3657	200.909	106.027
GT	Sense	Sense	-0.316	Comprom	0.316	Comprom	0.000	0.897	Detected	1.530	Detected	1.214	0.113	GT	Sens	contig199	contig199	Hydroxyc	GCAAAT	contig199	Solyc12g	Solyc12g	Hydroxyc	GO:0016	GO:0016	contig199	Solyc12g	Hydroxyc	GO:0016	SL2.40ch	AT2G025	ATHB21.	ATHB21	chr2:684	4.99376	9.20732	15.4978	14.3128	14.2257	18.5138
GT	Sense	Sense	0.366	Comprom	-0.366	Comprom	0.000	1.312	Detected	1.902	Detected	1.607	0.076	GT	Sens	contig199	contig199	Pentatric	AAATTT	contig199	Solyc02g	Solyc02g	Pentatric	GO:0003	GO:0003	contig199	Solyc02g	Pentatric	GO:0008	SL2.40ch	AT4G27890.1		nuclear r	chr4:138	4.93377	3.538	5.12169	3.13264	11.6834	14.7682
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	1.078	Detected	1.202	Detected	1.140	0.019	GT	Sens	contig200	contig200	DUF89 fa	TTTTTT	contig200	Solyc01g	Solyc01g	DUF89 family protein (Fragmen			contig200	Solyc01g	DUF89 family protei		SL2.40ch	AT2G17320.1		pantothe	chr2:753	111.467	108.397	192.766	206.792	261.432	239.089
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	0.845	Detected	1.177	Detected	1.011	0.027	GT	Sens	contig200	contig200	Cellulose	ATGAAG	contig200	Solyc09g	Solyc09g	Cellulose	GO:0016	GO:0016	contig200	Solyc08g	Late-emb	GO:0009	SL2.40ch	AT3G561	EIF3C. AT	EIF3C (E	chr3:208	911.357	1127.72	1559.32	1857.3	2050.93	2168.05
GT	Sense	Sense	0.447	Detected	-0.447	Detected	0.000	1.832	Detected	1.902	Detected	1.867	0.053	GT	Sens	contig200	contig200	Nitrate tra	AATGGA	contig200	Solyc08g	Solyc08g	Nitrate tra	GO:0016	GO:0016	contig200	Solyc08g	Nitrate tra	GO:0016	SL2.40ch	AT2G26690.1		nitrate tr	chr2:113	19.9372	12.7779	57.2092	23.2144	64.0325	56.4146
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	1.069	Detected	1.801	Detected	1.435	0.060	GT	Sens	contig201	contig201	Unknown	ATGGTC	contig201	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig201	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G65274.1		FUNCTIO	chr5:260	15.9453	18.4663	25.6739	17.9595	40.5581	56.5543
GT	Sense	Sense	0.363	Detected	-0.363	Detected	0.000	0.935	Detected	1.429	Detected	1.182	0.115	GT	Sens	contig201	contig201	Plant-spe	ATATCC	contig201	Solyc00g	Solyc00g	Plant-specific domain TIGR015			contig201	Solyc00g	Plant-specific doma		SL2.40ch	AT3G55240.1		Overexp	chr3:204	43.9688	31.644	83.2024	100.903	80.3309	94.9418
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	0.886	Detected	1.533	Detected	1.210	0.073	GT	Sens	contig201	contig201	Os03g08	GAAAAG	contig201	Solyc09g	Solyc09g	Os03g0816700 protein (Fragm			contig201	Solyc09g	Os03g0816700 prot		SL2.40ch	AT3G556	ATDFD	ATDFD (	chr3:206	2078.29	2092.36	4207.89	3881.31	4341.11	5707.01
GT	Sense	Sense	-0.065	Detected	0.065	Detected	0.000	3.504	Detected	3.203	Detected	3.354	0.002	GT	Sens	contig202	contig202	Glutathio	GGAATT	contig202	Solyc10g	Solyc10g	Glutathione S-transferase-like			contig202	Solyc10g	Glutathione S-transf		SL2.40ch	AT2G294	ATGSTU7	ATGSTU	chr2:126	48.3895	63.019	982.81	1030.49	705.977	480.933
GT	Sense	Sense	0.661	Detected	-0.661	Detected	0.000	1.246	Detected	1.649	Detected	1.447	0.171	GT	Sens	contig202	contig202	Polyprote	TTGTAA	contig202	Solyc12g	Solyc12g	Polyprotein (AHRD V1 *-*- O94I			contig202	Solyc12g	Polyprotein (AHRD V		SL2.40ch	AT2G32410.2				209.131	99.5661	395.633	353.402	385.472	427.913
GT	Sense	Sense	-0.115	Detected	0.115	Detected	0.000	1.490	Detected	0.886	Detected	1.188	0.067	GT	Sens	contig202	contig202	Unknown	AAAGTT	contig202	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig202	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G48710.1		EXPRES	chr3:180	4934.02	6887.68	14041.5	17872.9	18451.1	10189.6
GT	Sense	Sense	0.212	Detected	-0.212	Detected	0.000	2.016	Detected	1.061	Detected	1.539	0.098	GT	Sens	contig202	contig202	Cupin Rm	TGTCAAT	contig202	Solyc02g	Solyc02g	Cupin Rm	GO:0055	GO:0055	contig202	Solyc02g	Cupin Rm	GO:0055	SL2.40ch	AT5G15120.1		unknown	chr5:489	1670.34	1482.58	3588.61	2153.03	7170.97	3105.16
GT	Sense	Sense	-1.494	Comprom	1.494	Detected	0.000	0.969	Detected	1.055	Detected	1.012	0.568	GT	Sens	contig202	contig202	Cyclin B1	ACTTGG	contig202	Solyc01g	Solyc01g	Cyclin B1	GO:0005	GO:0005	contig202	Solyc01g	Cyclin B1	GO:0016	SL2.40ch	AT2G267	CYCB1:4	CYCB1:4	chr2:114	4.37184	41.3062	29.9561	13.4582	29.6304	26.4082
GT	Sense	Sense	-0.511	Comprom	0.511	Comprom	0.000	1.751	Detected	2.773	Detected	2.262	0.089	GT	Sens	contig202	contig202	Mutator-li	ACGGAC	contig202	Solyc01g	Solyc01g	Mutator-li	GO:0008	GO:0008	contig202	Solyc12g	Mutator-like transpo		SL2.40ch	AT3G52700.1		unknown	chr3:195	2.41857	5.84852	5.44383	4.72558	14.2625	24.3154
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	1.646	Detected	0.886	Detected	1.266	0.085	GT	Sens	contig203	contig203	1-aminoc	CAACCC	contig203	Solyc08g	Solyc08g	1-aminoc	GO:0030	GO:0030	contig203	Solyc08g	1-aminoc	GO:0009	SL2.40ch	AT5G283	ACS3	ACS3 (1-	chr5:103	20.7	21.3418	42.7806	32.3106	74.1019	36.7361
GT	Sense	Sense	0.268	Comprom	-0.268	Comprom	0.000	0.982	Detected	2.794	Detected	1.888	0.184	GT	Sens	contig203	contig203	Unknown	AATACA	contig203	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig203	Solyc09g	Unknown Protein (A		SL2.40ch	AT1G34480.1				6.10418	5.01252	4.52629	4.15332	12.3096	36.2808
GT	Sense	Sense	0.455	Detected	-0.455	Detected	0.000	1.906	Detected	1.440	Detected	1.673	0.082	GT	Sens	contig204	contig204	Membran	TTTGGA	contig204	Solyc09g	Solyc09g	Membrane protein-like protein			contig204	Solyc09g	Membrane protein-l		SL2.40ch	AT2G390	PIP2E. PI	PIP2E (P	chr2:162	4169.15	2640.41	5509.7	3284.13	14004.6	8510.69
GT	Sense	Sense	-0.701	Comprom	0.701	Comprom	0.000	1.057	Detected	2.618	Detected	1.838	0.222	GT	Sens	contig204	contig204	Unknown	AGAATC	contig204	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig204	Solyc00g055970.1.1				AT5G05290.1				2.39731	7.53852	5.0926	5.47162	9.96244	24.6797
GT	Sense	Sense	0.173	Detected	-0.173	Detected	0.000	1.747	Detected	1.894	Detected	1.820	0.010	GT	Sens	contig204	contig204	Disease r	GACCAC	contig204	Solyc04g	Solyc04g	Disease r	GO:0005	GO:0005	contig204	Solyc04g009120.1.1				AT5G66070.2				57.4212	53.7973	86.0324	59.3539	210.109	195.335
GT	Sense	Sense	-0.226	Comprom	0.226	Comprom	0.000	0.998	Detected	3.085	Detected	2.042	0.196	GT	Sens	contig204	contig204	Transpor	GTTTAA	contig204	Solyc06g	Solyc06g	Transpor	GO:0006	GO:0006	contig204	Solyc01g	Transpor	GO:0005	SL2.40ch	AT5G137	ZIF1	ZIF1 (ZIN	chr5:443	6.19308	10.0811	5.16327	4.72477	17.7773	63.4028
GT	Sense	Sense	-0.127	Comprom	0.127	Comprom	0.000	2.452	Detected	3.425	Detected	2.938	0.028	GT	Sens	contig204	contig204	Subtilisin	GAGGGA	contig204	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:0004	contig204	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT4G10520.1		subtilase	chr4:649	2.88312	4.09391	16.6125	5.34497	21.1715	34.8975
GT	Sense	Sense	-0.006	Detected	0.006	Detected	0.000	0.984	Detected	1.330	Detected	1.157	0.022	GT	Sens	contig204	contig204	Auxin-ind	AGTTTG	contig204	Solyc06g	Solyc06g	Auxin-ind	GO:0005	GO:0005	contig204	Solyc09g	Unknown Protein (A		SL2.40ch	AT1G36580.1				7309.55	8779.83	12318.3	13141.2	17851.7	19044.8
GT	Sense	Sense	-0.085	Comprom	0.085	Comprom	0.000	1.269	Detected	2.655	Detected	1.962	0.107	GT	Sens	contig206	contig206	MAP prot	GCTGCT	contig206	Solyc06g	Solyc06g	MAP prot	GO:0004	GO:0004	contig206	Solyc06g	MAP prot	GO:0004	SL2.40ch	AT3G057	RECOI1	RECOI1 (	chr3:169	4.56622	6.11942	15.0266	12.9001	14.3529	31.4902
GT	Sense	Sense	0.078	Comprom	-0.078	Comprom	0.000	0.832	Detected	1.226	Detected	1.029	0.040	GT	Sens	contig206	contig206	Unknown	AATACA	contig206	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig206	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G15680.1		binding	chr5:510	8.25368	8.81469	11.1124	9.07678	17.1027	18.8635
GT	Sense	Sense	-0.045	Comprom	0.045	Comprom	0.000	1.846	Detected	2.412	Detected	2.129	0.018	GT	Sens	contig206	contig206	Solute ca	GTGGAA	contig206	Solyc12g	Solyc12g	Solute ca	GO:0016	GO:0016	contig206	Solyc12g	Solute ca	GO:0016	SL2.40ch	AT5G62680.1		proton-d	chr5:251	3.66043	4.64143	11.745	5.51736	16.6894	20.7418
GT	Sense	Sense	-0.739	Detected	0.739	Detected	0.000	1.147	Detected	1.543	Detected	1.345	0.221	GT	Sens	contig206	contig206	Zinc finge	TTTTGA	contig206	Solyc02g	Solyc02g	Zinc finge	GO:0003	GO:0003	contig206	Solyc02g	Zinc finge	GO:0003	SL2.40ch	AT5G397	AtHB23	AtHB23 (	chr5:159	19.8872	65.9917	29.9156	56.4295	90.4033	99.795
GT	Sense	Sense	-0.151	Comprom	0.151	Comprom	0.000	2.490	Detected	2.865	Detected	2.677	0.008	GT	Sens	contig207	contig207	Os04g02	TATGCG	contig207	Solyc12g	Solyc12g	Os04g0226400 protein (Fragm			contig207	Solyc12g	Os04g0226400 prot		SL2.40ch	AT5G13500.3		unknown	chr5:433	2.51195	3.68851	2.39162	2.97831	19.2625	20.9671
GT	Sense	Sense	0.214	Comprom	-0.214	Comprom	0.000	1.238	Detected	2.459	Detected	1.848	0.104	GT	Sens	contig207	contig207	Unknown	AGACTG	contig207	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig207	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G133	BRL3	BRL3 (BF	chr3:434	4.04111	3.57367	9.31381	7.72789	10.0963	19.752
GT	Sense	Sense	-0.699	Detected	0.699	Detected	0.000	1.750	Detected	1.420	Detected	1.585	0.158	GT	Sens	contig207	contig207	Serine/thr	GTTTTG	contig207	Solyc06g	Solyc06g	Serine/thr	GO:0004	GO:0004	contig207	Solyc06g	Serine/thr	GO:0004	SL2.40ch	AT5G07140.1		protein k	chr5:221	34.7475	108.962	100.038	104.424	233.201	155.686
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	2.618	Detected	3.449	Detected	3.034	0.018	GT	Sens	contig207	contig207	Ribosoma	TGAGAA	contig207	Solyc11g	Solyc11g	Ribosoma	GO:0005	GO:0005	contig207	Solyc01g	Ribosoma	GO:0003	SL2.40ch	AT3G611	ARS27A	ARS27A	chr3:226	24.5045	30.2869	34.9663	44.3593	188.403	281.387
GT	Sense	Sense	0.156	Comprom	-0.156	Comprom	0.000	0.806	Detected	1.382	Detected	1.094	0.079	GT	Sens	contig208	contig208	Non-spec	TTGTGA	contig208	Solyc02g	Solyc02g	Non-spec	GO:0006	GO:0006	contig208	Solyc02g	Non-spec	GO:0005	SL2.40ch	AT2G29590.1		thioester	chr2:126	7.46864	7.16422	9.38838	5.85824	14.4047	18.0318
GT	Sense	Sense	-0.243	Comprom	0.243	Comprom	0.000	1.455	Detected	2.350	Detected	1.903	0.065	GT	Sens	contig208	contig208	Dihydroo	ACCTCC	contig208	Solyc02g	Solyc02g	Dihydroo	GO:0016	GO:0016	contig208	Solyc03g	Dihydroo	GO:0017	SL2.40ch	AT3G17810.1		dihydroo	chr3:609	3.09227	5.15687	9.31148	3.85553	12.3305	19.256
GT	Sense	Sense	0.411	Detected	-0.411	Comprom	0.000	1.546	Detected	1.338	Detected	1.442	0.077	GT	Sens	contig209	contig209	Receptor	CCTGCT	contig209	Solyc05g	Solyc05g	Receptor	GO:0006	GO:0006	contig209	Solyc05g	Receptor	GO:0006	SL2.40ch	AT1G25390.1		protein k	chr1:890	13.0903	8.81496	17.4286	18.4812	35.3257	25.6722
GT	Sense	Sense	0.370	Detected	-0.370	Detected	0.000	2.111	Detected	1.135	Detected	1.623	0.118	GT	Sens	contig209	contig209	UPF0497	ATTTCA	contig209	Solyc05g	Solyc05g	UPF0497 membrane protein 2			contig209	Solyc05g	UPF0497 membrane		SL2.40ch	AT2G310	ORP1A	ORP1A (	chr2:132	961.406	685.727	3069.56	2312.25	3949.98	1686.12
GT	Sense	Sense	0.234	Comprom	-0.234	Comprom	0.000	1.415	Detected	2.855	Detected	2.135	0.106	GT	Sens	contig209	contig209	Conserve	GGGATA	contig209	Solyc01g	Solyc01g	Conserve	GO:0016	GO:0016	contig209	Solyc01g	Conserve	GO:0016	SL2.40ch	AT2G46890.1		oxidored	chr2:192	3.61166	3.1067	3.98899	3.63997	10.0605	22.9146
GT	Sense	Sense	-0.489	Comprom	0.489	Detected	0.000	0.879	Detected	1.487	Detected	1.183	0.176	GT	Sens	contig209	contig209	Unknown	GAAGTT	contig209	Solyc04g	Solyc04g	Unknown	GO:0003	GO:0003	contig209	Solyc04g	Unknown	GO:0003	SL2.40ch	AT2G37670.1		WD-40 re	chr2:157	5.60478	13.1506	5.88558	9.88142	17.7849	22.7528
GT	Sense	Sense	0.285	Detected	-0.285	Detected	0.000	2.314	Detected	1.324	Detected	1.819	0.086	GT	Sens	contig209	contig209	Zinc finge	CTGAGA	contig209	Solyc03g	Solyc03g	Zinc finge	GO:0003	GO:0003	contig209	Solyc03g	Zinc finge	GO:0003	SL2.40ch	AT5G654	ATHB25.	HB25 (HO	chr5:261	107.245	85.9515	245.022	149.378	537.791	227.311
GT	Sense	Sense	-0.177	Detected	0.177	Detected	0.000	1.204	Detected	0.848	Detected	1.026	0.055	GT	Sens	contig210	contig210	Zinc finge	CATATT	contig210	Solyc03g	Solyc03g	Zinc finge	GO:0008	GO:0008	contig210	Solyc03g	Zinc finge	GO:0008	SL2.40ch	AT2G18480.1		mannitol	chr2:800	542.116	825.38	1308.57	1400.59	1736.31	1138.47
GT	Sense	Sense	-0.055	Comprom	0.055	Comprom	0.000	1.859	Detected	1.660	Detected	1.760	0.004	GT	Sens	contig210	contig210	WD-40 re	GAAATT	contig210	Solyc04g	Solyc04g	WD-40 re	GO:0000	GO:0000	contig210	Solyc04g	WD-40 re	GO:0000	SL2.40ch	AT1G24130.1		transduc	chr1:853	5.44895	6.9966	17.1024	5.32223	25.2398	18.4516
GT	Sense	Sense	-0.158	Comprom	0.158	Comprom	0.000	2.401	Detected	3.155	Detected	2.778	0.021	GT	Sens	contig210	contig210	Phototrop	AACAGT	contig210	Solyc06g	Solyc06g	Phototrop	GO:0005	GO:0005	contig210	Solyc06g	Phototrop	GO:0005	SL2.40ch	AT4G319	ASP5. AA	ASP5 (AS	chr4:154	3.6685	5.43301	3.17461	3.19249	26.5678	37.607
GT	Sense	Sense	0.459	Detected	-0.459	Detected	0.000	2.237	Detected	1.199	Detected	1.718	0.131	GT	Sens	contig210	contig210	Unknown	CCACCA	contig210	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig210	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G40250.1		zinc fing	chr5:160	710.463	447.649	1669.51	592.668	2995.09	1223.79
GT	Sense	Sense	-0.737	Detected	0.737	Detected	0.000	7.256	Detected	5.327	Detected	6.292	0.035	GT	Sens	contig211	contig211	1-aminoc	AAAGCT	contig211	Solyc07g	Solyc07g	1-aminoc	GO:0016	GO:0016	contig211	Solyc07g	1-aminoc	GO:0045	SL2.40ch	AT2G195	ACO1	ACO1 (AC	chr2:847	56.9881	188.502	4675.73	2950.77	17852.1	3933.68
GT	Sense	Sense	0.677	Detected	-0.677	Detected	0.000	1.025	Detected	1.145	Detected	1.085	0.251	GT	Sens	contig211	contig211	Phloem le	AGTATT	contig211	Solyc00g	Solyc00g	Phloem lectin (AHRD V1 ***- O8			contig211	Solyc00g	Phloem le	GO:0030	SL2.40ch	AT5G170	UGT78D2	UGT78D2	chr5:560	109.761	51.1191	396.89	121.782	171.728	156.595
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	2.283	Detected	1.104	Detected	1.693	0.103	GT	Sens	contig212	contig212	Ethylene	AGAAAG	contig212	Solyc03g	Solyc03g	Ethylene	GO:0003	GO:0003	contig212	Solyc03g	Ethylene	GO:0016	SL2.40ch	AT4G175	ATERF-1	ATERF-1	chr4:975	235.041	275.382	856.47	670.811	1394.65	517.067
GT	Sense	Sense	0.316	Comprom	-0.316	Comprom	0.000	1.415	Detected	1.736	Detected	1.576	0.047	GT	Sens	contig212	contig212	Plasma m	ATGCTT	contig212	Solyc09g	Solyc09g	Plasma membrane associated			contig212	Solyc09g	Plasma membrane a		SL2.40ch	AT1G04560.1		AWPM-1	chr1:124	6.98782	5.37046	14.6934	14.4947	18.3991	19.2991
GT	Sense	Sense	0.465	Detected	-0.465	Detected	0.000	1.084	Detected	1.919	Detected	1.502	0.138	GT	Sens	contig212	contig212	Unknown	TTTGCAT	contig212	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig212	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G44578.1		unknown	chr5:179	28.9725	18.0969	36.5137	33.7903	54.699	81.9016
GT	Sense	Sense	0.212	Detected	-0.212	Detected	0.000	1.526	Detected	1.706	Detected	1.616	0.020	GT	Sens	contig213	contig213	Unknown	TAGTTG	contig213	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig213	Solyc00g	Unknown Protein (A		SL2.40ch	AT1G049	ATPDIL2-	ATPDIL2	chr1:141	151.332	134.239	356.177	335.212	462.474	439.59
GT	Sense	Sense	0.850	Detected	-0.850	Detected	0.000	1.502	Detected	0.869	Detected	1.186	0.321	GT	Sens	contig213	contig213	Alcohol a	GGTTCC	contig213	Solyc07g	Solyc07g	Alcohol a	GO:0010	GO:0010	contig213	Solyc07g	Alcohol a	GO:0010	SL2.40ch	AT3G034	CHAT	CHAT (ac	chr3:828	2994.69	1097.54	5791.41	2552.91	5785.13	3131.73
GT	Sense	Sense	-0.011	Comprom	0.011	Comprom	0.000	5.820	Detected	2.467	Detected	4.143	0.132	GT	Sens	contig213	contig213	Unknown	AGATTG	contig213	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig213	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G428	DFR. TT3	DFR (DIH	chr5:171	2.51004	3.03479	3.51052	16.8157	175.592	14.4239
GT	Sense	Sense	0.494	Comprom	-0.494	Comprom	0.000	2.619	Detected	2.302	Detected	2.461	0.042	GT	Sens	contig213	contig213	Ulp1 prot	AGACGG	contig213	Solyc08g	Solyc08g	Ulp1 prot	GO:0006	GO:0006	contig213	Solyc08g	Ulp1 prot	GO:0006	SL2.40ch	AT1G220	TGA3	TGA3: DI	chr1:778	5.42771	3.25735	5.92408	15.3677	29.0983	19.6087
GT	Sense	Sense	0.320	Detected	-0.320	Detected	0.000	1.248	Detected	1.555	Detected	1.401	0.059	GT	Sens	contig213	contig213	PIF-like tr	GTGTTT	contig213	Solyc09g	Solyc09g	PIF-like transposase (AHRD V1			contig213	Solyc09g	PIF-like transposase		SL2.40ch	AT1G62450.1				80.2525	61.2687	78.2661	72.1607	187.55	194.797
GT	Sense	Sense	0.439	Comprom	-0.439	Comprom	0.000	1.258	Detected	2.055	Detected	1.656	0.108	GT	Sens	contig213	contig213	Dehydroc	AAGGTT	contig213	Solyc12g	Solyc12g	Dehydroc	GO:0008	GO:0008	contig213	Solyc12g	Dehydroc	GO:0008	SL2.40ch	AT5G61830.1		short-cha	chr5:248	5.85803	3.79565	6.7263	5.68472	12.7038	18.5235
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	1.221	Detected	1.295	Detected	1.258	0.001	GT	Sens	contig214	contig214	Glutathio	GGGCTG	contig214	Solyc09g	Solyc09g	Glutathio	GO:0004	GO:0004	contig214	Solyc09g	Glutathio	GO:0004	SL2.40ch	AT3G092	ATGSTU8	ATGSTU	chr3:284	178.893	211.802	419.175	412.171	511.234	451.675
GT	Sense	Sense	-0.460	Comprom	0.460	Comprom	0.000	1.038	Detected	2.814	Detected	1.926	0.194	GT	Sens	contig214	contig214	Glycosylt	TCAACG	contig214	Solyc06g	Solyc06g	Glycosyltransferase CAZy fam			contig214	Solyc06g	Glycosyltransferase		SL2.40ch	AT5G17930.1		binding /	chr5:594	3.0307	6.82265	2.0817	2.13718	10.5179	30.2288
GT	Sense	Sense	-0.300	Detected	0.300	Detected	0.000	1.804	Detected	1.552	Detected	1.678	0.036	GT	Sens	contig215	contig215	CM0216.2	AAGAAT	contig215	Solyc02g	Solyc02g	CM0216.240.nc protein (AHRD			contig215	Solyc02g	CM0216.240.nc prot		SL2.40ch	AT2G26620.1		glycosid	chr2:113	46.555	84.0176	98.6166	140.032	246.016	173.447
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	1.152	Detected	1.016	Detected	1.084	0.018	GT	Sens	contig215	contig215	Cytochro	TGCACA	contig215	Solyc04g	Solyc04g	Cytochro	GO:0010	GO:0010	contig215	Solyc04g	cytochro	GO:0010	SL2.40ch	AT5G259	GA3. CYP	GA3 (GA	chr5:903	111.541	158.764	204.596	208.178	333.11	254.488
GT	Sense	Sense	0.489	Detected	-0.489	Detected	0.000	1.006	Detected	1.792	Detected	1.399	0.155	GT	Sens	contig216	contig216	Subtilisin	GCAATT	contig216	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:0004	contig216	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT3G55580.1		regulator	chr3:206	24.9687	15.099	55.0776	40.2584	43.9121	63.5835
GT	Sense	Sense	-0.604	Detected	0.604	Detected	0.000	0.941	Detected	1.108	Detected	1.024	0.235	GT	Sens	contig216	contig216	Phospho	GAAAAT	contig216	Solyc06g	Solyc06g	Phospho	GO:0080	GO:0080	contig216	Solyc06g	Phospho	GO:0051	SL2.40ch	AT2G296	THIC	THIC (Th	chr2:126	487.958	1341.32	1073.35	1369.53	1749.99	1648.39
GT	Sense	Sense	0.523	Detected	-0.523	Detected	0.000	1.031	Detected	1.042	Detected	1.036	0.186	GT	Sens	contig216	contig216	Citrate tra	AAACTT	contig216	Solyc03g	Solyc03g	Citrate tra	GO:0016	GO:0016	contig216	Solyc03g	Citrate tra	GO:0016	SL2.40ch	AT1G02260.1		transmem	chr1:440	212.561	122.585	571.086	346.765	371.57	314.195
GT	Sense	Sense	0.436	Detected	-0.436	Detected	0.000	1.933	Detected	1.426	Detected	1.679	0.079	GT	Sens	contig217	contig217	Ethylene	TTGGAA	contig217	Solyc08g	Solyc08g	Ethylene	GO:0003	GO:0003	contig217	Solyc08g	Ethylene	GO:0003	SL2.40ch	AT5G472	ATERF2.	ERF2 (ET	chr5:191	26.5622	17.2867	98.3224	51.5841	92.1601	54.4484
GT	Sense	Sense	0.307	Comprom	-0.307	Comprom	0.000	2.470	Detected	1.025	Detected	1.747	0.156	GT	Sens	contig217	contig217	UDP-gluc	GTAGCT	contig217	Solyc11g	Solyc11g	UDP-gluc	GO:0080	GO:0080	contig217	Solyc11g	UDP-gluc	GO:0080	SL2.40ch	AT1G085	SYP111. I	SYP111 (	chr1:270	9.38993	7.30211	54.2289	22.6362	51.6857	15.9301
GT	Sense	Sense	-0.903	Detected	0.903	Detected	0.000	1.797	Detected	0.834	Detected	1.315	0.328	GT	Sens	contig217	contig217	Cortical c	ATTGGT	contig217	Solyc06g	Solyc06g	Cortical c	GO:0008	GO:0008	contig217	Solyc06g	Cortical c	GO:0008	SL2.40ch	AT5G46890.1		protease	chr5:190	54.2111	225.827	294.192	507.891	433.14	186.464
GT	Sense	Sense	0.455	Comprom	-0.455	Comprom	0.000	1.088	Detected	1.592	Detected	1.340	0.124	GT	Sens	contig217	contig217	BURP doi	TGCATC	contig217	Solyc08g	Solyc08g	BURP domain-containing prote			contig217	Solyc08g	BURP domain-conta		SL2.40ch	AT3G61660.1		unknown	chr3:228	8.00403	5.07013	15.1424	15.1815	15.2496	18.1536
GT	Sense	Sense	0.509	Detected	-0.509	Detected	0.000	1.426	Detected	2.099	Detected	1.763	0.102	GT	Sens	contig217	contig217	Resistanc	TTTATG	contig217	Solyc05g	Solyc05g	Resistanc	GO:0045	GO:0045	contig217	Solyc05g	Cc-nbs-lr	GO:0006	SL2.40ch	AT5G113	DXPS3	DXPS3 (1	chr5:363	37.4163	22.0093	92.7246	144.227	86.8741	116.256
GT	Sense	Sense	-0.140	Detected	0.140	Detected	0.000	4.946	Detected	2.779	Detected	3.862	0.072	GT	Sens	contig218	contig218	N-acetyltr	CTGTTG	contig218	Solyc00g	Solyc00g	N-acetyltr	GO:0008	GO:0008	contig218	Solyc00g	N-acetyltr	GO:0008	SL2.40ch	AT4G16563.1		aspartyl	chr4:932	15.8561	22.9345	113.18	151.267	662.319	123.729
GT	Sense	Sense	-0.284	Detected	0.284	Detected	0.000	0.956	Detected	1.679	Detected	1.318	0.103	GT	Sens	contig218	contig218	Cell numl	TTTTTAT	contig218	Solyc08g	Solyc08g	Cell number regulator 1 (AHRD			contig218	Solyc08g013920.2.1				AT4G147	IOD19	IOD19 (IC	chr4:847	15.7181	27.7467	38.8984	35.183	45.6246	63.2461
GT	Sense	Sense	0.040	Comprom	-0.040	Comprom	0.000	1.660	Detected	2.059	Detected	1.859	0.012	GT	Sens	contig218	contig218	Unknown	CCCCCA	contig218	Solyc02g	Solyc02g	Unknown	GO:0006	GO:0006	contig218	Solyc02g	Unknown	GO:0006	SL2.40ch	AT4G355	MLH3. AT	MLH3 (M	chr4:168	4.69008	5.28031	16.9426	15.6483	17.7108	19.6068
GT	Sense	Sense	0.319	Comprom	-0.319	Comprom	0.000	0.986	Detected	1.829	Detected	1.407	0.117	GT	Sens	contig219	contig219	Chromos	ATGCCC	contig219	Solyc09g	Solyc09g	Chromosome 14 open reading			contig219	Solyc09g	Chromosome 14 op		SL2.40ch	AT5G35970.1		DNA-bind	chr5:141	6.68237	5.11102	11.7102	17.075	13.0407	19.6279
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	1.872	Detected	1.904	Detected	1.888	0.000	GT	Sens	contig219	contig219	Harpin-in	AGGTTT	contig219	Solyc01g	Solyc01g	Harpin-induced protein-like (F			contig219	Solyc01g	Harpin-induced prot		SL2.40ch	AT2G02061.1		unknown	chr2:498	53.0805	60.7908	130.37	154.155	234.29	201.053
GT	Sense	Sense	0.581	Comprom	-0.581	Comprom	0.000	0.832	Detected	1.306	Detected	1.069	0.230	GT	Sens	contig220	contig220	Pentatric	GATCTG	contig220	Solyc11g	Solyc11g	Pentatricopeptide repeat-cont			contig220	Solyc11g	Pentatricopeptide r		SL2.40ch	AT1G74630.1		pentatric	chr1:280	7.70611	4.10084	6.47837	10.8011	11.2736	13.141
GT	Sense	Sense	0.157	Comprom	-0.157	Comprom	0.000	1.339	Detected	2.485	Detected	1.912	0.084	GT	Sens	contig220	contig220	Mutator-li	GACGGG	contig220	Solyc01g	Solyc01g	Mutator-li	GO:0008	GO:0008	contig220	Solyc01g	Mate efflu	GO:0005	SL2.40ch	AT5G662	CPK28	CPK28: A	chr5:264	3.66411	3.50954	2.10428	4.14777	10.2208	18.9885
GT	Sense	Sense	0.223	Detected	-0.223	Detected	0.000	1.073	Detected	1.012	Detected	1.043	0.043	GT	Sens	contig220	contig220	Calmodul	AGATCC	contig220	Solyc03g	Solyc03g	Calmodul	GO:0005	GO:0005	contig220	Solyc03g	Calmodul	GO:0005	SL2.40ch	AT1G18210.2		calcium-I	chr1:626	16906.3	14781.5	35267.9	26020.1	37467.5	30150.8
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	1.618	Detected	1.085	Detected	1.352	0.038	GT	Sens	contig220	contig220	RING fing	GGGTCA	contig220	Solyc10g	Solyc10g	RING fing	GO:0008	GO:0008	contig220	Solyc10g	RING fing	GO:0008	SL2.40ch	AT3G09770.1		zinc fing	chr3:299	72.8748	82.2513	140	98.4724	267.779	155.28
GT	Sense	Sense	0.867	Detected	-0.867	Detected	0.000	1.390	Detected	1.207	Detected	1.298	0.275	GT	Sens	contig220	contig220	Heat stres	AAGGAA	contig220	Solyc02g	Solyc02g	Heat stres	GO:0005	GO:0005	contig220	Solyc02g	Heat stres	GO:0003	SL2.40ch	AT5G620	AT-HSFB	AT-HSFB	chr5:249	183.094	65.5037	268.692	202.729	323.227	239.032
GT	Sense	Sense	0.386	Comprom	-0.386	Comprom	0.000	1.397	Detected	1.838	Detected	1.618	0.068	GT	Sens	contig221	contig221	Leucine-r	ACTTAT	contig221	Solyc04g	Solyc04g	Leucine-r	GO:0005	GO:0005	contig221	Solyc04g	LRR rece	GO:0004	SL2.40ch	AT3G23360.1		protein p	chr3:835	5.79276	4.03991	10.294	14.0214	14.3551	16.3502
GT	Sense	Sense	0.091	Detected	-0.091	Detected	0.000	1.755	Detected	2.280	Detected	2.018	0.018	GT	Sens	contig221	contig221	Unknown	ATTAGAT	contig221	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig221	Solyc11g	Unknown	GO:0005	SL2.40ch	AT4G18870.1		heat sho	chr4:103	83.747	87.9413	252.762	282.759	326.378	394.002
GT	Sense	Sense	0.368	Comprom	-0.368	Comprom	0.000	0.848	Detected	1.197	Detected	1.023	0.129	GT	Sens	contig221	contig221	Cold sho	TATTAGA	contig221	Solyc01g	Solyc01g	Cold sho	GO:0005	GO:0005	contig221	Solyc01g	Cold sho	GO:0030	SL2.40ch	AT5G59950.4		RNA and	chr5:241	7.98243	5.7048	10.9465	12.4812	13.6832	14.629
GT	Sense	Sense	-0.170	Detected	0.170	Detected	0.000	3.539	Detected	1.608	Detected	2.573	0.120	GT	Sens	contig222	contig222	Pectinest	TCAACT	contig222	Solyc03g	Solyc03g	Pectinest	GO:0030	GO:0030	contig222	Solyc03g	Pectinest	GO:0030	SL2.40ch	AT5G35230.1		unknown	chr5:134	51.0231	76.8882	377.531	137.572	820.197	180.467
GT	Sense	Sense	-0.372	Comprom	0.372	Comprom	0.000	1.071	Detected	2.697	Detected	1.884	0.170	GT	Sens	contig222	contig222	D-isomer	GCAGAT	contig222	Solyc03g	Solyc03g	D-isomer	GO:0008	GO:0008	contig222	Solyc03g	D-isomer	GO:0008	SL2.40ch	AT1G79870.1		oxidored	chr1:300	2.97458	5.93026	3.55353	6.25862	9.94251	25.7426
GT	Sense	Sense	-0.278	Detected	0.278	Detected	0.000	1.243	Detected	2.053	Detected	1.648	0.079	GT	Sens	contig222	contig222	Unknown	GGGAAT	contig222	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig222	Solyc05g	Unknown Protein (A		SL2.40ch	AT3G43850.1		unknown	chr3:157	18.8386	32.9569	88.0023	62.4231	66.4139	97.7711
GT	Sense	Sense	-0.295	Detected	0.295	Detected	0.000	2.415	Detected	0.850	Detected	1.633	0.190	GT	Sens	contig222	contig222	Gibberell	CTTAGG	contig222	Solyc10g	Solyc10g	Gibberell	GO:0004	GO:0004	contig222	Solyc10g	Gibberell	GO:0004	SL2.40ch	AT1G47480.1		hydrolas	chr1:174	82.1556	147.199	264.575	178.59	660.558	187.474
GT	Sense	Sense	-0.388	Comprom	0.388	Comprom	0.000	2.587	Detected	2.858	Detected	2.723	0.022	GT	Sens	contig222	contig222	Non-ltr re	TCAACG	contig222	Solyc00g	Solyc00g	Non-ltr retrotransposon revers			contig222	Solyc01g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	2.55929	5.2207	24.5113	4.05578	24.7396	25.0643
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	1.348	Detected	1.410	Detected	1.379	0.015	GT	Sens	contig222	contig222	LRR rece	AACGAA	contig222	Solyc11g	Solyc11g	LRR rece	GO:0004	GO:0004	contig222	Solyc11g	RLK. Rec	GO:0004	SL2.40ch	AT5G37450.1		leucine-r	chr5:148	287.946	271.944	444.922	640.723	802.282	703.261
GT	Sense	Sense	-0.280	Detected	0.280	Detected	0.000	0.920	Detected	1.437	Detected	1.178	0.090	GT	Sens	contig222	contig222	Unknown	TCGATC	contig222	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig222	Solyc06g	Unknown Protein (A		SL2.40ch	AT5G62510.1		F-box fa	chr5:250	38.7332	67.9555	107.988	91.1266	109.347	131.312
GT	Sense	Sense	0.387	Detected	-0.387	Detected	0.000	1.873	Detected	0.924	Detected	1.398	0.150	GT	Sens	contig223	contig223	Unknown	TGGTTT	contig223	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig223	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G52550.1		unknown	chr5:213	4124.39	2870.46	9683.43	7722.43	14195.6	6171.51
GT	Sense	Sense	0.203	Comprom	-0.203	Comprom	0.000	0.944	Detected	1.212	Detected	1.078	0.047	GT	Sens	contig223	contig223	Unknown	AGTTGA	contig223	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig223	Solyc05g	Unknown Protein (A		SL2.40ch	AT3G05950.1		germin-li	chr3:178	6.33487	5.69368	4.8235	13.5918	13.0165	13.1532
GT	Sense	Sense	0.225	Detected	-0.225	Detected	0.000	1.946	Detected	0.870	Detected	1.408	0.137	GT	Sens	contig223	contig223	Unknown	GCAGGT	contig223	Solyc12g	Solyc12g	Unknown Protein (AHRD V1):O			contig223	Solyc06g	DOMON c	GO:0004	SL2.40ch	AT3G19020.1		leucine-r	chr3:655	74.6658	65.0415	364.433	538.146	302.367	120.442
GT	Sense	Sense	-0.066	Detected	0.066	Detected	0.000	1.286	Detected	1.040	Detected	1.163	0.014	GT	Sens	contig224	contig224	Unknown	GTCACA	contig224	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig224	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G07610.1		F-box fa	chr5:240	124.933	162.889	247.022	278.875	391.858	277.356
GT	Sense	Sense	-0.149	Comprom	0.149	Comprom	0.000	1.483	Detected	2.877	Detected	2.180	0.092	GT	Sens	contig224	contig224	FAD-bind	CTAGAA	contig224	Solyc09g	Solyc09g	FAD-bind	GO:0050	GO:0050	contig224	Solyc09g	FAD-bind	GO:0016	SL2.40ch	AT2G46750.1		FAD-bind	chr2:192	3.70163	5.41764	15.2672	19.9395	14.1008	31.1036
GT	Sense	Sense	-0.486	Detected	0.486	Detected	0.000	1.651	Detected	1.900	Detected	1.776	0.071	GT	Sens	contig224	contig224	Ring H2 fi	AATCAT	contig224	Solyc04g	Solyc04g	Ring H2 fi	GO:0008	GO:0008	contig224	Solyc04g	Ring H2 fi	GO:0008	SL2.40ch	AT5G10380.1				79.6702	186.055	243.239	148.53	430.772	429.718
GT	Sense	Sense	-0.238	Detected	0.238	Detected	0.000	0.982	Detected	2.234	Detected	1.608	0.138	GT	Sens	contig224	contig224	Zinc finge	CAAGAG	contig224	Solyc05g	Solyc05g	Zinc finger family protein (AHR			contig224	Solyc04g	Ryanodin	GO:0008	SL2.40ch	AT5G44590.1		unknown	chr5:179	17.9476	29.731	16.7821	32.5758	51.3959	102.739
GT	Sense	Sense	0.271	Detected	-0.271	Detected	0.000	0.805	Detected	1.259	Detected	1.032	0.100	GT	Sens	contig224	contig224	Zinc finge	AGAAAG	contig224	Solyc00g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.143	Comprom	0.143	Comprom	0.000	1.739	Detected	2.351	Detected	2.045	0.026	GT	Sens	contig225	contig225	Cytochro	AAGAAA	contig225	Solyc01g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.258	Comprom	0.258	Comprom	0.000	1.363	Detected	2.393	Detected	1.878	0.083	GT	Sens	contig225	contig225	Unknown	TAAAAG	contig225	Solyc04g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.657	Detected	-0.657	Detected	0.000	1.358	Detected	0.941	Detected	1.150	0.237	GT	Sens	contig226	contig226	Glutathio	GAATTG	contig226	Solyc09g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.133	Detected	0.133	Detected	0.000	1.708	Detected	1.940	Detected	1.824	0.009	GT	Sens	contig226	contig226	Unknown	AGATTT	contig226	Solyc03g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.591	Detected	-0.591	Detected	0.000	1.242	Detected	0.879	Detected	1.060	0.229	GT	Sens	contig226	contig226	Unknown	TTATCA	contig226	Solyc10g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.100	Detected	0.100	Detected	0.000	1.419	Detected	2.336	Detected	1.877	0.057	GT	Sens	contig227	contig227	Transcrip	AGTAGG	contig227	Solyc00g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.483	Comprom	-0.483	Comprom	0.000	0.956	Detected	1.904	Detected	1.430	0.169	GT	Sens	contig227	contig227	Non-LTR	CAGGAG	contig227	Solyc01g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.538	Comprom	0.538	Detected	0.000	1.324	Detected	2.206	Detected	1.765	0.127	GT	Sens	contig227	contig227	Unknown	GTATTT	contig227	Solyc06g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.202	Comprom	-0.202	Comprom	0.000	1.854	Detected	2.246	Detected	2.050	0.018	GT	Sens	contig227	contig227	Unknown	GTCCAG	contig227	Solyc03g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.877	Detected	-0.877	Comprom	0.000	2.165	Detected	1.916	Detected	2.041	0.148	GT	Sens	contig228	contig228	MtN3-like	TTAACT	contig228	Solyc06g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	1.715	Detected	0.888	Detected	1.301	0.096	GT	Sens	contig228	contig228	Glycine-r	CGTCGG	contig228	Solyc01g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.217	Detected	-0.217	Detected	0.000	2.495	Detected	1.510	Detected	2.002	0.065	GT	Sens	contig228	contig228	Unknown	TCTCAAT	contig228	Solyc03g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	1.595	Detected	0.806	Detected	1.201	0.099	GT	Sens	contig228	contig228	Blight-ass	CCGCGC	contig228	Solyc08g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	1.623	Detected	-1.623	Comprom	0.000	1.450	Detected	2.438	Detected	1.944	0.370	GT	Sens	contig228	contig228	Histidine	TCAATT	contig228	Solyc08g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.255	Detected	0.255	Detected	0.000	1.138	Detected	0.868	Detected	1.003	0.074	GT	Sens	contig229	contig229	Unknown	AAACTC	contig229	Solyc05g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.199	Detected	-0.199	Detected	0.000	1.892	Detected	1.185	Detected	1.538	0.063	GT	Sens	contig229	contig229	Myb fami	ATGAACT	contig229	Solyc06g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.254	Detected	0.254	Detected	0.000	1.099	Detected	0.965	Detected	1.032	0.059	GT	Sens	contig230	contig230	Unknown	CAATAA	contig230	Solyc08g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.403	Detected	-0.403	Detected	0.000	3.868	Detected	2.369	Detected	3.119	0.067	GT	Sens	contig230	contig230	Cytochro	GCACCT	contig230	Solyc01g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-1.071	Comprom	1.071	Detected	0.000	2.468	Detected	1.620	Detected	2.044	0.218	GT	Sens	contig230	contig230	Os06g02	ATCCTT	contig230	Solyc07g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.207	Comprom	0.207	Comprom	0.000	1.142	Detected	3.302	Detected	2.222	0.181	GT	Sens	contig230	contig230	Unknown	CCTAAA	contig230	Solyc07g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.389	Detected	-0.389	Detected	0.000	1.005	Detected	1.343	Detected	1.174	0.110	GT	Sens	contig230	contig230	Unknown	TAAGAA	contig230	Solyc08g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.290	Comprom	0.290	Comprom	0.000	1.309	Detected	2.012	Detected	1.660	0.068	GT	Sens	contig230	contig230	F-box fan	TTGTTG	contig230	Solyc08g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.307	Comprom	-0.307	Comprom	0.000	0.916	Detected	1.748	Detected	1.332	0.123	GT	Sens	contig231	contig231	Unknown	GACCAG	contig231	Solyc03g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.373	Detected	-0.373	Detected	0.000	0.867	Detected	1.322	Detected	1.094	0.129	GT	Sens	contig231	contig231	Outer me	CTGCTT	contig231	Solyc12g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.330	Comprom	-0.330	Comprom	0.000	0.998	Detected	1.251	Detected	1.124	0.086	GT	Sens	contig231	contig231	Dof zinc f	AGAGGT	contig231	Solyc02g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.399	Detected	-0.399	Detected	0.000	1.696	Detected	0.898	Detected	1.297	0.148	GT	Sens	contig231	contig231	Receptor	AAATGG	contig231	Solyc09g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.271	Detected	0.271	Detected	0.000	1.840	Detected	1.044	Detected	1.442	0.096	GT	Sens	contig232	contig232	Hydroxyr	ATGCCA	contig232	Solyc03g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.311	Detected	-0.311	Detected	0.000	1.142	Detected	1.763	Detected	1.453	0.081	GT	Sens	contig232	contig232	Unknown	CCATTC	contig232	Solyc11g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.323	Detected	-0.323	Detected	0.000	1.077	Detected	1.392	Detected	1.234	0.075	GT	Sens	contig232	contig232	C2 domai	CCATTG	contig232	Solyc02g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.230	Comprom	-0.230	Comprom	0.000	2.538	Detected	2.516	Detected	2.527	0.008	GT	Sens	contig232	contig232	TIR-NBS	CCCAGC	contig232	Solyc07g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.066	Detected	0.066	Detected	0.000	1.131	Detected	0.876	Detected	1.004	0.020	GT	Sens	contig232	contig232	Unknown	TCACAT	contig232	Solyc06g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.439	Comprom	-0.439	Comprom	0.000	0.877	Detected	1.829	Detected	1.353	0.172	GT	Sens	contig232	contig232	Unknown	GAAATT	contig232	Solyc04g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	0.905	Detected	1.242	Detected	1.073	0.024	GT	Sens	contig233	contig233	1-AMINO	CTTTGA	contig233	Solyc11g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.289	Detected	-0.289	Detected	0.000	2.035	Detected	1.392	Detected	1.713	0.058	GT	Sens	contig233	contig233	Ethylene	TTCCAAT	contig233	Solyc01g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	4.175	Detected	0.874	Detected	2.524	0.266	GT	Sens	contig233	contig233	Homeobo	GGAGTA	contig233	Solyc02g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.224	Comprom	0.224	Comprom	0.000	1.771	Detected	2.318	Detected	2.045	0.029	GT	Sens	contig233	contig233	RRNA me	TTCTGA	contig233	Solyc11g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.203	Comprom	-0.203	Comprom	0.000	3.395	Detected	3.471	Detected	3.433	0.004	GT	Sens	contig234	contig234	Unknown	AATATCT	contig234	Solyc01g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.162	Detected	-0.162	Detected	0.000	1.694	Detected	1.925	Detected	1.809	0.012	GT	Sens	contig234	contig234	Receptor	AATGTG	contig234	Solyc03g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.137	Comprom	0.137	Comprom	0.000	1.205	Detected	2.048	Detected	1.627	0.067	GT	Sens	contig234	contig234	Unknown	TAGTTG	contig234	Solyc02g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.200	Comprom	-0.200	Comprom	0.000	1.422	Detected	2.280	Detected	1.851	0.060	GT	Sens	contig234	contig234	Proline-ri	GTTTCT	contig234	Solyc03g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.108	Comprom	-0.108	Comprom	0.000	2.026	Detected	2.766	Detected	2.396	0.025	GT	Sens	contig234	contig234	X1 (Fragr	ATCCAT	contig234	Solyc06g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	1.906	Detected	2.442	Detected	2.174	0.017	GT	Sens	contig235	contig235	Genomic	CATTGC	contig235	Solyc04g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.042	Comprom	0.042	Comprom	0.000	1.541	Detected	2.790	Detected	2.166	0.074	GT	Sens	contig235	contig235	cDNA clo	GGGTTG	contig235	Solyc07g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	0.834	Detected	1.380	Detected	1.107	0.056	GT	Sens	contig235	contig235	SRC2-like	AGTGTG	contig235	Solyc01g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.634	Comprom	-0.634	Comprom	0.000	1.589	Detected	2.414	Detected	2.002	0.118	GT	Sens	contig235	contig235	Serine ca	GTGATC	contig235	Solyc05g	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GT	Sense	Sense	0.589	Detected	-0.589	Detected	0.000	1.026	Detected	1.659	Detected	1.342	0.182	GT	Sens	contig236	contig236	Methionir	AAACCG	contig236	Solyc00g	Solyc00g	Methionir	GO:0046	GO:0046	contig236	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	623.744	328.283	1873.92	1665.1	1038.07	1350.76
GT	Sense	Sense	-0.803	Comprom	0.803	Comprom	0.000	1.070	Detected	2.660	Detected	1.865	0.241	GT	Sens	contig236	contig236	F-box fan	AGATTCT	contig236	Solyc08g	Solyc08g	F-box fan	GO:0004	GO:0004	contig236	Solyc08g	F-box fan	GO:0004	SL2.40ch	AT2G40240.1		pentatric	chr2:168	2.41885	8.76687	8.89967	6.05516	10.8929	27.516
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	1.145	Detected	2.005	Detected	1.575	0.073	GT	Sens	contig237	contig237	GDSL est	CTAGAT	contig237	Solyc04g	Solyc04g	GDSL est	GO:0016	GO:0016	contig237	Solyc04g	GDSL est	GO:0016	SL2.40ch	AT1G539	GLIP5	GLIP5: c	chr1:201	100.005	99.1048	209.338	205.22	248.05	377.773
GT	Sense	Sense	-0.357	Comprom	0.357	Comprom	0.000	0.956	Detected	2.167	Detected	1.561	0.156	GT	Sens	contig237	contig237	RING fing	GAAAAA	contig237	Solyc04g	Solyc04g	RING fing	GO:0008	GO:0008	contig237	Solyc09g	RING fing	GO:0008	SL2.40ch	AT2G18938.1				3.40792	6.65263	4.9508	5.32301	10.404	20.2207
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	1.289	Detected	1.217	Detected	1.253	0.006	GT	Sens	contig238	contig238	TIR-NBS-l	TGAACC	contig238	Solyc01g	Solyc01g	TIR-NBS-l	GO:0031	GO:0031	contig238	Solyc01g	Tir-nbs-lr	GO:0004	SL2.40ch	AT2G42760.1		unknown	chr2:177	112.209	118.141	397.757	363.867	316.921	253.103
GT	Sense	Sense	-0.391	Comprom	0.391	Comprom	0.000	1.147	Detected	2.227	Detected	1.687	0.127	GT	Sens	contig238	contig238	Unknown	GGGGAA	contig238	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig238	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G44230.1		pentatric	chr5:178	3.42173	7.00148	8.41907	5.32476	12.206	21.6643
GT	Sense	Sense	0.150	Comprom	-0.150	Comprom	0.000	2.285	Detected	2.983	Detected	2.634	0.020	GT	Sens	contig238	contig238	Unknown	CAAAGCT	contig238	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig238	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G08430.1		SWIB co	chr5:271	2.46517	2.38397	12.7612	10.5107	13.3105	18.1201
GT	Sense	Sense	-0.082	Detected	0.082	Detected	0.000	0.974	Detected	1.572	Detected	1.273	0.054	GT	Sens	contig238	contig238	Invertase	GCTAGT	contig238	Solyc12g	Solyc12g	Invertase	GO:0046	GO:0046	contig238	Solyc12g	Invertase	GO:0046	SL2.40ch	AT1G25320.1		leucine-r	chr1:887	328.05	437.365	492.431	482.699	838.222	1064.69
GT	Sense	Sense	0.019	Comprom	-0.019	Comprom	0.000	2.176	Detected	0.958	Detected	1.567	0.124	GT	Sens	contig239	contig239	Myb fami	GGTCCT	contig239	Solyc07g	Solyc07g	Myb fami	GO:0045449		contig239	Solyc07g	Myb fami	GO:0045	SL2.40ch	AT1G05360.1		unknown	chr1:156	9.65339	11.1868	17.0236	6.12471	52.8899	19.086
GT	Sense	Sense	0.757	Detected	-0.757	Detected	0.000	2.483	Detected	1.160	Detected	1.821	0.212	GT	Sens	contig239	contig239	Ethylene	TGCAAT	contig239	Solyc09g	Solyc09g	Ethylene	GO:0051	GO:0051	contig239	Solyc09g	Ethylene	GO:0051	SL2.40ch	AT3G045	EIN4	EIN4 (ET	chr3:123	58.3381	24.3129	94.4582	88.5649	237.153	79.557
GT	Sense	Sense	-0.309	Comprom	0.309	Comprom	0.000	1.794	Detected	2.743	Detected	2.269	0.057	GT	Sens	contig239	contig239	Ethylene-	ATGGCA	contig239	Solyc08g	Solyc08g	Ethylene-	GO:0016	GO:0016	contig239	Solyc08g	Ethylene-	GO:0016	SL2.40ch	AT2G44940.1		AP2 dom	chr2:185	2.71192	4.95316	32.1567	42.3721	14.3153	23.2052
GT	Sense	Sense	-0.664	Comprom	0.664	Detected	0.000	3.017	Detected	2.777	Detected	2.897	0.050	GT	Sens	contig239	contig239	Cytochro	AATGCT	contig239	Solyc09g	Solyc09g	Cytochro	GO:0019	GO:0019	contig239	Solyc09g	Cytochro	GO:0019	SL2.40ch	AT5G229	ATCHX9.	ATCHX9:	chr5:766	7.16689	21.4226	707.61	25.1816	112.973	80.2994
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	1.298	Detected	0.985	Detected	1.142	0.018	GT	Sens	contig240	contig240	Calmodul	CCAAGC	contig240	Solyc03g	Solyc03g	Calmodul	GO:0005	GO:0005	contig240	Solyc03g	Calmodul	GO:0005	SL2.40ch	AT5G18520.1		LOCATE	chr5:614	325.825	379.928	898.388	749.602	974.416	658.673
GT	Sense	Sense	0.362	Detected	-0.362	Detected	0.000	2.056	Detected	2.750	Detected	2.403	0.041	GT	Sens	contig240	contig240	Mutator-li	TGTATCT	contig240	Solyc04g	Solyc04g	Mutator-li	GO:0008	GO:0008	contig240	Solyc11g	F-box family protein		SL2.40ch	AT2G18938.1				82.6752	59.5585	178.917	99.1769	328.782	446.392
GT	Sense	Sense	0.254	Detected	-0.254	Detected	0.000	2.074	Detected	1.827	Detected	1.951	0.020	GT	Sens	contig240	contig240	Dehydroc	TTTGGA	contig240	Solyc05g	Solyc05g	Dehydroc	GO:0045	GO:0045	contig240	Solyc05g	Dehydroc	GO:0045	SL2.40ch	AT2G46900.1		FUNCTIO	chr2:192	40.3126	33.7624	86.0339	57.0656	175.022	123.791

GT	Sense	Sense	0.415	Comprom	-0.415	Comprom	0.000	1.869	Detected	3.376	Detected	2.622	0.093	GT	Sens
GT	Sense	Sense	-0.316	Comprom	0.316	Comprom	0.000	2.434	Detected	2.679	Detected	2.556	0.017	GT	Sens
GT	Sense	Sense	-0.078	Comprom	0.078	Comprom	0.000	5.379	Detected	2.761	Detected	4.070	0.090	GT	Sens
GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	1.159	Detected	1.087	Detected	1.123	0.010	GT	Sens
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	1.289	Detected	1.857	Detected	1.573	0.034	GT	Sens
GT	Sense	Sense	0.220	Detected	-0.220	Detected	0.000	0.855	Detected	1.409	Detected	1.132	0.085	GT	Sens
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	1.303	Detected	1.263	Detected	1.283	0.000	GT	Sens
GT	Sense	Sense	-0.283	Detected	0.283	Detected	0.000	1.094	Detected	1.710	Detected	1.402	0.079	GT	Sens
GT	Sense	Sense	-0.065	Comprom	0.065	Comprom	0.000	0.901	Detected	2.247	Detected	1.574	0.145	GT	Sens
GT	Sense	Sense	-0.173	Comprom	0.173	Comprom	0.000	1.625	Detected	3.761	Detected	2.693	0.131	GT	Sens
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	1.228	Detected	1.913	Detected	1.570	0.046	GT	Sens
GT	Sense	Sense	0.430	Detected	-0.430	Detected	0.000	1.545	Detected	1.338	Detected	1.441	0.083	GT	Sens
GT	Sense	Sense	0.018	Comprom	-0.018	Comprom	0.000	1.401	Detected	2.552	Detected	1.977	0.075	GT	Sens
GT	Sense	Sense	-0.238	Comprom	0.238	Comprom	0.000	1.146	Detected	1.646	Detected	1.396	0.056	GT	Sens
GT	Sense	Sense	0.536	Detected	-0.536	Detected	0.000	1.517	Detected	1.200	Detected	1.358	0.136	GT	Sens
GT	Sense	Sense	0.238	Comprom	-0.238	Comprom	0.000	2.197	Detected	2.878	Detected	2.538	0.026	GT	Sens
GT	Sense	Sense	0.324	Comprom	-0.324	Comprom	0.000	1.859	Detected	1.528	Detected	1.694	0.043	GT	Sens
GT	Sense	Sense	0.748	Detected	-0.748	Detected	0.000	1.098	Detected	0.932	Detected	1.015	0.310	GT	Sens
GT	Sense	Sense	0.049	Comprom	-0.049	Comprom	0.000	1.245	Detected	2.143	Detected	1.694	0.064	GT	Sens
GT	Sense	Sense	-0.030	Comprom	0.030	Comprom	0.000	1.974	Detected	2.558	Detected	2.266	0.016	GT	Sens
GT	Sense	Sense	0.971	Comprom	-0.971	Comprom	0.000	1.381	Detected	2.607	Detected	1.994	0.225	GT	Sens
GT	Sense	Sense	0.343	Detected	-0.343	Detected	0.000	2.168	Detected	1.430	Detected	1.799	0.070	GT	Sens
GT	Sense	Sense	0.472	Detected	-0.472	Detected	0.000	1.432	Detected	1.894	Detected	1.663	0.087	GT	Sens
GT	Sense	Sense	-0.357	Comprom	0.357	Detected	0.000	0.869	Detected	1.470	Detected	1.169	0.129	GT	Sens
GT	Sense	Sense	-0.316	Comprom	0.316	Comprom	0.000	0.849	Detected	2.027	Detected	1.438	0.165	GT	Sens
GT	Sense	Sense	-0.387	Comprom	0.387	Comprom	0.000	1.483	Detected	2.166	Detected	1.825	0.071	GT	Sens
GT	Sense	Sense	-0.132	Comprom	0.132	Comprom	0.000	1.579	Detected	1.599	Detected	1.589	0.007	GT	Sens
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	1.463	Detected	1.401	Detected	1.432	0.007	GT	Sens
GT	Sense	Sense	-0.315	Detected	0.315	Detected	0.000	1.550	Detected	2.048	Detected	1.799	0.046	GT	Sens
GT	Sense	Sense	0.469	Comprom	-0.469	Comprom	0.000	5.263	Detected	5.369	Detected	5.316	0.008	GT	Sens
GT	Sense	Sense	0.104	Comprom	-0.104	Comprom	0.000	6.694	Detected	2.596	Detected	4.645	0.152	GT	Sens
GT	Sense	Sense	-0.408	Detected	0.408	Detected	0.000	1.642	Detected	0.919	Detected	1.280	0.143	GT	Sens
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	1.703	Detected	1.895	Detected	1.799	0.004	GT	Sens
GT	Sense	Sense	-0.340	Comprom	0.340	Detected	0.000	0.865	Detected	2.198	Detected	1.531	0.177	GT	Sens
GT	Sense	Sense	-0.657	Comprom	0.657	Detected	0.000	1.141	Detected	1.056	Detected	1.099	0.237	GT	Sens
GT	Sense	Sense	0.379	Comprom	-0.379	Comprom	0.000	0.885	Detected	2.913	Detected	1.899	0.222	GT	Sens
GT	Sense	Sense	0.715	Comprom	-0.715	Comprom	0.000	1.817	Detected	1.866	Detected	1.842	0.124	GT	Sens
GT	Sense	Sense	0.052	Detected	-0.052	Detected	0.000	1.367	Detected	1.494	Detected	1.431	0.003	GT	Sens
GT	Sense	Sense	-0.433	Detected	0.433	Detected	0.000	1.460	Detected	1.449	Detected	1.454	0.078	GT	Sens
GT	Sense	Sense	-0.169	Detected	0.169	Detected	0.000	4.728	Detected	1.647	Detected	3.188	0.176	GT	Sens
GT	Sense	Sense	0.303	Comprom	-0.303	Comprom	0.000	1.047	Detected	1.876	Detected	1.462	0.104	GT	Sens
GT	Sense	Sense	-0.115	Comprom	0.115	Detected	0.000	1.206	Detected	1.019	Detected	1.113	0.017	GT	Sens
GT	Sense	Sense	1.873	Detected	-1.873	Comprom	0.000	0.940	Detected	2.112	Detected	1.526	0.518	GT	Sens
GT	Sense	Sense	-1.350	Comprom	1.350	Detected	0.000	1.971	Detected	2.001	Detected	1.986	0.279	GT	Sens
GT	Sense	Sense	-0.169	Comprom	0.169	Detected	0.000	0.949	Detected	1.118	Detected	1.033	0.032	GT	Sens
GT	Sense	Sense	0.380	Detected	-0.380	Detected	0.000	1.059	Detected	1.331	Detected	1.195	0.098	GT	Sens
GT	Sense	Sense	-0.164	Detected	0.164	Detected	0.000	1.031	Detected	1.699	Detected	1.365	0.067	GT	Sens
GT	Sense	Sense	0.717	Detected	-0.717	Comprom	0.000	0.859	Detected	1.820	Detected	1.340	0.261	GT	Sens
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	1.173	Detected	0.991	Detected	1.082	0.010	GT	Sens
GT	Sense	Sense	-0.585	Comprom	0.585	Detected	0.000	2.763	Detected	2.497	Detected	2.630	0.048	GT	Sens
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	1.284	Detected	1.134	Detected	1.209	0.010	GT	Sens
GT	Sense	Sense	-0.938	Comprom	0.938	Detected	0.000	1.015	Detected	1.815	Detected	1.415	0.299	GT	Sens
GT	Sense	Sense	0.874	Comprom	-0.874	Comprom	0.000	0.804	Detected	1.828	Detected	1.316	0.323	GT	Sens
GT	Sense	Sense	0.234	Comprom	-0.234	Comprom	0.000	5.143	Detected	5.624	Detected	5.383	0.004	GT	Sens
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	1.152	Detected	1.659	Detected	1.406	0.033	GT	Sens
GT	Sense	Sense	0.945	Detected	-0.945	Comprom	0.000	0.820	Detected	1.547	Detected	1.184	0.363	GT	Sens
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	1.211	Detected	0.980	Detected	1.095	0.023	GT	Sens
GT	Sense	Sense	-1.610	Comprom	1.610	Detected	0.000	1.334	Detected	0.835	Detected	1.084	0.574	GT	Sens
GT	Sense	Sense	0.027	Comprom	-0.027	Comprom	0.000	1.052	Detected	2.214	Detected	1.633	0.107	GT	Sens
GT	Sense	Sense	0.821	Detected	-0.821	Detected	0.000	3.981	Detected	1.053	Detected	2.517	0.272	GT	Sens
GT	Sense	Sense	0.214	Comprom	-0.214	Comprom	0.000	1.039	Detected	2.195	Detected	1.617	0.120	GT	Sens
GT	Sense	Sense	0.476	Detected	-0.476	Detected	0.000	1.266	Detected	1.314	Detected	1.290	0.114	GT	Sens
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	1.138	Detected	1.105	Detected	1.122	0.001	GT	Sens
GT	Sense	Sense	0.052	Detected	-0.052	Detected	0.000	2.115	Detected	2.118	Detected	2.116	0.001	GT	Sens
GT	Sense	Sense	-0.667	Comprom	0.667	Detected	0.000	1.035	Detected	1.180	Detected	1.108	0.240	GT	Sens
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	0.846	Detected	1.214	Detected	1.030	0.037	GT	Sens
GT	Sense	Sense	-0.729	Comprom	0.729	Detected	0.000	1.493	Detected	1.601	Detected	1.547	0.169	GT	Sens
GT	Sense	Sense	-0.168	Comprom	0.168	Comprom	0.000	1.817	Detected	2.132	Detected	1.974	0.013	GT	Sens
GT	Sense	Sense	0.477	Detected	-0.477	Detected	0.000	1.075	Detected	2.289	Detected	1.682	0.161	GT	Sens
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	0.804	Detected	1.467	Detected	1.136	0.077	GT	Sens
GT	Sense	Sense	-0.386	Comprom	0.386	Comprom	0.000	2.221	Detected	2.559	Detected	2.390	0.030	GT	Sens
GT	Sense	Sense	0.351	Detected	-0.351	Detected	0.000	1.065	Detected	1.311	Detected	1.188	0.086	GT	Sens
GT	Sense	Sense	-0.299	Detected	0.299	Detected	0.000	1.115	Detected	0.948	Detected	1.031	0.080	GT	Sens
GT	Sense	Sense	-0.667	Comprom	0.667	Comprom	0.000	0.943	Detected	2.046	Detected	1.494	0.226	GT	Sens
GT	Sense	Sense	0.085	Detected	-0.085	Detected	0.000	1.285	Detected	2.069	Detected	1.677	0.053	GT	Sens
GT	Sense	Sense	-0.217	Comprom	0.217	Comprom	0.000	0.885	Detected	1.707	Detected	1.296	0.108	GT	Sens
GT	Sense	Sense	-0.303	Detected	0.303	Detected	0.000	1.094	Detected	0.926	Detected	1.010	0.085	GT	Sens
GT	Sense	Sense	0.962	Detected	-0.962	Detected	0.000	2.717	Detected	1.329	Detected	2.023	0.230	GT	Sens
GT	Sense	Sense	-0.208	Detected	0.208	Detected	0.000	1.664	Detected	0.891	Detected	1.277	0.101	GT	Sens
GT	Sense	Sense	-0.561	Comprom	0.561	Detected	0.000	1.179	Detected	1.431	Detected	1.305	0.151	GT	Sens
GT	Sense	Sense	-0.293	Comprom	0.293	Comprom	0.000	1.858	Detected	2.862	Detected	2.360	0.056	GT	Sens
GT	Sense	Sense	0.542	Comprom	-0.542	Comprom	0.000	2.885	Detected	3.397	Detected	3.141	0.035	GT	Sens
GT	Sense	Sense	0.753	Detected	-0.753	Detected	0.000	0.842	Detected	1.507	Detected	1.175	0.290	GT	Sens
GT	Sense	Sense	-0.081	Detected	0.081	Detected	0.000	1.332	Detected	1.775	Detected	1.554	0.022	GT	Sens
GT	Sense	Sense	0.235	Comprom	-0.235	Comprom	0.000	1.387	Detected	2.887	Detected	2.137	0.113	GT	Sens
GT	Sense	Sense	-0.177	Detected	0.177	Detected	0.000	0.801	Detected	1.691	Detected	1.246	0.121	GT	Sens
GT	Sense	Sense	-0.875	Comprom	0.875	Detected	0.000	2.104	Detected	1.547	Detected	1.825	0.185	GT	Sens
GT	Sense	Sense	-0.091	Comprom	0.091	Comprom	0.000	1.355	Detected	2.307	Detected	1.831	0.064	GT	Sens
GT	Sense	Sense	0.062	Detected	-0.062	Detected	0.000	1.433	Detected	1.833	Detected	1.633	0.016	GT	Sens
GT	Sense	Sense	-0.215	Comprom	0.215	Comprom	0.000	1.632	Detected	2.269	Detected	1.950	0.037	GT	Sens
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	1.353	Detected	2.146	Detected	1.750	0.049	GT	Sens
GT	Sense	Sense	0.369	Detected	-0.369	Detected	0.000	1.126	Detected	1.801	Detected	1.464	0.100	GT	Sens
GT	Sense	Sense	0.066	Comprom	-0.066	Comprom	0.000	2.696	Detected	3.463	Detected	3.080	0.016	GT	Sens
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	1.704	Detected	2.046	Detected	1.875	0.009	GT	Sens
GT	Sense	Sense	-0.145	Detected	0.145	Detected	0.000	1.263	Detected	0.969	Detected	1.116	0.033	GT	Sens
GT	Sense	Sense	-0.526	Comprom	0.526	Detected	0.000	1.995	Detected	1.338	Detected	1.667	0.115	GT	Sens
GT	Sense	Sense	0.465	Comprom	-0.465	Comprom	0.000	3.352	Detected	2.486	Detected	2.919	0.044	GT	Sens
GT	Sense	Sense	0.234	Comprom	-0.234	Comprom	0.000	1.422	Detected	1.292	Detected	1.357	0.031	GT	Sens
GT	Sense	Sense	-0.440	Comprom	0.440	Comprom	0.000	1.157	Detected	2.140	Detected	1.648	0.130	GT	Sens
GT	Sense	Sense	0.001	Detected	-0.001	Detected	0.000	2.118	Detected	3.563	Detected	2.841	0.059	GT	Sens
GT	Sense	Sense	0.151	Comprom	-0.151	Comprom	0.000	2.634	Detected	3.867	Detected	3.250	0.036	GT	Sens
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	1.753	Detected	1.491	Detected	1.622	0.014	GT	Sens
GT	Sense	Sense	-0.556	Comprom	0.556	Comprom	0.000	1.292	Detected	3.766	Detected	2.529	0.203	GT	Sens
GT	Sense	Sense	0.008	Detected	-0.008	Detected	0.000	1.282	Detected	0.825	Detected	1.053	0.044	GT	Sens
GT	Sense	Sense	0.168	Comprom	-0.168	Comprom	0.000	1.903	Detected	2.708	Detected	2.305	0.034	GT	Sens
GT	Sense	Sense	-0.148	Detected	0.148	Detected	0.000	1.463	Detected	1.050	Detected	1.256	0.039	GT	Sens
GT	Sense	Sense	0.300	Detected	-0.300	Detected	0.000	0.980	Detected	1.152	Detected	1.066	0.076	GT	Sens
GT	Sense	Sense	-0.593	Comprom	0.593	Detected	0.000	0.877	Detected	1.463	Detected	1.170	0.219	GT	Sens
GT	Sense	Sense	0.371	Comprom	-0.371	Comprom	0.000	1.918	Detected	2.815	Detected	2.367	0.055	GT	Sens
GT	Sense	Sense	-0.215	Detected	0.215	Detected	0.000	2.073	Detected	1.288	Detected	1.680	0.064	GT	Sens
GT	Sense	Sense	0.606	Comprom	-0.606	Comprom	0.000	1.855	Detected	2.282	Detected	2.068	0.084	GT	Sens
GT	Sense	Sense	-0.096	Detected	0.096	Detected	0.000	1.191	Detected	0.842	Detected	1.017	0.036	GT	Sens
GT	Sense	Sense	-0.262	Detected	0.262	Detected	0.000	2.036	Detected	1.509	Detected	1.773	0.041	GT	Sens
GT	Sense	Sense	0.230	Comprom	-0.230	Comprom	0.000	0.981	Detected	2.172	Detected	1.577	0.132	GT	Sens
GT	Sense	Sense	0.702	Detected	-0.702	Detected	0.000	1.700	Detected	1.526	Detected	1.613	0.150	GT	Sens
GT	Sense	Sense	0.983	Detected	-0.983	Detected	0.000	1.534	Detected	1.075	Detected	1.305	0.325	GT	Sens
GT	Sense	Sense	0.190	Detected	-0.190	Detected	0.000	1.694	Detected	1.239	Detected	1.466	0.039	GT	Sens
GT	Sense	Sense	0.486	Detected	-0.486	Detected	0.000	1.542	Detected	1.375	Detected	1.459	0.098	GT	Sens
GT	Sense	Sense	0.436	Detected	-0.436	Detected	0.000	1.083	Detected	1.120	Detected	1.101	0.128	GT	Sens
GT	Sense	Sense	-0.613	Detected	0.613	Detected	0.000	0.893	Detected	1.442	Detected	1.167	0.224	GT	Sens
GT	Sense	Sense	-1.062	Comprom	1.062	Detected	0.000	1.854	Detected	1.652	Detected	1.753	0.242	GT	Sens
GT	Sense	Sense	-0.303	Comprom	0.303	Comprom	0.000	1.210	Detected	2.036	Detected	1.623	0.087	GT	Sens
GT	Sense	Sense	0.025	Comprom	-0.025	Comprom	0.000	1.173	Detected	2.346	Detected	1.760	0.096	GT	Sens
GT	Sense	Sense	0.649	Detected	-0.649	Detected	0.000	2.178	Detected	2.264	Detected	2.221	0.076	GT	Sens
GT	Sense	Sense	0.228	Detected	-0.228	Detected	0.000	0.899	Detected	1.122	Detected	1.011	0.058	GT	Sens
GT	Sense	Sense	0.767	Detected	-0.767	Detected	0.000	0.975	Detected	1.126	Detected	1.050	0.306	GT	Sens
GT	Sense	Sense	1.104	Detected	-1.104	Comprom	0.000	1.155	Detected	1.411	Detected	1.283	0.368	GT	Sens
GT	Sense	Sense	1.067	Comprom	-1.067	Comprom	0.000	1.914	Detected	1.986	Detected	1.950	0.209	GT	Sens
GT	Sense	Sense	-0.580	Comprom	0.580	Detected	0.000	1.776	Detected	1.943	Detected	1.859	0.087	GT	Sens
GT	Sense	Sense	0.304	Detected	-0.304	Detected	0.000	0.949	Detected	1.730	Detected	1.340	0.114	GT	Sens
GT	Sense	Sense	-0.155	Detected	0.155	Detected	0.000	1.246	Detected	1.397	Detected	1.322	0.017	GT	Sens
GT	Sense	Sense	0.789	Detected	-0.789	Comprom	0.000	1.242	Detected	0.990	Detected	1.116	0.297	GT	Sens
GT	Sense	Sense	-0.637	Comprom	0.637	Comprom	0.000	1.152	Detected	2.258	Detected	1.705	0.181	GT	Sens
GT	Sense	Sense	-0.783	Detected	0.783	Detected	0.000	0.961	Detected	1.635	Detected	1.298	0.267	GT	Sens
GT	Sense	Sense	-0.671	Comprom	0.671	Comprom	0.000	2.022	Detected	2.005	Detected	2.014	0.095	GT	Sens
GT	Sense	Sense	1.517	Detected	-1.517	Comprom	0.000	2.853	Detected	4.001	Detected	3.427	0.169	GT	Sens
GT	Sense	Sense	0.250	Comprom	-0.250	Comprom	0.000	1.056	Detected	2.083	Detected	1.570	0.111	GT	Sens
GT	Sense	Sense	0.079	Comprom	-0.079	Comprom	0.000	1.874	Detected	1.178	Detected	1.526	0.051	GT	Sens
GT	Sense	Sense	-0.228	Comprom	0.228	Comprom	0.000	1.958	Detected	2.370	Detected	2.164	0.020	GT	Sens
GT	Sense	Sense	0.187	Comprom	-0.187	Comprom	0.000	2.496	Detected	2.163	Detected	2.330	0.011	GT	Sens
GT	Sense	Sense	-0.136	Detected	0.136	Detected	0.000	2.065	Detected	1.166	Detected	1.616	0.075	GT	Sens
GT	Sense	Sense	-0.470	Detected	0.470	Detected	0.000	1.972	Detected	1.471	Detected	1.721	0.084	GT	Sens
GT	Sense	Sense	-0.493	Comprom	0.493	Comprom	0.000	1.498	Detected	2.385	Detected	1.941	0.100	GT	Sens
GT	Sense	Sense	-0.196	Detected	0.196	Detected	0.000	3.291	Detected	1.806	Detected	2.548	0.080	GT	Sens
GT	Sense	Sense	0.747	Comprom	-0.747	Comprom	0.000	0.931	Detected	1.842	Detected	1.386	0.254	GT	Sens
GT	Sense	Sense	-0.616	Comprom	0.616	Detected	0.000	1.475	Detected	2.198	Detected	1.836	0.124	GT	Sens
GT	Sense	Sense	-1.829	Comprom	1.829	Detected	0.000	2.345	Detected	4.668	Detected	3.506	0.247	GT	Sens
GT	Sense	Sense	0.166	Comprom	-0.166	Comprom	0.000	1.302	Detected	3.274	Detected	2.288	0.149	GT	Sens
GT	Sense	Sense	-0.030	Comprom	0.030	Comprom	0.000	1.146	Detected	2.481	Detected	1.813	0.113	GT	Sens
GT	Sense	Sense	0.054	Comprom	-0.054	Comprom	0.000	1.662	Detected	2.322	Detected	1.992	0.027	GT	Sens
GT	Sense	Sense	-0.423	Comprom	0.423	Comprom	0.000	2.151	Detected	2.549	Detected	2.350	0.037	GT	Sens
GT	Sense	Sense	0.980	Detected	-0.980	Detected	0.000	1.369	Detected	1.648	Detected	1.508	0.267	GT	Sens
GT	Sense	Sense	0.273	Comprom	-0.273	Comprom	0.000	1.502	Detected	2.741	Detected	2.122	0.088	GT	Sens
GT	Sense	Sense	0.685	Comprom	-0.685	Comprom	0.000	1.355	Detected	1.996	Detected	1.676	0.157	GT	Sens
GT	Sense	Sense	0.521	Comprom	-0.521	Comprom	0.000	1.464	Detected	2.647	Detected	2.055	0.121	GT	Sens
GT	Sense	Sense	0.396	Comprom	-0.396	Comprom	0.000	1.005	Detected	2.717	Detected	1.861	0.187	GT	Sens
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	1.095	Detected	1.144	Detected	1.120	0.003	GT	Sens
GT	Sense	Sense	1.497	Detected	-1.497	Comprom	0.000	1.266	Detected	1.116	Detected	1.191	0.510	GT	Sens
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	3.012	Detected	3.119	Detected	3.066	0.002	GT	Sens
GT	Sense	Sense	0.360	Comprom	-0.360	Comprom	0.000	0.842	Detected	1.787	Detected	1.315	0.157	GT	Sens
GT	Sense	Sense	-0.349	Detected	0.349	Detected	0.000	2.160	Detected	0.883	Detected	1.522	0.172	GT	Sens
GT	Sense	Sense	0.279	Detected	-0.279	Detected	0.000	2.768	Detected	1.854	Detected	2.311	0.050	GT	Sens
GT	Sense	Sense	0.222	Detected	-0.222	Detected	0.000	2.640	Detected	0.814	Detected	1.727	0.207	GT	Sens
GT	Sense	Sense	0.345	Detected	-0.345	Detected	0.000	0.832	Detected	1.757	Detected	1.294	0.154	GT	Sens
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	2.676	Detected	2.633	Detected	2.654	0.000	GT	Sens
GT	Sense	Sense	0.236	Comprom	-0.236	Comprom	0.000	1.099	Detected	1.277	Detected	1.188	0.042	GT	Sens
GT	Sense	Sense	0.521	Detected	-0.521	Detected	0.000	2.700	Detected	1.435	Detected	2.067	0.128	GT	Sens
GT	Sense	Sense	0.462	Comprom	-0.462	Comprom	0.000	1.181	Detected	1.945	Detected	1.563	0.121	GT	Sens
GT	Sense	Sense	0.143	Detected	-0.143	Detected	0.000	1.267	Detected	1.491	Detected	1.379	0.017	GT	Sens
GT	Sense	Sense	-0.717	Comprom	0.717	Detected	0.000	2.349	Detected	1.109	Detected	1.729	0.210	GT	Sens
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	1.376	Detected	0.995	Detected	1.185	0.030	GT	Sens
GT	Sense	Sense	0.263	Detected	-0.263	Detected	0.000	2.676	Detected	1.073	Detected	1.875	0.156	GT	Sens
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	0.835	Detected	1.336	Detected	1.085	0.050	GT	Sens
GT	Sense	Sense	0.351	Detected	-0.351	Detected	0.000	1.934	Detected	2.714	Detected	2.324	0.047	GT	Sens
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	1.219	Detected	1.820	Detected	1.520	0.066	GT	Sens
GT	Sense	Sense	0.321	Comprom	-0.321	Comprom	0.000	0.827	Detected	1.916	Detected	1.371	0.162	GT	Sens
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	1.271	Detected	0.968	Detected	1.120	0.027	GT	Sens
GT	Sense	Sense	-0.230	Comprom	0.230	Detected	0.000	1.120	Detected	1.520	Detected	1.320	0.049	GT	Sens
GT	Sense	Sense	0.054	Detected	-0.054	Detected	0.000	1.414	Detected	1.712	Detected	1.563	0.010	GT	Sens
GT	Sense	Sense	-0.108	Detected	0.108	Detected	0.000	1.571	Detected	1.313	Detected	1.442	0.013	GT	Sens
GT	Sense	Sense	0.379	Detected	-0.379	Detected	0.000	1.224	Detected	1.150	Detected	1.187	0.089	GT	Sens
GT	Sense	Sense	-0.391	Detected	0.391	Detected	0.000	1.024	Detected	1.126	Detected	1.075	0.113	GT	Sens
GT	Sense	Sense	0.447	Detected	-0.447	Detected	0.000	1.384	Detected	1.349	Detected	1.367	0.093	GT	Sens
GT	Sense	Sense	-0.344	Detected	0.344	Detected	0.000	1.679	Detected	1.183	Detected	1.431	0.078	GT	Sens
GT	Sense	Sense	-0.308	Comprom	0.308	Comprom	0.000	1.052	Detected	2.243	Detected	1.647	0.133	GT	Sens
GT	Sense	Sense	0.789	Detected	-0.789	Comprom	0.000	1.455	Detected	1.822	Detected	1.639	0.180	GT	Sens
GT	Sense	Sense	-0.764	Detected	0.764	Detected	0.000	0.896	Detected	1.435	Detected	1.166	0.287	GT	Sens
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	1.221	Detected	1.082	Detected	1.151	0.004	GT	Sens
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	1.438	Detected	1.637	Detected	1.537	0.009	GT	Sens
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	1.013	Detected	1.053	Detected	1.033	0.001	GT	Sens
GT	Sense	Sense	-0.398	Detected	0.398	Detected	0.000	0.841	Detected	1.875	Detected	1.358	0.173	GT	Sens
GT	Sense	Sense	0.225	Comprom	-0.225	Comprom	0.000	2.033	Detected	2.628	Detected	2.331	0.025	GT	Sens
GT	Sense	Sense	-0.335	Detected	0.335	Detected	0.000	2.487	Detected	2.116	Detected	2.301	0.027	GT	Sens
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	1.074	Detected	1.183	Detected	1.129	0.020	GT	Sens
GT	Sense	Sense	0.414	Detected	-0.414	Detected	0.000	2.896	Detected	2.052	Detected	2.474	0.053	GT	Sens
GT	Sense	Sense	0.521	Comprom	-0.521	Comprom	0.000	1.647	Detected	1.617	Detected	1.632	0.089	GT	Sens
GT	Sense	Sense	0.221	Detected	-0.221	Detected	0.000	1.443	Detected	1.965	Detected	1.704	0.038	GT	Sens
GT	Sense	Sense	-0.574	Comprom	0.574	Comprom	0.000	0.996	Detected	4.987	Detected	2.992	0.286	GT	Sens
GT	Sense	Sense	-0.148	Comprom	0.148	Comprom	0.000	1.022	Detected	2.845	Detected	1.933	0.171	GT	Sens
GT	Sense	Sense	-0.124	Detected	0.124	Detected	0.000	1.104	Detected	1.219	Detected	1.161	0.014	GT	Sens
GT	Sense	Sense	0.321	Detected	-0.321	Detected	0.000	1.311	Detected	1.354	Detected	1.333	0.054	GT	Sens
GT	Sense	Sense	-0.221	Comprom	0.221	Comprom	0.000	3.027	Detected	3.137	Detected	3.082	0.005	GT	Sens
GT	Sense	Sense	0.600	Comprom	-0.600	Comprom	0.000	1.472	Detected	2.105	Detected	1.788	0.119	GT	Sens
GT	Sense	Sense	0.129	Comprom	-0.129	Comprom	0.000	1.364	Detected	1.604	Detected	1.484	0.014	GT	Sens
GT	Sense	Sense	-0.115	Detected	0.115	Detected	0.000	2.081	Detected	2.105	Detected	2.093	0.003	GT	Sens
GT	Sense	Sense	1.181	Detected	-1.181	Detected	0.000	1.687	Detected	1.951	Detected	1.819	0.265	GT	Sens
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	0.865	Detected	1.278	Detected	1.072	0.040	GT	Sens
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	1.254	Detected	2.164	Detected	1.709	0.068	GT	Sens
GT	Sense	Sense	0.617	Detected	-0.617	Detected	0.000	0.987	Detected	1.078	Detected	1.033	0.237	GT	Sens
GT	Sense	Sense	0.446	Comprom	-0.446	Comprom	0.000	1.005	Detected	1.028	Detected	1.016	0.150	GT	Sens
GT	Sense	Sense	-0.608	Comprom	0.608	Detected	0.000	0.847	Detected	1.534	Detected	1.190	0.230	GT	Sens
GT	Sense	Sense	-0.368	Detected	0.368	Detected	0.000	0.894	Detected	1.149	Detected	1.022	0.119	GT	Sens
GT	Sense	Sense	0.031	Comprom	-0.031	Comprom	0.000	1.394	Detected	2.395	Detected	1.894	0.063	GT	Sens
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	1.400	Detected	0.922	Detected	1.161	0.044	GT	Sens
GT	Sense	Sense	-0.068	Comprom	0.068	Comprom	0.000	3.674	Detected	3.093	Detected	3.384	0.008	GT	Sens
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	1.708	Detected	2.112	Detected	1.910	0.016	GT	Sens
GT	Sense	Sense	0.467	Detected	-0.467	Comprom	0.000	1.425	Detected	1.664	Detected	1.545	0.085	GT	Sens
GT	Sense	Sense	0.751	Detected	-0.751	Comprom	0.000	1.039	Detected	2.339	Detected	1.689	0.231	GT	Sens
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	1.711	Detected	1.315	Detected	1.513	0.017	GT	Sens
GT	Sense	Sense	0.085	Detected	-0.085	Detected	0.000	1.052	Detected	1.087	Detected	1.069	0.006	GT	Sens
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	0.967	Detected	1.181	Detected	1.074	0.029	GT	Sens
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	1.594	Detected	1.349	Detected	1.471	0.009	GT	Sens
GT	Sense	Sense	-0.264	Comprom	0.264	Detected	0.000	1.643	Detected	1.544	Detected	1.593	0.027	GT	Sens
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	1.217	Detected	1.102	Detected	1.160	0.003	GT	Sens
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	1.769	Detected	1.241	Detected	1.505	0.029	GT	Sens
GT	Sense	Sense	-0.716	Comprom	0.716	Detected	0.000	1.855	Detected	2.614	Detected	2.234	0.110	GT	Sens
GT	Sense	Sense	-0.231	Comprom	0.231	Comprom	0.000	1.568	Detected	2.162	Detected	1.865	0.038	GT	Sens
GT	Sense	Sense	0.912	Comprom	-0.912	Comprom	0.000	2.445	Detected	2.551	Detected	2.498	0.112	GT	Sens
GT	Sense	Sense	0.263	Comprom	-0.263	Comprom	0.000	1.107	Detected	1.720	Detected	1.413	0.073	GT	Sens
GT	Sense	Sense	0.655	Comprom	-0.655	Comprom	0.000	1.201	Detected	2.845	Detected	2.023	0.194	GT	Sens
GT	Sense	Sense	0.667	Comprom	-0.667	Comprom	0.000	1.705	Detected	3.152	Detected	2.428	0.132	GT	Sens
GT	Sense	Sense	0.309	Comprom	-0.309	Comprom	0.000	1.323	Detected	1.630	Detected	1.477	0.051	GT	Sens
GT	Sense	Sense	-0.583	Comprom	0.583	Comprom	0.000	1.955	Detected	2.348	Detected	2.151	0.073	GT	Sens
GT	Sense	Sense	0.682	Comprom	-0.682	Comprom	0.000	1.665	Detected	2.840	Detected	2.252	0.129	GT	Sens
GT	Sense	Sense	0.208	Comprom	-0.208	Comprom	0.000	3.278	Detected	4.847	Detected	4.062	0.038	GT	Sens
GT	Sense	Sense	-0.411	Detected	0.411	Detected	0.000	2.185	Detected	2.031	Detected	2.108	0.037	GT	Sens
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	1.167	Detected	1.384	Detected	1.275	0.007	GT	Sens
GT	Sense	Sense	0.149	Comprom	-0.149	Comprom	0.000	2.164	Detected	2.605	Detected	2.384	0.012	GT	Sens
GT	Sense	Sense	0.355	Detected	-0.355	Detected	0.000	1.440	Detected	1.227	Detected	1.334	0.069	GT	Sens
GT	Sense	Sense	0.543	Detected	-0.543	Detected	0.000	1.325	Detected	1.067	Detected	1.196	0.165	GT	Sens
GT	Sense	Sense	-1.261	Comprom	1.261	Detected	0.000	0.840	Detected	1.212	Detected	1.026	0.505	GT	Sens
GT	Sense	Sense	-0.072	Comprom	0.072	Comprom	0.000	2.010	Detected	2.214	Detected	2.112	0.003	GT	Sens
GT	Sense	Sense	0.565	Detected	-0.565	Detected	0.000	0.973	Detected	1.727	Detected	1.350	0.185	GT	Sens
GT	Sense	Sense	0.281	Comprom	-0.281	Comprom	0.000	1.114	Detected	1.392	Detected	1.253	0.057	GT	Sens

GT	Sense	Sense	-0.076	Comprom	0.076	Comprom	0.000	1.128	Detected	2.293	Detected	1.710	0.100	GT	Sens	contig317	contig317	Unannota
GT	Sense	Sense	-0.338	Comprom	0.338	Comprom	0.000	1.481	Detected	2.230	Detected	1.856	0.067	GT	Sens	contig317	contig317	Unannota
GT	Sense	Sense	0.491	Comprom	-0.491	Comprom	0.000	2.606	Detected	2.755	Detected	2.681	0.033	GT	Sens	contig317	contig317	Unannota
GT	Sense	Sense	0.725	Detected	-0.725	Detected	0.000	3.538	Detected	1.125	Detected	2.331	0.239	GT	Sens	contig317	contig317	DUF599 f
GT	Sense	Sense	0.185	Detected	-0.185	Detected	0.000	1.381	Detected	1.508	Detected	1.444	0.018	GT	Sens	contig318	contig318	Unannota
GT	Sense	Sense	-1.453	Comprom	1.453	Detected	0.000	1.728	Detected	1.882	Detected	1.805	0.341	GT	Sens	contig318	contig318	Unannota
GT	Sense	Sense	-0.790	Comprom	0.790	Detected	0.000	0.927	Detected	1.146	Detected	1.036	0.323	GT	Sens	contig318	contig318	Unannota
GT	Sense	Sense	0.217	Comprom	-0.217	Comprom	0.000	2.028	Detected	3.077	Detected	2.552	0.046	GT	Sens	contig318	contig318	Unannota
GT	Sense	Sense	0.971	Detected	-0.971	Detected	0.000	1.172	Detected	1.215	Detected	1.194	0.344	GT	Sens	contig318	contig318	Unannota
GT	Sense	Sense	-0.744	Comprom	0.744	Detected	0.000	1.811	Detected	2.090	Detected	1.950	0.123	GT	Sens	contig319	contig319	Unannota
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	0.922	Detected	1.569	Detected	1.246	0.063	GT	Sens	contig319	contig319	Unannota
GT	Sense	Sense	0.485	Detected	-0.485	Detected	0.000	1.054	Detected	1.032	Detected	1.043	0.165	GT	Sens	contig319	contig319	Unannota
GT	Sense	Sense	0.642	Detected	-0.642	Detected	0.000	1.379	Detected	1.109	Detected	1.244	0.198	GT	Sens	contig319	contig319	Unannota
GT	Sense	Sense	0.199	Comprom	-0.199	Comprom	0.000	1.172	Detected	2.311	Detected	1.741	0.102	GT	Sens	contig320	contig320	Unannota
GT	Sense	Sense	0.940	Detected	-0.940	Comprom	0.000	0.977	Detected	1.110	Detected	1.043	0.383	GT	Sens	contig320	contig320	Unannota
GT	Sense	Sense	0.200	Detected	-0.200	Detected	0.000	1.406	Detected	1.658	Detected	1.532	0.023	GT	Sens	contig320	contig320	Unannota
GT	Sense	Sense	0.947	Detected	-0.947	Detected	0.000	1.000	Detected	1.303	Detected	1.151	0.353	GT	Sens	contig320	contig320	Unannota
GT	Sense	Sense	-0.585	Comprom	0.585	Comprom	0.000	1.824	Detected	1.277	Detected	1.550	0.138	GT	Sens	contig320	contig320	Unannota
GT	Sense	Sense	-0.147	Detected	0.147	Detected	0.000	1.884	Detected	1.316	Detected	1.600	0.038	GT	Sens	contig320	contig320	Unannota
GT	Sense	Sense	0.160	Detected	-0.160	Detected	0.000	1.063	Detected	1.199	Detected	1.131	0.023	GT	Sens	contig320	contig320	Unannota
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	1.108	Detected	0.944	Detected	1.026	0.006	GT	Sens	contig321	contig321	Unannota
GT	Sense	Sense	-0.291	Detected	0.291	Detected	0.000	1.706	Detected	1.834	Detected	1.770	0.027	GT	Sens	contig321	contig321	Unannota
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	1.375	Detected	0.990	Detected	1.182	0.029	GT	Sens	contig321	contig321	Unannota
GT	Sense	Sense	-0.144	Detected	0.144	Detected	0.000	1.504	Detected	1.434	Detected	1.469	0.010	GT	Sens	contig321	contig321	Unannota
GT	Sense	Sense	-0.596	Comprom	0.596	Comprom	0.000	0.850	Detected	1.618	Detected	1.234	0.224	GT	Sens	contig322	contig322	Unannota
GT	Sense	Sense	0.088	Comprom	-0.088	Comprom	0.000	0.935	Detected	1.100	Detected	1.018	0.014	GT	Sens	contig323	contig323	Ycf2 (AHF

GT	Sense	Sense	-0.457	Comprom	0.457	Detected	0.000	1.681	Detected	1.826	Detected	1.754	0.063	GT Sens	contig375	contig375	Unannota	CTCATTCACGATAGAGAACAAAATTATTCTCTATCCTTTTCTTCATCCA	contig375	Solyc12g	Cytochro	GO:0019	SL2.40ch	AT4G01810.1		protein t	chr4:776	5.49089	12.318	19.8672	13.5036	29.704	27.573
GT	Sense	Sense	-0.444	Detected	0.444	Detected	0.000	1.187	Detected	1.419	Detected	1.303	0.105	GT Sens	contig375	contig375	Unannota	TCTAGTTACAACATTGAAGAGATTTCGGCCAAATCTGGTGGTATGGCG	contig375	Solyc11g	Zinc finger protein (		SL2.40ch	AT3G227	SOL1	SOL1: tra	chr3:804	33.8862	74.7032	118.89	127.934	129.055	127.216
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	0.946	Detected	1.151	Detected	1.048	0.019	GT Sens	contig376	contig376	Unannota	AAAGTATCAGAAGGATAACATTTCTTGTGCATTATTTTATGTATATCAT	contig376	Solyc06g	Calcium/r	GO:0015	SL2.40ch	ATCG007	PETD	A chloro	chrC:764	390.558	401.815	640.192	622.884	859.418	831.596
GT	Sense	Sense	1.085	Detected	-1.085	Comprom	0.000	1.100	Detected	1.445	Detected	1.272	0.367	GT Sens	contig376	contig376	Unannota	ACACTCAGCAATATAATTACAGTCAGTCTACAAAGCAAGGCTGCAAAAT	contig376	Solyc12g	Lipoyl sy	GO:0008	SL2.40ch	AT3G140	RSH2. AT	RSH2 (RE	chr3:465	14.4324	3.81627	16.4175	12.318	17.917	19.1024
GT	Sense	Sense	0.311	Comprom	-0.311	Comprom	0.000	0.808	Detected	1.723	Detected	1.265	0.149	GT Sens	contig376	contig376	Unannota	ATACAAGATTAGCCAAAGGTGCAAGTAGCACACATTAAGGACAAATAAG	contig376	Solyc12g	Lipoyl sy	GO:0008	SL2.40ch	AT3G140	RSH2. AT	RSH2 (RE	chr3:465	7.64264	5.91212	8.1842	8.31904	13.2576	20.9786
GT	Sense	Sense	-0.065	Detected	0.065	Detected	0.000	1.726	Detected	2.051	Detected	1.889	0.009	GT Sens	contig376	contig376	Unannota	TAGACTTTAATATTTTGCTTTACAAACCAGAAAAAAGATTGAGAAAAGG	contig376	Solyc12g	RPM1 interacting pr		SL2.40ch	AT5G55660.1		LOCATE	chr5:225	47.0117	61.2771	94.7269	134.325	200.008	210.329
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	0.942	Detected	1.207	Detected	1.074	0.018	GT Sens	contig376	contig376	Unannota	GGTGGAAAATAATTAGTATTGGACTAAGAATAATGTTTGTGGGAAATGC	contig376	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G107	AHK5. CK	AHK5 (AH	chr5:338	126.464	137.889	219.114	215.852	285.714	288.264
GT	Sense	Sense	0.292	Detected	-0.292	Comprom	0.000	1.462	Detected	2.285	Detected	1.873	0.065	GT Sens	contig376	contig376	Unannota	ATTACAAAATAAGGAAAAAGGAAAATGTACAAATTTACCTGTGATATTT	contig376	Solyc12g	Histone-ly	GO:0005	SL2.40ch	AT5G61390.1		exonucle	chr5:246	15.0199	11.9333	39.5785	44.4699	41.5371	61.6852
GT	Sense	Sense	0.232	Comprom	-0.232	Comprom	0.000	1.422	Detected	1.725	Detected	1.574	0.030	GT Sens	contig377	contig377	Unknown	GGAACT contig377 Solyc09g Solyc09g Unknown Protein (AHRD V1)	contig377	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G17610.1		tRNA/rRN	chr4:980	5.70971	4.92753	11.1929	4.28009	16.0114	16.5811
GT	Sense	Sense	-0.215	Comprom	0.215	Comprom	0.000	2.591	Detected	2.596	Detected	2.594	0.007	GT Sens	contig377	contig377	Unannota	TTTAAGTACTTTGTAAGGGATGTGCTGAGTCAAACAAGGACGGAGAGA	contig377	Solyc06g	GDP-L-ga	GO:0080	SL2.40ch	AT3G28450.1		leucine-r	chr3:106	2.62275	4.20844	3.469	5.24084	22.5478	18.9951
GT	Sense	Sense	0.556	Detected	-0.556	Detected	0.000	1.663	Detected	2.417	Detected	2.040	0.093	GT Sens	contig377	contig377	Unannota	AATGGTATTTTAAAGTTTGTAAAATTCAAATTATGAGTTTATCTTCATAT	contig377	Solyc03g	Genomic DNA chror		SL2.40ch	AT5G168	ATTERT	ATTERT	chr5:553	603.264	332.378	1342.07	1322.6	1597.13	2261.81
GT	Sense	Sense	0.332	Detected	-0.332	Detected	0.000	1.086	Detected	1.099	Detected	1.093	0.081	GT Sens	contig377	contig377	Unannota	GTACAATTCCAGAGGGAATACAAAAGCAGTTTAACACAACAGAGATAAA	contig377	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G189	AHA1. PM	AHA1 (AH	chr2:822	89.8589	67.5261	172.978	109.281	186.256	157.802
GT	Sense	Sense	0.446	Comprom	-0.446	Comprom	0.000	1.162	Detected	1.830	Detected	1.496	0.115	GT Sens	contig378	contig378	Unannota	ATCATCTATCAAAGGAGCAAGGAAGCATCTCCGTAAGAGTTCACTTTGA	contig378	Solyc08g	Growth-re	GO:0005	SL2.40ch	AT1G20920.2		DEAD bo	chr1:728	5.9746	3.83226	11.5848	5.7299	12.0582	16.088
GT	Sense	Sense	0.362	Comprom	-0.362	Comprom	0.000	2.093	Detected	1.583	Detected	1.838	0.053	GT Sens	contig378	contig378	Unannota	TGCTTCATGGCAAGCACGTAAAAAACACAAAGGAGAAGAAATAACTGTG	contig378	Solyc05g	Unknown Protein (A		SL2.40ch	AT2G40960.1		nucleic a	chr2:170	9.87036	7.11496	14.7385	16.92	40.2764	23.7352
GT	Sense	Sense	0.338	Comprom	-0.338	Comprom	0.000	2.517	Detected	1.392	Detected	1.954	0.097	GT Sens	contig378	contig378	Unannota	GATCTATAGCAGGTAAAAATTTCAATATCACAACCACCATAGACTAGAT	contig378	Solyc08g	Nodulin-li	GO:0016	SL2.40ch	AT4G17660.1		protein k	chr4:983	6.43305	4.79414	14.7037	12.2405	35.7969	13.783
GT	Sense	Sense	-0.536	Detected	0.536	Detected	0.000	1.441	Detected	1.009	Detected	1.225	0.168	GT Sens	contig378	contig378	Unannota	AAGAATAGTTACTTATAAAAATATTGATTTTGAATAGACTCAACTTTGCT	contig378	Solyc01g	Elongatio	GO:0003	SL2.40ch	AT3G520	chx28	chx28 (ca	chr3:193	106.241	265.809	210.937	427.923	513.911	319.809
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	1.925	Detected	1.939	Detected	1.932	0.000	GT Sens	contig378	contig378	Unannota	TAAACCCTAACCACACCATTCAAATCCATATTATCGAACAGTTTCCGGT	contig378	Solyc02g	Cytochro	GO:0019	SL2.40ch	AT5G64816.2		unknown	chr5:259	69.8768	79.9196	138.908	124.578	319.66	271.028
GT	Sense	Sense	0.387	Comprom	-0.387	Comprom	0.000	1.258	Detected	1.523	Detected	1.390	0.077	GT Sens	contig378	contig378	Unannota	ATTGGTGAAATATGGGCGCGGACCCATTAGCTTTTGGTGTTTCCTGTT	contig378	Solyc09g	Pectate ly	GO:0016	SL2.40ch	AT4G28790.1				8.12875	5.66118	5.45601	4.07799	18.2707	18.4272
GT	Sense	Sense	-0.204	Detected	0.204	Detected	0.000	0.925	Detected	1.524	Detected	1.225	0.077	GT Sens	contig378	contig378	Unannota	CTCAAAGGAGAAAAATTATAGATCCATGAAATTAATTCTGCTTAATTATA	contig378	Solyc06g	Baculovir	GO:0008	SL2.40ch	AT5G109	CIPK5. Sn	CIPK5 (C	chr5:344	82.3026	130.036	174.639	386.862	221.343	281.25
GT	Sense	Sense	-0.140	Comprom	0.140	Comprom	0.000	0.940	Detected	1.838	Detected	1.389	0.098	GT Sens	contig378	contig378	Unannota	GCCATGAATAATAAGCATAAAGATATCATAATTCATATGTAAGAATGTCA	contig378	Solyc03g	CBL-inter	GO:0004	SL2.40ch	AT5G613	CYP89A3	CYP89A3	chr5:246	5.46078	7.89571	13.1248	14.3282	14.1929	22.1931
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	2.448	Detected	3.503	Detected	2.976	0.031	GT Sens	contig379	contig379	Unannota	CCAAACCAACTCCCCCGATAAGCCTAAACCTTCACAACACCGCCAGCC	contig379	Solyc05g018580.1.1				AT5G49120.1		senescen	chr5:199	18.6073	18.8127	37.102	39.9644	114.988	200.605
GT	Sense	Sense	0.165	Comprom	-0.165	Comprom	0.000	0.986	Detected	1.408	Detected	1.197	0.047	GT Sens	contig381	contig381	Unannota	CACTAATGGGGAGGTTGTTCTTTGAATTCTTGCAATAAAAAGATAATGA	contig381	Solyc02g	Palmitoyl	GO:0016	SL2.40ch	AT5G41060.1				6.43149	6.08939	7.60387	6.23614	13.9654	15.6999
GT	Sense	Sense	0.274	Detected	-0.274	Detected	0.000	2.521	Detected	1.232	Detected	1.877	0.116	GT Sens	contig381	contig381	Unannota	GGGGTGTTCCGATCGACATTGTAAAGAAATGGATTATAGATTGAATTCA	contig381	Solyc12g	Mutator-li	GO:0008	SL2.40ch	AT1G10880.1				773.859	630.394	1941.72	1059.77	4517.3	1550.9
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	2.938	Detected	1.436	Detected	2.187	0.106	GT Sens	contig381	contig381	Unannota	GTAAGGATATCTATGATGTCAATTGTTCATGTGAGACTTCTTTTAACAC	contig381	Solyc12g	Mutator-li	GO:0008	SL2.40ch	AT1G10880.1				249.552	227.354	734.241	375.78	2056.02	609.504
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	2.279	Detected	0.894	Detected	1.586	0.151	GT Sens	contig381	contig381	Unannota	CTGTCTAATAACTTGAGATTAAAAAACTTTGAGGCCTTGAGTAGGAGTG	contig381	Solyc10g	Unknown	GO:0016	SL2.40ch	AT3G140	CAX9. CC	CAX9 (CA	chr3:466	12.2293	12.7325	21.6638	21.1596	68.2208	21.9192
GT	Sense	Sense	-0.062	Comprom	0.062	Comprom	0.000	1.370	Detected	2.868	Detected	2.119	0.106	GT Sens	contig382	contig382	Unannota	CTATTATTTCAGACTCTGCAGTTGTCCTGATTCTCTTGGATCTTGTCAT	contig382	Solyc10g	Transcrip	GO:0006	SL2.40ch	AT1G54890.1				3.442	4.46769	2.56472	2.43749	11.4143	27.0757
GT	Sense	Sense	-0.056	Comprom	0.056	Comprom	0.000	2.498	Detected	2.151	Detected	2.324	0.006	GT Sens	contig382	contig382	Unannota	TGCACCAGATTGTTCTGACACCAACCAAATGAGGAAAAAAGGAGCACT	contig382	Solyc07g	Aldose 1-	GO:0047	SL2.40ch	AT1G505	HIT1. ATV	HIT1 (HE	chr1:187	3.11193	4.00434	2.04852	3.38265	22.4617	14.8214
GT	Sense	Sense	0.285	Detected	-0.285	Detected	0.000	1.254	Detected	1.044	Detected	1.149	0.063	GT Sens	contig382	contig382	Unannota	CACACGTTTGAAGCTGAAAATGCAGTTGATTCCAAATGAAAGAGTAGTT	contig382	Solyc02g	Os03g0395600 prot		SL2.40ch	AT3G04310.1				53.9598	43.2931	112.715	75.1946	129.815	94.2155
GT	Sense	Sense	0.545	Comprom	-0.545	Comprom	0.000	1.379	Detected	2.040	Detected	1.710	0.115	GT Sens	contig382	contig382	Unannota	ACGAACCTCATGGTGGACAACTTATTCCTGAAGAGGTGCAGTTGTCGA	contig382	Solyc04g	Nonsens	GO:0016	SL2.40ch	AT1G02305.1		cathepsi	chr1:455	5.81423	3.25272	7.27197	7.83212	12.7382	16.9141
GT	Sense	Sense	0.389	Detected	-0.389	Detected	0.000	1.322	Detected	1.673	Detected	1.498	0.072	GT Sens	contig382	contig382	Unannota	TGACAAAAAATTAAATAAACTAAATTGGATATCGCAGTTGGAGGAAAAT	contig382	Solyc12g098750.1.1				AT5G162	ATRAD21	SYN4 (SI	chr5:531	101.696	70.5931	208.614	218.511	238.678	255.487
GT	Sense	Sense	-0.055	Detected	0.055	Detected	0.000	1.278	Detected	1.446	Detected	1.362	0.005	GT Sens	contig382	contig382	Unannota	TAGATTTTATCGTCCTGGATCAGACATTTCGGACTGTCTCATTCTCTTG	contig382	Solyc11g	Interferon	GO:0005	SL2.40ch	AT5G19680.1		leucine-r	chr5:664	43.502	55.9161	83.8359	101.048	134.717	127.059
GT	Sense	Sense	-0.436	Comprom	0.436	Comprom	0.000	1.707	Detected	2.351	Detected	2.029	0.064	GT Sens	contig382	contig382	Unannota	ACGGAGAGAGAAGACAACTACTACTATATCAGATTAGAGAGAGAAAGT	contig382	Solyc12g	Cellulose synthase-		SL2.40ch	AT2G370	ATNAP12	ATNAP12	chr2:155	2.42411	5.27844	3.87032	5.10882	13.1584	17.2508
GT	Sense	Sense	-0.180	Comprom	0.180	Comprom	0.000	1.622	Detected	3.770	Detected	2.696	0.132	GT Sens	contig382	contig382	Unannota	AACCCTAGAGGGAGGAAAAAGAAGAAACCCTAACAAAACCTTGACAAAT	contig382	Solyc03g	RNA-bind	GO:0043	SL2.40ch	AT4G182	ATPUP10	ATPUP10	chr4:100	4.77413	7.29302	3.18477	3.74118	20.4642	76.0875
GT	Sense	Sense	0.555	Comprom	-0.555	Comprom	0.000	1.349	Detected	2.393	Detected	1.871	0.133	GT Sens	contig384	contig384	Unannota	TTGTCTTCCTCTATCTTTGAAGAACTGAACTATCTTCACAACAGTGTCT	contig384	Solyc04g	IST1 homolog (AHR		SL2.40ch	AT5G39460.1		F-box fa	chr5:157	5.34913	2.94921	13.2114	6.3499	11.4003	19.7251
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	1.591	Detected	1.003	Detected	1.297	0.065	GT Sens	contig384	contig384	Unannota	TAACATCTTTCATATTAGTTTCTGTCGTACAAATATAACTTGGTGGGCG	contig384	Solyc01g	Ribosoma	GO:0003	SL2.40ch	AT3G611	ARS27A	ARS27A	chr3:226	52.0661	80.4254	117.516	130.247	219.639	122.661
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	1.207	Detected	1.387	Detected	1.297	0.007	GT Sens	contig384	contig384	Unannota	ATGCCACATGTCTACTAACCATATCATAACTCTTCTTATATATATCTCTT	contig384	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G29075.1		glycine-r	chr3:110	139.991	152.617	315.599	290.522	380.068	361.38
GT	Sense	Sense	0.160	Detected	-0.160	Detected	0.000	2.236	Detected	2.416	Detected	2.326	0.006	GT Sens	contig384	contig384	Unannota	ATGATGAGAAAAAGAATCTATGAACTTTTTTGATTGGGGATGAAAATTT	contig384	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G29075.1		glycine-r	chr3:110	35.3677	33.7465	105.965	112.765	183.341	174.3
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	2.201	Detected	0.945	Detected	1.573	0.134	GT Sens	contig384	contig384	Unannota	TATTAAAGTGTCATCGGAAAATGGAAAGCGGCAGAGAAGATGACGGTG	contig384	Solyc03g115210.2.1				AT1G70140.1				185.525	183.679	1077.02	1544.9	955.83	336.046
GT	Sense	Sense	-0.024	Comprom	0.024	Comprom	0.000	1.051	Detected	3.279	Detected	2.165	0.191	GT Sens	contig384	contig384	Unannota	GAGATTACCATCTATTGAAGGAAATGAAGTGACAAAAAATGCTAACATC	contig384	Solyc08g	Os10g0422600 prot		SL2.40ch	AT2G40850.1				4.58602	5.64339	12.1311	8.5365	11.8736	46.6877
GT	Sense	Sense	0.404	Detected	-0.404	Detected	0.000	1.159	Detected	0.843	Detected	1.001	0.148	GT Sens	contig384	contig384	Unannota	CACCACACGTTACAAGACGAGTAGTGAGAACAGCAGCAACAAGTCATTA	contig384	Solyc03g	Sister chromatid co		SL2.40ch	AT5G65460.1		kinesin m	chr5:261	207.646	141.103	324.452	245.053	430.458	290.224
GT	Sense	Sense	0.225	Comprom	-0.225	Comprom	0.000	1.355	Detected	1.961	Detected	1.658	0.048	GT Sens	contig385	contig385	Unannota	GGAATTCGAATTCGAATCAATCAAATGAAGCAGAAACACAGAGAAAACG	contig385	Solyc03g	RNA polymerase II-a		SL2.40ch	AT3G52700.1		unknown	chr3:195	6.285	5.48097	7.51087	13.7356	16.9093	21.6107
GT	Sense	Sense	-0.544	Detected	0.544	Detected	0.000	1.242	Detected	1.296	Detected	1.269	0.145	GT Sens	contig385	contig385	Unannota	GATACGATATTTGGAGTTGTAAATTGTCAAAAAGTTTTTGTTGATAAATA	contig385	Solyc09g	Non-specific lipid-tra		SL2.40ch	AT4G33320.1				15.1789	38.4164	36.4748	46.9347	64.3347	56.0539
GT	Sense	Sense	0.163	Comprom	-0.163	Comprom	0.000	2.169	Detected	2.829	Detected	2.499	0.021	GT Sens	contig385	contig385	Unannota	CGACCAAACAAACTACAGCACATCAATAAAGAGTAAATGCAAAAGAGGA	contig385	Solyc02g	Succinate	GO:0000	SL2.40ch	AT5G406	SDH2-2	SDH2-2:	chr5:162	2.90283	2.75748	3.18006	2.53858	14.3288	19.0147
GT	Sense	Sense	-0.728	Comprom	0.728	Detected	0.000	0.860	Detected	1.378	Detected	1.119	0.285	GT Sens	contig386	contig386	Unannota	AAAGAGATGTGGAAATGAGATCTTAAAAGTATTCAATTGTTTGAAATAA	contig386	Solyc06g	Histone H	GO:0005	SL2.40ch	AT3G46320.1		histone H	chr3:170	3.99816	13.0598	8.26573	19.4622	14.7737	17.7638
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	0.893	Detected	1.190	Detected	1.041	0.021	GT Sens	contig387	contig387	Unannota	AAACAAAAAATGAACTGCCCTAAACCCCATGCTGGCTTTAACCATGCCAG	contig387	Solyc12g	1-aminocyclopropa		SL2.40ch	AT4G133	NIG	NIG (NSP	chr4:777	279.493	353.062	479.244	255.091	657.07	677.439
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	1.223	Detected	1.029	Detected	1.126	0.008	GT Sens	contig387	contig387	Unannota	TGTTATAGTGATGTTATGTCATGTAAATTGAAAAGATCGGAGTATCTTT	contig387	Solyc09g	Peptide tr	GO:0042	SL2.40ch	AT2G07815.1				15.916	19.4602	44.5511	49.953	46.2626	33.9539
GT	Sense	Sense	-0.211	Comprom	0.211	Comprom	0.000	0.991	Detected	2.088	Detected	1.540	0.120	GT Sens	contig387	contig387	Unannota	CAAGAGAGAGATGGTTGAAAAAGTTTATAAAGGGATGAAACTCTTTCTA	contig387	Solyc06g	Unknown Protein (A		SL2.40ch	AT5G649	ATATH13	ATATH13	chr5:259	4.8892	7.80288	13.5053	15.8723	13.8305	24.8284
GT	Sense	Sense	0.240	Comprom	-0.240	Comprom	0.000	1.600	Detected	2.952	Detected	2.276	0.087	GT Sens	contig387	contig387	Unannota	AGGAGAAAAAGTTGAAAAAGAAAGCTACAATTAAGGAAATCGGAGAAGA	contig387	Solyc02g	Binding protein (AH		SL2.40ch	AT5G20660.1		24 kDa v	chr5:698	4.4032	3.76051	3.45179	4.38984	13.8936	29.7728
GT	Sense	Sense	-0.363	Detected	0.363	Detected	0.000	1.376	Detected	1.191	Detected	1.284	0.076	GT Sens	contig387	contig387	Unannota	GTATTTTAAATTAAATTAAGCGGGACCCGCTAATCAATCTAACTTTGAA	contig387	Solyc11g	Ring finge	GO:0008	SL2.40ch	AT2G10970.1				15.0139	29.5625	51.4254	36.4561	61.6149	45.4866
GT	Sense	Sense	0.558	Comprom	-0.558	Comprom	0.000	1.206	Detected	2.528	Detected	1.867	0.163	GT Sens	contig388	contig388	Unannota	GCTGCAGCAAAACCCTAAGACATTTATAGGATCTTGAAATCCCTTTTAC	contig388	Solyc09g	F-box family protein		SL2.40ch	AT1G66840.1				7.27453	3.99718	6.39697	10.7827	14.0148	29.3983
GT	Sense	Sense	0.268	Detected	-0.268	Detected	0.000	1.463	Detected	1.022	Detected	1.243	0.070	GT Sens	contig388	contig388	Unannota	TCACGGAGATTGTGAAAATGATAAAGTGAAGTTACGTGGAGTAGTAGTT	contig388	Solyc09g	Ethylene	GO:0051	SL2.40ch	AT3G23870.1				31.5714	25.911	68.0482	85.0812	88.8317	54.9286
GT	Sense	Sense	0.117	Detected	-0.117	Detected	0.000	2.598	Detected	2.045	Detected	2.321	0.016	GT Sens	contig388	contig388	Unannota	TAAAATACTTTCTAATTCATATATTTTTATGAAAAATAACTGCCTTAACA	contig388	Solyc08g	Alpha glu	GO:0004	SL2.40ch	AT5G11550.1		binding	chr5:370	17.2441	17.4444	58.5536	63.6375	118.284	67.6583
GT	Sense	Sense	-0.429	Comprom	0.429	Detected	0.000	1.080	Detected	1.403	Detected	1.242	0.113	GT Sens	contig388	contig388	Serine/thr	TAGAAG contig388 Solyc12g Solyc12g Serine/thr GO:0016 GO:0016	contig388	Solyc12g	Serine/thr	GO:0016	SL2.40ch	AT5G638	PP7. ATP	PP7 (SER	chr5:255	7.30585	15.7541	14.0927	16.6482	25.5541	26.8337
GT	Sense	Sense	0.271	Detected	-0.271	Detected	0.000	1.640	Detected	0.930	Detected	1.285	0.102	GT Sens	contig389	contig389	Unannota	GCGAGTTATGAAGGAATTAAATCCTACATAAGTAATAGCATGTTTAGCG	contig389	Solyc12g	LRR rece	GO:0016	SL2.40ch	AT5G112	ATGLR2.5	ATGLR2.	chr5:357	37.6942	30.8275	79.8259	62.4149	119.645	61.4286
GT	Sense	Sense	-0.121	Detected	0.121	Detected	0.000	1.254	Detected	0.888	Detected	1.071	0.039	GT Sens	contig389	contig389	Unannota	TGAAAGAAACCCCATTCTTTGCAGGCAGCAGCAAGAGAAGATAGAGTA	contig389	Solyc01g	Gibberell	GO:0045	SL2.40ch	AT1G55290.1		oxidored	chr1:206	11.774	16.5822	35.694	31.3947	37.5278	24.4559
GT	Sense	Sense	-0.193	Comprom	0.193	Detected	0.000	1.319	Detected	1.042	Detected	1.181	0.038	GT Sens	contig389	contig389	Unannota	GGTTGGGAGATATCCAAAACAGGAAGTTGTAATGGTGATTAGGATTCA	contig389	Solyc01g	Gibberell	GO:0045	SL2.40ch	AT1G55290.1		oxidored	chr1:206	7.62594	11.8575	22.7159	25.1631	26.7256	18.5187
GT	Sense	Sense	0.312	Detected	-0.312	Detected	0.000	1.781	Detected	1.416	Detected	1.599	0.047	GT Sens	contig389	contig389	Unannota	AAGAGTAGGAACTACACGTAGTGAATGAGGGATCCTTTGGAGTAAGTG	contig389	Solyc12g	LRR rece	GO:0004	SL2.40ch	AT5G60720.1				127.743	98.6705	513.175	372.123	434.701	283.359
GT	Sense	Sense	0.277	Detected	-0.277	Detected	0.000	1.756	Detected	1.484	Detected	1.620	0.034	GT Sens	contig389	contig389	Unannota	TGAGAAGAGTGGTGCTTTGATCTTTGGGGCAAGGATGAGTTATGGATG	contig389	Solyc12g	LRR rece	GO:0004	SL2.40ch	AT5G60720.1				214.695	174.094	782.661	639.312	735.661	511.378
GT	Sense	Sense	0.334	Detected	-0.334	Detected	0.000	1.314	Detected	1.666	Detected	1.490	0.059	GT Sens	contig389	contig389	Receptor	TTATTAC contig389 Solyc04g Solyc04g Receptor GO:0005 GO:0005	contig389	Solyc04g	Receptor	GO:0004	SL2.40ch	AT4G34440.1		protein k	chr4:164	234.349	175.593	441.864	309.436	568.218	608.859
GT	Sense	Sense	-1.093	Comprom	1.093	Detected	0.000	1.253	Detected	1.277	Detected	1.265	0.367	GT Sens	contig390	contig390	Unannota	CTCGTCAACTTAAGCAATTCAGTACTAGTCGGTGTTGATATAAGCAAGA	contig390	Solyc12g	LRR rece	GO:0016	SL2.40ch	AT4G01810.1		protein t	chr4:776	2.88081	15.6009	5.99593	13.1973	18.0018	15.3585
GT	Sense	Sense	-0.570	Comprom	0.570	Comprom	0.000	2.149	Detected	1.967	Detected	2.058	0.070	GT Sens	contig390	contig390	Unannota	GGATGTCTTCCCAAATCAATTCAGTACTAGTGTATGTGTGAGGAAATAT	contig390	Solyc12g	LRR rece	GO:0016	SL2.40ch	AT4G01810.1		protein t	chr4:776	2.55573	6.70287	4.94228	12.6536	20.6816	15.2994
GT	Sense	Sense	-0.483	Comprom	0.483	Comprom	0.000	3.752	Detected	5.593	Detected	4.672	0.046	GT Sens	contig391	contig391	Unannota	ATAGGGTTTTCCAATATGCAACTCACACATCATACAATTAACCCAAAAC	contig391	Solyc05g	Transcrip	GO:0003	SL2.40ch	AT5G45310.1		unknown	chr5:183	2.51114	5.84186	17.7251	9.35397	58.1357	174.768
GT	Sense	Sense	0.838	Detected	-0.838	Detected	0.000	2.263	Detected	1.560	Detected	1.911	0.170	GT Sens	contig391	contig391	Unannota	CTACACAACAACTGGAGAAAATAGTAATGGGACAACAATTATATAGTGG	contig391	Solyc06g	Peroxida	GO:0005	SL2.40ch	AT5G22520.1				43.2552	16.1205	76.562	24.0309	142.746	73.6337
GT	Sense	Sense	0.911	Detected	-0.911	Detected	0.000	2.124	Detected	1.281	Detected	1.702	0.232	GT Sens	contig391	contig391	Unannota	CCTCCTACCACTGAATTGTTATACTTTTCCTTAGGAGATGGTTTATCCT	contig391	Solyc06g	Peroxida	GO:0005	SL2.40ch	AT5G22520.1				258.807	87.1432	442.359	116.635	737.281	344.954
GT	Sense	Sense	-0.302	Comprom	0.302	Comprom	0.000	1.118	Detected	1.938	Detected	1.528	0.095	GT Sens	contig391	contig391	Unannota	GCCAATAATGGACCAGAAATCAGAGGTACACTGAAGCTGATGGACAGT	contig391	Solyc04g	F-box family protein		SL2.40ch	AT5G501	ATFRO8.	FRO8 (FE	chr5:204	3.89482	7.05117	7.93127	9.08198	12.8121	18.9827
GT	Sense	Sense	0.382	Detected	-0.382	Detected	0.000	0.887	Detected	1.280	Detected	1.083	0.128	GT Sens	contig391	contig391	Unannota	GAATTTTTTTTAGGACAAACTTTTTCCTAGTCCAAGTGTGGTTGTTTGT	contig391	Solyc11g	Vacuolar	GO:0005	SL2.40ch	AT5G15170.1		tyrosyl-D	chr5:492	30.2766	21.2296	46.2451	30.9634	52.8218	58.1981
GT	Sense	Sense	0.309	Detected	-0.309	Detected	0.000	1.260	Detected	1.565	Detected	1.412	0.055	GT Sens	contig392	contig392	Unannota	CTATGATGCTTGAATTATTGGAATATTGTTGTTGTAGATATTGCGGATT	contig392	Solyc10g	Allene ox	GO:0019	SL2.40ch	AT4G01640.1				287.857	223.163	472.799	438.543	683.662	709.153
GT	Sense	Sense	0.722	Comprom	-0.722	Comprom	0.000	3.691	Detected	3.778	Detected	3.735	0.036	GT Sens	contig392	contig392	Unannota	TAATATAGTACTTACTATACATATAATTAAATACTTTTGAATTATGGTGT	contig392	Solyc10g	Allene ox	GO:0019	SL2.40ch	AT4G01640.1				5.38257	2.35526	25.6187	28.0655	51.8176	46.1809
GT	Sense	Sense	0.136	Comprom	-0.136	Comprom	0.000	0.816	Detected	1.485	Detected	1.150	0.086	GT Sens	contig392	contig392	Unannota	GATCTACAAGCTGGTGCAGAAAACAGCTATCAGAGCAACTTGTTTTAGC	contig392	Solyc09g	Regulato	GO:0003	SL2.40ch	AT3G22050.1				5.38504	5.30829	9.72137	11.4115	10.6041	14.1489
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	1.376	Detected	1.801	Detected	1.589	0.017	GT Sens	contig392	contig392	Unannota	TTTTCATGTAAATTAAATCTATCAAGTCACTTCCAAAATAGTATATAATA	contig392	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G42880.1		unknown	chr5:171	71.3619	84.2735	184.467	184.754	226.694	255.587
GT	Sense	Sense	0.452	Comprom	-0.452	Comprom	0.000	3.046	Detected	1.742	Detected	2.394	0.095	GT Sens	contig392	contig392	Unannota	GTTCTTCTCTAAGCAGTTGTTCTCTCTGGATCTCCTGTTCTAACTCTTT	contig392	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G08880.1				7.87608	5.00931	3.97376	10.1726	58.4328	19.8594
GT	Sense	Sense	-0.447	Detected	0.447	Detected	0.000	1.377	Detected	0.808	Detected	1.092	0.176	GT Sens	contig393	contig393	Unannota	CTGTTGTCAGGACAGAAATTCCCACCCATCCATTCTAACTCGAAGAATG	contig393	Solyc04g	Single-str	GO:0003	SL2.40ch	AT5G04380.1		S-adeno	chr5:123	56.6049	125.302	344.837	212.204	246.447	139.367
GT	Sense	Sense	-0.507	Detected	0.507	Detected	0.000	1.628	Detected	1.131	Detected	1.379	0.134	GT Sens	contig393	contig393	Unannota	CGACAACGAGTATCTTACAATAAGGTGCATTTTCCTAAGCTAAGTAAAA	contig393	Solyc04g	Single-str	GO:0003	SL2.40ch	AT5G04380.1		S-adeno	chr5:123	44.2974	106.43	302.592	210.676	239.117	142.146
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	1.341	Detected	0.882	Detected	1.111	0.048	GT Sens	contig393	contig393	Unannota	GAAGACAAGCCCAAGAATGAGAATGTGGTTATCAATTGAAATATATATC	contig393	Solyc11g	Pentatric	GO:0004	SL2.40ch	AT5G13950.2		unknown	chr5:449	62.0221	85.6018	104.696	89.642	207.91	126.931
GT	Sense	Sense	-0.147	Detected	0.147	Detected	0.000	1.256	Detected	0.951	Detected	1.104	0.035	GT Sens	contig393	contig393	Unannota	GTTGGTTTCACATTCTGACTACTCAGGGTTCTTATGATTATGATATTGT	contig393	Solyc11g	Pentatric	GO:0004	SL2.40ch	AT5G13950.2		unknown	chr5:449	72.4595	105.808	115.624	124.407	235.6	160.046
GT	Sense	Sense	0.268	Comprom	-0.268	Comprom	0.000	2.834	Detected	0.998	Detected	1.916	0.183	GT Sens	contig393	contig393	Unannota	GAGGTTTGATACCGGTGTACCGTACTGATTTATTTCAATTTCGATCAAG	contig393	Solyc09g	Alkaline p	GO:0003	SL2.40ch	AT3G627	ATMRP10	ATMRP1	chr3:231	12.0268	9.87072	62.8584	42.3676	87.5305	20.5761
GT	Sense	Sense	-0.051	Detected	0.051	Detected	0.000	1.391	Detected	0.990	Detected	1.191	0.029	GT Sens	contig393	contig393	Unannota	CCTCTCTCACATCTTCATTTTTCTCAATTTTGCGCCCTAGTTTTGACAC	contig393	Solyc10g	Genomic DNA chror		SL2.40ch	AT5G277	EMB2775	EMB2775	chr5:982	14.4595	18.484	43.8999	43.6862	48.3082	30.7111
GT	Sense	Sense	-0.400	Comprom	0.400	Comprom	0.000	1.551	Detected	3.625	Detected	2.588	0.145	GT Sens	contig393	contig393	Unannota	AAGATGAGCCACCAAACTTAAAGTTTCAAGCCTTCGTTGATTTTGGAGT	contig393	Solyc10g	Genomic DNA chror		SL2.40ch	AT5G277	EMB2775	EMB2775	chr5:982	2.6714	5.53506	12.625	12.9038	12.6953	44.8448
GT	Sense	Sense	-0.162	Comprom	0.162	Comprom	0.000	1.358	Detected	2.004	Detected	1.681	0.043	GT Sens	contig393	contig393	Unannota	GATGATTATAAGGTAAACTTTGATTGACTTCACTGTAAATTTGTTAAGG	contig393	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G16200.1		unknown	chr3:549	4.82105	7.18242	11.6149	7.94601	16.9928	22.3249
GT	Sense	Sense	-0.142	Comprom	0.142	Comprom	0.000	1.484	Detected	2.001	Detected	1.742	0.027	GT Sens	contig394	contig394	Mutator-li	ACAAAA contig394 Solyc12g Solyc12g Mutator-like transposase-like (	contig394	Solyc09g	Transpos	GO:0008	SL2.40ch	AT3G09770.2		zinc fing	chr3:299	3.09266	4.48476	5.10135	5.69635	11.7339	14.0911
GT	Sense	Sense	0.941	Comprom	-0.941	Comprom	0.000	1.417	Detected	2.447	Detected	1.932	0.213	GT Sens	contig394	contig394	Unannota	GCAGAGCAAGGAAGAAAACGGAGTACCTGAAAGTTTATAGTCAAAATTT	contig394	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G17070.1				7.23981	2.33933	9.18903	9.16109	12.3797	21.2179
GT	Sense	Sense	-0.344	Comprom	0.344	Detected	0.000	3.621	Detected	1.092	Detected	2.357	0.214	GT Sens	contig394	contig394	Unannota	GCTTCGAGATAAGTATTTTGTTTGAGAAAAGAAGAGGTTATCTAGTTGC	contig394	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G23260.1		ATP bind	chr4:121	7.09166	13.6051	13.6947	16.5732	136.167	19.7999
GT	Sense	Sense	0.418	Detected	-0.418	Detected	0.000	1.118	Detected	1.507	Detected	1.313	0.104	GT Sens	contig394	contig394	Unannota	GTTTACGTGGATTGATTTCTTCAACCTCATCTCAGCCAAACACACACAT	contig394	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G10070.1		RNase L	chr5:314	98.9215	65.9669	96.3206	97.426	197.569	217.103
GT	Sense	Sense	0.348	Detected	-0.348	Detected	0.000	1.207	Detected	1.463	Detected	1.335	0.069	GT Sens	contig394	contig394	Unannota	CTTCCACTCCAGCTAATGTTAATGAGGCTCATGCATCAGTTTCGGATGA	contig394	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G10070.1		RNase L	chr5:314	119.664	87.8797	130.284	129.219	266.685	267.244
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	1.623	Detected	0.920	Detected	1.271	0.069	GT Sens	contig394	contig394	Unannota	TTTCTAATATGATATGGAGTCTCCTTGTACCTGCCGGGCAACTGTAATT	contig394	Solyc03g	Heat stres	GO:0003	SL2.40ch	AT3G029	ATHSFA1	ATHSFA1	chr3:673	13.0156	16.0275	17.9862	5.79698	50.1096	25.8374
GT	Sense	Sense	0.161	Comprom	-0.161	Comprom	0.000	4.056	Detected	2.664	Detected	3.360	0.042	GT Sens	contig395	contig395	Unannota	TGAAATGGTAAGCTGGAGGATCAAAATCTGTTACTCAATGAACCGTGAA	contig395	Solyc09g	Splicing f	GO:0003	SL2.40ch	AT4G05080.1				2.42739	2.31193	2.07392	3.75165	44.3899	14.1923
GT	Sense	Sense	0.661	Detected	-0.661	Comprom	0.000	1.241	Detected	1.272	Detected	1.257	0.198	GT Sens	contig395	contig395	Unannota	TGAGAGTTCCACACATTAAATTGTGTGGTCTTCCTTTTCGTTATTATTG	contig395	Solyc11g008560.1.1				AT5G56800.1				14.0336	6.67896	25.707	16.8135	25.7729	22.1129
GT	Sense	Sense	-0.214	Comprom	0.214	Comprom	0.000	1.313	Detected	2.433	Detected	1.873	0.089	GT Sens	contig395	contig395	Unannota	CGTGTCTTGTAACAAATTCCTTTGTCAATAAAGAAGAACAAAAAGGCTA	contig395	Solyc11g008560.1.1				AT5G56800.1				4.23313	6.77719	15.3461	11.0963	14.9906	27.341
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	0.851	Detected	1.161	Detected	1.006	0.054	GT Sens	contig395	contig395	Unannota	GACCATGCTGATCTTCTCTGTATCGTTCAAATTTCAACATCGACTAATC	contig395	Solyc10g	Genomic DNA chror		SL2.40ch	AT1G53035.1		unknown	chr1:197	239.159	219.61	409.795	410.157	465.577	484.494
GT	Sense	Sense	0.109	Comprom	-0.109	Comprom	0.000	1.303	Detected	1.532	Detected	1.417	0.012	GT Sens	contig395	contig395	Unannota	CAAGATCCATATATGAAACAAAGGAAGTAAGGCAACATAGACTAATCAC	contig395	Solyc10g	Genomic DNA chror		SL2.40ch	AT1G53035.1		unknown	chr1:197	5.04342	5.16567	5.61356	2.82237	14.1832	13.9526
GT	Sense	Sense	0.139	Comprom	-0.139	Comprom	0.000	2.060	Detected	2.216	Detected	2.138	0.005	GT Sens	contig396	contig396	Unannota	TTTTGAATTTTTCTGATAAAATTGTGAAAAAGCTTCGATCTTGAAACTAT	contig396	Solyc01g	5'-A	GO:0019	SL2.40ch	AT5G46220.1		unknown	chr5:187	9.84809	9.67194	39.6577	47.0085	45.8486	42.8778
GT	Sense	Sense	0.201	Comprom	-0.201	Comprom	0.000	4.828	Detected	2.369	Detected	3.599	0.102	GT Sens	contig396	contig396	Unannota	CACAAGAGAGGGATAACAAAGTGTTAAAACTTAAAAGCCACCCACATCT	contig396	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G42900.3		unknown	chr5:171	4.31234	3.88747	4.16365	3.33611	131.043	20.002
GT	Sense	Sense	-0.358	Detected	0.358	Detected	0.000	3.220	Detected	3.155	Detected	3.188	0.012	GT Sens	contig397	contig397	Unknown	GGGACA contig397 Solyc04g Solyc04g Unknown Protein (AHRD V1)	contig397	Solyc04g	Unknown Protein (A		SL2.40ch	AT1G53040.2		unknown	chr1:197	14.736	28.8108	183.158	149.35	216.27	173.569
GT	Sense	Sense	-0.082	Comprom	0.082	Detected	0.000	1.348	Detected	1.634	Detected	1.491	0.012	GT Sens	contig397	contig397	Unannota	AAACATGACACCATGTTCAAGAGTCACAATACTCTTGCCTACACAGGG	contig397	Solyc02g	Protein SMG9 (AHR		SL2.40ch	AT4G158	ATRH1	ATRH1: A	chr4:900	8.29453	11.0696	25.669	17.8156	27.4727	28.1278
GT	Sense	Sense	-0.259	Comprom	0.259	Comprom	0.000	1.129	Detected	1.780	Detected	1.454	0.073	GT Sens	contig398	contig398	Unannota	TAAAGCTAAAATCTTTACCACAAGCTCTCCACAGAAGAGAGGGGTTATT	contig398	Solyc11g	Nedd8 ac	GO:0008	SL2.40ch	AT4G10370.1				4.48555	7.64803	7.3473	11.846	14.4319	19.0156
GT	Sense	Sense	-0.065	Comprom	0.065	Comprom	0.000	1.586	Detected	2.405	Detected	1.995	0.041	GT Sens	contig399	contig399	Unannota	TGATGATCGTTACCTATTTTATTGTACCATATTGCATCGTGTGCATTGT	contig399	Solyc11g	Os11g0198100 prot		SL2.40ch	AT1G078	ECA1. AT	ECA1 (EF	chr1:241	2.70087	3.51646	2.17988	2.98284	10.4187	15.4311
GT	Sense	Sense	-0.689	Comprom	0.689	Detected	0.000	3.162	Detected	3.981	Detected	3.572	0.047	GT Sens	contig399	contig399	Unannota	TCCTCAACCCTAAACTTTGTGATGAGGCTGTGATGATATTCTCCAGGAA	contig399	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G10290.1		leucine-r	chr5:323	8.20298	25.3647	61.6013	60.6214	145.478	215.327
GT	Sense	Sense	0.446	Detected	-0.446	Comprom	0.000	1.537	Detected	1.474	Detected	1.505	0.078	GT Sens	contig399	contig399	Unannota	TTTCAGAGCTGCTCTATTTTAAGCTATCAGGCAAGTGAGGGGACATTGA	contig399	Solyc12g	Unknown Protein (A		SL2.40ch	AT4G01400.2		FUNCTIO	chr4:573	13.2122	8.47497	5.70253	4.92384	34.5988	27.7848
GT	Sense	Sense	0.933	Detected	-0.933	Comprom	0.000	1.273	Detected	3.254	Detected	2.263	0.238	GT Sens	contig399	contig399	Unannota	GGAGAGGCACAGAAACAAGAAATTCAAGTTTACCCCTAAGCTATCAGAT	contig399	Solyc05g	WRKY tra	GO:0003	SL2.40ch	AT1G43260.1				15.2181	4.96732	5.15253	21.8328	23.6653	78.4163
GT	Sense	Sense	0.255	Comprom	-0.255	Comprom	0.000	1.579	Detected	3.359	Detected	2.469	0.117	GT Sens	contig400	contig400	Unannota	GAAGTTGAGCGCACATAAACTTTTGTAAACTTTTGTTGATCCACTTCGG	contig400	Solyc07g	14-3-3 pro	GO:0050	SL2.40ch	AT2G425	GRF9. GF	GRF9 (GE	chr2:177	5.99011	5.0091	9.4285	11.7288	18.4297	53.1374
GT	Sense	Sense	0.252	Detected	-0.252	Detected	0.000	1.620	Detected	2.051	Detected	1.836	0.031	GT Sens	contig400	contig400	Unannota	ATTAAGGATGAATTGAGAAATTTAATATTGAAATGAAGTAATTGTTTCTT	contig400	Solyc02g	Unknown	GO:0009	SL2.40ch	AT5G591	TOPP2. P	TOPP2: r	chr5:238	19.4803	16.3546	43.2472	47.5353	61.8213	69.9386
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	1.129	Detected	1.069	Detected	1.099	0.001	GT Sens	contig400	contig400	Unannota	CCTATGGTGCTTAATCTCATCACAGCATACTTTTCCATCAACAAACGAA	contig400	Solyc08g	Protein rai1 (AHRD V		SL2.40ch	AT5G639	CHR24	CHR24 (c	chr5:255	16.7779	19.2465	35.8299	36.1789	44.2658	35.6455
GT	Sense	Sense	-0.596	Comprom	0.596	Comprom	0.000	3.035	Detected	3.103	Detected	3.069	0.036	GT Sens	contig400	contig400	Unannota	TTCTGTGAAGAATTCCCCTTATTTCGTCCCATCCCAAAAGGGGAAAGG	contig400	Solyc01g057130.1.1				AT1G08230.2		amino ac	chr1:258	2.51268	6.83887	2.45992	2.07015	38.28	33.6651
GT	Sense	Sense	-0.146	Comprom	0.146	Comprom	0.000	3.169	Detected	1.897	Detected	2.533	0.060	GT Sens	contig400	contig400	Unannota	AGTTTAGTTAATCAAGTAAAAGAACTTCTTTTTTAAGGCGATTAATAATT	contig400	Solyc08g	Blight-associated pr		SL2.40ch	AT5G41120.1		esterase	chr5:164	5.53607	8.06977	43.5029	36.2649	67.7027	23.5323
GT	Sense	Sense	-0.435	Comprom	0.435	Comprom	0.000	1.333	Detected	2.048	Detected	1.690	0.095	GT Sens	contig400	contig400	Unannota	ACGAAGATCAAATGGCTCAGAATCACAGGGAAATATAGGTCACAAACCT	contig400	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G52700.1		unknown	chr3:195	4.37925	9.53427	15.7484	13.5076	18.339	25.2595
GT	Sense	Sense	0.307	Detected	-0.307	Comprom	0.000	2.027	Detected	0.910	Detected	1.468	0.148	GT Sens	contig400	contig400	Unannota	CTTTTGGTCAAAATATAAATAGGGGTTGAAAGAAAGAATCTTTCGATT	contig400	Solyc12g	Beta-1,3-(	GO:0016	SL2.40ch	AT5G59930.1		DC1 dom	chr5:241	13.1953	10.2679	14.4095	14.7033	53.4338	20.6777
GT	Sense	Sense	-0.159	Comprom	0.159	Comprom	0.000	1.948	Detected	2.518	Detected	2.233	0.021	GT Sens	contig401	contig401	Unannota	CACAAATAACTAACAAGTGAGAACCGACAACAATGATGAACGTAGGAAG	contig401	Solyc03g	DNA helic	GO:0043	SL2.40ch	AT1G30470.1		SIT4 pho	chr1:107	3.39187	5.03161	5.26963	2.40482	17.9587	22.373
GT	Sense	Sense	-0.659	Comprom	0.659	Detected	0.000	2.372	Detected	3.814	Detected	3.093	0.087	GT Sens	contig401	contig401	Unannota	CAGCGGAAACCCTAACACAGTAAGCCATACGTTTTCGTTCATCAAGGT	contig401	Solyc07g	Argonaut	GO:0035	SL2.40ch	AT3G52700.1		unknown	chr3:195	5.31202	15.7668	12.6665	6.16803	53.3608	121.739
GT	Sense	Sense	1.000	Comprom	-1.000	Comprom	0.000	1.271	Detected	1.451	Detected	1.361	0.308	GT Sens	contig401	contig401	Unannota	GTGAAACTGCTCCTTGTGATATCTGACGAAGCATTTTAATCTTTGATTG	contig401	Solyc05g	Transcriptional acti		SL2.40ch	AT5G53850.1		haloacid	chr5:218	9.99956	2.97556	17.0415	18.9724	14.8267	14.1039
GT	Sense	Sense	0.399	Comprom	-0.399	Comprom	0.000	1.653	Detected	3.042	Detected	2.347	0.099	GT Sens	contig401	contig401	Unannota	GAAGGTAACTGACTTATAAACCCCAAAGGAAAAATGTAGAAAAGAGAAG	contig401	Solyc09g	Vacuolar	GO:0008	SL2.40ch	AT4G14360.2		dehydrat	chr4:826	4.94484	3.38754	4.5949	3.05244	14.4967	31.8664
GT	Sense	Sense	-0.845	Comprom	0.845	Detected	0.000	1.119	Detected	2.157	Detected	1.638	0.240	GT Sens	contig402	contig402	Unannota	TTCTTGCTGGAGGTAGAGCTACTGGATGGCCGATGGGCCCGCGAGGG	contig402	Solyc09g	Glucose t	GO:0005	SL2.40ch	AT5G525	ATUSP	ATUSP (A	chr5:213	3.06932	11.7843	7.70161	3.73765	14.7191	25.3539
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	1.591	Detected	1.079	Detected	1.335	0.035	GT Sens	contig402	contig402	Unannota	GGATTACCACCGAAAAATGATGAAAACTCTAATTCTCTGTATATTCAAA	contig402	Solyc02g	RING fing	GO:0008	SL2.40ch	AT3G43960.1				43.8467	51.4913	72.31	82.0361	161.302	94.8913
GT	Sense	Sense	0.294	Comprom	-0.294	Comprom	0.000	1.032	Detected	1.574	Detected	1.303	0.083	GT Sens	contig402	contig402	Unannota	TAAATGAGCAGGAGCATCTTTAGCTTCTGGAAATGTGCATAAGAAAGAT	contig402	Solyc01g	PAP fibril	GO:0009	SL2.40ch	AT5G411	ATPUP12	ATPUP12	chr5:164	5.72248	4.53441	10.6428	6.97523	11.7361	14.3431
GT	Sense	Sense	-0.108	Detected	0.108	Detected	0.000	1.064	Detected	0.973	Detected	1.019	0.013	GT Sens	contig402	contig402	Unannota	ACTTTGAATTTGGACCTAGTTTAATAATATCATATATATAATATGTGGT	contig402	Solyc04g071170.1.1				AT5G40000.1				20.1175	27.8037	39.8541	41.7772	55.6846	43.9075
GT	Sense	Sense	0.274	Detected	-0.274	Detected	0.000	0.932	Detected	1.135	Detected	1.034	0.071	GT Sens	contig402	contig402	Unannota	ATGTATGTATATTTTCAAGGTGATATGATCCATTATGGACAAATATGTA	contig402	Solyc01g	Phospho	GO:0004	SL2.40ch	AT3G09550.1		protein b	chr3:293	100.78	82.0997	156.723	166.298	195.558	188.88
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	1.280	Detected	0.958	Detected	1.119	0.022	GT Sens	contig402	contig402	Unannota	CGTGAAGAGTGAAGAGATTTGAAGGAGACGGATATGAAGACCTTTTCT	contig402	Solyc09g	Ulp1 protease family		SL2.40ch	AT4G18500.1				15.0819	16.809	30.7673	33.1171	43.5524	29.2534
GT	Sense	Sense	0.908	Detected	-0.908	Comprom	0.000	0.955	Detected	1.161	Detected	1.058	0.366	GT Sens	contig402	contig402	Unannota	ACAGCCTCAAAAAGAGGCCTTACGTAAACAACGTACAGTTGGGTATATA	contig402	Solyc10g	Cc-nbs-lr	GO:0005	SL2.40ch	AT1G15610.1				13.0495	4.41465	10.0217	20.1235	16.5743	16.0493
GT	Sense	Sense	-0.268	Comprom	0.268	Comprom	0.000	1.072	Detected	2.203	Detected	1.637	0.120	GT Sens	contig403	contig403	Unannota	AAGAGTTCATATGCGATGCAATTAAGGCTGACAAAATCAAACCCAACCC	contig403	Solyc01g	Auxin Effl	GO:0009	SL2.40ch	AT5G048	RTM2	RTM2 (RI	chr5:142	4.30129	7.42738	5.09685	3.9884	13.3843	24.5985
GT	Sense	Sense	-0.203	Detected	0.203	Detected	0.000	1.799	Detected	0.867	Detected	1.333	0.120	GT Sens	contig403	contig403	Unannota	TAATGTTTTGTATATTTTCATTCGTTATTTCTGTTACAATGAGTATAATT	contig403	Solyc01g	RNA-bind	GO:0003	SL2.40ch	AT2G18200.1				20.8682	32.9218	62.7679	73.3015	102.76	45.1961
GT	Sense	Sense	0.808	Detected	-0.808	Detected	0.000	1.497	Detected	0.828	Detected	1.162	0.315	GT Sens	contig403	contig403	Unannota	GGATATGAATCTGAACTCAAAACAAGCCTTGTATGTGATTTAAATTATC	contig403	Solyc10g	Unknown Protein (A		SL2.40ch	ATCG007	PETB	Encodes	chrC:748	40.6035	15.759	44.3674	50.6865	80.4085	42.4611
GT	Sense	Sense	0.827	Detected	-0.827	Detected	0.000	1.241	Detected	0.819	Detected	1.030	0.351	GT Sens	contig403	contig403	Unannota	CAGAACATCGAGGCGTGAATTGACAGAGTTGCTAAAGATTTACAATTTC	contig403	Solyc10g	Unknown Protein (A		SL2.40ch	ATCG007	PETB	Encodes	chrC:748	63.5181	24.0427	60.0476	68.9148	104.043	65.1893
GT	Sense	Sense	-0.022	Comprom	0.022	Comprom	0.000	1.933	Detected	3.059	Detected	2.496	0.047	GT Sens	contig403	contig403	Unannota	AGTAAGAGTGTGACACACATTTAAGGGGCAAGTGCATTGGCATACAAA	contig403	Solyc04g	Binding p	GO:0008	SL2.40ch	AT4G21900.1		antiporte	chr4:116	3.0931	3.79617	22.5704	21.6924	14.7418	26.9983
GT	Sense	Sense	0.258	Detected	-0.258	Detected	0.000	1.282	Detected	1.039	Detected	1.160	0.056	GT Sens	contig403	contig403	Unannota	GGTTCGGTCCTCCGGTAACTGTTACGTCACTTTCAACCTGCTCATGGA	contig403	Solyc11g	Hypothetical chloro		SL2.40ch	AT3G099	PIP5K9	PIP5K9 (I	chr3:304	154.267	128.36	311.917	308.978	385.35	273.41
GT	Sense	Sense	0.325	Comprom	-0.325	Comprom	0.000	1.154	Detected	1.750	Detected	1.452	0.081	GT Sens	contig404	contig404	Unannota	AGGACTTGTTTGCAGGAAAATTTCAATACAGGTGTGTGTACCTATCTG	contig404	Solyc01g	Auxin-induced SAUI		SL2.40ch	AT2G21200.1				5.29429	4.01417	16.871	18.6202	11.5542	14.666
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	0.878	Detected	1.174	Detected	1.026	0.029	GT Sens	contig404	contig404	Unannota	ATAATGATATTTATGGATATTCAAATTTAAACAATTTACCAATTACTACT	contig404	Solyc05g	Zinc finge	GO:0003	SL2.40ch	AT3G256	CHUP1	CHUP1 (C	chr3:935	16.3903	16.9894	30.9537	32.0945	34.5497	35.5937
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	1.387	Detected	1.259	Detected	1.323	0.013	GT Sens	contig404	contig404	Unannota	GTTTGTTCATATTGATCTGTGTCAGTTAACCCTTAATACGTTACTTGAG	contig404	Solyc02g	Prolyl 4-h	GO:0004	SL2.40ch	AT4G16170.1		unknown	chr4:916	724.358	712.963	1287.01	819.145	2117.01	1626.12
GT	Sense	Sense	0.250	Detected	-0.250	Detected	0.000	1.271	Detected	0.980	Detected	1.126	0.060	GT Sens	contig404	contig404	Unannota	CCCATTACCCACAAAGCTCACCCCATCTTGCAGTAAAAAAGAAGTCTAA	contig404	Solyc02g	Prolyl 4-h	GO:0004	SL2.40ch	AT4G16170.1		unknown	chr4:916	964.165	811.919	1458.16	945.774	2405.82	1650.15
GT	Sense	Sense	0.040	Comprom	-0.040	Comprom	0.000	1.610	Detected	1.974	Detected	1.792	0.011	GT Sens	contig405	contig405	Unannota	CCACTAGTAACGATACATTCAAATGTCCACGTTCAATAAAGTAACAAGG	contig405	Solyc00g	Cytochrome P450 li		SL2.40ch	AT3G52700.1		unknown	chr3:195	5.87897	6.62224	12.4222	2.19779	21.4558	23.1802
GT	Sense	Sense	0.086	Comprom	-0.086	Comprom	0.000	1.557	Detected	1.912	Detected	1.734	0.013	GT Sens	contig405	contig405	Unannota	GAGAATGTGAGTTCTTCTCAAGATGTGAGTGTGTGAGAGAAACTTGTT	contig405	Solyc01g	Nucleolar	GO:0005	SL2.40ch	AT1G79630.3		protein p	chr1:299	4.09323	4.3267	13.1198	15.3599	13.9488	14.9714
GT	Sense	Sense	-0.328	Comprom	0.328	Comprom	0.000	1.353	Detected	3.201	Detected	2.277	0.146	GT Sens	contig405	contig405	Unannota	TGAGTGAATCAGTAAATGAGAGGAGGGTCTTGTTTTAATGGCAAAGAG	contig405	Solyc01g	Nucleolar	GO:0005	SL2.40ch	AT1G79630.3		protein p	chr1:299	2.57369	4.83015	4.66352	12.9787	10.1475	30.6592
GT	Sense	Sense	-0.138	Detected	0.138	Detected	0.000	1.780	Detected	2.334	Detected	2.057	0.022	GT Sens	contig406	contig406	Amino ac	TAGGAT contig406 Solyc03g Solyc03g Amino ac GO:0015 GO:0015	contig406	Solyc03g	Amino ac	GO:0015	SL2.40ch	AT5G15240.1		amino ac	chr5:494	261.428	376.779	422.319	356.155	1214.4	1496.21
GT	Sense	Sense	0.135	Comprom	-0.135	Comprom	0.000	0.989	Detected	1.241	Detected	1.115	0.026	GT Sens	contig406	contig406	Unannota	GTAGTTTTTGGGTTATATAATCTTCGTTTGGGTTTTTGGTTTGTGTGGA	contig406	Solyc08g	Polyprote	GO:0006	SL2.40ch	AT3G04732.1				7.86813	7.76861	18.3786	14.5195	17.4863	17.4724
GT	Sense	Sense	1.103	Detected	-1.103	Comprom	0.000	0.947	Detected	1.718	Detected	1.332	0.372	GT Sens	contig406	contig406	Unannota	GAGGCATTAATTATACATTAGCGGGGTGATTTACAGAGGGTGACATGC	contig406	Solyc05g	Cc-nbs-lr	GO:0006	SL2.40ch	AT4G159	PRL1	PRL1 (PL	chr4:902	16.5961	4.27967	3.94054	5.13059	18.2963	26.2175
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	1.086	Detected	0.944	Detected	1.015	0.005	GT Sens	contig406	contig406	Unannota	GGGCTTTCCCTCATAATAAAATCATCCCTCTTTCAAATACATCTTTCTC	contig406	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G15260.1		structura	chr5:495	111.876	132.143	203.595	185.161	290.672	221.212
GT	Sense	Sense	-0.074	Comprom	0.074	Comprom	0.000	5.673	Detected	3.015	Detected	4.344	0.082	GT Sens	contig406	contig406	Unannota	GAATGTTAAGAATATAACAAAAGAGCAATGAGAGGAGGGAGAGTGATGA	contig406	Solyc09g	Unknown Protein (A		SL2.40ch	AT2G43880.1		polygala	chr2:181	3.50391	4.61926	2.8125	2.72894	231.156	30.7485
GT	Sense	Sense	0.155	Comprom	-0.155	Comprom	0.000	3.505	Detected	3.488	Detected	3.497	0.002	GT Sens	contig406	contig406	Unannota	CATAATAACAACACAAAAGGCAACAAGCAAGCAAATATGCTACACATGC	contig406	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G51150.1		unknown	chr5:207	3.14059	3.01748	4.70337	3.75293	39.3765	32.6652
GT	Sense	Sense	0.223	Detected	-0.223	Detected	0.000	0.991	Detected	1.257	Detected	1.124	0.049	GT Sens	contig407	contig407	Unannota	ATTCTTGAGATGCACTTGTGCTTGAAGCTTGGTGAGTGACAGGTTAAG	contig407	Solyc11g	Pentatric	GO:0008	SL2.40ch	AT3G59830.1		ankyrin p	chr3:221	13.7407	12.0143	19.1647	19.1116	28.7702	29.025
GT	Sense	Sense	-0.365	Detected	0.365	Detected	0.000	0.959	Detected	1.075	Detected	1.017	0.110	GT Sens	contig407	contig407	Unannota	CGATGATGCAAGAATATTGGAATGTTATGAAGCAGCTACATATATTGTG	contig407	Solyc06g	Fimbrin-li	GO:0051	SL2.40ch	AT5G357	FIM2	FIM2 (FIM	chr5:138	16.2506	32.0796	28.5593	40.9009	50.0036	45.4942
GT	Sense	Sense	-0.241	Detected	0.241	Detected	0.000	1.129	Detected	1.287	Detected	1.208	0.041	GT Sens	contig407	contig407	Unannota	CATCTAATTGGTTCTTGTGAATAACTTTCTTTTCCATTGCTTCTCACTT	contig407	Solyc04g	Cysteine-	GO:0005	SL2.40ch	AT5G08310.1		pentatric	chr5:267	442.279	735.167	899.063	853.577	1405	1315.31
GT	Sense	Sense	0.450	Comprom	-0.450	Comprom	0.000	1.950	Detected	1.939	Detected	1.945	0.050	GT Sens	contig407	contig407	Unannota	AAACAATAAAGTGGATGGATTAATGTCCGAACAGAGAAAAATGAAATGA	contig407	Solyc01g	MADS-bo	GO:0005	SL2.40ch	AT5G66660.1				4.56082	2.9099	3.77134	3.75718	15.8538	13.2103
GT	Sense	Sense	1.072	Detected	-1.072	Comprom	0.000	1.974	Detected	1.456	Detected	1.715	0.260	GT Sens	contig408	contig408	Unannota	CTTCTTCAATCTTCAACGTACAGTTGAAATCTCGATAAGCAATCGTCAA	contig408	Solyc12g	Integral m	GO:0006	SL2.40ch	AT5G04550.1		unknown	chr5:130	30.8147	8.29535	51.573	38.4558	70.7538	41.4629
GT	Sense	Sense	-0.456	Comprom	0.456	Comprom	0.000	1.827	Detected	2.470	Detected	2.149	0.061	GT Sens	contig408	contig408	Unannota	CTCAGTAAACATGGGAGAGATGGATCAAGGTAGAAGGATCAAGAGAAC	contig408	Solyc04g	Calcium-t	GO:0005	SL2.40ch	AT2G34890.1		CTP syn	chr2:147	5.10704	11.4383	18.5146	22.3367	30.5558	40.0283
GT	Sense	Sense	0.317	Detected	-0.317	Detected	0.000	1.424	Detected	1.195	Detected	1.310	0.060	GT Sens	contig408	contig408	Unannota	GCTGGACTCAAAGGGGTAAGTAGACTGTAGAATTAGTTTGTTATGCTA	contig408	Solyc04g	Calcium-t	GO:0005	SL2.40ch	AT2G34890.1		CTP syn	chr2:147	20.8756	16.0242	26.9358	25.4169	55.2928	39.6013
GT	Sense	Sense	-0.452	Comprom	0.452	Detected	0.000	1.166	Detected	1.309	Detected	1.238	0.114	GT Sens	contig408	contig408	Unannota	GCAGTATGGTTGATTCACATATATTTGGGCTTTTTGTGTTCTTGAAATT	contig408	Solyc02g	ABC transporter C f		SL2.40ch	ATMG00610.1				9.60607	21.3971	20.6681	16.27	36.2392	33.5931
GT	Sense	Sense	-0.742	Comprom	0.742	Detected	0.000	1.498	Detected	1.212	Detected	1.355	0.215	GT Sens	contig409	contig409	Unannota	GTGAAAAGGTAATTGGGATAAGCCTGATTTTGCATCTAAAGTCAATCAA	contig409	Solyc02g	Uncharacterized me		SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:145	4.9456	16.4729	16.3273	19.6729	28.719	19.7722
GT	Sense	Sense	0.219	Detected	-0.219	Detected	0.000	0.987	Detected	1.298	Detected	1.142	0.051	GT Sens	contig409	contig409	Unannota	TTAGGTACGCAGAAGTCACATCATGCATAGATCAGTTTCGTTCTTCAGT	contig409	Solyc03g	Armadillo	GO:0005	SL2.40ch	AT5G03870.1		glutared	chr5:103	63.3506	55.7083	127.517	100.176	132.604	138.081
GT	Sense	Sense	-0.338	Comprom	0.338	Comprom	0.000	1.154	Detected	1.506	Detected	1.330	0.073	GT Sens	contig409	contig409	Unannota	GCAGCGATTTTGGGATGGTTGATGAGTTCAGAGAGACACTTCCACTAA	contig409	Solyc06g	Omega-3	GO:0042	SL2.40ch	AT2G241	PDE319.	SCA3 (SC	chr2:102	4.78518	9.09915	12.4613	4.91537	16.5377	17.7249
GT	Sense	Sense	0.972	Comprom	-0.972	Comprom	0.000	1.019	Detected	2.195	Detected	1.607	0.293	GT Sens	contig409	contig409	Unannota	ATTAATTTCATTTCACACCAGTGTCGAACTAGTGCAATCCCAAATGTGA	contig409	Solyc04g	MADS-bo	GO:0046	SL2.40ch	AT1G08190.1		vacuolar	chr1:256	9.47019	2.93087	12.0778	6.47824	12.0293	22.8018
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	0.977	Detected	1.037	Detected	1.007	0.013	GT Sens	contig409	contig409	Unannota	CAGAAGTGGGAATAGCGATTGCCATAGAAAATGAAATGAATTTGTATAT	contig409	Solyc08g	ATP-depe	GO:0008	SL2.40ch	AT5G11170.1		ATP bind	chr5:355	42.3581	58.9419	87.8382	64.9437	110.762	96.9396
GT	Sense	Sense	-0.242	Detected	0.242	Detected	0.000	1.086	Detected	1.622	Detected	1.354	0.064	GT Sens	contig409	contig409	Unannota	TGTACTAAATTTTATACATTAATGCTACCAAACATAATACTAGTTAGAAT	contig409	Solyc08g	Glycosyl	GO:0016	SL2.40ch	AT5G43570.1		serine-ty	chr5:175	18.5757	30.936	40.4399	48.2243	57.3386	69.7898
GT	Sense	Sense	-0.288	Comprom	0.288	Comprom	0.000	1.123	Detected	1.437	Detected	1.280	0.060	GT Sens	contig410	contig410	Unannota	GATGGTCTTTAGGAATGGTAATCCAAACTTGATTTTGGAGCATCCAATT	contig410	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G15030.1				5.30415	9.41001	18.6975	18.6475	17.3298	18.0924
GT	Sense	Sense	-0.338	Comprom	0.338	Comprom	0.000	1.289	Detected	1.715	Detected	1.502	0.064	GT Sens	contig410	contig410	Unannota	TGTTGAGAAGACAATAGAACTGTAAAATTGAACTTAAAGGTGCCAAGAA	contig410	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G15030.1				4.15931	7.91481	11.6036	8.15247	15.7902	17.8118
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	1.618	Detected	1.132	Detected	1.375	0.037	GT Sens	contig410	contig410	Unannota	GGTCAAAACAAAAACAAGAGATAATTTGGTTACATATGTCTATCTTAACT	contig410	Solyc03g	Gag-Pol p	GO:0008	SL2.40ch	AT3G496	UBP26. S	UBP26 (U	chr3:183	16.3558	16.4172	25.6623	20.5424	56.6735	33.9606
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	1.174	Detected	0.947	Detected	1.061	0.013	GT Sens	contig410	contig410	Unannota	CTACAAAGGAATTAATTCTTCTCAACAAGGAGAAGCTACTGACTTTTTA	contig410	Solyc03g	3-oxoacy	GO:0008	SL2.40ch	AT5G23360.1		GRAM do	chr5:786	25.1215	28.2083	44.6992	37.7404	67.6741	48.5295
GT	Sense	Sense	0.026	Comprom	-0.026	Comprom	0.000	4.405	Detected	2.628	Detected	3.517	0.058	GT Sens	contig411	contig411	Unannota	ACTCTACACAATGGGAATATGTACGTGCAAGCAAACCTACAAGAGACAC	contig411	Solyc00g228260.1.1				AT3G451	SETH2	SETH2: t	chr3:165	2.41991	2.77899	3.01353	4.03617	61.906	15.1608
GT	Sense	Sense	0.716	Detected	-0.716	Comprom	0.000	1.287	Detected	1.318	Detected	1.302	0.211	GT Sens	contig411	contig411	Unannota	CTCTATGTCATGGCCTAAAAGAATGTCAAGTCTAGCAGTTTTAAGAGTG	contig411	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G59440.1				17.4959	7.71683	14.5016	20.741	31.9316	27.3961
GT	Sense	Sense	0.222	Detected	-0.222	Detected	0.000	0.903	Detected	1.460	Detected	1.181	0.080	GT Sens	contig411	contig411	Unannota	CCATTAGTCACATTTTCAACGATTGTTATATAGCCAAGAAATTCTGGTT	contig411	Solyc11g	Multidrug	GO:0017	SL2.40ch	AT4G25340.1		immuno	chr4:129	19.0208	16.6532	31.2219	34.8018	37.4798	46.2865
GT	Sense	Sense	0.554	Detected	-0.554	Detected	0.000	0.950	Detected	1.651	Detected	1.300	0.186	GT Sens	contig411	contig411	Unannota	ATCCCTAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCC	contig411	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G13840.1		PHP dom	chr2:578	88.6684	48.972	125.734	100.121	143.386	195.615
GT	Sense	Sense	0.449	Detected	-0.449	Comprom	0.000	2.757	Detected	2.163	Detected	2.460	0.045	GT Sens	contig411	contig411	Unannota	CGTTTCGATGAGTGGAGACGAATTTAGGATTTGAATGTTGAAGTTCAAT	contig411	Solyc04g	WPP domain-associ		SL2.40ch	AT1G48660.1		auxin-res	chr1:179	16.3787	10.4615	21.3734	23.3718	99.6944	55.4482
GT	Sense	Sense	0.235	Detected	-0.235	Detected	0.000	1.600	Detected	1.923	Detected	1.762	0.025	GT Sens	contig411	contig411	LOB dom	TTACAG contig411 Solyc01g Solyc01g LOB dom GO:0005 GO:0005	contig411	Solyc01g	LOB dom	GO:0005	SL2.40ch	AT3G43930.2		FUNCTIO	chr3:157	274.078	235.658	400.817	374.222	867.814	911.433
GT	Sense	Sense	-0.685	Comprom	0.685	Detected	0.000	1.023	Detected	1.543	Detected	1.283	0.222	GT Sens	contig411	contig411	Unannota	GATTATGGTGAGGAGCAGAATATATGAGAGCATGAAAAGTTGTTCAGT	contig411	Solyc02g	Glucan e	GO:0005	SL2.40ch	AT5G038	EMB175.	EMB175	chr5:101	4.25473	13.0909	11.155	13.433	17.0883	20.5673
GT	Sense	Sense	1.251	Detected	-1.251	Comprom	0.000	0.871	Detected	1.498	Detected	1.185	0.455	GT Sens	contig411	contig411	Unannota	TAAAAGACTATGAGTCTTTACGACTCTCTCGAGATACGGAGAAGGAGA	contig411	Solyc02g090550.1.1				AT3G56160.1		bile acid	chr3:208	16.008	3.36264	14.8042	17.016	15.1189	19.5932
GT	Sense	Sense	-0.446	Comprom	0.446	Comprom	0.000	2.460	Detected	2.015	Detected	2.238	0.046	GT Sens	contig411	contig411	Unannota	CTCAAACGGATTTTACATGCCACAAAGTAAACGAAAGGAATTAATATAC	contig411	Solyc02g090550.1.1				AT3G56160.1		bile acid	chr3:208	2.45271	5.41623	5.39227	2.54777	22.595	13.93
GT	Sense	Sense	0.284	Detected	-0.284	Detected	0.000	1.300	Detected	1.359	Detected	1.330	0.043	GT Sens	contig411	contig411	Unannota	CCGAAATTCAGGACCACAACTTCAATGTTCTTGCTGAGATAGAATCTAT	contig411	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G04970.1		pectines	chr5:146	21.6037	17.3417	45.0184	43.8899	53.697	46.9496
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	1.749	Detected	1.555	Detected	1.652	0.006	GT Sens	contig411	contig411	Unannota	TTCAAGTAGGGTACCTTGATAGGCATTCATGGGTTCCGGTCAATGAAG	contig411	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G33170.1		pentatric	chr4:159	372.235	392.418	460.779	514.101	1447.04	1061.85
GT	Sense	Sense	0.099	Detected	-0.099	Detected	0.000	1.562	Detected	1.313	Detected	1.438	0.012	GT Sens	contig411	contig411	Unannota	GCGATGCCACTATCTAAATTATGGAGTTGCTTTTAGTTAAAGACTTCTA	contig411	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G33170.1		pentatric	chr4:159	377.545	391.579	553.113	561.029	1279.15	903.139
GT	Sense	Sense	0.664	Detected	-0.664	Detected	0.000	2.452	Detected	0.994	Detected	1.723	0.223	GT Sens	contig411	contig411	Unannota	ATAGTGTGAATCACACCTCCTCTAGCTACATGAATCACACCTCCTCGTA	contig411	Solyc01g049800.1.1				AT1G48800.1		terpene s	chr1:180	47.253	22.4056	145.592	93.2258	200.626	61.2904
GT	Sense	Sense	-0.279	Comprom	0.279	Comprom	0.000	1.679	Detected	2.996	Detected	2.337	0.082	GT Sens	contig411	contig411	Unannota	ATCAAAGGAAGCAACTTAATAACATCACATGGCTGAGTTGCTATGGAAA	contig411	Solyc03g	50S ribos	GO:0003	SL2.40ch	AT4G28730.1		glutared	chr4:141	4.93638	8.64605	6.12014	8.1808	23.5626	49.2657
GT	Sense	Sense	0.215	Comprom	-0.215	Comprom	0.000	3.459	Detected	3.604	Detected	3.531	0.004	GT Sens	contig412	contig412	Unannota	GAGCTCCTTATCTAATTTGCCTTACCTCAAGTCAAATGTTATATAAAGG	contig412	Solyc04g	Glycosyltransferase		SL2.40ch	AT3G19320.1				5.52351	4.88168	3.44433	3.95325	64.3221	59.6811
GT	Sense	Sense	-0.041	Comprom	0.041	Comprom	0.000	1.093	Detected	2.521	Detected	1.807	0.127	GT Sens	contig412	contig412	Unannota	CTTGGAGGAGAAAACAGACAAACAAAAACCGGGAGCCAAAATCCACGAT	contig412	Solyc06g	Dehydration-respor		SL2.40ch	AT5G23110.1		zinc fing	chr5:775	4.23172	5.32922	7.31411	5.1058	11.4086	25.7764
GT	Sense	Sense	0.547	Comprom	-0.547	Comprom	0.000	1.086	Detected	1.576	Detected	1.331	0.157	GT Sens	contig412	contig412	Unannota	CTCTGCTATCTGAATGACAAATCAGAACTTGAACAATGGAAAGACTGAA	contig412	Solyc02g	Equilibrat	GO:0005	SL2.40ch	AT1G36675.1				6.71914	3.74496	5.25212	3.2541	11.9987	14.1411
GT	Sense	Sense	0.349	Detected	-0.349	Detected	0.000	1.158	Detected	1.278	Detected	1.218	0.075	GT Sens	contig412	contig412	Unannota	TCAAATTTCCCCTTTATTATGCATAAGGGGCAATATCTTTTCCATGATT	contig412	Solyc02g	Unknown Protein (A		SL2.40ch	AT1G12300.1				22.3053	16.3781	33.5423	26.8599	48.0531	43.8247
GT	Sense	Sense	0.135	Comprom	-0.135	Comprom	0.000	1.384	Detected	1.483	Detected	1.433	0.010	GT Sens	contig412	contig412	Unannota	CCTTGACAATACGGTCGACCTCATATTTGGTGCCATTGTCCGTATTGT	contig412	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G35940.1		jacalin le	chr5:140	5.85092	5.77267	21.8096	23.7909	17.0865	15.3594
GT	Sense	Sense	0.690	Detected	-0.690	Comprom	0.000	2.378	Detected	1.511	Detected	1.944	0.140	GT Sens	contig412	contig412	Unannota	CCTTTGCACAATAATCCTTCAACATTTCAACATTGGCAGGAGTGTCTAA	contig412	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G35940.1		jacalin le	chr5:140	14.634	6.69219	29.6168	29.8448	57.9367	26.6594
GT	Sense	Sense	-0.183	Detected	0.183	Detected	0.000	1.303	Detected	0.917	Detected	1.110	0.053	GT Sens	contig413	contig413	Unannota	GTGTGAAAATAGTAGTCGGCGTTGGATTACGGAAACATTTTTCGCCAG	contig413	Solyc10g	Presenilin	GO:0016	SL2.40ch	AT1G747	CPK30. C	CPK30 (C	chr1:280	25.5156	39.1238	54.5109	52.6847	87.8218	56.4054
GT	Sense	Sense	0.397	Detected	-0.397	Detected	0.000	1.443	Detected	1.011	Detected	1.227	0.113	GT Sens	contig413	contig413	Unannota	CATCTTGAAGGGGAGTGTTGAAGTATGAAGATGATATGTTCAAGTAGA	contig413	Solyc03g	Gag-pol polyprotein		SL2.40ch	AT3G58020.1				42.8082	29.3845	60.4284	46.7014	108.621	67.5953
GT	Sense	Sense	0.754	Detected	-0.754	Detected	0.000	1.233	Detected	1.021	Detected	1.127	0.277	GT Sens	contig413	contig413	Unannota	CAGAATTGCCCAACTCTTAAAAAGAGTTCACACAAAGATCTGCTCTGAT	contig413	Solyc03g	Phospho	GO:0008	SL2.40ch	AT1G01670.1				29.5215	12.3544	28.5031	21.3565	50.5775	36.6477
GT	Sense	Sense	0.443	Comprom	-0.443	Comprom	0.000	1.414	Detected	1.668	Detected	1.541	0.079	GT Sens	contig413	contig413	Unannota	ACTAGCGGTAGGTGATCCTAGCTTTATGTTGTCCATATATCAAAGTTCC	contig413	Solyc11g	F-box family protein		SL2.40ch	AT3G58520.2		ubiquitin	chr3:216	9.8663	6.35389	17.9252	15.8121	23.7593	23.7866
GT	Sense	Sense	-0.316	Comprom	0.316	Detected	0.000	1.209	Detected	1.761	Detected	1.485	0.071	GT Sens	contig413	contig413	Unannota	GTAGGAAGCACGAACCACACCAAAACCCTACTTTTACTATGACTGCTG	contig413	Solyc09g	40S ribos	GO:0003	SL2.40ch	AT5G20290.1		40S ribo	chr5:685	9.40706	17.3564	11.8974	20.1081	33.2847	40.9474
GT	Sense	Sense	-0.110	Comprom	0.110	Comprom	0.000	0.833	Detected	1.950	Detected	1.392	0.134	GT Sens	contig413	contig413	Unannota	CTTGGGCAAGAGGAAACAGCTCATGAAGGGAAAAAACAAGCAATCAAA	contig413	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G05165.4				4.34493	6.02355	4.94426	5.39766	10.2656	18.6924

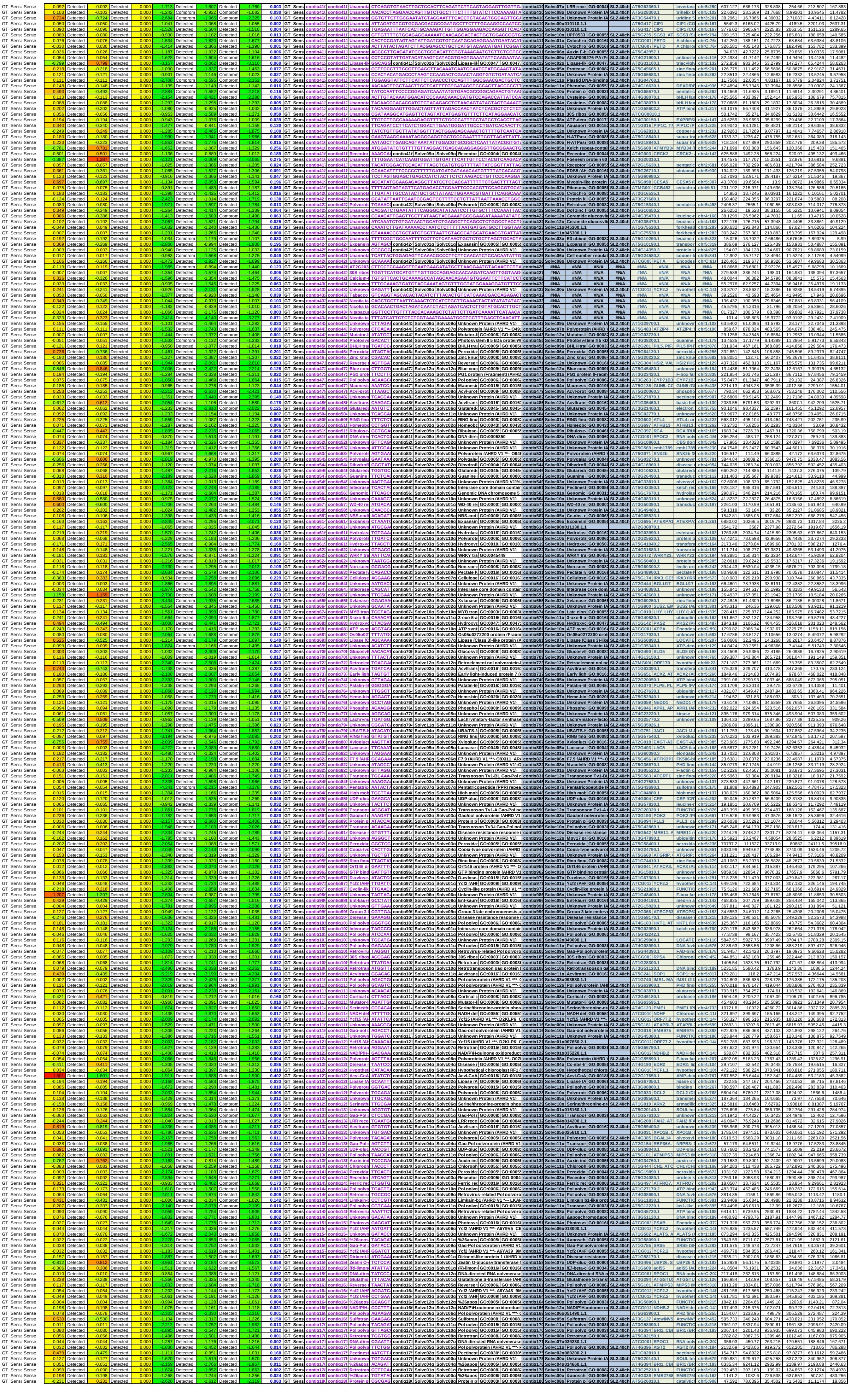
GT	Sense	Sense	-0.003	Comprom	0.003	Comprom	0.000	0.926	Detected	1.384	Detected	1.155	0.037	GT	Sens	contig426	contig426	Putative u	ACTCAAGCATCTGTGTAGGCAACGTAGCAAGGATACACAAGCATCATTA							contig426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	5.37203	6.41974	6.13345	6.94068	12.5672	14.4969
GT	Sense	Sense	0.739	Detected	-0.739	Comprom	0.000	1.679	Detected	1.649	Detected	1.664	0.153	GT	Sens	contig427	contig427	Probable	CATTCGTCTTTGTGCTGGAAAGCAGAAGACAATACAGGAACTATTTGCA							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	17.1394	7.32083	10.9667	6.46289	40.4121	33.2155
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	1.225	Detected	1.643	Detected	1.434	0.027	GT	Sens	contig427	contig427	Histone H	GGTGTTGAAGCAGGTTCATCCAGAATTCTTAGATTTAGATTTGTTTGTT							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	204.023	204.754	383.332	449.047	538.245	603.389
GT	Sense	Sense	0.048	Comprom	-0.048	Comprom	0.000	0.872	Detected	2.403	Detected	1.638	0.166	GT	Sens	contig428	contig428	AT5G509	AACCTGGAGGAAGACGAATAACGTACAATAATCGTTGATAATCGACGGC							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	5.56112	6.19209	13.9871	11.5377	12.1015	29.3534
GT	Sense	Sense	0.589	Comprom	-0.589	Comprom	0.000	1.017	Detected	1.711	Detected	1.364	0.184	GT	Sens	contig429	contig429	Vacuolar	AACAAAACCCTAGCAGATGACTTGATTGCTGGTGCTTTTCCCAACACAC							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	8.10255	4.26057	4.02899	4.34917	13.3928	18.1844
GT	Sense	Sense	-0.371	Comprom	0.371	Comprom	0.000	1.647	Detected	1.631	Detected	1.639	0.048	GT	Sens	contig429	contig429	AT3G208	GGCTTAGCTCTGTAGCTAAATGACAGATACAAGAGCTACAACAAGATAT							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	4.00566	7.97103	7.79154	6.77135	19.9402	16.5535
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	1.476	Detected	1.728	Detected	1.602	0.016	GT	Sens	contig429	contig429	Nicotia ta	CTACTCAGGAATCTGGATCACCGATCGTAAGCCTTCAACTTTACTGATA							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	56.9691	53.9523	146.726	138.495	173.749	173.643
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	1.516	Detected	0.871	Detected	1.193	0.066	GT	Sens	contig430	contig430	Gibberell	TTGGCC	contig430	Solyc06g	Solyc06g	Gibberellin-regulated protein (			contig430	Solyc06g	Gibberellin-regulate		SL2.40ch	AT1G74670.1		gibberell	chr1:280	15.2819	18.3899	63.5879	35.5686	53.9991	28.987
GT	Sense	Sense	0.376	Detected	-0.376	Detected	0.000	1.025	Detected	1.706	Detected	1.365	0.115	GT	Sens	contig430	contig430	Unknown	GTTTTTCGAGGAATACAAAGAATCACAAAATACCAAAGATCGTATGACA							contig430	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	25.378	17.9396	49.3333	60.6916	48.9022	65.8339
GT	Sense	Sense	0.455	Detected	-0.455	Detected	0.000	1.194	Detected	0.957	Detected	1.076	0.149	GT	Sens	contig431	contig431	Nicotia ta	GTTTGCTAGTGTAATTGCTTCCTTGTAAATACAGTTTAGAAGCACATCA							contig431	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	35912.3	22749	73304.3	61757.2	73681	52469.6
GT	Sense	Sense	0.509	Detected	-0.509	Detected	0.000	1.241	Detected	1.372	Detected	1.306	0.126	GT	Sens	contig431	contig431	TOBPAL1	ATTTTGGAGTTAAAAACTAAATATGAACTCTCTTGAATATATTGGTTTGT							contig431	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	3664.53	2153	6746.52	5378.42	7477.06	6873.76
GT	Sense	Sense	0.735	Detected	-0.735	Detected	0.000	1.592	Detected	1.699	Detected	1.646	0.155	GT	Sens	contig431	contig431	Nicotia ta	TATACAACAAGATCTGAGTGATTTTTTTCCAAAATAAATTGGGGAAAAT							contig431	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	148.928	63.9624	299.443	273.065	331.496	299.717
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	1.065	Detected	1.071	Detected	1.068	0.014	GT	Sens	contig432	contig432	Nicotia ta	TTGGTTACAAATTGAGTATCAAAGAGTAATGATGAATCTTAGTGACAGT							contig432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	980.183	978.287	2067.97	2075.58	2307.53	1945.26
GT	Sense	Sense	0.709	Detected	-0.709	Detected	0.000	0.992	Detected	1.497	Detected	1.245	0.240	GT	Sens	contig432	contig432	Nicotia ta	CTTGCTACCTAGTCAGGTTTTACTAATAGGGATACTGCAAATTCTTTTA							contig432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	12732.3	5672.09	11872.2	11007.1	19044.5	22679.7
GT	Sense	Sense	-0.111	Comprom	0.111	Comprom	0.000	2.289	Detected	2.079	Detected	2.184	0.005	GT	Sens	contig432	contig432	N.tabacu	GGAATGGTGGAGATAGAAGTCATATAATGGATAATCAAAACAGAATATC							contig432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	3.6357	5.04499	4.93832	11.4283	23.5824	17.1089
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	1.091	Detected	1.154	Detected	1.122	0.015	GT	Sens	contig432	contig432	Nicotia ta	TATGAGCTTCCATACTTGTATATTATGCAAGATGTGCAACTGTAGTATC							contig432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1829.57	1805.26	3436.4	2905	4360.64	3824.13
GT	Sense	Sense	-0.023	Comprom	0.023	Comprom	0.000	1.068	Detected	1.822	Detected	1.445	0.062	GT	Sens	contig433	contig433	Nicotia ta	TTACATTCCGCGCAACTCCAAGATAGTGTTAGTGACACCTTAAGTTAAA							contig433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	5.25134	6.45587	8.90183	6.22337	13.7463	19.4691
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	2.358	Detected	1.120	Detected	1.739	0.107	GT	Sens	contig433	contig433	TOBBY4I	TGGCTTTGAAGTGGACAGAAAATAGCAAATCATTCCACTAGGTGAGAAC							contig433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	142.495	168.879	576.529	445.119	895.619	318.742
GT	Sense	Sense	0.443	Detected	-0.443	Detected	0.000	1.076	Detected	1.142	Detected	1.109	0.130	GT	Sens	contig433	contig433	NTU6273	GTGTCGCCGCATCAGTTAAAATATCAAGGCATTATTTTTGAAATTTCCC							contig433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	4914.35	3166.73	12529.5	8041.34	9371.02	8231.79
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	1.506	Detected	1.746	Detected	1.626	0.007	GT	Sens	contig434	contig434	NTU6492	AGATGTAAAAATATGAAAAAGTTTGAAGATAAAGATACACCATTATGCTC							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	72.6761	79.7658	150.449	169.009	243.608	241.425
GT	Sense	Sense	0.135	Comprom	-0.135	Comprom	0.000	1.399	Detected	2.442	Detected	1.920	0.070	GT	Sens	contig436	contig436	Unknown	GGAGGA	contig436	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig436	Solyc06g	Unknown Protein (A		SL2.40ch	AT5G47740.1		FUNCTIC	chr5:193	3.83285	3.78407	2.98595	2.66653	11.3123	19.5636
GT	Sense	Sense	0.192	Comprom	-0.192	Comprom	0.000	2.430	Detected	2.823	Detected	2.627	0.011	GT	Sens	contig445	contig445	Unknown	CTCAGC	contig445	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig445	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G32375.1				2.61205	2.38211	2.16833	3.95249	15.1418	16.6941
GT	Sense	Sense	-0.220	Detected	0.220	Detected	0.000	1.873	Detected	1.928	Detected	1.901	0.013	GT	Sens	contig446	contig446	Fatty acy	TTTGTG	contig446	Solyc09g	Solyc09g	Fatty acy	GO:0080	GO:0080	contig446	Solyc09g	Fatty acy	GO:0080	SL2.40ch	AT1G65810.1		tRNA-spl	chr1:244	113.304	183.046	321.742	405.325	594.269	518.264
GT	Sense	Sense	-0.302	Comprom	0.302	Comprom	0.000	1.774	Detected	1.676	Detected	1.725	0.030	GT	Sens	contig448	contig448	Unknown	ACGTGA	contig448	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig448	Solyc05g	Unknown Protein (A		SL2.40ch	AT1G74720.1		C2 doma	chr1:280	5.77344	10.4455	15.9679	10.3941	29.9222	23.4594
GT	Sense	Sense	-0.948	Comprom	0.948	Detected	0.000	2.076	Detected	1.436	Detected	1.756	0.221	GT	Sens	contig449	contig449	Kelch do	AGTTCC	contig449	Solyc01g	Solyc01g	Kelch domain-containing prote			contig449	Solyc01g	Kelch domain-conta		SL2.40ch	AT3G243	chr40	chr40 (ch	chr3:883	3.91122	17.3316	19.8743	34.4832	39.1103	21.0574
GT	Sense	Sense	-0.057	Detected	0.057	Detected	0.000	1.577	Detected	2.096	Detected	1.836	0.020	GT	Sens	contig449	contig449	Geranylg	AGATAA	contig449	Solyc11g	Solyc11g	Geranylg	GO:0008	GO:0008	contig449	Solyc11g	Geranylg	GO:0008	SL2.40ch	AT3G14510.1		geranylg	chr3:486	161.768	208.481	849.971	512.498	617.024	742.27
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	0.898	Detected	2.698	Detected	1.798	0.184	GT	Sens	contig459	contig459	LINE-type	GGAGTG	contig459	Solyc06g	Solyc06g	LINE-type retrotransposon LIb			contig459	Solyc11g	Ycf1 (Fragment) (AH		SL2.40ch	AT5G59200.1		pentatric	chr5:238	24.95	27.5965	46.0982	49.2435	55.073	161.024

GT	Sense	Sense	0.289	Comprom	-0.289	Comprom	0.000	1.135	Detected	0.994	Detected	1.064	0.070	GT Sens	contig169	contig169	Ulp1 prot	AAATGA	contig169	Solyc01g	Solyc01g	Ulp1 protease family C-termina			contig169	Solyc12g	Ulp1 protease famil		SL2.40ch	AT3G445	FAR8	FAR8 (FA	chr3:161	10.733	8.55533	15.2927	17.8791	23.7049	18.0412
GT	Sense	Sense	-0.873	Comprom	0.873	Detected	0.000	7.272	Detected	7.857	Detected	7.564	0.014	GT Sens	contig170	contig170	Gag poly	CTGCAT	contig170	Solyc00g	Solyc00g	Gag poly	GO:0008	GO:00082	contig170	Solyc11g	Kinase fa	GO:0006	SL2.40ch	AT5G286	WRKY74.	WRKY74	chr5:106	3.33306	13.3006	2.8114	16.0217	1159.19	1459.51
GT	Sense	Sense	0.202	Detected	-0.202	Detected	0.000	1.379	Detected	1.539	Detected	1.459	0.022	GT Sens	contig171	contig171	Ulp1 prot	TGCAAC	contig171	Solyc12g	Solyc12g	Ulp1 prot	GO:0006	GO:00065	contig171	Solyc09g	Ulp1 protease famil		SL2.40ch	AT4G345	FAE1, KC	KCS18:	chr4:164	34.6806	31.1858	57.8462	40.7636	96.3595	90.3585
GT	Sense	Sense	-0.166	Detected	0.166	Detected	0.000	1.336	Detected	0.822	Detected	1.079	0.072	GT Sens	contig171	contig171	Ulp1 prot	CTCATA	contig171	Solyc05g	Solyc05g	Ulp1 protease family C-termina			contig171	Solyc11g	Ulp1 protease famil		SL2.40ch	AT5G28740.1		transcrip	chr5:107	1324.46	1983.64	3630.06	3453.28	4609.82	2709.9
GT	Sense	Sense	0.415	Detected	-0.415	Detected	0.000	2.117	Detected	1.405	Detected	1.761	0.084	GT Sens	contig172	contig172	Wound in	CCAAGA	contig172	Solyc07g	Solyc07g	Wound induced protein (AHRD			contig172	Solyc07g	Wound induced pro		SL2.40ch	AT4G10270.1		wound-r	chr4:637	58.199	38.982	115.761	56.9436	232.827	119.304
GT	Sense	Sense	-0.597	Comprom	0.597	Comprom	0.000	2.859	Detected	2.529	Detected	2.694	0.049	GT Sens	contig172	contig172	Receptor	CTGAGG	contig172	Solyc06g	Solyc06g	Receptor	GO:0019	GO:00191	contig172	Solyc12g	Peptidyl-t	GO:0006	SL2.40ch	AT4G01000.1		ubiquitin	chr4:432	2.45783	6.69877	37.9672	55.5826	33.1663	22.1413
GT	Sense	Sense	0.302	Detected	-0.302	Detected	0.000	1.455	Detected	1.310	Detected	1.382	0.047	GT Sens	contig174	contig174	Plant syn	ATCGGT	contig174	Solyc10g	Solyc10g	Plant synaptotagmin (AHRD V1			contig174	Solyc10g052520.1.1				AT3G610	NTMC2T	NTMC2T	chr3:225	58.939	46.1697	83.8571	99.3858	161.053	122.327
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	1.419	Detected	1.471	Detected	1.445	0.000	GT Sens	contig176	contig176	S-phase k	AGACAT	contig176	Solyc10g	Solyc10g	S-phase k	GO:0006	GO:00065	contig176	Solyc10g	S-phase k	GO:0005	SL2.40ch	AT1G759	SKP1, AS	SKP1 (S	chr1:285	80.3337	93.8424	122.768	131.266	261.556	227.538
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	0.979	Detected	1.126	Detected	1.053	0.007	GT Sens	contig180	contig180	Caffeoyl-	AGATTA	contig180	Solyc02g	Solyc02g	Caffeoyl-	GO:0042	GO:00424	contig180	Solyc02g	Caffeoyl-	GO:0042	SL2.40ch	AT4G34050.1		caffeoyl-	chr4:163	1567.63	1994.26	3819.58	3238.69	3926.39	3648.74
GT	Sense	Sense	0.130	Detected	-0.130	Detected	0.000	0.828	Detected	1.458	Detected	1.143	0.079	GT Sens	contig181	contig181	Aldehyde	TGTGGC	contig181	Solyc11g	Solyc11g	Aldehyde	GO:0050	GO:00506	contig181	Solyc11g	Aldehyde	GO:0009	SL2.40ch	AT1G045	AAO4, AT	AAO4 (A	chr1:125	338	335.953	607.079	763.882	673.765	875.114
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	1.353	Detected	1.292	Detected	1.323	0.046	GT Sens	contig182	contig182	Ubiquitin	TCTACC	contig182	Solyc10g	Solyc10g	Ubiquitin	GO:0006	GO:00064	contig182	Solyc12g	Ubiquitin-	GO:0006	SL2.40ch	AT2G18600.1		RUB1-co	chr2:807	1036.59	824.738	1769.1	1555.87	2661.17	2140.84
GT	Sense	Sense	0.483	Detected	-0.483	Detected	0.000	1.246	Detected	1.033	Detected	1.139	0.148	GT Sens	contig182	contig182	Unknown	TTATGT	contig182	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig182	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G46640.2		unknown	chr2:191	250.342	152.62	406.42	344.934	522.157	378.16
GT	Sense	Sense	0.446	Detected	-0.446	Detected	0.000	1.742	Detected	2.265	Detected	2.003	0.061	GT Sens	contig183	contig183	Photosys	CCTAGC	contig183	Solyc01g	Solyc01g	Photosys	GO:0030	GO:00300	contig183	Solyc01g097530.1.1				ATCG000	PSBA	Encodes	chrC:383	486.387	311.914	1067.62	891.597	1467.8	1769.77
GT	Sense	Sense	0.189	Comprom	-0.189	Comprom	0.000	2.027	Detected	4.489	Detected	3.258	0.120	GT Sens	contig185	contig185	Ethylene-	GTACAT	contig185	Solyc12g	Solyc12g	Ethylene-	GO:0006	GO:00063	contig185	Solyc01g	Ethylene	GO:0003	SL2.40ch	AT1G77640.1				2.46864	2.26004	2.03173	2.05756	10.8454	50.15
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	1.356	Detected	1.701	Detected	1.529	0.020	GT Sens	contig185	contig185	Unknown	GGAGTT	contig185	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig185	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G19200.1		unknown	chr3:664	483.809	478.581	1020.15	998.262	1387.73	1479.46
GT	Sense	Sense	-0.080	Detected	0.080	Detected	0.000	1.639	Detected	1.187	Detected	1.413	0.028	GT Sens	contig186	contig186	Ulp1 prot	GAGAAA	contig186	Solyc10g	Solyc10g	Ulp1 protease family C-termina			contig186	Solyc11g	Ulp1 protease famil		SL2.40ch	AT4G020	PRL, MC	PRL (PR	chr4:901	364.165	484.485	1046.24	1011.23	1473.8	903.985
GT	Sense	Sense	-0.285	Detected	0.285	Detected	0.000	1.907	Detected	2.223	Detected	2.065	0.024	GT Sens	contig187	contig187	Unknown	TAAAAA	contig187	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig187	Solyc03g	Unknown Protein (A		SL2.40ch	ATMG005	MATR	hypothet	chrM:144	79.8047	141.063	135.016	207.102	448.221	468.469
GT	Sense	Sense	-0.949	Comprom	0.949	Detected	0.000	3.593	Detected	3.102	Detected	3.348	0.076	GT Sens	contig19	contig19	Unknown	ATAGGA	contig19	Solyc07g	Solyc07g	Unknown	GO:0045449		contig19	Solyc10g045250.1.1				AT3G02900.1		unknown	chr3:645	2.9857	13.2531	9.91259	18.0183	85.5231	51.0843
GT	Sense	Sense	0.218	Detected	-0.218	Detected	0.000	0.983	Detected	1.607	Detected	1.295	0.077	GT Sens	contig190	contig190	PIF-like tr	CTAGGG	contig190	Solyc04g	Solyc04g	PIF-like transposase (AHRD V1			contig190	Solyc04g	PIF-like transposase		SL2.40ch	AT5G28950.1				43.5701	38.3402	44.0618	38.916	90.9968	117.716
GT	Sense	Sense	0.418	Detected	-0.418	Detected	0.000	0.920	Detected	1.779	Detected	1.349	0.153	GT Sens	contig190	contig190	Rhamnog	CAAAGT	contig190	Solyc04g	Solyc04g	Rhamnog	GO:0030	GO:00302	contig190	Solyc04g	Rhamnog	GO:0030	SL2.40ch	AT1G09890.1		lyase	chr1:321	1386.64	924.97	1489.2	1228.36	2413.51	3674.5
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	1.768	Detected	3.112	Detected	2.440	0.073	GT Sens	contig194	contig194	Auxin-res	ATCAAT	contig194	Solyc11g	Solyc11g	Auxin-responsive protein (AHF			contig194	Solyc11g	Auxin-responsive p		SL2.40ch	AT1G29450.1		auxin-res	chr1:103	20.8113	32.1706	217.917	360.875	99.2372	211.529
GT	Sense	Sense	-0.219	Detected	0.219	Detected	0.000	1.431	Detected	2.865	Detected	2.148	0.103	GT Sens	contig195	contig195	Auxin-ind	TGCTGT	contig195	Solyc11g	Solyc11g	Auxin-induced SAUR-like prote			contig195	Solyc11g	Auxin-induced SAU		SL2.40ch	AT1G29450.1		auxin-res	chr1:103	13.9809	22.543	114.064	181.752	53.9223	122.275
GT	Sense	Sense	-0.864	Detected	0.864	Detected	0.000	2.474	Detected	1.907	Detected	2.191	0.138	GT Sens	contig195	contig195	FAD-bind	GAGCTT	contig195	Solyc10g	Solyc10g	FAD-bind	GO:0050	GO:00506	contig195	Solyc02g	FAD-bind	GO:0009	SL2.40ch	AT5G44410.1		FAD-bind	chr5:178	164.698	649.187	431.109	1205.84	2046.5	1159.55
GT	Sense	Sense	-0.013	Detected	0.013	Detected	0.000	0.848	Detected	1.271	Detected	1.059	0.038	GT Sens	contig195	contig195	Unknown	TAAATT	contig195	Solyc12g	Solyc12g	Unknown	GO:0055	GO:00551	contig195	Solyc12g	Unknown	GO:0016	SL2.40ch	AT2G21420.1		zinc fing	chr2:916	235.854	285.814	396.062	614.25	526.271	592.455
GT	Sense	Sense	-0.487	Comprom	0.487	Detected	0.000	1.250	Detected	1.029	Detected	1.140	0.150	GT Sens	contig196	contig196	Cytochro	GTTGAG	contig196	Solyc02g	Solyc02g	Cytochro	GO:0019	GO:00198	contig196	Solyc02g065210.2.1				AT3G610	CYP76C7	CYP76C	chr3:225	10.2341	23.9443	29.0745	40.7943	41.9406	30.212
GT	Sense	Sense	-0.656	Comprom	0.656	Comprom	0.000	1.665	Detected	2.426	Detected	2.045	0.114	GT Sens	contig196	contig196	Peroxida	ATTCTA	contig196	Solyc07g	Solyc07g	Peroxida	GO:0005	GO:00055	contig196	Solyc07g	Peroxida	GO:0004	SL2.40ch	AT5G64100.1		peroxida	chr5:256	2.6151	7.73249	21.6591	5.96444	16.0635	22.8442
GT	Sense	Sense	-0.315	Comprom	0.315	Comprom	0.000	1.848	Detected	3.039	Detected	2.443	0.068	GT Sens	contig200	contig200	Leucine r	AAGACT	contig200	Solyc12g	Solyc12g	Leucine r	GO:0005	GO:00055	contig200	Solyc12g	LRR rece	GO:0004	SL2.40ch	AT5G41320.1		unknown	chr5:165	2.43442	4.48378	8.44494	12.0593	13.3943	25.6687
GT	Sense	Sense	0.486	Detected	-0.486	Detected	0.000	1.091	Detected	2.241	Detected	1.666	0.157	GT Sens	contig202	contig202	RING fing	TCGGTT	contig202	Solyc02g	Solyc02g	RING fing	GO:0008	GO:00082	contig202	Solyc02g	RING fing	GO:0008	SL2.40ch	AT4G11900.1		S-locus l	chr4:715	24645.3	14961	87310.3	89141.6	46078.7	85831
GT	Sense	Sense	-0.077	Detected	0.077	Detected	0.000	1.024	Detected	1.237	Detected	1.131	0.013	GT Sens	contig203	contig203	Unknown	AAATTA	contig203	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig203	Solyc06g	Unknown Protein (A		SL2.40ch	AT2G400	NRPD1B,	NRPD1B	chr2:167	343.839	455.666	634.143	657.495	906.717	882.277
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	0.969	Detected	1.502	Detected	1.235	0.067	GT Sens	contig203	contig203	Unknown	AATAGA	contig203	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig203	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G105	GTE2	GTE2 (G	chr5:333	34.4081	30.8454	63.9754	58.5353	71.8305	87.2475
GT	Sense	Sense	0.553	Comprom	-0.553	Comprom	0.000	4.211	Detected	1.655	Detected	2.933	0.170	GT Sens	contig204	contig204	Transcrip	TGTTTC	contig204	Solyc02g	Solyc02g	Transcrip	GO:0005	GO:00056	contig204	Solyc02g	Transcrip	GO:0003	SL2.40ch	AT3G28857.1		transcrip	chr3:108	9.58398	5.30273	18.2128	10.162	148.767	21.2324
GT	Sense	Sense	-0.509	Detected	0.509	Detected	0.000	2.739	Detected	1.136	Detected	1.938	0.178	GT Sens	contig205	contig205	Ovate pro	CATTAT	contig205	Solyc02g	Solyc02g	Ovate protein (AHRD V1 **-- O8			contig205	Solyc02g	Ovate protein (AHRI		SL2.40ch	AT5G16290.2		acetolac	chr5:533	129.758	312.868	541.286	461.245	1515.14	418.791
GT	Sense	Sense	0.057	Detected	-0.057	Detected	0.000	1.549	Detected	1.294	Detected	1.421	0.010	GT Sens	contig207	contig207	Unknown	TGTCAT	contig207	Solyc03g	Solyc03g	Unknown	GO:0005	GO:00056	contig207	Solyc03g	Unknown	GO:0005	SL2.40ch	AT1G042	SHY2, IAA	SHY2 (SH	chr1:112	82.1317	90.3089	131.949	196.526	283.89	199.657
GT	Sense	Sense	0.249	Detected	-0.249	Detected	0.000	1.094	Detected	1.766	Detected	1.430	0.076	GT Sens	contig208	contig208	Unknown	TGTTGC	contig208	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig208	Solyc07g	Unknown Protein (A		SL2.40ch	AT3G21390.1		mitochon	chr3:753	19.8503	16.7391	65.2338	89.8642	43.8424	58.6228
GT	Sense	Sense	-0.460	Detected	0.460	Detected	0.000	2.611	Detected	1.841	Detected	2.226	0.066	GT Sens	contig209	contig209	1-aminoc	GACTAC	contig209	Solyc09g	Solyc09g	1-aminocyclopropane-1-carbo			contig209	Solyc09g	1-aminocyclopropa		SL2.40ch	AT3G49030.1		F-box far	chr3:181	95.2779	214.698	353.34	603.73	984.604	484.361
GT	Sense	Sense	-0.489	Comprom	0.489	Detected	0.000	1.131	Detected	2.824	Detected	1.978	0.181	GT Sens	contig209	contig209	Exocyst c	CAGCAG	contig209	Solyc10g	Solyc10g	Exocyst c	GO:0005	GO:00057	contig209	Solyc04g	Transcrip	GO:0003	SL2.40ch	AT5G28610.1		FUNCTIO	chr5:106	7.56705	17.7428	13.8871	20.415	28.5794	77.6035
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	2.153	Detected	1.259	Detected	1.706	0.063	GT Sens	contig210	contig210	Wound in	TAGAAG	contig210	Solyc07g	Solyc07g	Wound induced protein (AHRD			contig210	Solyc07g	Wound induced pro		SL2.40ch	AT4G10270.1		wound-r	chr4:637	330.644	375.088	859.817	666.982	1764.65	796.797
GT	Sense	Sense	-0.146	Detected	0.146	Detected	0.000	1.050	Detected	1.966	Detected	1.508	0.088	GT Sens	contig210	contig210	1-aminoc	CCCAAT	contig210	Solyc04g	Solyc04g	1-aminoc	GO:0016	GO:00164	contig210	Solyc04g	1-aminoc	GO:0009	SL2.40ch	AT2G30840.1		2-oxoglu	chr2:131	513.572	748.953	1560.47	2091.59	1446.53	2291.26
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	1.292	Detected	0.911	Detected	1.102	0.033	GT Sens	contig212	contig212	NBS resis	TCCTTA	contig212	Solyc05g	Solyc05g	NBS resis	GO:0006	GO:00069	contig212	Solyc05g	Cc-nbs-lr	GO:0006	SL2.40ch	AT5G16880.2		VHS dom	chr5:554	20.1651	21.5905	2.17953	2.17818	57.5741	37.0856
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	1.307	Detected	1.585	Detected	1.446	0.010	GT Sens	contig212	contig212	Unknown	GGAGTT	contig212	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig212	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G19200.1		unknown	chr3:664	449.58	511.089	952.923	901.496	1336.2	1359.75
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	1.411	Detected	1.954	Detected	1.682	0.036	GT Sens	contig213	contig213	Cullin 1-li	GATAAC	contig213	Solyc01g	Solyc01g	Cullin 1-li	GO:0030	GO:00303	contig213	Solyc01g	Cullin 1-li	GO:0030	SL2.40ch	AT4G025	ATCUL1,	ATCUL1	chr4:112	45.2426	41.5538	61.7479	89.4594	129.841	158.789
GT	Sense	Sense	0.372	Detected	-0.372	Detected	0.000	1.983	Detected	2.417	Detected	2.200	0.036	GT Sens	contig214	contig214	Cortical c	TAGTTT	contig214	Solyc08g	Solyc08g	Cortical c	GO:0008	GO:00082	contig214	Solyc08g	Cortical c	GO:0008	SL2.40ch	AT2G45180.1		protease	chr2:186	118.955	84.5032	316.97	205.251	446.506	506.332
GT	Sense	Sense	0.049	Detected	-0.049	Detected	0.000	0.936	Detected	1.160	Detected	1.048	0.013	GT Sens	contig215	contig215	Unknown	CAATGC	contig215	Solyc03g	Solyc03g	Unknown	GO:0008	GO:00082	contig215	Solyc12g	Mutator-li	GO:0008	SL2.40ch	AT2G35880.1		FUNCTIO	chr2:150	61.9654	68.8864	98.4966	95.8442	140.847	138.009
GT	Sense	Sense	-0.173	Detected	0.173	Detected	0.000	1.197	Detected	0.807	Detected	1.002	0.062	GT Sens	contig216	contig216	Pentatric	TAATCT	contig216	Solyc02g	Solyc02g	Pentatricopeptide repeat-conta			contig216	Solyc02g	Pentatricopeptide re		SL2.40ch	AT4G36680.1				45.1999	68.4367	70.7997	112.216	143.611	92.021
GT	Sense	Sense	-0.064	Comprom	0.064	Comprom	0.000	1.324	Detected	7.083	Detected	4.203	0.282	GT Sens	contig217	contig217	Unknown	AGTAAG	contig217	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig217	Solyc10g	Nbs-lrr, resistance p		SL2.40ch	AT1G063	ACX6	ACX6 (AC	chr1:192	5.28684	6.87605	12.7951	8.7207	17.0032	772.801
GT	Sense	Sense	-0.341	Comprom	0.341	Comprom	0.000	1.997	Detected	2.230	Detected	2.114	0.028	GT Sens	contig219	contig219	Nitrate tra	GGAGTA	contig219	Solyc06g	Solyc06g	Nitrate tra	GO:0008	GO:00080	contig219	Solyc06g	Nitrate tra	GO:0008	SL2.40ch	AT3G45680.1		proton-d	chr3:167	2.94729	5.62747	2.28937	15.5798	18.3173	18.0709
GT	Sense	Sense	0.195	Detected	-0.195	Detected	0.000	0.913	Detected	1.242	Detected	1.077	0.052	GT Sens	contig220	contig220	Short-cha	GGTTAA	contig220	Solyc01g	Solyc01g	Short-cha	GO:0008	GO:00081	contig220	Solyc01g	Short-cha	GO:0008	SL2.40ch	AT4G265	ATOPT5,	OPT5 (O	chr4:134	23.4007	21.2491	36.4635	34.3242	47.309	49.853
GT	Sense	Sense	0.325	Detected	-0.325	Detected	0.000	1.144	Detected	1.103	Detected	1.124	0.075	GT Sens	contig221	contig221	Unknown	GAAAAT	contig221	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig221	Solyc07g041670.1.1				AT1G69550.1				61.6338	46.7844	104.211	92.4925	133.683	109.075
GT	Sense	Sense	-0.184	Detected	0.184	Detected	0.000	1.186	Detected	0.965	Detected	1.076	0.038	GT Sens	contig221	contig221	Unknown	TACATA	contig221	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig221	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G018	PEX11C	PEX11C	chr1:296	13.1029	20.1338	45.7246	42.0217	41.6373	29.9738
GT	Sense	Sense	-0.102	Detected	0.102	Detected	0.000	1.027	Detected	1.363	Detected	1.195	0.026	GT Sens	contig222	contig222	Subtilisin	TAGTTT	contig222	Solyc01g	Solyc01g	Subtilisin	GO:0006	GO:00065	contig222	Solyc01g	Subtilisin	GO:0006	SL2.40ch	AT5G59130.1		subtilase	chr5:238	1882.27	2581.37	4615.57	3538.99	5061.12	5360.33
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	0.916	Detected	1.684	Detected	1.300	0.078	GT Sens	contig222	contig222	Sister-chr	CTCATT	contig222	Solyc05g	Solyc05g	Sister-chromatide cohesion pr			contig222	Solyc05g	Sister-chromatide c		SL2.40ch	AT4G02410.1		lectin pro	chr4:106	13.4806	15.2612	23.2855	20.0529	30.4775	43.5633
GT	Sense	Sense	-0.388	Comprom	0.388	Comprom	0.000	2.320	Detected	2.933	Detected	2.626	0.034	GT Sens	contig223	contig223	Unknown	GATGAG	contig223	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig223	Solyc06g	En/Spm-like transpo		SL2.40ch	AT5G584	ATEXO70	ATEXO7	chr5:236	4.80727	9.80413	26.7755	23.3283	38.6053	49.5652
GT	Sense	Sense	0.552	Detected	-0.552	Detected	0.000	1.951	Detected	2.422	Detected	2.186	0.068	GT Sens	contig223	contig223	Transcrip	AGGAGA	contig223	Solyc03g	Solyc03g	Transcrip	GO:0045449		contig223	Solyc11g	Cellular n	GO:0008	SL2.40ch	AT4G37250.1		leucine-r	chr4:175	89.5906	49.6211	222.928	206.555	290.383	337.842
GT	Sense	Sense	0.246	Detected	-0.246	Comprom	0.000	0.917	Detected	1.091	Detected	1.004	0.062	GT Sens	contig223	contig223	Periaxin-l	AGGAAG	contig223	Solyc01g	Solyc01g	Periaxin-like protein (AHRD V1			contig223	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G42090.1		LOCATE	chr5:168	14.0596	11.8946	13.9019	9.41891	27.5104	26.0456
GT	Sense	Sense	0.213	Detected	-0.213	Detected	0.000	1.094	Detected	1.009	Detected	1.052	0.040	GT Sens	contig225	contig225	Subtilisin	AAGTTG	contig225	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:00042	contig225	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT3G52700.1		unknown	chr3:195	61.3616	54.356	95.0043	75.7378	138.869	109.904
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	1.081	Detected	2.301	Detected	1.691	0.109	GT Sens	contig225	contig225	Pathogen	TGAAGA	contig225	Solyc02g	Solyc02g	Pathogen-related protein relat			contig225	Solyc12g	Pathogenesis-relate		SL2.40ch	AT5G55620.1				59.5282	68.1208	190.536	131.767	151.728	296.722
GT	Sense	Sense	-0.825	Comprom	0.825	Comprom	0.000	1.977	Detected	2.396	Detected	2.186	0.124	GT Sens	contig225	contig225	Sulfotran	TGGAGG	contig225	Solyc05g	Solyc05g	Sulfotran	GO:0008	GO:00081	contig225	Solyc05g	Sulfotran	GO:0008	SL2.40ch	AT5G49260.1		unknown	chr5:199	2.82833	10.5614	8.01367	7.69121	24.2302	27.2077
GT	Sense	Sense	-0.166	Comprom	0.166	Comprom	0.000	0.800	Detected	1.985	Detected	1.393	0.152	GT Sens	contig226	contig226	Structura	TTCATT	contig226	Solyc02g	Solyc02g	Structural maintenance of chro			contig226	Solyc02g	Structural maintena		SL2.40ch	AT4G398	PXA1, PE	PXA1 (PE	chr4:184	4.38996	6.58095	7.75163	12.9455	10.5452	20.1163
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	0.931	Detected	1.135	Detected	1.033	0.025	GT Sens	contig227	contig227	Unknown	TATGAA	contig227	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig227	Solyc09g	Unknown Protein (A		SL2.40ch	AT3G11850.2		unknown	chr3:373	289.81	414.572	517.721	566.477	744.69	719.705
GT	Sense	Sense	0.155	Detected	-0.155	Detected	0.000	1.008	Detected	1.014	Detected	1.011	0.023	GT Sens	contig227	contig227	Transcrip	GTTGCT	contig227	Solyc06g	Solyc06g	Transcrip	GO:0005	GO:00056	contig227	Solyc06g	Transcrip	GO:0005	SL2.40ch	AT4G118	AGL14	AGL14 (a	chr4:714	123.901	118.993	153.821	258.462	275.062	231.879
GT	Sense	Sense	-0.180	Detected	0.180	Detected	0.000	2.146	Detected	2.064	Detected	2.105	0.008	GT Sens	contig228	contig228	Unknown	GAGATC	contig228	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig228	Solyc07g	Unknown Protein (A		SL2.40ch	AT3G19520.2				17.5759	26.8508	39.4257	63.5067	108.301	85.8692
GT	Sense	Sense	0.324	Detected	-0.324	Detected	0.000	1.129	Detected	1.212	Detected	1.170	0.070	GT Sens	contig228	contig228	Lysine ke	GCCTTT	contig228	Solyc07g	Solyc07g	Lysine ketoglutarate reductase			contig228	Solyc07g	Lysine ketoglutarate		SL2.40ch	AT5G023	PRT6	PRT6 (PF	chr5:474	117.743	89.4501	178.39	164.249	252.882	224.742
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	1.060	Detected	1.730	Detected	1.395	0.061	GT Sens	contig229	contig229	Receptor	AATAAT	contig229	Solyc02g	Solyc02g	Receptor	GO:0006	GO:00064	contig229	Solyc02g	Receptor	GO:0006	SL2.40ch	AT4G23240.1				40.2484	39.6261	180.228	125.903	93.7963	125.226
GT	Sense	Sense	0.744	Comprom	-0.744	Comprom	0.000	2.845	Detected	2.591	Detected	2.718	0.069	GT Sens	contig231	contig231	Omega-6	GCATGT	contig231	Solyc04g	Solyc04g	Omega-6	GO:0042	GO:00423	contig231	Solyc04g	Omega-6	GO:0042	SL2.40ch	AT5G61510.1		NADP-de	chr5:247	8.68687	3.68826	41.6068	8.94218	45.8131	32.2555
GT	Sense	Sense	0.250	Detected	-0.250	Comprom	0.000	0.990	Detected	1.041	Detected	1.015	0.056	GT Sens	contig231	contig231	Solute ca	GGGATT	contig231	Solyc02g	Solyc02g	Solute ca	GO:0015	GO:00155	contig231	Solyc02g	Solute ca	GO:0015	SL2.40ch	AT2G18480.1		mannitol	chr2:800	13.0725	11.0105	5.51161	9.68879	26.838	23.337
GT	Sense	Sense	0.112	Detected	-0.112	Detected	0.000	1.407	Detected	1.243	Detected	1.325	0.011	GT Sens	contig231	contig231	Unknown	CCAAAG	contig231	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig231	Solyc07g	Hypersen	GO:0033	SL2.40ch	AT5G202	DIN10	DIN10 (D	chr5:683	198.581	202.499	267.014	187.285	598.933	448.801
GT	Sense	Sense	0.487	Detected	-0.487	Detected	0.000	0.867	Detected	1.381	Detected	1.124	0.178	GT Sens	contig232	contig232	Cytochro	CTTTGT	contig232	Solyc07g	Solyc07g	Cytochro	GO:0019	GO:00198	contig232	Solyc07g	Cytochro	GO:0019	SL2.40ch	AT4G395	CYP96A1	CYP96A1	chr4:183	947.673	574.196	1458.54	1210.68	1515.68	1816.69
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	1.810	Detected	1.655	Detected	1.733	0.004	GT Sens	contig233	contig233	Endonuc	CTTAGA	contig233	Solyc07g	Solyc07g	Endonuclease/exonuclease/pl			contig233	Solyc07g	Endonuclease/exon		SL2.40ch	AT5G618	GUT1	GUT1: ca	chr5:248	1006.65	1351.23	2634.85	2493.96	4607.91	3472.39
GT	Sense	Sense	0.411	Detected	-0.411	Comprom	0.000	1.152	Detected	1.457	Detected	1.304	0.097	GT Sens	contig234	contig234	Alpha-hyd	GCATTG	contig234	Solyc01g	Solyc01g	Alpha-hyd	GO:0008	GO:00080	contig234	Solyc01g	Alpha-hyd	GO:0008	SL2.40ch	AT4G22720.2		glycopro	chr4:119	13.436	9.04983	19.8186	6.06089	27.6044	28.617
GT	Sense	Sense	-0.824	Detected	0.824	Detected	0.000	5.259	Detected	1.121	Detected	3.190	0.288	GT Sens	contig234	contig234	Hydroxyc	AATTCA	contig234	Solyc05g	Solyc05g	Hydroxyc	GO:0016	GO:00167	contig234	Solyc05g	Hydroxyc	GO:0016	SL2.40ch	AT2G39980.1		transfera	chr2:166	56.1903	209.773	811.211	661.295	4681.69	223.32
GT	Sense	Sense	-0.510	Detected	0.510	Detected	0.000	1.851	Detected	2.715	Detected	2.283	0.076	GT Sens	contig235	contig235	Subtilisin	CTACCA	contig235	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:00042	contig235	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT3G19540.1		unknown	chr3:678	92.9482	224.547	592.814	449.552	587.21	896.671
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	1.961	Detected	2.175	Detected	2.068	0.005	GT Sens	contig236	contig236	Unknown	AGAAGA	contig236	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig236	Solyc03g	Iron-sulfu	GO:0008	SL2.40ch	AT1G01240.3				133.536	136.528	299.544	318.496	592.213	576.598
GT	Sense	Sense	0.000	Comprom	0.000	Comprom	0.000	1.850	Detected	1.786	Detected	1.818	0.000	GT Sens	contig238	contig238	Unknown	AAACAG	contig238	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig238	Solyc12g	Unknown Protein (A		SL2.40ch	AT4G14970.1		unknown	chr4:855	5.27408	6.27869	7.69019	7.98673	23.3716	18.764
GT	Sense	Sense	-0.591	Detected	0.591	Detected	0.000	2.099	Detected	2.672	Detected	2.385	0.068	GT Sens	contig238	contig238	Chymotry	CCATAG	contig238	Solyc09g	Solyc09g	Chymotry	GO:0009	GO:00096	contig238	Solyc09g	Chymotry	GO:0009	SL2.40ch	AT5G28350.2		FUNCTIO	chr5:103	237.796	642.495	1082.11	254.311	1886.03	2354.77
GT	Sense	Sense	-0.640	Comprom	0.640	Comprom	0.000	1.704	Detected	2.311	Detected	2.008	0.105	GT Sens	contig238	contig238	Solute ca	TGAAGA	contig238	Solyc04g	Solyc04g	Solute ca	GO:0008	GO:00080	contig238	Solyc04g	Solute ca	GO:0008	SL2.40ch	AT5G46040.1		proton-d	chr5:186	2.42952	7.02332	12.4448	16.6217	15.1638	19.3866
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	1.813	Detected	2.874	Detected	2.343	0.048	GT Sens	contig239	contig239	Chromod	GAAGTG	contig239	Solyc07g	Solyc07g	Chromod	GO:0008	GO:00082	contig239	Solyc09g	UDP-gluc	GO:0008	SL2.40ch	AT3G52700.1		unknown	chr3:195	258.235	288.985	449.793	615.222	1081.12	1893.3
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	1.877	Detected	2.378	Detected	2.128	0.017	GT Sens	contig240	contig240	Calcium-l	GTTGAT	contig240	Solyc10g	Solyc10g	Calcium-l	GO:0005	GO:00052	contig240	Solyc10g	Calcium-l	GO:0005	SL2.40ch	AT5G544	PBP1	PBP1 (PI	chr5:221	616.689	616.66	2986.48	2876.54	2551.64	3031.56
GT	Sense	Sense	1.064	Detected	-1.064	Detected	0.000	2.934	Detected	1.371	Detected	2.153	0.245	GT Sens	contig240	contig240	EIN3-bind	CACAAG	contig240	Solyc05g	Solyc05g	EIN3-binding F-box protein 1 (/			contig240	Solyc07g	SCF E3 u	GO:0005	SL2.40ch	AT4G02750.1		pentatric	chr4:122	2313.01	629.823	3360.54	2724.77	10392.9	2951.45
GT	Sense	Sense	0.217	Detected	-0.217	Detected	0.000	0.981	Detected	1.105	Detected	1.043	0.044	GT Sens	contig243	contig243	Unknown	GCGTGG	contig243	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig243	Solyc02g	Unknown Protein (A		SL2.40ch	AT1G03300.1		agenet d	chr1:811	283.314	249.668	520.806	466.627	591.512	540.852
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	1.863	Detected	2.528	Detected	2.196	0.022	GT Sens	contig246	contig246	Unknown	GACTTG	contig246	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig246	Solyc05g024230.1.1				AT4G344	CHB3, AT	CHB3: DI	chr4:164	112.91	137.626	100.865	94.2237	510.9	679.711
GT	Sense	Sense	-0.578	Detected	0.578	Detected	0.000	1.664	Detected	2.795	Detected	2.229	0.110	GT Sens	contig247	contig247	Subtilisin	ACATTT	contig247	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:00042	contig247	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT3G19540.1		unknown	chr3:678	231.964	615.589	1592.57	1143.95	1348.51	2480.28
GT	Sense	Sense	0.478	Detected	-0.478	Detected	0.000	1.289	Detected	2.601	Detected	1.945	0.139	GT Sens	contig247	contig247	Unknown	CTGTAT	contig247	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig247	Solyc04g	Subtilisin	GO:0004	SL2.40ch	AT1G64300.2		protein k	chr1:238	15305.3	9398.31	74677.2	75993.2	33014.8	68823.1
GT	Sense	Sense	0.557	Comprom	-0.557	Comprom	0.000	5.115	Detected	2.729	Detected	3.922	0.097	GT Sens	contig248	contig248	Unknown	GACAGA	contig248	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig248	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G08510.1		pentatric	chr5:275	9.3104	5.11747	24.0424	14.8214	269.437	43.2842
GT	Sense	Sense	-0.005	Detected	0.005	Detected	0.000	3.316	Detected	0.963	Detected	2.139	0.211	GT Sens	contig249	contig249	Alcohol d	GAATTG	contig249	Solyc09g	Solyc09g	Alcohol dehydrogenase (AHRD			contig249	Solyc09g	Alcohol dehydroger		SL2.40ch	AT1G01760.1		RNA bind	chr1:276	16.3479	19.5956	28.1514	35.5671	200.73	32.987
GT	Sense	Sense	0.207	Detected	-0.207	Detected	0.000	1.372	Detected	1.965	Detected	1.668	0.044	GT Sens	contig249	contig249	Os03g08	GGAAGG	contig249	Solyc09g	Solyc09g	Os03g0816700 protein (Fragm			contig249	Solyc09g	Os03g0816700 prot		SL2.40ch	AT3G556	ATDFD	ATDFD (	chr3:206	76.7831	68.6248	160.989	166.672	211.589	267.919
GT	Sense	Sense	0.435	Detected	-0.435	Detected	0.000	1.091	Detected	2.482	Detected	1.787	0.161	GT Sens	contig251	contig251	Unknown	GAGTTG	contig251	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig251	Solyc01g	Unknown Protein (A		SL2.40ch	AT1G11500.1				19618.3	12779	91832.7	96919.6	38000.5	83628.3
GT	Sense	Sense	0.335	Detected	-0.335	Detected	0.000	1.807	Detected	1.997	Detected	1.902	0.032	GT Sens	contig252	contig252	Yippee-lik	CAGAAA	contig252	Solyc03g	Solyc03g	Yippee-lik	GO:0005	GO:00055	contig252	Solyc03g	Yippee-lik	GO:0005	SL2.40ch	AT2G40110.1		yippee fa	chr2:167	136.709	102.292	257.126	284.177	465.987	446.342
GT	Sense	Sense	0.418	Comprom	-0.418	Comprom	0.000	1.102	Detected	1.827	Detected	1.464	0.118	GT Sens	contig253	contig253	Amino ac	TGGTAT	contig253	Solyc05g	Solyc05g	Amino acid transporter (AHRD			contig253	Solyc05g	Amino ac	GO:0015	SL2.40ch	AT5G14470.1				11.3516	7.57396	2.173	4.17782	22.4149	31.1007
GT	Sense	Sense	-0.065	Detected	0.065	Detected	0.000	2.011	Detected	1.282	Detected	1.646	0.047	GT Sens	contig253	contig253	Cytochro	AAATGA	contig253	Solyc12g	Solyc12g	Cytochro	GO:0019	GO:00198	contig253	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT1G25360.1		pentatric	chr1:889	35.6651	46.4679	93.4848	67.7343	184.783	93.5964
GT	Sense	Sense	-0.077	Comprom	0.077	Comprom	0.000	1.364	Detected	1.912	Detected	1.638	0.029	GT Sens	contig255	contig255	2-isopren	TGAGTA	contig255	Solyc08g	Solyc08g	2-isopren	GO:0003	GO:00038	contig255	Solyc08g	2-isopren	GO:0003	SL2.40ch	AT3G08020.1		protein b	chr3:255	6.55766	8.68488	20.1535	18.8354	21.8766	26.8504
GT	Sense	Sense	-0.797	Comprom	0.797	Comprom	0.000	5.526	Detected	2.133	Detected	3.830	0.178	GT Sens	contig256	contig256	Unknown	GCCATT	contig256	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig256	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G136	PTAC5	PTAC5 (F	chr4:794	2.52191	9.06669	30.5758	19.1833	248.27	19.8374
GT	Sense	Sense	0.270	Comprom	-0.270	Comprom	0.000	0.861	Detected	1.181	Detected	1.021	0.083	GT Sens	contig256	contig256	Mutator-li	TATGGT	contig256	Solyc09g	Solyc09g	Mutator-li	GO:0008	GO:00082	contig256	Solyc10g	Mutator-li	GO:0008	SL2.40ch	#N/A	#N/A	#N/A	#N/A	9.53419	7.80738	12.5929	12.5141	17.6506	18.4919
GT	Sense	Sense	0.440	Detected	-0.440	Detected	0.000	1.259	Detected	1.438	Detected	1.349	0.095	GT Sens	contig256	contig256	Homeobo	ACTCAA	contig256	Solyc07g	Solyc07g	Homeobox-leucine zipper prot			contig256	Solyc09g	GTPase c	GO:0005	SL2.40ch	AT3G47833.1				4098.64	2651.76	6841.23	6542.11	8888.73	8448.52
GT	Sense	Sense	0.437	Comprom	-0.437	Comprom	0.000	1.252	Detected	1.871	Detected	1.562	0.100	GT Sens	contig256	contig256	Sister-chr	AATCAT	contig256	Solyc09g	Solyc09g	Sister-chromatide cohesion pr			contig256	Solyc09g037050.1.1				AT4G02410.1		lectin pro	chr4:106	8.72836	5.66845	9.4905	10.6804	18.8733	24.3352
GT	Sense	Sense	-0.232	Detected	0.232	Detected	0.000	1.800	Detected	1.692	Detected	1.746	0.018	GT Sens	contig261	contig261	Ribosoma	TTGAAG	contig261	Solyc11g	Solyc11g	Ribosoma	GO:0005	GO:00058	contig261	Solyc10g	30S ribos	GO:0005	SL2.40ch	AT5G02960.1		40S ribos	chr5:693	30.5274	50.1061	53.3353	75.4091	153.391	119.505
GT	Sense	Sense	-0.961	Comprom	0.961	Detected	0.000	2.138	Detected	2.040	Detected	2.089	0.162	GT Sens	contig262	contig262	Acid phos	CACTTA	contig262	Solyc06g	Solyc06g	Acid phos	GO:0003	GO:00039	contig262	Solyc06g	Acid phos	GO:0003	SL2.40ch	AT5G247	VSP2, AT	VSP2 (VE	chr5:850	3.46451	15.6281	22.595	21.2568	36.49	28.618
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	0.887	Detected	1.164	Detected	1.026	0.025	GT Sens	contig264	contig264	Receptor	AGCACT	contig264	Solyc02g	Solyc02g	Receptor	GO:0006	GO:00064	contig264	Solyc02g	S-receptor kinase (/		SL2.40ch	AT4G101	ATSPS4F	ATSPS4	chr4:631	150.209	158.346	323.35	275.408	321.316	326.785
GT	Sense	Sense	0.062	Comprom	-0.062	Comprom	0.000	1.529	Detected	2.020	Detected	1.774	0.020	GT Sens	contig264	contig264	Phenylala	GGTTTT	contig264	Solyc10g	Solyc10g	Phenylala	GO:0009	GO:00090	contig264	Solyc06g	Phenylala	GO:0009	SL2.40ch	AT2G370	pal1, ATP	pal1 (Phe	chr2:155	5.30281	5.79459	14.1385	15.3761	18.0151	21.261
GT	Sense	Sense	0.141	Detected	-0.141	Detected	0.000	1.305	Detected	1.329	Detected	1.317	0.011	GT Sens	contig266	contig266	Pyridine r	TTGATA	contig266	Solyc00g	Solyc00g	Pyridine nucleotide-disulfide o			contig266	Solyc06g	UPF0139	GO:0005	SL2.40ch	AT4G15010.2		mitochon	chr4:857	122.427	119.949	214.183	202.94	337.34	287.908
GT	Sense	Sense	0.318	Detected	-0.318	Detected	0.000	1.086	Detected	1.251	Detected	1.169	0.071	GT Sens	contig267	contig267	Mutator-l	ATGGGG	contig267	Solyc09g	Solyc09g	Mutator-li	GO:0008	GO:00082	contig267	Solyc10g	Mutator-like transpo		SL2.40ch	AT5G20980.2				92.5888	70.9448	124.661	122.711	193.818	182.417
GT	Sense	Sense	-0.146	Comprom	0.146	Detected	0.000	0.822	Detected	1.646	Detected	1.234	0.106	GT Sens	contig268	contig268	Thioester	ACAAAC	contig268	Solyc03g	Solyc03g	Thioester	GO:0005	GO:00055	contig268	Solyc03g	Thioester	GO:0005	SL2.40ch	AT2G47250.1				10.8676	15.8489	21.9924	20.0316	26.1291	38.8461
GT	Sense	Sense	0.451	Detected	-0.451	Detected	0.000	1.074	Detected	0.996	Detected	1.035	0.150	GT Sens	contig269	contig269	Aminotra	CCAGAA	contig269	Solyc07g	Solyc07g	Aminotra	GO:0030	GO:00301	contig269	Solyc07g	Aminotra	GO:0030	SL2.40ch	AT3G222	POP2, GA	POP2 (P	chr3:783	7792.78	4962.44	13893.5	9794.03	14750.7	11726.2
GT	Sense	Sense	-0.151	Detected	0.151	Detected	0.000	1.198	Detected	1.131	Detected	1.164	0.017	GT Sens	contig270	contig270	Cytochro	TTAGCA	contig270	Solyc00g	Solyc00g	Cytochro	GO:0019	GO:00198	contig270	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT1G25360.1		pentatric	chr1:889	13.4254	19.7002	30.0885	14.2086	42.0154	33.675
GT	Sense	Sense	0.380	Detected	-0.380	Detected	0.000	1.118	Detected	1.512	Detected	1.315	0.092	GT Sens	contig272	contig272	Unknown	ACCAGC	contig272	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig272	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G44440.1				70.9165	49.8203	96.3069	83.9566	145.344	160.342
GT	Sense	Sense	-0.241	Detected	0.241	Detected	0.000	1.565	Detected	1.742	Detected	1.653	0.023	GT Sens	contig273	contig273	Dof zinc f	GTCTTT	contig273	Solyc00g	Solyc00g	Dof zinc finger protein DOF2.4			contig273	Solyc02g	GDSL est	GO:0004	SL2.40ch	AT4G03153.1		kinase in	chr4:139	15.6704	26.0723	37.5518	42.1831	67.3518	63.9097
GT	Sense	Sense	0.226	Detected	-0.226	Detected	0.000	1.127	Detected	1.665	Detected	1.396	0.058	GT Sens	contig274	contig274	F-box fan	TTTTTT	contig274	Solyc04g	Solyc04g	F-box family protein (AHRD V1			contig274	Solyc11g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	1846.56	1605.93	3773.4	4017.45	4236.24	5164.23
GT	Sense	Sense	0.482	Detected	-0.482	Detected	0.000	1.965	Detected	2.308	Detected	2.137	0.053	GT Sens	contig274	contig274	Hydroxyp	TCTGAG	contig274	Solyc02g	Solyc02g	Hydroxyproline-rich glycoprot			contig274	Solyc02g	Hydroxyproline-rich		SL2.40ch	AT5G65660.1		hydroxyp	chr5:262	136.499	83.3342	182.823	185.409	469.097	499.514
GT	Sense	Sense	1.289	Detected	-1.289	Comprom	0.000	0.908	Detected	1.690	Detected	1.299	0.437	GT Sens	contig277	contig277	Cytochro	ATTCCG	contig277	Solyc03g	Solyc03g	Cytochro	GO:0020	GO:00200	contig277	Solyc03g	Cytochro	GO:0019	SL2.40ch	AT3G201	CYP705A	CYP705	chr3:702	45.9548	9.15791	17.2279	11.5819	43.3559	62.6073
GT	Sense	Sense	-0.287	Detected	0.287	Detected	0.000	1.237	Detected	2.787	Detected	2.012	0.135	GT Sens	contig277	contig277	Auxin-res	TTCTTG	contig277	Solyc11g	Solyc11g	Auxin-responsive protein (AHF			contig277	Solyc11g	Auxin-responsive p		SL2.40ch	AT1G29450.1		auxin-res	chr1:103	27.8208	49.3365	233.029	372.856	98.3591	241.746
GT	Sense	Sense	0.194	Detected	-0.194	Detected	0.000	3.949	Detected	3.207	Detected	3.578	0.013	GT Sens	contig278	contig278	Cellulose	CTTTTG	contig278	Solyc05g	Solyc05g	Cellulose	GO:0016	GO:00167	contig278	Solyc10g	Cytochro	GO:0019	SL2.40ch	AT2G43310.1				44.0259	40.0464	182.435	223.151	730.639	366.684
GT	Sense	Sense	0.009	Detected	-0.009	Detected	0.000	0.850	Detected	1.560	Detected	1.205	0.077	GT Sens	contig280	contig280	Cytochro	TAGTCC	contig280	Solyc09g	Solyc09g	Cytochro	GO:0019	GO:00198	contig280	Solyc09g	Cytochro	GO:0019	SL2.40ch	AT3G262	CYP71B2	CYP71B	chr3:963	205.29	241.367	529.923	463.265	452.127	620.609
GT	Sense	Sense	0.794	Comprom	-0.794	Comprom	0.000	2.332	Detected	5.429	Detected	3.880	0.156	GT Sens	contig280	contig280	Ethylene	GGGAAC	contig280	Solyc03g	Solyc03g	Ethylene	GO:0005	GO:00055	contig280	Solyc03g	Ethylene	GO:0005	SL2.40ch	AT5G472	ERF5, AT	ERF5 (ET	chr5:191	12.6049	4.99158	27.3376	17.3595	44.9819	323.101
GT	Sense	Sense	-0.056	Detected	0.056	Detected	0.000	2.571	Detected	2.691	Detected	2.631	0.001	GT Sens	contig282	contig282	F-box fan	GTTGAT	contig282	Solyc05g	Solyc05g	F-box family protein (AHRD V1			contig282	Solyc05g	F-box family protein		SL2.40ch	AT2G362	ABI5, GIA	ABI5 (AB	chr2:152	1542.79	1985.81	5207.79	5406.73	11716.4	10690.1
GT	Sense	Sense	0.363	Comprom	-0.363	Comprom	0.000	1.613	Detected	1.139	Detected	1.376	0.087	GT Sens	contig283	contig283	Mutator-li	TATTTAT	contig283	Solyc09g	Solyc09g	Mutator-li	GO:0008	GO:00082	contig283	Solyc09g	Mutator-li	GO:0008	SL2.40ch	AT1G604	ATVPS34	ATVPS3	chr1:222	7.73678	5.56888	10.408	5.9888	22.6134	13.6671
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	1.576	Detected	2.229	Detected	1.902	0.029	GT Sens	contig284	contig284	Unknown	GCTGAG	contig284	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig284	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G571	ATPAP28	PAP28 (F	chr5:231	122.923	137.504	153.178	132.536	436.654	576.257
GT	Sense	Sense	0.513	Comprom	-0.513	Comprom	0.000	1.099	Detected	2.349	Detected	1.724	0.167	GT Sens	contig284	contig284	Transpor	CATGGT	contig284	Solyc05g	Solyc05g	Transpor	GO:0055	GO:00550	contig284	Solyc05g	Transpor	GO:0005	SL2.40ch	AT5G10190.1		transpor	chr5:319	6.67491	3.90274	12.9283	9.33097	12.3135	24.5804
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	1.702	Detected	1.967	Detected	1.835	0.007	GT Sens	contig285	contig285	CTP synt	TGAAAG	contig285	Solyc02g	Solyc02g	CTP synthase (AHRD V1 *-*- D7			contig285	Solyc02g	CTP synthase (AHR		SL2.40ch	AT1G30820.1		CTP synt	chr1:109	166.487	179.708	361.434	238.248	634.021	639.424
GT	Sense	Sense	-0.116	Detected	0.116	Detected	0.000	1.581	Detected	1.635	Detected	1.608	0.005	GT Sens	contig285	contig285	Hcr2-p4.1	CAGAGT	contig285	Solyc01g	Solyc01g	Hcr2-p4.1 (AHRD V1 ***- O4G2V			contig285	Solyc01g	Hcr2-p4.1 (AHRD V1		SL2.40ch	AT4G22230.1				75.7202	105.863	238.45	208.026	301.789	262.84
GT	Sense	Sense	-0.566	Comprom	0.566	Comprom	0.000	1.337	Detected	2.090	Detected	1.713	0.128	GT Sens	contig286	contig286	Unknown	AATCTT	contig286	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig286	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G40030.1		protein k	chr5:160	3.34481	8.72793	8.61741	5.92446	15.3726	21.7469
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	1.518	Detected	1.195	Detected	1.356	0.029	GT Sens	contig287	contig287	MuDR far	GAGTTT	contig287	Solyc06g	Solyc06g	MuDR family transposase con			contig287	Solyc12g	Unknown	GO:0016	SL2.40ch	AT5G46470.1		disease r	chr5:188	3038.99	4587.82	4734.02	7163.3	12044.5	8082.04
GT	Sense	Sense	-0.534	Detected	0.534	Detected	0.000	2.360	Detected	3.020	Detected	2.690	0.050	GT Sens	contig288	contig288	Chymotry	CCATAT	contig288	Solyc09g	Solyc09g	Chymotry	GO:0009	GO:00096	contig288	Solyc09g	Chymotry	GO:0009	SL2.40ch	AT4G123	CYP706A	CYP706	chr4:731	120.228	299.973	578.967	141.198	1098.23	1456.73
GT	Sense	Sense	0.261	Detected	-0.261	Detected	0.000	1.254	Detected	2.147	Detected	1.701	0.081	GT Sens	contig290	contig290	Cytochro	TGACAC	contig290	Solyc09g	Solyc09g	Cytochrome P450 (AHRD V1 **			contig290	Solyc11g	Cytochro	GO:0019	SL2.40ch	AT5G64600.1		unknown	chr5:258	99.4992	82.519	228.079	204.902	243.521	379.478
GT	Sense	Sense	-0.081	Detected	0.081	Detected	0.000	3.120	Detected	1.870	Detected	2.495	0.058	GT Sens	contig291	contig291	Unknown	GTAACT	contig291	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig291	Solyc05g	Unknown Protein (A		SL2.40ch	AT1G19230.1		respirato	chr1:664	79.4129	105.83	372.298	229.202	897.942	316.916
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	1.045	Detected	1.583	Detected	1.314	0.040	GT Sens	contig291	contig291	Solute ca	GCTGCA	contig291	Solyc12g	Solyc12g	Solute ca	GO:0016	GO:00160	contig291	Solyc12g	Solute ca	GO:0016	SL2.40ch	AT2G020	ATPTR2-l	PTR2 (PE	chr2:487	476.532	555.642	934.798	958.634	1195.89	1457.45
GT	Sense	Sense	0.255	Comprom	-0.255	Comprom	0.000	1.784	Detected	2.851	Detected	2.318	0.059	GT Sens	contig291	contig291	Pentatric	GAAAAA	contig291	Solyc04g	Solyc04g	Pentatricopeptide repeat-conta			contig291	Solyc04g	Pentatricopeptide re		SL2.40ch	AT1G09220.1		pentatric	chr1:297	2.75755	2.30626	5.09646	6.96789	9.78344	17.2048
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	1.174	Detected	1.277	Detected	1.226	0.002	GT Sens	contig292	contig292	Storekeep	AGGTTG	contig292	Solyc07g	Solyc07g	Storekeeper protein (AHRD V1			contig292	Solyc07g	Storekeeper protein		SL2.40ch	AT5G30495.1		FUNCTIO	chr5:113	33.5816	41.2396	54.4548	56.8213	94.5806	85.29
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	1.387	Detected	0.838	Detected	1.113	0.057	GT Sens	contig292	contig292	UDP-gluc	AGAGAT	contig292	Solyc11g	Solyc11g	UDP-gluc	GO:0008	GO:00081	contig292	Solyc11g	UDP-gluc	GO:0008	SL2.40ch	AT3G262	CYP71B3	CYP71B3	chr3:959	3492.36	4422.37	9964.85	11512.4	11579.1	6643.16
GT	Sense	Sense	-0.300	Detected	0.300	Detected	0.000	2.058	Detected	1.720	Detected	1.889	0.032	GT Sens	contig295	contig295	60S ribos	GGCTTC	contig295	Solyc09g	Solyc09g	60S ribos	GO:0003	GO:00037	contig295	Solyc09g	60S ribos	GO:0003	SL2.40ch	AT2G34480.1		60S ribos	chr2:145	13.6606	24.649	36.3379	47.9765	86.0754	57.1687
GT	Sense	Sense	1.123	Detected	-1.123	Detected	0.000	1.961	Detected	1.998	Detected	1.979	0.220	GT Sens	contig296	contig296	Ulp1 prot	GAAAGG	contig296	Solyc05g	Solyc05g	Ulp1 protease family C-termina			contig296	Solyc05g	Ulp1 protease famil		SL2.40ch	AT1G63430.1		leucine-r	chr1:235	753.48	188.984	550.002	427.185	1655.19	1424.92
GT	Sense	Sense	0.444	Detected	-0.444	Detected	0.000	1.600	Detected	1.431	Detected	1.516	0.079	GT Sens	contig299	contig299	Mutator-li	GCAAGA	contig299	Solyc12g	Solyc12g	Mutator-li	GO:0008	GO:00082	contig299	Solyc10g	Mutator-like transpo		SL2.40ch	AT2G26210.1				42.2408	27.1811	81.6666	55.8029	115.705	86.3976
GT	Sense	Sense	-0.431	Comprom	0.431	Comprom	0.000	2.237	Detected	2.343	Detected	2.290	0.034	GT Sens	contig299	contig299	Unknown	TCGGTG	contig299	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig299	Solyc09g	Ethylene-	GO:0003	SL2.40ch	AT2G30280.1		unknown	chr2:129	2.53569	5.484	24.3484	9.99999	19.8067	17.8901
GT	Sense	Sense	-0.170	Comprom	0.170	Comprom	0.000	1.722	Detected	2.187	Detected	1.954	0.021	GT Sens	contig306	contig306	Ulp1 prot	CACTTT	contig306	Solyc07g	Solyc07g	Ulp1 prot	GO:0006	GO:00065	contig306	Solyc07g	Ulp1 prot	GO:0006	SL2.40ch	AT1G42470.1		patched	chr1:159	6.89871	10.3891	13.049	23.389	31.4506	36.4596
GT	Sense	Sense	-0.263	Comprom	0.263	Detected	0.000	1.468	Detected	0.842	Detected	1.155	0.106	GT Sens	contig307	contig307	Cytochro	CTCCAC	contig307	Solyc03g	Solyc03g	Cytochro	GO:0019	GO:00198	contig307	Solyc03g	Cytochro	GO:0019	SL2.40ch	AT5G50540.1		unknown	chr5:205	7.606	13.0375	69.8249	14.126	31.0217	16.8768
GT	Sense	Sense	-0.099	Detected	0.099	Detected	0.000	1.648	Detected	2.070	Detected	1.859	0.015	GT Sens	contig308	contig308	Transpor	ACTGCA	contig308	Solyc05g	Solyc05g	Transporter-like protein (AHRD			contig308	Solyc05g	Transporter-like pro		SL2.40ch	AT5G10190.1		transpor	chr5:319	28.6873	39.2007	80.2071	113.544	118.405	133.13
GT	Sense	Sense	0.491	Detected	-0.491	Detected	0.000	1.721	Detected	1.879	Detected	1.800	0.069	GT Sens	contig310	contig310	Yippee zi	TTGCCC	contig310	Solyc03g	Solyc03g	Yippee zi	GO:0005	GO:00055	contig310	Solyc03g	Yippee zi	GO:0005	SL2.40ch	AT2G40110.2		yippee fa	chr2:167	162.652	98.0335	298.476	301.52	468.807	439.244
GT	Sense	Sense	0.229	Detected	-0.229	Detected	0.000	0.984	Detected	1.136	Detected	1.060	0.048	GT Sens	contig311	contig311	Photosys	AAGAAA	contig311	Solyc01g	Solyc01g	Photosys	GO:0016	GO:00160	contig311	Solyc01g	Photosys	GO:0016	SL2.40ch	ATCG003	PSAA	Encodes	chrC:396	84.4799	73.2485	127.107	116.672	175.252	163.496
GT	Sense	Sense	-0.006	Detected	0.006	Detected	0.000	2.151	Detected	1.623	Detected	1.887	0.019	GT Sens	contig312	contig312	CER1 (AH	TGAGAA	contig312	Solyc00g	Solyc00g	CER1 (AHRD V1 **-- B6TFH3_M			contig312	Solyc00g278110.2.1				AT5G14700.1		cinnamo	chr5:474	5421.33	6507.25	17093.2	18537.8	29716.4	17298.2
GT	Sense	Sense	-0.480	Comprom	0.480	Detected	0.000	2.055	Detected	1.043	Detected	1.549	0.157	GT Sens	contig316	contig316	DNA-dire	AGCTCC	contig316	Solyc10g	Solyc10g	DNA-dire	GO:0006350		contig316	Solyc10g	DNA-dire	GO:0006	SL2.40ch	AT5G451	NRPC2	NRPC2:	chr5:182	7.50226	17.3752	28.1774	38.8204	53.4289	22.2379
GT	Sense	Sense	-0.224	Detected	0.224	Detected	0.000	1.352	Detected	1.658	Detected	1.505	0.031	GT Sens	contig329	contig329	cDNA clo	ACATCA	contig329	Solyc02g	Solyc02g	cDNA clone J023049H21 full in			contig329	Solyc02g	BZIP tran	GO:0005	SL2.40ch	AT4G12700.1		unknown	chr4:748	12.3498	20.0676	51.0527	64.3132	45.2836	46.9649
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	1.438	Detected	1.778	Detected	1.608	0.011	GT Sens	contig337	contig337	Unknown	GGGATG	contig337	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig337	Solyc11g	Mitochon	GO:0016	SL2.40ch	AT1G06900.1		catalytic/	chr1:211	3728.08	4398.68	7887.72	9317.99	12362.2	13132.4
GT	Sense	Sense	0.616	Detected	-0.616	Comprom	0.000	0.962	Detected	1.671	Detected	1.316	0.205	GT Sens	contig344	contig344	Serine/thr	ATCAAC	contig344	Solyc07g	Solyc07g	Serine/thr	GO:0019	GO:00191	contig344	Solyc07g	Serine/thr	GO:0019	SL2.40ch	AT1G11340.1		S-locus l	chr1:381	19.8888	10.0748	27.7542	15.9749	31.0559	42.6175
GT	Sense	Sense	-0.097	Comprom	0.097	Detected	0.000	2.037	Detected	2.239	Detected	2.138	0.004	GT Sens	contig345	contig345	Unknown	TGGAAA	contig345	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig345	Solyc09g	Unknown Protein (A		SL2.40ch	AT3G48670.2		XH/XS do	chr3:180	8.92621	12.1582	37.8401	36.3148	48.1756	46.5042
GT	Sense	Sense	0.369	Comprom	-0.369	Comprom	0.000	1.399	Detected	1.382	Detected	1.390	0.064	GT Sens	contig358	contig358	Cytochro	CCAACT	contig358	Solyc04g	Solyc04g	Cytochro	GO:0020	GO:00200	contig358	Solyc07g	Cytochro	GO:0019	SL2.40ch	AT3G16370.1		GDSL-mo	chr3:555	10.033	7.15682	28.9804	25.7357	25.1697	20.8766
GT	Sense	Sense	-0.085	Comprom	0.085	Detected	0.000	2.023	Detected	2.071	Detected	2.047	0.002	GT Sens	contig370	contig370	Legumin	AACCCA	contig370	Solyc11g	Solyc11g	Legumin	GO:0045	GO:00457	contig370	Solyc11g	Legumin	GO:0045	SL2.40ch	AT1G07750.1		cupin far	chr1:240	8.5361	11.4373	33.7245	25.1592	45.2378	39.2459
GT	Sense	Sense	0.379	Comprom	-0.379	Comprom	0.000	1.681	Detected	2.324	Detected	2.002	0.056	GT Sens	contig376	contig376	Pathogen	GAAAGA	contig376	Solyc02g	Solyc02g	Pathogenesis-related protein-l			contig376	Solyc04g	Pathogenesis-relate		SL2.40ch	AT3G52140.1		tetratrico	chr3:193	8.02519	5.65087	14.6418	5.42211	24.3191	31.873
GT	Sense	Sense	0.222	Detected	-0.222	Detected	0.000	1.011	Detected	1.818	Detected	1.415	0.091	GT Sens	contig386	contig386	Unknown	ATCGTT	contig386	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig386	Solyc06g009810.2.1				AT1G508	POLGAM	POLGAM	chr1:188	48.713	42.6592	55.9271	36.5123	103.524	151.945
GT	Sense	Sense	0.243	Detected	-0.243	Detected	0.000	2.190	Detected	2.630	Detected	2.410	0.018	GT Sens	contig387	contig387	Terminal	AATTGT	contig387	Solyc01g	Solyc01g	Terminal ear1-like 2 protein (A			contig387	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G53200.2				959.179	815.837	2559.81	2731.53	4546.09	5179.15
GT	Sense	Sense	-0.371	Comprom	0.371	Detected	0.000	2.043	Detected	3.118	Detected	2.581	0.058	GT Sens	contig405	contig405	Unannota	CCATAAGCGGCAGCATGGTGTTATGCTGTAATTTTACTATCTCAAGAAA							contig405	Solyc06g	Beta-fruc	GO:0005	SL2.40ch	AT3G45800.1				7.65574	15.2429	224.208	387.411	50.1654	88.6541
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	1.376	Detected	1.281	Detected	1.329	0.012	GT Sens	contig411	contig411	Unannota	AATAGATGTTGAATATTGATAGTTATTGAATTGGTTTTTATTAATGAGTT							contig411	Solyc03g	Polyprote	GO:0006	SL2.40ch	AT3G24530.1		AAA-type	chr3:894	53.7005	52.8475	90.0919	121.258	155.742	122.428
GT	Sense	Sense	-0.565	Comprom	0.565	Comprom	0.000	1.930	Detected	2.950	Detected	2.440	0.085	GT Sens	contig418	contig418	Mutator-li	GCTGAT	contig418	Solyc01g	Solyc01g	Mutator-like transposase (AHR			contig418	Solyc01g	Mutator-like transpo		SL2.40ch	AT4G29490.1		aminope	chr4:144	3.08298	8.03263	6.00214	12.634	21.3663	36.3677
GT	Sense	Sense	0.176	Comprom	-0.176	Comprom	0.000	4.407	Detected	3.408	Detected	3.908	0.018	GT Sens	contig419	contig419	Unannota	CTCACCATTCAAATTTGTACATCATCGAATGGGAAATCTCTATCTTCTA							contig419	Solyc03g	Polyprote	GO:0006	SL2.40ch	AT5G64667.1				2.39856	2.23743	4.35089	2.11507	55.378	23.2487
GT	Sense	Sense	-0.193	Comprom	0.193	Detected	0.000	1.084	Detected	1.023	Detected	1.054	0.033	GT Sens	contig461	contig461	Unknown	GGCTAC	contig461	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig461	Solyc00g	Unknown Protein (A		SL2.40ch	AT2G38160.1				9.47065	14.7338	3.9781	7.57126	28.2059	22.7003
GT	Sense	Sense	0.651	Detected	-0.651	Detected	0.000	0.992	Detected	1.082	Detected	1.037	0.253	GT Sens	contig462	contig462	Glutaredo	CAAACC	contig462	Solyc04g	Solyc04g	Glutaredo	GO:0045	GO:00454	contig462	Solyc04g	Glutaredo	GO:0045	SL2.40ch	ATMG009	NAD3	NADH de	chrM:26	35.529	17.1541	16.3622	35.4234	55.3053	49.4314
GT	Sense	Sense	-0.594	Comprom	0.594	Detected	0.000	1.086	Detected	1.820	Detected	1.453	0.173	GT Sens	contig489	contig489	Unknown	AGTGAT	contig489	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig489	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G55660.1		LOCATE	chr5:225	4.7334	12.8378	12.2055	12.776	18.6456	26.0246
GT	Sense	Sense	1.126	Detected	-1.126	Detected	0.000	2.786	Detected	1.199	Detected	1.993	0.285	GT Sens	contig497	contig497	EIN3-bind	GCTGCT	contig497	Solyc05g	Solyc05g	EIN3-binding F-box protein 1 (/			contig497	Solyc07g	SCF E3 u	GO:0005	SL2.40ch	AT4G30020.1		subtilase	chr4:146	2958.58	739.82	4091.07	3206.59	11495.7	3212.6
GT	Sense	Sense	0.802	Comprom	-0.802	Comprom	0.000	1.731	Detected	2.095	Detected	1.913	0.146	GT Sens	contig499	contig499	Unknown	TCAAAT	contig499	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig499	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G35330.1				8.98328	3.5168	19.6272	19.3845	21.019	22.7019
GT	Sense	Sense	-0.189	Comprom	0.189	Comprom	0.000	2.048	Detected	2.489	Detected	2.269	0.016	GT Sens	contig500	contig500	Cytochro	GCAGGA	contig500	Solyc09g	Solyc09g	Cytochro	GO:0019	GO:00198	contig500	Solyc09g066370.1.1				AT3G50220.1		unknown	chr3:186	4.33561	6.70486	133.209	5.38936	25.1213	28.6212
GT	Sense	Sense	0.392	Comprom	-0.392	Comprom	0.000	1.191	Detected	1.332	Detected	1.262	0.087	GT Sens	contig516	contig516	Phenylco	GATGGC	contig516	Solyc10g	Solyc10g	Phenylco	GO:0008	GO:00081	contig516	Solyc10g	Phenylco	GO:0032	SL2.40ch	AT1G75280.1		isoflavor	chr1:282	8.93086	6.17131	14.7927	15.4225	19.0915	17.6741
GT	Sense	Sense	-0.139	Comprom	0.139	Detected	0.000	1.722	Detected	1.454	Detected	1.588	0.014	GT Sens	contig518	contig518	Glutathio	AGGAAT	contig518	Solyc09g	Solyc09g	Glutathio	GO:0004	GO:00043	contig518	Solyc09g	Glutathio	GO:0004	SL2.40ch	AT3G092	ATGSTU8	ATGSTU	chr3:284	9.15624	13.2164	14.7506	36.1482	40.8728	28.5049
GT	Sense	Sense	0.535	Comprom	-0.535	Comprom	0.000	1.079	Detected	1.441	Detected	1.260	0.156	GT Sens	contig521	contig521	Disease r	AGCAGA	contig521	Solyc07g	Solyc07g	Disease r	GO:0006	GO:00069	contig521	Solyc07g	Nbs-lrr, re	GO:0006	SL2.40ch	AT3G51080.1		zinc fing	chr3:189	8.90234	5.04747	12.6071	9.95218	15.9487	17.2031
GT	Sense	Sense	0.186	Detected	-0.186	Detected	0.000	1.387	Detected	0.822	Detected	1.104	0.082	GT Sens	contig577	contig577	Myb-relat	CTCCAA	contig577	Solyc07g	Solyc07g	Myb-relat	GO:0045449		contig577	Solyc07g	Myb-relat	GO:0003	SL2.40ch	AT5G542	MYB49, A	MYB49 (	chr5:220	79.8358	73.4376	84.9952	94.6993	225.6	127.976
GT	Sense	Sense	-0.229	Detected	0.229	Detected	0.000	3.177	Detected	2.508	Detected	2.842	0.020	GT Sens	contig582	contig582	Helicase-	CAATGG	contig582	Solyc01g	Solyc01g	Helicase-like protein (AHRD V1			contig582	Solyc01g	Helicase-like protein		SL2.40ch	AT3G20700.1				141.029	230.566	574.328	530.718	1836.88	969.733
GT	Sense	Sense	0.853	Detected	-0.853	Detected	0.000	1.460	Detected	1.399	Detected	1.429	0.236	GT Sens	contig584	contig584	Epoxide h	GTATTG	contig584	Solyc01g	Solyc01g	Epoxide h	GO:0003	GO:00038	contig584	Solyc01g	Epoxide h	GO:0004	SL2.40ch	AT4G02489.1		unknown	chr4:109	5682.63	2072.2	7083.17	4663.54	10634.3	8554.85
GT	Sense	Sense	0.173	Comprom	-0.173	Comprom	0.000	2.396	Detected	3.332	Detected	2.864	0.029	GT Sens	contig584	contig584	Nonribos	GTTATT	contig584	Solyc02g	Solyc02g	Nonribosomal peptide synthet			contig584	Solyc02g	Nonribosomal pepti		SL2.40ch	AT4G18540.1		unknown	chr4:102	2.37392	2.2246	15.8641	11.5183	13.6225	21.8804
GT	Sense	Sense	-0.209	Comprom	0.209	Comprom	0.000	3.551	Detected	3.069	Detected	3.310	0.009	GT Sens	contig608	contig608	Aldo/keto	TGGTAT	contig608	Solyc09g	Solyc09g	Aldo/keto	GO:0055	GO:00551	contig608	Solyc09g	Aldo/keto	GO:0055	SL2.40ch	AT1G60680.1		aldo/keto	chr1:223	2.48091	3.94692	4.16988	7.03987	41.3101	24.8357
GT	Sense	Sense	0.019	Detected	-0.019	Detected	0.000	1.239	Detected	1.310	Detected	1.275	0.001	GT Sens	contig614	contig614	Unknown	GACTCC	contig614	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig614	Solyc08g	Unknown Protein (A		SL2.40ch	AT4G14580.1				1084.9	1257.19	2023.86	2056.76	3106.11	2738.78
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	1.373	Detected	1.546	Detected	1.459	0.004	GT Sens	contig618	contig618	Cyclin-de	ACTTAT	contig618	Solyc10g	Solyc10g	Cyclin-de	GO:0004	GO:00046	contig618	Solyc10g	Cyclin-de	GO:0004	SL2.40ch	AT4G187	BIN2, DW	BIN2 (BR	chr4:102	20.3458	24.7395	41.3438	57.9997	65.4407	61.9411
GT	Sense	Sense	-0.161	Detected	0.161	Detected	0.000	1.350	Detected	0.828	Detected	1.089	0.071	GT Sens	contig642	contig642	Ulp1 prot	AGAAGG	contig642	Solyc06g	Solyc06g	Ulp1 protease family C-termina			contig642	Solyc09g	Ulp1 protease famil		SL2.40ch	AT5G651	ACX2, AT	ACX2 (AC	chr5:260	1806.39	2689.26	4914.66	4736.41	6328.21	3700.61
GT	Sense	Sense	-0.173	Detected	0.173	Detected	0.000	1.385	Detected	0.877	Detected	1.131	0.066	GT Sens	contig645	contig645	Ulp1 prot	CCTCAA	contig645	Solyc08g	Solyc08g	Ulp1 prot	GO:0006	GO:00065	contig645	Solyc11g	Ulp1 protease famil		SL2.40ch	AT5G38360.1		catalytic	chr5:153	1144.83	1731.51	3103.17	3119.36	4141.54	2445.7
GT	Sense	Sense	-0.667	Detected	0.667	Detected	0.000	1.153	Detected	1.296	Detected	1.225	0.209	GT Sens	contig690	contig690	Proteinas	CAGGAT	contig690	Solyc09g	Solyc09g	Proteinas	GO:0009	GO:00096	contig690	Solyc09g	Proteinas	GO:0009	SL2.40ch	AT5G58830.1		identical	chr5:237	5619.85	16867.3	16343.8	10869.7	24390	22606.5
GT	Sense	Sense	0.244	Comprom	-0.244	Comprom	0.000	0.826	Detected	1.805	Detected	1.315	0.138	GT Sens	contig696	contig696	Peroxida	TTCAGA	contig696	Solyc01g	Solyc01g	Peroxida	GO:0055	GO:00551	contig696	Solyc01g	Peroxida	GO:0004	SL2.40ch	AT5G37620.1				6.22453	5.28182	7.98636	5.27802	11.4494	18.938
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	0.808	Detected	2.275	Detected	1.541	0.175	GT Sens	contig705	contig705	Unknown	ACAAAA	contig705	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig705	Solyc05g	Unknown Protein (A		SL2.40ch	AT3G52700.1		unknown	chr3:195	937.784	1344.81	1774.75	2509.73	2214.24	5140.11
GT	Sense	Sense	-0.148	Comprom	0.148	Comprom	0.000	1.793	Detected	1.893	Detected	1.843	0.007	GT Sens	contig712	contig712	Unknown	AACTAA	contig712	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig712	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G144	anac085	anac085	chr5:467	4.47461	6.53853	9.46436	2.08789	21.1143	18.9959
GT	Sense	Sense	-0.294	Detected	0.294	Detected	0.000	3.010	Detected	1.792	Detected	2.401	0.071	GT Sens	contig715	contig715	Wound in	GCACAA	contig715	Solyc07g	Solyc07g	Wound induced protein (AHRD			contig715	Solyc07g	Wound induced pro		SL2.40ch	AT4G10270.1		wound-r	chr4:637	491.031	879.238	2335.57	1459.51	5964.43	2151.51
GT	Sense	Sense	-0.350	Detected	0.350	Detected	0.000	1.214	Detected	0.807	Detected	1.011	0.130	GT Sens	contig736	contig736	Unknown	CGGATG	contig736	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)%			contig736	Solyc04g	Unknown Protein (A		SL2.40ch	AT1G59990.1		DEAD/DE	chr1:220	70.7152	136.802	165.429	188.265	257.107	162.758
GT	Sense	Sense	-0.009	Comprom	0.009	Comprom	0.000	2.027	Detected	3.571	Detected	2.799	0.068	GT Sens	contig739	contig739	Unknown	ATGTTG	contig739	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)%			contig739	Solyc06g	Unknown Protein (A		SL2.40ch	AT4G27520.1		plastocy	chr4:137	2.61222	3.15087	2.38018	3.91988	13.1707	32.2392
GT	Sense	Sense	1.118	Detected	-1.118	Comprom	0.000	1.024	Detected	1.434	Detected	1.229	0.393	GT Sens	contig752	contig752	Phosphat	AGAGTA	contig752	Solyc09g	Solyc09g	Phosphatidylinositol 3-kinase			contig752	Solyc09g	Phosphatidylinosito		SL2.40ch	AT2G479	SCC3, AT	SCC3 (SI	chr2:196	12.4652	3.15041	16.6572	12.3715	14.3583	16.0061
GT	Sense	Sense	-0.640	Detected	0.640	Detected	0.000	0.934	Detected	1.169	Detected	1.052	0.247	GT Sens	contig754	contig754	Proteinas	AGAGTT	contig754	Solyc09g	Solyc09g	Proteinas	GO:0009	GO:00096	contig754	Solyc09g	Proteinas	GO:0009	SL2.40ch	AT3G08947.1		binding /	chr3:272	11144.2	32197.7	31081.8	20356.1	40764.7	40277.7
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	1.176	Detected	1.288	Detected	1.232	0.005	GT Sens	contig763	contig763	Developn	TTATGG	contig763	Solyc12g	Solyc12g	Developmentally regulated GT			contig763	Solyc12g	Developmentally re		SL2.40ch	AT1G72660.3		developm	chr1:273	13.2294	17.412	13.1772	24.3866	38.6293	35.049
GT	Sense	Sense	0.802	Detected	-0.802	Detected	0.000	0.850	Detected	1.289	Detected	1.069	0.327	GT Sens	contig776	contig776	Cytochro	AAACTC	contig776	Solyc10g	Solyc10g	Cytochro	GO:0020	GO:00200	contig776	Solyc10g	Cytochro	GO:0046	SL2.40ch	AT2G408	CYP98A3	CYP98A3	chr2:170	983.363	385.306	1597.2	1300.14	1249.9	1421.87
GT	Sense	Sense	-0.633	Comprom	0.633	Detected	0.000	1.015	Detected	1.843	Detected	1.429	0.199	GT Sens	contig777	contig777	Unknown	GTAAAT	contig777	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig777	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G23240.1		DNAJ he	chr5:782	8.68018	24.8426	14.2428	19.6235	33.4279	49.8153
GT	Sense	Sense	0.335	Detected	-0.335	Detected	0.000	1.689	Detected	1.017	Detected	1.353	0.104	GT Sens	contig782	contig782	Ankyrin r	GCAAGT	contig782	Solyc01g	Solyc01g	Ankyrin repeat protein-like (AH			contig782	Solyc01g	Ankyrin repeat prot		SL2.40ch	AT2G317	UGT74D1	UGT74D	chr2:134	52.4106	39.1965	95.3618	76.1986	164.651	86.7135
GT	Sense	Sense	0.967	Detected	-0.967	Comprom	0.000	1.963	Detected	1.425	Detected	1.694	0.233	GT Sens	contig802	contig802	Glutathio	GATGAG	contig802	Solyc09g	Solyc09g	Glutathione S-transferase-like			contig802	Solyc09g	Glutathio	GO:0004	SL2.40ch	AT1G76790.1				36.0007	11.2214	82.8591	58.7125	88.2443	51.0153
GT	Sense	Sense	0.150	Comprom	-0.150	Comprom	0.000	1.669	Detected	2.085	Detected	1.877	0.018	GT Sens	contig817	contig817	Ulp1 prot	AGCGCA	contig817	Solyc04g	Solyc04g	Ulp1 protease family C-termina			contig817	Solyc10g	Ulp1 protease famil		SL2.40ch	AT4G14746.1				5.01933	4.85216	8.93116	22.654	17.6834	19.8043
GT	Sense	Sense	0.909	Detected	-0.909	Comprom	0.000	1.924	Detected	1.623	Detected	1.774	0.194	GT Sens	contig827	contig827	Hydrolase	CAACTT	contig827	Solyc01g	Solyc01g	Hydrolase alpha/beta fold fami			contig827	Solyc01g	Hydrolase	GO:0008	SL2.40ch	AT5G575	BIO1	BIO1 (bic	chr5:233	24.1213	8.14276	32.6596	25.2526	59.9207	40.8087
GT	Sense	Sense	0.242	Detected	-0.242	Detected	0.000	0.939	Detected	1.212	Detected	1.076	0.061	GT Sens	contig828	contig828	Yippee zi	CTGAAA	contig828	Solyc03g	Solyc03g	Yippee zi	GO:0008	GO:00082	contig828	Solyc03g	Yippee zi	GO:0008	SL2.40ch	AT2G40110.2		yippee fa	chr2:167	1246.09	1061.13	2461.61	2182.22	2483.69	2518.64
GT	Sense	Sense	-0.338	Detected	0.338	Detected	0.000	0.905	Detected	2.444	Detected	1.675	0.185	GT Sens	contig849	contig849	Auxin-ind	TGCTGT	contig849	Solyc11g	Solyc11g	Auxin-induced SAUR-like prote			contig849	Solyc11g	Auxin-induced SAU		SL2.40ch	AT5G01881.1		unknown	chr5:339	26.432	50.2988	179.759	274.204	76.9091	187.616
GT	Sense	Sense	1.015	Comprom	-1.015	Comprom	0.000	1.362	Detected	2.814	Detected	2.088	0.236	GT Sens	contig875	contig875	Mutator-li	GAAAAT	contig875	Solyc10g	Solyc10g	Mutator-li	GO:0008	GO:00082	contig875	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G60810.2				10.6675	3.10823	5.32261	7.77545	16.6721	38.2979
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	2.050	Detected	1.842	Detected	1.946	0.005	GT Sens	contig890	contig890	Ribose-pl	AAAGCT	contig890	Solyc07g	Solyc07g	Ribose-pl	GO:0009	GO:00091	contig890	Solyc07g	Ribose-pl	GO:0042	SL2.40ch	AT2G42910.1		ribose-pl	chr2:178	114.755	119.287	220.864	224.641	545.898	396.534
GT	Sense	Sense	0.540	Detected	-0.540	Comprom	0.000	1.143	Detected	1.411	Detected	1.277	0.149	GT Sens	contig895	contig895	Mutator-li	GTGAAG	contig895	Solyc10g	Solyc10g	Mutator-li	GO:0008	GO:00082	contig895	Solyc10g	Mutator-li	GO:0008	SL2.40ch	AT5G656	bHLH093	bHLH093	chr5:262	20.1526	11.3486	29.5692	35.6573	37.6267	38.0355
GT	Sense	Sense	1.067	Detected	-1.067	Comprom	0.000	1.841	Detected	1.722	Detected	1.782	0.237	GT Sens	contig900	contig900	Ulp1 prot	ATGCAG	contig900	Solyc02g	Solyc02g	Ulp1 protease family C-termina			contig900	Solyc02g	Ulp1 protease famil		SL2.40ch	AT3G439	DCL3, AT	ribonucl	chr3:157	71.1075	19.2791	41.5605	28.4608	149.408	115.512
GT	Sense	Sense	0.113	Comprom	-0.113	Detected	0.000	0.873	Detected	1.315	Detected	1.094	0.048	GT Sens	contig904	contig904	Ulp1 prot	AAATCG	contig904	Solyc00g	Solyc00g	Ulp1 protease family C-termina			contig904	Solyc00g	Ulp1 protease famil		SL2.40ch	AT4G255	MSH3, AT	MSH3 (A	chr4:130	11.4786	11.6913	12.9673	10.6659	23.9032	27.2429
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	2.470	Detected	1.913	Detected	2.192	0.016	GT Sens	contig906	contig906	1-aminoc	GTCCAG	contig906	Solyc09g	Solyc09g	1-aminoc	GO:0016	GO:00164	contig906	Solyc09g	1-aminoc	GO:0009	SL2.40ch	AT1G06640.1		2-oxoglu	chr1:203	16.6532	20.3559	37.202	107.213	114.941	65.5705
GT	Sense	Sense	-0.610	Comprom	0.610	Comprom	0.000	1.998	Detected	2.551	Detected	2.274	0.077	GT Sens	contig909	contig909	Inosine-u	GCATAC	contig909	Solyc01g	Solyc01g	Inosine-u	GO:0016	GO:00167	contig909	Solyc01g	Inosine-u	GO:0016	SL2.40ch	AT5G18890.1		inosine-u	chr5:630	2.55431	7.08099	19.7073	2.20051	19.1397	23.5584
GT	Sense	Sense	-0.414	Detected	0.414	Detected	0.000	1.284	Detected	0.807	Detected	1.045	0.160	GT Sens	contig934	contig934	Fatty acic	TGTAGA	contig934	Solyc12g	Solyc12g	Fatty acid desaturase (AHRD V			contig934	Solyc12g	Fatty acid desatura		SL2.40ch	AT3G121	FAD2	FAD2 (FA	chr3:386	886.641	1873.77	2521.09	1643.75	3535.8	2131.91
GT	Sense	Sense	-0.397	Comprom	0.397	Comprom	0.000	2.457	Detected	3.407	Detected	2.932	0.042	GT Sens	contig949	contig949	Unknown	GAAAAT	contig949	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig949	Solyc02g	Auxin-repressed pr		SL2.40ch	AT5G44578.1		unknown	chr5:179	2.5966	5.35861	8.57927	10.9164	23.0755	37.4055
GT	Sense	Sense	0.044	Comprom	-0.044	Comprom	0.000	1.320	Detected	1.870	Detected	1.595	0.029	GT Sens	contig950	contig950	Unknown	AAACAA	contig950	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig950	Solyc07g	Unknown Protein (A		SL2.40ch	AT4G24200.1		LOCATE	chr4:125	4.86168	5.44828	13.177	15.5522	14.4726	17.7834
GT	Sense	Sense	0.099	Detected	-0.099	Detected	0.000	1.432	Detected	1.343	Detected	1.387	0.006	GT Sens	contig956	contig956	Subtilisin	TACCAA	contig956	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:00042	contig956	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT5G673	ARA12	ARA12: s	chr5:268	371.595	385.692	792.271	940.997	1150.84	907.888
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	1.815	Detected	1.890	Detected	1.852	0.001	GT Sens	contig993	contig993	Glutathio	CACGCA	contig993	Solyc09g	Solyc09g	Glutathio	GO:0004	GO:00043	contig993	Solyc09g	Glutathio	GO:0004	SL2.40ch	AT3G21940.1		receptor	chr3:772	126.375	162.083	353.898	467.658	567.172	501.441
GT	Sense	Sense	-0.237	Detected	0.237	Detected	0.000	2.517	Detected	2.034	Detected	2.276	0.021	GT Sens	contig993	contig993	Unknown	TATTAG	contig993	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig993	Solyc04g	30S ribos	GO:0005	SL2.40ch	AT3G460	RPS15AD	RPS15A	chr3:169	304.187	503.111	978.679	1519.54	2523.09	1515.07
GT	Sense	Sense	0.733	Detected	-0.733	Comprom	0.000	1.477	Detected	1.256	Detected	1.366	0.206	GT Sens	contig998	contig998	E3 ubiqui	GGATTC	contig998	Solyc03g	Solyc03g	E3 ubiqui	GO:0005	GO:00056	contig998	Solyc03g	E3 ubiqui	GO:0004	SL2.40ch	AT4G31430.2		unknown	chr4:152	24.2428	10.4523	39.8899	35.0386	49.9011	35.945

ProbeNar	Orientatic	20h_AZ_Control Fold 20h	Flag 20h	Fold 20h	Flag 20h	Geomean	20h_AZ_TAPG + TPRP vs. 20h_AZ_Control Fold 20h	Flag 20h	Fold 20h	Flag 20h	Geomean	P-value
A 96 P00	Sense	-1.335	Detected	1.335	Detected	0.000	-1.452	Detected	-2.550	Detected	-2.001	0.300
A 96 P00	Sense	-0.058	Detected	0.058	Detected	0.000	-0.885	Detected	-1.516	Detected	-1.200	0.064
A 96 P00	Sense	0.122	Detected	-0.122	Detected	0.000	-1.284	Detected	-1.567	Detected	-1.425	0.017
A 96 P00	Sense	0.607	Detected	-0.607	Detected	0.000	-1.136	Detected	-1.044	Detected	-1.090	0.215
A 96 P01	Sense	-0.428	Detected	0.428	Detected	0.000	-1.208	Detected	-1.518	Detected	-1.363	0.096
A 96 P02	Sense	0.163	Detected	-0.163	Detected	0.000	-1.220	Detected	-1.437	Detected	-1.329	0.021
A 96 P02	Sense	0.011	Detected	-0.011	Detected	0.000	-1.177	Detected	-1.470	Detected	-1.323	0.012
A 96 P02	Sense	0.173	Detected	-0.173	Detected	0.000	-1.124	Detected	-1.004	Detected	-1.064	0.028
A 96 P02	Sense	-0.104	Detected	0.104	Detected	0.000	-0.864	Detected	-1.243	Detected	-1.054	0.040
A 96 P02	Sense	0.581	Detected	-0.581	Detected	0.000	-1.219	Detected	-2.926	Comprom	-2.072	0.183
A 96 P02	Sense	-0.099	Detected	0.099	Detected	0.000	-0.983	Detected	-1.232	Detected	-1.107	0.020
A 96 P02	Sense	-0.041	Detected	0.041	Detected	0.000	-1.459	Detected	-1.069	Detected	-1.264	0.024
A 96 P03	Sense	0.086	Detected	-0.086	Detected	0.000	-1.366	Detected	-1.534	Detected	-1.450	0.007
A 96 P03	Sense	0.199	Detected	-0.199	Detected	0.000	-1.600	Comprom	-1.692	Comprom	-1.646	0.015
A 96 P03	Sense	-0.084	Detected	0.084	Detected	0.000	-1.027	Detected	-1.199	Detected	-1.113	0.011
A 96 P03	Sense	-1.152	Detected	1.152	Detected	0.000	-4.323	Comprom	-2.245	Comprom	-3.284	0.169
A 96 P03	Sense	0.242	Detected	-0.242	Detected	0.000	-1.646	Detected	-2.029	Detected	-1.838	0.027
A 96 P03	Sense	0.074	Detected	-0.074	Detected	0.000	-0.959	Detected	-2.018	Detected	-1.489	0.108
A 96 P03	Sense	0.041	Detected	-0.041	Detected	0.000	-1.260	Detected	-1.075	Detected	-1.168	0.007
A 96 P04	Sense	-0.114	Detected	0.114	Detected	0.000	-1.367	Detected	-1.030	Detected	-1.198	0.028
A 96 P04	Sense	-0.070	Detected	0.070	Detected	0.000	-1.524	Detected	-0.828	Detected	-1.176	0.080
A 96 P04	Sense	-0.094	Detected	0.094	Detected	0.000	-3.021	Detected	-0.900	Detected	-1.961	0.207
A 96 P05	Sense	-0.269	Detected	0.269	Detected	0.000	-1.896	Detected	-1.401	Detected	-1.648	0.046
A 96 P05	Sense	-0.941	Detected	0.941	Detected	0.000	-2.872	Detected	-2.112	Detected	-2.492	0.134
A 96 P05	Sense	0.050	Detected	-0.050	Detected	0.000	-1.158	Detected	-1.503	Detected	-1.331	0.018
A 96 P05	Sense	-0.271	Detected	0.271	Detected	0.000	-1.193	Comprom	-2.434	Comprom	-1.814	0.116
A 96 P06	Sense	0.242	Detected	-0.242	Detected	0.000	-1.229	Detected	-0.894	Detected	-1.062	0.069
A 96 P06	Sense	0.064	Detected	-0.064	Detected	0.000	-3.332	Detected	-2.045	Detected	-2.689	0.053
A 96 P06	Sense	-0.060	Detected	0.060	Detected	0.000	-1.095	Detected	-0.974	Detected	-1.034	0.007
A 96 P06	Sense	0.374	Detected	-0.374	Detected	0.000	-1.187	Detected	-5.298	Detected	-3.243	0.261
A 96 P06	Sense	-0.066	Detected	0.066	Detected	0.000	-0.873	Detected	-1.246	Detected	-1.060	0.033
A 96 P07	Sense	-0.351	Detected	0.351	Detected	0.000	-1.106	Detected	-2.257	Comprom	-1.681	0.130
A 96 P07	Sense	0.016	Detected	-0.016	Detected	0.000	-1.310	Detected	-1.215	Detected	-1.263	0.002
A 96 P07	Sense	-0.054	Detected	0.054	Detected	0.000	-1.484	Detected	-1.132	Comprom	-1.308	0.019
A 96 P07	Sense	-0.624	Detected	0.624	Detected	0.000	-1.929	Detected	-1.032	Detected	-1.481	0.194
A 96 P07	Sense	-0.460	Detected	0.460	Detected	0.000	-1.081	Detected	-1.519	Detected	-1.300	0.125
A 96 P07	Sense	0.020	Detected	-0.020	Detected	0.000	-1.059	Detected	-1.030	Detected	-1.044	0.001
A 96 P07	Sense	0.369	Detected	-0.369	Detected	0.000	-1.217	Detected	-1.651	Detected	-1.434	0.079
A 96 P07	Sense	-0.057	Detected	0.057	Detected	0.000	-1.172	Detected	-2.326	Comprom	-1.749	0.095
A 96 P08	Sense	-0.110	Detected	0.110	Detected	0.000	-1.199	Detected	-1.685	Detected	-1.442	0.032
A 96 P08	Sense	0.216	Detected	-0.216	Detected	0.000	-0.887	Detected	-1.166	Detected	-1.026	0.058
A 96 P08	Sense	0.125	Detected	-0.125	Detected	0.000	-1.650	Detected	-1.877	Detected	-1.763	0.009
A 96 P08	Sense	0.184	Detected	-0.184	Detected	0.000	-1.632	Detected	-0.883	Detected	-1.258	0.095
A 96 P08	Sense	0.439	Detected	-0.439	Detected	0.000	-1.913	Detected	-1.383	Detected	-1.648	0.085
A 96 P08	Sense	0.422	Detected	-0.422	Detected	0.000	-0.879	Detected	-4.026	Detected	-2.452	0.271
A 96 P08	Sense	0.237	Detected	-0.237	Detected	0.000	-0.969	Detected	-1.133	Detected	-1.051	0.052
A 96 P08	Sense	0.235	Detected	-0.235	Detected	0.000	-0.985	Detected	-1.037	Detected	-1.011	0.051
A 96 P08	Sense	-0.580	Detected	0.580	Detected	0.000	-1.951	Detected	-0.808	Detected	-1.379	0.232
A 96 P09	Sense	-0.963	Detected	0.963	Detected	0.000	-1.257	Detected	-1.780	Detected	-1.518	0.268
A 96 P09	Sense	-0.224	Detected	0.224	Detected	0.000	-1.604	Detected	-1.739	Detected	-1.671	0.019
A 96 P09	Sense	0.263	Detected	-0.263	Detected	0.000	-0.898	Detected	-1.382	Detected	-1.140	0.086
A 96 P09	Sense	-0.033	Detected	0.033	Detected	0.000	-1.345	Detected	-0.810	Detected	-1.078	0.057
A 96 P10	Sense	0.076	Detected	-0.076	Detected	0.000	-1.808	Detected	-0.943	Detected	-1.376	0.089
A 96 P10	Sense	-0.184	Detected	0.184	Detected	0.000	-1.383	Detected	-1.526	Detected	-1.454	0.018
A 96 P10	Sense	-0.194	Detected	0.194	Detected	0.000	-2.099	Detected	-1.419	Detected	-1.759	0.046
A 96 P10	Sense	0.292	Detected	-0.292	Detected	0.000	-1.451	Detected	-1.957	Detected	-1.704	0.048
A 96 P10	Sense	-0.043	Detected	0.043	Detected	0.000	-1.250	Detected	-1.206	Detected	-1.228	0.002
A 96 P11	Sense	-0.278	Detected	0.278	Detected	0.000	-1.608	Detected	-1.532	Detected	-1.570	0.031
A 96 P12	Sense	-0.355	Detected	0.355	Detected	0.000	-2.511	Comprom	-1.567	Comprom	-2.039	0.075
A 96 P12	Sense	-0.404	Detected	0.404	Detected	0.000	-1.397	Detected	-1.623	Detected	-1.510	0.069
A 96 P12	Sense	0.090	Detected	-0.090	Detected	0.000	-1.206	Detected	-0.986	Detected	-1.096	0.016
A 96 P12	Sense	-0.064	Detected	0.064	Detected	0.000	-1.511	Detected	-2.648	Detected	-2.079	0.068
A 96 P12	Sense	0.139	Detected	-0.139	Detected	0.000	-1.129	Detected	-1.086	Detected	-1.108	0.016
A 96 P12	Sense	0.521	Detected	-0.521	Detected	0.000	-1.217	Detected	-1.700	Detected	-1.459	0.126
A 96 P12	Sense	-0.583	Detected	0.583	Detected	0.000	-1.363	Detected	-1.196	Detected	-1.280	0.162
A 96 P13	Sense	-0.025	Detected	0.025	Detected	0.000	-1.136	Detected	-1.125	Detected	-1.131	0.001
A 96 P13	Sense	0.556	Detected	-0.556	Detected	0.000	-1.340	Detected	-1.833	Detected	-1.587	0.121
A 96 P13	Sense	0.050	Detected	-0.050	Detected	0.000	-1.257	Detected	-0.955	Detected	-1.106	0.020
A 96 P13	Sense	-0.796	Detected	0.796	Detected	0.000	-3.368	Comprom	-2.304	Comprom	-2.836	0.098
A 96 P13	Sense	-0.228	Detected	0.228	Detected	0.000	-0.875	Detected	-1.539	Detected	-1.207	0.096
A 96 P13	Sense	0.260	Detected	-0.260	Detected	0.000	-1.361	Detected	-2.415	Detected	-1.888	0.085
A 96 P13	Sense	-1.374	Detected	1.374	Detected	0.000	-1.386	Detected	-2.588	Detected	-1.987	0.316
A 96 P13	Sense	-0.156	Detected	0.156	Detected	0.000	-0.866	Detected	-1.558	Detected	-1.212	0.086
A 96 P13	Sense	-0.277	Detected	0.277	Detected	0.000	-1.130	Detected	-1.973	Detected	-1.552	0.091
A 96 P14	Sense	0.516	Detected	-0.516	Detected	0.000	-1.062	Detected	-4.480	Detected	-2.771	0.261
A 96 P14	Sense	-0.199	Detected	0.199	Detected	0.000	-1.132	Detected	-2.009	Detected	-1.570	0.083
A 96 P15	Sense	-0.178	Detected	0.178	Detected	0.000	-1.404	Detected	-1.693	Comprom	-1.549	0.021
A 96 P16	Sense	0.214	Detected	-0.214	Detected	0.000	-1.291	Detected	-1.129	Detected	-1.210	0.034
A 96 P16	Sense	-0.663	Detected	0.663	Detected	0.000	-2.271	Detected	-1.072	Detected	-1.671	0.202
A 96 P16	Sense	0.466	Detected	-0.466	Detected	0.000	-0.876	Detected	-1.356	Detected	-1.116	0.167
A 96 P16	Sense	-0.097	Detected	0.097	Detected	0.000	-0.900	Detected	-1.475	Detected	-1.187	0.060
A 96 P16	Sense	-0.011	Detected	0.011	Detected	0.000	-1.156	Detected	-1.137	Detected	-1.146	0.000
A 96 P17	Sense	0.572	Detected	-0.572	Detected	0.000	-1.256	Detected	-1.804	Detected	-1.530	0.137
A 96 P17	Sense	0.187	Detected	-0.187	Detected	0.000	-1.693	Detected	-1.915	Detected	-1.804	0.014
A 96 P17	Sense	-0.154	Detected	0.154	Detected	0.000	-1.264	Detected	-1.645	Detected	-1.455	0.027
A 96 P17	Sense	-0.170	Detected	0.170	Detected	0.000	-1.022	Detected	-1.508	Detected	-1.265	0.051
A 96 P17	Sense	-0.003	Detected	0.003	Detected	0.000	-1.268	Detected	-1.158	Detected	-1.213	0.002
A 96 P17	Sense	-1.326	Detected	1.326	Detected	0.000	-1.763	Detected	-2.875	Detected	-2.319	0.248
A 96 P17	Sense	0.190	Detected	-0.190	Detected	0.000	-1.230	Detected	-0.868	Detected	-1.049	0.057
A 96 P17	Sense	0.513	Detected	-0.513	Detected	0.000	-0.831	Detected	-3.226	Detected	-2.029	0.260
A 96 P17	Sense	-0.105	Detected	0.105	Detected	0.000	-1.018	Detected	-1.708	Detected	-1.363	0.063
A 96 P17	Sense	-0.231	Detected	0.231	Detected	0.000	-1.769	Detected	-1.896	Comprom	-1.832	0.017
A 96 P18	Sense	-0.075	Detected	0.075	Detected	0.000	-1.068	Detected	-1.826	Comprom	-1.447	0.064
A 96 P18	Sense	0.514	Detected	-0.514	Detected	0.000	-1.059	Detected	-1.011	Detected	-1.035	0.182
A 96 P18	Sense	0.169	Detected	-0.169	Detected	0.000	-1.876	Detected	-2.129	Detected	-2.002	0.011
A 96 P18	Sense	-0.184	Detected	0.184	Detected	0.000	-0.975	Detected	-1.451	Detected	-1.213	0.056
A 96 P18	Sense	0.579	Detected	-0.579	Detected	0.000	-0.925	Detected	-1.089	Detected	-1.007	0.227
A 96 P19	Sense	-1.333	Detected	1.333	Detected	0.000	-1.657	Detected	-2.680	Detected	-2.168	0.268
A 96 P19	Sense	-0.520	Detected	0.520	Detected	0.000	-4.222	Detected	-2.194	Detected	-3.208	0.106
A 96 P20	Sense	-0.185	Detected	0.185	Detected	0.000	-0.852	Detected	-1.540	Detected	-1.196	0.092
A 96 P20	Sense	-0.669	Detected	0.669	Detected	0.000	-1.332	Detected	-1.307	Detected	-1.320	0.188
A 96 P20	Sense	-0.066	Detected	0.066	Detected	0.000	-1.664	Detected	-2.368	Comprom	-2.016	0.030
A 96 P20	Sense	0.465	Detected	-0.465	Detected	0.000	-1.094	Detected	-1.654	Detected	-1.374	0.127
A 96 P20	Sense	-0.267	Detected	0.267	Detected	0.000	-1.416	Detected	-2.261	Detected	-1.839	0.067
A 96 P20	Sense	0.154	Detected	-0.154	Detected	0.000	-1.532	Detected	-1.389	Comprom	-1.461	0.013
A 96 P21	Sense	0.020	Detected	-0.020	Detected	0.000	-1.744	Detected	-2.479	Detected	-2.112	0.029
A 96 P21	Sense	0.107	Detected	-0.107	Detected	0.000	-2.534	Comprom	-2.182	Comprom	-2.358	0.008
A 96 P21	Sense	0.260	Detected	-0.260	Detected	0.000	-1.289	Detected	-1.897	Detected	-1.593	0.058
A 96 P21	Sense	0.428	Detected	-0.428	Detected	0.000	-1.241	Detected	-0.802	Detected	-1.021	0.168
A 96 P21	Sense	0.150	Detected	-0.150	Detected	0.000	-1.684	Detected	-1.816	Detected	-1.750	0.009
A 96 P21	Sense	-0.113	Detected	0.113	Detected	0.000	-2.692	Detected	-1.412	Detected	-2.052	0.087
A 96 P22	Sense	0.035	Detected	-0.035	Detected	0.000	-0.956	Detected	-1.482	Detected	-1.219	0.044
A 96 P22	Sense	0.218	Detected	-0.218	Detected	0.000	-1.020	Detected	-0.989	Detected	-1.004	0.044
A 96 P22	Sense	-0.245	Detected	0.245	Detected	0.000	-1.049	Detected	-1.091	Detected	-1.070	0.049
A 96 P22	Sense	-0.490	Detected	0.490	Detected	0.000	-1.308	Comprom	-1.861	Comprom	-1.585	0.106
A 96 P22	Sense	-0.202	Detected	0.202	Detected	0.000	-1.227	Detected	-1.715	Detected	-1.471	0.043
A 96 P22	Sense	-0.076	Detected	0.076	Detected	0.000	-1.929	Detected	-2.056	Detected	-1.993	0.002
A 96 P23	Sense	0.145	Detected	-0.145	Detected	0.000	-1.021	Detected	-1.062	Detected	-1.041	0.019
A 96 P23	Sense	0.457	Detected	-0.457	Detected	0.000	-1.352	Detected	-1.885	Comprom	-1.619	0.092
A 96 P23	Sense	0.185	Detected	-0.185	Detected	0.000	-0.992	Detected	-1.234	Detected	-1.113	0.037
A 96 P23	Sense	0.583	Detected	-0.583	Detected	0.000	-1.058	Detected	-1.102	Detected	-1.080	0.205
A 96 P24	Sense	-1.099	Detected	1.099	Detected	0.000	-2.478	Detected	-3.096	Comprom	-2.787	0.135
A 96 P25	Sense	0.058	Detected	-0.058	Detected	0.000	-1.880	Detected	-1.212	Detected	-1.546	0.045
A 96 P25	Sense	-0.058	Detected	0.058	Detected	0.000	-1.720	Detected	-1.617	Detected	-1.669	0.002
A 96 P26	Sense	0.690	Detected	-0.690	Detected	0.000	-0.906	Detected	-1.170	Detected	-1.038	0.278
A 96 P26	Sense	-0.007	Detected	0.007	Detected	0.000	-1.414	Detected	-1.332	Detected	-1.373	0.001
A 96 P26	Sense	-1.030	Detected	1.030	Detected	0.000	-2.689	Detected	-2.646	Detected	-2.667	0.122
GT Sense	Sense	0.658	Detected	-0.658	Detected	0.000	-1.175	Detected	-1.739	Detected	-1.457	0.179
GT Sense	Sense	0.388	Detected	-0.388	Detected	0.000	-1.181	Detected	-1.081	Detected	-1.131	0.102
GT Sense	Sense	0.262	Detected	-0.262	Detected	0.000	-1.223	Detected	-1.521	Detected	-1.372	0.045
GT Sense	Sense	-0.427	Detected	0.427	Detected	0.000	-1.392	Detected	-0.871	Detected	-1.132	0.152
GT Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-0.895	Detected	-1.370	Detected	-1.132	0.053
GT Sense	Sense	0.237	Detected	-0.237	Detected	0.000	-1.553	Detected	-1.596	Detected	-1.575	0.022
GT Sense	Sense	0.502	Detected	-0.502	Detected	0.000	-3.099	Detected	-2.335	Detected	-2.717	0.050
GT Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.642	Detected	-1.788	Detected	-1.715	0.002
GT Sense	Sense	0.044	Detected	-0.044	Detected	0.000	-1.601	Detected	-2.181	Detected	-1.891	0.023
GT Sense	Sense	0.399	Detected	-0.399	Detected	0.000	-1.099	Detected	-1.558	Comprom	-1.329	0.102
GT Sense	Sense	-0.213	Detected	0.213	Detected	0.000	-1.999	Detected	-1.483	Detected	-1.741	0.035
GT Sense	Sense	0.100	Detected	-0.100	Detected	0.000	-1.732	Detected	-0.874	Detected	-1.303	0.098
GT Sense	Sense	-0.128	Detected	0.128	Detected	0.000	-1.483	Detected	-1.102	Detected	-1.293	0.030
GT Sense	Sense	2.536	Detected	-2.536	Detected	0.000	-1.438	Detected	-1.292	Detected	-1.365	0.644
GT Sense	Sense	-0.707	Detected	0.707	Detected	0.000	-1.200	Detected	-2.144	Detected	-1.672	0.188
GT Sense	Sense	0.261	Detected	-0.261	Detected	0.000	-0.826	Detected	-1.219	Detected	-1.023	0.089
GT Sense	Sense	0.165	Detected	-0.165	Detected	0.000	-1.456	Detected	-1.588	Detected	-1.522	0.013
GT Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-0.940	Detected	-1.195	Detected	-1.067	0.033
GT Sense	Sense	-0.206	Detected	0.206	Detected	0.000	-0.934	Detected	-1.468	Comprom	-1.201	0.070
GT Sense	Sense	-0.178	Detected	0.178	Detected	0.000	-2.652	Detected	-1.217	Detected	-1.934	0.120
GT Sense	Sense	-0.893	Detected	0.893	Detected	0.000	-3.561	Detected	-2.031	Detected	-2.796	0.141
GT Sense	Sense	0.018	Detected	-0.018	Detected	0.000	-1.216	Comprom	-0.934	Comprom	-1.075	0.017
GT Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-1.610	Detected	-1.820	Detected	-1.715	0.008
GT Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.112	Detected	-1.107	Detected	-1.109	0.004
GT Sense	Sense	-0.070	Detected	0.070	Detected	0.000	-2.045	Comprom	-2.422	Comprom	-2.233	0.008
GT Sense	Sense	-1.395	Detected	1.395	Detected	0.000	-3.526	Detected	-1.462	Detected	-2.494	0.287
GT Sense	Sense	-0.247	Detected	0.247	Detected	0.000	-0.817	Detected	-1.270	Detected	-1.043	0.089
GT Sense	Sense	-1.371	Detected	1.371	Detected	0.000	-1.773	Detected	-2.308	Comprom	-2.040	0.282
GT Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-0.984	Detected	-1.699	Detected	-1.341	0.067
GT Sense	Sense	-0.185	Detected	0.185	Detected	0.000	-1.312	Detected	-0.923	Comprom	-1.118	0.053
GT Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-0.840	Detected	-1.181	Detected	-1.010	0.033
GT Sense	Sense	0.207	Detected	-0.207	Detected	0.000	-0.890	Detected	-1.894	Comprom	-1.392	0.124
GT Sense	Sense	0.138	Detected	-0.138	Detected	0.000	-1.358	Detected	-1.220	Detected	-1.289	0.014
GT Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-1.323	Detected	-1.467	Detected	-1.395	0.005
GT Sense	Sense	0.140	Detected	-0.140	Detected	0.000	-1.447	Detected	-1.141	Detected	-1.294	0.025
GT Sense	Sense	-0.046	Detected	0.046	Detected	0.000	-2.367	Detected	-2.501	Detected	-2.434	0.001
GT Sense	Sense	-0.562	Detected	0.562	Detected	0.000	-1.606	Detected	-1.307	Detected	-1.456	0.129
GT Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-1.229	Detected	-0.956	Detected	-1.092	0.020
GT Sense	Sense	-1.023	Detected	1.023	Detected	0.000	-2.546	Detected	-2.852	Detected	-2.699	0.121
GT Sense	Sense	0.516	Detected	-0.516	Detected	0.000	-1.367	Detected	-1.818	Detected	-1.593	0.106
GT Sense	Sense	0.231	Detected	-0.231	Detected	0.000	-1.462	Detected	-1.245	Detected	-1.353	0.034
GT Sense	Sense	-0.270	Detected	0.270	Detected	0.000	-3.070	Comprom	-1.142	Comprom	-2.106	0.170
GT Sense	Sense	-0.590	Detected	0.590	Detected	0.000	-1.724	Detected	-2.522	Detected	-2.123	0.096
GT Sense	Sense	-0.020	Detected	0.020	Detected	0.000	-1.474	Detected	-1.412	Detected	-1.443	0.001
GT Sense	Sense	-0.278	Detected	0.278	Detected	0.000	-2.673	Detected	-1.048	Detected	-1.860	0.163
GT Sense	Sense	-0.286	Detected	0.286	Detected	0.000	-1.417	Comprom	-1.337	Comprom	-1.377	0.041
GT Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-1.782	Detected	-1.625	Detected	-1.704	0.004
GT Sense	Sense	1.112	Detected	-1.112	Detected	0.000	-1.359	Detected	-1.196	Detected	-1.278	0.370
GT Sense	Sense	-0.250	Detected	0.250	Detected	0.000	-1.775	Detected	-0.835	Detected	-1.305	0.134
GT Sense	Sense	-0.749	Detected	0.749	Detected	0.000	-1.141	Detected	-1.065	Detected	-1.103	0.279
GT Sense	Sense	0.322	Detected	-0.322	Detected	0.000	-1.998	Comprom	-1.085	Comprom	-1.541	0.110
GT Sense	Sense	0.449	Detected	-0.449	Detected	0.000	-2.344	Comprom	-0.983	Comprom	-1.663	0.178
GT Sense	Sense	0.260	Detected	-0.260	Detected	0.000	-1.413	Comprom	-1.864	Comprom	-1.639	0.041
GT Sense	Sense	0.009	Detected	-0.009	Detected	0.000	-2.975	Detected	-5.011	Detected	-3.993	0.059
GT Sense	Sense	0.086	Detected	-0.086	Detected	0.000	-2.063	Detected	-1.920	Detected	-1.992	0.003
GT Sense	Sense	-0.621	Detected	0.621	Detected	0.000	-1.043	Detected	-1.230	Detected	-1.137	0.212
GT Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-0.964	Detected	-1.897	Comprom	-1.431	0.092
GT Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-1.350	Detected	-1.045	Detected	-1.197	0.019
GT Sense	Sense	-1.044	Detected	1.044	Detected	0.000	-1.631	Detected	-1.120	Detected	-1.375	0.329
GT Sense	Sense	-0.180	Detected	0.180	Detected	0.000	-1.144	Detected	-1.050	Detected	-1.097	0.028
GT Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-1.068	Detected	-1.661	Detected	-1.364	0.044
GT Sense	Sense	0.144	Detected	-0.144	Detected	0.000	-1.579	Comprom	-0.862	Comprom	-1.220	0.087
GT Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-3.603	Comprom	-1.895	Comprom	-2.749	0.087
GT Sense	Sense	-0.329	Detected	0.329	Detected	0.000	-1.313	Detected	-1.318	Detected	-1.315	0.057
GT Sense	Sense	-1.039	Detected	1.039	Detected	0.000	-0.874	Detected	-1.198	Detected	-1.036	0.428
GT Sense	Sense	-0.132	Detected	0.132	Detected	0.000	-1.237	Detected	-1.529	Detected	-1.383	0.020
GT Sense	Sense	-0.322	Detected	0.322	Detected	0.000	-1.206	Detected	-1.126	Detected	-1.166	0.070
GT Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-2.036	Detected	-0.929	Detected	-1.482	0.119
GT Sense	Sense	-0.622	Detected	0.622	Detected	0.000	-2.048	Detected	-1.120	Detected	-1.584	0.178
GT Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-1.628	Detected	-1.325	Detected	-1.476	0.019
GT Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.219	Detected	-2.580	Detected	-1.899	0.108
GT Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-2.176	Detected	-1.456	Detected	-1.816	0.039
GT Sense	Sense	0.103	Detected	-0.103	Detected	0.000	-1.776	Detected	-1.875	Detected	-1.826	0.004
GT Sense	Sense	-0.011	Detected	0.011	Detected	0.000	-3.370	Detected	-1.456	Detected	-2.413	0.128
GT Sense	Sense	-0.337	Detected	0.337	Detected	0.000	-1.106	Detected	-0.986	Detected	-1.046	0.093
GT Sense	Sense	0.065	Detected	-0.065	Detected	0.000	-2.171	Detected	-1.828	Detected	-1.999	0.008
GT Sense	Sense	0.001	Detected	-0.001	Detected	0.000	-1.016	Detected	-1.412	Detected	-1.214	0.026
GT Sense	Sense	-0.021	Detected	0.021	Detected	0.000	-1.312	Detected	-1.722	Detected	-1.517	0.018
GT Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.656	Detected	-1.696	Detected	-1.676	0.003
GT Sense	Sense	-0.388	Detected	0.388	Detected	0.000	-1.792	Detected	-1.881	Detected	-1.836	0.042
GT Sense	Sense	0.035	Detected	-0.035	Detected	0.000	-1.356	Detected	-0.809	Detected	-1.083	0.059
GT Sense	Sense	0.413	Detected	-0.413	Detected	0.000	-1.669	Comprom	-0.985	Comprom	-1.327	0.132
GT Sense	Sense	0.167	Detected	-0.167	Detected	0.000	-1.618	Detected	-1.759	Detected	-1.688	0.011
GT Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.736	Detected	-2.034	Detected	-1.885	0.009
GT Sense	Sense	0.262	Detected	-0.262	Detected	0.000	-2.076	Comprom	-1.825	Comprom	-1.950	0.022
GT Sense	Sense	-0.203	Detected	0.203	Detected	0.000	-1.137	Detected	-0.956	Comprom	-1.046	0.042
GT Sense	Sense	-0.100	Detected	0.100	Detected	0.000	-1.375	Detected	-2.636	Detected	-2.006	0.088
GT Sense	Sense	-0.194	Detected	0.194	Detected	0.000	-1.245	Detected	-1.753	Detected	-1.499	0.042
GT Sense	Sense	0.109	Detected	-0.109	Detected	0.000	-1.947	Detected	-2.053	Detected	-2.000	0.004
GT Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-1.287	Detected	-1.739	Detected	-1.513	0.025
GT Sense	Sense	-0.126	Detected	0.126	Detected	0.000	-2.816	Detected	-1.323	Detected	-2.069	0.112
GT Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-2.005	Detected	-0.854	Detected	-1.430	0.139
GT Sense	Sense	0.065	Detected	-0.065	Detected	0.000	-1.431	Detected	-1.110	Detected	-1.271	0.018
GT Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-2.789	Detected	-1.825	Detected	-2.307	0.042
GT Sense	Sense	0.069	Detected	-0.069	Detected	0.000	-1.106	Detected	-1.350	Detected	-1.228	0.013
GT Sense	Sense	-0.156	Detected	0.156	Detected	0.000	-1.161	Detected	-0.845	Detected	-1.003	0.046
GT Sense	Sense	-0.429	Detected	0.429	Detected	0.000	-1.152	Detected	-1.375	Detected	-1.263	0.104
GT Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-0.856	Detected	-1.279	Detected	-1.067	0.038
GT Sense	Sense	-0.057	Detected	0.057	Detected	0.000	-1.520	Detected	-1.938	Detected	-1.729	0.015
GT Sense	Sense	-0.027	Detected	0.027	Detected	0.000	-1.096	Detected	-1.095	Comprom	-1.096	0.001
GT Sense	Sense	0.022	Detected	-0.022	Detected	0.000	-1.484	Detected	-1.001	Detected	-1.243	0.036
GT Sense	Sense	0.050	Detected	-0.050	Detected	0.000	-1.316	Detected	-1.624	Detected	-1.470	0.012
GT Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-2.045	Detected	-2.345	Detected	-2.195	0.005
GT Sense	Sense	-0.307	Detected	0.307	Detected	0.000	-2.810	Detected	-1.092	Detected	-1.951	0.166
GT Sense	Sense	-0.002	Detected	0.002	Detected	0.000	-1.255	Detected	-1.388	Detected	-1.322	0.003
GT Sense	Sense	0.017	Detected	-0.017	Detected	0.000	-1.106	Detected	-1.015	Detected	-1.060	0.002
GT Sense	Sense	-0.199	Detected	0.199	Detected	0.000	-0.983	Detected	-1.152	Detected	-1.067	0.039
GT Sense	Sense	-0.601	Detected	0.601	Detected	0.000	-2.120	Detected	-1.481	Detected	-1.800	0.118
GT Sense	Sense	0.253	Detected	-0.253	Detected	0.000	-1.182	Detected	-0.914	Comprom	-1.048	0.067
GT Sense	Sense	0.800	Detected	-0.800	Detected	0.000	-2.275	Comprom	-1.465	Detected	-1.870	0.172
GT Sense	Sense	0.157	Detected	-0.157	Detected	0.000	-1.204	Detected	-0.941	Detected	-1.073	0.035
GT Sense	Sense	-0.522	Detected	0.522	Detected	0.000	-2.792	Detected	-0.935	Detected	-1.864	0.222
GT Sense	Sense	0.836	Detected	-0.836	Detected	0.000	-4.285	Comprom	-1.543	Detected	-2.914	0.211
GT Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-1.968	Detected	-1.946	Detected	-1.957	0.008
GT Sense	Sense	0.225	Detected	-0.225	Detected	0.000	-1.228	Detected	-1.152	Detected	-1.190	0.035

GT	Sens	Sense	-0.217	Detected	0.217	Detected	0.000	-1.215	Detected	-0.894	Detected	-1.055	0.060
GT	Sens	Sense	0.448	Detected	-0.448	Detected	0.000	-0.852	Detected	-1.818	Comprom	-1.335	0.180
GT	Sens	Sense	0.048	Detected	-0.048	Detected	0.000	-2.124	Detected	-0.984	Detected	-1.554	0.113
GT	Sens	Sense	-0.006	Detected	0.006	Detected	0.000	-1.029	Detected	-1.138	Detected	-1.083	0.003
GT	Sens	Sense	0.243	Detected	-0.243	Detected	0.000	-1.311	Detected	-1.656	Detected	-1.483	0.038
GT	Sens	Sense	0.423	Detected	-0.423	Detected	0.000	-2.672	Comprom	-1.329	Comprom	-2.001	0.128
GT	Sens	Sense	-0.320	Detected	0.320	Detected	0.000	-1.296	Detected	-0.858	Detected	-1.077	0.109
GT	Sens	Sense	0.097	Detected	-0.097	Detected	0.000	-2.087	Detected	-2.027	Detected	-2.057	0.002
GT	Sens	Sense	-0.090	Detected	0.090	Detected	0.000	-1.023	Comprom	-1.699	Comprom	-1.361	0.060
GT	Sens	Sense	0.163	Detected	-0.163	Detected	0.000	-1.157	Detected	-1.259	Detected	-1.208	0.019
GT	Sens	Sense	-0.555	Detected	0.555	Detected	0.000	-2.287	Detected	-1.242	Detected	-1.764	0.147
GT	Sens	Sense	-0.030	Detected	0.030	Detected	0.000	-2.086	Comprom	-0.876	Comprom	-1.481	0.134
GT	Sens	Sense	-0.093	Detected	0.093	Detected	0.000	-1.850	Detected	-0.896	Detected	-1.373	0.106
GT	Sens	Sense	0.014	Detected	-0.014	Detected	0.000	-1.226	Detected	-1.509	Detected	-1.367	0.011
GT	Sens	Sense	-1.323	Detected	1.323	Detected	0.000	-3.505	Comprom	-2.210	Comprom	-2.858	0.192
GT	Sens	Sense	-0.009	Detected	0.009	Detected	0.000	-2.789	Detected	-1.966	Detected	-2.378	0.029
GT	Sens	Sense	-0.212	Detected	0.212	Detected	0.000	-1.113	Detected	-1.020	Detected	-1.066	0.039
GT	Sens	Sense	0.031	Detected	-0.031	Detected	0.000	-1.240	Detected	-0.926	Detected	-1.083	0.021
GT	Sens	Sense	-0.291	Detected	0.291	Detected	0.000	-1.604	Detected	-1.072	Detected	-1.338	0.077
GT	Sens	Sense	0.148	Detected	-0.148	Detected	0.000	-1.014	Detected	-1.098	Detected	-1.056	0.021
GT	Sens	Sense	-0.032	Detected	0.032	Detected	0.000	-1.199	Detected	-1.913	Detected	-1.556	0.049
GT	Sens	Sense	-0.613	Detected	0.613	Detected	0.000	-1.255	Detected	-1.999	Detected	-1.627	0.151
GT	Sens	Sense	-0.789	Detected	0.789	Detected	0.000	-1.230	Detected	-1.029	Detected	-1.129	0.291
GT	Sens	Sense	-0.548	Detected	0.548	Detected	0.000	-2.668	Detected	-0.912	Detected	-1.790	0.226
GT	Sens	Sense	0.277	Detected	-0.277	Detected	0.000	-1.245	Detected	-1.278	Detected	-1.261	0.045
GT	Sens	Sense	-0.504	Detected	0.504	Detected	0.000	-3.835	Detected	-2.090	Detected	-2.963	0.099
GT	Sens	Sense	-0.466	Detected	0.466	Detected	0.000	-0.852	Detected	-1.820	Detected	-1.336	0.185
GT	Sens	Sense	-0.054	Detected	0.054	Detected	0.000	-1.093	Detected	-1.233	Detected	-1.163	0.006
GT	Sens	Sense	0.579	Detected	-0.579	Detected	0.000	-1.235	Detected	-1.286	Detected	-1.261	0.161
GT	Sens	Sense	-0.414	Detected	0.414	Detected	0.000	-1.196	Detected	-1.042	Detected	-1.119	0.117
GT	Sens	Sense	-0.095	Detected	0.095	Detected	0.000	-1.830	Detected	-1.235	Detected	-1.532	0.039
GT	Sens	Sense	-0.446	Detected	0.446	Detected	0.000	-3.849	Detected	-2.888	Detected	-3.369	0.036
GT	Sens	Sense	1.032	Detected	-1.032	Detected	0.000	-1.639	Detected	-1.178	Detected	-1.409	0.314
GT	Sens	Sense	0.111	Detected	-0.111	Detected	0.000	-1.200	Detected	-1.756	Detected	-1.478	0.039
GT	Sens	Sense	-0.087	Detected	0.087	Detected	0.000	-1.455	Detected	-1.014	Detected	-1.235	0.035
GT	Sens	Sense	-1.311	Detected	1.311	Detected	0.000	-2.047	Detected	-3.050	Detected	-2.549	0.211
GT	Sens	Sense	-0.154	Detected	0.154	Detected	0.000	-1.035	Detected	-1.247	Detected	-1.141	0.026
GT	Sens	Sense	0.075	Detected	-0.075	Detected	0.000	-1.172	Detected	-1.200	Detected	-1.186	0.004
GT	Sens	Sense	0.112	Detected	-0.112	Detected	0.000	-1.667	Comprom	-2.381	Comprom	-2.024	0.032
GT	Sens	Sense	0.050	Detected	-0.050	Detected	0.000	-2.277	Detected	-1.912	Detected	-2.094	0.008
GT	Sens	Sense	-0.214	Detected	0.214	Detected	0.000	-1.546	Detected	-0.874	Detected	-1.210	0.094
GT	Sens	Sense	-0.092	Detected	0.092	Detected	0.000	-1.328	Detected	-0.980	Detected	-1.154	0.028
GT	Sens	Sense	-0.376	Detected	0.376	Detected	0.000	-1.565	Detected	-1.634	Detected	-1.599	0.051
GT	Sens	Sense	-0.004	Detected	0.004	Detected	0.000	-1.164	Detected	-1.483	Detected	-1.324	0.014
GT	Sens	Sense	0.073	Detected	-0.073	Detected	0.000	-1.753	Comprom	-1.930	Comprom	-1.842	0.004
GT	Sens	Sense	0.182	Detected	-0.182	Detected	0.000	-1.391	Comprom	-0.806	Comprom	-1.098	0.086
GT	Sens	Sense	-0.090	Detected	0.090	Detected	0.000	-1.010	Detected	-1.057	Detected	-1.034	0.008
GT	Sens	Sense	-0.002	Detected	0.002	Detected	0.000	-1.674	Detected	-0.997	Detected	-1.336	0.059
GT	Sens	Sense	-0.756	Detected	0.756	Detected	0.000	-1.263	Detected	-0.840	Detected	-1.052	0.312
GT	Sens	Sense	0.060	Detected	-0.060	Detected	0.000	-1.828	Detected	-1.680	Detected	-1.754	0.003
GT	Sens	Sense	-0.119	Detected	0.119	Detected	0.000	-1.891	Detected	-0.916	Detected	-1.404	0.107
GT	Sens	Sense	0.066	Detected	-0.066	Detected	0.000	-1.315	Detected	-1.908	Detected	-1.612	0.034
GT	Sens	Sense	0.028	Detected	-0.028	Detected	0.000	-2.356	Detected	-1.600	Detected	-1.978	0.035
GT	Sens	Sense	0.028	Detected	-0.028	Detected	0.000	-3.990	Detected	-1.501	Detected	-2.746	0.158
GT	Sens	Sense	0.146	Detected	-0.146	Detected	0.000	-0.887	Detected	-1.256	Detected	-1.071	0.045
GT	Sens	Sense	-0.742	Detected	0.742	Detected	0.000	-2.414	Detected	-1.737	Detected	-2.075	0.126
GT	Sens	Sense	0.116	Detected	-0.116	Detected	0.000	-1.758	Detected	-1.625	Detected	-1.692	0.006
GT	Sens	Sense	0.190	Detected	-0.190	Detected	0.000	-1.623	Comprom	-0.821	Comprom	-1.222	0.110
GT	Sens	Sense	-0.568	Detected	0.568	Detected	0.000	-2.663	Detected	-0.823	Detected	-1.743	0.248
GT	Sens	Sense	-0.143	Detected	0.143	Detected	0.000	-1.716	Detected	-1.260	Detected	-1.488	0.031
GT	Sens	Sense	0.149	Detected	-0.149	Detected	0.000	-2.466	Comprom	-2.537	Comprom	-2.501	0.004
GT	Sens	Sense	0.101	Detected	-0.101	Detected	0.000	-1.899	Detected	-1.505	Detected	-1.702	0.017
GT	Sens	Sense	-0.697	Detected	0.697	Detected	0.000	-0.914	Detected	-1.409	Detected	-1.162	0.257
GT	Sens	Sense	-0.036	Detected	0.036	Detected	0.000	-1.099	Detected	-1.150	Detected	-1.125	0.002
GT	Sens	Sense	-0.328	Detected	0.328	Detected	0.000	-2.322	Detected	-1.557	Detected	-1.940	0.061
GT	Sens	Sense	0.466	Detected	-0.466	Detected	0.000	-1.059	Detected	-1.447	Detected	-1.253	0.131
GT	Sens	Sense	-0.360	Detected	0.360	Detected	0.000	-3.563	Comprom	-0.848	Detected	-2.206	0.257
GT	Sens	Sense	-0.145	Detected	0.145	Detected	0.000	-1.025	Detected	-1.027	Detected	-1.026	0.019
GT	Sens	Sense	0.107	Detected	-0.107	Detected	0.000	-1.579	Detected	-1.463	Detected	-1.521	0.006
GT	Sens	Sense	-0.293	Detected	0.293	Detected	0.000	-2.086	Detected	-2.409	Detected	-2.247	0.021
GT	Sens	Sense	0.402	Detected	-0.402	Detected	0.000	-2.684	Comprom	-1.330	Comprom	-2.007	0.126
GT	Sens	Sense	0.214	Detected	-0.214	Detected	0.000	-2.175	Detected	-1.534	Detected	-1.855	0.041
GT	Sens	Sense	0.247	Detected	-0.247	Detected	0.000	-1.075	Detected	-0.966	Detected	-1.021	0.056
GT	Sens	Sense	-0.392	Detected	0.392	Detected	0.000	-1.084	Detected	-1.002	Detected	-1.043	0.118
GT	Sens	Sense	-0.047	Detected	0.047	Detected	0.000	-1.683	Detected	-2.153	Detected	-1.918	0.015
GT	Sens	Sense	-0.670	Detected	0.670	Detected	0.000	-1.218	Detected	-1.772	Detected	-1.495	0.175
GT	Sens	Sense	0.064	Detected	-0.064	Detected	0.000	-2.806	Detected	-3.096	Detected	-2.951	0.003
GT	Sens	Sense	-0.661	Detected	0.661	Detected	0.000	-2.701	Detected	-1.604	Detected	-2.153	0.129
GT	Sens	Sense	-0.280	Detected	0.280	Detected	0.000	-1.557	Detected	-1.013	Detected	-1.285	0.081
GT	Sens	Sense	0.215	Detected	-0.215	Detected	0.000	-1.176	Detected	-0.963	Detected	-1.070	0.047
GT	Sens	Sense	0.196	Detected	-0.196	Detected	0.000	-1.281	Detected	-0.907	Detected	-1.094	0.056
GT	Sens	Sense	-0.229	Detected	0.229	Detected	0.000	-1.748	Detected	-0.918	Detected	-1.333	0.107
GT	Sens	Sense	-0.307	Detected	0.307	Detected	0.000	-1.196	Detected	-0.820	Detected	-1.008	0.108
GT	Sens	Sense	-0.686	Detected	0.686	Detected	0.000	-2.813	Detected	-1.166	Detected	-1.989	0.204
GT	Sens	Sense	0.330	Detected	-0.330	Detected	0.000	-1.722	Comprom	-1.454	Comprom	-1.588	0.047
GT	Sens	Sense	0.086	Detected	-0.086	Detected	0.000	-1.711	Detected	-1.895	Detected	-1.803	0.005
GT	Sens	Sense	0.036	Detected	-0.036	Detected	0.000	-1.604	Detected	-1.649	Detected	-1.626	0.001
GT	Sens	Sense	0.427	Detected	-0.427	Detected	0.000	-1.023	Detected	-1.379	Detected	-1.201	0.122
GT	Sens	Sense	0.600	Detected	-0.600	Detected	0.000	-1.072	Detected	-1.279	Detected	-1.176	0.193
GT	Sens	Sense	0.164	Detected	-0.164	Detected	0.000	-1.235	Detected	-1.350	Detected	-1.293	0.018
GT	Sens	Sense	-0.507	Detected	0.507	Detected	0.000	-1.948	Detected	-0.873	Detected	-1.410	0.197
GT	Sens	Sense	0.094	Detected	-0.094	Detected	0.000	-2.168	Detected	-2.054	Detected	-2.111	0.003
GT	Sens	Sense	-0.208	Detected	0.208	Detected	0.000	-1.669	Detected	-0.843	Detected	-1.256	0.113
GT	Sens	Sense	-0.505	Detected	0.505	Detected	0.000	-1.440	Detected	-0.880	Detected	-1.160	0.182
GT	Sens	Sense	1.717	Detected	-1.717	Detected	0.000	-1.567	Detected	-1.499	Detected	-1.533	0.466
GT	Sens	Sense	0.147	Detected	-0.147	Detected	0.000	-1.263	Detected	-3.046	Comprom	-2.155	0.140
GT	Sens	Sense	-0.260	Detected	0.260	Detected	0.000	-0.849	Detected	-1.250	Detected	-1.049	0.086
GT	Sens	Sense	0.073	Detected	-0.073	Detected	0.000	-1.883	Detected	-1.161	Detected	-1.522	0.054
GT	Sens	Sense	0.147	Detected	-0.147	Detected	0.000	-1.290	Detected	-1.297	Comprom	-1.293	0.013
GT	Sens	Sense	0.077	Detected	-0.077	Detected	0.000	-1.907	Detected	-1.058	Detected	-1.482	0.075
GT	Sens	Sense	0.093	Detected	-0.093	Detected	0.000	-1.224	Detected	-1.205	Detected	-1.215	0.006
GT	Sens	Sense	-0.395	Detected	0.395	Detected	0.000	-3.523	Detected	-1.545	Detected	-2.534	0.140
GT	Sens	Sense	0.993	Detected	-0.993	Detected	0.000	-1.899	Detected	-1.399	Detected	-1.649	0.249
GT	Sens	Sense	-0.224	Detected	0.224	Detected	0.000	-2.390	Detected	-1.061	Detected	-1.725	0.133
GT	Sens	Sense	0.021	Detected	-0.021	Detected	0.000	-0.834	Detected	-1.239	Detected	-1.036	0.036
GT	Sens	Sense	-0.435	Detected	0.435	Detected	0.000	-1.085	Detected	-1.983	Comprom	-1.534	0.133
GT	Sens	Sense	-0.287	Detected	0.287	Detected	0.000	-2.188	Detected	-0.954	Detected	-1.571	0.147
GT	Sens	Sense	0.219	Detected	-0.219	Detected	0.000	-1.117	Comprom	-1.369	Comprom	-1.243	0.039
GT	Sens	Sense	-0.357	Detected	0.357	Detected	0.000	-1.676	Detected	-1.252	Detected	-1.464	0.072
GT	Sens	Sense	-0.519	Detected	0.519	Detected	0.000	-2.087	Detected	-0.943	Detected	-1.515	0.189
GT	Sens	Sense	-0.079	Detected	0.079	Detected	0.000	-1.140	Detected	-1.270	Detected	-1.205	0.007
GT	Sens	Sense	-0.885	Detected	0.885	Detected	0.000	-3.230	Detected	-1.675	Detected	-2.452	0.173
GT	Sens	Sense	0.176	Detected	-0.176	Detected	0.000	-1.067	Detected	-1.158	Detected	-1.112	0.026
GT	Sens	Sense	0.168	Detected	-0.168	Detected	0.000	-1.134	Detected	-1.704	Detected	-1.419	0.050
GT	Sens	Sense	-0.050	Detected	0.050	Detected	0.000	-1.494	Detected	-1.074	Detected	-1.284	0.027
GT	Sens	Sense	0.208	Detected	-0.208	Detected	0.000	-0.998	Detected	-1.391	Detected	-1.195	0.053
GT	Sens	Sense	-0.086	Detected	0.086	Detected	0.000	-1.076	Detected	-1.028	Detected	-1.052	0.007
GT	Sens	Sense	0.245	Detected	-0.245	Detected	0.000	-1.942	Detected	-1.293	Detected	-1.618	0.058
GT	Sens	Sense	-0.090	Detected	0.090	Detected	0.000	-1.205	Detected	-1.481	Detected	-1.343	0.015
GT	Sens	Sense	-0.327	Detected	0.327	Detected	0.000	-1.247	Detected	-0.941	Detected	-1.094	0.094
GT	Sens	Sense	-0.264	Detected	0.264	Detected	0.000	-3.516	Comprom	-2.795	Comprom	-3.156	0.019
GT	Sens	Sense	0.801	Detected	-0.801	Detected	0.000	-1.065	Detected	-1.032	Detected	-1.049	0.321
GT	Sens	Sense	-0.356	Detected	0.356	Detected	0.000	-1.673	Detected	-0.836	Detected	-1.254	0.150
GT	Sens	Sense	0.104	Detected	-0.104	Detected	0.000	-1.353	Detected	-1.920	Detected	-1.637	0.032
GT	Sens	Sense	0.185	Detected	-0.185	Detected	0.000	-1.397	Detected	-1.323	Detected	-1.360	0.019
GT	Sens	Sense	0.044	Detected	-0.044	Detected	0.000	-2.513	Detected	-1.188	Detected	-1.850	0.108
GT	Sens	Sense	-0.056	Detected	0.056	Detected	0.000	-2.615	Comprom	-1.773	Comprom	-2.194	0.036
GT	Sens	Sense	-0.430	Detected	0.430	Detected	0.000	-1.815	Detected	-1.089	Detected	-1.452	0.123
GT	Sens	Sense	0.173	Detected	-0.173	Detected	0.000	-0.914	Detected	-1.231	Detected	-1.072	0.045
GT	Sens	Sense	-0.241	Detected	0.241	Detected	0.000	-2.499	Comprom	-1.375	Comprom	-1.937	0.087
GT	Sens	Sense	-0.127	Detected	0.127	Detected	0.000	-3.076	Detected	-1.691	Detected	-2.383	0.077
GT	Sens	Sense	0.228	Detected	-0.228	Detected	0.000	-0.937	Detected	-1.445	Detected	-1.191	0.073
GT	Sens	Sense	0.954	Detected	-0.954	Detected	0.000	-2.769	Detected	-2.907	Detected	-2.838	0.097
GT	Sens	Sense	0.086	Detected	-0.086	Detected	0.000	-1.698	Detected	-1.853	Detected	-1.776	0.004
GT	Sens	Sense	0.863	Detected	-0.863	Detected	0.000	-1.325	Detected	-1.142	Detected	-1.234	0.291
GT	Sens	Sense	-0.622	Detected	0.622	Detected	0.000	-2.283	Detected	-1.262	Detected	-1.773	0.159
GT	Sens	Sense	-0.219	Detected	0.219	Detected	0.000	-2.426	Detected	-1.485	Detected	-1.956	0.064
GT	Sens	Sense	0.039	Detected	-0.039	Detected	0.000	-1.381	Detected	-1.223	Detected	-1.302	0.005
GT	Sens	Sense	0.068	Detected	-0.068	Detected	0.000	-2.851	Comprom	-1.271	Comprom	-2.061	0.122
GT	Sens	Sense	-0.351	Detected	0.351	Detected	0.000	-1.603	Detected	-1.517	Detected	-1.560	0.048
GT	Sens	Sense	-0.087	Detected	0.087	Detected	0.000	-2.240	Detected	-1.394	Detected	-1.817	0.052
GT	Sens	Sense	0.143	Detected	-0.143	Detected	0.000	-0.922	Detected	-1.086	Detected	-1.004	0.026
GT	Sens	Sense	-0.126	Detected	0.126	Detected	0.000	-3.019	Detected	-1.188	Detected	-2.103	0.151
GT	Sens	Sense	-0.230	Detected	0.230	Detected	0.000	-1.297	Detected	-1.102	Detected	-1.200	0.041
GT	Sens	Sense	0.044	Detected	-0.044	Detected	0.000	-2.451	Detected	-2.226	Detected	-2.338	0.003
GT	Sens	Sense	-0.271	Detected	0.271	Detected	0.000	-1.060	Detected	-1.932	Detected	-1.496	0.100
GT	Sens	Sense	-0.119	Detected	0.119	Detected	0.000	-1.117	Detected	-1.125	Detected	-1.121	0.011
GT	Sens	Sense	-0.398	Detected	0.398	Detected	0.000	-1.027	Detected	-1.482	Comprom	-1.254	0.112
GT	Sens	Sense	-0.553	Detected	0.553	Detected	0.000	-1.698	Detected	-0.932	Detected	-1.315	0.190
GT	Sens	Sense	-0.176	Detected	0.176	Detected	0.000	-2.375	Detected	-1.372	Detected	-1.873	0.072
GT	Sens	Sense	-0.026	Detected	0.026	Detected	0.000	-1.201	Detected	-0.880	Detected	-1.040	0.024
GT	Sens	Sense	-1.131	Detected	1.131	Detected	0.000	-2.222	Detected	-2.279	Detected	-2.250	0.185
GT	Sens	Sense	-0.492	Detected	0.492	Detected	0.000	-1.866	Detected	-2.099	Comprom	-1.983	0.059
GT	Sens	Sense	-0.128	Detected	0.128	Detected	0.000	-1.287	Detected	-0.815	Detected	-1.051	0.059
GT	Sens	Sense	0.228	Detected	-0.228	Detected	0.000	-1.324	Detected	-1.221	Detected	-1.272	0.032
GT	Sens	Sense	-0.309	Detected	0.309	Detected	0.000	-1.878	Detected	-0.981	Detected	-1.430	0.120
GT	Sens	Sense	-0.002	Detected	0.002	Detected	0.000	-2.259	Detected	-1.914	Detected	-2.087	0.007
GT	Sens	Sense	0.139	Detected	-0.139	Detected	0.000	-0.985	Detected	-1.660	Detected	-1.322	0.068
GT	Sens	Sense	-0.319	Detected	0.319	Detected	0.000	-1.050	Detected	-1.383	Detected	-1.217	0.077
GT	Sens	Sense	0.189	Detected	-0.189	Detected	0.000	-3.340	Comprom	-2.313	Comprom	-2.827	0.036
GT	Sens	Sense	0.029	Detected	-0.029	Detected	0.000	-1.451	Detected	-1.272	Detected	-1.361	0.005
GT	Sens	Sense	0.880	Detected	-0.880	Detected	0.000	-1.683	Detected	-1.948	Detected	-1.816	0.178
GT	Sens	Sense	-0.041	Detected	0.041	Detected	0.000	-3.060	Detected	-2.266	Detected	-2.663	0.022
GT	Sens	Sense	0.596	Detected	-0.596	Detected	0.000	-1.262	Detected	-0.871	Detected	-1.067	0.231
GT	Sens	Sense	-0.169	Detected	0.169	Detected	0.000	-1.499	Detected	-0.819	Detected	-1.159	0.093
GT	Sens	Sense	1.510	Detected	-1.510	Detected	0.000	-1.202	Detected	-1.567	Detected	-1.384	0.459
GT	Sens	Sense	-0.025	Detected	0.025	Detected	0.000	-1.969	Detected	-1.098	Detected	-1.533	0.072
GT	Sens	Sense	-0.046	Detected	0.046	Detected	0.000	-1.253	Detected	-0.885	Detected	-1.069	0.030
GT	Sens	Sense	-0.154	Detected	0.154	Detected	0.000	-1.358	Detected	-0.890	Detected	-1.124	0.057
GT	Sens	Sense	0.178	Detected	-0.178	Detected	0.000	-2.706	Detected	-0.989	Detected	-1.847	0.170
GT	Sens	Sense	-0.922	Detected	0.922	Detected	0.000	-2.068	Detected	-0.917	Detected	-1.493	0.303
GT	Sens	Sense	0.404	Detected	-0.404	Detected	0.000	-1.066	Detected	-1.194	Detected	-1.130	0.110
GT	Sens	Sense	0.144	Detected	-0.144	Detected	0.000	-2.173	Detected	-1.963	Detected	-2.068	0.007
GT	Sens	Sense	0.014	Detected	-0.014	Detected	0.000	-1.232	Detected	-1.372	Detected	-1.302	0.003
GT	Sens	Sense	-0.040	Detected	0.040	Detected	0.000	-1.119	Detected	-0.988	Detected	-1.053	0.005
GT	Sens	Sense	-0.100	Detected	0.100	Detected	0.000	-2.342	Detected	-1.336	Detected	-1.839	0.070
GT	Sens	Sense	0.054	Detected	-0.054	Detected	0.000	-1.612	Detected	-1.922	Detected	-1.767	0.009
GT	Sens	Sense	0.206	Detected	-0.206	Detected	0.000	-1.006	Detected	-1.430	Comprom	-1.218	0.054
GT	Sens	Sense	-0.415	Detected	0.415	Detected	0.000	-2.175	Detected	-0.948	Detected	-1.561	0.170
GT	Sens	Sense	0.088	Detected	-0.088	Detected	0.000	-2.345	Comprom	-1.773	Comprom	-2.059	0.020
GT	Sens	Sense	0.084	Detected	-0.084	Detected	0.000	-2.049	Detected	-1.443	Detected	-1.746	0.031
GT	Sens	Sense	0.188	Detected	-0.188	Detected	0.000	-2.775	Detected	-1.982	Detected	-2.379	0.032
GT	Sens	Sense	-0.330	Detected	0.330	Detected	0.000	-1.380	Detected	-1.005	Detected	-1.192	0.088
GT	Sens	Sense	-0.246	Detected	0.246	Detected	0.000	-1.589	Detected	-1.141	Detected	-1.365	0.055
GT	Sens	Sense	-0.849	Detected	0.849	Detected	0.000	-1.834	Detected	-1.257	Detected	-1.545	0.227
GT	Sens	Sense	-0.122	Detected	0.122	Detected	0.000	-1.402	Detected	-1.237	Detected	-1.320	0.012
GT	Sens	Sense	0.088	Detected	-0.088	Detected	0.000	-1.192	Detected	-1.478	Detected	-1.335	0.015
GT	Sens	Sense	-0.151	Detected	0.151	Detected	0.000	-1.131	Detected	-1.484	Detected	-1.307	0.030
GT	Sens	Sense	-0.566	Detected	0.566	Detected	0.000	-2.292	Detected	-0.947	Detected	-1.619	0.207
GT	Sens	Sense	-0.292	Detected	0.292	Detected	0.000	-1.414	Detected	-0.846	Detected	-1.130	0.109
GT	Sens	Sense	0.257	Detected	-0.257	Detected	0.000	-1.499	Comprom	-1.059	Comprom	-1.279	0.063
GT	Sens	Sense	-0.260	Detected	0.260	Detected	0.000	-2.581	Detected	-0.913	Detected	-1.747	0.184
GT	Sens	Sense	0.013	Detected	-0.013	Detected	0.000	-1.823	Detected	-2.422	Detected	-2.122	0.019
GT	Sens	Sense	-0.830	Detected	0.830	Detected	0.000	-1.152	Detected	-1.123	Detected	-1.138	0.304
GT	Sens	Sense	-0.177	Detected	0.177	Detected	0.000	-2.369	Comprom	-1.082	Comprom	-1.726	0.123
GT	Sens	Sense	-0.457	Detected	0.457	Detected	0.000	-2.265	Detected	-0.912	Detected	-1.589	0.191
GT	Sens	Sense	-0.119	Detected	0.119	Detected	0.000	-1.193	Detected	-1.247	Detected	-1.220	0.010
GT	Sens	Sense	0.146	Detected	-0.146	Detected	0.000	-1.065	Detected	-1.464	Detected	-1.265	0.036
GT	Sens	Sense	-0.568	Detected	0.568	Detected	0.000	-2.020	Detected	-1.342	Detected	-1.681	0.126
GT	Sens	Sense	-0.898	Detected	0.898	Detected	0.000	-5.237	Comprom	-3.136	Comprom	-4.187	0.094
GT	Sens	Sense	-0.043	Detected	0.043	Detected	0.000	-1.261	Detected	-1.472	Detected	-1.367	0.007
GT	Sens	Sense	-0.390	Detected	0.390	Detected	0.000	-2.565	Detected	-1.457	Detected	-2.011	0.097
GT	Sens	Sense	-0.129	Detected	0.129	Detected	0.000	-1.235	Detected	-1.131	Detected	-1.183	0.013
GT	Sens	Sense	-0.265	Detected	0.265	Detected	0.000	-1.353	Detected	-1.161	Detected	-1.257	0.047
GT	Sens	Sense	-0.553	Detected	0.553	Detected	0.000	-1.747	Detected	-1.242	Detected	-1.495	0.133
GT	Sens	Sense	-0.647	Detected	0.647	Detected	0.000	-1.885	Detected	-1.038	Detected	-1.462	0.199
GT	Sens	Sense	0.163	Detected	-0.163	Detected	0.000	-1.308	Detected	-0.897	Detected	-1.103	0.052
GT	Sens	Sense	-0.019	Detected	0.019	Detected	0.000	-0.868	Detected	-1.536	Detected	-1.202	0.069
GT	Sens	Sense	0.079	Detected	-0.079	Detected	0.000	-2.199	Detected	-2.129	Detected	-2.164	0.002
GT	Sens	Sense	-0.293	Detected	0.293	Detected	0.000	-1.159	Detected	-0.911	Detected	-1.035	0.083
GT	Sens	Sense	0.085	Detected	-0.085	Detected	0.000	-1.156	Comprom	-1.558	Comprom	-1.357	0.025
GT	Sens	Sense	0.009	Detected	-0.009	Detected	0.000	-1.721	Comprom	-1.779	Comprom	-1.750	0.000
GT	Sens	Sense	0.325	Detected	-0.325	Detected	0.000	-0.953	Detected	-1.761	Detected	-1.357	0.120
GT	Sens	Sense	0.844	Detected	-0.844	Detected	0.000	-0.875	Detected	-1.138	Detected	-1.006	0.360
GT	Sens	Sense	-0.303	Detected	0.303	Detected	0.000	-0.816	Detected	-1.845	Detected	-1.331	0.156
GT	Sens	Sense	0.018	Detected	-0.018	Detected	0.000	-1.177	Detected	-0.899	Detected	-1.038	0.018
GT	Sens	Sense	-1.533	Detected	1.533	Detected	0.000	-1.674	Detected	-1.449	Detected	-1.561	0.416
GT	Sens	Sense	0.390	Detected	-0.390	Detected	0.000	-0.930	Detected	-1.250	Detected	-1.090	0.123
GT	Sens	Sense	0.291	Detected	-0.291	Detected	0.000	-1.411	Detected	-0.942	Detected	-1.177	0.088
GT	Sens	Sense	-0.459	Detected	0.459	Detected	0.000	-1.148	Detected	-1.579	Detected	-1.364	0.115
GT	Sens	Sense	-0.103	Detected	0.103	Detected	0.000	-0.939	Detected	-1.270	Detected	-1.104	0.030
GT	Sens	Sense	0.144	Detected	-0.144	Detected	0.000	-0.865	Detected	-1.505	Comprom	-1.185	0.078
GT	Sens	Sense	0.076	Detected	-0.076	Detected	0.000	-2.248	Detected	-2.270	Detected	-2.259	0.001
GT	Sens	Sense	-0.010	Detected	0.010	Detected	0.000	-1.134	Detected	-0.991	Detected	-1.062	0.005
GT	Sens	Sense	0.165	Detected	-0.165	Detected	0.000	-1.026	Detected	-1.101	Detected	-1.064	0.024
GT	Sens	Sense	-0.210	Detected	0.210	Detected	0.000	-1.716	Detected	-1.539	Detected	-1.628	0.019
GT	Sens	Sense	0.032	Detected	-0.032	Detected	0.000	-1.386	Detected	-0.803	Detected	-1.095	0.065
GT	Sens	Sense	0.827	Detected	-0.827	Detected	0.000	-1.314	Detected	-0.828	Detected	-1.071	0.340
GT	Sens	Sense	-0.008	Detected	0.008	Detected	0.000	-1.780	Detected	-1.264	Detected	-1.522	0.028
GT	Sens	Sense	-0.075	Detected	0.075	Detected	0.000	-1.004	Detected	-1.531	Detected	-1.267	0.044
GT	Sens	Sense	-0.274	Detected	0.274	Detected	0.000	-1.749	Detected	-0.886	Detected	-1.317	0.123
GT	Sens	Sense	-0.279	Detected	0.279	Detected	0.000	-1.278	Detected	-2.514	Detected	-1.896	0.108
GT	Sens	Sense	-0.566	Detected	0.566	Detected	0.000	-3.401	Detected	-1.081	Detected	-2.241	0.225
GT	Sens	Sense	0.036	Detected	-0.036	Detected	0.000	-0.843	Detected	-1.466	Detected	-1.155	0.066
GT	Sens	Sense	0.006	Detected	-0.006	Detected	0.000	-1.594	Detected	-1.768	Detected	-1.681	0.003
GT	Sens	Sense	0.757	Detected	-0.757	Detected	0.000	-1.108	Detected	-1.857	Comprom	-1.483	0.221
GT	Sens	Sense	0.011	Detected	-0.011	Detected	0.000	-1.294	Detected	-1.502	Detected	-1.398	0.006
GT	Sens	Sense	-0.268	Detected	0.268	Detected	0.000	-2.855	Detected	-2.223	Detected	-2.539	0.026
GT	Sens	Sense	0.166	Detected	-0.166	Detected	0.000	-1.300	Detected	-1.560	Comprom	-1.430	0.021
GT	Sens	Sense	-0.284	Detected	0.284	Detected	0.000	-0.960	Detected	-1.126	Detected	-1.043	0.072
GT	Sens	Sense	0.154	Detected	-0.154	Detected	0.000	-1.070	Detected	-1.075	Detected	-1.073	0.020
GT	Sens	Sense	-0.389	Detected	0.389	Detected	0.000	-1.595	Detected	-1.321	Detected	-1.458	0.071
GT	Sens	Sense	0.065	Detected	-0.065	Detected	0.000	-0.937	Detected	-2.745	Comprom	-1.841	0.179
GT	Sens	Sense	0.247	Detected	-0.247	Detected	0.000	-2.730	Detected	-1.707	Detected	-2.218	0.060

GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-0.937	Detected	-2.771	Detected	-1.854	0.184	GT	Sens	contig293
GT	Sense	Sense	0.506	Detected	-0.506	Detected	0.000	-1.165	Detected	-1.003	Detected	-1.084	0.169	GT	Sens	contig293
GT	Sense	Sense	0.305	Detected	-0.305	Detected	0.000	-1.378	Comprom	-0.861	Comprom	-1.120	0.107	GT	Sens	contig293
GT	Sense	Sense	0.336	Detected	-0.336	Detected	0.000	-1.019	Detected	-1.209	Detected	-1.114	0.086	GT	Sens	contig294
GT	Sense	Sense	-0.286	Detected	0.286	Detected	0.000	-2.938	Detected	-1.389	Detected	-2.164	0.120	GT	Sens	contig294
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-1.064	Detected	-1.274	Detected	-1.169	0.013	GT	Sens	contig296
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-1.762	Detected	-1.489	Detected	-1.625	0.007	GT	Sens	contig296
GT	Sense	Sense	0.184	Detected	-0.184	Detected	0.000	-1.584	Comprom	-2.319	Comprom	-1.952	0.042	GT	Sens	contig297
GT	Sense	Sense	-0.026	Detected	0.026	Detected	0.000	-2.227	Comprom	-1.321	Comprom	-1.774	0.060	GT	Sens	contig297
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-0.904	Detected	-1.809	Detected	-1.357	0.104	GT	Sens	contig300
GT	Sense	Sense	0.148	Detected	-0.148	Detected	0.000	-0.821	Detected	-1.591	Comprom	-1.206	0.100	GT	Sens	contig300
GT	Sense	Sense	-0.130	Detected	0.130	Detected	0.000	-2.486	Detected	-1.610	Detected	-2.048	0.046	GT	Sens	contig300
GT	Sense	Sense	-0.859	Detected	0.859	Detected	0.000	-1.216	Detected	-1.195	Detected	-1.206	0.295	GT	Sens	contig300
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	-1.099	Detected	-1.270	Detected	-1.185	0.029	GT	Sens	contig300
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-1.355	Detected	-0.886	Detected	-1.121	0.050	GT	Sens	contig301
GT	Sense	Sense	-0.444	Detected	0.444	Detected	0.000	-2.891	Detected	-1.485	Detected	-2.188	0.119	GT	Sens	contig301
GT	Sense	Sense	-0.208	Detected	0.208	Detected	0.000	-1.375	Detected	-1.676	Detected	-1.526	0.027	GT	Sens	contig301
GT	Sense	Sense	0.409	Detected	-0.409	Detected	0.000	-2.854	Detected	-1.106	Detected	-1.980	0.177	GT	Sens	contig303
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-1.672	Detected	-1.459	Detected	-1.565	0.007	GT	Sens	contig304
GT	Sense	Sense	-0.351	Detected	0.351	Detected	0.000	-1.767	Detected	-1.290	Detected	-1.529	0.069	GT	Sens	contig304
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-1.131	Detected	-1.064	Detected	-1.098	0.003	GT	Sens	contig304
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	-1.440	Detected	-2.142	Detected	-1.791	0.036	GT	Sens	contig305
GT	Sense	Sense	-1.296	Detected	1.296	Detected	0.000	-2.299	Detected	-2.122	Comprom	-2.210	0.231	GT	Sens	contig305
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	-1.328	Detected	-1.561	Detected	-1.445	0.006	GT	Sens	contig305
GT	Sense	Sense	-0.278	Detected	0.278	Detected	0.000	-1.354	Detected	-0.911	Detected	-1.132	0.086	GT	Sens	contig306
GT	Sense	Sense	-0.344	Detected	0.344	Detected	0.000	-2.275	Detected	-1.022	Detected	-1.649	0.147	GT	Sens	contig306
GT	Sense	Sense	-0.246	Detected	0.246	Detected	0.000	-1.964	Detected	-2.192	Comprom	-2.078	0.017	GT	Sens	contig307
GT	Sense	Sense	0.581	Detected	-0.581	Detected	0.000	-1.185	Detected	-1.291	Detected	-1.238	0.168	GT	Sens	contig307
GT	Sense	Sense	-0.651	Detected	0.651	Detected	0.000	-1.409	Detected	-1.108	Detected	-1.258	0.201	GT	Sens	contig307
GT	Sense	Sense	0.328	Detected	-0.328	Detected	0.000	-1.309	Detected	-1.619	Comprom	-1.464	0.056	GT	Sens	contig307
GT	Sense	Sense	-0.149	Detected	0.149	Detected	0.000	-1.134	Detected	-1.223	Detected	-1.179	0.017	GT	Sens	contig307
GT	Sense	Sense	-0.225	Detected	0.225	Detected	0.000	-1.424	Detected	-0.821	Detected	-1.122	0.097	GT	Sens	contig307
GT	Sense	Sense	0.623	Detected	-0.623	Detected	0.000	-1.594	Detected	-0.994	Detected	-1.294	0.202	GT	Sens	contig308
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-3.386	Detected	-1.920	Detected	-2.653	0.069	GT	Sens	contig308
GT	Sense	Sense	0.343	Detected	-0.343	Detected	0.000	-2.027	Comprom	-1.751	Comprom	-1.889	0.036	GT	Sens	contig309
GT	Sense	Sense	1.041	Detected	-1.041	Detected	0.000	-1.925	Detected	-1.519	Detected	-1.722	0.246	GT	Sens	contig309
GT	Sense	Sense	0.326	Detected	-0.326	Detected	0.000	-1.059	Detected	-1.084	Detected	-1.072	0.082	GT	Sens	contig309
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	-0.956	Detected	-2.268	Comprom	-1.612	0.138	GT	Sens	contig310
GT	Sense	Sense	0.074	Detected	-0.074	Detected	0.000	-1.533	Detected	-1.431	Detected	-1.482	0.004	GT	Sens	contig311
GT	Sense	Sense	-0.274	Detected	0.274	Detected	0.000	-0.995	Detected	-1.528	Detected	-1.261	0.081	GT	Sens	contig311
GT	Sense	Sense	0.935	Detected	-0.935	Detected	0.000	-1.991	Detected	-1.240	Detected	-1.615	0.250	GT	Sens	contig312
GT	Sense	Sense	0.323	Detected	-0.323	Detected	0.000	-1.501	Detected	-0.877	Detected	-1.189	0.118	GT	Sens	contig313
GT	Sense	Sense	-0.018	Detected	0.018	Detected	0.000	-2.147	Detected	-2.326	Detected	-2.236	0.002	GT	Sens	contig313
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-1.036	Detected	-1.194	Detected	-1.115	0.020	GT	Sens	contig314
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-1.522	Comprom	-1.970	Comprom	-1.746	0.017	GT	Sens	contig315
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.718	Detected	-2.212	Detected	-1.965	0.018	GT	Sens	contig316
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	-1.953	Detected	-2.244	Detected	-2.098	0.006	GT	Sens	contig316
GT	Sense	Sense	-0.197	Detected	0.197	Detected	0.000	-0.849	Detected	-2.299	Comprom	-1.574	0.171	GT	Sens	contig316
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.446	Detected	-1.666	Detected	-1.556	0.008	GT	Sens	contig317
GT	Sense	Sense	-0.903	Detected	0.903	Detected	0.000	-1.508	Detected	-2.384	Comprom	-1.946	0.192	GT	Sens	contig317
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	-1.544	Comprom	-1.961	Comprom	-1.753	0.015	GT	Sens	contig318
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-1.380	Detected	-1.844	Detected	-1.612	0.026	GT	Sens	contig319
GT	Sense	Sense	0.163	Detected	-0.163	Detected	0.000	-1.695	Detected	-1.976	Detected	-1.836	0.013	GT	Sens	contig319
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-1.098	Detected	-1.398	Detected	-1.248	0.024	GT	Sens	contig319
GT	Sense	Sense	0.506	Detected	-0.506	Detected	0.000	-1.034	Detected	-1.522	Comprom	-1.278	0.151	GT	Sens	contig319
GT	Sense	Sense	0.000	Detected	0.000	Detected	0.000	-1.207	Comprom	-1.229	Comprom	-1.218	0.000	GT	Sens	contig320
GT	Sense	Sense	-0.220	Detected	0.220	Detected	0.000	-1.608	Detected	-1.761	Detected	-1.685	0.019	GT	Sens	contig321
GT	Sense	Sense	0.669	Detected	-0.669	Detected	0.000	-1.081	Detected	-1.301	Detected	-1.191	0.221	GT	Sens	contig321
GT	Sense	Sense	-0.207	Detected	0.207	Detected	0.000	-1.138	Detected	-1.466	Detected	-1.302	0.039	GT	Sens	contig321
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	-5.745	Comprom	-5.470	Comprom	-5.608	0.001	GT	Sens	contig322
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-4.373	Comprom	-3.588	Comprom	-3.980	0.010	GT	Sens	contig322
GT	Sense	Sense	0.253	Detected	-0.253	Detected	0.000	-1.261	Comprom	-1.600	Comprom	-1.431	0.042	GT	Sens	contig322
GT	Sense	Sense	-0.020	Detected	0.020	Detected	0.000	-0.882	Detected	-1.692	Comprom	-1.287	0.086	GT	Sens	contig322
GT	Sense	Sense	-0.364	Detected	0.364	Detected	0.000	-1.607	Detected	-1.048	Detected	-1.327	0.101	GT	Sens	contig322
GT	Sense	Sense	-1.360	Detected	1.360	Detected	0.000	-3.965	Comprom	-2.711	Comprom	-3.338	0.156	GT	Sens	contig323
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	-1.074	Detected	-0.999	Detected	-1.036	0.001	GT	Sens	contig323
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	-0.940	Detected	-1.077	Detected	-1.008	0.012	GT	Sens	contig323
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	-0.947	Detected	-1.297	Detected	-1.122	0.033	GT	Sens	contig324
GT	Sense	Sense	-0.510	Detected	0.510	Detected	0.000	-1.230	Detected	-2.262	Comprom	-1.746	0.138	GT	Sens	contig325
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	-1.736	Detected	-1.184	Detected	-1.460	0.035	GT	Sens	contig325
GT	Sense	Sense	-0.172	Detected	0.172	Detected	0.000	-1.631	Detected	-1.151	Detected	-1.391	0.042	GT	Sens	contig325
GT	Sense	Sense	-0.053	Detected	0.053	Detected	0.000	-1.110	Detected	-1.327	Detected	-1.219	0.010	GT	Sens	contig326
GT	Sense	Sense	0.007	Detected	-0.007	Detected	0.000	-1.349	Detected	-1.153	Detected	-1.251	0.006	GT	Sens	contig326
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	-1.785	Detected	-1.543	Detected	-1.664	0.005	GT	Sens	contig327
GT	Sense	Sense	-0.437	Detected	0.437	Detected	0.000	-4.569	Comprom	-3.850	Comprom	-4.209	0.018	GT	Sens	contig327
GT	Sense	Sense	0.555	Detected	-0.555	Detected	0.000	-0.963	Detected	-1.359	Detected	-1.161	0.188	GT	Sens	contig327
GT	Sense	Sense	-0.602	Detected	0.602	Detected	0.000	-1.112	Detected	-2.218	Detected	-1.665	0.179	GT	Sens	contig328
GT	Sense	Sense	0.262	Detected	-0.262	Detected	0.000	-1.542	Detected	-1.658	Detected	-1.600	0.027	GT	Sens	contig329
GT	Sense	Sense	0.232	Detected	-0.232	Detected	0.000	-1.832	Detected	-1.861	Detected	-1.846	0.015	GT	Sens	contig329
GT	Sense	Sense	0.095	Detected	-0.095	Detected	0.000	-1.501	Detected	-2.147	Detected	-1.824	0.032	GT	Sens	contig332
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-1.858	Detected	-2.574	Detected	-2.216	0.027	GT	Sens	contig332
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.469	Detected	-1.787	Detected	-1.628	0.009	GT	Sens	contig332
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.422	Detected	-1.781	Detected	-1.601	0.013	GT	Sens	contig332
GT	Sense	Sense	0.176	Detected	-0.176	Detected	0.000	-1.069	Detected	-1.871	Detected	-1.470	0.078	GT	Sens	contig332
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	-1.254	Detected	-1.527	Detected	-1.391	0.014	GT	Sens	contig332
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-0.880	Detected	-1.251	Detected	-1.066	0.034	GT	Sens	contig332
GT	Sense	Sense	-0.158	Detected	0.158	Detected	0.000	-1.509	Detected	-1.518	Detected	-1.513	0.011	GT	Sens	contig333
GT	Sense	Sense	-0.156	Detected	0.156	Detected	0.000	-1.298	Detected	-0.920	Detected	-1.109	0.046	GT	Sens	contig333
GT	Sense	Sense	-0.084	Detected	0.084	Detected	0.000	-1.834	Detected	-1.179	Detected	-1.507	0.047	GT	Sens	contig333
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-1.771	Detected	-1.865	Detected	-1.818	0.004	GT	Sens	contig333
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-2.124	Comprom	-2.505	Comprom	-2.315	0.007	GT	Sens	contig333
GT	Sense	Sense	0.447	Detected	-0.447	Detected	0.000	-1.112	Detected	-1.121	Detected	-1.117	0.130	GT	Sens	contig333
GT	Sense	Sense	0.397	Detected	-0.397	Detected	0.000	-1.387	Comprom	-1.164	Comprom	-1.275	0.091	GT	Sens	contig334
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-1.342	Detected	-1.292	Detected	-1.317	0.012	GT	Sens	contig334
GT	Sense	Sense	0.181	Detected	-0.181	Detected	0.000	-1.398	Detected	-1.071	Detected	-1.235	0.037	GT	Sens	contig334
GT	Sense	Sense	0.191	Detected	-0.191	Detected	0.000	-1.410	Comprom	-1.930	Comprom	-1.670	0.035	GT	Sens	contig334
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	-1.124	Detected	-1.447	Detected	-1.285	0.028	GT	Sens	contig335
GT	Sense	Sense	1.764	Detected	-1.764	Detected	0.000	-2.032	Detected	-1.058	Detected	-1.545	0.487	GT	Sens	contig335
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.501	Detected	-1.843	Detected	-1.672	0.014	GT	Sens	contig336
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.494	Detected	-2.200	Detected	-1.847	0.035	GT	Sens	contig336
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	-1.528	Detected	-2.030	Detected	-1.779	0.020	GT	Sens	contig336
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-1.888	Detected	-2.239	Detected	-2.064	0.009	GT	Sens	contig338
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-1.907	Detected	-2.118	Detected	-2.013	0.003	GT	Sens	contig338
GT	Sense	Sense	-0.289	Detected	0.289	Detected	0.000	-1.039	Comprom	-2.237	Comprom	-1.638	0.133	GT	Sens	contig338
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-1.948	Comprom	-3.114	Comprom	-2.531	0.051	GT	Sens	contig338
GT	Sense	Sense	0.194	Detected	-0.194	Detected	0.000	-3.596	Comprom	-2.217	Comprom	-2.907	0.056	GT	Sens	contig338
GT	Sense	Sense	-0.352	Detected	0.352	Detected	0.000	-1.197	Detected	-0.881	Detected	-1.039	0.115	GT	Sens	contig339
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	-1.073	Comprom	-1.333	Comprom	-1.203	0.011	GT	Sens	contig340
GT	Sense	Sense	-0.573	Detected	0.573	Detected	0.000	-2.149	Detected	-0.910	Detected	-1.530	0.212	GT	Sens	contig341
GT	Sense	Sense	-1.107	Detected	1.107	Detected	0.000	-2.205	Detected	-2.291	Detected	-2.248	0.180	GT	Sens	contig341
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	-1.408	Detected	-1.875	Detected	-1.641	0.034	GT	Sens	contig341
GT	Sense	Sense	0.192	Detected	-0.192	Detected	0.000	-1.691	Detected	-1.313	Detected	-1.502	0.031	GT	Sens	contig341
GT	Sense	Sense	-0.280	Detected	0.280	Detected	0.000	-0.937	Detected	-1.211	Detected	-1.074	0.075	GT	Sens	contig341
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	-0.865	Comprom	-2.225	Comprom	-1.545	0.153	GT	Sens	contig342
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	-1.806	Detected	-1.356	Detected	-1.581	0.020	GT	Sens	contig344
GT	Sense	Sense	-0.018	Detected	0.018	Detected	0.000	-1.359	Detected	-1.413	Detected	-1.386	0.001	GT	Sens	contig344
GT	Sense	Sense	-0.280	Detected	0.280	Detected	0.000	-1.047	Detected	-1.357	Detected	-1.202	0.064	GT	Sens	contig345
GT	Sense	Sense	1.620	Detected	-1.620	Detected	0.000	-0.932	Detected	-1.976	Comprom	-1.454	0.483	GT	Sens	contig345
GT	Sense	Sense	0.151	Detected	-0.151	Detected	0.000	-1.070	Detected	-1.833	Comprom	-1.451	0.072	GT	Sens	contig345
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	-0.906	Detected	-1.411	Comprom	-1.159	0.048	GT	Sens	contig345
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	-1.272	Comprom	-0.810	Comprom	-1.041	0.058	GT	Sens	contig346
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-1.910	Detected	-2.057	Detected	-1.984	0.004	GT	Sens	contig346
GT	Sense	Sense	0.180	Detected	-0.180	Detected	0.000	-1.564	Detected	-1.890	Detected	-1.727	0.019	GT	Sens	contig346
GT	Sense	Sense	0.085	Detected	-0.085	Detected	0.000	-1.969	Detected	-2.016	Detected	-1.993	0.002	GT	Sens	contig347
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	-1.825	Detected	-2.052	Detected	-1.938	0.004	GT	Sens	contig347
GT	Sense	Sense	0.303	Detected	-0.303	Detected	0.000	-1.038	Detected	-1.556	Comprom	-1.297	0.083	GT	Sens	contig347
GT	Sense	Sense	0.153	Detected	-0.153	Detected	0.000	-1.311	Comprom	-1.935	Comprom	-1.623	0.043	GT	Sens	contig347
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-1.481	Comprom	-1.123	Comprom	-1.302	0.023	GT	Sens	contig348
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-2.403	Detected	-2.230	Detected	-2.316	0.002	GT	Sens	contig348
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-2.053	Detected	-2.027	Detected	-2.040	0.001	GT	Sens	contig348
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	-1.089	Detected	-0.913	Detected	-1.001	0.023	GT	Sens	contig349
GT	Sense	Sense	-0.206	Detected	0.206	Detected	0.000	-1.067	Detected	-1.057	Detected	-1.062	0.036	GT	Sens	contig350
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-1.660	Comprom	-1.241	Comprom	-1.451	0.028	GT	Sens	contig351
GT	Sense	Sense	0.049	Detected	-0.049	Detected	0.000	-0.958	Detected	-1.348	Detected	-1.153	0.029	GT	Sens	contig351
GT	Sense	Sense	0.166	Detected	-0.166	Detected	0.000	-1.299	Detected	-1.594	Detected	-1.446	0.023	GT	Sens	contig351
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-2.292	Comprom	-1.676	Comprom	-1.984	0.025	GT	Sens	contig351
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.574	Comprom	-0.889	Comprom	-1.231	0.072	GT	Sens	contig352
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-1.494	Comprom	-1.060	Comprom	-1.277	0.028	GT	Sens	contig353
GT	Sense	Sense	0.074	Detected	-0.074	Detected	0.000	-1.648	Detected	-2.530	Comprom	-2.089	0.043	GT	Sens	contig353
GT	Sense	Sense	-0.091	Detected	0.091	Detected	0.000	-1.386	Comprom	-1.757	Comprom	-1.572	0.017	GT	Sens	contig354
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	-1.452	Comprom	-2.417	Comprom	-1.935	0.058	GT	Sens	contig356
GT	Sense	Sense	0.191	Detected	-0.191	Detected	0.000	-0.988	Comprom	-2.001	Comprom	-1.495	0.110	GT	Sens	contig356
GT	Sense	Sense	-0.420	Detected	0.420	Detected	0.000	-1.368	Detected	-0.987	Comprom	-1.177	0.125	GT	Sens	contig356
GT	Sense	Sense	0.246	Detected	-0.246	Detected	0.000	-1.856	Detected	-1.006	Detected	-1.431	0.100	GT	Sens	contig357
GT	Sense	Sense	0.184	Detected	-0.184	Detected	0.000	-2.270	Detected	-1.037	Detected	-1.654	0.124	GT	Sens	contig357
GT	Sense	Sense	1.446	Detected	-1.446	Detected	0.000	-1.252	Detected	-1.060	Detected	-1.156	0.509	GT	Sens	contig358
GT	Sense	Sense	0.380	Detected	-0.380	Detected	0.000	-1.115	Detected	-1.971	Comprom	-1.543	0.114	GT	Sens	contig360
GT	Sense	Sense	-0.332	Detected	0.332	Detected	0.000	-1.017	Detected	-1.239	Comprom	-1.128	0.084	GT	Sens	contig360
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	-1.011	Detected	-1.927	Comprom	-1.469	0.094	GT	Sens	contig360
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	-1.560	Detected	-1.916	Detected	-1.738	0.011	GT	Sens	contig361
GT	Sense	Sense	-0.050	Detected	0.050	Detected	0.000	-1.531	Comprom	-2.574	Comprom	-2.053	0.059	GT	Sens	contig361
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.272	Detected	-0.922	Detected	-1.097	0.038	GT	Sens	contig362
GT	Sense	Sense	0.238	Detected	-0.238	Detected	0.000	-1.534	Detected	-1.703	Detected	-1.618	0.023	GT	Sens	contig362
GT	Sense	Sense	0.143	Detected	-0.143	Detected	0.000	-1.175	Detected	-1.347	Detected	-1.261	0.017	GT	Sens	contig362
GT	Sense	Sense	0.855	Detected	-0.855	Detected	0.000	-1.834	Comprom	-1.389	Comprom	-1.611	0.210	GT	Sens	contig364
GT	Sense	Sense	-0.240	Detected	0.240	Detected	0.000	-1.159	Comprom	-1.150	Comprom	-1.155	0.041	GT	Sens	contig365
GT	Sense	Sense	0.347	Detected	-0.347	Detected	0.000	-1.632	Detected	-1.807	Detected	-1.720	0.041	GT	Sens	contig368
GT	Sense	Sense	0.270	Detected	-0.270	Detected	0.000	-1.253	Comprom	-1.713	Comprom	-1.483	0.053	GT	Sens	contig369
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	-1.874	Detected	-2.300	Detected	-2.087	0.016	GT	Sens	contig370
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.612	Detected	-2.318	Detected	-1.965	0.031	GT	Sens	contig370
GT	Sense	Sense	0.030	Detected	-0.030	Detected	0.000	-0.899	Detected	-1.147	Detected	-1.023	0.015	GT	Sens	contig370
GT	Sense	Sense	0.124	Detected	-0.124	Detected	0.000	-2.342	Detected	-2.322	Detected	-2.332	0.003	GT	Sens	contig370
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	-1.944	Detected	-2.438	Comprom	-2.191	0.021	GT	Sens	contig370
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	-1.755	Detected	-2.068	Detected	-1.911	0.014	GT	Sens	contig371
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-1.709	Detected	-1.259	Detected	-1.484	0.026	GT	Sens	contig371
GT	Sense	Sense	-0.196	Detected	0.196	Detected	0.000	-1.408	Detected	-1.249	Detected	-1.328	0.024	GT	Sens	contig372
GT	Sense	Sense	-0.253	Detected	0.253	Detected	0.000	-1.401	Detected	-1.255	Detected	-1.328	0.037	GT	Sens	contig372
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	-1.702	Detected	-2.505	Detected	-2.104	0.035	GT	Sens	contig372
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-1.505	Detected	-2.689	Detected	-2.097	0.071	GT	Sens	contig372
GT	Sense	Sense	0.345	Detected	-0.345	Detected	0.000	-1.082	Detected	-1.316	Comprom	-1.199	0.081	GT	Sens	contig372
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-1.229	Detected	-1.438	Detected	-1.334	0.012	GT	Sens	contig372
GT	Sense	Sense	1.528	Detected	-1.528	Detected	0.000	-1.410	Detected	-2.979	Comprom	-2.194	0.330	GT	Sens	contig373
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	-1.063	Detected	-1.110	Detected	-1.086	0.016	GT	Sens	contig373
GT	Sense	Sense	-0.016	Detected	0.016	Detected	0.000	-1.577	Detected	-1.264	Detected	-1.421	0.012	GT	Sens	contig373
GT	Sense	Sense	0.116	Detected	-0.116	Detected	0.000	-1.556	Detected	-1.605	Detected	-1.581	0.006	GT	Sens	contig373
GT	Sense	Sense	0.319	Detected	-0.319	Detected	0.000	-1.878	Comprom	-2.698	Comprom	-2.288	0.048	GT	Sens	contig373
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-0.866	Detected	-1.549	Detected	-1.208	0.078	GT	Sens	contig374
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-1.856	Comprom	-0.936	Comprom	-1.396	0.095	GT	Sens	contig374
GT	Sense	Sense	0.823	Detected	-0.823	Detected	0.000	-2.628	Comprom	-1.253	Comprom	-1.941	0.212	GT	Sens	contig375
GT	Sense	Sense	0.384	Detected	-0.384	Detected	0.000	-1.445	Detected	-1.683	Comprom	-1.564	0.060	GT	Sens	contig375
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-2.697	Comprom	-1.465	Comprom	-2.081	0.078	GT	Sens	contig376
GT	Sense	Sense	-0.360	Detected	0.360	Detected	0.000	-0.823	Detected	-1.284	Comprom	-1.054	0.133	GT	Sens	contig377
GT	Sense	Sense	-1.016	Detected	1.016	Detected	0.000	-1.202	Detected	-1.175	Detected	-1.188	0.363	GT	Sens	contig378
GT	Sense	Sense	-0.247	Detected	0.247	Detected	0.000	-1.271	Detected	-0.958	Detected	-1.115	0.063	GT	Sens	contig378
GT	Sense	Sense	-0.098	Detected	0.098	Detected	0.000	-1.822	Detected	-1.899	Comprom	-1.860	0.003	GT	Sens	contig378
GT	Sense	Sense	0.130	Detected	-0.130	Detected	0.000	-1.283	Detected	-1.570	Detected	-1.427	0.018	GT	Sens	contig379
GT	Sense	Sense	0.166	Detected	-0.166	Detected	0.000	-1.212	Detected	-0.909	Detected	-1.060	0.042	GT	Sens	contig379
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	-0.928	Detected	-1.216	Detected	-1.072	0.040	GT	Sens	contig381
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	-0.950	Detected	-1.521	Detected	-1.235	0.072	GT	Sens	contig381
GT	Sense	Sense	0.355	Detected	-0.355	Detected	0.000	-1.167	Detected	-1.047	Detected	-1.107	0.091	GT	Sens	contig382
GT	Sense	Sense	-0.304	Detected	0.304	Detected	0.000	-1.717	Detected	-1.401	Detected	-1.559	0.045	GT	Sens	contig383
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.385	Detected	-1.685	Detected	-1.535	0.012	GT	Sens	contig385
GT	Sense	Sense	0.083	Detected	-0.083	Detected	0.000	-1.586	Detected	-1.905	Detected	-1.745	0.010	GT	Sens	contig385
GT	Sense	Sense	-0.392	Detected	0.392	Detected	0.000	-1.419	Detected	-1.013	Comprom	-1.216	0.110	GT	Sens	contig386
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-2.601	Detected	-1.308	Detected	-1.955	0.096	GT	Sens	contig386
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-0.802	Detected	-1.281	Comprom	-1.042	0.055	GT	Sens	contig386
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-2.172	Detected	-1.863	Detected	-2.018	0.006	GT	Sens	contig387
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-2.543	Detected	-2.345	Detected	-2.444	0.003	GT	Sens	contig387
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-1.483	Detected	-1.885	Detected	-1.684	0.017	GT	Sens	contig387
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-0.990	Detected	-1.066	Comprom	-1.028	0.015	GT	Sens	contig388
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	-0.882	Detected	-1.731	Comprom	-1.307	0.107	GT	Sens	contig389
GT	Sense	Sense	-0.380	Detected	0.380	Detected	0.000	-1.831	Detected	-1.362	Detected	-1.597	0.070	GT	Sens	contig394
GT	Sense	Sense	-0.099	Detected	0.099	Detected	0.000	-1.184	Detected	-1.228	Detected	-1.206	0.007	GT	Sens	contig394
GT	Sense	Sense	-0.616	Detected	0.616	Detected	0.000	-1.673	Detected	-2.354	Comprom	-2.013	0.103	GT	Sens	contig394
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-1.755	Detected	-1.511	Detected	-1.633	0.011	GT	Sens	contig396
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-2.319	Detected	-2.320	Detected	-2.319	0.002	GT	Sens	contig396
GT	Sense	Sense	-0.066	Detected	0.066	Detected	0.000	-1.701	Detected	-1.600	Detected	-1.651	0.003	GT	Sens	contig397
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-3.202	Detected	-6.097	Comprom	-4.650	0.085	GT	Sens	contig399
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	-4.976	Comprom	-4.575	Comprom	-4.775	0.002	GT	Sens	contig399
GT	Sense	Sense	-0.181	Detected	0.181	Detected	0.000	-1.533	Comprom	-1.048	Comprom	-1.291	0.051	GT	Sens	contig400
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-1.086	Detected	-1.305	Comprom	-1.195	0.009	GT	Sens	contig400
GT	Sense	Sense	-0.426	Detected	0.426	Detected	0.000	-3.623	Detected	-2.689	Detected	-3.156	0.038	GT	Sens	contig400
GT	Sense	Sense	-0.387	Detected	0.387	Detected	0.000	-3.421	Detected	-2.434	Detected	-2.927	0.043	GT	Sens	contig400
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	-1.840	Comprom	-0.972	Comprom	-1.406	0.092	GT	Sens	contig401
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-0.969	Detected	-1.322	Detected	-1.146	0.024	GT	Sens	contig401
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.141	Detected	-1.092	Detected	-1.117	0.001	GT	Sens	contig401
GT	Sense	Sense	-0.014	Detected	0.014	Detected	0.000	-1.540	Comprom	-0.809	Comprom	-1.175	0.085	GT	Sens	contig401
GT	Sense	Sense	0.793	Detected	-0.793	Detected	0.000	-2.159	Comprom	-2.865	Comprom	-2.512	0.102	GT	Sens	contig402
GT	Sense	Sense	0.173	Detected	-0.173	Detected	0.000	-1.446	Comprom	-2.352	Comprom	-1.899	0.059	GT	Sens	contig402
GT	Sense	Sense	-0.170	Detected	0.170	Detected	0.000	-1.862	Detected	-2.976	Comprom	-2.419	0.053	GT	Sens	contig402
GT	Sense	Sense	-0.159	Detected	0.159	Detected	0.000	-1.235	Detected	-1.206	Detected	-1.221	0.017	GT	Sens	contig403
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.053	Detected	-1.045	Detected	-1.049	0.001	GT	Sens	contig403
GT	Sense	Sense	0.265	Detected	-0.265	Detected	0.000	-1.218	Detected	-1.795	Comprom	-1.506	0.061	GT	Sens	contig403
GT	Sense	Sense	-1.399	Detected	1.399	Detected	0.000	-1.268	Detected	-2.123	Detected	-1.696	0.366	GT	Sens	contig404
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-1.946	Detected	-2.230	Detected	-2.088	0.006	GT	Sens	contig405
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.096	Detected	-1.579	Detected	-1.338	0.035	GT	Sens	contig405
GT	Sense	Sense	0.099	Detected	-0.099	Detected	0.000	-1.389	Detected	-1.860	Detected	-1.624	0.024	GT	Sens	contig405
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	-1.437	Detected	-0.998	Detected	-1.217	0.035	GT	Sens	contig405
GT	Sense	Sense	0.218	Detected	-0.218	Detected	0.000	-1.636	Detected	-1.761	Detected	-1.699	0.017	GT	Sens	contig405
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.521	Detected	-2.490	Comprom	-2.006	0.056	GT	Sens	contig405
GT	Sense	Sense	0.085	Detected	-0.085	Detected	0.000	-1.621	Detected	-1.745	Detected	-1.683	0.004	GT	Sens	contig405
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-1.814	Detected	-1.831	Detected	-1.822	0.004	GT	Sens	contig405
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-0.969	Detected	-1.157	Detected	-1.063	0.014	GT	Sens	contig405
GT	Sense	Sense	0.278	Detected	-0.278	Detected	0.000	-1.143	Comprom	-2.490	Comprom	-1.816	0.130	GT	Sens	contig405
GT	Sense	Sense	0.105	Detected	-0.105	Detected	0.000	-1.899	Detected	-1.923	Detected	-1.911	0.003	GT	Sens	contig405
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-1.717	Detected	-1.582	Detected	-1.650	0.003	GT	Sens	contig406
GT	Sense	Sense	0.112	Detected	-0.112	Detected	0.000	-1.266	Detected	-1.100	Detected	-1.183	0.014	GT	Sens	contig406
GT	Sense	Sense	-1.066	Detected	1.066	Detected	0.000	-1.547	Detected	-2.084	Comprom	-1.815	0.240	GT	Sens	contig406
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	-1.835	Detected	-1.794	Detected	-1.814	0.000	GT	Sens	contig407
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-1.820	Detected	-1.552	Detected	-1.686	0.008	GT	Sens	contig407
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-1.063	Detected	-1.272	Detected	-1.167	0.011	GT	Sens	contig407
GT	Sense	Sense	0.168	Detected	-0.168	Detected	0.000	-1.476	Detected	-1.347	Detected	-1.412	0.016	GT	Sens	contig409
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-1.584	Detected	-1.445	Detected	-1.514	0.015	GT	Sens	contig409
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	-1.109	Detected	-1.579	Detected	-1.344	0.036	GT	Sens	contig410



GT	Sense	Sense	0.092	Detected	-0.092	Detected	0.000	-1.713	Detected	-1.807	Detected	-1.760	0.003	GT	Sens	contig410	contig410	Unannota	CTCAGGTGTAACTTGCTCCACTTCAGATTCTTCAGTAGGAGTTGGTTGA	contig410	Solyc07g	LRR rece	GO:00046	SL2.40ch	AT5G62360.1		invertase	chr5:250	607.127	636.173	328.808	254.66	213.507	167.883
GT	Sense	Sense	0.103	Detected	-0.103	Detected	0.000	-1.242	Comprom	-0.922	Comprom	-1.082	0.030	GT	Sens	contig410	contig410	Unannota	AACACCTAGGAACCAGTTGTCTGCCTTTCTTTTGTATCTTCCAAAAGTA	contig410	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G28300.1		trihelix D	chr5:102	22.6392	23.3669	21.7668	8.99201	10.9545	11.4782
GT	Sense	Sense	0.724	Detected	-0.724	Detected	0.000	-2.684	Comprom	-1.965	Comprom	-2.325	0.103	GT	Sens	contig410	contig410	Unannota	GGTGTTCTTGCGAATATCTACGAATTTCACCTCTACACTCGCAGTTCCA	contig410	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G54470.1		uridine 5	chr3:201	38.2961	16.7066	4.30032	2.71083	4.43411	6.12428
GT	Sense	Sense	0.050	Detected	-0.050	Detected	0.000	-1.041	Detected	-1.068	Detected	-1.055	0.002	GT	Sens	contig410	contig410	Unannota	ATTAGATGTCGTGCGACGACGCCGATGCCTTCTTTGCAAGGCCAATCC	contig410	Solyc00g010110.1.1				AT5G417	CIP1	CIP1 (CO	chr5:167	5549.3	6165.02	4425.79	4189.5	3201.03	2637.31
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-1.528	Detected	-1.504	Detected	-1.516	0.004	GT	Sens	contig410	contig410	Unannota	TGAGAATTTAATCACTGCAAAGATTGTTGGAGGAAGACCAAGGTTCACA	contig410	Solyc00g010110.1.1				AT5G417	CIP1	CIP1 (CO	chr5:167	3776.02	3965.94	2225.83	2063.55	1511.26	1289.65
GT	Sense	Sense	0.080	Detected	-0.080	Detected	0.000	-0.930	Detected	-1.102	Detected	-1.016	0.013	GT	Sens	contig410	contig410	Unannota	GTTGTTTTCTGGAGAGGAAAAATCAAGAGGACTACTGCTGGACCGGTG	contig410	Solyc10g	UPF0533	GO:00055	SL2.40ch	AT5G235	SGS3. AT	SGS3 (SU	chr5:794	309.153	329.404	222.256	185.881	188.658	140.585
GT	Sense	Sense	-0.076	Detected	0.076	Detected	0.000	-1.534	Detected	-1.820	Detected	-1.677	0.009	GT	Sens	contig411	contig411	Unannota	CACTCCGATAGTAGTATTGATCGTGTCAATGCAGAGGAAATGAATACAT	contig411	Solyc01g	Cytochro	GO:00160	SL2.40ch	ATCG007	PETD	A chloro	chrC:764	142.263	188.151	74.7273	68.684	63.6384	43.8106
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-1.414	Detected	-1.366	Detected	-1.390	0.001	GT	Sens	contig411	contig411	Unannota	ACTTATACTAGATCTTACGGAGCCTGCTCATGTACAACATGATTCGGAT	contig411	Solyc01g	Cytochro	GO:00160	SL2.40ch	ATCG007	PETD	A chloro	chrC:764	326.581	405.143	176.873	182.498	153.782	133.399
GT	Sense	Sense	-0.026	Detected	0.026	Detected	0.000	-1.187	Detected	-1.022	Detected	-1.104	0.006	GT	Sens	contig411	contig411	Unannota	AGCCCTTGAGATATCCCTCCCACATTGTGTAAACAATCTCTTCTCGTCG	contig411	Solyc06g	Auxin F-b	GO:00055	SL2.40ch	AT5G42957.1				34.633	42.7222	25.8735	29.859	19.0335	17.9081
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	-1.628	Detected	-1.604	Comprom	-1.616	0.001	GT	Sens	contig412	contig412	Unannota	CCTCCGTATTGATACATAAGTCATACGTGAGTGAAATATTCAAGAATAA	contig412	Solyc09g	AGAP009276-PA (Fr		SL2.40ch	AT4G21900.1		antiporte	chr4:116	32.4934	41.7142	16.7499	14.9494	13.4186	11.4482
GT	Sense	Sense	-0.799	Detected	0.799	Detected	0.000	-3.157	Detected	-3.062	Detected	-3.110	0.060	GT	Sens	contig412	contig412	Lipase-lik	GGCAGG contig412 Solyc02g Solyc02g Lipase-lik GO:00477 GO:00477	contig412	Solyc02g	Lipase-lik	GO:00477	SL2.40ch	AT2G31100.1		triacylgly	chr2:132	272.858	983.345	53.2799	147.277	65.4244	58.6263
GT	Sense	Sense	0.218	Detected	-0.218	Detected	0.000	-1.090	Detected	-1.837	Detected	-1.463	0.077	GT	Sens	contig412	contig412	Unannota	CCTTCCCTTTCCGTTGAGCTTACAAATCAATGCAATCTATGCAAGTATA	contig412	Solyc05g	Protease	GO:00082	SL2.40ch	AT5G49665.1		zinc fing	chr5:201	126.775	111.492	56.5606	50.8675	62.9187	31.4631
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-0.901	Detected	-1.146	Comprom	-1.023	0.027	GT	Sens	contig412	contig412	Unannota	CCACTACATGACCCTAAGTCCAAGACTCGAACTAGGTGTCTGATAATCA	contig412	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G65683.1		zinc fing	chr5:262	22.3513	22.4866	12.6583	16.2332	13.5245	9.57958
GT	Sense	Sense	0.111	Detected	-0.111	Detected	0.000	-2.708	Comprom	-1.595	Comprom	-2.152	0.063	GT	Sens	contig412	contig412	Unannota	TGGAGGTATTCTTCATTCTCAACCCTCCAGTTTGGCGAACGACTGCTCT	contig412	Solyc11g	Plastid DNA-binding		SL2.40ch	AT3G04760.1				11.7566	12.0054	4.83167	10.6779	2.04824	3.71751
GT	Sense	Sense	0.148	Detected	-0.148	Detected	0.000	-1.135	Detected	-1.149	Detected	-1.142	0.016	GT	Sens	contig412	contig412	Unannota	AACAAGTTGCTAACTTGCTCATTTTGTGATAGGTCCCAGTTACCCCCTT	contig412	Solyc11g	Pheophor	GO:00551	SL2.40ch	AT4G16630.1		DEAD/DE	chr4:936	57.4894	55.7345	32.3964	28.8566	29.0307	24.1367
GT	Sense	Sense	0.493	Detected	-0.493	Detected	0.000	-2.884	Comprom	-1.552	Comprom	-2.218	0.116	GT	Sens	contig413	contig413	Unannota	TATCCAATTCCCCGGAGATCAAATATGTGAACGCCGGCAGAACTGTAAC	contig413	Solyc10g	Protein pl	GO:00038	SL2.40ch	AT5G65570.1		pentatric	chr5:262	19.4668	11.6935	3.18911	11.6914	2.30291	4.86401
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-2.154	Detected	-2.421	Detected	-2.288	0.006	GT	Sens	contig413	contig413	Unannota	ACTTGTACAAATGGACATCCCAAACAAACCATGTCCAGACCATTATCCA	contig413	Solyc04g	Cysteine-	GO:00082	SL2.40ch	AT4G38070.1		bHLH fan	chr4:178	425.565	433.097	152.414	105.953	108.679	75.7815
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-1.292	Detected	-1.295	Detected	-1.293	0.005	GT	Sens	contig413	contig413	Unannota	TACAACCCACACGATGTCTACAGACCTCTAAGAGTATAGTAGTGAAACT	contig413	Solyc04g	Cysteine-	GO:00082	SL2.40ch	AT4G38070.1		bHLH fan	chr4:178	77.0685	81.1808	29.1832	17.8034	36.3815	30.4889
GT	Sense	Sense	0.202	Detected	-0.202	Detected	0.000	-1.080	Detected	-0.925	Detected	-1.002	0.044	GT	Sens	contig413	contig413	Unannota	TACAAGGAAGTTGGACTAGTTATTAGACCAACTATCTCACGCTCTCTCT	contig413	Solyc04g	Unknown Protein (A		SL2.40ch	AT1G58602.2		ATP bind	chr1:217	63.1075	56.7408	41.1927	36.1375	31.8959	29.8023
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-0.953	Detected	-1.589	Detected	-1.271	0.059	GT	Sens	contig414	contig414	Unannota	CGATAAGGCATGAGTTCTAGTATCATGAGTGTTTCTTCATAGGAACATC	contig414	Solyc01g	30S ribos	GO:00058	SL2.40ch	ATCG00810.1				50.1742	55.271	34.6629	31.5131	30.6442	16.5552
GT	Sense	Sense	0.194	Detected	-0.194	Detected	0.000	-0.943	Detected	-1.076	Detected	-1.009	0.039	GT	Sens	contig415	contig415	Unannota	TTGTCTTGCCAAAAAGAGGTTTTCTGCCCATTTCCTATCCTCACCTTAG	contig415	Solyc08g	ATP-depe	GO:00171	SL2.40ch	AT4G30150.1		EXPRES	chr4:147	40.6259	36.9693	35.6299	29.436	22.7109	17.3864
GT	Sense	Sense	0.340	Detected	-0.340	Detected	0.000	-1.477	Detected	-0.841	Detected	-1.159	0.130	GT	Sens	contig416	contig416	Unannota	TTCAGATCCTTCATCTGGACTTGAATGGGATTGCCCTGATCACAACTTC	contig416	Solyc03g	Aquapori	GO:00152	SL2.40ch	AT1G016	PIP1C. TI	PIP1C (P	chr1:225	84.9043	63.1281	48.4821	68.2114	29.6355	38.6332
GT	Sense	Sense	-0.249	Detected	0.249	Detected	0.000	-1.285	Comprom	-2.465	Comprom	-1.875	0.100	GT	Sens	contig416	contig416	Unannota	TATCTGTTGCTTATATGGTTTACTGGAGAGCAAACTCTTTTGTCAATCA	contig416	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G62810.1		copper a	chr1:232	12.9263	21.7269	9.07797	11.4041	7.74657	2.86918
GT	Sense	Sense	0.180	Detected	-0.180	Detected	0.000	-1.990	Detected	-1.941	Detected	-1.966	0.008	GT	Sens	contig416	contig416	Unannota	GAAGTAAGGAAAATAGGGGAGGTGCTGCCGAATTTTCGTTAGATTATTA	contig416	Solyc00g	H-ATPase	GO:00085	SL2.40ch	AT5G18840.1		sugar tra	chr5:628	1333.37	1236.47	478.755	392.681	364.089	316.143
GT	Sense	Sense	0.223	Detected	-0.223	Detected	0.000	-1.853	Detected	-1.775	Detected	-1.814	0.015	GT	Sens	contig416	contig416	Unannota	AATAGCTTGAGCAGTAAATATTGGACGTGCGGCTCAATTATACGGTGTA	contig416	Solyc00g	H-ATPase	GO:00085	SL2.40ch	AT5G18840.1		sugar tra	chr5:628	718.184	627.899	290.859	202.778	209.38	185.572
GT	Sense	Sense	-0.781	Detected	0.781	Detected	0.000	-1.652	Detected	-1.007	Detected	-1.329	0.256	GT	Sens	contig416	contig416	Unannota	ATGGATATCTGTTTTGTTAGGACTGAGCACAGGAGGGTTGCGGAACTG	contig416	Solyc05g	Kelch repeat-contai		SL2.40ch	AT5G608	ATMYB34	MYB34 (I	chr5:244	171.699	603.808	156.643	120.368	115.433	151.465
GT	Sense	Sense	-0.501	Detected	0.501	Detected	0.000	-1.136	Detected	-0.889	Detected	-1.012	0.189	GT	Sens	contig416	contig416	Receptor	AAAGCA contig416 Solyc09g Solyc09g Receptor GO:00046 GO:00046	contig416	Solyc09g	Receptor	GO:00046	SL2.40ch	AT4G003	CRCK2	CRCK2:	chr4:142	625.588	1492.28	566.224	920.07	495.132	493.466

GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.420	Detected	-2.095	Detected	-1.757	0.037	GT	Sens	contig182	contig182	DNA-dire	TGAATC	contig182	Solyc04g	Solyc04g	DNA-dire	GO:0006350		contig182	Solyc04g049730.1.1				ATCG001	RPOC2	RNA poly	chrC:15	317.627	418.11	156.206	148.97	153.463	80.6648
GT	Sense	Sense	0.117	Detected	-0.117	Detected	0.000	-1.243	Detected	-1.010	Detected	-1.126	0.021	GT	Sens	contig184	contig184	Unknown	GATGGG	contig184	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig184	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G26749.1				171.615	173.666	126.635	112.479	82.1611	81.0589
GT	Sense	Sense	0.080	Detected	-0.080	Detected	0.000	-1.623	Detected	-1.113	Detected	-1.368	0.036	GT	Sens	contig186	contig186	Pol polyp	TGAGAG	contig186	Solyc01g	Solyc01g	Pol polyprotein (AHRD V1 ***- (			contig186	Solyc01g	Pol polyprotein (AH		SL2.40ch	AT3G52561.1				109.6	116.861	62.459	50.1946	41.3913	49.4893
GT	Sense	Sense	0.018	Detected	-0.018	Detected	0.000	-1.484	Detected	-1.661	Detected	-1.572	0.003	GT	Sens	contig187	contig187	Ycf2 (AHF	TGTGGG	contig187	Solyc04g	Solyc04g	Ycf2 (AHF	GO:0009	GO:0009	contig187	Solyc01g	Ycf2 (AHF	GO:0005	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:14	570.316	661.955	270.027	209.615	247.447	183.745
GT	Sense	Sense	0.555	Detected	-0.555	Detected	0.000	-0.957	Detected	-1.076	Detected	-1.016	0.210	GT	Sens	contig188	contig188	Sulfotran	GAAGAG	contig188	Solyc05g	Solyc05g	Sulfotran	GO:0008	GO:0008	contig188	Solyc05g	Sulfotran	GO:0080	SL2.40ch	AT3G137	AtcwINV5	AtcwINV	chr3:452	794.788	438.259	730.575	491.262	342.496	264.685
GT	Sense	Sense	-0.092	Detected	0.092	Detected	0.000	-1.519	Detected	-1.142	Detected	-1.331	0.024	GT	Sens	contig189	contig189	Unknown	TGAATC	contig189	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)%			contig189	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G099	EMB1691	EMB169	chr4:624	39.9784	54.0862	27.0886	26.2868	18.2743	19.9228
GT	Sense	Sense	-0.180	Detected	0.180	Detected	0.000	-1.676	Detected	-0.937	Detected	-1.306	0.086	GT	Sens	contig190	contig190	Unknown	CATGGG	contig190	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig190	Solyc01g	Disease resistance		SL2.40ch	AT3G13650.1				4724.41	7213.83	3695.05	9402.31	2058.2	2882.91
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-1.738	Detected	-1.552	Detected	-1.645	0.007	GT	Sens	contig190	contig190	Gag-Pol p	CATTTG	contig190	Solyc01g	Solyc01g	Gag-Pol polyprotein (AHRD V1			contig190	Solyc01g	Gag-Pol polyprotein		SL2.40ch	AT3G52561.1				280.694	288.668	130.144	112.142	96.1526	91.8055
GT	Sense	Sense	-0.472	Detected	0.472	Detected	0.000	-2.015	Detected	-2.018	Detected	-2.016	0.051	GT	Sens	contig193	contig193	Alcohol d	GGTAAT	contig193	Solyc12g	Solyc12g	Alcohol d	GO:0008	GO:0008	contig193	Solyc12g	Alcohol d	GO:0008	SL2.40ch	AT5G16980.1		NADP-de	chr5:557	1285.15	2943.73	1015.6	2083.96	542.28	453.951
GT	Sense	Sense	-0.510	Detected	0.510	Detected	0.000	-1.783	Detected	-0.908	Detected	-1.346	0.183	GT	Sens	contig193	contig193	Purple ac	ATGTGG	contig193	Solyc01g	Solyc01g	Purple ac	GO:0046	GO:0046	contig193	Solyc01g	Purple ac	GO:0004	SL2.40ch	AT2G164	PAP10. A	PAP10 (P	chr2:712	2296.97	5543.04	1096.29	3126.67	1167.59	1798.18
GT	Sense	Sense	0.530	Detected	-0.530	Detected	0.000	-1.064	Detected	-1.102	Detected	-1.083	0.178	GT	Sens	contig194	contig194	UDP-gluc	AAACAT	contig194	Solyc12g	Solyc12g	UDP-gluc	GO:0008	GO:0008	contig194	Solyc12g	UDP-gluc	GO:0008	SL2.40ch	AT1G223	AtUGT85	AtUGT85	chr1:789	881.322	502.972	365.628	572.149	358.787	293.212
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.262	Detected	-1.414	Detected	-1.338	0.003	GT	Sens	contig194	contig194	Gag-Pol p	TCATCT	contig194	Solyc07g	Solyc07g	Gag-Pol polyprotein (AHRD V1			contig194	Solyc10g	Gag-Pol polyprotein		SL2.40ch	AT5G11250.1		disease r	chr5:358	563.296	651.672	295.264	231.774	284.621	215.003
GT	Sense	Sense	0.162	Detected	-0.162	Detected	0.000	-1.199	Detected	-1.562	Detected	-1.381	0.030	GT	Sens	contig195	contig195	Ycf1 (AHF	AAGCGA	contig195	Solyc01g	Solyc01g	Ycf1 (AHRD V1 *--- D2KLR1_OL			contig195	Solyc11g	Unknown Protein (A		SL2.40ch	AT2G45380.1		FUNCTIO	chr2:186	192.54	183.007	88.7853	82.9515	92.0897	60.1204
GT	Sense	Sense	0.080	Detected	-0.080	Detected	0.000	-2.014	Comprom	-1.829	Comprom	-1.921	0.004	GT	Sens	contig195	contig195	Mutator-li	ACAAAA	contig195	Solyc01g	Solyc01g	Mutator-li	GO:0008	GO:0008	contig195	Solyc04g054620.1.1				AT4G23230.1		protein k	chr4:121	15.7461	16.7787	6.51092	9.43809	4.53427	4.32635
GT	Sense	Sense	0.099	Detected	-0.099	Detected	0.000	-1.680	Detected	-1.624	Detected	-1.652	0.004	GT	Sens	contig199	contig199	Unknown	CCTGTG	contig199	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig199	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G297	NFC5. MS	NFC5 (Nu	chr4:145	6965.77	7225.97	3590.84	2822.47	2494.12	2176.98
GT	Sense	Sense	0.019	Detected	-0.019	Detected	0.000	-1.013	Detected	-1.350	Detected	-1.182	0.020	GT	Sens	contig202	contig202	Ycf2 (AHF	GCAATT	contig202	Solyc04g	Solyc04g	Ycf2 (AHF	GO:0009	GO:0009	contig202	Solyc01g	Ycf2 (AHF	GO:0005	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:14	1311.81	1520.81	732.776	701.874	788.339	523.881
GT	Sense	Sense	-0.061	Detected	0.061	Detected	0.000	-1.188	Detected	-1.474	Detected	-1.331	0.013	GT	Sens	contig203	contig203	Orf146 pr	TGAAGT	contig203	Solyc11g	Solyc11g	Orf146 protein (AHRD V1 ***- O			contig203	Solyc11g	Orf146 protein (AHR		SL2.40ch	AT1G452	ABF2. AR	ABF2 (AE	chr1:171	172.097	222.879	96.5204	76.1345	96.8612	66.643
GT	Sense	Sense	0.154	Detected	-0.154	Detected	0.000	-1.944	Detected	-1.879	Detected	-1.912	0.007	GT	Sens	contig205	contig205	%26apos	GCCAAC	contig205	Solyc04g	Solyc04g	%26aposchromo%26apos dor			contig205	Solyc04g	&aposchromo&apo		SL2.40ch	AT3G51120.1		DNA bind	chr3:189	2799	2692.41	1237.17	899.893	803.886	705.486
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-1.954	Detected	-1.857	Detected	-1.905	0.002	GT	Sens	contig205	contig205	%26apos	AATTGT	contig205	Solyc07g	Solyc07g	%26apos	GO:0008	GO:0008	contig205	Solyc07g	&aposchi	GO:0008	SL2.40ch	AT1G20220.1		nucleic a	chr1:700	2557.64	2732.7	1050.29	773.055	768.753	690.275
GT	Sense	Sense	-0.947	Detected	0.947	Detected	0.000	-2.430	Detected	-1.120	Detected	-1.775	0.263	GT	Sens	contig206	contig206	Peroxida	GAAACC	contig206	Solyc05g	Solyc05g	Peroxida	GO:0005	GO:0005	contig206	Solyc05g	Peroxida	GO:0004	SL2.40ch	AT3G21770.1		peroxida	chr3:767	289.364	1280.59	360.881	951.95	127.26	264.906
GT	Sense	Sense	0.117	Detected	-0.117	Detected	0.000	-0.925	Detected	-1.078	Detected	-1.001	0.019	GT	Sens	contig207	contig207	Sieve ele	GCATAC	contig207	Solyc03g	Solyc03g	Sieve element-occluding prote			contig207	Solyc03g	Sieve element-occlu		SL2.40ch	AT5G01320.1		pyruvate	chr5:129	8599.71	8699.02	9699.08	7322.25	5132.66	3874.52
GT	Sense	Sense	1.162	Detected	-1.162	Detected	0.000	-0.907	Detected	-1.164	Detected	-1.036	0.469	GT	Sens	contig210	contig210	Endochiti	TTCTTT	contig210	Solyc10g	Solyc10g	Endochiti	GO:0005	GO:0005	contig210	Solyc10g	Endochiti	GO:0008	SL2.40ch	AT3G125	ATHCHIB	ATHCHIB	chr3:396	77.2414	18.3605	26.6455	19.0216	22.6285	15.8861
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.230	Detected	-1.071	Detected	-1.151	0.006	GT	Sens	contig210	contig210	Polyprote	AGTGAA	contig210	Solyc05g	Solyc05g	Polyprotein (AHRD V1 ***- O9X			contig210	Solyc05g	Polyprotein (AHRD V		SL2.40ch	AT3G185	RTFL20. I	RTFL20 (	chr3:636	325.985	366.456	210.703	150.887	165.944	155.546
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-1.538	Detected	-1.245	Detected	-1.392	0.019	GT	Sens	contig210	contig210	Unknown	AAATGA	contig210	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig210	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G17920.2		protein b	chr3:613	66964.9	66513.4	38051.3	28870.6	25891.3	26618.5
GT	Sense	Sense	0.050	Detected	-0.050	Detected	0.000	-1.436	Detected	-0.900	Detected	-1.168	0.050	GT	Sens	contig213	contig213	Gag-Pol p	TGATAG	contig213	Solyc09g	Solyc09g	Gag-Pol polyprotein (AHRD V1			contig213	Solyc09g	Gag-Pol polyprotein		SL2.40ch	AT1G09750.1		chloropla	chr1:315	43.954	48.8147	30.5692	21.5815	19.2871	23.4654
GT	Sense	Sense	-0.623	Detected	0.623	Detected	0.000	-0.863	Detected	-1.770	Detected	-1.317	0.230	GT	Sens	contig214	contig214	Proline-ri	CTTAGC	contig214	Solyc08g	Solyc08g	Proline-ri	GO:0008	GO:0008	contig214	Solyc08g078920.1.1				AT2G45180.1		protease	chr2:186	1420.67	4011.32	864.39	2358.87	1478.38	661.786
GT	Sense	Sense	0.019	Detected	-0.019	Detected	0.000	-2.862	Comprom	-3.163	Comprom	-3.013	0.003	GT	Sens	contig214	contig214	Unknown	GCAGTT	contig214	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)%			contig214	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G16010.1		pentatric	chr3:543	55.9995	64.911	6.26477	8.03918	9.34292	6.36341
GT	Sense	Sense	-1.097	Detected	1.097	Detected	0.000	-3.087	Detected	-2.896	Detected	-2.992	0.113	GT	Sens	contig215	contig215	Hydroxyc	ACAACG	contig215	Solyc12g	Solyc12g	Hydroxyc	GO:0016	GO:0016	contig215	Solyc12g	Hydroxyc	GO:0016	SL2.40ch	AT4G15390.1		transfera	chr4:879	246.233	1341	122.443	285.878	76.1806	72.9898
GT	Sense	Sense	0.184	Detected	-0.184	Detected	0.000	-1.737	Detected	-1.415	Detected	-1.576	0.023	GT	Sens	contig216	contig216	Mutator-li	AGTATC	contig216	Solyc01g	Solyc01g	Mutator-li	GO:0008	GO:0008	contig216	Solyc12g	Mutator-li	GO:0008	SL2.40ch	AT5G59450.1		scarecro	chr5:239	65.1488	60.0793	28.8367	22.3823	21.144	22.1892
GT	Sense	Sense	-0.106	Detected	0.106	Detected	0.000	-1.500	Detected	-1.518	Detected	-1.509	0.005	GT	Sens	contig216	contig216	NAD(P)H-	CTACTA	contig216	Solyc11g	Solyc11g	NAD(P)H-quinone oxidoreduct			contig216	Solyc11g	NAD(P)H-quinone o		SL2.40ch	ATCG012	NDHB.2	NADH de	chrC:14	296.612	409.253	173.231	167.638	138.763	115.017
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	-1.148	Detected	-1.462	Detected	-1.305	0.024	GT	Sens	contig217	contig217	Pol polyp	ATAGCT	contig217	Solyc07g	Solyc07g	Pol polyprotein (AHRD V1 ***- (			contig217	Solyc07g	Pol polyprotein (AH		SL2.40ch	AT5G11250.1		disease r	chr5:358	374.658	371.685	201.641	181.603	189.7	128.049
GT	Sense	Sense	-0.525	Detected	0.525	Detected	0.000	-1.632	Detected	-0.930	Detected	-1.281	0.180	GT	Sens	contig218	contig218	Aldose-1-	AAGTCA	contig218	Solyc02g	Solyc02g	Aldose-1-	GO:0019	GO:0019	contig218	Solyc02g	Aldose-1-	GO:0005	SL2.40ch	AT3G47800.1		aldose 1-	chr3:176	928.615	2287.49	763.253	1158.54	529.54	723.314
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	-1.914	Detected	-2.061	Detected	-1.988	0.004	GT	Sens	contig220	contig220	Pol polyp	TTGACA	contig220	Solyc11g	Solyc11g	Pol polyprotein (AHRD V1 ***- (			contig220	Solyc12g	Transposon Ty1-A (		SL2.40ch	AT1G623	STM. BU	STM (SH	chr1:230	888.821	918.961	411.654	272.484	270.066	204.744
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-1.259	Detected	-1.556	Detected	-1.408	0.012	GT	Sens	contig221	contig221	NADH-qui	TTATTT	contig221	Solyc01g	Solyc01g	NADH-qui	GO:0055	GO:0055	contig221	Solyc01g	NADH-qui	GO:0055	SL2.40ch	ATCG010	NDHF	Chloropl	chrC:11	456.304	502.304	256.641	229.005	225.318	153.956
GT	Sense	Sense	1.112	Detected	-1.112	Detected	0.000	-1.706	Detected	-1.140	Detected	-1.423	0.341	GT	Sens	contig222	contig222	FAD-bind	GTCTAC	contig222	Solyc02g	Solyc02g	FAD-bind	GO:0050	GO:0050	contig222	Solyc02g070160.1.1				AT5G44400.1		FAD-bind	chr5:178	6131.25	1562.8	2669.5	2384.64	1068.77	1328.4
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	-1.756	Detected	-2.141	Detected	-1.949	0.011	GT	Sens	contig223	contig223	Unknown	GGGCAA	contig223	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig223	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G064	EMB2750	EMB275	chr3:195	230.31	248.374	138.374	103.635	79.7436	51.2629
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	-1.420	Detected	-1.664	Detected	-1.542	0.010	GT	Sens	contig224	contig224	Unknown	CAGGCA	contig224	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig224	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G370	PLP4. PL	PLP4 (PA	chr4:174	2451.36	2532.88	1558.76	1236.18	1048.92	743.272
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-0.941	Detected	-1.129	Detected	-1.035	0.011	GT	Sens	contig226	contig226	NADH-qui	AGAATT	contig226	Solyc12g	Solyc12g	NADH-qui	GO:0055	GO:0055	contig226	Solyc12g	NADH-qui	GO:0055	SL2.40ch	ATCG011	NDHH	Encodes	chrC:12	505.702	647.281	387.64	385.087	335.66	247.291
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.527	Detected	-1.244	Detected	-1.386	0.019	GT	Sens	contig227	contig227	Pol polyp	ATGTGT	contig227	Solyc11g	Solyc11g	Pol polyp	GO:0006	GO:0006	contig227	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT3G237	NRPD2A.	NRPD2A:	chr3:856	602.303	596.137	314.193	227.861	234.187	239.135
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-1.060	Detected	-1.034	Detected	-1.047	0.013	GT	Sens	contig228	contig228	UDP-gluc	ATAGTG	contig228	Solyc10g	Solyc10g	UDP-gluc	GO:0008	GO:0008	contig228	Solyc10g	UDP-gluc	GO:0008	SL2.40ch	AT5G38040.1		UDP-gluc	chr5:151	31.5518	31.8377	24.7209	28.9363	17.1204	14.6317
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-2.215	Detected	-1.710	Detected	-1.962	0.017	GT	Sens	contig230	contig230	Unknown	GCTACG	contig230	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig230	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G18570.1		GTP1/OB	chr5:617	1763.34	1979.8	602.408	335.666	453.384	540.172
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-2.351	Detected	-1.981	Detected	-2.166	0.007	GT	Sens	contig231	contig231	Pro-Pol p	ATTCAG	contig231	Solyc01g	Solyc01g	Pro-Pol p	GO:0015	GO:0015	contig231	Solyc11g	Pol polyp	GO:0003	SL2.40ch	AT4G394	BRI1. CBI	BRI1 (BR	chr4:183	8895.6	10259.5	3139.6	2203.13	2109.37	2288.25
GT	Sense	Sense	0.136	Detected	-0.136	Detected	0.000	-1.523	Detected	-1.479	Detected	-1.501	0.008	GT	Sens	contig232	contig232	Unknown	CACGCA	contig232	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig232	Solyc11g	Unknown Protein (A		SL2.40ch	AT2G30870.1				24776.1	24439.4	15457.1	14343	9646.69	8344.77
GT	Sense	Sense	0.141	Detected	-0.141	Detected	0.000	-1.581	Detected	-1.367	Detected	-1.474	0.014	GT	Sens	contig235	contig235	Reverse t	ATGAGT	contig235	Solyc01g	Solyc01g	Reverse transcriptase (Fragm			contig235	Solyc10g	Polyprote	GO:0006	SL2.40ch	AT4G211	ATERDJ2	ATERDJ	chr4:112	2407.08	2357.22	1181.01	740.626	897.001	873.304
GT	Sense	Sense	0.129	Detected	-0.129	Detected	0.000	-1.329	Detected	-0.971	Detected	-1.150	0.035	GT	Sens	contig238	contig238	Unknown	ACACGG	contig238	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig238	Solyc00g	Unknown Protein (A		SL2.40ch	AT1G27850.1		unknown	chr1:969	33627.3	33456.2	18265.2	14351.8	15036.8	16179
GT	Sense	Sense	-0.841	Detected	0.841	Detected	0.000	-1.224	Detected	-1.102	Detected	-1.163	0.302	GT	Sens	contig239	contig239	Histone-l	CTGAGG	contig239	Solyc08g	Solyc08g	Histone-lysine N-methyltransfe			contig239	Solyc08g	Histone-lysine N-me		SL2.40ch	AT5G468	HB-7. HD	HB-7 (HO	chr5:190	238.065	910.027	140.463	430.136	224.514	205.057
GT	Sense	Sense	-0.211	Detected	0.211	Detected	0.000	-0.915	Detected	-1.203	Detected	-1.059	0.054	GT	Sens	contig240	contig240	ATP synt	TAGTAA	contig240	Solyc11g	Solyc11g	ATP synt	GO:0045	GO:0045	contig240	Solyc11g	ATP synt	GO:0045	SL2.40ch	ATCG001	ATPA	Encodes	chrC:99	4833.9	7708.66	6225.66	5999.84	3647.65	2507.51
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-2.060	Detected	-2.256	Detected	-2.158	0.003	GT	Sens	contig240	contig240	Reverse t	AGCTAA	contig240	Solyc06g	Solyc06g	Reverse t	GO:0006	GO:0006	contig240	Solyc03g	Pol polyp	GO:0006	SL2.40ch	AT4G099	EMB1691	EMB169	chr4:624	75.7668	83.4734	22.1099	23.7661	21.4846	15.7455
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-1.500	Detected	-2.031	Detected	-1.765	0.026	GT	Sens	contig240	contig240	Transpos	CAAGAT	contig240	Solyc01g	Solyc01g	Transpos	GO:0003	GO:0003	contig240	Solyc01g	Transpos	GO:0003	SL2.40ch	AT1G493	ATPI4K A	ATPI4K A	chr1:182	87.8988	89.5089	45.804	27.2572	35.3363	20.5271
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-1.202	Detected	-1.533	Detected	-1.368	0.017	GT	Sens	contig240	contig240	Receptor	GCTATG	contig240	Solyc12g	Solyc12g	Receptor-like kinase (AHRD V1			contig240	Solyc12g	Receptor-like kinase		SL2.40ch	AT2G37050.3		kinase	chr2:155	62.2299	66.4285	70.6755	92.7354	31.4726	21.0124
GT	Sense	Sense	-0.852	Detected	0.852	Detected	0.000	-2.545	Detected	-1.084	Detected	-1.815	0.247	GT	Sens	contig241	contig241	Peroxida	AAGAAT	contig241	Solyc05g	Solyc05g	Peroxida	GO:0005	GO:0005	contig241	Solyc05g046020.2.1				AT3G21770.1		peroxida	chr3:767	223.316	866.731	265.153	644.633	84.935	196.179
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-2.249	Detected	-2.304	Detected	-2.276	0.001	GT	Sens	contig241	contig241	Pol polyp	TCACAA	contig241	Solyc09g	Solyc09g	Pol polyprotein (AHRD V1 ***- (			contig241	Solyc09g	Pol polyprotein (AH		SL2.40ch	AT3G09120.1		unknown	chr3:279	745.533	807.938	278.96	161.064	183.965	148.65
GT	Sense	Sense	0.140	Detected	-0.140	Detected	0.000	-1.688	Detected	-3.151	Comprom	-2.419	0.083	GT	Sens	contig245	contig245	Transpos	ACAGCG	contig245	Solyc03g	Solyc03g	Transpos	GO:0015	GO:0015	contig245	Solyc03g043670.1.1				AT2G40935.3		unknown	chr2:170	41.8646	41.0515	21.6251	16.8307	14.4924	4.4138
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-1.896	Detected	-1.480	Detected	-1.688	0.016	GT	Sens	contig245	contig245	Gag-pol (	AGAAAA	contig245	Solyc11g	Solyc11g	Gag-pol (	GO:0005	GO:0005	contig245	Solyc11g	Gag-pol (	GO:0005	SL2.40ch	AT3G58090.1		FUNCTIO	chr3:215	2427.58	3108.05	1089.66	799.478	831.582	931.078
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-1.067	Detected	-1.616	Detected	-1.341	0.040	GT	Sens	contig247	contig247	DNA-dire	CACAAT	contig247	Solyc10g	Solyc10g	DNA-dire	GO:0006350		contig247	Solyc10g	DNA-dire	GO:0006	SL2.40ch	ATCG001	RPOC2	RNA poly	chrC:15	262.525	325.032	161.01	143.686	157.024	90.1314
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-1.844	Detected	-1.447	Detected	-1.645	0.018	GT	Sens	contig248	contig248	Polyprote	CTTGTG	contig248	Solyc01g	Solyc01g	Polyprote	GO:0006	GO:0006	contig248	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT5G101	ATMIPS3	MIPS3 (M	chr5:318	3098.7	3194.2	1377.38	819.279	987.232	1091.26
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	-1.747	Detected	-1.191	Detected	-1.469	0.036	GT	Sens	contig248	contig248	Aldose-1-	TCCTTA	contig248	Solyc02g	Solyc02g	Aldose-1-	GO:0005	GO:0005	contig248	Solyc02g	Aldose-1-	GO:0005	SL2.40ch	AT3G47800.1		aldose 1-	chr3:176	590.083	778.058	407.991	550.387	227.457	280.543
GT	Sense	Sense	-0.445	Detected	0.445	Detected	0.000	-2.597	Detected	-1.238	Detected	-1.917	0.142	GT	Sens	contig251	contig251	Cyclopro	ATTTCA	contig251	Solyc09g	Solyc09g	Cyclopro	GO:0005	GO:0005	contig251	Solyc09g	Cyclopro	GO:0005	SL2.40ch	AT3G23510.1		cyclopro	chr3:842	2008.82	4430.12	1219.14	1731.9	555.501	1196.01
GT	Sense	Sense	0.092	Detected	-0.092	Detected	0.000	-2.490	Detected	-2.059	Detected	-2.274	0.010	GT	Sens	contig251	contig251	Unknown	AGACAA	contig251	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig251	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G115	MYB3R-4	MYB3R-4	chr5:368	1931.46	2024.67	583.708	387.43	396.416	448.861
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	-1.391	Detected	-1.736	Detected	-1.563	0.012	GT	Sens	contig253	contig253	Elongatio	AGTAGT	contig253	Solyc12g	Solyc12g	Elongatio	GO:0005	GO:0005	contig253	Solyc08g	Elongatio	GO:0003	SL2.40ch	AT1G627	ATSCO1.	SCO1 (S	chr1:232	1330	1661.18	794.355	1110.7	638.667	421.967
GT	Sense	Sense	0.700	Detected	-0.700	Detected	0.000	-3.186	Comprom	-1.821	Comprom	-2.504	0.125	GT	Sens	contig257	contig257	Alpha-gal	TTTCAT	contig257	Solyc03g	Solyc03g	Alpha-gal	GO:0047	GO:0047	contig257	Solyc03g	Alpha-gal	GO:0047	SL2.40ch	AT5G403	SIP1	SIP1 (see	chr5:161	25.7073	11.5896	9.53034	12.4442	2.1362	4.61975
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-1.286	Detected	-1.000	Detected	-1.143	0.015	GT	Sens	contig259	contig259	NAD(P)H-	ATCGAA	contig259	Solyc01g	Solyc01g	NAD(P)H-	GO:0055	GO:0055	contig259	Solyc12g	NAD(P)H-quinone o		SL2.40ch	ATCG012	NDHB.2	NADH de	chrC:14	139.042	164.289	92.1758	93.4484	69.8325	71.4458
GT	Sense	Sense	-0.007	Detected	0.007	Detected	0.000	-1.142	Detected	-1.457	Detected	-1.300	0.014	GT	Sens	contig260	contig260	Unknown	CTTAGT	contig260	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig260	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G18570.1		GTP1/OB	chr5:617	861.191	1035.93	636.149	400.725	482.038	325.195
GT	Sense	Sense	-0.010	Detected	0.010	Detected	0.000	-1.073	Detected	-1.088	Detected	-1.080	0.000	GT	Sens	contig260	contig260	Peptide tr	ATTGGC	contig260	Solyc09g	Solyc09g	Peptide tr	GO:0042	GO:0042	contig260	Solyc05g	Peptide tr	GO:0042	SL2.40ch	AT5G46040.1		proton-d	chr5:186	264.285	319.185	228.107	347.972	155.561	129.213
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-1.138	Detected	-0.967	Detected	-1.052	0.007	GT	Sens	contig261	contig261	Unknown	ACTCCA	contig261	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig261	Solyc11g021100.1.1				ATCG012	NDHB.2	NADH de	chrC:14	992.87	1195.2	713.783	714.399	557.549	527.004
GT	Sense	Sense	0.141	Detected	-0.141	Detected	0.000	-1.950	Detected	-1.920	Detected	-1.935	0.005	GT	Sens	contig261	contig261	Early ligh	CTAGCT	contig261	Solyc09g	Solyc09g	Early light-induced protein 7 (A			contig261	Solyc09g	Early ligh	GO:0016	SL2.40ch	AT4G146	ELIP2	ELIP2 (E	chr4:841	2040.94	1999.07	1480.87	1121.47	588.808	504.829
GT	Sense	Sense	-0.273	Detected	0.273	Detected	0.000	-1.051	Detected	-1.436	Detected	-1.244	0.065	GT	Sens	contig262	contig262	ATP synt	GTATAT	contig262	Solyc06g	Solyc06g	ATP synthase subunit alpha c			contig262	Solyc06g	ATP synthase subu		SL2.40ch	ATCG001	ATPA	Encodes	chrC:99	5337.66	9273.49	6449.61	6998.67	3823.98	2458.69
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	-1.129	Detected	-1.265	Detected	-1.197	0.010	GT	Sens	contig264	contig264	Unknown	TGGCTG	contig264	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig264	Solyc11g	Unknown Protein (A		SL2.40ch	AT4G16880.1				99.0156	102.6	87.7266	64.6556	51.9051	39.6452
GT	Sense	Sense	0.122	Detected	-0.122	Detected	0.000	-1.731	Detected	-0.840	Detected	-1.286	0.108	GT	Sens	contig266	contig266	Unknown	ATGGAA	contig266	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)%			contig266	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G14819.1		unknown	chr4:850	146.668	147.38	157.961	165.712	49.8892	77.6394
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-2.094	Detected	-1.912	Detected	-2.003	0.003	GT	Sens	contig267	contig267	Pol polyp	CCGCGA	contig267	Solyc01g	Solyc01g	Pol polyprotein (AHRD V1 ***- F			contig267	Solyc01g020250.1.1				AT4G211	ATERDJ2	ATERDJ	chr4:112	7736.94	8320.78	3188.1	2382.85	2117.01	2016.53
GT	Sense	Sense	-0.283	Detected	0.283	Detected	0.000	-2.233	Detected	-0.966	Detected	-1.600	0.148	GT	Sens	contig268	contig268	Hydroxyc	TTCAGC	contig268	Solyc03g	Solyc03g	Hydroxycinnamoyl-CoA shikin			contig268	Solyc03g	Hydroxycinnamoyl-		SL2.40ch	AT5G65460.1		kinesin m	chr5:261	2743.52	4832.98	2293.69	3776.66	872.343	1762.83
GT	Sense	Sense	0.092	Detected	-0.092	Detected	0.000	-1.299	Detected	-0.905	Detected	-1.102	0.037	GT	Sens	contig268	contig268	Pol polyp	CAGTAC	contig268	Solyc10g	Solyc10g	Pol polyprotein (AHRD V1 ***- F			contig268	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT4G29750.1		RNA bind	chr4:145	458.154	479.998	255.721	197.06	214.703	236.774
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	-1.620	Detected	-1.299	Detected	-1.459	0.012	GT	Sens	contig27	contig27	Retrotran	AAATCT	contig27	Solyc01g	Solyc01g	Retrotran	GO:0005	GO:0005	contig27	Solyc01g049700.2.1				AT3G58090.1		FUNCTIO	chr3:215	6203.97	7264.83	3297.88	2361.67	2460.49	2580.35
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-1.180	Detected	-1.252	Detected	-1.216	0.002	GT	Sens	contig270	contig270	Tir-nbs-lr	TCACTT	contig270	Solyc12g	Solyc12g	Tir-nbs-lr	GO:0031	GO:0031	contig270	Solyc12g	Tir. resist	GO:0031	SL2.40ch	AT2G271	AAO3	AAO3 (A	chr2:116	100.841	126.414	93.5271	210.814	56.1457	44.8377
GT	Sense	Sense	-0.751	Detected	0.751	Detected	0.000	-0.917	Detected	-1.663	Detected	-1.290	0.264	GT	Sens	contig270	contig270	Purple ac	TATAAG	contig270	Solyc07g	Solyc07g	Purple ac	GO:0005	GO:0005	contig270	Solyc07g	Purple ac	GO:0004	SL2.40ch	AT5G504	ATPAP27	PAP27 (P	chr5:205	958.971	3231.5	997.862	1067.53	1050.27	525.727
GT	Sense	Sense	-0.058	Detected	0.058	Detected	0.000	-1.213	Detected	-0.995	Detected	-1.104	0.012	GT	Sens	contig271	contig271	Zinc finge	TGCTAA	contig271	Solyc10g	Solyc10g	Zinc finge	GO:0003	GO:0003	contig271	Solyc10g	Zinc finge	GO:0003	SL2.40ch	AT3G51950.2		zinc fing	chr3:192	164.289	212.093	153.763	166.801	90.7103	88.5313
GT	Sense	Sense	1.872	Detected	-1.872	Detected	0.000	-2.160	Detected	-1.657	Detected	-1.908	0.419	GT	Sens	contig272	contig272	Acyl-CoA	ATCTTG	contig272	Solyc07g	Solyc07g	Acyl-CoA	GO:0008	GO:0008	contig272	Solyc07g	Acyl-CoA	GO:0015	SL2.40ch	AT2G17650.1		AMP-dep	chr2:767	1036.15	92.0047	265.83	195.893	77.8238	92.5835
GT	Sense	Sense	0.039	Detected	-0.039	Detected	0.000	-1.831	Detected	-1.229	Detected	-1.530	0.037	GT	Sens	contig272	contig272	Pol polyp	CTATTC	contig272	Solyc10g	Solyc10g	Pol polyp	GO:0015	GO:0015	contig272	Solyc00g	Pol polyp	GO:0003	SL2.40ch	AT5G59980.2		RNase P	chr5:241	720.269	812.34	269.364	173.044	242.164	308.588
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-0.971	Detected	-1.382	Detected	-1.176	0.029	GT	Sens	contig273	contig273	Ycf2 (AHF	GATCTC	contig273	Solyc11g	Solyc11g	Ycf2 (AHRD V1 ***- D2KLP5_OL			contig273	Solyc11g062050.1.1				ATCG012	YCF2.2	hypothet	chrC:14	560.822	663.303	392.306	368.622	350.482	221.286
GT	Sense	Sense	0.085	Detected	-0.085	Detected	0.000	-1.397	Detected	-1.468	Detected	-1.433	0.004	GT	Sens	contig274	contig274	Gag-Pol p	GTCTTG	contig274	Solyc06g	Solyc06g	Gag-Pol polyprotein (AHRD V1			contig274	Solyc06g	Gag-Pol polyprotein		SL2.40ch	AT5G05400.1		disease r	chr5:159	346.004	366.181	221.36	166.506	152.239	121.667
GT	Sense	Sense	0.116	Detected	-0.116	Detected	0.000	-2.247	Detected	-1.704	Detected	-1.976	0.022	GT	Sens	contig276	contig276	Unknown	ACAAGA	contig276	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig276	Solyc03g051630.1.1				AT5G25580.1		FUNCTIO	chr5:890	625.65	634.316	216.394	145.49	149.448	182.85
GT	Sense	Sense	-0.197	Detected	0.197	Detected	0.000	-3.452	Detected	-1.216	Detected	-2.334	0.176	GT	Sens	contig278	contig278	MYB tran	TTGGAA	contig278	Solyc12g	Solyc12g	MYB tran	GO:0045449		contig278	Solyc02g	MYB tran	GO:0003	SL2.40ch	AT2G359	BLH1	BLH1 (BE	chr2:150	93.8691	146.884	46.7971	129.443	12.0902	47.7938
GT	Sense	Sense	0.083	Detected	-0.083	Detected	0.000	-1.841	Detected	-1.388	Detected	-1.615	0.022	GT	Sens	contig281	contig281	Pol polyp	ACATTG	contig281	Solyc00g	Solyc00g	Pol polyp	GO:0015	GO:0015	contig281	Solyc08g	Pol polyp	GO:0008	SL2.40ch	AT3G01880.1		unknown	chr3:307	443.045	470.275	210.951	149.835	143.496	164.91
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	-1.353	Detected	-1.791	Detected	-1.572	0.019	GT	Sens	contig281	contig281	NADH del	TTTGTT	contig281	Solyc05g	Solyc05g	NADH del	GO:0055	GO:0055	contig281	Solyc01g	NADH del	GO:0055	SL2.40ch	AT5G18350.1		ATP bind	chr5:607	377.068	442.358	182.768	184.708	180.071	111.56
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-0.940	Detected	-1.064	Detected	-1.002	0.013	GT	Sens	contig282	contig282	Cytochro	TTTTTG	contig282	Solyc02g	Solyc02g	Cytochrome c biogenesis prot			contig282	Solyc02g	Cytochrome c bioge		SL2.40ch	ATCG010	YCF5	hypothet	chrC:11	37.0285	50.2848	22.1733	22.0307	25.3303	19.5153
GT	Sense	Sense	-0.780	Detected	0.780	Detected	0.000	-2.126	Detected	-0.801	Detected	-1.463	0.289	GT	Sens	contig284	contig284	Cytochro	ATTAAG	contig284	Solyc07g	Solyc07g	Cytochro	GO:0019	GO:0019	contig284	Solyc07g055440.1.1				AT3G146	CYP72A9	CYP72A	chr3:491	100.637	353.437	95.295	330.759	48.6661	102.372
GT	Sense	Sense	0.117	Detected	-0.117	Detected	0.000	-1.814	Detected	-1.383	Detected	-1.598	0.023	GT	Sens	contig284	contig284	Polyprote	CTACTG	contig284	Solyc11g	Solyc11g	Polyprotein (AHRD V1 ***- O6A			contig284	Solyc11g	Pol polyp	GO:0003	SL2.40ch	AT4G29750.1		RNA bind	chr4:145	1671.76	1691.81	647.245	489.767	538.818	609.736
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	-2.119	Detected	-1.735	Detected	-1.927	0.010	GT	Sens	contig284	contig284	Polyprote	TTTTGT	contig284	Solyc12g	Solyc12g	Polyprotein (Fragment) (AHRD			contig284	Solyc11g	Pol polyp	GO:0003	SL2.40ch	ATMG00750.1				4122.13	4653.87	1457.69	1046.38	1135.51	1244.41
GT	Sense	Sense	0.194	Detected	-0.194	Detected	0.000	-1.120	Detected	-1.413	Detected	-1.266	0.035	GT	Sens	contig286	contig286	Mutator-li	GTGCGT	contig286	Solyc03g	Solyc03g	Mutator-like transposase (AHF			contig286	Solyc11g	Mutator-li	GO:0008	SL2.40ch	AT3G48630.1				48.6261	44.2338	27.5548	13.6115	24.0367	16.4704
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-2.124	Detected	-1.692	Detected	-1.908	0.014	GT	Sens	contig287	contig287	Retrotran	GCATGG	contig287	Solyc08g	Solyc08g	Retrotran	GO:0015	GO:0015	contig287	Solyc11g	Pol polyp	GO:0003	SL2.40ch	AT4G266	WRKY20.	WRKY20	chr4:134	5918.06	6476.07	2267.42	1557.53	1599.76	1811.72
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-1.184	Detected	-1.120	Detected	-1.152	0.004	GT	Sens	contig287	contig287	Unknown	AGATTC	contig287	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig287	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G098	CESA5	CESA5 (	chr5:307	96.1725	104.434	57.9785	46.166	49.6895	43.5895
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.483	Detected	-1.340	Detected	-1.412	0.011	GT	Sens	contig288	contig288	LINE-type	CAGCCG	contig288	Solyc00g	Solyc00g	LINE-type retrotransposon LIb			contig288	Solyc09g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	266.679	263.979	134.812	80.2809	106.895	99.0803
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	-1.894	Detected	-1.676	Detected	-1.785	0.006	GT	Sens	contig289	contig289	Pol polyp	GGATGT	contig289	Solyc12g	Solyc12g	Pol polyp	GO:0006	GO:0006	contig289	Solyc12g	Pol polyp	GO:0006	SL2.40ch	AT4G36210.3		unknown	chr4:171	1727.79	1835.43	727.155	607.453	539.921	526.853
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-0.946	Detected	-1.072	Detected	-1.009	0.004	GT	Sens	contig291	contig291	Photosys	TGGGCC	contig291	Solyc12g	Solyc12g	Photosys	GO:0016	GO:0016	contig291	Solyc12g	Photosys	GO:0016	SL2.40ch	ATCG003	PSAB	Encodes	chrC:37	369.548	453.843	288.891	290.34	239.464	184.132
GT	Sense	Sense	-0.222	Detected	0.222	Detected	0.000	-1.252	Detected	-0.917	Detected	-1.084	0.060	GT	Sens	contig292	contig292	Acetyl co	CTACTC	contig292	Solyc05g	Solyc05g	Acetyl co	GO:0010	GO:0010	contig292	Solyc05g	Acetyl co	GO:0010	SL2.40ch	AT5G17540.1		transfera	chr5:578	33.6014	54.4359	15.1834	44.4973	20.2295	21.4228
GT	Sense	Sense	0.162	Detected	-0.162	Detected	0.000	-1.924	Detected	-1.610	Detected	-1.767	0.016	GT	Sens	contig294	contig294	Unknown	AAACCT	contig294	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig294	Solyc10g035570.1.1				AT3G51120.1		DNA bind	chr3:189	5678.35	5401.05	2442.12	1697.78	1644.42	1715.96
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.651	Detected	-1.300	Detected	-1.475	0.015	GT	Sens	contig294	contig294	Gag-Pol p	ACGTAC	contig294	Solyc07g	Solyc07g	Gag-Pol polyprotein (AHRD V1			contig294	Solyc07g	Gag-Pol polyprotein		SL2.40ch	AT5G012	CPL2. AT	CPL2: do	chr5:108	75.5181	84.3916	45.2054	48.1664	28.6446	30.6493
GT	Sense	Sense	-0.290	Detected	0.290	Detected	0.000	-1.182	Detected	-1.101	Detected	-1.141	0.060	GT	Sens	contig295	contig295	Serine ca	AGCTCC	contig295	Solyc06g	Solyc06g	Serine ca	GO:0006	GO:0006	contig295	Solyc06g	Serine ca	GO:0042	SL2.40ch	AT4G129	scpl20	scpl20 (s	chr4:755	1273.14	2265.59	940.758	1201	843.355	748.5
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-2.127	Detected	-1.758	Detected	-1.942	0.011	GT	Sens	contig296	contig296	Pro-Pol p	ACTTTA	contig296	Solyc05g	Solyc05g	Pro-Pol p	GO:0015	GO:0015	contig296	Solyc05g	Pro-Pol p	GO:0003	SL2.40ch	AT1G79990.5		protein b	chr1:300	4144.54	4374.4	1607.18	1133.64	1098.35	1190.53
GT	Sense	Sense	0.001	Detected	-0.001	Detected	0.000	-1.165	Detected	-1.378	Detected	-1.271	0.007	GT	Sens	contig296	contig296	Ycf2 (AHF	ATCAAA	contig296	Solyc09g	Solyc09g	Ycf2 (AHF	GO:0009	GO:0009	contig296	Solyc09g	Ycf2 (AHF	GO:0009	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:14	574.684	683.587	362.107	344.374	314.948	228.092
GT	Sense	Sense	-0.216	Detected	0.216	Detected	0.000	-0.972	Detected	-1.191	Detected	-1.082	0.047	GT	Sens	contig299	contig299	CONSTAI	GGAGTA	contig299	Solyc02g	Solyc02g	CONSTAI	GO:0003	GO:0003	contig299	Solyc02g	Tomato C	GO:0003	SL2.40ch	AT5G158	COL1. AT	COL1 (co	chr5:517	132.067	212.029	196.973	188.02	96.1012	69.2975
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	-1.289	Detected	-1.340	Comprom	-1.314	0.011	GT	Sens	contig303	contig303	Transpos	ACTCTT	contig303	Solyc07g	Solyc07g	Transposase (AHRD V1 **-- O6			contig303	Solyc08g	Transposase (AHRD		SL2.40ch	AT3G28510.1		AAA-type	chr3:106	26.3946	25.9145	10.2652	9.36813	12.0554	9.77058
GT	Sense	Sense	-0.091	Detected	0.091	Detected	0.000	-1.716	Detected	-1.333	Detected	-1.525	0.019	GT	Sens	contig305	contig305	Reverse t	AGCATG	contig305	Solyc06g	Solyc06g	Reverse t	GO:0006	GO:0006	contig305	Solyc03g	Pol polyp	GO:0006	SL2.40ch	AT5G425	XRN2	XRN2 (E	chr5:170	63.4617	85.6602	38.6969	37.6022	25.2789	27.6662
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.856	Detected	-1.458	Detected	-1.657	0.017	GT	Sens	contig306	contig306	Pol polyp	TCTCCT	contig306	Solyc08g	Solyc08g	Pol polyp	GO:0006	GO:0006	contig306	Solyc08g	Pol polyp	GO:0006	SL2.40ch	AT5G035	ATEXO70	ATEXO7	chr5:890	2869.89	2999.45	1076.36	779.647	913.21	1009.56
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	-1.541	Detected	-1.077	Detected	-1.309	0.030	GT	Sens	contig306	contig306	Pol polyp	AGTTTA	contig306	Solyc00g	Solyc00g	Pol polyp	GO:0003	GO:0003	contig306	Solyc00g	Pol polyp	GO:0003	SL2.40ch	AT5G43110.1				1509.31	1735.69	827.183	505.074	626.695	725.624
GT	Sense	Sense	0.044	Detected	-0.044	Detected	0.000	-1.247	Detected	-0.865	Detected	-1.056	0.033	GT	Sens	contig308	contig308	Unknown	AATGCA	contig308	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig308	Solyc07g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	79.3337	88.8419	43.4737	28.2611	39.8343	43.582
GT	Sense	Sense	0.189	Detected	-0.189	Detected	0.000	-1.216	Detected	-2.016	Comprom	-1.616	0.067	GT	Sens	contig308	contig308	Gag-Pol p	AAGACA	contig308	Solyc02g	Solyc02g	Gag-Pol p	GO:0008	GO:0008	contig308	Solyc12g	Transpos	GO:0003	SL2.40ch	AT5G45510.2		leucine-r	chr5:184	48.7462	44.6476	24.3325	23.643	22.6212	10.9093
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-1.839	Detected	-1.422	Detected	-1.631	0.016	GT	Sens	contig310	contig310	Polyprote	TTGATC	contig310	Solyc10g	Solyc10g	Polyprote	GO:0003	GO:0003	contig310	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT2G03740.1				531.218	627.732	220.892	151.633	181.778	203.818
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-1.178	Detected	-1.264	Detected	-1.221	0.012	GT	Sens	contig311	contig311	Unknown	ACAGAC	contig311	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig311	Solyc11g	Unknown Protein (A		SL2.40ch	AT4G067	RAP2.9	RAP2.9 (	chr4:407	2354.42	2356.23	1609.16	1260.43	1173.02	927.453
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-1.633	Detected	-1.472	Detected	-1.552	0.005	GT	Sens	contig314	contig314	Pol polyp	ATCTGA	contig314	Solyc00g	Solyc00g	Pol polyp	GO:0003	GO:0003	contig314	Solyc00g	Pol polyp	GO:0003	SL2.40ch	AT3G127	ALIS1	ALIS1 (A	chr3:404	5882.24	6280.6	3292.79	2282.3	2207.8	2071.77
GT	Sense	Sense	-0.244	Detected	0.244	Detected	0.000	-1.176	Detected	-1.088	Detected	-1.132	0.045	GT	Sens	contig323	contig323	Indole-3-a	AATGGG	contig323	Solyc00g	Solyc00g	Indole-3-acetic acid-amido syn			contig323	Solyc10g	GH3 famil	GO:0080	SL2.40ch	AT5G38340.1		disease r	chr5:153	143.758	239.994	191.39	179.496	92.5731	82.6145
GT	Sense	Sense	-0.630	Detected	0.630	Detected	0.000	-1.860	Detected	-1.299	Detected	-1.580	0.149	GT	Sens	contig323	contig323	Beta-gala	TTAATG	contig323	Solyc11g	Solyc11g	Beta-gala	GO:0005	GO:0005	contig323	Solyc11g	Beta-gala	GO:0005	SL2.40ch	AT5G638	MUM2. B	MUM2 (M	chr5:255	51.2114	146.111	35.4549	83.3052	26.842	33.2391
GT	Sense	Sense	-0.098	Detected	0.098	Detected	0.000	-1.033	Detected	-1.225	Detected	-1.129	0.014	GT	Sens	contig329	contig329	Ycf1 (Fra	CTGGAA	contig329	Solyc11g	Solyc11g	Ycf1 (Fragment) (AHRD V1 ***-			contig329	Solyc10g	Hypothetical chloro		SL2.40ch	ATMG003	ORF199	hypothet	chrM:10	159.308	217.155	147.311	119.577	102.364	75.2119
GT	Sense	Sense	0.184	Detected	-0.184	Detected	0.000	-1.471	Detected	-1.568	Detected	-1.519	0.015	GT	Sens	contig330	contig330	Unknown	CCATTG	contig330	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig330	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G05840.1		unknown	chr5:175	12029	11090.4	7155.25	5874.69	4692.86	3684.41
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	-2.423	Detected	-2.597	Detected	-2.510	0.002	GT	Sens	contig333	contig333	Transcrip	GGAAGA	contig333	Solyc02g	Solyc02g	Transcription factor CYCLOID			contig333	Solyc02g	Transcription factor		SL2.40ch	AT1G54740.1		FUNCTIO	chr1:204	1692.15	1877.82	659.403	919.719	374.389	278.633
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-1.467	Detected	-1.144	Detected	-1.306	0.029	GT	Sens	contig348	contig348	Unknown	CGTCGG	contig348	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig348	Solyc06g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	29035.2	27753.7	15451.5	11923.7	11568.2	12143.1
GT	Sense	Sense	0.017	Detected	-0.017	Detected	0.000	-1.337	Detected	-0.987	Detected	-1.162	0.022	GT	Sens	contig361	contig361	Ycf2 (AHF	GGTTAT	contig361	Solyc00g	Solyc00g	Ycf2 (AHRD V1 ***- A6YA23_9M			contig361	Solyc01g	Ycf2 (AHF	GO:0005	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:14	494.711	574.858	263.988	254.821	237.802	254.323
GT	Sense	Sense	0.146	Detected	-0.146	Detected	0.000	-1.459	Detected	-1.654	Detected	-1.557	0.012	GT	Sens	contig365	contig365	Unknown	GCATGG	contig365	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig365	Solyc12g	Unknown Protein (A		SL2.40ch	AT2G181	ATMPK7.	ATMPK7	chr2:790	4154.67	4042.06	3012.77	2245.04	1678.74	1231.2
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-2.034	Detected	-1.600	Detected	-1.817	0.015	GT	Sens	contig366	contig366	Pol polyp	ATGCTT	contig366	Solyc11g	Solyc11g	Pol polyp	GO:0008	GO:0008	contig366	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT5G036	PTL	PTL (PET	chr5:957	2454.14	2685.84	1014.62	733.468	706.203	800.808
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	-2.307	Detected	-1.816	Detected	-2.061	0.015	GT	Sens	contig371	contig371	Pol polyp	TCGCTA	contig371	Solyc08g	Solyc08g	Pol polyp	GO:0006	GO:0006	contig371	Solyc08g	Pol polyp	GO:0008	SL2.40ch	AT5G40450.2		unknown	chr5:161	3759.67	4097.68	1285.49	1001.41	893.74	1054.2
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-1.546	Detected	-1.478	Detected	-1.512	0.005	GT	Sens	contig374	contig374	Unknown	AACCTC	contig374	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig374	Solyc11g	Unknown Protein (A		SL2.40ch	AT2G45990.4		unknown	chr2:189	737.528	768.101	386.515	206.708	290.37	255.47
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-1.601	Detected	-1.278	Detected	-1.439	0.019	GT	Sens	contig381	contig381	Unknown	GGGGCT	contig381	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig381	Solyc09g	Unknown Protein (A		SL2.40ch	AT1G14225.1				39719.3	40136.7	22021.9	14714.8	14823.9	15572.1
GT	Sense	Sense	0.141	Detected	-0.141	Detected	0.000	-1.550	Detected	-1.191	Detected	-1.370	0.027	GT	Sens	contig383	contig383	Gag-pol p	GATCTT	contig383	Solyc12g	Solyc12g	Gag-pol polyprotein (AHRD V1			contig383	Solyc12g	Gag-pol polyprotein		SL2.40ch	AT5G65910.1		BSD dom	chr5:263	95.0827	93.1119	28.8829	25.5765	36.1979	38.9746
GT	Sense	Sense	-0.289	Detected	0.289	Detected	0.000	-2.466	Detected	-2.341	Detected	-2.403	0.015	GT	Sens	contig383	contig383	Pol polyp	CAACCA	contig383	Solyc00g	Solyc00g	Pol polyp	GO:0006	GO:0006	contig383	Solyc00g	Pol polyp	GO:0006	SL2.40ch	AT2G350	URED	URED (u	chr2:147	76.7376	136.404	27.3742	32.7437	20.8615	19.093
GT	Sense	Sense	0.174	Detected	-0.174	Detected	0.000	-1.637	Detected	-0.926	Detected	-1.282	0.084	GT	Sens	contig387	contig387	Lipoxyge	TTGGTT	contig387	Solyc01g	Solyc01g	Lipoxyge	GO:0016	GO:0016	contig387	Solyc01g	Lipoxyge	GO:0016	SL2.40ch	AT3G224	LOX5	LOX5: el	chr3:792	18658.7	17440.2	7762.73	9556.62	6532.3	8975.29
GT	Sense	Sense	-0.376	Detected	0.376	Detected	0.000	-2.185	Detected	-1.581	Detected	-1.883	0.060	GT	Sens	contig402	contig402	Long-cha	ATAGCA	contig402	Solyc09g	Solyc09g	Long-cha	GO:0008	GO:0008	contig402	Solyc09g	Long-cha	GO:0004	SL2.40ch	AT3G059	LACS6. A	LACS6 (l	chr3:178	72.6853	145.829	106.648	128.48	25.4969	32.5422
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	-1.157	Detected	-1.399	Detected	-1.278	0.019	GT	Sens	contig405	contig405	Unannota	TAATCTCCTTTGCAAAATTTATGTCTCAACACAGAGAACCCCTTTTCTC							contig405	Solyc07g	LRR rece	GO:0004	SL2.40ch	AT5G27240.1		DNAJ he	chr5:959	38.1818	37.8434	17.5589	10.6976	19.1992	13.6258
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-0.958	Detected	-1.414	Detected	-1.186	0.038	GT	Sens	contig409	contig409	Ycf2 (AHF	TGCAGA	contig409	Solyc03g	Solyc03g	Ycf2 (AHRD V1 ***- D2KLP5_OL			contig409	Solyc12g	Ycf2 (AHF	GO:0005	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:14	1178	1272.61	769.108	690.351	710.243	434.434
GT	Sense	Sense	0.181	Detected	-0.181	Detected	0.000	-1.244	Detected	-2.071	Detected	-1.657	0.067	GT	Sens	contig413	contig413	Unannota	GAAGAACCGAAGTCAAGCAACTACTTCTCCAATGCCTTTCCTTTTCTTA							contig413	Solyc02g014100.1.1				AT4G24880.1		unknown	chr4:128	126.24	116.976	68.4189	61.8296	57.8101	27.3511
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-2.056	Detected	-1.808	Detected	-1.932	0.006	GT	Sens	contig422	contig422	Unannota	ATAGGGATCTGGCGAGGTTAAATTCCCATATACGCTAGCATGTTATTGA							contig422	Solyc02g	Lipase (A	GO:0004	SL2.40ch	AT5G02850.1		hydroxy	chr5:652	478.817	511.25	259.241	211.973	134.045	133.607
GT	Sense	Sense	0.219	Detected	-0.219	Detected	0.000	-1.633	Detected	-1.045	Detected	-1.339	0.067	GT	Sens	contig426	contig426	Lipoxyge	TTGCAA	contig426	Solyc01g	Solyc01g	Lipoxyge	GO:0016	GO:0016	contig426	Solyc01g099150.2.1				AT3G224	LOX5	LOX5: el	chr3:792	5518.67	4852.1	2098.86	2426.35	1879.75	2370.81
GT	Sense	Sense	-2.003	Detected	2.003	Detected	0.000	-1.920	Detected	-1.152	Detected	-1.536	0.530	GT	Sens	contig427	contig427	ORMDL d	ACAGTGATATGTGACAAGGAAATGAGCGAGATTGACAATAGTCCATGC							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	22.1152	422.818	32.8952	42.4711	28.7934	41.1538
GT	Sense	Sense	-0.311	Detected	0.311	Detected	0.000	-1.659	Detected	-1.190	Detected	-1.424	0.067	GT	Sens	contig427	contig427	Uncharac	ATTAGGCGTCGAAAAATCCGGGAGAAATGCTGAAGGAGATTCATGGTT							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	115.516	211.571	115.463	125.217	55.7486	64.809
GT	Sense	Sense	-0.296	Detected	0.296	Detected	0.000	-1.226	Detected	-0.818	Detected	-1.022	0.105	GT	Sens	contig429	contig429	Probable	GAGAGGTTGAGTTACTTTGGTATAGCCACAAGTTTGATCATTTACCTAA							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	159.563	286.272	102.448	268.364	102.899	114.654
GT	Sense	Sense	-0.543	Detected	0.543	Detected	0.000	-1.424	Detected	-1.291	Detected	-1.358	0.131	GT	Sens	contig429	contig429	Nicotia ta	CAAGTAAGAATCCTTCTCAAATTGTTATTTGTGCATCTTGATCATCATG							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	139.34	352.301	116.58	236.542	93.0157	85.6065
GT	Sense	Sense	-0.507	Detected	0.507	Detected	0.000	-1.657	Detected	-1.038	Detected	-1.348	0.151	GT	Sens	contig430	contig430	Nicotia ta	AGAGGCCATACCATCCTCCACCAACACCATATCATCCCACACCAGTTTA							contig430	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	298.101	717.087	155.487	425.861	165.147	212.844
GT	Sense	Sense	-0.373	Detected	0.373	Detected	0.000	-1.043	Detected	-1.265	Detected	-1.154	0.097	GT	Sens	contig446	contig446	Auxin-ind	CATGAT	contig446	Solyc03g	Solyc03g	Auxin-ind	GO:0005	GO:0005	contig446	Solyc03g	Auxin-ind	GO:0005	SL2.40ch	AT2G21220.1		auxin-res	chr2:908	466.926	932.387	536.755	798.584	360.68	259.636
GT	Sense	Sense	0.062	Detected	-0.062	Detected	0.000	-1.628	Detected	-1.799	Detected	-1.713	0.004	GT	Sens	contig454	contig454	Gag-Pol p	AAGGTT	contig454	Solyc10g	Solyc10g	Gag-Pol polyprotein (AHRD V1			contig454	Solyc05g	Nucleore	GO:0004	SL2.40ch	AT2G28940.2		protein k	chr2:124	316.408	345.627	155.022	95.349	120.529	89.8639
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-1.449	Detected	-1.544	Detected	-1.496	0.002	GT	Sens	contig456	contig456	Ycf2 (AHF	GGGGAT	contig456	Solyc04g	Solyc04g	Ycf2 (AHRD V1 ***- A6Y9X1_HA			contig456	Solyc04g024580.1.1				ATCG012	YCF2.2	hypothet	chrC:14	641.488	807.692	295.619	279.884	296.997	233.477
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	-1.555	Detected	-1.485	Detected	-1.520	0.003	GT	Sens	contig457	contig457	NAD(P)H-	ACTATA	contig457	Solyc09g	Solyc09g	NAD(P)H-quinone oxidoreduct			contig457	Solyc09g	NAD(P)H-quinone o		SL2.40ch	ATCG012	NDHB.2	NADH de	chrC:14	296.778	393.594	171.525	166.36	130.985	115.467
GT	Sense	Sense	0.118	Detected	-0.118	Detected	0.000	-1.481	Detected	-1.060	Detected	-1.271	0.034	GT	Sens	contig460	contig460	Reverse t	TATACT	contig460	Solyc02g	Solyc02g	Reverse t	GO:0006	GO:0006	contig460	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT4G292	PFK1	PFK1 (P	chr4:144	215.707	217.948	131.858	93.2477	87.4955	98.3309
GT	Sense	Sense	0.545	Detected	-0.545	Detected	0.000	-1.166	Detected	-1.220	Detected	-1.193	0.160	GT	Sens	contig484	contig484	UDP-gluc	AATAGG	contig484	Solyc12g	Solyc12g	UDP-gluc	GO:0008	GO:0008	contig484	Solyc12g	UDP-gluc	GO:0008	SL2.40ch	AT1G223	AtUGT85	AtUGT85	chr1:789	327.61	183.223	149.986	210.169	123.011	99.4376
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	-1.298	Detected	-0.950	Detected	-1.124	0.027	GT	Sens	contig504	contig504	Pol polyp	TTGTGA	contig504	Solyc10g	Solyc10g	Pol polyp	GO:0006	GO:0006	contig504	Solyc10g	Pol polyp	GO:0006	SL2.40ch	AT5G40450.2		unknown	chr5:161	563.843	608.278	311.547	211.807	268.323	286.653
GT	Sense	Sense	-0.018	Detected	0.018	Detected	0.000	-1.021	Detected	-1.244	Detected	-1.132	0.010	GT	Sens	contig512	contig512	Topoison	TTGAGA	contig512	Solyc11g	Solyc11g	Topoisomerase 6 subunit B-lik			contig512	Solyc11g	Topoisomerase 6 s		SL2.40ch	AT3G294	ATEXO70	ATEXO7	chr3:112	56.004	68.3825	40.9997	41.9468	34.3585	24.7059
GT	Sense	Sense	0.157	Detected	-0.157	Detected	0.000	-1.298	Detected	-0.966	Detected	-1.132	0.038	GT	Sens	contig526	contig526	Reverse t	AGAATG	contig526	Solyc01g	Solyc01g	Reverse t	GO:0006	GO:0006	contig526	Solyc09g	Polyprote	GO:0008	SL2.40ch	AT5G124	CPK7	CPK7 (ca	chr5:404	755.483	723.942	417.779	342.223	338.827	357.843
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.928	Detected	-1.698	Detected	-1.813	0.005	GT	Sens	contig545	contig545	Retrotran	ATATTG	contig545	Solyc08g	Solyc08g	Retrotransposon gag protein (			contig545	Solyc08g022190.1.1				AT5G14050.1		transduc	chr5:453	2908.74	3219.09	1187.03	862.575	906.105	891.45
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-1.745	Detected	-1.651	Detected	-1.698	0.005	GT	Sens	contig545	contig545	Polyprote	ACACTT	contig545	Solyc05g	Solyc05g	Polyprote	GO:0006	GO:0006	contig545	Solyc08g	Pol polyp	GO:0008	SL2.40ch	AT5G40450.2		unknown	chr5:161	2540.93	2586.57	1297.11	930.394	861.288	771.661
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-2.261	Detected	-1.982	Detected	-2.121	0.004	GT	Sens	contig547	contig547	Unknown	GGCGGG	contig547	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig547	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G18570.1		GTP1/OB	chr5:617	1633.63	1903.89	626.935	418.22	414.555	422.111
GT	Sense	Sense	0.183	Detected	-0.183	Detected	0.000	-1.578	Comprom	-0.849	Comprom	-1.214	0.097	GT	Sens	contig555	contig555	Transpos	AACAAT	contig555	Solyc10g	Solyc10g	Transposase (AHRD V1 *--- O6			contig555	Solyc08g	Transposase (AHRD		SL2.40ch	AT1G75900.1		family II e	chr1:284	24.4972	22.6203	6.046	5.52805	8.88024	12.3564
GT	Sense	Sense	0.670	Detected	-0.670	Detected	0.000	-3.837	Detected	-3.155	Detected	-3.496	0.043	GT	Sens	contig600	contig600	Acyltrans	CCAAGT	contig600	Solyc11g	Solyc11g	Acyltrans	GO:0016	GO:0016	contig600	Solyc11g	Acyltrans	GO:0016	SL2.40ch	AT4G37950.1		lyase	chr4:178	2621.55	1232.23	3795.89	5116.28	141.644	190.843
GT	Sense	Sense	-0.068	Detected	0.068	Detected	0.000	-1.865	Comprom	-1.182	Comprom	-1.524	0.048	GT	Sens	contig605	contig605	Retroviru	GTTTGA	contig605	Solyc07g	Solyc07g	Retrovirus-related Pol polypro			contig605	Solyc07g	Retrovirus-related P		SL2.40ch	AT2G326	AtRLP23	AtRLP23	chr2:138	17.6388	23.063	13.8752	16.295	6.23725	8.40318
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	-1.800	Detected	-1.626	Detected	-1.713	0.003	GT	Sens	contig606	contig606	Unknown	ACAGAC	contig606	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig606	Solyc12g	Unknown Protein (A		SL2.40ch	AT4G291	IOD25	IOD25 (I	chr4:143	3290.6	3692.22	1654.82	1277.75	1127.36	1067.53
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	-0.835	Detected	-2.540	Comprom	-1.688	0.189	GT	Sens	contig617	contig617	Mutator-li	AGTCCA	contig617	Solyc10g	Solyc10g	Mutator-li	GO:0008	GO:0008	contig617	Solyc12g	Mutator-li	GO:0008	SL2.40ch	AT3G227	SOL1	SOL1: tr	chr3:804	15.1204	21.5123	15.3171	10.279	11.3853	2.93119
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-0.950	Detected	-1.120	Detected	-1.035	0.018	GT	Sens	contig640	contig640	Unknown	TAAGCG	contig640	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig640	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G174	IRX3. CE	IRX3 (IR	chr5:573	48.9892	49.775	45.4128	43.437	28.7859	21.4793
GT	Sense	Sense	0.070	Detected	-0.070	Detected	0.000	-1.649	Comprom	-1.384	Comprom	-1.517	0.010	GT	Sens	contig644	contig644	Unknown	TCTGCT	contig644	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig644	Solyc05g	Unknown Protein (A		SL2.40ch	AT4G170	CT-BMY.	CT-BMY	chr4:960	15.3761	16.6022	5.39323	18.802	5.73978	5.78714
GT	Sense	Sense	0.405	Detected	-0.405	Detected	0.000	-1.627	Detected	-2.082	Detected	-1.855	0.057	GT	Sens	contig689	contig689	Protease	TACTGC	contig689	Solyc10g	Solyc10g	Protease inhibitor/seed storag			contig689	Solyc10g	Protease inhibitor/s		SL2.40ch	AT5G35370.1		ATP bind	chr5:135	460.29	312.416	334.941	207.412	138.273	84.6586
GT	Sense	Sense	-0.439	Detected	0.439	Detected	0.000	-1.372	Detected	-1.505	Detected	-1.438	0.083	GT	Sens	contig691	contig691	Serine ca	AGACAG	contig691	Solyc06g	Solyc06g	Serine ca	GO:0005	GO:0005	contig691	Solyc06g	Serine ca	GO:0005	SL2.40ch	AT4G129	scpl20	scpl20 (s	chr4:755	442.052	967.109	289.378	403.951	284.548	217.874
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.309	Detected	-1.063	Detected	-1.186	0.011	GT	Sens	contig694	contig694	NAD(P)H-	TTCCTC	contig694	Solyc09g	Solyc09g	NAD(P)H-	GO:0055	GO:0055	contig694	Solyc01g	NAD(P)H-	GO:0055	SL2.40ch	ATCG012	NDHB.2	NADH de	chrC:14	241.866	297.757	127.667	154.203	121.969	121.49
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.348	Detected	-0.828	Detected	-1.088	0.059	GT	Sens	contig698	contig698	ABC tran	TGCTAG	contig698	Solyc06g	Solyc06g	ABC tran	GO:0017	GO:0017	contig698	Solyc03g	ABC tran	GO:0008	SL2.40ch	AT1G178	WBC11. A	WBC11 (	chr1:614	90.7408	94.785	77.0277	78.5848	41.039	49.3951
GT	Sense	Sense	-0.200	Detected	0.200	Detected	0.000	-0.963	Detected	-1.054	Detected	-1.009	0.039	GT	Sens	contig702	contig702	Sulfotran	TGTTCT	contig702	Solyc09g	Solyc09g	Sulfotran	GO:0008	GO:0008	contig702	Solyc09g	Sulfotran	GO:0080	SL2.40ch	AT5G059	DHS	DHS (DE	chr5:177	28.1062	44.1759	28.4655	24.426	20.3642	16.0427
GT	Sense	Sense	-0.115	Detected	0.115	Detected	0.000	-2.038	Detected	-3.187	Detected	-2.613	0.047	GT	Sens	contig725	contig725	Salicylic	TCCTTG	contig725	Solyc09g	Solyc09g	Salicylic a	GO:0008	GO:0008	contig725	Solyc09g	Salicylic a	GO:0008	SL2.40ch	AT4G36470.1		S-adeno	chr4:172	202.097	282.133	63.4818	121.481	65.4938	24.7904
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-1.736	Detected	-1.475	Detected	-1.605	0.007	GT	Sens	contig729	contig729	Pol polyp	CCTCCG	contig729	Solyc08g	Solyc08g	Pol polyprotein (AHRD V1 ***- F			contig729	Solyc08g	Pol polyp	GO:0008	SL2.40ch	AT2G43110.1				1551.39	1728.08	782.102	514.096	553.823	557.003
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-2.460	Detected	-1.768	Detected	-2.114	0.026	GT	Sens	contig730	contig730	Retrotran	TAGTAC	contig730	Solyc09g	Solyc09g	Retrotran	GO:0015	GO:0015	contig730	Solyc09g	Retrotran	GO:0003	SL2.40ch	AT3G63320.1				945.359	1085.56	361.34	244.901	207.373	281.274
GT	Sense	Sense	-0.077	Detected	0.077	Detected	0.000	-0.922	Detected	-1.338	Detected	-1.130	0.036	GT	Sens	contig737	contig737	NADH-qui	TGCTTA	contig737	Solyc03g	Solyc03g	NADH-qui	GO:0055	GO:0055	contig737	Solyc03g	NADH-qui	GO:0055	SL2.40ch	ATCG010	NDHF	Chloropl	chrC:11	88.2075	116.792	57.37	53.9125	60.3519	37.9668
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.536	Detected	-1.544	Detected	-1.540	0.000	GT	Sens	contig739	contig739	Retrotran	CTTTGT	contig739	Solyc10g	Solyc10g	Retrotran	GO:0008	GO:0008	contig739	Solyc10g	Retrotran	GO:0006	SL2.40ch	AT2G181	ATMPK7.	ATMPK7	chr2:790	1420.95	1682.89	863.534	715.678	600.597	501.566
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	-1.728	Detected	-2.073	Detected	-1.900	0.008	GT	Sens	contig744	contig744	Ycf1 (Fra	ATCAAT	contig744	Solyc05g	Solyc05g	Ycf1 (Fragment) (AHRD V1 ***-			contig744	Solyc05g	Ycf1 (Fragment) (AH		SL2.40ch	ATMG003	ORF199	hypothet	chrM:10	604.388	734.221	320.89	314.72	226.524	149.713
GT	Sense	Sense	-0.197	Detected	0.197	Detected	0.000	-2.233	Detected	-0.911	Detected	-1.572	0.150	GT	Sens	contig756	contig756	Peroxida	TTTTCA	contig756	Solyc02g	Solyc02g	Peroxida	GO:0005	GO:0005	contig756	Solyc02g	Peroxida	GO:0004	SL2.40ch	AT1G14540.1		anionic p	chr1:497	28728.6	44954.3	15039.3	30105.4	8614.23	18070.9
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	-1.468	Detected	-1.440	Detected	-1.454	0.004	GT	Sens	contig768	contig768	Unknown	GAAGAG	contig768	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig768	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G13820.1				3360.93	3511.56	1547.33	1175.64	1399.19	1197.25
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-1.949	Detected	-1.646	Detected	-1.798	0.011	GT	Sens	contig791	contig791	Polyprote	GAATGG	contig791	Solyc01g	Solyc01g	Polyprotein (AHRD V1 ***- A5J			contig791	Solyc01g	Polyprotein (AHRD V		SL2.40ch	AT4G192	CYP707A	CYP707A	chr4:105	2216.84	2254.25	976.943	675.602	652.287	675.187
GT	Sense	Sense	0.107	Detected	-0.107	Detected	0.000	-1.664	Detected	-1.628	Detected	-1.646	0.004	GT	Sens	contig812	contig812	Unknown	TGCAGG	contig812	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig812	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G63750.1				5299.13	5442.36	2989.27	2401.89	1908.94	1642.78
GT	Sense	Sense	-0.231	Detected	0.231	Detected	0.000	-1.148	Detected	-1.634	Detected	-1.391	0.054	GT	Sens	contig815	contig815	CONSTAI	TGGAAT	contig815	Solyc02g	Solyc02g	CONSTAI	GO:0003	GO:0003	contig815	Solyc02g	Tomato C	GO:0003	SL2.40ch	AT5G158	COL1. AT	COL1 (co	chr5:517	230.535	378.201	329.826	316.562	150.082	89.9642
GT	Sense	Sense	0.148	Detected	-0.148	Detected	0.000	-1.872	Detected	-1.786	Detected	-1.829	0.007	GT	Sens	contig816	contig816	Unknown	TTCAGA	contig816	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig816	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G067	RAP2.9	RAP2.9 (	chr4:407	1635.72	1585.85	743.637	521.192	495.771	441.595
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-3.129	Detected	-3.185	Detected	-3.157	0.002	GT	Sens	contig843	contig843	Glutathio	GGCGTA	contig843	Solyc01g	Solyc01g	Glutathione-S-transferase (AH			contig843	Solyc01g	Glutathione-S-trans		SL2.40ch	AT3G492	emb1796	emb1796	chr3:182	6549.22	6501.04	1369.5	1256.64	840.406	678.168
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	-1.584	Detected	-1.555	Detected	-1.569	0.003	GT	Sens	contig875	contig875	Unknown	TGCCGT	contig875	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig875	Solyc00g010110.1.1				AT4G24680.1		FUNCTIO	chr4:127	4983.52	5304.55	3019.55	2319.58	1932.15	1654.4
GT	Sense	Sense	0.418	Detected	-0.418	Detected	0.000	-1.568	Detected	-1.834	Detected	-1.701	0.060	GT	Sens	contig883	contig883	Protease	AATGCG	contig883	Solyc05g	Solyc05g	Protease	GO:0008	GO:0008	contig883	Solyc05g	Protease	GO:0008	SL2.40ch	AT3G60270.1		uclacyan	chr3:222	141.218	94.2301	89.4861	65.0235	43.8148	30.5829
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	-1.143	Detected	-1.218	Detected	-1.181	0.027	GT	Sens	contig883	contig883	Unknown	AGCAGA	contig883	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig883	Solyc04g	Unknown Protein (A		SL2.40ch	AT2G37420.1		kinesin m	chr2:157	236.368	215.459	205.153	203.377	115.121	91.7161
GT	Sense	Sense	-0.076	Detected	0.076	Detected	0.000	-1.295	Detected	-1.280	Detected	-1.287	0.003	GT	Sens	contig903	contig903	Ribulose	AGATGA	contig903	Solyc12g	Solyc12g	Ribulose	GO:0009	GO:0009	contig903	Solyc12g	Ribulose	GO:0009	SL2.40ch	ATCG001	RPOC1	RNA poly	chrC:20	127.105	168.069	79.9916	84.6881	67.1159	56.9146
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.521	Detected	-1.722	Detected	-1.622	0.005	GT	Sens	contig907	contig907	NADH-qui	TACACG	contig907	Solyc01g	Solyc01g	NADH-qui	GO:0055	GO:0055	contig907	Solyc03g	NADH-qui	GO:0055	SL2.40ch	ATCG010	NDHF	Chloropl	chrC:11	290.628	324.757	142.827	136.721	120.577	88.0329
GT	Sense	Sense	0.313	Detected	-0.313	Detected	0.000	-1.118	Detected	-1.424	Detected	-1.271	0.067	GT	Sens	contig921	contig921	Reverse t	GATCGC	contig921	Solyc11g	Solyc11g	Reverse transcriptase (Fragm			contig921	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT1G33030.1		O-methyl	chr1:119	60.3842	46.6124	25.0431	20.424	27.5409	18.7001
GT	Sense	Sense	0.054	Detected	-0.054	Detected	0.000	-1.994	Detected	-1.958	Detected	-1.976	0.001	GT	Sens	contig922	contig922	Retrotran	CGGAGT	contig922	Solyc02g	Solyc02g	Retrotran	GO:0015	GO:0015	contig922	Solyc12g	Retrotran	GO:0003	SL2.40ch	AT5G52000.1				170.641	188.494	81.4958	68.2986	50.7216	43.661
GT	Sense	Sense	-0.041	Detected	0.041	Detected	0.000	-1.656	Detected	-0.891	Detected	-1.274	0.080	GT	Sens	contig927	contig927	Unknown	AGGATT	contig927	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig927	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G145	NTMC2T	NTMC2T	chr3:490	234.139	294.924	2017.22	3388.18	93.9365	133.957
GT	Sense	Sense	-0.016	Detected	0.016	Detected	0.000	-1.639	Detected	-0.936	Detected	-1.288	0.067	GT	Sens	contig930	contig930	Mutator-li	ATAGTG	contig930	Solyc08g	Solyc08g	Mutator-li	GO:0008	GO:0008	contig930	Solyc12g	Mutator-li	GO:0008	SL2.40ch	AT1G03720.1				56.0811	68.223	27.2946	17.3425	22.3726	30.5609
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	-2.295	Detected	-1.796	Detected	-2.045	0.016	GT	Sens	contig931	contig931	Pol polyp	ACATCT	contig931	Solyc03g	Solyc03g	Pol polyp	GO:0015	GO:0015	contig931	Solyc10g	Pol polyp	GO:0003	SL2.40ch	AT3G58090.1		FUNCTIO	chr3:215	7333.23	7746.62	2470.67	1812.14	1729.98	2052.91
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.487	Detected	-1.287	Detected	-1.387	0.006	GT	Sens	contig931	contig931	Pol polyp	GTGACT	contig931	Solyc07g	Solyc07g	Pol polyp	GO:0015	GO:0015	contig931	Solyc10g	Pol polyp	GO:0003	SL2.40ch	AT5G56460.1		protein k	chr5:228	338.597	380.615	166.221	139.311	144.264	139.119
GT	Sense	Sense	-0.238	Detected	0.238	Detected	0.000	-2.366	Detected	-1.039	Detected	-1.702	0.137	GT	Sens	contig938	contig938	Laccase	GTTATT	contig938	Solyc05g	Solyc05g	Laccase (	GO:0048	GO:0048	contig938	Solyc07g	Laccase (	GO:0005	SL2.40ch	AT5G589	LAC16	LAC16 (la	chr5:237	582.943	965.204	534.921	894.7	163.959	345.254
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-1.917	Detected	-1.510	Detected	-1.713	0.015	GT	Sens	contig943	contig943	Polyprote	TTCTTG	contig943	Solyc11g	Solyc11g	Polyprotein (AHRD V1 ***- O0ZI			contig943	Solyc08g	Pol polyp	GO:0008	SL2.40ch	AT4G396	AGT2	AGT2 (A	chr4:184	8348.68	9064.31	3580.34	2661.63	2594.6	2888.64

GO ID	GO ACCESSION	GO Term	p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
11776	GO:0019825	oxygen binding	**0.00**	22	3.7225041	389	1.1234008
3048	GO:0004364	glutathione transferase activi	**0.00**	9	1.5228426	84	0.24258527
25094	GO:0050789|GO:0050791	regulation of biological proce	**0.00**	108	18.27411	4315	12.461374
11931	GO:0020037	heme binding	**0.00**	24	4.0609136	550	1.5883559
3872	GO:0005506	iron ion binding	**0.00**	24	4.0609136	563	1.6258988
28364	GO:0065007	biological regulation	**0.00**	108	18.27411	4376	12.637537
25098	GO:0050794|GO:0051244	regulation of cellular process	**0.00**	100	16.920473	3987	11.514136
11224	GO:0019222	regulation of metabolic proce	**0.00**	81	13.705584	3115	8.995871
4530	GO:0006355|GO:0032583|G	regulation of transcription, DI	**0.00**	70	11.844332	2591	7.4826
25544	GO:0051252	regulation of RNA metabolic	**0.00**	70	11.844332	2593	7.488376
22409	GO:0046906	tetrapyrrole binding	**0.00**	24	4.0609136	596	1.7212002
32213	GO:2000112	regulation of cellular macrom	**0.00**	70	11.844332	2605	7.523031
13756	GO:0031326	regulation of cellular biosynth	**0.00**	70	11.844332	2605	7.523031
7141	GO:0009889	regulation of biosynthetic pro	**0.00**	70	11.844332	2605	7.523031
7772	GO:0010556	regulation of macromolecule	**0.00**	70	11.844332	2605	7.523031
7692	GO:0010468	regulation of gene expressio	**0.00**	70	11.844332	2635	7.6096687
19590	GO:0043295	glutathione binding	**0.00**	5	0.8460237	31	0.08952551
7074	GO:0009815	1-aminocyclopropane-1-carb	**0.00**	6	1.0152284	49	0.14150807
27228	GO:0060255	regulation of macromolecule	**0.00**	70	11.844332	2660	7.6818666
13753	GO:0031323	regulation of cellular metabo	**0.00**	72	12.182741	2770	7.999538
25468	GO:0051171	regulation of nitrogen compo	**0.00**	70	11.844332	2675	7.7251854
11221	GO:0019219	regulation of nucleobase, nu	**0.00**	70	11.844332	2675	7.7251854
31465	GO:0080090	regulation of primary metabo	**0.00**	70	11.844332	2710	7.826263
19479	GO:0043176	amine binding	**0.00**	7	1.1844332	80	0.2310336
9682	GO:0016597	amino acid binding	**0.00**	7	1.1844332	80	0.2310336
30700	GO:0072341	modified amino acid binding	**0.00**	6	1.0152284	59	0.17038727
2986	GO:0004252	serine-type endopeptidase a	**0.00**	9	1.5228426	144	0.41586044
6888	GO:0009611|GO:0002245	response to wounding	**0.00**	6	1.0152284	66	0.1906027
9722	GO:0016641	oxidoreductase activity, actin	**0.00**	6	1.0152284	69	0.19926646
5766	GO:0008236	serine-type peptidase activity	**0.00**	11	1.8612521	214	0.6180149
4641	GO:0006508	proteolysis	**0.00**	30	5.0761423	965	2.7868426
13829	GO:0031406	carboxylic acid binding	**0.00**	7	1.1844332	98	0.28301615
10103	GO:0017171	serine hydrolase activity	**0.00**	11	1.8612521	220	0.63534236
9768	GO:0016706	oxidoreductase activity, actin	**0.00**	9	1.5228426	175	0.505386
9719	GO:0016638	oxidoreductase activity, actin	**0.00**	6	1.0152284	89	0.25702485
9767	GO:0016705	oxidoreductase activity, actin	**0.00**	13	2.1996615	329	0.95012563
9818	GO:0016765|GO:0016766	transferase activity, transferr	**0.00**	9	1.5228426	185	0.53426516
5704	GO:0008150|GO:0000004|G	biological_process	**0.01**	409	69.204735	22215	64.155136
20342	GO:0044092	negative regulation of molec	**0.01**	9	1.5228426	188	0.54292893
19393	GO:0043086	negative regulation of catalyt	**0.01**	9	1.5228426	188	0.54292893
22375	GO:0046872	metal ion binding	**0.01**	69	11.675127	2985	8.6204405
19470	GO:0043167	ion binding	**0.01**	69	11.675127	2997	8.655096
19472	GO:0043169	cation binding	**0.01**	69	11.675127	2997	8.655096
716	GO:0001071	nucleic acid binding transcrip	**0.01**	37	6.2605753	1417	4.0921826
2643	GO:0003700|GO:0000130	sequence-specific DNA bind	**0.01**	37	6.2605753	1417	4.0921826
3356	GO:0004737	pyruvate decarboxylase activ	**0.01**	2	0.33840948	8	0.023103358
9600	GO:0016491	oxidoreductase activity	**0.01**	43	7.2758036	1724	4.9787736
5097	GO:0007049	cell cycle	**0.01**	4	0.67681897	52	0.15017183
5678	GO:0008113|GO:0033742	peptide-methionine-(S)-S-ox	**0.01**	2	0.33840948	10	0.0288792
4526	GO:0006351|GO:0006350|G	transcription, DNA-depender	**0.01**	39	6.5989847	1575	4.548474
15176	GO:0032774	RNA biosynthetic process	**0.01**	39	6.5989847	1575	4.548474
2870	GO:0004064	arylesterase activity	**0.01**	3	0.5076142	30	0.086637594
13809	GO:0031386	protein tag	**0.01**	2	0.33840948	11	0.03176712
26959	GO:0055114	oxidation-reduction process	**0.01**	57	9.6446705	2490	7.1909204
5715	GO:0008171	O-methyltransferase activity	**0.02**	4	0.67681897	57	0.16461143
12516	GO:0022804	active transmembrane trans	**0.02**	22	3.7225041	787	2.2727928
3464	GO:0004857	enzyme inhibitor activity	**0.02**	7	1.1844332	157	0.4534034
18633	GO:0042277	peptide binding	**0.02**	5	0.8460237	95	0.27435237
3318	GO:0004693|GO:0016537	cyclin-dependent protein kina	**0.03**	3	0.5076142	37	0.10685303
12805	GO:0030246	carbohydrate binding	**0.03**	9	1.5228426	251	0.7248679
3801	GO:0005342	organic acid transmembrane	**0.03**	6	1.0152284	136	0.3927571
22444	GO:0046943	carboxylic acid transmembra	**0.03**	6	1.0152284	136	0.3927571
13435	GO:0030976	thiamine pyrophosphate bind	**0.03**	2	0.33840948	16	0.046206716
18757	GO:0042409	caffeoyl-CoA O-methyltransf	**0.03**	2	0.33840948	16	0.046206716
22412	GO:0046910	pectinesterase inhibitor activi	**0.03**	2	0.33840948	16	0.046206716
22415	GO:0046914	transition metal ion binding	**0.03**	57	9.6446705	2599	7.5057034
18738	GO:0042389	omega-3 fatty acid desatura	**0.03**	2	0.33840948	17	0.049094636
3719	GO:0005201	extracellular matrix structural	**0.03**	1	0.16920474	2	0.00577584
5907	GO:0008413	8-oxo-7,8-dihydroguanosine	**0.03**	1	0.16920474	2	0.00577584
7409	GO:0010177	2-(2'-methylthio)ethylmalate	**0.03**	1	0.16920474	2	0.00577584
7470	GO:0010241	ent-kaurene oxidation to kau	**0.03**	1	0.16920474	2	0.00577584
8509	GO:0015093	ferrous iron transmembrane	**0.03**	1	0.16920474	2	0.00577584
8612	GO:0015204|GO:0015287	urea transmembrane transpo	**0.03**	1	0.16920474	2	0.00577584
8953	GO:0015684	ferrous iron transport	**0.03**	1	0.16920474	2	0.00577584
9106	GO:0015840	urea transport	**0.03**	1	0.16920474	2	0.00577584
11186	GO:0019177	dihydroneopterin triphosphat	**0.03**	1	0.16920474	2	0.00577584
15726	GO:0033331	ent-kaurene metabolic proce	**0.03**	1	0.16920474	2	0.00577584
19204	GO:0042887	amide transmembrane trans	**0.03**	1	0.16920474	2	0.00577584
30280	GO:0071918	urea transmembrane transpo	**0.03**	1	0.16920474	2	0.00577584
10899	GO:0018858	benzoate-CoA ligase activity	**0.04**	2	0.33840948	18	0.051982556
22917	GO:0047429	nucleoside-triphosphate diph	**0.04**	2	0.33840948	18	0.051982556
31431	GO:0080054	low affinity nitrate transmem	**0.04**	3	0.5076142	45	0.1299564
2975	GO:0004175|GO:0016809	endopeptidase activity	**0.05**	10	1.6920474	320	0.9241344
19758	GO:0043492	ATPase activity, coupled to	**0.05**	8	1.3536379	235	0.67866117
5921	GO:0008428	ribonuclease inhibitor activity	**0.05**	1	0.16920474	3	0.00866376
11784	GO:0019838	growth factor binding	**0.05**	3	0.5076142	49	0.14150807
31421	GO:0080044	quercetin 7-O-glucosyltransf	**0.05**	3	0.5076142	49	0.14150807
3874	GO:0005509	calcium ion binding	**0.05**	9	1.5228426	279	0.8057296
9114	GO:0015849	organic acid transport	**0.05**	6	1.0152284	156	0.45051548
22443	GO:0046942	carboxylic acid transport	**0.05**	6	1.0152284	156	0.45051548
8584	GO:0015171|GO:0015359	amino acid transmembrane	**0.05**	5	0.8460237	118	0.34077454
2521	GO:0003333	amino acid transmembrane	**0.05**	5	0.8460237	118	0.34077454
8489	GO:0015066	alpha-amylase inhibitor activi	**0.05**	2	0.33840948	22	0.06353424
12608	GO:0030001	metal ion transport	0.06	11	1.8612521	374	1.080082
9806	GO:0016752	sinapoyltransferase activity	0.06	2	0.33840948	23	0.06642216
9807	GO:0016753	O-sinapoyltransferase activit	0.06	2	0.33840948	23	0.06642216
9808	GO:0016754	sinapoylglucose-malate O-si	0.06	2	0.33840948	23	0.06642216
4951	GO:0006865|GO:0006866	amino acid transport	0.06	5	0.8460237	123	0.35521415
19473	GO:0043170|GO:0043283	macromolecule metabolic pr	0.06	127	21.489002	6553	18.92454
8559	GO:0015146	pentose transmembrane tra	0.06	2	0.33840948	24	0.06931008
8561	GO:0015148	D-xylose transmembrane tra	0.06	2	0.33840948	24	0.06931008
8829	GO:0015519	D-xylose:hydrogen symporte	0.06	2	0.33840948	24	0.06931008
9019	GO:0015750	pentose transport	0.06	2	0.33840948	24	0.06931008
9022	GO:0015753	D-xylose transport	0.06	2	0.33840948	24	0.06931008
5702	GO:0008146	sulfotransferase activity	0.06	3	0.5076142	54	0.15594767
3761	GO:0005275|GO:0005279	amine transmembrane trans	0.07	5	0.8460237	126	0.3638779
11522	GO:0019538|GO:0006411	protein metabolic process	0.07	83	14.043993	4134	11.938661
4039	GO:0005751|GO:0005752	mitochondrial respiratory cha	0.07	1	0.16920474	4	0.011551679
7511	GO:0010285|GO:0043742	L,L-diaminopimelate aminotr	0.07	1	0.16920474	4	0.011551679
8594	GO:0015184	L-cystine transmembrane tra	0.07	1	0.16920474	4	0.011551679
9080	GO:0015811	L-cystine transport	0.07	1	0.16920474	4	0.011551679
20901	GO:0045277|GO:0045287	respiratory chain complex IV	0.07	1	0.16920474	4	0.011551679
21300	GO:0045703	ketoreductase activity	0.07	1	0.16920474	4	0.011551679
31418	GO:0080041	ADP-ribose pyrophosphohyd	0.07	1	0.16920474	4	0.011551679
31507	GO:0080132	fatty acid alpha-hydroxylase	0.07	1	0.16920474	4	0.011551679

75	GO:0000099	sulfur amino acid transmemb	0.07	1	0.16920474	4	0.011551679
77	GO:0000101	sulfur amino acid transport	0.07	1	0.16920474	4	0.011551679
21145	GO:0045543	gibberellin 2-beta-dioxygenas	0.07	2	0.33840948	25	0.072197996
18956	GO:0042626	ATPase activity, coupled to t	0.07	7	1.1844332	211	0.6093511
17024	GO:0034645|GO:0034961	cellular macromolecule biosy	0.07	43	7.2758036	1999	5.7729516
30066	GO:0071702	organic substance transport	0.07	14	2.3688664	529	1.5277096
9744	GO:0016671	oxidoreductase activity, actin	0.07	2	0.33840948	26	0.075085916
9861	GO:0016820	hydrolase activity, acting on a	0.07	7	1.1844332	212	0.612239
6428	GO:0009059|GO:0043284	macromolecule biosynthetic	0.07	43	7.2758036	2003	5.7845035
9308	GO:0016070	RNA metabolic process	0.08	40	6.7681894	1855	5.3570914
8749	GO:0015399	primary active transmembrar	0.08	8	1.3536379	260	0.75085914
8753	GO:0015405	P-P-bond-hydrolysis-driven t	0.08	8	1.3536379	260	0.75085914
17617	GO:0035251	UDP-glucosyltransferase act	0.08	7	1.1844332	218	0.62956655
9103	GO:0015837	amine transport	0.08	5	0.8460237	135	0.38986918
14850	GO:0032442	phenylcoumaran benzylic eth	0.08	1	0.16920474	5	0.0144396
21949	GO:0046424	ferulate 5-hydroxylase activit	0.08	1	0.16920474	5	0.0144396
11787	GO:0019842	vitamin binding	0.08	6	1.0152284	177	0.5111618
8526	GO:0015112	nitrate transmembrane trans	0.09	3	0.5076142	61	0.1761631
8975	GO:0015706|GO:0006872	nitrate transport	0.09	3	0.5076142	61	0.1761631
16430	GO:0034046	poly(G) RNA binding	0.09	4	0.67681897	100	0.28879198
3603	GO:0005030	neurotrophin receptor activity	0.09	2	0.33840948	30	0.086637594
6216	GO:0008810	cellulase activity	0.09	2	0.33840948	30	0.086637594
19425	GO:0043121	neurotrophin binding	0.09	2	0.33840948	30	0.086637594
22049	GO:0046527	glucosyltransferase activity	0.09	8	1.3536379	270	0.77973837
25820	GO:0051536	iron-sulfur cluster binding	0.10	3	0.5076142	64	0.18482687
25824	GO:0051540	metal cluster binding	0.10	3	0.5076142	64	0.18482687
3197	GO:0004550	nucleoside diphosphate kinas	0.10	1	0.16920474	6	0.01732752
3413	GO:0004802	transketolase activity	0.10	1	0.16920474	6	0.01732752
4375	GO:0006165	nucleoside diphosphate phos	0.10	1	0.16920474	6	0.01732752
7250	GO:0010012	steroid 22-alpha hydroxylase	0.10	1	0.16920474	6	0.01732752
9333	GO:0016101	diterpenoid metabolic proces	0.10	1	0.16920474	6	0.01732752
9772	GO:0016710	trans-cinnamate 4-monooxyg	0.10	1	0.16920474	6	0.01732752
19203	GO:0042886	amide transport	0.10	1	0.16920474	6	0.01732752
30707	GO:0072348	sulfur compound transport	0.10	1	0.16920474	6	0.01732752
2702	GO:0003852	2-isopropylmalate synthase a	0.10	1	0.16920474	6	0.01732752
2713	GO:0003863	3-methyl-2-oxobutanoate del	0.10	1	0.16920474	6	0.01732752
3073	GO:0004397	histidine ammonia-lyase activ	0.10	1	0.16920474	6	0.01732752
5732	GO:0008194	UDP-glycosyltransferase act	0.10	9	1.5228426	322	0.9299102
21041	GO:0045431	flavonol synthase activity	0.10	2	0.33840948	32	0.09241343
25836	GO:0051552	flavone metabolic process	0.10	2	0.33840948	32	0.09241343
25837	GO:0051553	flavone biosynthetic process	0.10	2	0.33840948	32	0.09241343
25838	GO:0051554	flavonol metabolic process	0.10	2	0.33840948	32	0.09241343
25839	GO:0051555	flavonol biosynthetic process	0.10	2	0.33840948	32	0.09241343
3473	GO:0004867	serine-type endopeptidase in	0.10	3	0.5076142	66	0.1906027
23515	GO:0048037	cofactor binding	0.11	9	1.5228426	327	0.94434977
24968	GO:0050662	coenzyme binding	0.11	6	1.0152284	191	0.5515927
7691	GO:0010467	gene expression	0.11	41	6.937394	1974	5.7007537
5114	GO:0007067	mitosis	0.11	1	0.16920474	7	0.020215439
16115	GO:0033729	anthocyanidin reductase acti	0.11	1	0.16920474	7	0.020215439
21149	GO:0045548	phenylalanine ammonia-lyas	0.11	1	0.16920474	7	0.020215439
23710	GO:0048285	organelle fission	0.11	1	0.16920474	7	0.020215439
64	GO:0000087	M phase of mitotic cell cycle	0.11	1	0.16920474	7	0.020215439
213	GO:0000279	M phase	0.11	1	0.16920474	7	0.020215439
214	GO:0000280	nuclear division	0.11	1	0.16920474	7	0.020215439
31420	GO:0080043	quercetin 3-O-glucosyltransfe	0.11	3	0.5076142	69	0.19926646
7690	GO:0010466	negative regulation of peptida	0.12	4	0.67681897	110	0.31767118
12946	GO:0030414	peptidase inhibitor activity	0.12	4	0.67681897	110	0.31767118
25636	GO:0051346	negative regulation of hydrola	0.12	4	0.67681897	110	0.31767118
8679	GO:0015297	antiporter activity	0.12	5	0.8460237	152	0.4389638
8682	GO:0015300	solute:solute antiporter activi	0.12	5	0.8460237	152	0.4389638
21146	GO:0045544	gibberellin 20-oxidase activity	0.12	2	0.33840948	35	0.10107719
9740	GO:0016667	oxidoreductase activity, actin	0.13	3	0.5076142	72	0.20793022
26711	GO:0052547	regulation of peptidase activi	0.13	4	0.67681897	112	0.32344702
28100	GO:0061134	peptidase regulator activity	0.13	4	0.67681897	112	0.32344702
29081	GO:0070717	poly-purine tract binding	0.13	4	0.67681897	112	0.32344702
8739	GO:0015385|GO:0015502	sodium:hydrogen antiporter a	0.13	2	0.33840948	36	0.10396511
3402	GO:0004791	thioredoxin-disulfide reductas	0.13	1	0.16920474	8	0.023103358
3803	GO:0005344|GO:0015033	oxygen transporter activity	0.13	1	0.16920474	8	0.023103358
4035	GO:0005746	mitochondrial respiratory cha	0.13	1	0.16920474	8	0.023103358
6497	GO:0009132	nucleoside diphosphate meta	0.13	1	0.16920474	8	0.023103358
7003	GO:0009737	response to abscisic acid stir	0.13	1	0.16920474	8	0.023103358
7843	GO:0010628	positive regulation of gene ex	0.13	1	0.16920474	8	0.023103358
8725	GO:0015367	oxoglutarate:malate antiporte	0.13	1	0.16920474	8	0.023103358
8940	GO:0015669	gas transport	0.13	1	0.16920474	8	0.023103358
8942	GO:0015671	oxygen transport	0.13	1	0.16920474	8	0.023103358
9011	GO:0015742	alpha-ketoglutarate transport	0.13	1	0.16920474	8	0.023103358
9680	GO:0016595	glutamate binding	0.13	1	0.16920474	8	0.023103358
21461	GO:0045893|GO:0043193|G	positive regulation of transcri	0.13	1	0.16920474	8	0.023103358
22702	GO:0047209	coniferyl-alcohol glucosyltran	0.13	1	0.16920474	8	0.023103358
28833	GO:0070469	respiratory chain	0.13	1	0.16920474	8	0.023103358
30696	GO:0072337	modified amino acid transpo	0.13	1	0.16920474	8	0.023103358
30708	GO:0072349	modified amino acid transme	0.13	1	0.16920474	8	0.023103358
3022	GO:0004338	glucan exo-1,3-beta-glucosid	0.13	1	0.16920474	8	0.023103358
9832	GO:0016782	transferase activity, transferr	0.13	3	0.5076142	74	0.21370606
30069	GO:0071705	nitrogen compound transport	0.13	6	1.0152284	202	0.5833598
26845	GO:0052689	carboxylic ester hydrolase ac	0.13	13	2.1996615	538	1.5537009
9637	GO:0016538|GO:0003751|G	cyclin-dependent protein kina	0.14	2	0.33840948	38	0.10974095
24966	GO:0050660	flavin adenine dinucleotide bi	0.14	4	0.67681897	118	0.34077454
7225	GO:0009978	allene oxide synthase activity	0.14	1	0.16920474	9	0.025991278
13224	GO:0030755	quercetin 3-O-methyltransfer	0.14	1	0.16920474	9	0.025991278
19342	GO:0043027	caspase inhibitor activity	0.14	1	0.16920474	9	0.025991278
19343	GO:0043028	caspase regulator activity	0.14	1	0.16920474	9	0.025991278
19458	GO:0043154|GO:0001719	negative regulation of caspas	0.14	1	0.16920474	9	0.025991278
19579	GO:0043281|GO:0043026	regulation of caspase activity	0.14	1	0.16920474	9	0.025991278
5891	GO:0008395|GO:0008394	steroid hydroxylase activity	0.15	2	0.33840948	40	0.1155168
7072	GO:0009813	flavonoid biosynthetic proces	0.15	2	0.33840948	40	0.1155168
21058	GO:0045454|GO:0030503|G	cell redox homeostasis	0.15	6	1.0152284	211	0.6093511
3856	GO:0005471|GO:0005349	ATP:ADP antiporter activity	0.16	1	0.16920474	10	0.0288792
4878	GO:0006772	thiamine metabolic process	0.16	1	0.16920474	10	0.0288792
6592	GO:0009228	thiamine biosynthetic proces	0.16	1	0.16920474	10	0.0288792
7175	GO:0009924	octadecanal decarbonylase a	0.16	1	0.16920474	10	0.0288792
9741	GO:0016668|GO:0016654	oxidoreductase activity, actin	0.16	1	0.16920474	10	0.0288792
26022	GO:0051740	ethylene binding	0.16	1	0.16920474	10	0.0288792
30135	GO:0071771	aldehyde decarbonylase acti	0.16	1	0.16920474	10	0.0288792
30687	GO:0072328	alkene binding	0.16	1	0.16920474	10	0.0288792
22376	GO:0046873	metal ion transmembrane tra	0.16	6	1.0152284	213	0.6151269
3718	GO:0005200	structural constituent of cytos	0.16	2	0.33840948	42	0.121292636
4911	GO:0006812|GO:0006819|G	cation transport	0.16	15	2.5380712	662	1.9118029
9849	GO:0016803	ether hydrolase activity	0.17	1	0.16920474	11	0.03176712
12469	GO:0022402	cell cycle process	0.17	1	0.16920474	11	0.03176712
12470	GO:0022403	cell cycle phase	0.17	1	0.16920474	11	0.03176712
16183	GO:0033799	myricetin 3'-O-methyltransfer	0.17	1	0.16920474	11	0.03176712
212	GO:0000278	mitotic cell cycle	0.17	1	0.16920474	11	0.03176712
2989	GO:0004301	epoxide hydrolase activity	0.17	1	0.16920474	11	0.03176712
7071	GO:0009812	flavonoid metabolic process	0.17	2	0.33840948	44	0.12706847
3476	GO:0004872|GO:0019041	receptor activity	0.18	15	2.5380712	672	1.9406822
8666	GO:0015276	ligand-gated ion channel acti	0.18	2	0.33840948	45	0.1299564
12530	GO:0022834	ligand-gated channel activity	0.18	2	0.33840948	45	0.1299564
4786	GO:0006664	glycolipid metabolic process	0.19	1	0.16920474	12	0.03465504
6610	GO:0009247	glycolipid biosynthetic proces	0.19	1	0.16920474	12	0.03465504
7526	GO:0010301|GO:0033710	xanthoxin dehydrogenase ac	0.19	1	0.16920474	12	0.03465504
9704	GO:0016621	cinnamoyl-CoA reductase ac	0.19	1	0.16920474	12	0.03465504

14848	GO:0032440	2-alkenal reductase activity	0.19	1	0.16920474	12	0.03465504
19047	GO:0042723	thiamine-containing compour	0.19	1	0.16920474	12	0.03465504
19048	GO:0042724	thiamine-containing compour	0.19	1	0.16920474	12	0.03465504
21503	GO:0045935	positive regulation of nucleob	0.19	1	0.16920474	12	0.03465504
21992	GO:0046467	membrane lipid biosynthetic	0.19	1	0.16920474	12	0.03465504
25470	GO:0051173	positive regulation of nitroger	0.19	1	0.16920474	12	0.03465504
25546	GO:0051254	positive regulation of RNA m	0.19	1	0.16920474	12	0.03465504
6427	GO:0009058	biosynthetic process	0.19	54	9.137055	2796	8.074624
4032	GO:0005743	mitochondrial inner membrar	0.19	3	0.5076142	88	0.25413695
3475	GO:0004871|GO:0005062|G	signal transducer activity	0.19	17	2.8764806	787	2.2727928
27063	GO:0060089	molecular transducer activity	0.19	17	2.8764806	787	2.2727928
12547	GO:0022857|GO:0005386|G	transmembrane transporter a	0.19	30	5.0761423	1483	4.282785
4990	GO:0006915|GO:0008632	apoptosis	0.19	6	1.0152284	227	0.6555578
21331	GO:0045735	nutrient reservoir activity	0.19	3	0.5076142	89	0.25702485
3449	GO:0004842|GO:0004840|G	ubiquitin-protein ligase activit	0.20	8	1.3536379	326	0.94146186
7551	GO:0010327	acetyl CoA:(Z)-3-hexen-1-ol	0.20	1	0.16920474	13	0.037542958
8149	GO:0010941	regulation of cell death	0.20	1	0.16920474	13	0.037542958
13443	GO:0030984	kininogen binding	0.20	1	0.16920474	13	0.037542958
19298	GO:0042981	regulation of apoptosis	0.20	1	0.16920474	13	0.037542958
19381	GO:0043067|GO:0043070	regulation of programmed ce	0.20	1	0.16920474	13	0.037542958
25095	GO:0050790	regulation of catalytic activity	0.20	11	1.8612521	480	1.3862015
4909	GO:0006810|GO:0015457|G	transport	0.20	45	7.614213	2315	6.6855345
25529	GO:0051234	establishment of localization	0.20	45	7.614213	2315	6.6855345
3844	GO:0005451	monovalent cation:hydrogen	0.20	2	0.33840948	49	0.14150807
6483	GO:0009116	nucleoside metabolic proces	0.20	2	0.33840948	49	0.14150807
25476	GO:0051179	localization	0.20	45	7.614213	2319	6.697086
28366	GO:0065009	regulation of molecular funct	0.21	11	1.8612521	484	1.3977532
9654	GO:0016567	protein ubiquitination	0.21	8	1.3536379	332	0.9587894
14854	GO:0032446	protein modification by small	0.21	8	1.3536379	332	0.9587894
29011	GO:0070647	protein modification by small	0.21	8	1.3536379	332	0.9587894
4408	GO:0006200	ATP catabolic process	0.21	14	2.3688664	641	1.8511566
9918	GO:0016887|GO:0004002	ATPase activity	0.21	14	2.3688664	641	1.8511566
21600	GO:0046034	ATP metabolic process	0.21	14	2.3688664	641	1.8511566
4910	GO:0006811	ion transport	0.21	20	3.3840947	959	2.769515
28378	GO:0070011	peptidase activity, acting on	0.21	12	2.0304568	537	1.550813
11695	GO:0019725	cellular homeostasis	0.21	6	1.0152284	234	0.67577326
5195	GO:0007165|GO:0023033	signal transduction	0.21	20	3.3840947	961	2.775291
12602	GO:0023052|GO:0023046	signaling	0.21	20	3.3840947	961	2.775291
7660	GO:0010436	carotenoid dioxygenase activ	0.21	1	0.16920474	14	0.040430877
8553	GO:0015140	malate transmembrane trans	0.21	1	0.16920474	14	0.040430877
8859	GO:0015556	C4-dicarboxylate transmemb	0.21	1	0.16920474	14	0.040430877
9009	GO:0015740	C4-dicarboxylate transport	0.21	1	0.16920474	14	0.040430877
9012	GO:0015743	malate transport	0.21	1	0.16920474	14	0.040430877
9399	GO:0016174	NAD(P)H oxidase activity	0.21	1	0.16920474	14	0.040430877
9847	GO:0016801	hydrolase activity, acting on	0.21	1	0.16920474	14	0.040430877
9879	GO:0016841	ammonia-lyase activity	0.21	1	0.16920474	14	0.040430877
11157	GO:0019144	ADP-sugar diphosphatase a	0.21	1	0.16920474	14	0.040430877
17616	GO:0035250	UDP-galactosyltransferase a	0.21	1	0.16920474	14	0.040430877
21150	GO:0045549	9-cis-epoxycarotenoid dioxy	0.21	1	0.16920474	14	0.040430877
24970	GO:0050664	oxidoreductase activity, actin	0.21	1	0.16920474	14	0.040430877
29787	GO:0071423	malate transmembrane trans	0.21	1	0.16920474	14	0.040430877
31408	GO:0080031	methyl salicylate esterase ac	0.21	1	0.16920474	14	0.040430877
3808	GO:0005351|GO:0005403	sugar:hydrogen symporter a	0.22	3	0.5076142	94	0.27146447
3835	GO:0005402	cation:sugar symporter activi	0.22	3	0.5076142	94	0.27146447
11803	GO:0019866	organelle inner membrane	0.22	3	0.5076142	94	0.27146447
2657	GO:0003727|GO:0003728	single-stranded RNA binding	0.22	5	0.8460237	188	0.54292893
3472	GO:0004866	endopeptidase inhibitor activ	0.22	3	0.5076142	95	0.27435237
8159	GO:0010951	negative regulation of endop	0.22	3	0.5076142	95	0.27435237
11712	GO:0019748	secondary metabolic proces	0.22	3	0.5076142	95	0.27435237
26712	GO:0052548	regulation of endopeptidase	0.22	3	0.5076142	95	0.27435237
28101	GO:0061135	endopeptidase regulator acti	0.22	3	0.5076142	95	0.27435237
6965	GO:0009699	phenylpropanoid biosynthetic	0.22	2	0.33840948	52	0.15017183
2809	GO:0003993	acid phosphatase activity	0.22	2	0.33840948	52	0.15017183
18925	GO:0042592	homeostatic process	0.22	6	1.0152284	238	0.68732494
11747	GO:0019787|GO:0008639|G	small conjugating protein liga	0.22	8	1.3536379	339	0.9790048
5756	GO:0008219	cell death	0.23	6	1.0152284	239	0.69021285
8209	GO:0012501|GO:0016244	programmed cell death	0.23	6	1.0152284	239	0.69021285
9462	GO:0016265	death	0.23	6	1.0152284	239	0.69021285
7520	GO:0010294	abscisic acid glucosyltransfe	0.23	1	0.16920474	15	0.043318797
10079	GO:0017134	fibroblast growth factor bindi	0.23	1	0.16920474	15	0.043318797
14101	GO:0031683	G-protein beta/gamma-subu	0.23	1	0.16920474	15	0.043318797
2868	GO:0004062	aryl sulfotransferase activity	0.23	1	0.16920474	15	0.043318797
8677	GO:0015295	solute:hydrogen symporter a	0.23	3	0.5076142	98	0.28301615
8681	GO:0015299	solute:hydrogen antiporter a	0.23	3	0.5076142	98	0.28301615
20499	GO:0044249	cellular biosynthetic process	0.24	50	8.460237	2635	7.6096687
2897	GO:0004091|GO:0004302|G	carboxylesterase activity	0.24	5	0.8460237	194	0.5602564
3382	GO:0004768|GO:0016214|G	stearoyl-CoA 9-desaturase a	0.24	1	0.16920474	16	0.046206716
3742	GO:0005242	inward rectifier potassium ch	0.24	1	0.16920474	16	0.046206716
3782	GO:0005310|GO:0005312|G	dicarboxylic acid transmemb	0.24	1	0.16920474	16	0.046206716
3829	GO:0005381|GO:0005382|G	iron ion transmembrane tran	0.24	1	0.16920474	16	0.046206716
4767	GO:0006643	membrane lipid metabolic pr	0.24	1	0.16920474	16	0.046206716
4928	GO:0006835|GO:0006841	dicarboxylic acid transport	0.24	1	0.16920474	16	0.046206716
7178	GO:0009927	histidine phosphotransfer kin	0.24	1	0.16920474	16	0.046206716
9386	GO:0016157	sucrose synthase activity	0.24	1	0.16920474	16	0.046206716
9427	GO:0016215	CoA desaturase activity	0.24	1	0.16920474	16	0.046206716
9878	GO:0016840	carbon-nitrogen lyase activity	0.24	1	0.16920474	16	0.046206716
17134	GO:0034755	iron ion transmembrane tran	0.24	1	0.16920474	16	0.046206716
31396	GO:0080019	fatty-acyl-CoA reductase (al	0.24	1	0.16920474	16	0.046206716
9533	GO:0016405	CoA-ligase activity	0.24	2	0.33840948	55	0.15883559
5874	GO:0008374	O-acyltransferase activity	0.25	3	0.5076142	102	0.29456782
12794	GO:0030234	enzyme regulator activity	0.25	9	1.5228426	403	1.1638317
4446	GO:0006241	CTP biosynthetic process	0.25	1	0.16920474	17	0.049094636
6507	GO:0009142	nucleoside triphosphate bios	0.25	1	0.16920474	17	0.049094636
6513	GO:0009148	pyrimidine nucleoside triphos	0.25	1	0.16920474	17	0.049094636
6565	GO:0009201	ribonucleoside triphosphate	0.25	1	0.16920474	17	0.049094636
6572	GO:0009208	pyrimidine ribonucleoside trip	0.25	1	0.16920474	17	0.049094636
6573	GO:0009209	pyrimidine ribonucleoside trip	0.25	1	0.16920474	17	0.049094636
8585	GO:0015172	acidic amino acid transmem	0.25	1	0.16920474	17	0.049094636
9069	GO:0015800	acidic amino acid transport	0.25	1	0.16920474	17	0.049094636
21602	GO:0046036|GO:0006243	CTP metabolic process	0.25	1	0.16920474	17	0.049094636
9910	GO:0016878	acid-thiol ligase activity	0.25	2	0.33840948	57	0.16461143
4913	GO:0006814|GO:0006834|G	sodium ion transport	0.26	2	0.33840948	58	0.16749935
8499	GO:0015081|GO:0022816	sodium ion transmembrane t	0.26	2	0.33840948	58	0.16749935
8558	GO:0015145	monosaccharide transmemb	0.26	2	0.33840948	58	0.16749935
9018	GO:0015749	monosaccharide transport	0.26	2	0.33840948	58	0.16749935
11820	GO:0019887	protein kinase regulator activ	0.26	2	0.33840948	58	0.16749935
18086	GO:0035725	sodium ion transmembrane t	0.26	2	0.33840948	58	0.16749935
29800	GO:0071436	sodium ion export	0.26	2	0.33840948	58	0.16749935
5763	GO:0008233	peptidase activity	0.26	12	2.0304568	565	1.6316746
4357	GO:0006139|GO:0055134	nucleobase, nucleoside, nuc	0.26	61	10.321489	3285	9.486816
8673	GO:0015291|GO:0015290|G	secondary active transmemb	0.26	9	1.5228426	407	1.1753833
26931	GO:0055085	transmembrane transport	0.26	30	5.0761423	1548	4.4705
3832	GO:0005388	calcium-transporting ATPase	0.27	1	0.16920474	18	0.051982556
4134	GO:0005874	microtubule	0.27	1	0.16920474	18	0.051982556
4225	GO:0005985	sucrose metabolic process	0.27	1	0.16920474	18	0.051982556
7773	GO:0010557	positive regulation of macron	0.27	1	0.16920474	18	0.051982556
12887	GO:0030332	cyclin binding	0.27	1	0.16920474	18	0.051982556
19253	GO:0042936	dipeptide transporter activity	0.27	3	0.5076142	105	0.3032316
19255	GO:0042938	dipeptide transport	0.27	3	0.5076142	105	0.3032316
3333	GO:0004712	protein serine/threonine/tyros	0.27	2	0.33840948	59	0.17038727
31895	GO:0090304	nucleic acid metabolic proce	0.27	44	7.4450083	2340	6.7577324
4840	GO:0006720|GO:0016096	isoprenoid metabolic process	0.27	2	0.33840948	60	0.17327519

6964	GO:0009698	phenylpropanoid metabolic p	0.27		2	0.33840948	60	0.17327519
14811	GO:0032403	protein complex binding	0.27		2	0.33840948	60	0.17327519
28375	GO:0070008	serine-type exopeptidase act	0.27		2	0.33840948	60	0.17327519
2980	GO:0004185	serine-type carboxypeptidase	0.27		2	0.33840948	60	0.17327519
3290	GO:0004656	procollagen-proline 4-dioxyge	0.28		1	0.16920474	19	0.054870475
11752	GO:0019798	procollagen-proline dioxygen	0.28		1	0.16920474	19	0.054870475
13966	GO:0031543	peptidyl-proline dioxygenase	0.28		1	0.16920474	19	0.054870475
13968	GO:0031545	peptidyl-proline 4-dioxygenas	0.28		1	0.16920474	19	0.054870475
5705	GO:0008152	metabolic process	0.28		305	51.607445	17432	50.34222
4954	GO:0006869	lipid transport	0.28		5	0.8460237	208	0.6006873
8085	GO:0010876	lipid localization	0.28		5	0.8460237	208	0.6006873
20488	GO:0044238	primary metabolic process	0.28		163	27.580372	9167	26.47356
3888	GO:0005529	sugar binding	0.28		4	0.67681897	158	0.45629135
6018	GO:0008559|GO:0005226|G	xenobiotic-transporting ATPa	0.29		2	0.33840948	62	0.17905103
11210	GO:0019207	kinase regulator activity	0.29		2	0.33840948	62	0.17905103
19225	GO:0042908	xenobiotic transport	0.29		2	0.33840948	62	0.17905103
19227	GO:0042910	xenobiotic transporter activity	0.29		2	0.33840948	62	0.17905103
2978	GO:0004180	carboxypeptidase activity	0.29		2	0.33840948	62	0.17905103
4921	GO:0006826|GO:0015681	iron ion transport	0.29		1	0.16920474	20	0.0577584
9707	GO:0016624	oxidoreductase activity, actin	0.29		1	0.16920474	20	0.0577584
9799	GO:0016744|GO:0016745	transferase activity, transferr	0.29		1	0.16920474	20	0.0577584
8680	GO:0015298	solute:cation antiporter activi	0.30		3	0.5076142	112	0.32344702
9730	GO:0016651	oxidoreductase activity, actin	0.30		3	0.5076142	112	0.32344702
3364	GO:0004745	retinol dehydrogenase activit	0.30		1	0.16920474	21	0.060646318
3474	GO:0004869|GO:0004870	cysteine-type endopeptidase	0.30		1	0.16920474	21	0.060646318
4420	GO:0006213	pyrimidine nucleoside metab	0.30		1	0.16920474	21	0.060646318
5878	GO:0008378	galactosyltransferase activity	0.30		1	0.16920474	21	0.060646318
6582	GO:0009218	pyrimidine ribonucleotide me	0.30		1	0.16920474	21	0.060646318
6584	GO:0009220	pyrimidine ribonucleotide bio	0.30		1	0.16920474	21	0.060646318
21697	GO:0046131	pyrimidine ribonucleoside me	0.30		1	0.16920474	21	0.060646318
9933	GO:0016903	oxidoreductase activity, actin	0.30		3	0.5076142	113	0.32633495
9710	GO:0016628	oxidoreductase activity, actin	0.30		2	0.33840948	65	0.18771479
14379	GO:0031966	mitochondrial membrane	0.31		3	0.5076142	114	0.32922286
9422	GO:0016209	antioxidant activity	0.31		4	0.67681897	165	0.47650677
5840	GO:0008324	cation transmembrane transp	0.31		11	1.8612521	538	1.5537009
7143	GO:0009891	positive regulation of biosynt	0.32		1	0.16920474	22	0.06353424
8774	GO:0015431	glutathione S-conjugate-expo	0.32		1	0.16920474	22	0.06353424
10032	GO:0017075	syntaxin-1 binding	0.32		1	0.16920474	22	0.06353424
12660	GO:0030077	plasma membrane light-harv	0.32		1	0.16920474	22	0.06353424
13038	GO:0030551	cyclic nucleotide binding	0.32		1	0.16920474	22	0.06353424
13758	GO:0031328	positive regulation of cellular	0.32		1	0.16920474	22	0.06353424
18438	GO:0042054	histone methyltransferase ac	0.32		1	0.16920474	22	0.06353424
19040	GO:0042716	plasma membrane-derived c	0.32		1	0.16920474	22	0.06353424
19325	GO:0043008	ATP-dependent protein bindi	0.32		1	0.16920474	22	0.06353424
30359	GO:0071997	glutathione S-conjugate-trans	0.32		1	0.16920474	22	0.06353424
4609	GO:0006464	protein modification process	0.32		51	8.629441	2781	8.031305
2674	GO:0003824	catalytic activity	0.32		189	31.979696	10750	31.045137
3986	GO:0005681	spliceosomal complex	0.33		1	0.16920474	23	0.06642216
5636	GO:0008061	chitin binding	0.33		1	0.16920474	23	0.06642216
6512	GO:0009147	pyrimidine nucleoside triphos	0.33		1	0.16920474	23	0.06642216
7527	GO:0010302	2-oxoglutarate-dependent dio	0.33		1	0.16920474	23	0.06642216
22414	GO:0046912	transferase activity, transferr	0.33		1	0.16920474	23	0.06642216
25416	GO:0051119	sugar transmembrane transp	0.33		3	0.5076142	118	0.34077454
9795	GO:0016740	transferase activity	0.33		68	11.505922	3764	10.870131
3620	GO:0005057	receptor signaling protein act	0.33		2	0.33840948	69	0.19926646
21710	GO:0046148	pigment biosynthetic process	0.33		2	0.33840948	69	0.19926646
8943	GO:0015672	monovalent inorganic cation	0.33		8	1.3536379	383	1.1060733
3156	GO:0004497	monooxygenase activity	0.34		4	0.67681897	172	0.49672222
3213	GO:0004568	chitinase activity	0.34		1	0.16920474	24	0.06931008
6248	GO:0008843	endochitinase activity	0.34		1	0.16920474	24	0.06931008
9779	GO:0016717	oxidoreductase activity, actin	0.34		1	0.16920474	24	0.06931008
22440	GO:0046939	nucleotide phosphorylation	0.34		1	0.16920474	24	0.06931008
31407	GO:0080030	methyl indole-3-acetate este	0.34		1	0.16920474	24	0.06931008
2821	GO:0004012|GO:0008557	phospholipid-translocating AT	0.34		1	0.16920474	24	0.06931008
8494	GO:0015075	ion transmembrane transpor	0.34		16	2.7072759	827	2.3883097
8675	GO:0015293	symporter activity	0.34		4	0.67681897	173	0.49961013
3723	GO:0005215|GO:0005478	transporter activity	0.35		34	5.752961	1844	5.325324
9482	GO:0016291|GO:0008778|G	acyl-CoA thioesterase activit	0.35		1	0.16920474	25	0.072197996
31493	GO:0080118	brassinosteroid sulfotransfera	0.35		1	0.16920474	25	0.072197996
16603	GO:0034220	ion transmembrane transpor	0.35		16	2.7072759	833	2.4056373
9913	GO:0016881	acid-amino acid ligase activit	0.35		8	1.3536379	391	1.1291766
9812	GO:0016758	transferase activity, transferr	0.35		10	1.6920474	501	1.4468478
9703	GO:0016620	oxidoreductase activity, actin	0.35		2	0.33840948	73	0.21081814
18786	GO:0042440	pigment metabolic process	0.35		2	0.33840948	73	0.21081814
11202	GO:0019199	transmembrane receptor pro	0.36		10	1.6920474	504	1.4555116
9194	GO:0015935	small ribosomal subunit	0.36		1	0.16920474	26	0.075085916
9421	GO:0016208	AMP binding	0.36		1	0.16920474	26	0.075085916
9658	GO:0016571	histone methylation	0.36		1	0.16920474	26	0.075085916
126	GO:0000160	two-component signal transd	0.36		1	0.16920474	26	0.075085916
13082	GO:0030599	pectinesterase activity	0.36		4	0.67681897	178	0.5140497
12741	GO:0030170	pyridoxal phosphate binding	0.36		3	0.5076142	126	0.3638779
28643	GO:0070279	vitamin B6 binding	0.36		3	0.5076142	126	0.3638779
8810	GO:0015491	cation:cation antiporter activi	0.37		2	0.33840948	75	0.21659398
4612	GO:0006468	protein phosphorylation	0.37		40	6.7681894	2205	6.367863
3329	GO:0004708	MAP kinase kinase activity	0.37		1	0.16920474	27	0.077973835
3725	GO:0005217	intracellular ligand-gated ion	0.37		1	0.16920474	27	0.077973835
8919	GO:0015645	fatty acid ligase activity	0.37		1	0.16920474	27	0.077973835
9541	GO:0016413	O-acetyltransferase activity	0.37		1	0.16920474	27	0.077973835
12573	GO:0022891	substrate-specific transmem	0.37		23	3.8917089	1241	3.5839086
6563	GO:0009199	ribonucleoside triphosphate r	0.37		15	2.5380712	790	2.2814567
3877	GO:0005516	calmodulin binding	0.38		5	0.8460237	236	0.6815491
6529	GO:0009165	nucleotide biosynthetic proce	0.38		2	0.33840948	77	0.22236982
4916	GO:0006818	hydrogen transport	0.38		6	1.0152284	292	0.84327257
9246	GO:0015992	proton transport	0.38		6	1.0152284	292	0.84327257
3284	GO:0004650	polygalacturonase activity	0.38		1	0.16920474	28	0.080861755
4374	GO:0006164	purine nucleotide biosyntheti	0.38		1	0.16920474	28	0.080861755
7145	GO:0009893	positive regulation of metabo	0.38		1	0.16920474	28	0.080861755
7819	GO:0010604	positive regulation of macron	0.38		1	0.16920474	28	0.080861755
9827	GO:0016776	phosphotransferase activity,	0.38		1	0.16920474	28	0.080861755
13634	GO:0031177	phosphopantetheine binding	0.38		1	0.16920474	28	0.080861755
13755	GO:0031325	positive regulation of cellular	0.38		1	0.16920474	28	0.080861755
6506	GO:0009141	nucleoside triphosphate meta	0.38		15	2.5380712	796	2.2987843
9909	GO:0016877	ligase activity, forming carbo	0.39		2	0.33840948	78	0.22525774
30865	GO:0072509	divalent inorganic cation tran	0.39		2	0.33840948	78	0.22525774
25998	GO:0051716	cellular response to stimulus	0.39		21	3.5532994	1138	3.2864528
25195	GO:0050896|GO:0051869	response to stimulus	0.39		34	5.752961	1881	5.432177
20510	GO:0044260|GO:0034960	cellular macromolecule meta	0.39		98	16.582064	5577	16.105928
4427	GO:0006221	pyrimidine nucleotide biosynt	0.39		1	0.16920474	29	0.083749674
4841	GO:0006721	terpenoid metabolic process	0.39		1	0.16920474	29	0.083749674
11834	GO:0019905	syntaxin binding	0.39		1	0.16920474	29	0.083749674
3955	GO:0005634	nucleus	0.40		26	4.399323	1433	4.138389
18674	GO:0042325	regulation of phosphorylation	0.40		2	0.33840948	81	0.23392151
5916	GO:0008422|GO:0016983	beta-glucosidase activity	0.40		1	0.16920474	30	0.086637594
6814	GO:0009526	plastid envelope	0.40		1	0.16920474	30	0.086637594
7188	GO:0009941	chloroplast envelope	0.40		1	0.16920474	30	0.086637594
8683	GO:0015301|GO:0015380|G	anion:anion antiporter activity	0.40		1	0.16920474	30	0.086637594
5712	GO:0008168|GO:0004480	methyltransferase activity	0.40		5	0.8460237	244	0.7046524
3242	GO:0004601|GO:0016685|G	peroxidase activity	0.41		3	0.5076142	135	0.38986918
9754	GO:0016684	oxidoreductase activity, actin	0.41		3	0.5076142	135	0.38986918
29202	GO:0070838	divalent metal ion transport	0.41		2	0.33840948	82	0.23680943
4373	GO:0006163	purine nucleotide metabolic p	0.41		15	2.5380712	810	2.339215
30884	GO:0072528	pyrimidine-containing compo	0.41		1	0.16920474	31	0.08952551

6622	GO:0009259|GO:0009121	ribonucleotide metabolic pro	0.41	15	2.5380712	812	2.344991
3787	GO:0005319	lipid transporter activity	0.42	2	0.33840948	83	0.23969735
4912	GO:0006813|GO:0015458	potassium ion transport	0.42	2	0.33840948	84	0.24258527
30168	GO:0071804	cellular potassium ion transp	0.42	2	0.33840948	84	0.24258527
30169	GO:0071805	potassium ion transmembrar	0.42	2	0.33840948	84	0.24258527
30867	GO:0072511	divalent inorganic cation tran	0.42	2	0.33840948	84	0.24258527
3304	GO:0004672|GO:0050222	protein kinase activity	0.42	24	4.0609136	1333	3.8495972
3265	GO:0004630	phospholipase D activity	0.42	1	0.16920474	32	0.09241343
4614	GO:0006470	protein dephosphorylation	0.42	1	0.16920474	32	0.09241343
6942	GO:0009674	potassium:sodium symporter	0.42	1	0.16920474	32	0.09241343
12522	GO:0022820	potassium ion symporter acti	0.42	1	0.16920474	32	0.09241343
23914	GO:0048522|GO:0051242	positive regulation of cellular	0.42	1	0.16920474	32	0.09241343
4942	GO:0006855	drug transmembrane transpo	0.42	3	0.5076142	139	0.40142086
8607	GO:0015197|GO:0015637	peptide transporter activity	0.42	3	0.5076142	139	0.40142086
8608	GO:0015198	oligopeptide transporter activ	0.42	3	0.5076142	139	0.40142086
8642	GO:0015238|GO:0015239|G	drug transmembrane transpo	0.42	3	0.5076142	139	0.40142086
9154	GO:0015893	drug transport	0.42	3	0.5076142	139	0.40142086
18832	GO:0042493|GO:0017035	response to drug	0.42	3	0.5076142	139	0.40142086
11222	GO:0019220	regulation of phosphate meta	0.43	2	0.33840948	85	0.24547319
25471	GO:0051174	regulation of phosphorus me	0.43	2	0.33840948	85	0.24547319
25626	GO:0051336	regulation of hydrolase activi	0.43	4	0.67681897	196	0.5660323
19684	GO:0043412	macromolecule modification	0.43	51	8.629441	2900	8.374968
5768	GO:0008238	exopeptidase activity	0.43	2	0.33840948	86	0.24836111
4944	GO:0006857	oligopeptide transport	0.43	3	0.5076142	141	0.4071967
8676	GO:0015294	solute:cation symporter activ	0.43	3	0.5076142	141	0.4071967
9099	GO:0015833	peptide transport	0.43	3	0.5076142	141	0.4071967
4493	GO:0006298|GO:0006300	mismatch repair	0.43	1	0.16920474	33	0.09530135
30878	GO:0072522	purine-containing compound	0.43	1	0.16920474	33	0.09530135
18953	GO:0042623	ATPase activity, coupled	0.43	10	1.6920474	537	1.550813
30877	GO:0072521	purine-containing compound	0.44	15	2.5380712	827	2.3883097
8557	GO:0015144	carbohydrate transmembran	0.44	3	0.5076142	143	0.41297254
16602	GO:0034219	carbohydrate transmembran	0.44	3	0.5076142	143	0.41297254
3749	GO:0005249	voltage-gated potassium cha	0.44	1	0.16920474	34	0.09818927
5270	GO:0007264	small GTPase mediated sigr	0.44	1	0.16920474	34	0.09818927
6486	GO:0009119	ribonucleoside metabolic pro	0.44	1	0.16920474	34	0.09818927
11208	GO:0019205	nucleobase, nucleoside, nucl	0.44	1	0.16920474	34	0.09818927
11831	GO:0019902	phosphatase binding	0.44	1	0.16920474	34	0.09818927
11832	GO:0019903	protein phosphatase binding	0.44	1	0.16920474	34	0.09818927
12574	GO:0022892	substrate-specific transporte	0.44	26	4.399323	1463	4.2250266
26932	GO:0055086	nucleobase, nucleoside and	0.45	17	2.8764806	944	2.7261963
4405	GO:0006195	purine nucleotide catabolic p	0.45	14	2.3688664	773	2.232362
6508	GO:0009143	nucleoside triphosphate cata	0.45	14	2.3688664	773	2.232362
6509	GO:0009144	purine nucleoside triphospha	0.45	14	2.3688664	773	2.232362
6511	GO:0009146	purine nucleoside triphospha	0.45	14	2.3688664	773	2.232362
6519	GO:0009154	purine ribonucleotide catabol	0.45	14	2.3688664	773	2.232362
6530	GO:0009166	nucleotide catabolic process	0.45	14	2.3688664	773	2.232362
6567	GO:0009203	ribonucleoside triphosphate c	0.45	14	2.3688664	773	2.232362
6569	GO:0009205	purine ribonucleoside triphos	0.45	14	2.3688664	773	2.232362
6571	GO:0009207	purine ribonucleoside triphos	0.45	14	2.3688664	773	2.232362
6624	GO:0009261	ribonucleotide catabolic proc	0.45	14	2.3688664	773	2.232362
17034	GO:0034655	nucleobase, nucleoside, nucl	0.45	14	2.3688664	773	2.232362
17035	GO:0034656	nucleobase, nucleoside and	0.45	14	2.3688664	773	2.232362
22209	GO:0046700	heterocycle catabolic proces	0.45	14	2.3688664	773	2.232362
30879	GO:0072523	purine-containing compound	0.45	14	2.3688664	773	2.232362
14380	GO:0031967	organelle envelope	0.45	4	0.67681897	201	0.5804719
4426	GO:0006220	pyrimidine nucleotide metab	0.45	1	0.16920474	35	0.10107719
9480	GO:0016289	CoA hydrolase activity	0.45	1	0.16920474	35	0.10107719
12806	GO:0030247	polysaccharide binding	0.45	1	0.16920474	35	0.10107719
1169	GO:0001871	pattern binding	0.45	1	0.16920474	35	0.10107719
28365	GO:0065008	regulation of biological qualit	0.45	6	1.0152284	316	0.9125827
20520	GO:0044270	cellular nitrogen compound c	0.46	14	2.3688664	777	2.2439137
6071	GO:0008643|GO:0006861|G	carbohydrate transport	0.46	3	0.5076142	147	0.42452422
9796	GO:0016741	transferase activity, transferr	0.46	5	0.8460237	261	0.7537471
6794	GO:0009505	plant-type cell wall	0.46	1	0.16920474	36	0.10396511
12626	GO:0030029	actin filament-based process	0.46	1	0.16920474	36	0.10396511
12633	GO:0030036	actin cytoskeleton organizati	0.46	1	0.16920474	36	0.10396511
20649	GO:0044455	mitochondrial membrane par	0.46	1	0.16920474	36	0.10396511
9579	GO:0016462	pyrophosphatase activity	0.46	17	2.8764806	954	2.7550755
14387	GO:0031975	envelope	0.46	4	0.67681897	205	0.59202355
9859	GO:0016818	hydrolase activity, acting on a	0.47	17	2.8764806	956	2.7608514
16785	GO:0034404	nucleobase, nucleoside and	0.47	2	0.33840948	92	0.26568863
17033	GO:0034654	nucleobase, nucleoside, nucl	0.47	2	0.33840948	92	0.26568863
11426	GO:0019438	aromatic compound biosynth	0.47	3	0.5076142	149	0.43030006
3758	GO:0005267	potassium channel activity	0.47	1	0.16920474	37	0.10685303
8934	GO:0015662	ATPase activity, coupled to t	0.47	1	0.16920474	37	0.10685303
8980	GO:0015711	organic anion transport	0.47	1	0.16920474	37	0.10685303
9858	GO:0016817	hydrolase activity, acting on a	0.47	17	2.8764806	959	2.769515
5018	GO:0006950	response to stress	0.47	11	1.8612521	611	1.764519
9811	GO:0016757|GO:0016932	transferase activity, transferr	0.48	13	2.1996615	729	2.1052935
4029	GO:0005740	mitochondrial envelope	0.48	3	0.5076142	151	0.4360759
5066	GO:0007010	cytoskeleton organization	0.48	1	0.16920474	38	0.10974095
6749	GO:0009414	response to water deprivatio	0.48	1	0.16920474	38	0.10974095
8501	GO:0015085	calcium ion transmembrane	0.48	1	0.16920474	38	0.10974095
8588	GO:0015175	neutral amino acid transmem	0.48	1	0.16920474	38	0.10974095
9073	GO:0015804	neutral amino acid transport	0.48	1	0.16920474	38	0.10974095
12538	GO:0022843	voltage-gated cation channel	0.48	1	0.16920474	38	0.10974095
117	GO:0000149	SNARE binding	0.48	1	0.16920474	38	0.10974095
6515	GO:0009150	purine ribonucleotide metab	0.48	14	2.3688664	791	2.2843447
6623	GO:0009260	ribonucleotide biosynthetic p	0.49	1	0.16920474	39	0.11262887
30883	GO:0072527	pyrimidine-containing compo	0.49	1	0.16920474	39	0.11262887
6424	GO:0009055|GO:0009053|G	electron carrier activity	0.49	3	0.5076142	154	0.44473964
8517	GO:0015103	inorganic anion transmembra	0.49	3	0.5076142	154	0.44473964
4867	GO:0006753	nucleoside phosphate metab	0.49	16	2.7072759	914	2.6395588
6484	GO:0009117	nucleotide metabolic process	0.49	16	2.7072759	914	2.6395588
8495	GO:0015077	monovalent inorganic cation	0.50	4	0.67681897	214	0.6180149
23910	GO:0048518|GO:0043119	positive regulation of biologic	0.50	1	0.16920474	40	0.1155168
12572	GO:0022890|GO:0015082	inorganic cation transmembr	0.50	6	1.0152284	332	0.9587894
22007	GO:0046483	heterocycle metabolic proces	0.50	19	3.21489	1094	3.1593843
20627	GO:0044433	cytoplasmic vesicle part	0.51	1	0.16920474	41	0.118404716
3716	GO:0005198	structural molecule activity	0.51	7	1.1844332	393	1.1349525
17020	GO:0034641	cellular nitrogen compound n	0.51	63	10.659899	3678	10.621769
3490	GO:0004888|GO:0004926	transmembrane receptor act	0.51	10	1.6920474	571	1.6490022
4874	GO:0006767	water-soluble vitamin metab	0.51	1	0.16920474	42	0.121292636
8461	GO:0015020|GO:0003981	glucuronosyltransferase activ	0.51	1	0.16920474	42	0.121292636
12659	GO:0030076	light-harvesting complex	0.51	1	0.16920474	42	0.121292636
13884	GO:0031461	cullin-RING ubiquitin ligase c	0.51	1	0.16920474	42	0.121292636
18713	GO:0042364	water-soluble vitamin biosynt	0.51	1	0.16920474	42	0.121292636
8496	GO:0015078	hydrogen ion transmembran	0.52	3	0.5076142	160	0.4620672
9911	GO:0016879	ligase activity, forming carbo	0.52	8	1.3536379	456	1.3168914
9870	GO:0016830	carbon-carbon lyase activity	0.52	3	0.5076142	161	0.4649551
3900	GO:0005548|GO:0008497	phospholipid transporter activ	0.52	1	0.16920474	43	0.124180555
8589	GO:0015179	L-amino acid transmembran	0.52	1	0.16920474	43	0.124180555
9076	GO:0015807	L-amino acid transport	0.52	1	0.16920474	43	0.124180555
9174	GO:0015914	phospholipid transport	0.52	1	0.16920474	43	0.124180555
13833	GO:0031410	cytoplasmic vesicle	0.52	1	0.16920474	43	0.124180555
14393	GO:0031982	vesicle	0.52	1	0.16920474	43	0.124180555
4873	GO:0006766	vitamin metabolic process	0.53	1	0.16920474	44	0.12706847
4914	GO:0006816	calcium ion transport	0.53	1	0.16920474	44	0.12706847
5797	GO:0008276	protein methyltransferase ac	0.53	1	0.16920474	44	0.12706847
6477	GO:0009110	vitamin biosynthetic process	0.53	1	0.16920474	44	0.12706847
9186	GO:0015926	glucosidase activity	0.53	1	0.16920474	44	0.12706847
9753	GO:0016682	oxidoreductase activity, actin	0.53	1	0.16920474	44	0.12706847

20522	GO:0044272	sulfur compound biosyntheti	0.53		1	0.16920474	44	0.12706847
28952	GO:0070588	calcium ion transmembrane	0.53		1	0.16920474	44	0.12706847
9709	GO:0016627	oxidoreductase activity, actin	0.53		2	0.33840948	104	0.30034366
5055	GO:0006996	organelle organization	0.53		3	0.5076142	164	0.47361887
20623	GO:0044429	mitochondrial part	0.54		3	0.5076142	165	0.47650677
14667	GO:0032259	methylation	0.54		5	0.8460237	285	0.8230572
5692	GO:0008134	transcription factor binding	0.54		1	0.16920474	45	0.1299564
8787	GO:0015450	P-P-bond-hydrolysis-driven p	0.54		1	0.16920474	45	0.1299564
11780	GO:0019829	cation-transporting ATPase a	0.54		1	0.16920474	45	0.1299564
4476	GO:0006278	RNA-dependent DNA replica	0.54		3	0.5076142	166	0.4793947
3942	GO:0005618	cell wall	0.55		2	0.33840948	107	0.30900744
4906	GO:0006807	nitrogen compound metaboli	0.55		63	10.659899	3725	10.757502
8497	GO:0015079|GO:0022817	potassium ion transmembrar	0.55		1	0.16920474	47	0.13573223
4188	GO:0005938	cell cortex	0.56		1	0.16920474	48	0.13862015
14591	GO:0032183	SUMO binding	0.56		1	0.16920474	48	0.13862015
20642	GO:0044448	cell cortex part	0.56		1	0.16920474	48	0.13862015
113	GO:0000145	exocyst	0.56		1	0.16920474	48	0.13862015
20498	GO:0044248	cellular catabolic process	0.56		15	2.5380712	894	2.5818002
12868	GO:0030312	external encapsulating struct	0.57		2	0.33840948	111	0.3205591
9906	GO:0016874	ligase activity	0.57		10	1.6920474	597	1.7240882
3756	GO:0005261|GO:0015281|G	cation channel activity	0.57		1	0.16920474	49	0.14150807
6750	GO:0009415	response to water	0.57		1	0.16920474	49	0.14150807
8909	GO:0015630	microtubule cytoskeleton	0.57		1	0.16920474	49	0.14150807
9493	GO:0016310	phosphorylation	0.57		42	7.106599	2504	7.2313514
4622	GO:0006479	protein methylation	0.58		1	0.16920474	50	0.14439599
5750	GO:0008213	protein alkylation	0.58		1	0.16920474	50	0.14439599
20517	GO:0044267	cellular protein metabolic pro	0.58		54	9.137055	3225	9.313541
8967	GO:0015698	inorganic anion transport	0.58		3	0.5076142	176	0.5082739
9871	GO:0016831	carboxy-lyase activity	0.59		2	0.33840948	115	0.3321108
6166	GO:0008757	S-adenosylmethionine-deper	0.60		3	0.5076142	180	0.5198256
20532	GO:0044282	small molecule catabolic pro	0.60		14	2.3688664	854	2.4662836
9750	GO:0016679	oxidoreductase activity, actin	0.60		1	0.16920474	53	0.15305975
9836	GO:0016787	hydrolase activity	0.60		62	10.490694	3723	10.751725
5981	GO:0008509	anion transmembrane transp	0.60		4	0.67681897	245	0.70754033
17918	GO:0035556|GO:0007242|G	intracellular signal transducti	0.61		1	0.16920474	54	0.15594767
4917	GO:0006820|GO:0006822	anion transport	0.61		4	0.67681897	247	0.7133162
20505	GO:0044255	cellular lipid metabolic proce	0.61		3	0.5076142	184	0.53137726
4894	GO:0006790	sulfur compound metabolic p	0.61		1	0.16920474	55	0.15883559
4844	GO:0006725	cellular aromatic compound	0.61		3	0.5076142	185	0.53426516
3200	GO:0004553|GO:0016800	hydrolase activity, hydrolyzin	0.62		5	0.8460237	312	0.90103096
12532	GO:0022836	gated channel activity	0.62		2	0.33840948	122	0.3523262
4224	GO:0005984	disaccharide metabolic proc	0.62		1	0.16920474	56	0.16172351
9369	GO:0016137	glycoside metabolic process	0.62		1	0.16920474	56	0.16172351
7229	GO:0009987|GO:0008151|G	cellular process	0.62		178	30.118443	10601	30.614838
5964	GO:0008483	transaminase activity	0.63		1	0.16920474	57	0.16461143
9813	GO:0016759	cellulose synthase activity	0.63		1	0.16920474	57	0.16461143
9821	GO:0016769	transferase activity, transferr	0.63		1	0.16920474	57	0.16461143
3323	GO:0004702	receptor signaling protein se	0.63		1	0.16920474	58	0.16749935
5819	GO:0008299|GO:0009241	isoprenoid biosynthetic proce	0.63		1	0.16920474	58	0.16749935
6665	GO:0009311	oligosaccharide metabolic pr	0.63		1	0.16920474	58	0.16749935
2831	GO:0004022	alcohol dehydrogenase (NAI	0.64		1	0.16920474	59	0.17038727
2626	GO:0003674|GO:0005554	molecular_function	0.64		413	69.88155	24394	70.447914
10058	GO:0017111	nucleoside-triphosphatase a	0.64		14	2.3688664	878	2.5355935
3306	GO:0004674|GO:0004695|G	protein serine/threonine kina	0.64		17	2.8764806	1062	3.0669708
30206	GO:0071842	cellular component organiza	0.64		3	0.5076142	193	0.5573685
5652	GO:0008081|GO:0004434|G	phosphoric diester hydrolase	0.64		1	0.16920474	60	0.17327519
9824	GO:0016773	phosphotransferase activity,	0.65		24	4.0609136	1493	4.311664
2818	GO:0004003	ATP-dependent DNA helicas	0.65		1	0.16920474	61	0.1761631
4849	GO:0006730|GO:0019753|G	one-carbon metabolic proce	0.65		5	0.8460237	325	0.93857396
9488	GO:0016301	kinase activity	0.65		28	4.737733	1740	5.0249805
22479	GO:0046983	protein dimerization activity	0.66		8	1.3536379	517	1.4930545
3340	GO:0004721	phosphoprotein phosphatase	0.66		3	0.5076142	199	0.57469606
10244	GO:0018130	heterocycle biosynthetic pro	0.66		3	0.5076142	199	0.57469606
19126	GO:0042803	protein homodimerization ac	0.66		4	0.67681897	265	0.7652988
22416	GO:0046915	transition metal ion transme	0.67		1	0.16920474	64	0.18482687
15436	GO:0033036	macromolecule localization	0.67		6	1.0152284	397	1.1465042
9838	GO:0016790	thiolester hydrolase activity	0.67		1	0.16920474	65	0.18771479
5791	GO:0008270	zinc ion binding	0.67		30	5.0761423	1880	5.4292893
9765	GO:0016702	oxidoreductase activity, actin	0.68		1	0.16920474	66	0.1906027
2629	GO:0003678|GO:0003679	DNA helicase activity	0.68		1	0.16920474	67	0.19349062
4897	GO:0006793	phosphorus metabolic proce	0.69		47	7.952623	2925	8.4471655
4900	GO:0006796	phosphate metabolic proces	0.69		47	7.952623	2925	8.4471655
18955	GO:0042625	ATPase activity, coupled to t	0.69		1	0.16920474	68	0.19637854
32	GO:0000041	transition metal ion transport	0.69		1	0.16920474	68	0.19637854
3724	GO:0005216	ion channel activity	0.69		2	0.33840948	140	0.40430877
6046	GO:0008610	lipid biosynthetic process	0.70		2	0.33840948	141	0.4071967
5726	GO:0008187	poly-pyrimidine tract binding	0.70		1	0.16920474	70	0.20215438
5788	GO:0008266	poly(U) RNA binding	0.70		1	0.16920474	70	0.20215438
5838	GO:0008320	protein transmembrane trans	0.70		1	0.16920474	70	0.20215438
12568	GO:0022884	macromolecule transmembr	0.70		1	0.16920474	70	0.20215438
9771	GO:0016709	oxidoreductase activity, actin	0.71		1	0.16920474	71	0.2050423
3744	GO:0005244	voltage-gated ion channel a	0.71		1	0.16920474	72	0.20793022
9764	GO:0016701	oxidoreductase activity, actin	0.71		1	0.16920474	72	0.20793022
12528	GO:0022832	voltage-gated channel activi	0.71		1	0.16920474	72	0.20793022
15280	GO:0032879	regulation of localization	0.71		1	0.16920474	72	0.20793022
17141	GO:0034762	regulation of transmembrane	0.71		1	0.16920474	72	0.20793022
17144	GO:0034765	regulation of ion transmemb	0.71		1	0.16920474	72	0.20793022
19568	GO:0043269	regulation of ion transport	0.71		1	0.16920474	72	0.20793022
25348	GO:0051049	regulation of transport	0.71		1	0.16920474	72	0.20793022
3311	GO:0004683|GO:0004684|G	calmodulin-dependent protei	0.72		1	0.16920474	74	0.21370606
20628	GO:0044434	chloroplast part	0.72		1	0.16920474	74	0.21370606
20629	GO:0044435	plastid part	0.72		1	0.16920474	74	0.21370606
4028	GO:0005739	mitochondrion	0.72		3	0.5076142	219	0.63245445
25510	GO:0051213	dioxygenase activity	0.73		1	0.16920474	75	0.21659398
5019	GO:0006952|GO:0002217|G	defense response	0.73		3	0.5076142	221	0.63823026
5663	GO:0008094|GO:0004011	DNA-dependent ATPase act	0.73		1	0.16920474	76	0.2194819
5604	GO:0008017	microtubule binding	0.73		1	0.16920474	77	0.22236982
13656	GO:0031224	intrinsic to membrane	0.74		18	3.0456853	1193	3.4452884
4460	GO:0006260|GO:0055133	DNA replication	0.74		3	0.5076142	224	0.64689404
13547	GO:0031090	organelle membrane	0.74		3	0.5076142	224	0.64689404
9697	GO:0016614	oxidoreductase activity, actin	0.74		4	0.67681897	293	0.84616053
5681	GO:0008116	prostaglandin-I synthase acti	0.74		1	0.16920474	78	0.22525774
9800	GO:0016746	transferase activity, transferr	0.75		7	1.1844332	498	1.438184
9655	GO:0016568	chromatin modification	0.75		1	0.16920474	80	0.2310336
9656	GO:0016569	covalent chromatin modificat	0.75		1	0.16920474	80	0.2310336
9657	GO:0016570	histone modification	0.75		1	0.16920474	80	0.2310336
9875	GO:0016836	hydro-lyase activity	0.75		1	0.16920474	80	0.2310336
3307	GO:0004675	transmembrane receptor pro	0.75		5	0.8460237	367	1.0598665
19526	GO:0043227	membrane-bounded organel	0.75		33	5.5837564	2142	6.185924
19530	GO:0043231	intracellular membrane-boun	0.75		33	5.5837564	2142	6.185924
6991	GO:0009725	response to hormone stimul	0.76		1	0.16920474	82	0.23680943
20487	GO:0044237	cellular metabolic process	0.76		133	22.50423	8185	23.637625
4643	GO:0006511	ubiquitin-dependent protein	0.76		1	0.16920474	84	0.24258527
11864	GO:0019941	modification-dependent prot	0.76		1	0.16920474	84	0.24258527
19898	GO:0043632	modification-dependent mac	0.76		1	0.16920474	84	0.24258527
20507	GO:0044257	cellular protein catabolic pro	0.76		1	0.16920474	84	0.24258527
25887	GO:0051603	proteolysis involved in cellula	0.76		1	0.16920474	84	0.24258527
9837	GO:0016788	hydrolase activity, acting on	0.77		23	3.8917089	1534	4.430069
2628	GO:0003677	DNA binding	0.77		18	3.0456853	1224	3.534814
6985	GO:0009719	response to endogenous stir	0.77		1	0.16920474	86	0.24836111
12734	GO:0030163	protein catabolic process	0.77		1	0.16920474	86	0.24836111
19952	GO:0043687	post-translational protein mo	0.77		1	0.16920474	86	0.24836111

20515	GO:0044265|GO:0034962	cellular macromolecule catab	0.77		1	0.16920474	86	0.24836111
9267	GO:0016021	integral to membrane	0.78		16	2.7072759	1103	3.1853757
20624	GO:0044430	cytoskeletal part	0.78		1	0.16920474	88	0.25413695
119	GO:0000151	ubiquitin ligase complex	0.78		1	0.16920474	88	0.25413695
14590	GO:0032182	small conjugating protein bin	0.79		1	0.16920474	90	0.2599128
2982	GO:0004197	cysteine-type endopeptidase	0.79		1	0.16920474	90	0.2599128
3644	GO:0005102	receptor binding	0.79		1	0.16920474	91	0.2628007
3341	GO:0004722|GO:0000158|G	protein serine/threonine phos	0.79		2	0.33840948	171	0.4938343
9801	GO:0016747	transferase activity, transferr	0.79		6	1.0152284	456	1.3168914
2660	GO:0003735|GO:0003736|G	structural constituent of ribos	0.79		3	0.5076142	246	0.7104283
6425	GO:0009056	catabolic process	0.79		15	2.5380712	1051	3.0352037
4067	GO:0005783	endoplasmic reticulum	0.80		2	0.33840948	174	0.50249803
18582	GO:0042221	response to chemical stimulu	0.81		4	0.67681897	328	0.94723773
9845	GO:0016798	hydrolase activity, acting on	0.82		5	0.8460237	401	1.1580559
5809	GO:0008289	lipid binding	0.82		3	0.5076142	258	0.74508333
30306	GO:0071944	cell periphery	0.82		3	0.5076142	259	0.74797124
7271	GO:0010033	response to organic substan	0.82		1	0.16920474	100	0.28879198
5280	GO:0007275	multicellular organismal deve	0.82		1	0.16920474	101	0.2916799
9285	GO:0016043	cellular component organizat	0.82		3	0.5076142	261	0.7537471
9486	GO:0016298	lipase activity	0.83		2	0.33840948	185	0.53426516
9699	GO:0016616	oxidoreductase activity, actin	0.83		3	0.5076142	266	0.7681867
14909	GO:0032501|GO:0050874	multicellular organismal proc	0.84		1	0.16920474	105	0.3032316
9823	GO:0016772	transferase activity, transferr	0.84		28	4.737733	1932	5.579461
6426	GO:0009057|GO:0043285	macromolecule catabolic pro	0.84		1	0.16920474	106	0.3061195
9869	GO:0016829	lyase activity	0.84		6	1.0152284	488	1.4093049
8910	GO:0015631	tubulin binding	0.84		1	0.16920474	107	0.30900744
9494	GO:0016311	dephosphorylation	0.85		5	0.8460237	425	1.227366
4512	GO:0006325	chromatin organization	0.86		1	0.16920474	112	0.32344702
5070	GO:0007017	microtubule-based process	0.86		1	0.16920474	112	0.32344702
5071	GO:0007018	microtubule-based movemen	0.86		1	0.16920474	112	0.32344702
25568	GO:0051276|GO:0007001|G	chromosome organization	0.86		1	0.16920474	112	0.32344702
19686	GO:0043414	macromolecule methylation	0.86		1	0.16920474	113	0.32633495
22478	GO:0046982	protein heterodimerization ac	0.86		1	0.16920474	114	0.32922286
6020	GO:0008565|GO:0015463	protein transporter activity	0.86		1	0.16920474	115	0.3321108
9535	GO:0016407	acetyltransferase activity	0.86		1	0.16920474	115	0.3321108
30205	GO:0071841	cellular component organizat	0.87		3	0.5076142	285	0.8230572
14910	GO:0032502	developmental process	0.88		1	0.16920474	121	0.3494383
18912	GO:0042578	phosphoric ester hydrolase a	0.88		5	0.8460237	444	1.2822365
4755	GO:0006629	lipid metabolic process	0.88		7	1.1844332	590	1.7038727
3260	GO:0004620	phospholipase activity	0.88		1	0.16920474	123	0.35521415
4121	GO:0005856	cytoskeleton	0.89		1	0.16920474	126	0.3638779
13018	GO:0030529	ribonucleoprotein complex	0.89		9	1.5228426	741	2.1399486
12533	GO:0022838	substrate-specific channel ac	0.89		2	0.33840948	221	0.63823026
9839	GO:0016791|GO:0016302	phosphatase activity	0.89		4	0.67681897	383	1.1060733
4109	GO:0005840|GO:0033279	ribosome	0.90		8	1.3536379	682	1.9695613
8660	GO:0015267|GO:0015249|G	channel activity	0.90		2	0.33840948	226	0.6526699
12515	GO:0022803	passive transmembrane tran	0.90		2	0.33840948	226	0.6526699
6796	GO:0009507	chloroplast	0.90		2	0.33840948	229	0.6613336
20531	GO:0044281	small molecule metabolic pro	0.91		24	4.0609136	1788	5.1636004
19125	GO:0042802	identical protein binding	0.91		8	1.3536379	697	2.01288
3873	GO:0005507	copper ion binding	0.92		1	0.16920474	146	0.42163628
9895	GO:0016860	intramolecular oxidoreductas	0.92		1	0.16920474	146	0.42163628
5909	GO:0008415	acyltransferase activity	0.92		3	0.5076142	330	0.95301354
4478	GO:0006281	DNA repair	0.92		1	0.16920474	149	0.43030006
5037	GO:0006974|GO:0034984	response to DNA damage st	0.92		1	0.16920474	149	0.43030006
6824	GO:0009536	plastid	0.93		2	0.33840948	247	0.7133162
19525	GO:0043226	organelle	0.93		42	7.106599	3013	8.701303
19528	GO:0043229	intracellular organelle	0.93		42	7.106599	3013	8.701303
19831	GO:0043565	sequence-specific DNA bind	0.94		1	0.16920474	159	0.45917925
20533	GO:0044283	small molecule biosynthetic p	0.94		3	0.5076142	347	1.0021082
5764	GO:0008234|GO:0004220	cysteine-type peptidase activ	0.94		1	0.16920474	163	0.47073093
20619	GO:0044425	membrane part	0.94		19	3.21489	1523	4.398302
3178	GO:0004519	endonuclease activity	0.94		3	0.5076142	356	1.0280994
6899	GO:0009628	response to abiotic stimulus	0.95		1	0.16920474	170	0.49094638
30204	GO:0071840	cellular component organizat	0.95		3	0.5076142	362	1.045427
4605	GO:0006457|GO:0007022|G	protein folding	0.95		1	0.16920474	173	0.49961013
15949	GO:0033554	cellular response to stress	0.95		1	0.16920474	173	0.49961013
20521	GO:0044271	cellular nitrogen compound b	0.95		3	0.5076142	367	1.0598665
4215	GO:0005975	carbohydrate metabolic proc	0.95		11	1.8612521	990	2.8590407
3904	GO:0005576	extracellular region	0.95		1	0.16920474	178	0.5140497
20622	GO:0044428	nuclear part	0.95		1	0.16920474	178	0.5140497
4572	GO:0006412|GO:0006416|G	translation	0.96		1	0.16920474	180	0.5198256
5610	GO:0008026	ATP-dependent helicase act	0.96		1	0.16920474	183	0.52848935
28401	GO:0070035	purine NTP-dependent helica	0.96		1	0.16920474	183	0.52848935
8466	GO:0015031|GO:0015831	protein transport	0.96		1	0.16920474	185	0.53426516
20820	GO:0045184	establishment of protein loca	0.96		1	0.16920474	185	0.53426516
20640	GO:0044446	intracellular organelle part	0.96		7	1.1844332	710	2.0504231
20616	GO:0044422	organelle part	0.96		7	1.1844332	712	2.0561988
5669	GO:0008104	protein localization	0.96		1	0.16920474	189	0.54581684
3068	GO:0004386	helicase activity	0.96		1	0.16920474	189	0.54581684
9874	GO:0016835	carbon-oxygen lyase activity	0.97		1	0.16920474	202	0.5833598
4459	GO:0006259|GO:0055132	DNA metabolic process	0.97		4	0.67681897	493	1.4237444
3863	GO:0005488	binding	0.97		215	36.379017	13903	40.15075
9266	GO:0016020	membrane	0.98		50	8.460237	3741	10.803708
19527	GO:0043228	non-membrane-bounded org	0.98		9	1.5228426	923	2.66555
19531	GO:0043232	intracellular non-membrane-	0.98		9	1.5228426	923	2.66555
4558	GO:0006396|GO:0006394	RNA processing	0.98		1	0.16920474	219	0.63245445
3177	GO:0004518	nuclease activity	0.98		3	0.5076142	427	1.2331418
13531	GO:0031072	heat shock protein binding	0.98		1	0.16920474	230	0.6642216
2627	GO:0003676	nucleic acid binding	0.98		30	5.0761423	2453	7.0840673
11828	GO:0019899	enzyme binding	0.98		1	0.16920474	237	0.684437
2653	GO:0003723	RNA binding	0.98		7	1.1844332	797	2.3016722
13041	GO:0030554	adenyl nucleotide binding	0.99		4	0.67681897	550	1.5883559
14965	GO:0032559	adenyl ribonucleotide binding	0.99		4	0.67681897	550	1.5883559
20512	GO:0044262|GO:0006092	cellular carbohydrate metabo	0.99		1	0.16920474	248	0.7162041
5661	GO:0008092	cytoskeletal protein binding	0.99		1	0.16920474	249	0.719092
4649	GO:0006520|GO:0006519	cellular amino acid metabolic	0.99		1	0.16920474	277	0.7999538
3884	GO:0005524	ATP binding	0.99		3	0.5076142	524	1.51327
20356	GO:0044106	cellular amine metabolic pro	0.99		1	0.16920474	303	0.8750397
9889	GO:0016853	isomerase activity	0.99		1	0.16920474	306	0.8837035
6662	GO:0009308	amine metabolic process	1.00		1	0.16920474	314	0.9068068
20638	GO:0044444	cytoplasmic part	1.00		16	2.7072759	1644	4.7477403
19533	GO:0043234	protein complex	1.00		6	1.0152284	848	2.448956
15392	GO:0032991	macromolecular complex	1.00		15	2.5380712	1616	4.666878
4320	GO:0006082	organic acid metabolic proce	1.00		1	0.16920474	369	1.0656425
11716	GO:0019752	carboxylic acid metabolic pro	1.00		1	0.16920474	369	1.0656425
19707	GO:0043436	oxoacid metabolic process	1.00		1	0.16920474	369	1.0656425
20618	GO:0044424	intracellular part	1.00		45	7.614213	3853	11.127155
18541	GO:0042180	cellular ketone metabolic pro	1.00		1	0.16920474	375	1.0829699
3945	GO:0005622	intracellular	1.00		56	9.475466	4751	13.720507
14959	GO:0032553	ribonucleotide binding	1.00		4	0.67681897	795	2.2958963
14961	GO:0032555	purine ribonucleotide binding	1.00		4	0.67681897	795	2.2958963
10033	GO:0017076	purine nucleotide binding	1.00		4	0.67681897	797	2.3016722
3876	GO:0005515|GO:0045308	protein binding	1.00		88	14.890017	6933	20.021948
4027	GO:0005737	cytoplasm	1.00		17	2.8764806	2001	5.7787275
18000	GO:0035639	purine ribonucleoside triphos	1.00		3	0.5076142	769	2.2208104
3946	GO:0005623	cell	1.00		105	17.766497	8227	23.758917
20657	GO:0044464	cell part	1.00		105	17.766497	8227	23.758917
3903	GO:0005575|GO:0008372	cellular_component	1.00		108	18.27411	8515	24.590637
131	GO:0000166	nucleotide binding	1.00		6	1.0152284	1213	3.5030468

GO ID	GO ACCESSION	GO Term	p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
6427	GO:0009058	biosynthetic process	0.00	42	15.730337	2796	8.074624
17024	GO:0034645|GO:003496	cellular macromolecule bi	0.00	31	11.610487	1999	5.7729516
6428	GO:0009059|GO:004328	macromolecule biosynthe	0.00	31	11.610487	2003	5.7845035
20499	GO:0044249	cellular biosynthetic proce	0.00	37	13.857677	2635	7.6096687
4476	GO:0006278	RNA-dependent DNA rep	0.00	7	2.621723	166	0.4793947
4109	GO:0005840|GO:003327	ribosome	0.00	14	5.243446	682	1.9695613
6613	GO:0009250	glucan biosynthetic proce	0.00	2	0.7490637	8	0.023103358
4460	GO:0006260|GO:005513	DNA replication	0.00	7	2.621723	224	0.64689404
13018	GO:0030529	ribonucleoprotein comple	0.00	14	5.243446	741	2.1399486
2837	GO:0004028	3-chloroallyl aldehyde deh	0.00	2	0.7490637	9	0.025991278
31895	GO:0090304	nucleic acid metabolic pro	0.00	31	11.610487	2340	6.7577324
6275	GO:0008878	glucose-1-phosphate ade	0.00	2	0.7490637	10	0.0288792
26959	GO:0055114	oxidation-reduction proce	0.00	32	11.985019	2490	7.1909204
5624	GO:0008047	enzyme activator activity	0.00	4	1.4981273	85	0.24547319
4459	GO:0006259|GO:005513	DNA metabolic process	0.01	10	3.7453184	493	1.4237444
19527	GO:0043228	non-membrane-bounded	0.01	15	5.6179776	923	2.66555
19531	GO:0043232	intracellular non-membra	0.01	15	5.6179776	923	2.66555
8493	GO:0015074	DNA integration	0.01	3	1.1235955	47	0.13573223
16081	GO:0033692	cellular polysaccharide bi	0.01	2	0.7490637	15	0.043318797
206	GO:0000271	polysaccharide biosynthe	0.01	2	0.7490637	16	0.046206716
25635	GO:0051345	positive regulation of hyd	0.01	3	1.1235955	53	0.15305975
19392	GO:0043085	positive regulation of cata	0.01	4	1.4981273	104	0.30034366
20343	GO:0044093	positive regulation of mol	0.01	4	1.4981273	104	0.30034366
2662	GO:0003746|GO:000818	translation elongation fact	0.01	2	0.7490637	22	0.06353424
4574	GO:0006414|GO:000644	translational elongation	0.01	2	0.7490637	22	0.06353424
4357	GO:0006139|GO:005513	nucleobase, nucleoside,	0.01	37	13.857677	3285	9.486816
17016	GO:0034637	cellular carbohydrate bios	0.01	3	1.1235955	63	0.18193895
9293	GO:0016051|GO:000609	carbohydrate biosynthetic	0.01	3	1.1235955	64	0.18482687
9767	GO:0016705	oxidoreductase activity, a	0.01	7	2.621723	329	0.95012563
4311	GO:0006073	cellular glucan metabolic	0.01	2	0.7490637	24	0.06931008
20293	GO:0044042	glucan metabolic process	0.01	2	0.7490637	24	0.06931008
3309	GO:0004677	DNA-dependent protein k	0.02	1	0.37453184	2	0.00577584
4600	GO:0006448	regulation of translational	0.02	1	0.37453184	2	0.00577584
4602	GO:0006450|GO:000002	regulation of translational	0.02	1	0.37453184	2	0.00577584
14849	GO:0032441	pheophorbide a oxygenas	0.02	1	0.37453184	2	0.00577584
24925	GO:0050619	phytochromobilin:ferredox	0.02	1	0.37453184	2	0.00577584
26020	GO:0051738	xanthophyll binding	0.02	1	0.37453184	2	0.00577584
5809	GO:0008289	lipid binding	0.02	6	2.247191	258	0.74508333
17020	GO:0034641	cellular nitrogen compoun	0.02	40	14.981274	3678	10.621769
3896	GO:0005544	calcium-dependent phosp	0.02	2	0.7490637	26	0.075085916
9194	GO:0015935	small ribosomal subunit	0.02	2	0.7490637	26	0.075085916
9771	GO:0016709	oxidoreductase activity, a	0.02	3	1.1235955	71	0.2050423
9703	GO:0016620	oxidoreductase activity, a	0.02	3	1.1235955	73	0.21081814
4906	GO:0006807	nitrogen compound meta	0.02	40	14.981274	3725	10.757502
20487	GO:0044237	cellular metabolic process	0.02	78	29.213484	8185	23.637625
4526	GO:0006351|GO:000635	transcription, DNA-depen	0.02	20	7.490637	1575	4.548474
15176	GO:0032774	RNA biosynthetic process	0.02	20	7.490637	1575	4.548474
20510	GO:0044260|GO:003496	cellular macromolecule m	0.02	56	20.973783	5577	16.105928
11827	GO:0019898|GO:003039	extrinsic to membrane	0.02	2	0.7490637	30	0.086637594
3895	GO:0005543	phospholipid binding	0.02	4	1.4981273	140	0.40430877
20514	GO:0044264	cellular polysaccharide m	0.02	2	0.7490637	31	0.08952551
4358	GO:0006140	regulation of nucleotide m	0.02	3	1.1235955	80	0.2310336
7146	GO:0009894	regulation of catabolic pro	0.02	3	1.1235955	80	0.2310336
13278	GO:0030811	regulation of nucleotide c	0.02	3	1.1235955	80	0.2310336
13759	GO:0031329	regulation of cellular cata	0.02	3	1.1235955	80	0.2310336
15521	GO:0033121	regulation of purine nucle	0.02	3	1.1235955	80	0.2310336
2632	GO:0003682	chromatin binding	0.03	2	0.7490637	33	0.09530135
2985	GO:0004222	metalloendopeptidase act	0.03	2	0.7490637	34	0.09818927
2805	GO:0003989	acetyl-CoA carboxylase a	0.03	1	0.37453184	4	0.011551679
3033	GO:0004349	glutamate 5-kinase activit	0.03	1	0.37453184	4	0.011551679
3057	GO:0004373	glycogen (starch) synthas	0.03	1	0.37453184	4	0.011551679
3100	GO:0004430	1-phosphatidylinositol 4-k	0.03	1	0.37453184	4	0.011551679
3466	GO:0004859	phospholipase inhibitor a	0.03	1	0.37453184	4	0.011551679
3640	GO:0005098	Ran GTPase activator act	0.03	1	0.37453184	4	0.011551679
4218	GO:0005978	glycogen biosynthetic pro	0.03	1	0.37453184	4	0.011551679
4859	GO:0006743	ubiquinone metabolic pro	0.03	1	0.37453184	4	0.011551679
4860	GO:0006744	ubiquinone biosynthetic p	0.03	1	0.37453184	4	0.011551679
5729	GO:0008191	metalloendopeptidase inh	0.03	1	0.37453184	4	0.011551679
7792	GO:0010576	metalloenzyme regulator	0.03	1	0.37453184	4	0.011551679
8911	GO:0015633	zinc transporting ATPase	0.03	1	0.37453184	4	0.011551679
9718	GO:0016636	oxidoreductase activity, a	0.03	1	0.37453184	4	0.011551679
9790	GO:0016730	oxidoreductase activity, a	0.03	1	0.37453184	4	0.011551679
10039	GO:0017084	delta1-pyrroline-5-carbox	0.03	1	0.37453184	4	0.011551679
11781	GO:0019834	phospholipase A2 inhibito	0.03	1	0.37453184	4	0.011551679
11857	GO:0019932	second-messenger-medi	0.03	1	0.37453184	4	0.011551679
14425	GO:0032015	regulation of Ran protein	0.03	1	0.37453184	4	0.011551679
14724	GO:0032316	regulation of Ran GTPase	0.03	1	0.37453184	4	0.011551679
15254	GO:0032853	positive regulation of Ran	0.03	1	0.37453184	4	0.011551679
20918	GO:0045300	acyl-[acyl-carrier-protein]	0.03	1	0.37453184	4	0.011551679
23493	GO:0048015	phosphatidylinositol-medi	0.03	1	0.37453184	4	0.011551679
23495	GO:0048017	inositol lipid-mediated sig	0.03	1	0.37453184	4	0.011551679
23942	GO:0048551	metalloenzyme inhibitor a	0.03	1	0.37453184	4	0.011551679
26947	GO:0055102	lipase inhibitor activity	0.03	1	0.37453184	4	0.011551679
7691	GO:0010467	gene expression	0.03	23	8.614232	1974	5.7007537
13791	GO:0031361	integral to thylakoid mem	0.04	1	0.37453184	5	0.0144396
3638	GO:0005096	GTPase activator activity	0.04	2	0.7490637	41	0.118404716
19813	GO:0043547	positive regulation of GT	0.04	2	0.7490637	41	0.118404716
5607	GO:0008022	protein C-terminus bindin	0.04	2	0.7490637	42	0.121292636
3029	GO:0004345	glucose-6-phosphate deh	0.05	1	0.37453184	6	0.01732752
3208	GO:0004563	beta-N-acetylhexosamini	0.05	1	0.37453184	6	0.01732752
3342	GO:0004723|GO:000859	calcium-dependent protei	0.05	1	0.37453184	6	0.01732752
5810	GO:0008290	F-actin capping protein c	0.05	1	0.37453184	6	0.01732752
7220	GO:0009973	adenylyl-sulfate reductas	0.05	1	0.37453184	6	0.01732752
9248	GO:0015994	chlorophyll metabolic pro	0.05	1	0.37453184	6	0.01732752
9249	GO:0015995	chlorophyll biosynthetic p	0.05	1	0.37453184	6	0.01732752
9435	GO:0016231	beta-N-acetylglucosamini	0.05	1	0.37453184	6	0.01732752
9825	GO:0016774	phosphotransferase activ	0.05	1	0.37453184	6	0.01732752
13832	GO:0031409	pigment binding	0.05	1	0.37453184	6	0.01732752
14264	GO:0031849	olfactory receptor binding	0.05	1	0.37453184	6	0.01732752
18724	GO:0042375	quinone cofactor metabol	0.05	1	0.37453184	6	0.01732752
21036	GO:0045426	quinone cofactor biosynth	0.05	1	0.37453184	6	0.01732752
9600	GO:0016491	oxidoreductase activity	0.05	20	7.490637	1724	4.9787736
14726	GO:0032318	regulation of Ras GTPase	0.05	2	0.7490637	45	0.1299564
22096	GO:0046578	regulation of Ras protein	0.05	2	0.7490637	45	0.1299564
25355	GO:0051056	regulation of small GTPa	0.05	2	0.7490637	45	0.1299564
19253	GO:0042936	dipeptide transporter activ	0.05	3	1.1235955	105	0.3032316
19255	GO:0042938	dipeptide transport	0.05	3	1.1235955	105	0.3032316

3904	GO:0005576	extracellular region	**0.05**	4	1.4981273	178	0.5140497
9308	GO:0016070	RNA metabolic process	**0.05**	21	7.8651686	1855	5.3570914
20638	GO:0044444	cytoplasmic part	**0.05**	19	7.116105	1644	4.7477403
28930	GO:0070566	adenylyltransferase activi	**0.05**	2	0.7490637	48	0.13862015
4216	GO:0005976	polysaccharide metabolic	0.06	2	0.7490637	50	0.14439599
5096	GO:0007047	cellular cell wall organizat	0.06	2	0.7490637	50	0.14439599
6932	GO:0009664	plant-type cell wall organiz	0.06	2	0.7490637	50	0.14439599
9783	GO:0016722	oxidoreductase activity, o	0.06	2	0.7490637	50	0.14439599
20857	GO:0045229	external encapsulating str	0.06	2	0.7490637	50	0.14439599
30033	GO:0071669	plant-type cell wall organiz	0.06	2	0.7490637	50	0.14439599
9933	GO:0016903	oxidoreductase activity, a	0.06	3	1.1235955	113	0.32633495
18912	GO:0042578	phosphoric ester hydrolas	0.06	7	2.621723	444	1.2822365
7213	GO:0009966|GO:0035466	regulation of signal transd	0.06	2	0.7490637	51	0.14728391
12601	GO:0023051	regulation of signaling	0.06	2	0.7490637	51	0.14728391
3051	GO:0004367	glycerol-3-phosphate deh	0.06	1	0.37453184	8	0.023103358
3257	GO:0004617	phosphoglycerate dehydro	0.06	1	0.37453184	8	0.023103358
5635	GO:0008060	ARF GTPase activator ac	0.06	1	0.37453184	8	0.023103358
6684	GO:0009331	glycerol-3-phosphate deh	0.06	1	0.37453184	8	0.023103358
9549	GO:0016421	CoA carboxylase activity	0.06	1	0.37453184	8	0.023103358
9916	GO:0016885	ligase activity, forming ca	0.06	1	0.37453184	8	0.023103358
29246	GO:0070882	cellular cell wall organizat	0.06	2	0.7490637	53	0.15305975
25626	GO:0051336	regulation of hydrolase ac	0.07	4	1.4981273	196	0.5660323
3158	GO:0004499|GO:0047076	flavin-containing monooxy	0.07	1	0.37453184	9	0.025991278
6670	GO:0009317	acetyl-CoA carboxylase c	0.07	1	0.37453184	9	0.025991278
11785	GO:0019840	isoprenoid binding	0.07	1	0.37453184	9	0.025991278
19254	GO:0042937	tripeptide transporter activ	0.07	1	0.37453184	9	0.025991278
3340	GO:0004721	phosphoprotein phosphat	0.07	4	1.4981273	199	0.57469606
5767	GO:0008237	metallopeptidase activity	0.07	2	0.7490637	56	0.16172351
23973	GO:0048583	regulation of response to	0.07	2	0.7490637	57	0.16461143
29919	GO:0071555	cell wall organization	0.07	2	0.7490637	58	0.16749935
11205	GO:0019202	amino acid kinase activity	0.07	1	0.37453184	10	0.0288792
15183	GO:0032781	positive regulation of ATP	0.07	1	0.37453184	10	0.0288792
19728	GO:0043462	regulation of ATPase acti	0.07	1	0.37453184	10	0.0288792
21148	GO:0045547	dehydrodolichyl diphosph	0.07	1	0.37453184	10	0.0288792
27563	GO:0060590	ATPase regulator activity	0.07	1	0.37453184	10	0.0288792
31441	GO:0080065	4-alpha-methyl-delta7-ste	0.07	1	0.37453184	10	0.0288792
196	GO:0000254	C-4 methylsterol oxidase	0.07	1	0.37453184	10	0.0288792
983	GO:0001664	G-protein-coupled recepto	0.07	1	0.37453184	10	0.0288792
989	GO:0001671	ATPase activator activity	0.07	1	0.37453184	10	0.0288792
9839	GO:0016791|GO:0016302	phosphatase activity	0.08	6	2.247191	383	1.1060733
25095	GO:0050790	regulation of catalytic acti	0.08	7	2.621723	480	1.3862015
12579	GO:0022900	electron transport chain	0.08	1	0.37453184	11	0.03176712
19256	GO:0042939	tripeptide transport	0.08	1	0.37453184	11	0.03176712
19473	GO:0043170|GO:0043283	macromolecule metabolic	0.08	60	22.47191	6553	18.92454
28366	GO:0065009	regulation of molecular fu	0.08	7	2.621723	484	1.3977532
6018	GO:0008559|GO:0005226	xenobiotic-transporting AT	0.08	2	0.7490637	62	0.17905103
19225	GO:0042908	xenobiotic transport	0.08	2	0.7490637	62	0.17905103
19227	GO:0042910	xenobiotic transporter acti	0.08	2	0.7490637	62	0.17905103
25820	GO:0051536	iron-sulfur cluster binding	0.09	2	0.7490637	64	0.18482687
25824	GO:0051540	metal cluster binding	0.09	2	0.7490637	64	0.18482687
3386	GO:0004773	steryl-sulfatase activity	0.09	1	0.37453184	12	0.03465504
4217	GO:0005977	glycogen metabolic proce	0.09	1	0.37453184	12	0.03465504
4344	GO:0006112	energy reserve metabolic	0.09	1	0.37453184	12	0.03465504
5965	GO:0008484	sulfuric ester hydrolase ac	0.09	1	0.37453184	12	0.03465504
8607	GO:0015197|GO:0015637	peptide transporter activity	0.09	3	1.1235955	139	0.40142086
8608	GO:0015198	oligopeptide transporter a	0.09	3	1.1235955	139	0.40142086
12794	GO:0030234	enzyme regulator activity	0.09	6	2.247191	403	1.1638317
2628	GO:0003677	DNA binding	0.09	14	5.243446	1224	3.534814
7551	GO:0010327	acetyl CoA:(Z)-3-hexen-1-	0.10	1	0.37453184	13	0.037542958
4944	GO:0006857	oligopeptide transport	0.10	3	1.1235955	141	0.4071967
9099	GO:0015833	peptide transport	0.10	3	1.1235955	141	0.4071967
21710	GO:0046148	pigment biosynthetic proc	0.10	2	0.7490637	69	0.19926646
15524	GO:0033124	regulation of GTP catabol	0.10	2	0.7490637	70	0.20215438
19394	GO:0043087	regulation of GTPase acti	0.10	2	0.7490637	70	0.20215438
3641	GO:0005099	Ras GTPase activator act	0.10	1	0.37453184	14	0.040430877
14728	GO:0032320	positive regulation of Ras	0.10	1	0.37453184	14	0.040430877
25040	GO:0050734	hydroxycinnamoyltransfer	0.10	1	0.37453184	14	0.040430877
9740	GO:0016667	oxidoreductase activity, a	0.11	2	0.7490637	72	0.20793022
5705	GO:0008152	metabolic process	0.11	145	54.307117	17432	50.34222
18786	GO:0042440	pigment metabolic proces	0.11	2	0.7490637	73	0.21081814
9494	GO:0016311	dephosphorylation	0.11	6	2.247191	425	1.227366
27562	GO:0060589	nucleoside-triphosphatase	0.11	3	1.1235955	152	0.4389638
3382	GO:0004768|GO:0016214	stearoyl-CoA 9-desaturas	0.12	1	0.37453184	16	0.046206716
7521	GO:0010295	(+)-abscisic acid 8'-hydrox	0.12	1	0.37453184	16	0.046206716
9189	GO:0015929	hexosaminidase activity	0.12	1	0.37453184	16	0.046206716
9427	GO:0016215	CoA desaturase activity	0.12	1	0.37453184	16	0.046206716
19338	GO:0043022|GO:0030376	ribosome binding	0.12	1	0.37453184	16	0.046206716
15392	GO:0032991	macromolecular complex	0.12	17	6.367041	1616	4.666878
3885	GO:0005525	GTP binding	0.12	4	1.4981273	245	0.70754033
11032	GO:0019001	guanyl nucleotide binding	0.12	4	1.4981273	245	0.70754033
14967	GO:0032561	guanyl ribonucleotide bind	0.12	4	1.4981273	245	0.70754033
9923	GO:0016892	endoribonuclease activity	0.12	1	0.37453184	17	0.049094636
9925	GO:0016894	endonuclease activity, act	0.12	1	0.37453184	17	0.049094636
16281	GO:0033897	ribonuclease T2 activity	0.12	1	0.37453184	17	0.049094636
15189	GO:0032787	monocarboxylic acid meta	0.13	2	0.7490637	81	0.23392151
2659	GO:0003730	mRNA 3'-UTR binding	0.13	1	0.37453184	18	0.051982556
4576	GO:0006417|GO:0006445	regulation of translation	0.13	1	0.37453184	18	0.051982556
5776	GO:0008252	nucleotidase activity	0.13	1	0.37453184	18	0.051982556
8469	GO:0015036	disulfide oxidoreductase a	0.13	1	0.37453184	18	0.051982556
2658	GO:0003729	mRNA binding	0.13	2	0.7490637	82	0.23680943
3290	GO:0004656	procollagen-proline 4-diox	0.14	1	0.37453184	19	0.054870475
11752	GO:0019798	procollagen-proline dioxyg	0.14	1	0.37453184	19	0.054870475
13966	GO:0031543	peptidyl-proline dioxygena	0.14	1	0.37453184	19	0.054870475
13968	GO:0031545	peptidyl-proline 4-dioxyge	0.14	1	0.37453184	19	0.054870475
2627	GO:0003676	nucleic acid binding	0.14	24	8.988764	2453	7.0840673
4327	GO:0006091	generation of precursor m	0.14	2	0.7490637	84	0.24258527
18000	GO:0035639	purine ribonucleoside tripl	0.14	9	3.3707864	769	2.2208104
4027	GO:0005737	cytoplasm	0.14	20	7.490637	2001	5.7787275
9784	GO:0016723	oxidoreductase activity, o	0.14	1	0.37453184	20	0.0577584
225	GO:0000293	ferric-chelate reductase a	0.14	1	0.37453184	20	0.0577584
3341	GO:0004722|GO:0000158	protein serine/threonine p	0.15	3	1.1235955	171	0.4938343
3156	GO:0004497	monooxygenase activity	0.15	3	1.1235955	172	0.49672222
4605	GO:0006457|GO:0007022	protein folding	0.15	3	1.1235955	173	0.49961013
9768	GO:0016706	oxidoreductase activity, a	0.15	3	1.1235955	175	0.505386
3831	GO:0005385	zinc ion transmembrane t	0.16	1	0.37453184	22	0.06353424
4882	GO:0006778	porphyrin metabolic proce	0.16	1	0.37453184	22	0.06353424
4883	GO:0006779	porphyrin biosynthetic pro	0.16	1	0.37453184	22	0.06353424
4924	GO:0006829	zinc ion transport	0.16	1	0.37453184	22	0.06353424
7823	GO:0010608	posttranscriptional regulat	0.16	1	0.37453184	22	0.06353424
29941	GO:0071577	zinc ion transmembrane t	0.16	1	0.37453184	22	0.06353424
5693	GO:0008135	translation factor activity,	0.16	2	0.7490637	92	0.26568863
14959	GO:0032553	ribonucleotide binding	0.16	9	3.3707864	795	2.2958963

14961	GO:0032555	purine ribonucleotide bind	0.16	9	3.3707864	795	2.2958963
10033	GO:0017076	purine nucleotide binding	0.17	9	3.3707864	797	2.3016722
3262	GO:0004622|GO:004512	lysophospholipase activity	0.17	1	0.37453184	24	0.06931008
8559	GO:0015146	pentose transmembrane t	0.17	1	0.37453184	24	0.06931008
8561	GO:0015148	D-xylose transmembrane	0.17	1	0.37453184	24	0.06931008
8829	GO:0015519	D-xylose:hydrogen sympo	0.17	1	0.37453184	24	0.06931008
9019	GO:0015750	pentose transport	0.17	1	0.37453184	24	0.06931008
9022	GO:0015753	D-xylose transport	0.17	1	0.37453184	24	0.06931008
9779	GO:0016717	oxidoreductase activity, a	0.17	1	0.37453184	24	0.06931008
13657	GO:0031225	anchored to membrane	0.17	1	0.37453184	24	0.06931008
25578	GO:0051287|GO:005128	NAD binding	0.17	1	0.37453184	24	0.06931008
22357	GO:0046854|GO:004683	phosphatidylinositol phos	0.18	1	0.37453184	25	0.072197996
19393	GO:0043086	negative regulation of cat	0.18	3	1.1235955	188	0.54292893
20342	GO:0044092	negative regulation of mo	0.18	3	1.1235955	188	0.54292893
3415	GO:0004805	trehalose-phosphatase ac	0.18	1	0.37453184	26	0.075085916
9884	GO:0016847|GO:003410	1-aminocyclopropane-1-c	0.18	1	0.37453184	26	0.075085916
10911	GO:0018871	1-aminocyclopropane-1-c	0.18	1	0.37453184	26	0.075085916
18579	GO:0042218	1-aminocyclopropane-1-c	0.18	1	0.37453184	26	0.075085916
30689	GO:0072330	monocarboxylic acid bios	0.18	1	0.37453184	26	0.075085916
24968	GO:0050662	coenzyme binding	0.18	3	1.1235955	191	0.5515927
9541	GO:0016413	O-acetyltransferase activi	0.19	1	0.37453184	27	0.077973835
22340	GO:0046834	lipid phosphorylation	0.19	1	0.37453184	27	0.077973835
1029	GO:0001727	lipid kinase activity	0.19	1	0.37453184	27	0.077973835
9238	GO:0015980	energy derivation by oxida	0.19	1	0.37453184	28	0.080861755
19337	GO:0043021	ribonucleoprotein binding	0.20	1	0.37453184	29	0.083749674
2870	GO:0004064	arylesterase activity	0.21	1	0.37453184	30	0.086637594
3009	GO:0004322	ferroxidase activity	0.21	1	0.37453184	30	0.086637594
9785	GO:0016724	oxidoreductase activity, o	0.21	1	0.37453184	30	0.086637594
15414	GO:0033013	tetrapyrrole metabolic pro	0.21	1	0.37453184	30	0.086637594
15415	GO:0033014	tetrapyrrole biosynthetic p	0.21	1	0.37453184	30	0.086637594
3626	GO:0005083	small GTPase regulator a	0.21	2	0.7490637	111	0.3205591
14422	GO:0032012	regulation of ARF protein	0.21	1	0.37453184	31	0.08952551
14720	GO:0032312	regulation of ARF GTPas	0.21	1	0.37453184	31	0.08952551
29918	GO:0071554	cell wall organization or bi	0.21	2	0.7490637	112	0.32344702
3265	GO:0004630	phospholipase D activity	0.22	1	0.37453184	32	0.09241343
4757	GO:0006633|GO:000003	fatty acid biosynthetic pro	0.22	1	0.37453184	32	0.09241343
6942	GO:0009674	potassium:sodium sympo	0.22	1	0.37453184	32	0.09241343
12522	GO:0022820	potassium ion symporter a	0.22	1	0.37453184	32	0.09241343
21041	GO:0045431	flavonol synthase activity	0.22	1	0.37453184	32	0.09241343
25836	GO:0051552	flavone metabolic process	0.22	1	0.37453184	32	0.09241343
25837	GO:0051553	flavone biosynthetic proce	0.22	1	0.37453184	32	0.09241343
25838	GO:0051554	flavonol metabolic proces	0.22	1	0.37453184	32	0.09241343
25839	GO:0051555	flavonol biosynthetic proc	0.22	1	0.37453184	32	0.09241343
7229	GO:0009987|GO:000815	cellular process	0.22	88	32.9588	10601	30.614838
18956	GO:0042626	ATPase activity, coupled	0.22	3	1.1235955	211	0.6093511
9861	GO:0016820	hydrolase activity, acting	0.22	3	1.1235955	212	0.612239
24966	GO:0050660	flavin adenine dinucleotid	0.23	2	0.7490637	118	0.34077454
11206	GO:0019203	carbohydrate phosphatas	0.24	1	0.37453184	35	0.10107719
12817	GO:0030258	lipid modification	0.24	1	0.37453184	35	0.10107719
22012	GO:0046488|GO:003038	phosphatidylinositol meta	0.24	1	0.37453184	35	0.10107719
4232	GO:0005992	trehalose biosynthetic pro	0.24	1	0.37453184	36	0.10396511
9393	GO:0016165	lipoxygenase activity	0.24	1	0.37453184	36	0.10396511
3260	GO:0004620	phospholipase activity	0.25	2	0.7490637	123	0.35521415
25485	GO:0051188	cofactor biosynthetic proc	0.25	2	0.7490637	123	0.35521415
20488	GO:0044238	primary metabolic process	0.25	76	28.46442	9167	26.47356
4231	GO:0005991	trehalose metabolic proce	0.25	1	0.37453184	38	0.10974095
7072	GO:0009813	flavonoid biosynthetic pro	0.27	1	0.37453184	40	0.1155168
4851	GO:0006733	oxidoreduction coenzyme	0.27	1	0.37453184	41	0.118404716
19758	GO:0043492	ATPase activity, coupled	0.27	3	1.1235955	235	0.67866117
3877	GO:0005516	calmodulin binding	0.27	3	1.1235955	236	0.6815491
2653	GO:0003723	RNA binding	0.27	8	2.9962547	797	2.3016722
4756	GO:0006631	fatty acid metabolic proce	0.28	1	0.37453184	42	0.121292636
6666	GO:0009312	oligosaccharide biosynthe	0.28	1	0.37453184	42	0.121292636
9370	GO:0016138	glycoside biosynthetic pro	0.28	1	0.37453184	42	0.121292636
21880	GO:0046351	disaccharide biosynthetic	0.28	1	0.37453184	42	0.121292636
14676	GO:0032268	regulation of cellular prote	0.28	1	0.37453184	43	0.124180555
25538	GO:0051246	regulation of protein meta	0.28	1	0.37453184	43	0.124180555
7071	GO:0009812	flavonoid metabolic proce	0.29	1	0.37453184	44	0.12706847
9753	GO:0016682	oxidoreductase activity, a	0.29	1	0.37453184	44	0.12706847
4942	GO:0006855	drug transmembrane tran	0.29	2	0.7490637	139	0.40142086
8642	GO:0015238|GO:001523	drug transmembrane tran	0.29	2	0.7490637	139	0.40142086
9154	GO:0015893	drug transport	0.29	2	0.7490637	139	0.40142086
18832	GO:0042493|GO:001703	response to drug	0.29	2	0.7490637	139	0.40142086
31431	GO:0080054	low affinity nitrate transme	0.29	1	0.37453184	45	0.1299564
13164	GO:0030695	GTPase regulator activity	0.30	2	0.7490637	142	0.4100846
20512	GO:0044262|GO:000609	cellular carbohydrate met	0.30	3	1.1235955	248	0.7162041
9396	GO:0016168	chlorophyll binding	0.30	1	0.37453184	46	0.13284431
4773	GO:0006650|GO:000665	glycerophospholipid meta	0.31	1	0.37453184	47	0.13573223
8497	GO:0015079|GO:002281	potassium ion transmemb	0.31	1	0.37453184	47	0.13573223
22010	GO:0046486	glycerolipid metabolic pro	0.31	1	0.37453184	47	0.13573223
3307	GO:0004675	transmembrane receptor	0.31	4	1.4981273	367	1.0598665
31421	GO:0080044	quercetin 7-O-glucosyltra	0.32	1	0.37453184	49	0.14150807
9829	GO:0016779	nucleotidyltransferase act	0.32	2	0.7490637	148	0.42741212
8749	GO:0015399	primary active transmemb	0.32	3	1.1235955	260	0.75085914
8753	GO:0015405	P-P-bond-hydrolysis-drive	0.32	3	1.1235955	260	0.75085914
4897	GO:0006793	phosphorus metabolic pro	0.32	25	9.363296	2925	8.4471655
4900	GO:0006796	phosphate metabolic proc	0.32	25	9.363296	2925	8.4471655
3099	GO:0004428	inositol or phosphatidylino	0.33	1	0.37453184	51	0.14728391
3293	GO:0004659	prenyltransferase activity	0.33	1	0.37453184	51	0.14728391
8908	GO:0015629	actin cytoskeleton	0.33	1	0.37453184	51	0.14728391
18541	GO:0042180	cellular ketone metabolic	0.33	4	1.4981273	375	1.0829699
2809	GO:0003993	acid phosphatase activity	0.33	1	0.37453184	52	0.15017183
6965	GO:0009699	phenylpropanoid biosynth	0.33	1	0.37453184	52	0.15017183
6424	GO:0009055|GO:000905	electron carrier activity	0.33	2	0.7490637	154	0.44473964
131	GO:0000166	nucleotide binding	0.33	11	4.11985	1213	3.5030468
9750	GO:0016679	oxidoreductase activity, a	0.34	1	0.37453184	53	0.15305975
9699	GO:0016616	oxidoreductase activity, a	0.34	3	1.1235955	266	0.7681867
3464	GO:0004857	enzyme inhibitor activity	0.34	2	0.7490637	157	0.4534034
17918	GO:0035556|GO:000724	intracellular signal transdu	0.34	1	0.37453184	54	0.15594767
4224	GO:0005984	disaccharide metabolic pr	0.35	1	0.37453184	56	0.16172351
9369	GO:0016137	glycoside metabolic proce	0.35	1	0.37453184	56	0.16172351
9883	GO:0016846	carbon-sulfur lyase activit	0.35	1	0.37453184	56	0.16172351
6441	GO:0009072	aromatic amino acid famil	0.36	1	0.37453184	57	0.16461143
25483	GO:0051186	cofactor metabolic proces	0.36	2	0.7490637	164	0.47361887
6665	GO:0009311	oligosaccharide metabolic	0.36	1	0.37453184	58	0.16749935
8558	GO:0015145	monosaccharide transme	0.36	1	0.37453184	58	0.16749935
9018	GO:0015749	monosaccharide transpor	0.36	1	0.37453184	58	0.16749935
18981	GO:0042651	thylakoid membrane	0.37	1	0.37453184	59	0.17038727
2980	GO:0004185	serine-type carboxypeptid	0.37	1	0.37453184	60	0.17327519
5652	GO:0008081|GO:000443	phosphoric diester hydrol	0.37	1	0.37453184	60	0.17327519
6964	GO:0009698	phenylpropanoid metaboli	0.37	1	0.37453184	60	0.17327519
28375	GO:0070008	serine-type exopeptidase	0.37	1	0.37453184	60	0.17327519
4768	GO:0006644	phospholipid metabolic pr	0.38	1	0.37453184	61	0.1761631

8526	GO:0015112	nitrate transmembrane tra	0.38	1	0.37453184	61	0.1761631
8975	GO:0015706|GO:000687	nitrate transport	0.38	1	0.37453184	61	0.1761631
3884	GO:0005524	ATP binding	0.38	5	1.8726592	524	1.51327
2978	GO:0004180	carboxypeptidase activity	0.38	1	0.37453184	62	0.17905103
17457	GO:0035091	phosphatidylinositol bindi	0.38	1	0.37453184	62	0.17905103
8675	GO:0015293	symporter activity	0.39	2	0.7490637	173	0.49961013
5704	GO:0008150|GO:000000	biological_process	0.39	174	65.16854	22215	64.155136
22416	GO:0046915	transition metal ion transn	0.39	1	0.37453184	64	0.18482687
9697	GO:0016614	oxidoreductase activity, a	0.39	3	1.1235955	293	0.84616053
11616	GO:0019637	organophosphate metabo	0.40	1	0.37453184	65	0.18771479
25314	GO:0051015	actin filament binding	0.40	1	0.37453184	65	0.18771479
18953	GO:0042623	ATPase activity, coupled	0.40	5	1.8726592	537	1.550813
3180	GO:0004521	endoribonuclease activity	0.40	1	0.37453184	66	0.1906027
9765	GO:0016702	oxidoreductase activity, a	0.40	1	0.37453184	66	0.1906027
9837	GO:0016788	hydrolase activity, acting	0.40	13	4.8689137	1534	4.430069
4572	GO:0006412|GO:000641	translation	0.40	2	0.7490637	180	0.5198256
32	GO:0000041	transition metal ion transp	0.41	1	0.37453184	68	0.19637854
5610	GO:0008026	ATP-dependent helicase	0.41	2	0.7490637	183	0.52848935
28401	GO:0070035	purine NTP-dependent he	0.41	2	0.7490637	183	0.52848935
20505	GO:0044255	cellular lipid metabolic pr	0.42	2	0.7490637	184	0.53137726
4844	GO:0006725	cellular aromatic compou	0.42	2	0.7490637	185	0.53426516
9486	GO:0016298	lipase activity	0.42	2	0.7490637	185	0.53426516
5726	GO:0008187	poly-pyrimidine tract bindi	0.42	1	0.37453184	70	0.20215438
5788	GO:0008266	poly(U) RNA binding	0.42	1	0.37453184	70	0.20215438
23522	GO:0048046	apoplast	0.42	1	0.37453184	70	0.20215438
13041	GO:0030554	adenyl nucleotide binding	0.42	5	1.8726592	550	1.5883559
14965	GO:0032559	adenyl ribonucleotide bin	0.42	5	1.8726592	550	1.5883559
6475	GO:0009108	coenzyme biosynthetic pr	0.43	1	0.37453184	72	0.20793022
9764	GO:0016701	oxidoreductase activity, a	0.43	1	0.37453184	72	0.20793022
3068	GO:0004386	helicase activity	0.43	2	0.7490637	189	0.54581684
3306	GO:0004674|GO:000469	protein serine/threonine k	0.43	9	3.3707864	1062	3.0669708
3311	GO:0004683|GO:000468	calmodulin-dependent pro	0.44	1	0.37453184	74	0.21370606
25510	GO:0051213	dioxygenase activity	0.44	1	0.37453184	75	0.21659398
28365	GO:0065008	regulation of biological qu	0.44	3	1.1235955	316	0.9125827
2897	GO:0004091|GO:000430	carboxylesterase activity	0.44	2	0.7490637	194	0.5602564
2819	GO:0004004	ATP-dependent RNA heli	0.45	1	0.37453184	78	0.22525774
5725	GO:0008186|GO:000401	RNA-dependent ATPase	0.45	1	0.37453184	78	0.22525774
30865	GO:0072509	divalent inorganic cation t	0.45	1	0.37453184	78	0.22525774
2654	GO:0003724	RNA helicase activity	0.46	1	0.37453184	80	0.2310336
23515	GO:0048037	cofactor binding	0.46	3	1.1235955	327	0.94434977
29202	GO:0070838	divalent metal ion transpo	0.47	1	0.37453184	82	0.23680943
16738	GO:0034357	photosynthetic membrane	0.47	1	0.37453184	83	0.23969735
4954	GO:0006869	lipid transport	0.48	2	0.7490637	208	0.6006873
8085	GO:0010876	lipid localization	0.48	2	0.7490637	208	0.6006873
4912	GO:0006813|GO:001545	potassium ion transport	0.48	1	0.37453184	84	0.24258527
30168	GO:0071804	cellular potassium ion tra	0.48	1	0.37453184	84	0.24258527
30169	GO:0071805	potassium ion transmemb	0.48	1	0.37453184	84	0.24258527
30867	GO:0072511	divalent inorganic cation t	0.48	1	0.37453184	84	0.24258527
9295	GO:0016053	organic acid biosynthetic	0.49	2	0.7490637	211	0.6093511
21058	GO:0045454|GO:003050	cell redox homeostasis	0.49	2	0.7490637	211	0.6093511
21922	GO:0046394	carboxylic acid biosynthet	0.49	2	0.7490637	211	0.6093511
5768	GO:0008238	exopeptidase activity	0.49	1	0.37453184	86	0.24836111
22376	GO:0046873	metal ion transmembrane	0.49	2	0.7490637	213	0.6151269
20624	GO:0044430	cytoskeletal part	0.49	1	0.37453184	88	0.25413695
20630	GO:0044436	thylakoid part	0.50	1	0.37453184	90	0.2599128
17617	GO:0035251	UDP-glucosyltransferase	0.50	2	0.7490637	218	0.62956655
3644	GO:0005102	receptor binding	0.51	1	0.37453184	91	0.2628007
3808	GO:0005351|GO:000540	sugar:hydrogen symporte	0.52	1	0.37453184	94	0.27146447
3835	GO:0005402	cation:sugar symporter ac	0.52	1	0.37453184	94	0.27146447
6863	GO:0009579	thylakoid	0.52	1	0.37453184	94	0.27146447
10058	GO:0017111	nucleoside-triphosphatase	0.52	7	2.621723	878	2.5355935
3472	GO:0004866	endopeptidase inhibitor a	0.52	1	0.37453184	95	0.27435237
8159	GO:0010951	negative regulation of en	0.52	1	0.37453184	95	0.27435237
11712	GO:0019748	secondary metabolic proc	0.52	1	0.37453184	95	0.27435237
26712	GO:0052548	regulation of endopeptida	0.52	1	0.37453184	95	0.27435237
28101	GO:0061135	endopeptidase regulator a	0.52	1	0.37453184	95	0.27435237
6796	GO:0009507	chloroplast	0.53	2	0.7490637	229	0.6613336
13531	GO:0031072	heat shock protein binding	0.53	2	0.7490637	230	0.6642216
8677	GO:0015295	solute:hydrogen symporte	0.53	1	0.37453184	98	0.28301615
25379	GO:0051082	unfolded protein binding	0.53	1	0.37453184	98	0.28301615
4612	GO:0006468	protein phosphorylation	0.54	17	6.367041	2205	6.367863
11695	GO:0019725	cellular homeostasis	0.54	2	0.7490637	234	0.67577326
4320	GO:0006082	organic acid metabolic pr	0.54	3	1.1235955	369	1.0656425
11716	GO:0019752	carboxylic acid metabolic	0.54	3	1.1235955	369	1.0656425
19707	GO:0043436	oxoacid metabolic proces	0.54	3	1.1235955	369	1.0656425
11202	GO:0019199	transmembrane receptor	0.55	4	1.4981273	504	1.4555116
5874	GO:0008374	O-acyltransferase activity	0.55	1	0.37453184	102	0.29456782
18925	GO:0042592	homeostatic process	0.55	2	0.7490637	238	0.68732494
4405	GO:0006195	purine nucleotide catabol	0.55	6	2.247191	773	2.232362
6508	GO:0009143	nucleoside triphosphate c	0.55	6	2.247191	773	2.232362
6509	GO:0009144	purine nucleoside triphos	0.55	6	2.247191	773	2.232362
6511	GO:0009146	purine nucleoside triphos	0.55	6	2.247191	773	2.232362
6519	GO:0009154	purine ribonucleotide cata	0.55	6	2.247191	773	2.232362
6530	GO:0009166	nucleotide catabolic proce	0.55	6	2.247191	773	2.232362
6567	GO:0009203	ribonucleoside triphospha	0.55	6	2.247191	773	2.232362
6569	GO:0009205	purine ribonucleoside trip	0.55	6	2.247191	773	2.232362
6571	GO:0009207	purine ribonucleoside trip	0.55	6	2.247191	773	2.232362
6624	GO:0009261	ribonucleotide catabolic p	0.55	6	2.247191	773	2.232362
17034	GO:0034655	nucleobase, nucleoside, r	0.55	6	2.247191	773	2.232362
17035	GO:0034656	nucleobase, nucleoside a	0.55	6	2.247191	773	2.232362
22209	GO:0046700	heterocycle catabolic pro	0.55	6	2.247191	773	2.232362
30879	GO:0072523	purine-containing compou	0.55	6	2.247191	773	2.232362
4408	GO:0006200	ATP catabolic process	0.55	5	1.8726592	641	1.8511566
9918	GO:0016887|GO:000400	ATPase activity	0.55	5	1.8726592	641	1.8511566
21600	GO:0046034	ATP metabolic process	0.55	5	1.8726592	641	1.8511566
19525	GO:0043226	organelle	0.55	23	8.614232	3013	8.701303
19528	GO:0043229	intracellular organelle	0.55	23	8.614232	3013	8.701303
9709	GO:0016627	oxidoreductase activity, a	0.55	1	0.37453184	104	0.30034366
20520	GO:0044270	cellular nitrogen compoun	0.56	6	2.247191	777	2.2439137
2668	GO:0003779	actin binding	0.56	1	0.37453184	105	0.3032316
3195	GO:0004540	ribonuclease activity	0.56	1	0.37453184	106	0.3061195
9493	GO:0016310	phosphorylation	0.56	19	7.116105	2504	7.2313514
6824	GO:0009536	plastid	0.57	2	0.7490637	247	0.7133162
6563	GO:0009199	ribonucleoside triphospha	0.57	6	2.247191	790	2.2814567
6515	GO:0009150	purine ribonucleotide met	0.57	6	2.247191	791	2.2843447
7690	GO:0010466	negative regulation of pep	0.57	1	0.37453184	110	0.31767118
12946	GO:0030414	peptidase inhibitor activity	0.57	1	0.37453184	110	0.31767118
25636	GO:0051346	negative regulation of hyd	0.57	1	0.37453184	110	0.31767118
6506	GO:0009141	nucleoside triphosphate m	0.58	6	2.247191	796	2.2987843
3304	GO:0004672|GO:005022	protein kinase activity	0.58	10	3.7453184	1333	3.8495972
26711	GO:0052547	regulation of peptidase ac	0.58	1	0.37453184	112	0.32344702
28100	GO:0061134	peptidase regulator activit	0.58	1	0.37453184	112	0.32344702
4850	GO:0006732|GO:000675	coenzyme metabolic proc	0.58	1	0.37453184	113	0.32633495

9535	GO:0016407	acetyltransferase activity	0.59	1	0.37453184	115	0.3321108
4373	GO:0006163	purine nucleotide metabol	0.60	6	2.247191	810	2.339215
26845	GO:0052689	carboxylic ester hydrolase	0.60	4	1.4981273	538	1.5537009
6622	GO:0009259|GO:0009121	ribonucleotide metabolic p	0.60	6	2.247191	812	2.344991
9285	GO:0016043	cellular component organi	0.60	2	0.7490637	261	0.7537471
25416	GO:0051119	sugar transmembrane tra	0.60	1	0.37453184	118	0.34077454
9824	GO:0016773	phosphotransferase activi	0.60	11	4.11985	1493	4.311664
9579	GO:0016462	pyrophosphatase activity	0.61	7	2.621723	954	2.7550755
9859	GO:0016818	hydrolase activity, acting	0.61	7	2.621723	956	2.7608514
19126	GO:0042803	protein homodimerization	0.61	2	0.7490637	265	0.7652988
22007	GO:0046483	heterocycle metabolic pro	0.61	8	2.9962547	1094	3.1593843
9858	GO:0016817	hydrolase activity, acting	0.61	7	2.621723	959	2.769515
6884	GO:0009607	response to biotic stimulu	0.61	1	0.37453184	122	0.3523262
30877	GO:0072521	purine-containing compou	0.62	6	2.247191	827	2.3883097
22049	GO:0046527	glucosyltransferase activi	0.62	2	0.7490637	270	0.77973837
4121	GO:0005856	cytoskeleton	0.62	1	0.37453184	126	0.3638779
19125	GO:0042802	identical protein binding	0.63	5	1.8726592	697	2.01288
4649	GO:0006520|GO:0006519	cellular amino acid metab	0.63	2	0.7490637	277	0.7999538
9823	GO:0016772	transferase activity, transf	0.63	14	5.243446	1932	5.579461
3874	GO:0005509	calcium ion binding	0.64	2	0.7490637	279	0.8057296
2758	GO:0003924	GTPase activity	0.64	1	0.37453184	132	0.3812054
4394	GO:0006184	GTP catabolic process	0.64	1	0.37453184	132	0.3812054
21605	GO:0046039	GTP metabolic process	0.64	1	0.37453184	132	0.3812054
4215	GO:0005975	carbohydrate metabolic p	0.64	7	2.621723	990	2.8590407
3490	GO:0004888|GO:0004926	transmembrane receptor a	0.64	4	1.4981273	571	1.6490022
20532	GO:0044282	small molecule catabolic	0.65	6	2.247191	854	2.4662836
30205	GO:0071841	cellular component organi	0.65	2	0.7490637	285	0.8230572
9811	GO:0016757|GO:0016932	transferase activity, transf	0.66	5	1.8726592	729	2.1052935
6046	GO:0008610	lipid biosynthetic process	0.67	1	0.37453184	141	0.4071967
8676	GO:0015294	solute:cation symporter ac	0.67	1	0.37453184	141	0.4071967
8557	GO:0015144	carbohydrate transmembr	0.67	1	0.37453184	143	0.41297254
16602	GO:0034219	carbohydrate transmembr	0.67	1	0.37453184	143	0.41297254
3873	GO:0005507	copper ion binding	0.68	1	0.37453184	146	0.42163628
20356	GO:0044106	cellular amine metabolic p	0.68	2	0.7490637	303	0.8750397
6071	GO:0008643|GO:0006861	carbohydrate transport	0.68	1	0.37453184	147	0.42452422
20517	GO:0044267	cellular protein metabolic	0.68	23	8.614232	3225	9.313541
9801	GO:0016747	transferase activity, transf	0.69	3	1.1235955	456	1.3168914
11426	GO:0019438	aromatic compound biosy	0.69	1	0.37453184	149	0.43030006
20498	GO:0044248	cellular catabolic process	0.69	6	2.247191	894	2.5818002
9488	GO:0016301	kinase activity	0.69	12	4.494382	1740	5.0249805
3200	GO:0004553|GO:0016800	hydrolase activity, hydroly	0.70	2	0.7490637	312	0.90103096
5791	GO:0008270	zinc ion binding	0.70	13	4.8689137	1880	5.4292893
8517	GO:0015103	inorganic anion transmem	0.70	1	0.37453184	154	0.44473964
11224	GO:0019222	regulation of metabolic pr	0.70	22	8.2397	3115	8.995871
6662	GO:0009308	amine metabolic process	0.70	2	0.7490637	314	0.9068068
13656	GO:0031224	intrinsic to membrane	0.70	8	2.9962547	1193	3.4452884
2975	GO:0004175|GO:0016809	endopeptidase activity	0.71	2	0.7490637	320	0.9241344
4867	GO:0006753	nucleoside phosphate me	0.71	6	2.247191	914	2.6395588
6484	GO:0009117	nucleotide metabolic proc	0.71	6	2.247191	914	2.6395588
5732	GO:0008194	UDP-glycosyltransferase	0.71	2	0.7490637	322	0.9299102
18582	GO:0042221	response to chemical stim	0.72	2	0.7490637	328	0.94723773
12572	GO:0022890|GO:0015082	inorganic cation transmen	0.73	2	0.7490637	332	0.9587894
12516	GO:0022804	active transmembrane tra	0.73	5	1.8726592	787	2.2727928
20618	GO:0044424	intracellular part	0.73	27	10.11236	3853	11.127155
6077	GO:0008652	cellular amino acid biosyn	0.73	1	0.37453184	169	0.48805845
26932	GO:0055086	nucleobase, nucleoside a	0.74	6	2.247191	944	2.7261963
9800	GO:0016746	transferase activity, transf	0.74	3	1.1235955	498	1.438184
4067	GO:0005783	endoplasmic reticulum	0.74	1	0.37453184	174	0.50249803
20619	GO:0044425	membrane part	0.74	10	3.7453184	1523	4.398302
8967	GO:0015698	inorganic anion transport	0.74	1	0.37453184	176	0.5082739
20533	GO:0044283	small molecule biosynthet	0.75	2	0.7490637	347	1.0021082
6166	GO:0008757	S-adenosylmethionine-de	0.75	1	0.37453184	180	0.5198256
5195	GO:0007165|GO:0023033	signal transduction	0.75	6	2.247191	961	2.775291
12602	GO:0023052|GO:0023046	signaling	0.75	6	2.247191	961	2.775291
6663	GO:0009309	amine biosynthetic proces	0.75	1	0.37453184	181	0.5227135
9818	GO:0016765|GO:0016766	transferase activity, transf	0.76	1	0.37453184	185	0.53426516
22479	GO:0046983	protein dimerization activi	0.76	3	1.1235955	517	1.4930545
3476	GO:0004872|GO:0019041	receptor activity	0.76	4	1.4981273	672	1.9406822
2657	GO:0003727|GO:0003728	single-stranded RNA bind	0.77	1	0.37453184	188	0.54292893
30204	GO:0071840	cellular component organi	0.77	2	0.7490637	362	1.045427
30066	GO:0071702	organic substance transpo	0.78	3	1.1235955	529	1.5277096
20521	GO:0044271	cellular nitrogen compoun	0.78	2	0.7490637	367	1.0598665
31465	GO:0080090	regulation of primary meta	0.78	18	6.741573	2710	7.826263
28378	GO:0070011	peptidase activity, acting	0.79	3	1.1235955	537	1.550813
12608	GO:0030001	metal ion transport	0.79	2	0.7490637	374	1.080082
5840	GO:0008324	cation transmembrane tra	0.79	3	1.1235955	538	1.5537009
10244	GO:0018130	heterocycle biosynthetic p	0.79	1	0.37453184	199	0.57469606
9836	GO:0016787	hydrolase activity	0.80	25	9.363296	3723	10.751725
8943	GO:0015672	monovalent inorganic cati	0.80	2	0.7490637	383	1.1060733
9266	GO:0016020	membrane	0.80	25	9.363296	3741	10.803708
13753	GO:0031323	regulation of cellular meta	0.81	18	6.741573	2770	7.999538
5766	GO:0008236	serine-type peptidase acti	0.81	1	0.37453184	214	0.6180149
8495	GO:0015077	monovalent inorganic cati	0.81	1	0.37453184	214	0.6180149
25094	GO:0050789|GO:0050791	regulation of biological pro	0.81	29	10.8614235	4315	12.461374
4609	GO:0006464	protein modification proce	0.81	18	6.741573	2781	8.031305
15436	GO:0033036	macromolecule localizatio	0.81	2	0.7490637	397	1.1465042
5763	GO:0008233	peptidase activity	0.81	3	1.1235955	565	1.6316746
9845	GO:0016798	hydrolase activity, acting	0.82	2	0.7490637	401	1.1580559
4558	GO:0006396|GO:0006394	RNA processing	0.82	1	0.37453184	219	0.63245445
20531	GO:0044281	small molecule metabolic	0.82	11	4.11985	1788	5.1636004
10103	GO:0017171	serine hydrolase activity	0.82	1	0.37453184	220	0.63534236
6425	GO:0009056	catabolic process	0.82	6	2.247191	1051	3.0352037
8673	GO:0015291|GO:0015290	secondary active transme	0.82	2	0.7490637	407	1.1753833
11221	GO:0019219	regulation of nucleobase,	0.83	17	6.367041	2675	7.7251854
25468	GO:0051171	regulation of nitrogen com	0.83	17	6.367041	2675	7.7251854
4990	GO:0006915|GO:0008632	apoptosis	0.83	1	0.37453184	227	0.6555578
28364	GO:0065007	biological regulation	0.83	29	10.8614235	4376	12.637537
4755	GO:0006629	lipid metabolic process	0.84	3	1.1235955	590	1.7038727
9906	GO:0016874	ligase activity	0.84	3	1.1235955	597	1.7240882
11828	GO:0019899	enzyme binding	0.84	1	0.37453184	237	0.684437
5756	GO:0008219	cell death	0.84	1	0.37453184	239	0.69021285
8209	GO:0012501|GO:0016244	programmed cell death	0.84	1	0.37453184	239	0.69021285
9462	GO:0016265	death	0.84	1	0.37453184	239	0.69021285
25098	GO:0050794|GO:0051244	regulation of cellular proc	0.84	26	9.737827	3987	11.514136
11522	GO:0019538|GO:0006411	protein metabolic process	0.85	27	10.11236	4134	11.938661
5712	GO:0008168|GO:0004480	methyltransferase activity	0.85	1	0.37453184	244	0.7046524
5981	GO:0008509	anion transmembrane tra	0.85	1	0.37453184	245	0.70754033
4917	GO:0006820|GO:0006822	anion transport	0.85	1	0.37453184	247	0.7133162
5661	GO:0008092	cytoskeletal protein bindir	0.86	1	0.37453184	249	0.719092
12805	GO:0030246	carbohydrate binding	0.86	1	0.37453184	251	0.7248679
3475	GO:0004871|GO:0005062	signal transducer activity	0.86	4	1.4981273	787	2.2727928
27063	GO:0060089	molecular transducer acti	0.86	4	1.4981273	787	2.2727928
19684	GO:0043412	macromolecule modificati	0.86	18	6.741573	2900	8.374968

9795	GO:0016740	transferase activity	0.86	24	8.988764	3764	10.870131
9796	GO:0016741	transferase activity, transf	0.87	1	0.37453184	261	0.7537471
25998	GO:0051716	cellular response to stimu	0.88	6	2.247191	1138	3.2864528
8494	GO:0015075	ion transmembrane transp	0.88	4	1.4981273	827	2.3883097
16603	GO:0034220	ion transmembrane transp	0.89	4	1.4981273	833	2.4056373
4911	GO:0006812|GO:0006819	cation transport	0.89	3	1.1235955	662	1.9118029
14667	GO:0032259	methylation	0.89	1	0.37453184	285	0.8230572
4916	GO:0006818	hydrogen transport	0.90	1	0.37453184	292	0.84327257
9246	GO:0015992	proton transport	0.90	1	0.37453184	292	0.84327257
9812	GO:0016758	transferase activity, transf	0.90	2	0.7490637	501	1.4468478
22415	GO:0046914	transition metal ion bindin	0.91	15	5.6179776	2599	7.5057034
7141	GO:0009889	regulation of biosynthetic	0.91	15	5.6179776	2605	7.523031
7772	GO:0010556	regulation of macromolec	0.91	15	5.6179776	2605	7.523031
13756	GO:0031326	regulation of cellular biosy	0.91	15	5.6179776	2605	7.523031
32213	GO:2000112	regulation of cellular macr	0.91	15	5.6179776	2605	7.523031
20640	GO:0044446	intracellular organelle par	0.91	3	1.1235955	710	2.0504231
20616	GO:0044422	organelle part	0.91	3	1.1235955	712	2.0561988
7692	GO:0010468	regulation of gene expres	0.92	15	5.6179776	2635	7.6096687
4849	GO:0006730|GO:0019753	one-carbon metabolic pro	0.92	1	0.37453184	325	0.93857396
3449	GO:0004842|GO:0004840	ubiquitin-protein ligase ac	0.92	1	0.37453184	326	0.94146186
27228	GO:0060255	regulation of macromolec	0.92	15	5.6179776	2660	7.6818666
5909	GO:0008415	acyltransferase activity	0.92	1	0.37453184	330	0.95301354
2643	GO:0003700|GO:0000130	sequence-specific DNA b	0.92	7	2.621723	1417	4.0921826
716	GO:0001071	nucleic acid binding trans	0.92	7	2.621723	1417	4.0921826
9654	GO:0016567	protein ubiquitination	0.92	1	0.37453184	332	0.9587894
14854	GO:0032446	protein modification by sm	0.92	1	0.37453184	332	0.9587894
29011	GO:0070647	protein modification by sm	0.92	1	0.37453184	332	0.9587894
3903	GO:0005575|GO:0008372	cellular_component	0.93	56	20.973783	8515	24.590637
22375	GO:0046872	metal ion binding	0.93	17	6.367041	2985	8.6204405
11747	GO:0019787|GO:0008639	small conjugating protein	0.93	1	0.37453184	339	0.9790048
9267	GO:0016021	integral to membrane	0.93	5	1.8726592	1103	3.1853757
19470	GO:0043167	ion binding	0.93	17	6.367041	2997	8.655096
19472	GO:0043169	cation binding	0.93	17	6.367041	2997	8.655096
2674	GO:0003824	catalytic activity	0.94	72	26.966291	10750	31.045137
3178	GO:0004519	endonuclease activity	0.94	1	0.37453184	356	1.0280994
4910	GO:0006811	ion transport	0.94	4	1.4981273	959	2.769515
4530	GO:0006355|GO:0032583	regulation of transcription	0.94	14	5.243446	2591	7.4826
25544	GO:0051252	regulation of RNA metabo	0.94	14	5.243446	2593	7.488376
4641	GO:0006508	proteolysis	0.94	4	1.4981273	965	2.7868426
12547	GO:0022857|GO:0005386	transmembrane transporte	0.94	7	2.621723	1483	4.282785
22409	GO:0046906	tetrapyrrole binding	0.95	2	0.7490637	596	1.7212002
3723	GO:0005215|GO:0005478	transporter activity	0.95	9	3.3707864	1844	5.325324
9913	GO:0016881	acid-amino acid ligase ac	0.95	1	0.37453184	391	1.1291766
3945	GO:0005622	intracellular	0.95	28	10.486892	4751	13.720507
26931	GO:0055085	transmembrane transport	0.96	7	2.621723	1548	4.4705
25195	GO:0050896|GO:0051869	response to stimulus	0.96	9	3.3707864	1881	5.432177
3946	GO:0005623	cell	0.96	52	19.475655	8227	23.758917
20657	GO:0044464	cell part	0.96	52	19.475655	8227	23.758917
19533	GO:0043234	protein complex	0.96	3	1.1235955	848	2.448956
3177	GO:0004518	nuclease activity	0.96	1	0.37453184	427	1.2331418
12574	GO:0022892	substrate-specific transpo	0.97	6	2.247191	1463	4.2250266
9911	GO:0016879	ligase activity, forming ca	0.97	1	0.37453184	456	1.3168914
4909	GO:0006810|GO:0015457	transport	0.97	11	4.11985	2315	6.6855345
25529	GO:0051234	establishment of localizati	0.97	11	4.11985	2315	6.6855345
25476	GO:0051179	localization	0.97	11	4.11985	2319	6.697086
3863	GO:0005488	binding	0.98	92	34.45693	13903	40.15075
9869	GO:0016829	lyase activity	0.98	1	0.37453184	488	1.4093049
11931	GO:0020037	heme binding	0.99	1	0.37453184	550	1.5883559
3955	GO:0005634	nucleus	0.99	5	1.8726592	1433	4.138389
12573	GO:0022891	substrate-specific transme	0.99	4	1.4981273	1241	3.5839086
3872	GO:0005506	iron ion binding	0.99	1	0.37453184	563	1.6258988
19526	GO:0043227	membrane-bounded orga	0.99	8	2.9962547	2142	6.185924
19530	GO:0043231	intracellular membrane-bo	0.99	8	2.9962547	2142	6.185924
3876	GO:0005515|GO:0045308	protein binding	1.00	34	12.734082	6933	20.021948
2626	GO:0003674|GO:0005554	molecular_function	1.00	157	58.8015	24394	70.447914