Table S4. Differentially regulated genes (up and down regulated) in the control compared with THyPRP silenced plants in FAZ at 8 h along with their expression values, fold changes, annotations, GO ids and terms.

Worksheet 2 & 3

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.

Set3					
Line	Array	Details	Time	Treated vs. Con	Set
Control – New Yorker	254331010026_1_1	8h_5_AZ	8h	Control	Set 3
Control – New Yorker	254331010026_1_2	8h_6_AZ	8h		
TAPG + TPRP	254331010035_1_1	8h_41_AZ	8h	Treated	
TAPG + TPRP	254331010035_1_2	8h_42_AZ	8h		

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

Differentially Regulated Probes

Sample	Up	Down
8h_TPRP_ AZ vs. 8h_Control_AZ_Sense	1314	2139
8h_TPRP_ AZ vs. 8h_Control_AZ_Antisense	424	1983

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.

		8h_AZ_Control					8h_AZ_TAPG + TPRP vs. 8h_AZ_Control					
ProbeNar	Orientatio	Fold 8h	Flag 8h	Fold 8h	Flag 8h	Geomean	Fold 8h	Flag 8h	Fold 8h	Flag 8h	Geomean	P-value
A 96 P00	Sense	-0.258	Detected	0.258	Detected	0.000	0.934	Detected	1.130	Detected	1.032	0.065
A 96 P00	Sense	-0.518	Detected	0.518	Detected	0.000	3.917	Detected	1.676	Detected	2.796	0.152
A 96 P00	Sense	0.030	Detected	-0.030	Detected	0.000	1.607	Detected	1.029	Detected	1.318	0.045
A 96 P00	Sense	-0.462	Detected	0.462	Detected	0.000	1.670	Detected	1.278	Detected	1.474	0.099
A 96 P00	Sense	0.204	Detected	-0.204	Detected	0.000	1.288	Detected	1.298	Detected	1.293	0.024
A 96 P00	Sense	-0.070	Detected	0.070	Detected	0.000	1.490	Detected	1.642	Detected	1.566	0.004
A 96 P01	Sense	-0.023	Detected	0.023	Detected	0.000	1.612	Detected	1.610	Detected	1.611	0.000
A 96 P01	Sense	0.106	Detected	-0.106	Detected	0.000	1.581	Detected	0.966	Detected	1.274	0.059
A 96 P01	Sense	-0.113	Detected	0.113	Detected	0.000	1.539	Detected	1.004	Detected	1.272	0.048
A 96 P02	Sense	-0.078	Detected	0.078	Detected	0.000	1.530	Detected	1.320	Detected	1.425	0.008
A 96 P02	Sense	0.117	Detected	-0.117	Detected	0.000	1.309	Detected	1.180	Detected	1.244	0.011
A 96 P02	Sense	0.020	Detected	-0.020	Detected	0.000	1.364	Detected	1.075	Detected	1.219	0.014
A 96 P02	Sense	0.420	Detected	-0.420	Detected	0.000	1.247	Detected	1.436	Detected	1.342	0.089
A 96 P02	Sense	-0.079	Detected	0.079	Detected	0.000	1.247	Detected	1.035	Detected	1.141	0.013
A 96 P02	Sense	-0.152	Detected	0.152	Detected	0.000	1.611	Detected	1.141	Detected	1.376	0.039
A 96 P02	Sense	-0.170	Comprom	0.170	Comprom	0.000	1.859	Detected	1.739	Detected	1.799	0.010
A 96 P02	Sense	0.190	Detected	-0.190	Detected	0.000	2.908	Detected	1.912	Detected	2.410	0.046
A 96 P02	Sense	-0.033	Detected	0.033	Detected	0.000	1.555	Detected	1.225	Detected	1.390	0.014
A 96 P02	Sense	-0.178	Comprom	0.178	Comprom	0.000	2.171	Detected	1.726	Detected	1.948	0.021
A 96 P02	Sense	0.017	Detected	-0.017	Detected	0.000	1.437	Detected	1.007	Detected	1.222	0.030
A 96 P02	Sense	-0.088	Detected	0.088	Detected	0.000	1.369	Detected	1.051	Detected	1.210	0.022
A 96 P02	Sense	-0.230	Detected	0.230	Detected	0.000	1.839	Detected	1.234	Detected	1.536	0.056
A 96 P02	Sense	0.256	Detected	-0.256	Detected	0.000	1.597	Detected	0.964	Detected	1.280	0.088
A 96 P03	Sense	0.167	Detected	-0.167	Detected	0.000	1.823	Detected	1.674	Detected	1.749	0.011
A 96 P03	Sense	-0.388	Detected	0.388	Detected	0.000	1.264	Detected	0.815	Detected	1.039	0.146
A 96 P03	Sense	0.137	Detected	-0.137	Detected	0.000	1.173	Detected	1.219	Detected	1.196	0.013
A 96 P03	Sense	0.169	Detected	-0.169	Detected	0.000	1.289	Detected	0.996	Detected	1.143	0.036
A 96 P03	Sense	-0.196	Detected	0.196	Detected	0.000	1.661	Detected	1.317	Detected	1.489	0.029
A 96 P03	Sense	0.100	Detected	-0.100	Detected	0.000	1.240	Detected	0.905	Detected	1.072	0.031
A 96 P03	Sense	-0.181	Detected	0.181	Detected	0.000	1.139	Detected	0.924	Detected	1.031	0.039
A 96 P03	Sense	0.050	Detected	-0.050	Detected	0.000	1.791	Detected	1.338	Detected	1.564	0.021
A 96 P03	Sense	0.334	Detected	-0.334	Comprom	0.000	1.791	Detected	1.237	Detected	1.514	0.073
A 96 P03	Sense	-0.147	Detected	0.147	Detected	0.000	1.974	Detected	1.607	Detected	1.791	0.017
A 96 P04	Sense	0.117	Detected	-0.117	Detected	0.000	1.289	Detected	1.020	Detected	1.154	0.023
A 96 P04	Sense	0.396	Detected	-0.396	Detected	0.000	1.234	Detected	0.947	Detected	1.091	0.122
A 96 P04	Sense	0.202	Detected	-0.202	Detected	0.000	1.121	Detected	1.036	Detected	1.079	0.035
A 96 P04	Sense	0.084	Detected	-0.084	Detected	0.000	1.120	Detected	0.932	Detected	1.026	0.015
A 96 P04	Sense	0.140	Detected	-0.140	Detected	0.000	1.222	Detected	1.152	Detected	1.187	0.014
A 96 P05	Sense	-0.461	Comprom	0.461	Detected	0.000	1.438	Detected	1.088	Detected	1.263	0.125
A 96 P05	Sense	0.113	Detected	-0.113	Detected	0.000	1.484	Detected	1.206	Detected	1.345	0.017
A 96 P05	Sense	0.130	Detected	-0.130	Detected	0.000	1.803	Detected	0.916	Detected	1.359	0.099
A 96 P05	Sense	-0.230	Detected	0.230	Detected	0.000	1.650	Detected	1.333	Detected	1.491	0.033
A 96 P05	Sense	0.054	Detected	-0.054	Detected	0.000	1.474	Detected	1.224	Detected	1.349	0.010
A 96 P06	Sense	0.500	Detected	-0.500	Detected	0.000	2.012	Detected	1.944	Detected	1.978	0.059
A 96 P06	Sense	-0.012	Detected	0.012	Detected	0.000	1.087	Detected	0.954	Detected	1.020	0.004
A 96 P06	Sense	-0.178	Detected	0.178	Detected	0.000	1.105	Detected	0.997	Detected	1.051	0.030
A 96 P06	Sense	0.083	Detected	-0.083	Detected	0.000	1.235	Detected	1.139	Detected	1.187	0.006
A 96 P06	Sense	-0.006	Detected	0.006	Detected	0.000	1.397	Detected	0.974	Detected	1.185	0.030
A 96 P06	Sense	0.427	Comprom	-0.427	Comprom	0.000	3.711	Detected	3.046	Detected	3.379	0.025
A 96 P06	Sense	0.589	Detected	-0.589	Comprom	0.000	1.827	Detected	1.585	Detected	1.706	0.105
A 96 P06	Sense	0.099	Detected	-0.099	Detected	0.000	1.437	Detected	0.968	Detected	1.202	0.042
A 96 P07	Sense	-0.344	Detected	0.344	Detected	0.000	1.688	Detected	1.020	Detected	1.354	0.106
A 96 P07	Sense	-0.217	Detected	0.217	Detected	0.000	1.966	Detected	0.923	Detected	1.444	0.125
A 96 P07	Sense	0.036	Detected	-0.036	Detected	0.000	1.872	Detected	1.693	Detected	1.783	0.003
A 96 P07	Sense	-1.056	Detected	1.056	Detected	0.000	2.523	Detected	1.322	Detected	1.922	0.254
A 96 P07	Sense	-0.022	Detected	0.022	Detected	0.000	1.893	Detected	0.916	Detected	1.404	0.103
A 96 P07	Sense	0.023	Detected	-0.023	Detected	0.000	1.480	Detected	1.335	Detected	1.408	0.003
A 96 P07	Sense	0.206	Detected	-0.206	Detected	0.000	1.510	Detected	1.177	Detected	1.343	0.037
A 96 P07	Sense	-0.166	Detected	0.166	Detected	0.000	2.904	Detected	2.774	Detected	2.839	0.004
A 96 P08	Sense	0.065	Detected	-0.065	Detected	0.000	2.059	Detected	1.105	Detected	1.582	0.081
A 96 P08	Sense	-0.191	Detected	0.191	Detected	0.000	1.539	Detected	1.190	Detected	1.364	0.034
A 96 P08	Sense	0.294	Detected	-0.294	Detected	0.000	1.449	Detected	1.300	Detected	1.375	0.045
A 96 P08	Sense	-0.386	Detected	0.386	Detected	0.000	1.976	Detected	1.621	Detected	1.798	0.052
A 96 P08	Sense	-0.342	Detected	0.342	Detected	0.000	1.852	Detected	0.868	Detected	1.360	0.151
A 96 P08	Sense	0.156	Detected	-0.156	Detected	0.000	1.622	Detected	1.352	Detected	1.487	0.019
A 96 P08	Sense	0.090	Detected	-0.090	Detected	0.000	1.535	Detected	1.276	Detected	1.405	0.012
A 96 P08	Sense	0.179	Detected	-0.179	Detected	0.000	1.602	Detected	1.350	Detected	1.476	0.021
A 96 P08	Sense	-0.107	Detected	0.107	Detected	0.000	1.246	Detected	1.327	Detected	1.286	0.008
A 96 P09	Sense	0.166	Detected	-0.166	Detected	0.000	1.067	Detected	0.935	Detected	1.001	0.030
A 96 P09	Sense	0.057	Detected	-0.057	Detected	0.000	1.642	Detected	1.628	Detected	1.635	0.001
A 96 P09	Sense	0.022	Detected	-0.022	Detected	0.000	2.235	Detected	1.776	Detected	2.005	0.013
A 96 P09	Sense	0.010	Detected	-0.010	Detected	0.000	1.448	Detected	0.965	Detected	1.207	0.038
A 96 P09	Sense	0.126	Detected	-0.126	Detected	0.000	2.216	Detected	2.151	Detected	2.183	0.004
A 96 P09	Sense	0.326	Detected	-0.326	Detected	0.000	2.542	Detected	2.651	Detected	2.597	0.016
A 96 P09	Sense	0.035	Detected	-0.035	Detected	0.000	1.175	Detected	1.198	Detected	1.187	0.001
A 96 P09	Sense	-0.048	Detected	0.048	Detected	0.000	1.043	Detected	0.966	Detected	1.004	0.004
A 96 P09	Sense	-0.192	Detected	0.192	Detected	0.000	1.152	Detected	1.028	Detected	1.090	0.033
A 96 P09	Sense	0.177	Detected	-0.177	Detected	0.000	1.148	Detected	0.992	Detected	1.070	0.031
A 96 P10	Sense	0.010	Detected	-0.010	Detected	0.000	1.350	Detected	0.931	Detected	1.141	0.032
A 96 P10	Sense	-0.023	Detected	0.023	Detected	0.000	1.266	Detected	1.079	Detected	1.173	0.007
A 96 P10	Sense	0.189	Detected	-0.189	Detected	0.000	1.765	Detected	1.090	Detected	1.428	0.066
A 96 P10	Sense	-0.217	Detected	0.217	Detected	0.000	1.164	Detected	1.322	Detected	1.243	0.033
A 96 P10	Sense	0.006	Detected	-0.006	Detected	0.000	1.713	Detected	1.629	Detected	1.671	0.001
A 96 P10	Sense	0.060	Detected	-0.060	Detected	0.000	1.451	Detected	2.608	Detected	2.030	0.073
A 96 P11	Sense	-0.255	Detected	0.255	Detected	0.000	1.103	Detected	0.912	Detected	1.008	0.066
A 96 P11	Sense	0.036	Detected	-0.036	Detected	0.000	1.058	Detected	1.054	Detected	1.056	0.001
A 96 P11	Sense	0.501	Detected	-0.501	Comprom	0.000	1.481	Detected	1.448	Detected	1.464	0.100
A 96 P11	Sense	0.121	Detected	-0.121	Detected	0.000	1.020	Detected	0.999	Detected	1.009	0.014
A 96 P11	Sense	0.099	Detected	-0.099	Detected	0.000	1.590	Detected	1.042	Detected	1.316	0.046
A 96 P11	Sense	-0.088	Detected	0.088	Detected	0.000	1.278	Detected	0.968	Detected	1.123	0.024
A 96 P11	Sense	0.119	Detected	-0.119	Detected	0.000	1.239	Detected	1.207	Detected	1.223	0.010
A 96 P11	Sense	-0.007	Detected	0.007	Detected	0.000	1.070	Detected	0.967	Detected	1.019	0.003
A 96 P12	Sense	0.004	Detected	-0.004	Detected	0.000	1.464	Detected	1.210	Detected	1.337	0.009
A 96 P12	Sense	0.065	Detected	-0.065	Detected	0.000	1.320	Detected	1.139	Detected	1.230	0.008
A 96 P12	Sense	-0.326	Comprom	0.326	Comprom	0.000	1.419	Detected	1.503	Detected	1.461	0.047
A 96 P13	Sense	0.376	Detected	-0.376	Detected	0.000	1.269	Detected	1.099	Detected	1.184	0.091
A 96 P13	Sense	0.285	Detected	-0.285	Detected	0.000	1.221	Detected	1.281	Detected	1.251	0.049
A 96 P13	Sense	0.524	Detected	-0.524	Detected	0.000	1.151	Detected	0.891	Detected	1.021	0.199
A 96 P13	Sense	-0.462	Detected	0.462	Detected	0.000	1.949	Detected	1.261	Detected	1.605	0.108
A 96 P13	Sense	0.133	Detected	-0.133	Detected	0.000	2.751	Detected	2.732	Detected	2.742	0.002
A 96 P13	Sense	-0.687	Comprom	0.687	Detected	0.000	4.724	Detected	2.397	Detected	3.561	0.119
A 96 P13	Sense	0.194	Detected	-0.194	Detected	0.000	1.118	Detected	1.120	Detected	1.119	0.029
A 96 P13	Sense	-0.082	Detected	0.082	Detected	0.000	1.404	Detected	0.824	Detected	1.114	0.066
A 96 P13	Sense	-0.223	Detected	0.223	Detected	0.000	1.054	Detected	1.215	Detected	1.134	0.041
A 96 P14	Sense	0.219	Detected	-0.219	Detected	0.000	2.144	Detected	2.167	Detected	2.156	0.010
A 96 P14	Sense	0.086	Detected	-0.086	Detected	0.000	1.724	Detected	0.944	Detected	1.334	0.079
A 96 P14	Sense	-0.037	Detected	0.037	Detected	0.000	1.500	Detected	0.804	Detected	1.152	0.081
A 96 P15	Sense	0.343	Detected	-0.343	Detected	0.000	2.237	Detected	2.314	Detected	2.275	0.022
A 96 P15	Sense	-0.548	Detected	0.548	Detected	0.000	1.675	Detected	1.673	Detected	1.674	0.092
A 96 P15	Sense	0.245	Detected	-0.245	Detected	0.000	1.707	Detected	1.407	Detected	1.557	0.032
A 96 P15	Sense	0.356	Detected	-0.356	Detected	0.000	1.515	Detected	2.124	Detected	1.820	0.060
A 96 P15	Sense	0.080	Detected	-0.080	Detected	0.000	1.213	Detected	0.953	Detected	1.083	0.019
A 96 P16	Sense	0.269	Detected	-0.269	Detected	0.000	1.270	Detected	1.019	Detected	1.144	0.061
A 96 P16	Sense	0.090	Detected	-0.090	Detected	0.000	1.049	Detected	0.964	Detected	1.007	0.010
A 96 P16	Sense	0.071	Detected	-0.071	Detected	0.000	1.594	Detected	0.929	Detected	1.262	0.065
A 96 P16	Sense	-0.199	Detected	0.199	Detected	0.000	1.686	Detected	1.314	Detected	1.500	0.031
A 96 P16	Sense	-0.125	Detected	0.125	Detected	0.000	1.246	Detected	1.278	Detected	1.262	0.010
A 96 P16	Sense	-0.066	Detected	0.066	Detected	0.000	1.368	Detected	0.961	Detected	1.164	0.032
A 96 P16	Sense	0.477	Detected	-0.477	Detected	0.000	1.269	Detected	1.074	Detected	1.172	0.138
A 96 P16	Sense	0.575	Detected	-0.575	Comprom	0.000	1.807	Detected	1.218	Detected	1.513	0.144
A 96 P17	Sense	0.730	Detected	-0.730	Detected	0.000	1.071	Detected	1.021	Detected	1.046	0.288
A 96 P17	Sense	-0.015	Comprom	0.015	Comprom	0.000	1.187	Detected	1.502	Detected	1.345	0.014
A 96 P17	Sense	-0.101	Detected	0.101	Detected	0.000	1.702	Detected	1.197	Detected	1.450	0.033
A 96 P17	Sense	-0.213	Detected	0.213	Detected	0.000	1.137	Detected	0.946	Detected	1.041	0.047
A 96 P17	Sense	-0.035	Detected	0.035	Detected	0.000	1.079	Detected	1.226	Detected	1.152	0.005
A 96 P17	Sense	0.067	Detected	-0.067	Detected	0.000	1.605	Detected	1.490	Detected	1.547	0.003
A 96 P17	Sense	-0.211	Detected	0.211	Detected	0.000	0.959	Detected	1.316	Detected	1.138	0.054
A 96 P17	Sense	-0.280	Detected	0.280	Detected	0.000	0.834	Detected	1.245	Detected	1.039	0.096
A 96 P17	Sense	0.153	Detected	-0.153	Detected	0.000	1.489	Detected	1.243	Detected	1.366	0.020
A 96 P17	Sense	-0.281	Detected	0.281	Detected	0.000	0.981	Detected	1.283	Detected	1.132	0.071
A 96 P17	Sense	-0.030	Detected	0.030	Detected	0.000	1.661	Detected	0.819	Detected	1.240	0.099
A 96 P17	Sense	-0.650	Detected	0.650	Detected	0.000	4.783	Detected	2.627	Detected	3.705	0.099
A 96 P17	Sense	0.110	Detected	-0.110	Detected	0.000	1.099	Detected	0.984	Detected	1.041	0.014
A 96 P17	Sense	0.134	Detected	-0.134	Detected	0.000	1.232	Detected	0.904	Detected	1.068	0.037
A 96 P17	Sense	-0.136	Detected	0.136	Detected	0.000	1.673	Detected	1.215	Detected	1.444	0.032
A 96 P18	Sense	-0.074	Detected	0.074	Comprom	0.000	1.382	Detected	0.805	Detected	1.094	0.067
A 96 P18	Sense	0.390	Detected	-0.390	Detected	0.000	1.437	Detected	1.097	Detected	1.267	0.097
A 96 P18	Sense	0.358	Detected	-0.358	Detected	0.000	1.173	Detected	0.934	Detected	1.053	0.108
A 96 P19	Sense	0.186	Detected	-0.186	Detected	0.000	1.966	Detected	1.084	Detected	1.525	0.086
A 96 P19	Sense	0.150	Detected	-0.150	Detected	0.000	1.409	Detected	1.597	Detected	1.503	0.014
A 96 P19	Sense	0.239	Detected	-0.239	Detected	0.000	1.196	Detected	0.856	Detected	1.026	0.073
A 96 P19	Sense	-0.090	Detected	0.090	Detected	0.000	1.479	Detected	1.032	Detected	1.256	0.035
A 96 P19	Sense	0.540	Detected	-0.540	Detected	0.000	1.290	Detected	1.012	Detected	1.151	0.175
A 96 P19	Sense	-0.673	Detected	0.673	Detected	0.000	4.472	Detected	2.051	Detected	3.262	0.143
A 96 P20	Sense	0.127	Detected	-0.127	Detected	0.000	0.901	Detected	1.208	Detected	1.055	0.034
A 96 P20	Sense	-0.086	Detected	0.086	Detected	0.000	1.465	Detected	1.340	Detected	1.403	0.006
A 96 P20	Sense	0.211	Detected	-0.211	Detected	0.000	1.519	Detected	1.390	Detected	1.454	0.022
A 96 P20	Sense	0.329	Detected	-0.329	Detected	0.000	1.803	Detected	1.832	Detected	1.818	0.031
A 96 P20	Sense	-0.002	Detected	0.002	Detected	0.000	1.619	Detected	1.484	Detected	1.552	0.002
A 96 P20	Sense	-0.053	Detected	0.053	Detected	0.000	1.617	Detected	1.041	Detected	1.329	0.045
A 96 P20	Sense	0.258	Detected	-0.258	Comprom	0.000	1.826	Detected	1.747	Detected	1.787	0.021
A 96 P20	Sense	0.412	Detected	-0.412	Comprom	0.000	1.982	Detected	1.680	Detected	1.831	0.053
A 96 P20	Sense	0.040	Detected	-0.040	Detected	0.000	1.719	Detected	1.136	Detected	1.427	0.040
A 96 P21	Sense	-0.106	Detected	0.106	Detected	0.000	1.416	Detected	1.294	Detected	1.355	0.008
A 96 P21	Sense	0.338	Detected	-0.338	Detected	0.000	2.453	Detected	2.435	Detected	2.444	0.019
A 96 P21	Sense	0.067	Detected	-0.067	Detected	0.000	1.405	Detected	0.918	Detected	1.161	0.044
A 96 P21	Sense	0.039	Detected	-0.039	Detected	0.000	1.311	Detected	1.163	Detected	1.237	0.005
A 96 P21	Sense	0.206	Detected	-0.206	Detected	0.000	1.772	Detected	1.394	Detected	1.583	0.030
A 96 P21	Sense	0.001	Detected	-0.001	Detected	0.000	1.860	Detected	1.725	Detected	1.793	0.001
A 96 P21	Sense	0.086	Detected	-0.086	Detected	0.000	1.421	Detected	1.374	Detected	1.397	0.004
A 96 P21	Sense	-0.242	Detected	0.242	Detected	0.000	1.234	Detected	1.471	Detected	1.352	0.038
A 96 P21	Sense	-0.172	Detected	0.172	Detected	0.000	1.380	Detected	1.393	Detected	1.387	0.015
A 96 P21	Sense	-0.166	Detected	0.166	Detected	0.000	1.525	Detected	1.083	Detected	1.304	0.042
A 96 P21	Sense	0.217	Detected	-0.217	Detected	0.000	1.425	Detected	1.272	Detected	1.348	0.028
A 96 P21	Sense	0.082	Detected	-0.082	Detected	0.000	2.611	Detected	2.581	Detected	2.596	0.001
A 96 P21	Sense	-0.056	Comprom	0.056	Comprom	0.000	3.430	Detected	3.218	Detected	3.324	0.001
A 96 P21	Sense	-0.101	Detected	0.101	Detected	0.000	1.317	Detected	0.920	Detected	1.118	0.037
A 96 P21	Sense	0.137	Detected	-0.137	Detected	0.000	2.070	Detected	2.024	Detected	2.047	0.005
A 96 P21	Sense	-0.249	Detected	0.249	Detected	0.000	0.999	Detected	1.358	Detected	1.179	0.062
A 96 P22	Sense	0.094	Detected	-0.094	Detected	0.000	1.534	Detected	1.052	Detected	1.293	0.038
A 96 P22	Sense	0.020	Detected	-0.020	Detected	0.000	1.417	Detected	1.072	Detected	1.244	0.019
A 96 P22	Sense	0.058	Detected	-0.058	Detected	0.000	2.086	Detected	2.026	Detected	2.056	0.001
A 96 P22	Sense	0.081	Detected	-0.081	Detected	0.000	1.004	Detected	1.065	Detected	1.035	0.007
A 96 P22	Sense	-0.080	Detected	0.080	Detected	0.000	1.009	Detected	1.150	Detected	1.080	0.010
A 96 P22	Sense	0.219	Detected	-0.219	Detected	0.000	1.497	Detected	1.482	Detected	1.490	0.021
A 96 P22	Sense	0.138	Detected	-0.138	Detected	0.000	1.854	Detected	1.558	Detected	1.706	0.014
A 96 P22	Sense	0.124	Detected	-0.124	Detected	0.000	1.418	Detected	1.081	Detected	1.249	0.027
A 96 P22	Sense	0.235	Comprom	-0.235	Comprom	0.000	1.866	Detected	1.808	Detected	1.837	0.016
A 96 P22	Sense	-0.030	Detected	0.030	Detected	0.000	1.750	Detected	1.519	Detected	1.634	0.005
A 96 P22	Sense	-0.471	Detected	0.471	Detected	0.000	1.517	Detected	1.372	Detected	1.445	0.094
A 96 P22	Sense	-0.039	Detected	0.039	Detected	0.000	1.454	Detected	1.025	Detected	1.240	0.030
A 96 P22	Sense	-0.188	Detected	0.188	Detected	0.000	1.291	Detected	1.213	Detected	1.252	0.023
A 96 P23	Sense	0.213	Detected	-0.213	Detected	0.000	1.382	Detected	0.909	Detected	1.145	0.069
A 96 P23	Sense	-0.128	Detected	0.128	Detected	0.000	1.099	Detected	0.969	Detected	1.034	0.019
A 96 P23	Sense	-0.043	Detected	0.043	Detected	0.000	1.198	Detected	0.916	Detected	1.057	0.019
A 96 P23	Sense	0.356	Detected	-0.356	Detected	0.000	1.128	Detected	0.876	Detected	1.002	0.118
A 96 P23	Sense	0.283	Detected	-0.283	Detected	0.000	2.025	Detected	1.905	Detected	1.965	0.021
A 96 P23	Sense	-0.008	Detected	0.008	Detected	0.000	1.153	Detected	1.074	Detected	1.113	0.001
A 96 P23	Sense	-0.256	Comprom	0.256	Comprom	0.000	1.934	Detected	1.689	Detected	1.812	0.024
A 96 P23	Sense	0.045	Detected	-0.045	Detected	0.000	1.240	Detected	0.960	Detected	1.100	0.017
A 96 P23	Sense	0.131	Detected	-0.131	Detected	0.000	1.606	Detected	1.583	Detected	1.594	0.007
A 96 P24	Sense	-0.194	Comprom	0.194	Comprom	0.000	1.986	Detected	1.293	Detected	1.639	0.054
A 96 P24	Sense	0.506	Detected	-0.506	Detected	0.000	1.253	Detected	0.940	Detected	1.097	0.174
A 96 P25	Sense	-0.101	Detected	0.101	Detected	0.000	1.497	Detected	0.832	Detected	1.165	0.079
A 96 P25	Sense	0.147	Detected	-0.147	Detected	0.000	1.572	Detected	1.351	Detected	1.461	0.015
A 96 P25	Sense	-0.065	Detected	0.065	Detected	0.000	1.299	Detected	0.849	Detected	1.074	0.044
A 96 P25	Sense	-0.270	Detected	0.270	Detected	0.000	1.699	Detected	1.119	Detected	1.409	0.071
A 96 P25	Sense	-0.030	Detected	0.030	Comprom	0.000	2.054	Detected	0.913	Detected	1.484	0.122
A 96 P25	Sense	-0.291	Detected	0.291	Detected	0.000	1.769	Detected	1.372	Detected	1.570	0.047
A 96 P26	Sense	-0.231	Detected	0.231	Detected	0.000	2.110	Detected	1.756	Detected	1.933	0.022
GT Sense	Sense	-0.646	Comprom	0.646	Detected	0.000	1.741	Detected	1.712	Detected	1.727	0.116
GT Sense	Sense	-0.339	Comprom	0.339	Comprom	0.000	1.496	Detected	1.774	Detected	1.635	0.047
GT Sense	Sense	0.075	Detected	-0.075	Detected	0.000	1.052	Detected	0.975	Detected	1.014	0.007
GT Sense	Sense	-0.646	Detected	0.646	Detected	0.000	0.973	Detected	1.144	Detected	1.058	0.246
GT Sense	Sense	-0.240	Detected	0.240	Detected	0.000	1.150	Detected	0.989	Detected	1.069	0.052
GT Sense	Sense	0.396	Detected	-0.396	Comprom	0.000	0.991	Detected	1.083	Detected	1.037	0.122
GT Sense	Sense	0.110	Detected	-0.110	Detected	0.000	1.104	Detected	1.266	Detected	1.185	0.013
GT Sense	Sense	-0.159	Detected	0.159	Detected	0.000	1.061	Detected	1.450	Detected	1.255	0.038
GT Sense	Sense	0.396	Comprom	-0.396	Comprom	0.000	1.273	Detected	1.089	Detected	1.181	0.101
GT Sense	Sense	0.199	Detected	-0.199	Detected	0.000	1.085	Detected	1.216	Detected	1.151	0.032
GT Sense	Sense	0.724	Comprom	-0.724	Comprom	0.000	1.517	Detected	1.456	Detected	1.486	0.177
GT Sense	Sense	0.431	Detected	-0.431	Comprom	0.000	0.926	Detected	1.512	Detected	1.219	0.144
GT Sense	Sense	-0.788	Detected	0.788	Detected	0.000	1.083	Detected	1.143	Detected	1.113	0.293
GT Sense	Sense	0.723	Comprom	-0.723	Comprom	0.000	0.991	Detected	1.345	Detected	1.168	0.257
GT Sense	Sense	0.503	Detected	-0.503	Detected	0.000	1.310	Detected	2.213	Detected	1.761	0.121
GT Sense	Sense	0.682	Detected	-0.682	Detected	0.000	1.062	Detected	1.055	Detected	1.059	0.261
GT Sense	Sense	0.075	Detected	-0.075	Detected	0.000	1.681	Detected	1.684	Detected	1.683	0.002
GT Sense	Sense	-0.119	Detected	0.119	Detected	0.000	1.039	Detected	1.431	Detected	1.235	0.033
GT Sense	Sense	0.033	Detected	-0.033	Detected	0.000	1.272	Detected	1.028	Detected	1.150	0.012
GT Sense	Sense	0.370	Detected	-0.370	Detected	0.000	1.104	Detected	1.090	Detected	1.097	0.097
GT Sense	Sense	0.483	Detected	-0.483	Detected	0.000	1.575	Detected	2.684	Detected	2.130	0.101
GT Sense	Sense	0.589	Detected	-0.589	Detected	0.000	1.169	Detected	0.847	Detected	1.008	0.241
GT Sense	Sense	0.060	Detected	-0.060	Detected	0.000	1.380	Detected	1.047	Detected	1.214	0.021
GT Sense	Sense	0.378	Detected	-0.378	Detected	0.000	1.139	Detected	1.489	Detected	1.314	0.088
GT Sense	Sense	0.242	Comprom	-0.242	Comprom	0.000	2.049	Detected	1.355	Detected	1.702	0.057
GT Sense	Sense	-0.069	Detected	0.069	Detected	0.000	1.169	Detected	0.861	Detected	1.015	0.026
GT Sense	Sense	0.281	Detected	-0.281	Detected	0.000	1.558	Detected	1.222	Detected	1.390	0.051
GT Sense	Sense	-0.589	Comprom	0.589	Comprom	0.000	2.553	Detected	1.236	Detected	1.895	0.165
GT Sense	Sense	0.513	Comprom	-0.513	Comprom	0.000	1.264	Detected	1.471	Detected	1.368	0.120
GT Sense	Sense	0.672	Detected	-0.672	Detected	0.000	1.328	Detected	0.920	Detected	1.124	0.251
GT Sense	Sense	-0.424	Detected	0.424	Detected	0.000	1.273	Detected	0.968	Detected	1.121	0.131
GT Sense	Sense	-0.070	Detected	0.070	Detected	0.000	1.150	Detected	1.033	Detected	1.091	0.007
GT Sense	Sense	0.236	Detected	-0.236	Detected	0.000	1.181	Detected	1.252	Detected	1.216	0.036
GT Sense	Sense	-0.166	Comprom	0.166	Comprom	0.000	2.382	Detected	1.698	Detected	2.040	0.033
GT Sense	Sense	0.142	Detected	-0.142	Detected	0.000	2.523	Detected	1.824	Detected	2.173	0.029
GT Sense	Sense	-0.634	Detected	0.634	Detected	0.000	1.054	Detected	1.221	Detected	1.137	0.217
GT Sense	Sense	0.095	Comprom	-0.095	Comprom	0.000	1.992	Detected	1.337	Detected	1.664	0.040
GT Sense	Sense	-0.032	Detected	0.032	Detected	0.000	1.552	Detected	1.208	Detected	1.380	0.016
GT Sense	Sense	0.322	Detected	-0.322	Detected	0.000	1.870	Detected	1.437	Detected	1.654	0.051
GT Sense	Sense	0.048	Detected	-0.048	Detected	0.000	1.130	Detected	0.971	Detected	1.051	0.008
GT Sense	Sense	0.545	Detected	-0.545	Detected	0.000	1.279	Detected	1.385	Detected	1.332	0.136
GT Sense	Sense	0.816	Detected	-0.816	Comprom	0.000	1.537	Detected	1.728	Detected	1.632	0.185

GT	Sense	Sense	-0.435	Detected	0.435	Detected	0.000	2.316	Detected	0.901	Detected	1.608	0.192	GT	Sens	contig11	contig11	Solute ca	CAATGC	contig11	Solyc01g	Solyc01g	Solute ca	GO:0016	GO:0016	contig11	Solyc01g	Solute ca	GO:0016	SL2
GT	Sense	Sense	0.269	Detected	-0.269	Detected	0.000	1.626	Detected	1.499	Detected	1.562	0.030	GT	Sens	contig117	contig117	Late elon	TTTAAG	contig117	Solyc10g	Solyc10g	Late elongated hypocotyl and			contig117	Solyc10g	Late elon	GO:0005	SL2
GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	1.705	Detected	1.524	Detected	1.614	0.007	GT	Sens	contig117	contig117	IBR finge	TATTTA	contig117	Solyc06g	Solyc06g	IBR finge	GO:0008	GO:0008	contig117	Solyc06g	IBR finge	GO:0008	SL2
GT	Sense	Sense	0.305	Detected	-0.305	Detected	0.000	1.532	Detected	1.153	Detected	1.343	0.065	GT	Sens	contig117	contig117	Sodium/c	TAATAG	contig117	Solyc03g	Solyc03g	Sodium/c	GO:0005	GO:0005	contig117	Solyc03g	Sodium/c	GO:0005	SL2
GT	Sense	Sense	-0.215	Comprom	0.215	Comprom	0.000	1.526	Detected	1.649	Detected	1.588	0.019	GT	Sens	contig118	contig118	Cell morp	TTTCTG	contig118	Solyc02g	Solyc02g	Cell morphogenesis protein (A			contig118	Solyc02g	Cell morphogenesis		SL2
GT	Sense	Sense	0.428	Detected	-0.428	Comprom	0.000	1.634	Detected	0.988	Detected	1.311	0.135	GT	Sens	contig119	contig119	Unknown	GGCATG	contig119	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig119	Solyc06g	Unknown Protein (A		SL2
GT	Sense	Sense	0.052	Detected	-0.052	Detected	0.000	1.381	Detected	1.331	Detected	1.356	0.002	GT	Sens	contig120	contig120	Cytochro	CACATC	contig120	Solyc04g	Solyc04g	Cytochro	GO:0019	GO:0019	contig120	Solyc04g	Cytochro	GO:0019	SL2
GT	Sense	Sense	-0.149	Detected	0.149	Detected	0.000	1.496	Detected	1.589	Detected	1.542	0.010	GT	Sens	contig120	contig120	Unknown	GCTTGT	contig120	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig120	Solyc05g	Unknown Protein (A		SL2
GT	Sense	Sense	0.159	Detected	-0.159	Detected	0.000	1.241	Detected	1.039	Detected	1.140	0.026	GT	Sens	contig120	contig120	Unknown	AATTTG	contig120	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig120	Solyc05g	Unknown Protein (A		SL2
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	1.502	Detected	1.254	Detected	1.378	0.008	GT	Sens	contig120	contig120	Magnesiu	GAGTGA	contig120	Solyc10g	Solyc10g	Magnesiu	GO:0048	GO:0048	contig120	Solyc10g	Magnesiu	GO:0003	SL2
GT	Sense	Sense	-0.038	Detected	0.038	Detected	0.000	1.018	Detected	1.001	Detected	1.010	0.001	GT	Sens	contig121	contig121	RNA ligas	TTTCTT	contig121	Solyc11g	Solyc11g	RNA ligase isoform 2 (Fragmen			contig121	Solyc11g	RNA ligas	GO:0004	SL2
GT	Sense	Sense	0.577	Comprom	-0.577	Comprom	0.000	2.306	Detected	1.658	Detected	1.982	0.096	GT	Sens	contig122	contig122	Pentatric	GAGGTT	contig122	Solyc01g	Solyc01g	Pentatricopeptide repeat-cont			contig122	Solyc01g	Pentatricopeptide re		SL2
GT	Sense	Sense	-0.255	Comprom	0.255	Comprom	0.000	1.036	Detected	0.986	Detected	1.011	0.059	GT	Sens	contig122	contig122	Os01g09	AAGGAT	contig122	Solyc09g	Solyc09g	Os01g09	GO:0003	GO:0003	contig122	Solyc09g	Os01g09	GO:0003	SL2
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	1.755	Detected	1.470	Detected	1.613	0.008	GT	Sens	contig122	contig122	Uncharac	CCTTGT	contig122	Solyc02g	Solyc02g	Uncharac	GO:0016	GO:0016	contig122	Solyc02g	Uncharac	GO:0016	SL2
GT	Sense	Sense	0.243	Detected	-0.243	Detected	0.000	1.651	Detected	1.597	Detected	1.624	0.022	GT	Sens	contig123	contig123	Os01g04	TTGGCT	contig123	Solyc04g	Solyc04g	Os01g0498200 protein (Fragm			contig123	Solyc04g	Os01g0498200 prot		SL2
GT	Sense	Sense	0.225	Detected	-0.225	Detected	0.000	1.035	Detected	1.229	Detected	1.132	0.044	GT	Sens	contig123	contig123	Aldose-1-	TATGCA	contig123	Solyc02g	Solyc02g	Aldose-1-	GO:0005	GO:0005	contig123	Solyc02g	Aldose-1-	GO:0005	SL2
GT	Sense	Sense	0.886	Detected	-0.886	Detected	0.000	1.199	Detected	1.183	Detected	1.191	0.311	GT	Sens	contig123	contig123	Nodulin-li	CAATCG	contig123	Solyc09g	Solyc09g	Nodulin-li	GO:0016	GO:0016	contig123	Solyc09g	Nodulin-li	GO:0016	SL2
GT	Sense	Sense	-0.459	Detected	0.459	Detected	0.000	1.389	Detected	0.819	Detected	1.104	0.178	GT	Sens	contig123	contig123	Myb fami	GTTGCA	contig123	Solyc07g	Solyc07g	Myb fami	GO:0003	GO:0003	contig123	Solyc07g	Myb fami	GO:0005	SL2
GT	Sense	Sense	-0.694	Detected	0.694	Detected	0.000	1.340	Detected	0.852	Detected	1.096	0.275	GT	Sens	contig123	contig123	Histidine	ACTAGC	contig123	Solyc01g	Solyc01g	Histidine	GO:0009	GO:0009	contig123	Solyc01g	Histidine	GO:0009	SL2
GT	Sense	Sense	-0.488	Detected	0.488	Detected	0.000	1.203	Detected	0.924	Detected	1.064	0.171	GT	Sens	contig123	contig123	Transcrip	AATTGT	contig123	Solyc03g	Solyc03g	Transcrip	GO:0005	GO:0005	contig123	Solyc03g	Transcrip	GO:0005	SL2
GT	Sense	Sense	0.433	Detected	-0.433	Detected	0.000	1.850	Detected	1.880	Detected	1.865	0.050	GT	Sens	contig124	contig124	Unknown	CACGAA	contig124	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig124	Solyc05g	Unknown Protein (A		SL2
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	1.489	Detected	1.791	Detected	1.640	0.019	GT	Sens	contig125	contig125	Acidic ch	ATAGCA	contig125	Solyc01g	Solyc01g	Acidic ch	GO:0005	GO:0005	contig125	Solyc01g	Acidic ch	GO:0005	SL2
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	1.210	Detected	0.908	Detected	1.059	0.023	GT	Sens	contig125	contig125	Cc-nbs-lr	ATTGCA	contig125	Solyc10g	Solyc10g	Cc-nbs-lr	GO:0006	GO:0006	contig125	Solyc10g	Cc-nbs-lr	GO:0005	SL2
GT	Sense	Sense	0.371	Detected	-0.371	Detected	0.000	2.226	Detected	1.807	Detected	2.016	0.042	GT	Sens	contig125	contig125	CONSTA	AAGATG	contig125	Solyc12g	Solyc12g	CONSTA	GO:0005	GO:0005	contig125	Solyc12g	CONSTA	GO:0005	SL2
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	1.224	Detected	1.302	Detected	1.263	0.020	GT	Sens	contig127	contig127	RING fing	ACAAGT	contig127	Solyc12g	Solyc12g	RING fing	GO:0008	GO:0008	contig127	Solyc12g	RING fing	GO:0008	SL2
GT	Sense	Sense	-0.118	Detected	0.118	Detected	0.000	1.443	Detected	1.144	Detected	1.294	0.021	GT	Sens	contig127	contig127	Photosys	AGAGGC	contig127	Solyc06g	Solyc06g	Photosys	GO:0009	GO:0009	contig127	Solyc06g	Photosys	GO:0009	SL2
GT	Sense	Sense	-0.509	Detected	0.509	Detected	0.000	1.808	Detected	1.162	Detected	1.485	0.133	GT	Sens	contig128	contig128	Strictosid	AATTTG	contig128	Solyc07g	Solyc07g	Strictosid	GO:0004	GO:0004	contig128	Solyc07g	Strictosid	GO:0004	SL2
GT	Sense	Sense	0.708	Detected	-0.708	Comprom	0.000	1.285	Detected	1.350	Detected	1.318	0.204	GT	Sens	contig128	contig128	Targeting	TATCAA	contig128	Solyc07g	Solyc07g	Targeting	GO:0008	GO:0008	contig128	Solyc07g	Targeting	GO:0008	SL2

GT	Sense	Sense	-0.056	Detected	0.056	Detected	0.000	1.272	Detected	0.927	Detected	1.100	0.026	GT	Sens	contig218	contig218	ATP-depe	ATACCA	contig218	Solyc03g	Solyc03g	ATP-depe	GO:0030	GO:0030	contig218	Solyc03g	ATP-depe	GO:0030	SL2.40ch	AT1G68660.1		FUNCTIO	chr1:257	717.528	605.872	1290.76	1534.29	1682.36	1279.48
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	1.568	Detected	1.000	Detected	1.284	0.058	GT	Sens	contig218	contig218	Signal pe	TTTAAA	contig218	Solyc03g	Solyc03g	Signal pe	GO:0006	GO:0006	contig218	Solyc03g	Signal pe	GO:0006	SL2.40ch	AT1G739	SPPA	SPPA: se	chr1:278	31.1054	19.5774	49.3072	40.7126	77.3528	50.3748
GT	Sense	Sense	0.276	Detected	-0.276	Detected	0.000	1.199	Detected	1.248	Detected	1.223	0.048	GT	Sens	contig218	contig218	Macropha	TCAAGA	contig218	Solyc10g	Solyc10g	Macropha	GO:0004	GO:0004	contig218	Solyc10g	Macropha	GO:0004	SL2.40ch	AT3G51660.1		macroph	chr3:191	522.673	278.484	469.699	589.348	925.439	924.781
GT	Sense	Sense	0.244	Detected	-0.244	Detected	0.000	1.121	Detected	1.087	Detected	1.104	0.046	GT	Sens	contig218	contig218	BHLH tra	TATGAT	contig218	Solyc02g	Solyc02g	BHLH tra	GO:0045449		contig218	Solyc02g	BHLH tra	GO:0005	SL2.40ch	AT3G192	ATRAD54	ATRAD5	chr3:665	199.209	111.041	297.27	253.17	341.919	322.452
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	1.444	Detected	1.239	Detected	1.342	0.015	GT	Sens	contig219	contig219	LRR rece	TGTTCG	contig219	Solyc03g	Solyc03g	LRR rece	GO:0004	GO:0004	contig219	Solyc03g	Receptor	GO:0004	SL2.40ch	AT4G36180.1		leucine-r	chr4:171	21.4039	13.9605	38.7759	19.7872	49.7192	41.634
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	1.579	Detected	1.092	Detected	1.336	0.032	GT	Sens	contig220	contig220	Fasciclin	AACTCT	contig220	Solyc01g	Solyc01g	Fasciclin-	GO:0005	GO:0005	contig220	Solyc01g	Fasciclin-	GO:0005	SL2.40ch	AT2G454	FLA8, AG	FLA8 (FA	chr2:187	870.236	643.95	1491.98	1041.1	2364.13	1628.44
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	1.335	Detected	0.867	Detected	1.101	0.043	GT	Sens	contig220	contig220	BHLH tra	CCTCAAT	contig220	Solyc03g	Solyc03g	BHLH tra	GO:0045449		contig220	Solyc03g	BHLH tra	GO:0005	SL2.40ch	AT4G000	UNE10	UNE10 (u	chr4:178	256.286	197.3	359.407	460.272	599.594	418.356
GT	Sense	Sense	-1.921	Comprom	1.921	Detected	0.000	1.495	Detected	1.845	Detected	1.670	0.478	GT	Sens	contig221	contig221	Unknown	GATAAA	contig221	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig221	Solyc07g	Unknown Protein (A		SL2.40ch	AT1G74055.1		unknowr	chr1:278	5.04814	56.5693	113.757	68.2294	50.3422	61.9651
GT	Sense	Sense	0.148	Detected	-0.148	Detected	0.000	1.303	Detected	0.858	Detected	1.080	0.056	GT	Sens	contig221	contig221	Cold sho	TATTAG	contig221	Solyc01g	Solyc01g	Cold sho	GO:0005	GO:0005	contig221	Solyc01g	Cold sho	GO:0030	SL2.40ch	AT5G59950.4		RNA and	chr5:241	18.7458	11.9326	19.185	22.8608	38.9911	27.662
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	1.388	Detected	1.085	Detected	1.236	0.015	GT	Sens	contig222	contig222	GDSL est	GAAGCT	contig222	Solyc02g	Solyc02g	GDSL est	GO:0006	GO:0006	contig222	Solyc02g	GDSL est	GO:0006	SL2.40ch	AT1G31550.2				104.541	80.5862	194.12	199.387	253.808	198.667
GT	Sense	Sense	-0.245	Detected	0.245	Detected	0.000	1.067	Detected	1.149	Detected	1.108	0.047	GT	Sens	contig222	contig222	Defective	TAATCA	contig222	Solyc10g	Solyc10g	Defective in exine formation (A			contig222	Solyc10g	Defective in exine fo		SL2.40ch	AT3G090	DEX1	DEX1 (DE	chr3:278	106.932	117.388	183.128	175.098	248.022	253.541
GT	Sense	Sense	-0.173	Comprom	0.173	Comprom	0.000	1.151	Detected	1.047	Detected	1.099	0.026	GT	Sens	contig224	contig224	Unknown	TCAACA	contig224	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig224	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G102	ASN3	ASN3 (AS	chr5:321	8.59169	8.53409	29.1599	22.1742	20.0912	18.0562
GT	Sense	Sense	-0.390	Comprom	0.390	Comprom	0.000	4.203	Detected	2.520	Detected	3.362	0.068	GT	Sens	contig224	contig224	Pectinest	AACACT	contig224	Solyc01g	Solyc01g	Pectinest	GO:0005	GO:0005	contig224	Solyc01g	Pectinest	GO:0005	SL2.40ch	AT4G100	AtHSD5	AtHSD5 (	chr4:626	3.95282	5.30696	2.00839	33.8508	89.1753	26.8049
GT	Sense	Sense	0.111	Detected	-0.111	Detected	0.000	1.760	Detected	1.722	Detected	1.741	0.004	GT	Sens	contig224	contig224	Auxin eff	TGTGAT	contig224	Solyc12g	Solyc12g	Auxin effl	GO:0009	GO:0009	contig224	Solyc12g	Auxin effl	GO:0009	SL2.40ch	AT1G76520.2		auxin eff	chr1:287	164.614	110.315	221.261	283.873	482.499	453.748
GT	Sense	Sense	-0.058	Detected	0.058	Detected	0.000	1.289	Detected	1.068	Detected	1.178	0.011	GT	Sens	contig225	contig225	Bzip tran	TTTGTC	contig225	Solyc10g	Solyc10g	Bzip transcription factor-like (/			contig225	Solyc10g	Bzip transcription fa		SL2.40ch	AT2G17110.1		unknowr	chr2:744	31.5226	26.716	57.7384	52.367	74.9356	62.0578
GT	Sense	Sense	-1.683	Detected	1.683	Detected	0.000	1.449	Detected	1.797	Detected	1.623	0.439	GT	Sens	contig225	contig225	Chaperon	ATGAAG	contig225	Solyc06g	Solyc06g	Chaperon	GO:0051	GO:0051	contig225	Solyc06g	Chaperon	GO:0051	SL2.40ch	AT3G47940.1		DNAJ he	chr3:176	57.4983	463.345	488	420.074	470.855	578.551
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	1.657	Detected	1.348	Detected	1.502	0.012	GT	Sens	contig225	contig225	CAS1 dor	TTTATT	contig225	Solyc01g	Solyc01g	CAS1 dor	GO:0016	GO:0016	contig225	Solyc01g	CAS1 dor	GO:0016	SL2.40ch	AT5G46340.1		O-acetylt	chr5:187	38.838	32.7226	88.0319	65.9218	118.822	92.5727
GT	Sense	Sense	-0.753	Comprom	0.753	Comprom	0.000	1.167	Detected	1.477	Detected	1.322	0.228	GT	Sens	contig226	contig226	Receptor	TTTGAT	contig226	Solyc04g	Solyc04g	Receptor	GO:0005	GO:0005	contig226	Solyc04g	LRR rece	GO:0042	SL2.40ch	AT1G17750.1		leucine-r	chr1:610	3.36084	7.45791	7.74739	7.50658	11.8829	14.2155
GT	Sense	Sense	0.586	Detected	-0.586	Comprom	0.000	0.916	Detected	1.086	Detected	1.001	0.233	GT	Sens	contig227	contig227	F-box fam	TCGTGG	contig227	Solyc07g	Solyc07g	F-box family protein (AHRD V1			contig227	Solyc07g	F-box family protein		SL2.40ch	AT3G226	ATSFL61	CEG (CE	chr3:801	18.3859	6.38154	26.0093	23.5673	21.6073	23.4634
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	2.431	Detected	1.059	Detected	1.745	0.128	GT	Sens	contig227	contig227	Hydroxy	TAAAAA	contig227	Solyc07g	Solyc07g	Hydroxyc	GO:0016	GO:0016	contig227	Solyc07g	Hydroxyc	GO:0016	SL2.40ch	AT5G484	ATGLR1.	ATGLR1.	chr5:196	284.391	250.959	901.586	451.365	1523.09	568.004
GT	Sense	Sense	-0.643	Comprom	0.643	Comprom	0.000	1.589	Detected	0.820	Detected	1.205	0.249	GT	Sens	contig228	contig228	Clathrin a	TGTACC	contig228	Solyc01g	Solyc01g	Clathrin a	GO:0005	GO:0005	contig228	Solyc01g	Clathrin a	GO:0030	SL2.40ch	AT4G31710.1				4.77161	9.0974	16.6898	10.242	20.9459	11.8703
GT	Sense	Sense	0.214	Detected	-0.214	Detected	0.000	1.182	Detected	0.848	Detected	1.015	0.065	GT	Sens	contig228	contig228	Receptor	ATGTGG	contig228	Solyc02g	Solyc02g	Receptor protein kinase-like p			contig228	Solyc02g	Receptor protein kir		SL2.40ch	AT4G17080.1		FUNCTIO	chr4:960	216.293	125.696	174.628	140.155	395.43	302.933
GT	Sense	Sense	-0.055	Detected	0.055	Detected	0.000	1.109	Detected	0.911	Detected	1.010	0.012	GT	Sens	contig228	contig228	Pentatric	AATATT	contig228	Solyc08g	Solyc08g	Pentatricopeptide repeat-conta			contig228	Solyc08g	Pentatricopeptide re		SL2.40ch	AT4G31180.2		aspartyl-	chr4:151	149.342	125.914	254.442	230.368	312.531	263.017
GT	Sense	Sense	-0.236	Comprom	0.236	Comprom	0.000	2.582	Detected	1.730	Detected	2.156	0.047	GT	Sens	contig228	contig228	Chloroph	ATCCAC	contig228	Solyc05g	Solyc05g	Chloroph	GO:0016	GO:0016	contig228	Solyc05g	Chloroph	GO:0016	SL2.40ch	AT3G548	LHCA1	LHCA1: c	chr3:203	6.44147	6.98613	14.0525	25.4408	42.4516	22.7102
GT	Sense	Sense	-1.336	Comprom	1.336	Detected	0.000	3.451	Detected	1.871	Detected	2.661	0.229	GT	Sens	contig229	contig229	Lysine/hi	GGCTTT	contig229	Solyc12g	Solyc12g	Lysine/histidine transporter (A			contig229	Solyc12g	Lysine/histidine trar		SL2.40ch	AT1G244	LHT2, AA	LHT2 (LY	chr1:865	2.72999	13.6004	6.25402	30.7722	70.4049	22.7456
GT	Sense	Sense	-0.049	Detected	0.049	Detected	0.000	0.871	Detected	1.488	Detected	1.180	0.063	GT	Sens	contig229	contig229	Myb famil	ATGAAC	contig229	Solyc06g	Solyc06g	Myb fami	GO:0045449		contig229	Solyc06g	Myb famil	GO:0045	SL2.40ch	AT5G45580.1		transcrip	chr5:184	186.297	155.926	296.535	158.505	329.497	487.806
GT	Sense	Sense	0.163	Detected	-0.163	Detected	0.000	1.158	Detected	1.049	Detected	1.103	0.023	GT	Sens	contig230	contig230	Novel pro	CAGAAT	contig230	Solyc10g	Solyc10g	Novel protein (AHRD V1 *-*- B8			contig230	Solyc10g	Novel protein (AHRD		SL2.40ch	AT5G44670.1		unknowr	chr5:180	54.7425	34.1273	63.4233	56.0393	101.963	91.2229

GT	Sens	Sense	-0.702	Comprom	0.702	Detected	0.000	0.918	Detected	1.485	Detected	1.202	0.253	GT	Sens	contig327	contig327	Unannota	CCCTTTGAATTCACCATTTGTATGATTGGGAAGTAAATAGCAGTTCACC							contig327	Solyc08g	Signal pe	GO:0008	SL2.40ch	AT3G53380.1		lectin pro	chr3:197	5.91244	12.2262	15.5653	10.7916	16.9808	24.2831
GT	Sens	Sense	0.023	Detected	-0.023	Detected	0.000	1.502	Detected	1.362	Detected	1.432	0.003	GT	Sens	contig327	contig327	Unannota	TCCGATGTGAAGCATATACTCTTTGTCAAGGAGCCATTACTATGTGAAC							contig327	Solyc10g	Receptor-	GO:0004	SL2.40ch	AT5G35400.1		tRNA pse	chr5:135	40.0845	30.3434	72.5296	79.9652	104.378	91.4748
GT	Sens	Sense	0.068	Detected	-0.068	Detected	0.000	1.410	Detected	1.050	Detected	1.230	0.024	GT	Sens	contig327	contig327	Unannota	GGCCGAGGATACCATGGTTACCATTTTAGATCACAACTAAATGGATTAC							contig327	Solyc10g	Receptor-	GO:0004	SL2.40ch	AT5G35400.1		tRNA pse	chr5:135	63.9925	45.5294	104.812	113.922	151.579	114.075
GT	Sens	Sense	-0.732	Comprom	0.732	Comprom	0.000	0.972	Detected	1.289	Detected	1.130	0.270	GT	Sens	contig327	contig327	Unannota	GGGAATCTTGCTTATGTTATACAGTTCCAATAGGGCAGGATTAGTCTG							contig327	Solyc02g	Unknown Protein (A		SL2.40ch	AT2G11626.1				3.19198	6.88545	14.957	4.7982	9.71784	11.6882
GT	Sens	Sense	0.237	Comprom	-0.237	Comprom	0.000	1.315	Detected	0.862	Detected	1.089	0.080	GT	Sens	contig327	contig327	Unannota	AAACCTCATGACACAAAAGAAGGGTCAAACTAGAGCAAACTCGACATTC							contig327	Solyc12g	Ethylene-	GO:0003	SL2.40ch	AT4G04950.1		thioredo	chr4:251	9.0785	5.10886	12.1037	16.306	17.909	12.6295
GT	Sens	Sense	0.254	Comprom	-0.254	Comprom	0.000	1.262	Detected	1.164	Detected	1.213	0.043	GT	Sens	contig327	contig327	Unannota	AGGAGAATAAAAAAGAAGAGGAAGGTGGAGAGAGAGTTACGCCTTCGC							contig327	Solyc08g029040.1.1				AT4G12050.1		DNA-bind	chr4:722	6.22527	3.41949	15.6166	10.7971	11.6914	10.5466
GT	Sens	Sense	0.196	Comprom	-0.196	Comprom	0.000	2.204	Detected	1.619	Detected	1.911	0.032	GT	Sens	contig328	contig328	Unannota	CTGTATTCAAATTCCATTCCCCATGATTTATCCCCAAACAATTTACAATT							contig328	Solyc06g	Myosin X	GO:0006	SL2.40ch	AT1G23360.2				4.86936	2.89858	6.34189	10.2318	18.2926	11.7747
GT	Sens	Sense	-0.542	Detected	0.542	Detected	0.000	1.078	Detected	1.146	Detected	1.112	0.177	GT	Sens	contig328	contig328	Unannota	GAAGAAGCTAGCATGGTGGAAAGCCCAATACTTATCACTTGAGGGAAA							contig328	Solyc03g	Kunitz try	GO:0004	SL2.40ch	AT5G05570.1		transduc	chr5:165	14.5135	24.0532	35.922	67.6461	41.6733	42.1903
GT	Sens	Sense	0.064	Detected	-0.064	Detected	0.000	1.577	Detected	1.140	Detected	1.358	0.027	GT	Sens	contig328	contig328	Unannota	TCAGGACCTCTTACATCTCATTGCGTGTAGGACTATGTTGTTCCACACT							contig328	Solyc01g	Nucleic a	GO:0003	SL2.40ch	AT4G03200.2		catalytic	chr4:140	15.2875	10.9419	31.1796	29.459	40.7825	29.0738
GT	Sens	Sense	0.804	Detected	-0.804	Comprom	0.000	1.348	Detected	1.195	Detected	1.271	0.256	GT	Sens	contig329	contig329	Unannota	CTGAGGAAATTTCAAATATTTGTGACATGAATATCTCTCGTGGTCGATC							contig329	Solyc02g	Pyrroline	GO:0042	SL2.40ch	AT1G305	NF-YA7	NF-YA7 (	chr1:108	16.6224	4.26219	18.4319	18.9701	22.637	19.6599
GT	Sens	Sense	-0.412	Detected	0.412	Detected	0.000	1.349	Detected	1.452	Detected	1.401	0.078	GT	Sens	contig329	contig329	Unannota	CAAGCCACTTTGAGCTGATTGAACAAAACCAATTGCTACACAAGATTGA							contig329	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G575	BIO1	BIO1 (bio	chr5:233	23.4411	32.4517	65.6673	55.7972	74.2662	76.9867
GT	Sens	Sense	-0.256	Detected	0.256	Detected	0.000	1.293	Detected	1.558	Detected	1.426	0.038	GT	Sens	contig329	contig329	Unannota	GGGAGCTACACTTGAAGAAAGTGAAAATTGAGAGCAATTGGGAAGATA							contig329	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G575	BIO1	BIO1 (bio	chr5:233	24.8789	27.7189	79.0955	56.0034	68.027	78.9232
GT	Sens	Sense	0.769	Detected	-0.769	Detected	0.000	1.341	Detected	0.914	Detected	1.128	0.293	GT	Sens	contig331	contig331	Unannota	CCATATCACATTAGATCCGTGACAGAAAAACCCTAAAGCTTACAAGAAG							contig331	Solyc12g019900.1.1				AT5G16550.1		unknown	chr5:540	44.4067	11.9457	14.8196	14.1769	61.6648	44.2958
GT	Sens	Sense	-0.073	Comprom	0.073	Comprom	0.000	1.213	Detected	1.065	Detected	1.139	0.008	GT	Sens	contig331	contig331	Unannota	TCAGAGAGGCCCAGTGGCAATTTCTTCAAGGGACCATAGTTCATGGCT							contig331	Solyc01g	Acyl-CoA	GO:0006	SL2.40ch	AT4G00520.3		acyl-CoA	chr4:227	5.77066	4.99422	4.3368	14.2048	13.1542	11.4638
GT	Sens	Sense	0.735	Detected	-0.735	Comprom	0.000	0.953	Detected	2.900	Detected	1.926	0.255	GT	Sens	contig332	contig332	Unannota	AATAGATTCATCTACATATACAAAAATCTTCAATAAACCCTTAATTTTGA							contig332	Solyc01g	Subtilisin	GO:0006	SL2.40ch	AT4G04320.2		malonyl-	chr4:211	14.4891	4.08608	18.0744	12.6613	15.7411	58.5936
GT	Sens	Sense	0.219	Detected	-0.219	Detected	0.000	1.471	Detected	0.987	Detected	1.229	0.064	GT	Sens	contig332	contig332	Peptide tr	TTAGCA	contig332	Solyc03g	Solyc03g	Peptide tr	GO:0016	GO:0016	contig332	Solyc03g	Peptide tr	GO:0042	SL2.40ch	AT3G47960.1		proton-d	chr3:176	4792.2	2764.93	8854.04	9327.51	10663.1	7360.11
GT	Sens	Sense	-0.110	Comprom	0.110	Comprom	0.000	0.975	Detected	1.027	Detected	1.001	0.012	GT	Sens	contig332	contig332	Endonuc	AAGGAA	contig332	Solyc11g	Solyc11g	Endonuclease/exonuclease/pl			contig332	Solyc11g	Endonuclease/exon		SL2.40ch	AT1G02020.2		nitroredu	chr1:353	5.66095	5.15192	13.6648	6.24296	11.217	11.2306
GT	Sens	Sense	0.083	Detected	-0.083	Detected	0.000	1.230	Detected	0.859	Detected	1.044	0.036	GT	Sens	contig332	contig332	Unannota	CTTGAAACACTATTTTTGGCTTTGGATTTTCAGACATCTCTAAGAGATT							contig332	Solyc06g	Unknown Protein (A		SL2.40ch	AT3G02450.1		cell divis	chr3:502	26.0084	18.1306	37.4156	47.2778	53.8321	40.182
GT	Sens	Sense	0.393	Comprom	-0.393	Comprom	0.000	1.797	Detected	1.418	Detected	1.607	0.067	GT	Sens	contig333	contig333	Unannota	CATCTTGTAGACTGACCATTACTAACTTGATATGGTTTTATACCGTAGA							contig333	Solyc06g	Baculovir	GO:0008	SL2.40ch	AT3G52700.1		unknown	chr3:195	5.40911	2.45042	3.33927	11.379	13.3723	9.92298
GT	Sens	Sense	0.324	Detected	-0.324	Detected	0.000	1.964	Detected	1.810	Detected	1.887	0.030	GT	Sens	contig333	contig333	Unknown	TTATTG	contig333	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig333	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G466	B5 #1. AT	CB5-C (C	chr2:191	2900.8	1447.87	5671.18	5764.31	8451.55	7332.43
GT	Sens	Sense	0.118	Detected	-0.118	Detected	0.000	1.307	Detected	0.908	Detected	1.107	0.041	GT	Sens	contig333	contig333	Unannota	AGTTGCTTTAGTTTGGTCTGAGCATGTGCTAGAGCTATAGCTGATGTG							contig333	Solyc05g	Inositol-3	GO:0042	SL2.40ch	AT4G398	MI-1-P SY	MIPS1 (M	chr4:184	188.757	125.246	173.265	317.716	401.955	294.375
GT	Sens	Sense	0.050	Detected	-0.050	Detected	0.000	1.444	Detected	1.007	Detected	1.226	0.032	GT	Sens	contig333	contig333	Unannota	GTAATTTCCTTCATCTGTGGTCCAAGATAAATTAGAAATGATGCCAACA							contig333	Solyc05g	Inositol-3	GO:0042	SL2.40ch	AT4G398	MI-1-P SY	MIPS1 (M	chr4:184	132.943	96.9205	143.174	255.083	326.479	232.726
GT	Sens	Sense	1.030	Detected	-1.030	Comprom	0.000	0.979	Detected	2.941	Detected	1.960	0.302	GT	Sens	contig333	contig333	Unannota	CGACCAAGAGCTACAAGGATACTGTTTACTCTAATATTTGGCATGTTAT							contig333	Solyc12g	Ribosoma	GO:0005	SL2.40ch	AT5G11870.1		FUNCTIO	chr5:382	11.9158	2.23266	8.78136	11.8523	10.7433	40.4275
GT	Sens	Sense	-0.019	Comprom	0.019	Comprom	0.000	1.831	Detected	1.021	Detected	1.426	0.072	GT	Sens	contig334	contig334	Unannota	CGACTTGCCATCGTTGTTCACTTAACTATGATGTTTTCAGAGTCCACGT							contig334	Solyc02g	DNA misn	GO:0005	SL2.40ch	AT4G04480.1		LOCATE	chr4:222	6.27117	5.03249	6.46506	6.24851	21.1227	11.6336
GT	Sens	Sense	-0.260	Comprom	0.260	Comprom	0.000	1.054	Detected	1.500	Detected	1.277	0.065	GT	Sens	contig335	contig335	Unannota	TTCCTTGCCCACAAAAAGATACCAACTACGTATATTGCTCTATATAGCA							contig335	Solyc05g	Alpha-sol	GO:0019	SL2.40ch	AT5G186	CHR17	CHR17 (C	chr5:619	3.81262	4.27109	6.68179	7.57065	8.85326	11.6439
GT	Sens	Sense	-0.174	Detected	0.174	Detected	0.000	1.744	Detected	1.166	Detected	1.455	0.050	GT	Sens	contig335	contig335	Rhodane	AAGTAT	contig335	Solyc10g	Solyc10g	Rhodane	GO:0005	GO:0005	contig335	Solyc10g	Rhodane	GO:0005	SL2.40ch	AT4G01050.1		hydroxy	chr4:455	169.317	168.409	423.994	437.263	597.891	386.506
GT	Sens	Sense	-0.171	Comprom	0.171	Comprom	0.000	2.471	Detected	2.288	Detected	2.380	0.007	GT	Sens	contig335	contig335	Unannota	TAATTCACCTGAAGGCTCTTATGTTATTACTTTGGCTTATTTACAATAT							contig335	Solyc02g	Protein tr	GO:0005	SL2.40ch	AT5G22920.1		zinc fing	chr5:766	2.65106	2.62481	12.8838	9.38871	15.4592	13.147
GT	Sens	Sense	0.036	Detected	-0.036	Detected	0.000	1.589	Detected	1.482	Detected	1.535	0.002	GT	Sens	contig335	contig335	Unannota	GAAACTGCATACGCTATCCTTGAAGTGCATTGAAGGTAATCTTTAAGTA							contig335	Solyc11g	Magnesiu	GO:0016	SL2.40ch	AT5G17640.1		unknown	chr5:581	88.4665	65.7493	173.007	227.775	242.452	217.379
GT	Sens	Sense	-0.242	Detected	0.242	Detected	0.000	1.233	Detected	1.139	Detected	1.186	0.040	GT	Sens	contig335	contig335	Unannota	GCCAGGCTGCCCTATACATTAAAATATATCTATCATAACCTAAATTTGA							contig335	Solyc09g	Lysine ketoglutarat		SL2.40ch	AT3G18970.1				29.5951	32.335	67.3698	60.8306	76.8526	69.5323
GT	Sens	Sense	-0.712	Comprom	0.712	Comprom	0.000	1.157	Detected	1.195	Detected	1.176	0.240	GT	Sens	contig336	contig336	Unannota	AGTTCCCACACCAGCAGGAACACAAAGAGAAGAGGACACATAGGTAGA							contig336	Solyc12g	Arginine/serine-rich		SL2.40ch	AT3G56720.1		unknown	chr3:210	2.92142	6.12525	10.6065	5.23273	9.97117	9.87846
GT	Sens	Sense	-0.144	Comprom	0.144	Comprom	0.000	1.425	Detected	1.072	Detected	1.249	0.032	GT	Sens	contig337	contig337	Unannota	CGTTGTTCACTCTCTTCTGGCCATTTACATGTTTTTAGTTATTAATACA							contig337	Solyc10g	FAD dependent oxi		SL2.40ch	AT3G23730.1		xylogluca	chr3:855	6.96519	6.64699	17.1061	18.9244	19.3131	14.5962
GT	Sens	Sense	-0.582	Comprom	0.582	Comprom	0.000	1.467	Detected	1.899	Detected	1.683	0.113	GT	Sens	contig338	contig338	Unannota	CCTTGTACTGATGATGCATAGATTATCCAAATCAACTATGGATAGACTT							contig338	Solyc05g	Phosphat	GO:0016	SL2.40ch	AT3G30200.1				2.71263	4.75398	8.18614	10.455	10.4921	13.6703
GT	Sens	Sense	0.353	Comprom	-0.353	Comprom	0.000	1.796	Detected	1.776	Detected	1.786	0.037	GT	Sens	contig338	contig338	Unannota	CGAGCTGACAAATAGTAAACATCAACATTACACATGTAACTTCTTGGTT							contig338	Solyc05g	Phosphat	GO:0016	SL2.40ch	AT3G30200.1				7.40244	3.54875	12.9843	14.7553	18.8061	17.9134
GT	Sens	Sense	0.446	Detected	-0.446	Comprom	0.000	1.748	Detected	1.922	Detected	1.835	0.056	GT	Sens	contig338	contig338	Unannota	TACCAACTGCAATCCTGAGGTGGAGTATGTTCCCAAATATCATCATTTT							contig338	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G37160.1		tRNA-spli	chr5:147	15.2572	6.42377	20.9335	13.4415	35.1482	38.2772
GT	Sens	Sense	-0.091	Detected	0.091	Detected	0.000	1.331	Detected	0.826	Detected	1.079	0.057	GT	Sens	contig338	contig338	Unannota	AAGCTTGCAAATCAAATGCACTGGAGAATCCACAGCATTAGCACTGGTT							contig338	Solyc11g	Os01g0873900 prot		SL2.40ch	AT5G48945.1				25.365	22.5034	56.46	73.508	63.5179	43.2293
GT	Sens	Sense	-0.268	Detected	0.268	Detected	0.000	1.549	Detected	1.382	Detected	1.466	0.035	GT	Sens	contig338	contig338	Unannota	CTCTCATTGTAACCTTGGGCTAGTTCTGCTATTTATTGCTTATTACTCA							contig338	Solyc03g	Hydrolase	GO:0004	SL2.40ch	AT4G11900.1		S-locus l	chr4:715	49.5202	56.1342	97.013	137.236	163.092	140.221
GT	Sens	Sense	-0.172	Detected	0.172	Detected	0.000	1.788	Detected	1.270	Detected	1.529	0.039	GT	Sens	contig338	contig338	Unannota	TGTAACGTGTAAATAGTTCTTTACCAATTTTAATCCTTTGGGAATGTCG							contig338	Solyc03g	Hydrolase	GO:0004	SL2.40ch	AT4G11900.1		S-locus l	chr4:715	16.9508	16.8264	39.3345	48.0756	61.6592	41.5434
GT	Sens	Sense	-0.066	Detected	0.066	Detected	0.000	1.175	Detected	1.003	Detected	1.089	0.010	GT	Sens	contig339	contig339	Unannota	TGAAAATGACTCTCTCCAGTGGCACCACAAAGGGCATGTATGATACA							contig339	Solyc02g	Cyclin delta-3 (AHRD		SL2.40ch	AT2G320	PUR ALPI	PUR ALP	chr2:136	17.3938	14.9056	16.5539	22.5186	38.4153	32.9263
GT	Sens	Sense	-0.478	Comprom	0.478	Comprom	0.000	1.666	Detected	1.871	Detected	1.768	0.069	GT	Sens	contig339	contig339	NBS-codi	ATGGAC	contig339	Solyc04g	Solyc04g	NBS-codi	GO:0006	GO:0006	contig339	Solyc04g	Cc-nbs-lr	GO:0006	SL2.40ch	AT5G45200.1		disease r	chr5:182	2.48794	3.77363	3.76441	4.78808	10.2733	11.4345
GT	Sens	Sense	0.110	Detected	-0.110	Detected	0.000	1.049	Detected	1.295	Detected	1.172	0.019	GT	Sens	contig339	contig339	Heat shoc	GGAAAT	contig339	Solyc03g	Solyc03g	Heat shoc	GO:0005	GO:0005	contig339	Solyc03g	Heat shoc	GO:0005	SL2.40ch	AT2G18938.1				48.3338	32.4548	72.5969	66.0177	86.6284	99.1839
GT	Sens	Sense	1.546	Detected	-1.546	Comprom	0.000	1.297	Detected	1.459	Detected	1.378	0.467	GT	Sens	contig340	contig340	Unannota	CATTAATGTTTTCATTCTAGAGCCTGACTCAACCCTAAATCCTCTTCAA							contig340	Solyc04g	Transposase family		SL2.40ch	AT5G151	WRKY72.	WRKY72	chr5:490	50.7761	4.65479	16.4753	20.0247	39.9125	43.1274
GT	Sens	Sense	-0.223	Comprom	0.223	Comprom	0.000	1.324	Detected	3.689	Detected	2.506	0.173	GT	Sens	contig341	contig341	Unannota	GTATCATTGTGTAGAGAACATTATGAGACAATTGAGCTCATAAGTGACA							contig341	Solyc03g	CYCLOIDEA-like (Fr		SL2.40ch	AT2G03500.1		myb fam	chr2:105	3.98414	4.24392	6.11519	5.22184	10.8804	54.1107
GT	Sens	Sense	0.081	Detected	-0.081	Detected	0.000	0.877	Detected	1.574	Detected	1.225	0.076	GT	Sens	contig341	contig341	Endogluc	TTGTTG	contig341	Solyc09g	Solyc09g	Endogluc	GO:0005	GO:0005	contig341	Solyc09g	Endogluc	GO:0004	SL2.40ch	AT1G707	ATGH9B1	ATGH9B	chr1:266	771.018	538.929	668.689	498.959	1251.32	1957.89
GT	Sens	Sense	0.242	Detected	-0.242	Comprom	0.000	0.997	Detected	1.023	Detected	1.010	0.053	GT	Sens	contig341	contig341	Unannota	CTTGCTGTGCATTCTAAATTGCTTAAGCAATCTTTTGCAATTCATGCAC							contig341	Solyc09g	Aromatic	GO:0004	SL2.40ch	AT2G20240.1				17.1614	9.59559	20.4844	17.1576	27.071	26.6094
GT	Sens	Sense	0.445	Detected	-0.445	Comprom	0.000	0.812	Detected	1.712	Detected	1.262	0.184	GT	Sens	contig341	contig341	Unannota	ATCTTTTTAGGGGAAGGATCTGGGACAACGAGCTTAACCACAAAGAGC							contig341	Solyc01g066790.1.1				AT3G45800.1				14.7108	6.20454	66.0258	35.4883	17.7317	31.94
GT	Sens	Sense	0.180	Detected	-0.180	Comprom	0.000	0.923	Detected	1.381	Detected	1.152	0.058	GT	Sens	contig342	contig342	Unannota	TTTAACAACCTCCGAGTTAGCTGAAAGTAGCTTTTTGAAACCCTTTTAC							contig342	Solyc11g044640.1.1				AT1G69280.1		unknown	chr1:260	14.0064	8.53353	22.9104	26.8922	21.9133	29.0562
GT	Sens	Sense	-0.180	Detected	0.180	Detected	0.000	1.212	Detected	0.887	Detected	1.049	0.049	GT	Sens	contig342	contig342	Unannota	TTAAATTTTAAATTTTGACTTCGCTTTGTGTGACTATACAATTACAGAA							contig342	Solyc10g	Plant-specific doma		SL2.40ch	AT5G036	SBE2.2	SBE2.2 (	chr5:931	14.9101	14.964	24.565	44.6385	36.5613	28.1911
GT	Sens	Sense	-0.252	Detected	0.252	Detected	0.000	1.292	Detected	0.848	Detected	1.070	0.086	GT	Sens	contig342	contig342	Unannota	CCATTGTTGAAAGAGAGGGTGGAATTTGTAAGTCAAGAAACAGGTTACT							contig342	Solyc10g	Plant-specific doma		SL2.40ch	AT5G036	SBE2.2	SBE2.2 (	chr5:931	153.252	169.869	283.281	427.324	417.485	296.353
GT	Sens	Sense	0.000	Comprom	0.000	Comprom	0.000	3.522	Detected	2.466	Detected	2.994	0.030	GT	Sens	contig343	contig343	Unannota	GCTCTTGATAGGTTGAATGGTTCAAACCCATATTAGCAGACCTAAATTC							contig343	Solyc07g	Polyprotein (AHRD V		SL2.40ch	AT1G80130.1		binding	chr1:301	3.087	2.414	2.28443	2.04564	33.1359	15.3922
GT	Sens	Sense	0.175	Comprom	-0.175	Comprom	0.000	3.313	Detected	2.575	Detected	2.944	0.019	GT	Sens	contig343	contig343	Unannota	GTGGGTTCGGCCCAATCCAGTAGCTAGCTTTAATCCAATATATTTGTAT							contig343	Solyc07g	Polyprotein (AHRD V		SL2.40ch	AT1G80130.1		binding	chr1:301	5.93124	3.63748	3.22994	6.35221	48.7727	28.2412
GT	Sens	Sense	0.245	Detected	-0.245	Detected	0.000	1.029	Detected	1.094	Detected	1.061	0.050	GT	Sens	contig343	contig343	MutL DN	ACTTGAT	contig343	Solyc09g	Solyc09g	MutL DN	GO:0006	GO:0006	contig343	Solyc09g	MutL DN	GO:0006	SL2.40ch	AT4G024	PMS1	PMS1 (P	chr4:107	123.868	68.9277	133.748	145.998	199.222	201.192
GT	Sens	Sense	0.982	Detected	-0.982	Comprom	0.000	1.175	Detected	1.126	Detected	1.150	0.362	GT	Sens	contig343	contig343	Unannota	TTTTACCACGTACCTTATTTGTGTGTATTGCATTTAAAAGCACAACTTT							contig343	Solyc04g	RNA-bind	GO:0008	SL2.40ch	AT5G20470.1		myosin.	chr5:691	15.1352	3.03265	13.5257	11.7106	16.1697	15.0822
GT	Sens	Sense	0.028	Comprom	-0.028	Comprom	0.000	2.305	Detected	1.465	Detected	1.885	0.046	GT	Sens	contig344	contig344	Unannota	CCAGCCAAAACAGCGTTTACTTTTTGAGTTAGAAAATGCAGTAATGACG							contig344	Solyc03g	PAR-1c protein (AH		SL2.40ch	AT5G61140.1		DEAD bo	chr5:245	4.51129	3.39226	13.9831	11.2497	20.4334	11.0198
GT	Sens	Sense	0.156	Detected	-0.156	Detected	0.000	1.121	Detected	1.517	Detected	1.319	0.035	GT	Sens	contig345	contig345	Unannota	GGACTTTGTTTAGTTCCCATTTCATGTACCCCTCAAATATATCATGAGA							contig345	Solyc06g	BHLH tra	GO:0030	SL2.40ch	AT1G31050.1				101.292	63.7956	95.692	116.499	184.753	234.673
GT	Sens	Sense	0.305	Comprom	-0.305	Comprom	0.000	1.927	Detected	1.807	Detected	1.867	0.027	GT	Sens	contig345	contig345	Unannota	GTGGTATGCATGAAGTAGTCGTCTTGTTACTGGCAGGTGAGTTCATAG							contig345	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G132	AK-LYS1.	AK-LYS1	chr5:424	5.29299	2.71141	2.9049	10.9298	15.2222	13.5281
GT	Sens	Sense	0.066	Detected	-0.066	Detected	0.000	1.399	Detected	1.054	Detected	1.226	0.022	GT	Sens	contig345	contig345	Unannota	CATCTATGAGGTTGCGTTGGACTGGTTTTCCTGAGCTAAGGACTCAGA							contig345	Solyc01g	Nitroredu	GO:0016	SL2.40ch	AT5G15560.1		unknown	chr5:506	26.95	19.2238	36.0939	34.8804	63.4276	48.2268
GT	Sens	Sense	0.286	Detected	-0.286	Comprom	0.000	0.988	Detected	1.059	Detected	1.024	0.071	GT	Sens	contig345	contig345	Unannota	CGGCTTCAGTACCATCTCTGTCACATGTTATTCATTTACCTATCTTGTC							contig345	Solyc12g	Jasmona	GO:0005	SL2.40ch	AT4G14820.1		pentatric	chr4:850	15.3619	8.07918	16.8955	11.0393	23.3589	23.681
GT	Sens	Sense	-0.139	Detected	0.139	Detected	0.000	1.564	Detected	1.069	Detected	1.317	0.043	GT	Sens	contig345	contig345	Uncharac	CAAAAA	contig345	Solyc09g	Solyc09g	Uncharac	GO:0006	GO:0006	contig345	Solyc09g	Uncharac	GO:0006	SL2.40ch	AT3G24190.1		ABC1 far	chr3:874	1919.74	1818.45	2903.23	3659.38	5839.26	4000.66
GT	Sens	Sense	0.072	Comprom	-0.072	Comprom	0.000	2.047	Detected	1.765	Detected	1.906	0.007	GT	Sens	contig345	contig345	Unannota	TGTTTAGTCCAAGAATCTACTTCTACCCCTTATACCTGAGCAATCACTT							contig345	Solyc03g	Uncharac	GO:0016	SL2.40ch	AT2G405	KT2. ATK	KT2 (PO	chr2:169	6.04122	4.27152	17.1116	16.9883	22.1903	17.6137
GT	Sens	Sense	0.027	Comprom	-0.027	Comprom	0.000	1.225	Detected	1.448	Detected	1.337	0.007	GT	Sens	contig346	contig346	Unannota	ATAGACTATACTGCCGAGGACATCAAGCATGCGGATCTGTCTGTTGTG							contig346	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G37550.2		formamid	chr4:176	4.67447	3.51835	16.9112	7.17254	10.0205	11.2904
GT	Sens	Sense	0.325	Detected	-0.325	Detected	0.000	1.711	Detected	1.429	Detected	1.570	0.047	GT	Sens	contig346	contig346	Unannota	AATTGTCCACCAGATGCATGCAGGAATGGTATCCTACCGTTCTGTTTG							contig346	Solyc08g	Processi	GO:0046	SL2.40ch	AT1G03760.1		prefoldin	chr1:941	34.3224	17.0974	60.387	51.0191	83.8323	66.5724
GT	Sens	Sense	0.306	Detected	-0.306	Detected	0.000	1.322	Detected	1.107	Detected	1.215	0.065	GT	Sens	contig347	contig347	Unannota	GAGTGCTTTTAGTTCTTGTAGCATTTCAGAATAGGTATTGTTCTAGTGT							contig347	Solyc00g	Unknown Protein (A		SL2.40ch	AT2G28620.1				43.7425	22.3608	35.0081	33.2453	82.6579	68.7194
GT	Sens	Sense	-0.197	Comprom	0.197	Comprom	0.000	1.526	Detected	1.167	Detected	1.346	0.037	GT	Sens	contig347	contig347	Unannota	CCCATTTTAGTGTCCATGACCCAAACTCAATTAGAAGAGTTAAAATAAC							contig347	Solyc02g	Riboflavi	GO:0003	SL2.40ch	AT1G78480.1		prenyltra	chr1:295	4.51362	4.63544	4.61273	6.61464	13.9197	10.4779
GT	Sens	Sense	0.607	Comprom	-0.607	Comprom	0.000	1.189	Detected	1.695	Detected	1.442	0.160	GT	Sens	contig348	contig348	Unannota	TCATACAAACAAGCTCTGATTAATGGTGGACATTAGTGGTGGAAGAACT							contig348	Solyc04g054620.1.1				AT4G23500.1		glycosid	chr4:122	7.92778	2.67272	13.0107	18.5091	11.0903	15.2028
GT	Sens	Sense	0.079	Comprom	-0.079	Comprom	0.000	1.170	Detected	1.143	Detected	1.156	0.005	GT	Sens	contig348	contig348	Unannota	CGAAGCATCTCAAAATCGCAGTGTAAACTAGTTCCACTTGACAATGTAG							contig348	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT2G24810.1				7.1157	4.98768	4.42108	6.7716	14.1624	13.4276
GT	Sens	Sense	-0.148	Comprom	0.148	Comprom	0.000	1.414	Detected	1.192	Detected	1.303	0.020	GT	Sens	contig349	contig349	Unannota	AGGCCTTGTCATTTATTGTGTCCCCTCTTACTGAAACTTGAAGTTCCAT							contig349	Solyc09g	Genomic DNA chrom		SL2.40ch	AT1G55720.1				8.75169	8.39646	8.62913	4.43817	24.1462	19.9801
GT	Sens	Sense	0.323	Detected	-0.323	Comprom	0.000	1.872	Detected	1.670	Detected	1.771	0.035	GT	Sens	contig350	contig350	Unknown	AGGATA	contig350	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig350	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G42720.1		glycosyl	chr5:171	15.2461	7.61371	27.9877	24.5286	41.6758	34.9898
GT	Sens	Sense	0.959	Detected	-0.959	Comprom	0.000	2.088	Detected	1.456	Detected	1.772	0.221	GT	Sens	contig351	contig351	Unannota	CTAAACCCCATTTCTCTATATGGTATCATAGAAAGTCATTATCAACCCC							contig351	Solyc12g027570.1.1				AT3G28560.1				15.5495	3.21521	13.5406	15.8508	31.7604	19.7923
GT	Sens	Sense	0.384	Detected	-0.384	Comprom	0.000	1.476	Detected	1.292	Detected	1.384	0.073	GT	Sens	contig352	contig352	Unannota	TCTACAAGTCTTTCTTATTTTGAGGTGTTCAAGAAGACCTTATTGCAGG							contig352	Solyc10g	UDP-gluc	GO:0008	SL2.40ch	AT5G149	GMII. ATC	GMII (GO	chr5:483	11.5783	5.31259	24.1248	15.5166	23.0547	19.6012
GT	Sens	Sense	0.005	Detected	-0.005	Detected	0.000	0.967	Detected	1.053	Detected	1.010	0.002	GT	Sens	contig352	contig352	Unannota	GGAGTGATTGGAGTTAAACCATGTAGCTATCAGTTGTAGTTGTACTTTT							contig352	Solyc10g	UDP-gluc	GO:0008	SL2.40ch	AT5G149	GMII. ATC	GMII (GO	chr5:483	27.6369	21.4674	38.3135	28.0367	50.3057	51.5679
GT	Sens	Sense	-0.550	Comprom	0.550	Detected	0.000	0.907	Detected	1.476	Detected	1.191	0.194	GT	Sens	contig353	contig353	Unannota	GGCGACACTTTTCAGTCTTTGTTTCTAGTTATTACATGACTAGCTTTAG							contig353	Solyc10g	Transcrip	GO:0006	SL2.40ch	AT2G313	emb1381	emb1381	chr2:133	9.9639	16.7055	29.8096	19.5118	25.5623	36.6252
GT	Sens	Sense	0.035	Detected	-0.035	Comprom	0.000	1.418	Detected	1.504	Detected	1.461	0.001	GT	Sens	contig353	contig353	Unannota	AAACATGTATGAAATAATCTTCCTGACGTTCAAAACTTCTGATCATTTC							contig353	Solyc10g	Transcrip	GO:0006	SL2.40ch	AT2G313	emb1381	emb1381	chr2:133	12.8312	9.55947	20.5464	15.4686	31.2831	32.0523
GT	Sens	Sense	0.275	Comprom	-0.275	Comprom	0.000	1.258	Detected	1.017	Detected	1.138	0.063	GT	Sens	contig353	contig353	Unannota	CTTCACTCCATTACAAACCACCTAAATGAAGTTAAAGTTTCCAACTTCC							contig353	Solyc10g	Unknown Protein (A		SL2.40ch	AT3G162	TRZ4	TRZ4 (TR	chr3:550	7.83768	4.18294	10.928	10.4192	14.4717	11.8259
GT	Sens	Sense	0.136	Comprom	-0.136	Comprom	0.000	1.568	Detected	1.096	Detected	1.332	0.039	GT	Sens	contig354	contig354	Unannota	ACTTGAAGGCTTTAGATGCAGACAACCAACTTTATCCTCTTCACAAGGC							contig354	Solyc09g	TspO and	GO:0016	SL2.40ch	AT2G05210.3				7.71658	4.99755	12.5249	7.36206	19.4622	13.548
GT	Sens	Sense	0.683	Detected	-0.683	Comprom	0.000	0.848	Detected	1.280	Detected	1.064	0.276	GT	Sens	contig354	contig354	Unannota	CATTTACTTCCATTTTTAGCTTCTAATTGGGTTCACTTTGCAACATGAG							contig354	Solyc03g	Kelch-like	GO:0005	SL2.40ch	AT2G38740.1		haloacid	chr2:161	14.0894	4.27228	16.0133	19.0572	14.7611	19.221
GT	Sens	Sense	0.115	Detected	-0.115	Detected	0.000	1.087	Detected	0.923	Detected	1.005	0.019	GT	Sens	contig355	contig355	Unannota	AGCTCACAGCCTAGGTCATTCATGGCCCAGCTTCATATGTTTTGAGTTC							contig355	Solyc09g	Os08g0482100 prot		SL2.40ch	AT3G05920.1				73.3559	48.9115	104.65	109.008	134.479	115.91
GT	Sens	Sense	0.042	Comprom	-0.042	Comprom	0.000	1.020	Detected	1.087	Detected	1.053	0.003	GT	Sens	contig356	contig356	Low-temp	GAAAAC	contig356	Solyc01g	Solyc01g	Low-temperature-induced 65 k			contig356	Solyc12g	Serine/threonine-pr		SL2.40ch	AT1G645	ATGCN3	ATGCN3	chr1:239	6.0275	4.44752	5.36456	11.0443	11.0948	11.2242
GT	Sens	Sense	-0.477	Comprom	0.477	Comprom	0.000	2.814	Detected	3.214	Detected	3.014	0.028	GT	Sens	contig356	contig356	Unannota	ATAACCTTTAGTTCATGACAAGTGACAAATTAAGTCGAGTGTGAAAAGG							contig356	Solyc09g	Tir-nbs-lr	GO:0006	SL2.40ch	AT4G37850.1				1.99771	3.02635	1.89607	2.16691	18.272	23.2807
GT	Sens	Sense	-0.208	Comprom	0.208	Comprom	0.000	1.426	Detected	1.908	Detected	1.667	0.035	GT	Sens	contig356	contig356	Unannota	GCTTTACTGAACTGGCATGTCATTTATAACAATTTCAGTACTATGACCT							contig356	Solyc01g	DNA poly	GO:0003	SL2.40ch	AT3G12640.1		RNA bind	chr3:401	4.01728	4.18708	7.22166	4.94926	11.6441	15.7061
GT	Sens	Sense	0.768	Detected	-0.768	Comprom	0.000	0.839	Detected	1.167	Detected	1.003	0.330	GT	Sens	contig357	contig357	Unannota	GAGTAGTACAATTAACTATATAAGAAATAGATAACCCCAAGGCCCTCAT							contig357	Solyc07g	Heavy me	GO:0030	SL2.40ch	AT1G61240.4		unknown	chr1:225	9.94605	2.68195	3.9746	4.62335	9.7624	11.8331
GT	Sens	Sense	-0.168	Detected	0.168	Detected	0.000	1.402	Detected	0.993	Detected	1.198	0.045	GT	Sens	contig357	contig357	Unannota	GCTAAGTAGAACTATATTTAAGTGGGAAATTGGCTCAGTGATGAAGCTC							contig357	Solyc12g	Arf-GAP v	GO:0030	SL2.40ch	AT2G17670.1		pentatric	chr2:767	46.4705	45.8647	94.4917	104.926	128.913	93.7818
GT	Sens	Sense	0.045	Detected	-0.045	Detected	0.000	2.157	Detected	1.886	Detected	2.022	0.005	GT	Sens	contig357	contig357	Unannota	ACCCTTTTTCTGAATTTTCTGTAAAACGGGATGTTCTGTGTACCGAACT							contig357	Solyc12g	Unknown	GO:0016	SL2.40ch	AT5G094	EICBP.B	EICBP.B	chr5:292	151.685	111.433	421.382	611.651	612.937	490.328
GT	Sens	Sense	0.075	Detected	-0.075	Detected	0.000	2.162	Detected	1.804	Detected	1.983	0.009	GT	Sens	contig357	contig357	Unannota	CGATAAATTTGTTTCCGTGTGATTTATACGTCAAGGGTTCAAGCCGTGC							contig357	Solyc12g	Unknown	GO:0016	SL2.40ch	AT5G094	EICBP.B	EICBP.B	chr5:292	124.995	88.0462	330.617	508.669	496.231	373.646
GT	Sens	Sense	0.806	Comprom	-0.806	Comprom	0.000	1.478	Detected	3.030	Detected	2.254	0.182	GT	Sens	contig358	contig358	Unannota	CCCTTTGTTTATTTGATTATTTCAGCTCTCTGGTATACCAGAGGAGTCA							contig358	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G50010.1		transcrip	chr5:203	8.57039	2.19236	10.5797	12.9167	12.7584	36.1372
GT	Sens	Sense	-0.211	Comprom	0.211	Comprom	0.000	2.329	Detected	2.116	Detected	2.223	0.011	GT	Sens	contig358	contig358	Unannota	GTAGATCATTTGTCGAGTTTTCATAGGAGACGACGGGTAATAATGTTTC							contig358	Solyc12g	Cytochro	GO:0019	SL2.40ch	AT3G49400.1				2.41268	2.52519	2.3487	2.25021	13.104	10.9207
GT	Sens	Sense	-0.049	Comprom	0.049	Comprom	0.000	1.851	Detected	2.035	Detected	1.943	0.003	GT	Sens	contig358	contig358	Unannota	GTGATAAAGAAGCTAAGAAGTTTGACAAATTGCTGGAAGAAACAGGACC							contig358	Solyc12g	Cytochro	GO:0019	SL2.40ch	AT3G49400.1				2.95905	2.47587	2.17231	1.91659	10.3194	11.3148
GT	Sens	Sense	0.362	Detected	-0.362	Detected	0.000	0.882	Detected	1.372	Detected	1.127	0.123	GT	Sens	contig360	contig360	Unannota	GTTCCTCAACCAAACAAGCATATGCAAGTGTCTAAATACCTAATTGTAC							contig360	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G215	UGT84A2	UGT84A2	chr3:759	63.5368	30.0581	63.1218	58.0676	85.1256	115.415
GT	Sens	Sense	0.203	Detected	-0.203	Detected	0.000	0.995	Detected	1.504	Detected	1.250	0.062	GT	Sens	contig360	contig360	Unannota	CTTCTGAATTTGACACAGCAGATGTCAGCAACGTAATTGGAACCATGCC							contig360	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G215	UGT84A2	UGT84A2	chr3:759	39.7616	23.4554	42.0121	39.4602	64.345	88.3779
GT	Sens	Sense	0.467	Detected	-0.467	Comprom	0.000	0.928	Detected	1.801	Detected	1.365	0.166	GT	Sens	contig361	contig361	Malate sy	AGCTAT	contig361	Solyc03g	Solyc03g	Malate sy	GO:0006	GO:0006	contig361	Solyc03g	Malate sy	GO:0004	SL2.40ch	AT5G038	MLS	MLS (MA	chr5:103	14.937	6.11047	14.3713	21.7237	19.2117	33.9732
GT	Sens	Sense	-0.618	Comprom	0.618	Comprom	0.000	1.129	Detected	1.056	Detected	1.092	0.219	GT	Sens	contig362	contig362	Unannota	TATGAAAAACGGAAGGCATAGTCCTTGCTCCATAGAAAACGCTAAGTTA							contig362	Solyc11g	Pectinest	GO:0005	SL2.40ch	AT3G52700.1		unknown	chr3:195	3.44701	6.34228	1.84053	3.57744	10.8054	9.91879
GT	Sens	Sense	-0.140	Detected	0.140	Detected	0.000	1.248	Detected	1.092	Detected	1.170	0.018	GT	Sens	contig364	contig364	UDP-gluc	CAATCCT	contig364	Solyc11g	Solyc11g	UDP-gluc	GO:0008	GO:0008	contig364	Solyc11g	UDP-gluc	GO:0008	SL2.40ch	AT1G10400.1		UDP-glyc	chr1:341	17.6634	16.7643	29.9834	22.4153	43.2024	37.4326
GT	Sens	Sense	-0.632	Comprom	0.632	Comprom	0.000	0.979	Detected	1.142	Detected	1.061	0.238	GT	Sens	contig364	contig364	Unannota	TGTTTAGATTCTGAGTTTAGTTAATCAGGTGCTTAAAGCCCTAAATT							contig364	Solyc09g	Mitochon	GO:0015	SL2.40ch	AT1G780	SULTR1::	SULTR1:	chr1:293	3.18435	7.16281	14.3344	13.1684	10.8919	11.7717
GT	Sens	Sense	0.002	Detected	-0.002	Detected	0.000	1.416	Detected	1.051	Detected	1.233	0.021	GT	Sens	contig365	contig365	Phytoene	AGATTC	contig365	Solyc03g	Solyc03g	Phytoene	GO:0009	GO:0009	contig365	Solyc03g	Phytoene	GO:0046	SL2.40ch	AT5G172	PSY	phytoene	chr5:565	5167.07	4030.25	7708.26	10084.4	12870.1	9646.45
GT	Sens	Sense	-0.121	Detected	0.121	Detected	0.000	1.251	Detected	0.984	Detected	1.118	0.025	GT	Sens	contig366	contig366	Unannota	TAGGATGTTGCAGGTATCCAGTAGATTCGTCAAGATCGTGCTAGTTAAC							contig366	Solyc03g	Aldo/keto	GO:0055	SL2.40ch	AT1G19980.1				29.3169	27.1112	47.024	47.7417	70.9245	56.9138
GT	Sens	Sense	-0.389	Detected	0.389	Detected	0.000	1.114	Detected	0.915	Detected	1.015	0.127	GT	Sens	contig366	contig366	Unannota	TGTTAACACCACCGATTCAAGCATTGTTAGTGGTCATCAAATACCAATA							contig366	Solyc03g	Aldo/keto	GO:0055	SL2.40ch	AT1G19980.1				19.5524	26.1914	35.0133	38.9885	51.7799	43.547
GT	Sens	Sense	-0.155	Detected	0.155	Detected	0.000	1.029	Detected	1.062	Detected	1.046	0.021	GT	Sens	contig366	contig366	Unannota	TAAAAATTGATTCCCGTGGTCGACTTCTACTGTTGTTTCTTACTGTCTT							contig366	Solyc11g	BZIP tran	GO:0005	SL2.40ch	AT5G49870.1		jacalin le	chr5:202	24.1714	23.411	40.4421	38.985	51.3197	50.6708
GT	Sens	Sense	0.515	Detected	-0.515	Comprom	0.000	1.003	Detected	1.875	Detected	1.439	0.166	GT	Sens	contig366	contig366	Unannota	GAGTGACAGAGTTCTTACAGATCCTACAAAGTATCAGAGACTTGTAGGC							contig366	Solyc06g	Unknown Protein (A		SL2.40ch	AT2G02380.1				20.0615	7.68319	31.53	25.5785	26.3018	46.4522
GT	Sens	Sense	0.004	Detected	-0.004	Detected	0.000	1.576	Detected	1.977	Detected	1.776	0.013	GT	Sens	contig366	contig366	Unannota	TCTCACCATGACAAGACCAGACTTAGCTTTCTCTACTCAAGTTTTAAGT							contig366	Solyc06g	Unknown Protein (A		SL2.40ch	AT2G02380.1				28.5477	22.1845	81.0735	63.5347	79.2831	101.087
GT	Sens	Sense	-0.059	Detected	0.059	Detected	0.000	1.056	Detected	1.128	Detected	1.092	0.004	GT	Sens	contig367	contig367	Unannota	ACACAAAGTTACGCTTCGCATCTAAAGTATTGGGTTTAGATGATCATGC							contig367	Solyc11g	Metal ion	GO:0030	SL2.40ch	AT3G01980.3				19.2528	16.3361	25.0649	17.1717	38.9777	39.5362
GT	Sens	Sense	-0.115	Detected	0.115	Detected	0.000	1.342	Detected	1.223	Detected	1.283	0.010	GT	Sens	contig367	contig367	Alpha ma	GAACTC	contig367	Solyc06g	Solyc06g	Alpha ma	GO:0051	GO:0051	contig367	Solyc06g	Alpha ma	GO:0051	SL2.40ch	AT5G43710.1		glycosid	chr5:175	126.266	115.719	184.562	161.264	323.938	287.838
GT	Sens	Sense	-0.941	Detected	0.941	Detected	0.000	1.517	Detected	1.682	Detected	1.599	0.232	GT	Sens	contig369	contig369	HAT famil	CAAAAT	contig369	Solyc12g	Solyc12g	HAT famil	GO:0003	GO:0003	contig369	Solyc12g	HAT famil	GO:0003	SL2.40ch	AT3G42170.1		DNA bind	chr3:143	217.457	626.215	959.817	644.544	1116.22	1208.03
GT	Sens	Sense	-0.022	Detected	0.022	Detected	0.000	1.462	Detected	1.526	Detected	1.494	0.001	GT	Sens	contig369	contig369	Unannota	AGTTACACACTTGTAGATTTGTGTATACTTCTGGATGACCTTTTTCGTG							contig369	Solyc04g	Receptor	GO:0003	SL2.40ch	AT5G051	CESA3. I	CEV1 (C	chr5:153	40.4323	32.5791	63.5881	72.4416	105.646	106.682
GT	Sens	Sense	0.212	Detected	-0.212	Detected	0.000	1.403	Detected	1.381	Detected	1.392	0.022	GT	Sens	contig369	contig369	Unannota	TGCAAGAGGTAGTCAAGTGATCCAGTATATATAGGTGGTCATATATGTT							contig369	Solyc04g	Receptor	GO:0003	SL2.40ch	AT5G051	CESA3. I	CEV1 (C	chr5:153	59.8307	34.8748	93.6079	92.4297	127.63	121.404
GT	Sens	Sense	0.266	Detected	-0.266	Comprom	0.000	1.100	Detected	1.144	Detected	1.122	0.052	GT	Sens	contig369	contig369	Unannota	GCTCTATGTACAGAATTTCCCTGAAGTTTCTTGAGTTGATAATGAAGG							contig369	Solyc01g	Phospho	GO:0004	SL2.40ch	AT1G071	F2KP. AT	F2KP (FF	chr1:217	11.5343	6.23889	22.5006	19.0149	19.2235	19.1334
GT	Sens	Sense	-0.025	Detected	0.025	Detected	0.000	1.315	Detected	1.129	Detected	1.222	0.006	GT	Sens	contig371	contig371	Unannota	TCATATTCTTGGACATGGGAGGGGCAATTTCGGACGGTCTTCACTATT							contig371	Solyc12g	Class III homeodom		SL2.40ch	AT3G553	PGP20	PGP20 (F	chr3:205	41.6602	33.6978	77.0015	68.1338	98.5464	83.5892
GT	Sens	Sense	-0.494	Comprom	0.494	Comprom	0.000	1.665	Detected	2.677	Detected	2.171	0.092	GT	Sens	contig371	contig371	Unannota	GGTATCATTGCATCTTTGAGACTTCACACTCGTATTGATGCAATAAAAA							contig371	Solyc09g031670.1.1				AT4G35270.1		RWP-RK	chr4:167	2.12693	3.29758	2.05834	2.35984	8.87589	17.2796
GT	Sens	Sense	-0.088	Comprom	0.088	Comprom	0.000	1.073	Detected	1.044	Detected	1.058	0.007	GT	Sens	contig371	contig371	Unannota	ATCAGAAAGACGCACAACGCTTCGCAACTCAAATGATTGAAAGTTGTTT							contig371	Solyc12g	Nup205 protein (Fra		SL2.40ch	AT2G385	TFIIS	TFIIS (TF	chr2:161	8.45218	7.45976	16.0192	12.7757	17.6504	16.7087
GT	Sens	Sense	0.233	Comprom	-0.233	Comprom	0.000	1.816	Detected	1.232	Detected	1.524	0.055	GT	Sens	contig371	contig371	Unannota	TGAGGCGAAGTTTTTACTTGGTCAATGAGAGTTACATGTTGATCACAC							contig371	Solyc01g	Receptor-	GO:0005	SL2.40ch	AT4G11845.1				6.95921	3.93691	12.9115	7.72694	19.4817	12.5452
GT	Sens	Sense	0.363	Comprom	-0.363	Comprom	0.000	2.714	Detected	2.495	Detected	2.605	0.021	GT	Sens	contig372	contig372	Unannota	GCATGCATGCAATCCCATTAGTACTGTACTACACTACTAATGAAGTAGA							contig372	Solyc08g	Unknown	GO:0005	SL2.40ch	AT5G154	GAUT14	GAUT14	chr5:502	6.8743	3.24783	16.4866	36.3654	32.7771	27.1798
GT	Sens	Sense	0.991	Detected	-0.991	Comprom	0.000	2.644	Detected	2.959	Detected	2.802	0.108	GT	Sens	contig372	contig372	Unannota	GCCACGGTGGCTACATTCCTTGAACTTTCATAACTTTGTACTATAAAAG							contig372	Solyc08g	Unknown	GO:0005	SL2.40ch	AT5G154	GAUT14	GAUT14	chr5:502	11.5242	2.27881	28.9567	47.3598	33.8622	40.6596
GT	Sens	Sense	0.068	Comprom	-0.068	Comprom	0.000	2.045	Detected	2.533	Detected	2.289	0.012	GT	Sens	contig372	contig372	Unannota	CTGACAAAGTCTAAGTACTCCGAATAACTTCAAATTTAGCCCAAACATG							contig372	Solyc01g	Unknown Protein (A		SL2.40ch	AT1G53350.1		ATP bind	chr1:199	5.22213	3.71351	20.8194	29.2624	19.2113	26.0066
GT	Sens	Sense	0.426	Detected	-0.426	Detected	0.000	1.541	Detected	1.533	Detected	1.537	0.069	GT	Sens	contig372	contig372	Unannota	AAACACTCGCCACTGAAAATCAATACTCACGGAGAACTTCGCCGGAGAT							contig372	Solyc01g	Unknown Protein (A		SL2.40ch	AT1G53350.1		ATP bind	chr1:199	46.5071	20.1383	64.677	71.2061	94.1272	90.3358
GT	Sens	Sense	0.396	Detected	-0.396	Comprom	0.000	1.196	Detected	1.130	Detected	1.163	0.100	GT	Sens	contig372	contig372	Unannota	GATTTTAATGTGGTTGCGGAAAACGTAAAGGAAACTGACGTCAATATTT							contig372	Solyc06g	YbaK/prolyl-tRNA sy		SL2.40ch	AT3G61960.2		protein k	chr3:229	14.9036	6.73004	15.9496	16.9815	24.2455	22.3645
GT	Sens	Sense	-0.086	Comprom	0.086	Comprom	0.000	1.026	Detected	1.713	Detected	1.369	0.061	GT	Sens	contig372	contig372	Unannota	TCGATGTTGCATCCTTTTTGTTCCTTAGCTGTGCATCGAACCTTTAGGT							contig372	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G07610.1		F-box far	chr5:240	7.05151	6.20932	23.7885	15.5869	14.236	22.1412
GT	Sens	Sense	0.071	Detected	-0.071	Detected	0.000	1.140	Detected	1.255	Detected	1.197	0.006	GT	Sens	contig373	contig373	Unannota	GGTAGGGTTGATGTCCAAAAGTCAGTAACTATAGTGACATTAACATCTC							contig373	Solyc06g	Conserve	GO:0016	SL2.40ch	ATMG000	RPL16	encodes	chrM:25	320.536	227.043	437.403	564.686	628.149	656.732
GT	Sens	Sense	0.174	Detected	-0.174	Detected	0.000	1.260	Detected	1.308	Detected	1.284	0.018	GT	Sens	contig373	contig373	Unannota	TGGATCTGGTATTTGAACATTATGCTTGGAAGAGATCTAGAGAGCGGC							contig373	Solyc06g	Conserve	GO:0016	SL2.40ch	ATMG000	RPL16	encodes	chrM:25	513.073	314.974	666.131	863.233	1017.46	1015.53
GT	Sens	Sense	0.246	Detected	-0.246	Detected	0.000	1.765	Detected	1.407	Detected	1.586	0.035	GT	Sens	contig373	contig373	Unannota	GTTCTTGGATGCACCTTTTTTACTTCAAGATAAAGTGGATGTTCATGAC							contig373	Solyc05g	Ovarian cancer-ass		SL2.40ch	AT5G259	TGG2. B	TGG2 (G	chr5:907	45.8478	25.4692	67.9931	118.069	122.769	92.4846
GT	Sens	Sense	0.294	Detected	-0.294	Detected	0.000	1.727	Detected	1.336	Detected	1.532	0.049	GT	Sens	contig373	contig373	Unannota	CCCTACTATGAATGGTTCCAATCTACTGAGGACTTCAAGGAAATTTACA							contig373	Solyc05g	Ovarian cancer-ass		SL2.40ch	AT5G259	TGG2. B	TGG2 (G	chr5:907	86.04	44.7664	113.592	182.8	217.174	159.856
GT	Sens	Sense	0.462	Comprom	-0.462	Comprom	0.000	1.244	Detected	0.957	Detected	1.101	0.151	GT	Sens	contig373	contig373	Unannota	ATGCTCAACGAGAAAAGTAGATATTATCATAGAGCTAGCTGAGACCATT							contig373	Solyc03g	B3 domain-containi		SL2.40ch	AT2G018	EMB975	EMB975	chr2:388	9.71548	4.00213	12.4879	12.6672	15.6125	12.351
GT	Sens	Sense	0.016	Comprom	-0.016	Comprom	0.000	3.144	Detected	1.308	Detected	2.226	0.136	GT	Sens	contig376	contig376	Unannota	ACGAGCCATAGCCATTGAACTTGTATCCTGTACAAAGAAGGAGAATTGT							contig376	Solyc07g	Phosphat	GO:0005	SL2.40ch	AT1G53800.2		endonuc	chr1:200	4.29857	3.28623	10.5745	7.08033	35.1161	9.49679
GT	Sens	Sense	0.102	Detected	-0.102	Detected	0.000	1.035	Detected	1.022	Detected	1.028	0.010	GT	Sens	contig376	contig376	Unannota	TCATAGATGGTTACAGTGACTTATGCGAAGTTGAGATTACTTCCAAACC							contig376	Solyc07g054610.2.1				AT2G27610.1		pentatric	chr2:117	45.6336	30.9554	64.414	63.9302	81.388	77.8759
GT	Sens	Sense	0.894	Detected	-0.894	Comprom	0.000	1.577	Detected	1.685	Detected	1.631	0.210	GT	Sens	contig378	contig378	Unannota	CAGTGTTACAAAATTGTTGGTTACCCTGCTGATTTTAAGGCTAAAAGAA							contig378	Solyc06g	NAC dom	GO:0003	SL2.40ch	AT1G135	LAG13	LAG13 (L	chr1:464	23.4575	5.30628	45.3193	24.7328	35.1893	36.5994
GT	Sens	Sense	-0.094	Detected	0.094	Detected	0.000	1.049	Detected	1.118	Detected	1.084	0.008	GT	Sens	contig379	contig379	Unannota	AACTTGAAATATGCCGGCGAAAGTCAAAAGGGTGCATATATTTTTATGT							contig379	Solyc12g	Homeobo	GO:0005	SL2.40ch	AT5G30520.1				99.2895	88.3636	155.978	213.227	204.897	207.448
GT	Sens	Sense	0.083	Detected	-0.083	Detected	0.000	1.634	Detected	1.394	Detected	1.514	0.009	GT	Sens	contig379	contig379	Unannota	CAACATTTGGCAATTAGTGTTAGATAAATCGCAAGTTCTGAATGCTTTG							contig379	Solyc02g	COL domain class t		SL2.40ch	AT4G38960.2		zinc fing	chr4:181	1156.15	805.135	2145.62	2783.69	3165.24	2586.38
GT	Sens	Sense	0.096	Detected	-0.096	Detected	0.000	1.630	Detected	1.282	Detected	1.456	0.018	GT	Sens	contig379	contig379	Unannota	TTAAGAAATTGCCTGCTGAAAGTAGCTGATGTAACTGAAGTTTATGATG							contig379	Solyc02g	COL domain class t		SL2.40ch	AT4G38960.2		zinc fing	chr4:181	1188.94	813.241	2084.88	2805.23	3217.33	2439.87
GT	Sens	Sense	0.707	Comprom	-0.707	Comprom	0.000	1.230	Detected	1.519	Detected	1.374	0.197	GT	Sens	contig379	contig379	Unannota	AGATGTAACACTTCCTTTGAGATGTGATCACCTTTAAATTGGGGAAACA							contig379	Solyc02g	Wound responsive		SL2.40ch	AT1G145	MIOX1	MIOX1 (M	chr1:496	7.26136	2.13026	10.6028	19.329	9.75101	11.4975
GT	Sens	Sense	0.481	Detected	-0.481	Comprom	0.000	1.321	Detected	0.959	Detected	1.140	0.157	GT	Sens	contig379	contig379	Unannota	GCTGTAGCAAATGTTCACCAACATGAGAGAGATTAAATGGGTGAAATTA							contig379	Solyc07g	Dimethyla	GO:0004	SL2.40ch	AT5G14290.1				13.2102	5.3009	14.9929	12.3324	22.0998	16.6025
GT	Sens	Sense	-0.288	Comprom	0.288	Comprom	0.000	1.073	Detected	1.151	Detected	1.112	0.062	GT	Sens	contig379	contig379	Unannota	TTTTGGTACTGCAGGTTCTTAACCACACTGCAGTTTATTTGGTAATTGC							contig379	Solyc02g	ATP-depe	GO:0008	SL2.40ch	AT5G672	SKIP2. VF	SKIP2 (S	chr5:268	4.94781	5.76522	9.8067	10.9344	11.8792	12.1034
GT	Sens	Sense	0.116	Comprom	-0.116	Comprom	0.000	2.344	Detected	2.190	Detected	2.267	0.004	GT	Sens	contig380	contig380	Unannota	ACAGTCTCAATATTTCTTGATAATCTTGCTCTTCTCCAGACCATGGAGG							contig380	Solyc05g	Pto-like. S	GO:0004	SL2.40ch	AT5G48205.1				3.23692	2.15562	10.9146	4.81143	14.1785	12.2975
GT	Sens	Sense	-0.911	Comprom	0.911	Comprom	0.000	1.251	Detected	1.524	Detected	1.387	0.271	GT	Sens	contig381	contig381	Unannota	CACTAGGTGGGTCTAAATTTAACCTGGAGCAAACTGCTATACTTCAATT							contig381	Solyc02g	Palmitoyl	GO:0016	SL2.40ch	AT5G41060.1				3.32135	9.18309	27.2558	9.21909	13.8944	16.2011
GT	Sens	Sense	0.229	Detected	-0.229	Detected	0.000	1.292	Detected	1.171	Detected	1.231	0.035	GT	Sens	contig381	contig381	Unannota	AGAGGAACATGTAACAAACAGACATTGGAAACAAATGATCCACCTGCCT							contig381	Solyc12g	Unknown	GO:0009	SL2.40ch	AT5G56120.1		unknown	chr5:227	426.961	243.113	708.35	824.446	833.791	740.171
GT	Sens	Sense	-0.527	Comprom	0.527	Comprom	0.000	1.019	Detected	1.042	Detected	1.030	0.190	GT	Sens	contig382	contig382	Unannota	GAGGCAGTAGCGGATCCAGGATTATCATTAAGGAGTGTTAATTGTTGT							contig382	Solyc07g	Riboflavi	GO:0004	SL2.40ch	AT5G28220.1				4.78778	7.76816	4.62405	10.4487	13.0647	12.8092
GT	Sens	Sense	0.200	Detected	-0.200	Detected	0.000	1.179	Detected	1.068	Detected	1.124	0.032	GT	Sens	contig383	contig383	Aquapori	CTTGTC	contig383	Solyc03g	Solyc03g	Aquapori	GO:0016	GO:0016	contig383	Solyc03g	Aquapori	GO:0015	SL2.40ch	AT1G016	PIP1C. TI	PIP1C (P	chr1:225	6798.11	4028.94	8426.13	7799.78	12522.7	11197.8
GT	Sens	Sense	-0.263	Detected	0.263	Detected	0.000	1.160	Detected	1.031	Detected	1.095	0.056	GT	Sens	contig386	contig386	Unannota	TCGTATTCTGGCATGTTAGCTACTCAGTAGGCTGGAGTGCAATCTATG							contig386	Solyc07g	Pit1 protein (AHRD V		SL2.40ch	AT2G24740.1				134.33	151.128	139.233	162.483	336.374	297.085
GT	Sens	Sense	-0.994	Comprom	0.994	Comprom	0.000	2.117	Detected	1.113	Detected	1.615	0.284	GT	Sens	contig386	contig386	Unannota	CCCATTTTGAATCAGTACTTGGTAGAGAAGACCATTTAAACGAAAAGAA							contig386	Solyc07g	ATP-bind	GO:0005	SL2.40ch	AT4G20840.1		FAD-bind	chr4:111	2.71505	8.42109	13.6043	15.8384	21.9182	10.5531
GT	Sens	Sense	0.527	Detected	-0.527	Comprom	0.000	1.308	Detected	1.712	Detected	1.510	0.116	GT	Sens	contig388	contig388	Unannota	CTTATGAACAGCAGGTGGAAGTGGACAGAACTAGAGTGTGTGCTAGAT							contig388	Solyc01g	Zinc finge	GO:0008	SL2.40ch	AT5G55330.1				10.9745	4.13336	11.494	10.461	17.6278	22.5067
GT	Sens	Sense	0.281	Detected	-0.281	Comprom	0.000	1.374	Detected	1.305	Detected	1.340	0.042	GT	Sens	contig389	contig389	Unannota	TGCAATAATCCACAGTAAACAGATAACAAAATGCTTGCATTGTCATCTT							contig389	Solyc09g	tRNA-spe	GO:0004	SL2.40ch	AT4G02405.2				10.4472	5.53082	15.5378	23.7206	20.825	19.1644
GT	Sens	Sense	0.265	Detected	-0.265	Detected	0.000	1.154	Detected	0.942	Detected	1.048	0.067	GT	Sens	contig390	contig390	Unannota	GCTAACCCTTCTTTGTATTAGTCCTCTGTATGTGTATTGATATATCAAG							contig390	Solyc04g	ABC-1 do	GO:0005	SL2.40ch	AT2G20030.1				2779.6	1503.82	3039.44	3594.65	4807.91	4008.57
GT	Sens	Sense	-0.197	Comprom	0.197	Comprom	0.000	1.035	Detected	1.160	Detected	1.098	0.034	GT	Sens	contig391	contig391	Unannota	GCCAATAATGGACCAGAAATCAGAGGTACACTGAAGCTGATGGACAGT							contig391	Solyc04g	F-box family protein		SL2.40ch	AT5G501	ATFRO8.	FRO8 (FE	chr5:204	6.50678	6.67885	11.8226	11.4773	14.2779	15.0325
GT	Sens	Sense	0.406	Comprom	-0.406	Comprom	0.000	1.081	Detected	1.289	Detected	1.185	0.106	GT	Sens	contig392	contig392	Unannota	CACAAGACTTCAGTAATGCCTAAATGATCTTTGATCCATGACATAACAA							contig392	Solyc02g	PsaB tran	GO:0003	SL2.40ch	AT1G28210.2				8.75419	3.89512	15.3865	17.6189	13.0586	14.5627
GT	Sens	Sense	0.307	Detected	-0.307	Detected	0.000	1.161	Detected	1.122	Detected	1.141	0.065	GT	Sens	contig392	contig392	Unannota	TTTTCATGTAAATTAAATCTATCAAGTCACTTCCAAAATAGTATATAATA							contig392	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G42880.1		unknown	chr5:171	47.0378	24.0389	29.5777	66.3918	79.4436	74.6879
GT	Sens	Sense	0.259	Detected	-0.259	Detected	0.000	1.457	Detected	1.404	Detected	1.430	0.032	GT	Sens	contig392	contig392	Unannota	CAGGGGTTTATCATGCATGTGGTATCATGTACTGTCTCTTCTTCTTTAA							contig392	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G42880.1		unknown	chr5:171	657.075	358.696	504.432	940.07	1408.16	1311.23
GT	Sens	Sense	0.822	Detected	-0.822	Comprom	0.000	1.280	Detected	1.033	Detected	1.156	0.299	GT	Sens	contig392	contig392	Unannota	CCCTACTTCACTAGCATCACCCTCTTATCCGAAAATGACATTTAATTTG							contig392	Solyc03g	(-)-ent-kau	GO:0016	SL2.40ch	AT1G687	ATPPC4	ATPPC4:	chr1:258	11.2737	2.81924	15.8153	17.9104	14.469	11.7688
GT	Sens	Sense	0.052	Comprom	-0.052	Comprom	0.000	2.000	Detected	3.248	Detected	2.624	0.053	GT	Sens	contig392	contig392	F-box fan	GAGTAA	contig392	Solyc02g	Solyc02g	F-box fan	GO:0032	GO:0032	contig392	Solyc02g	F-box fan	GO:0032	SL2.40ch	AT2G18193.1		AAA-type	chr2:791	2.96924	2.15944	1.84616	2.70422	10.7042	24.5478
GT	Sens	Sense	0.066	Detected	-0.066	Detected	0.000	1.416	Detected	1.446	Detected	1.431	0.002	GT	Sens	contig393	contig393	LRR rece	TCATGG	contig393	Solyc12g	Solyc12g	LRR rece	GO:0005	GO:0005	contig393	Solyc12g	LRR rece	GO:0004	SL2.40ch	AT3G01240.1		unknown	chr3:785	15.3567	10.9558	29.2944	25.4219	36.5711	36.056
GT	Sens	Sense	0.046	Comprom	-0.046	Comprom	0.000	1.095	Detected	1.159	Detected	1.127	0.002	GT	Sens	contig393	contig393	Unannota	ATAGTCATTAAGGAGGATAGGGGTTGAAGAAAATCTTGAGGCTGGTGT							contig393	Solyc08g	Phosphat	GO:0004	SL2.40ch	AT4G23940.1		FtsH pro	chr4:124	6.18359	4.53242	6.89402	6.33379	11.9494	12.0619
GT	Sens	Sense	-0.206	Comprom	0.206	Comprom	0.000	1.614	Detected	2.091	Detected	1.853	0.028	GT	Sens	contig393	contig393	Unannota	TGTCTATCCATTAGTTAAGGATTCAACTAAACTGACTTCCAGATTGTCG							contig393	Solyc12g	Pheophor	GO:0055	SL2.40ch	AT5G46250.3		RNA reco	chr5:187	3.54693	3.69027	10.3706	13.4912	11.7058	15.7329
GT	Sens	Sense	-0.103	Detected	0.103	Detected	0.000	1.173	Detected	0.866	Detected	1.020	0.031	GT	Sens	contig393	contig393	Unannota	CCTCTCTCACATCTTCATTTTTCTCAATTTTGCGCCCTAGTTTTGACAC							contig393	Solyc10g	Genomic DNA chrom		SL2.40ch	AT5G277	EMB2775	EMB277	chr5:982	69.3401	62.5563	95.119	91.3635	156.962	122.474
GT	Sens	Sense	0.120	Comprom	-0.120	Comprom	0.000	2.201	Detected	1.992	Detected	2.097	0.006	GT	Sens	contig393	contig393	Unknown	ATATTT	contig393	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig393	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G19050.1		unknown	chr5:636	6.33498	4.19273	6.94778	1.89147	25.0413	20.9242
GT	Sens	Sense	0.082	Detected	-0.082	Detected	0.000	1.128	Detected	1.015	Detected	1.072	0.009	GT	Sens	contig394	contig394	Unannota	CTTCCACTCCAGCTAATGTTAATGAGGCTCATGCATCAGTTTCGGATG							contig394	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G10070.1		RNase L	chr5:314	97.1727	67.8144	100.334	110.176	187.528	167.376
GT	Sens	Sense	0.699	Comprom	-0.699	Comprom	0.000	0.875	Detected	1.255	Detected	1.065	0.279	GT	Sens	contig395	contig395	Unannota	CTGGGATGAAAAATCATCTCAAACATCTCAATTTAAACACAGGCAAGAA							contig395	Solyc07g	Glutathio	GO:0015	SL2.40ch	AT5G52050.1				9.19257	2.72646	16.5203	11.5964	9.70139	12.193
GT	Sens	Sense	0.385	Detected	-0.385	Comprom	0.000	2.102	Detected	1.173	Detected	1.638	0.113	GT	Sens	contig395	contig395	Unannota	TATTTTCTAAGGCAGGTGGCAGAGCCATCTATCCTTTTGTATTTCCCTC							contig395	Solyc05g050870.2.1				AT5G52120.1				18.4368	8.45413	30.5855	25.7791	56.6606	28.7267
GT	Sens	Sense	0.103	Detected	-0.103	Detected	0.000	1.053	Detected	1.083	Detected	1.068	0.009	GT	Sens	contig396	contig396	Solute ca	CAACAA	contig396	Solyc07g	Solyc07g	Solute carrier family 35 memb			contig396	Solyc07g	Solute carrier family		SL2.40ch	AT5G55950.1		transpor	chr5:226	424.915	287.764	583.501	466.145	767.01	756.061
GT	Sens	Sense	0.214	Detected	-0.214	Detected	0.000	1.450	Detected	0.814	Detected	1.132	0.098	GT	Sens	contig396	contig396	Unannota	AATTTCATTGGCTTTGCAAGAGCCACGTGGATGTCTAATGGACTCAGC							contig396	Solyc12g	Unknown Protein (A		SL2.40ch	AT4G00960.1		protein k	chr4:414	65.2599	37.9363	76.9788	53.1908	143.686	89.2336
GT	Sens	Sense	0.405	Comprom	-0.405	Comprom	0.000	4.364	Detected	3.345	Detected	3.855	0.027	GT	Sens	contig397	contig397	Unannota	TCTACCATGGATATAGCTGCAGATTCACAGTAGTTCTTGTATTCACCCC							contig397	Solyc11g	Unknown Protein (A		SL2.40ch	AT2G04030.2				4.83438	2.15614	1.85262	4.03905	70.2483	33.482
GT	Sens	Sense	-0.183	Detected	0.183	Detected	0.000	1.130	Detected	0.873	Detected	1.001	0.047	GT	Sens	contig397	contig397	Unannota	CTTGGTAACGATTATTCCACCTTGTGATAACGATAACCTATTCCAGTAC							contig397	Solyc07g	Squamos	GO:0003	SL2.40ch	AT2G384	ATIREG1	ATIREG1	chr2:161	28.5673	28.7899	44.4952	21.304	66.3385	53.5772
GT	Sens	Sense	-0.071	Detected	0.071	Detected	0.000	1.757	Detected	1.535	Detected	1.646	0.006	GT	Sens	contig397	contig397	Unannota	CTGCCAAGATTAATAACCAAACAAAACAGGGCTATTTATGCTTCTGACA							contig397	Solyc07g	Squamos	GO:0003	SL2.40ch	AT2G384	ATIREG1	ATIREG1	chr2:161	22.3342	19.2765	34.8331	26.9327	74.144	61.3411
GT	Sens	Sense	-0.443	Detected	0.443	Detected	0.000	0.967	Detected	1.243	Detected	1.105	0.140	GT	Sens	contig397	contig397	Unannota	GACAGCGGATGTATCATCTTTATTAAGTTCTAATAAGAGTAGCACATGA							contig397	Solyc01g	NAD depe	GO:0004	SL2.40ch	AT5G157	GLIP7	GLIP7: c	chr5:512	851.34	1230.37	2000.23	1641.08	2114.76	2471.62
GT	Sens	Sense	-1.035	Detected	1.035	Detected	0.000	1.365	Detected	1.498	Detected	1.432	0.302	GT	Sens	contig397	contig397	Unannota	GGCTGCACAAATTTACCTGACTAGAGTGTGATATTTTATTACTTGGTAG							contig397	Solyc07g	Fanconi anemia E (A		SL2.40ch	AT5G604	ATSIZ1. S	SIZ1: DN	chr5:242	347.127	1139.78	1741.23	1875.15	1712.58	1812.61
GT	Sens	Sense	1.162	Detected	-1.162	Comprom	0.000	2.356	Detected	1.946	Detected	2.151	0.210	GT	Sens	contig397	contig397	Unannota	GCTGTTGTAAGCTCAGTTTGAGTTTTTACTAGGCTTAGTTTGAACCTTC							contig397	Solyc08g	ATP-depe	GO:0005	SL2.40ch	ATCG010	YCF5	hypothet	chrC:11	17.838	2.78297	26.7343	30.2469	38.1117	27.7063
GT	Sens	Sense	-0.135	Detected	0.135	Detected	0.000	1.975	Detected	1.565	Detected	1.770	0.019	GT	Sens	contig397	contig397	Unannota	GGGTATGTTATGTATCAGTATGCACCTATTCATAACAATCCACCTTTGA							contig397	Solyc03g	Auxin-ind	GO:0005	SL2.40ch	AT3G04210.1		disease r	chr3:110	13.8634	13.0579	12.9942	23.5574	55.9051	40.619
GT	Sens	Sense	0.095	Detected	-0.095	Detected	0.000	2.068	Detected	1.995	Detected	2.031	0.002	GT	Sens	contig397	contig397	Unannota	TAAGGATGCAAAATCAACAGCAGAATGTAGGTCTCGTACCGTAGTAAG							contig397	Solyc03g	Auxin-ind	GO:0005	SL2.40ch	AT3G04210.1		disease r	chr3:110	24.6746	16.9148	27.5111	38.2443	90.5049	83.1075
GT	Sens	Sense	0.875	Detected	-0.875	Comprom	0.000	4.846	Detected	4.668	Detected	4.757	0.033	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	26.1947	6.0865	316.225	269.373	383.885	327.613
GT	Sens	Sense	0.047	Detected	-0.047	Detected	0.000	1.060	Detected	1.015	Detected	1.038	0.003	GT	Sens	contig399	contig399	Unannota	GGAATCTTTTTTCAGCAGGCCAAGGATTGAGCAGTGCTTATTCTTAAGT							contig399	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G05340.1		peroxida	chr5:157	81.6906	59.7943	135.008	106.818	154.002	144.127
GT	Sens	Sense	0.209	Detected	-0.209	Detected	0.000	1.762	Detected	1.524	Detected	1.643	0.021	GT	Sens	contig400	contig400	Unannota	ATGAGAGATATCACCAAGGCCTTTGTAAGTGGCAATGTTTAGTTTGTCT							contig400	Solyc10g	HAD supe	GO:0008	SL2.40ch	AT1G041	XIB. ATXI	XIB (MY	chr1:108	5119.83	2997.14	7640.71	9111.18	14045.5	11493.2
GT	Sens	Sense	0.109	Detected	-0.109	Detected	0.000	1.804	Detected	1.620	Detected	1.712	0.007	GT	Sens	contig400	contig400	Unannota	GCTACAGAAATTTGGTCTCTCAATGCCCTATTTTTGTAGCCTCTTTTG							contig400	Solyc10g	HAD supe	GO:0008	SL2.40ch	AT1G041	XIB. ATXI	XIB (MY	chr1:108	4925.01	3307.75	7263.97	8830.69	14898	12656.9
GT	Sens	Sense	-0.279	Comprom	0.279	Comprom	0.000	1.568	Detected	2.049	Detected	1.809	0.039	GT	Sens	contig401	contig401	Unannota	GTCATCTCTATCATTAAGTTTTATTCCCAGTCAAGAAGATTTGATAACG							contig401	Solyc11g	Sentrin si	GO:0006	SL2.40ch	AT3G17770.1		dihydrox	chr3:608	2.82266	3.24904	7.48614	10.3395	9.49191	12.7897
GT	Sens	Sense	-1.623	Comprom	1.623	Detected	0.000	1.163	Detected	1.319	Detected	1.241	0.525	GT	Sens	contig401	contig401	Unknown	ATATTAC	contig401	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig401	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G14370.1		LOCATE	chr5:463	2.02002	14.9714	1.89712	1.95002	13.0175	14.0037
GT	Sens	Sense	-0.243	Detected	0.243	Detected	0.000	1.216	Detected	1.141	Detected	1.179	0.041	GT	Sens	contig401	contig401	Unannota	CATTGTCGTTTTTTGATTCTCGAGTTTTGATTTCTCAGATGGTCACTTA							contig401	Solyc10g	BEL1-like	GO:0003	SL2.40ch	AT2G237	BLH4. SA	BLH4 (B	chr2:101	16.4755	18.0432	39.2526	41.0853	42.3311	38.7962
GT	Sens	Sense	-0.226	Detected	0.226	Detected	0.000	1.287	Detected	0.910	Detected	1.099	0.065	GT	Sens	contig401	contig401	Unannota	TCTGAGAAATCGACTCTTGGATTCTCTGGTTTCTGGTTTTTACTAAGTT							contig401	Solyc10g	BEL1-like	GO:0003	SL2.40ch	AT2G237	BLH4. SA	BLH4 (B	chr2:101	32.6346	34.8745	64.442	71.0477	87.0087	64.6683
GT	Sens	Sense	-1.147	Comprom	1.147	Detected	0.000	1.995	Detected	0.974	Detected	1.484	0.359	GT	Sens	contig401	contig401	Unannota	CTTCTAAACTCAAAACTGGTTTGAAATGCCCATTTTGAGCTGGTTCAGC							contig401	Solyc10g	ATP synt	GO:0045	SL2.40ch	AT5G55770.1		DC1 dom	chr5:225	3.01725	11.5562	4.79469	4.62365	24.8787	11.8402
GT	Sens	Sense	-1.295	Comprom	1.295	Detected	0.000	1.115	Detected	1.677	Detected	1.396	0.403	GT	Sens	contig401	contig401	Unannota	CGCTTATCTAGATTCACTAATTGTGAGCTTCTGTTATTTGGTCATTT							contig401	Solyc10g	ATP synt	GO:0045	SL2.40ch	AT5G55770.1		DC1 dom	chr5:225	2.77741	13.0727	9.71469	5.78618	13.7942	19.6566
GT	Sens	Sense	-0.070	Comprom	0.070	Comprom	0.000	1.983	Detected	1.875	Detected	1.929	0.002	GT	Sens	contig401	contig401	Unannota	ATCAAGTTGTAATCTACAGAAAATCTTACAGTTTTCTTATTACTACTCA							contig401	Solyc01g	Os01g0498200 prot		SL2.40ch	AT4G04790.1		FUNCTIO	chr4:243	6.86096	5.90804	25.6148	34.8945	26.5918	23.8295
GT	Sens	Sense	0.836	Detected	-0.836	Comprom	0.000	1.771	Detected	1.642	Detected	1.707	0.179	GT	Sens	contig401	contig401	Unannota	GAAGCTTTGAGAAATTTGCGCGAAAATCATTTTTAACAGCAATTGATGTT							contig401	Solyc01g	Os01g0498200 prot		SL2.40ch	AT4G04790.1		FUNCTIO	chr4:243	16.3884	4.02088	26.9582	17.798	29.2808	25.8549
GT	Sens	Sense	-0.151	Detected	0.151	Comprom	0.000	1.040	Detected	1.331	Detected	1.186	0.030	GT	Sens	contig402	contig402	Unannota	GGTGTGAAACCATGCTGAAACAGGATAGATCTAAAATCACATTGAATGA							contig402	Solyc10g	Os06g0207500 prot		SL2.40ch	AT5G41390.2		FUNCTIO	chr5:165	5.05341	4.86827	14.1917	15.0823	10.7799	12.735
GT	Sens	Sense	0.078	Comprom	-0.078	Comprom	0.000	2.069	Detected	2.036	Detected	2.053	0.002	GT	Sens	contig402	contig402	Unannota	GGGCGTTGAGTTACGCAACCCAAGATCCATTCTTTAACAACTATTATTA							contig402	Solyc07g	Glycosylt	GO:0016	SL2.40ch	AT4G31550.2				4.3001	3.01627	12.4217	7.23857	15.9747	15.0671
GT	Sens	Sense	0.242	Detected	-0.242	Detected	0.000	1.775	Detected	1.516	Detected	1.646	0.027	GT	Sens	contig402	contig402	HAD supe	TTCATGT	contig402	Solyc10g	Solyc10g	HAD supe	GO:0008	GO:0008	contig402	Solyc10g	HAD supe	GO:0008	SL2.40ch	AT2G41250.1		haloacid	chr2:172	4737	2645.99	6362.21	7719.59	12804.3	10334.6
GT	Sens	Sense	0.290	Detected	-0.290	Comprom	0.000	1.748	Detected	1.344	Detected	1.546	0.048	GT	Sens	contig402	contig402	Unannota	ACTATCCAATCTTTTGTCAAAATTTCCTAGCTCATTTCTGGATGTTCAT							contig402	Solyc02g	Oxygen-e	GO:0008	SL2.40ch	AT3G508	PSBO2. F	PSBO2 (	chr3:188	11.7833	6.16528	15.9967	29.282	30.2503	22.0696
GT	Sens	Sense	0.567	Comprom	-0.567	Comprom	0.000	1.977	Detected	2.146	Detected	2.062	0.069	GT	Sens	contig402	contig402	Unannota	GACAAGCATCAATAGTTCTATAAAGATGAACTAGTTGCAGATTCTGTC							contig402	Solyc02g	Oxygen-e	GO:0008	SL2.40ch	AT3G508	PSBO2. F	PSBO2 (	chr3:188	7.91845	2.81984	12.2159	11.8948	19.6622	21.3441
GT	Sens	Sense	0.319	Comprom	-0.319	Comprom	0.000	1.406	Detected	1.296	Detected	1.351	0.053	GT	Sens	contig403	contig403	Unannota	TACTGTAATAGAATGGATTAGACCTTGTTTCACTTCTCGTCTTATAAAT							contig403	Solyc02g	Kinesin-li	GO:0005	SL2.40ch	AT1G20460.1		unknown	chr1:709	7.13922	3.58513	16.3141	14.7581	14.7135	12.6723
GT	Sens	Sense	0.136	Comprom	-0.136	Comprom	0.000	1.120	Detected	1.429	Detected	1.274	0.025	GT	Sens	contig403	contig403	Unannota	TCAGCATGAAGTAAACCTCTCTGATTCTCATCATCAGAGTCAAAATTGT							contig403	Solyc03g	Lipid a ex	GO:0042	SL2.40ch	AT5G390	ATTAP2.	ATTAP2:	chr5:156	6.4395	4.1699	9.86327	15.4514	11.9026	14.2356
GT	Sens	Sense	-0.077	Detected	0.077	Detected	0.000	0.803	Detected	1.447	Detected	1.125	0.077	GT	Sens	contig403	contig403	Unannota	TCAGATTGTGCTTCTATAGCCAGTCACATCCCACAAGATTAAAACAAGT							contig403	Solyc03g	Lipid a ex	GO:0042	SL2.40ch	AT5G390	ATTAP2.	ATTAP2:	chr5:156	14.3689	12.4917	29.3781	26.0386	24.7056	37.2788
GT	Sens	Sense	0.091	Detected	-0.091	Detected	0.000	1.338	Detected	0.927	Detected	1.132	0.037	GT	Sens	contig403	contig403	Unannota	GCTCTTTTTACATAGTATTGTCGCGGGGTTAATTATTGGTGACAATAAC							contig403	Solyc11g	Protein tyrosine pho		SL2.40ch	AT4G010	ATCNGC1	ATCNGC	chr4:434	49.0465	33.8057	102.558	91.69	108.764	78.9792
GT	Sens	Sense	-0.344	Comprom	0.344	Comprom	0.000	1.466	Detected	0.826	Detected	1.146	0.135	GT	Sens	contig404	contig404	Unannota	ATTAACAATTTCTCCTATGATGATAATGTTTCTCATAAGTACTTATCTTT							contig404	Solyc12g	Alcohol d	GO:0008	SL2.40ch	AT5G045	DME	DME (DE	chr5:130	4.90557	6.17565	16.8178	14.1949	16.072	9.95848
GT	Sens	Sense	0.221	Detected	-0.221	Detected	0.000	1.159	Detected	1.148	Detected	1.154	0.035	GT	Sens	contig405	contig405	Unannota	CTGCATTCTTCAGACTATTTGAAACCAGTTTGTAACGTATTCCTCTTTT							contig405	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G11000.1		unknown	chr5:347	29.3746	16.9081	59.6339	47.4464	52.6082	50.3948
GT	Sens	Sense	-0.083	Comprom	0.083	Comprom	0.000	1.064	Detected	1.089	Detected	1.076	0.006	GT	Sens	contig405	contig405	Unannota	GGTTAGACCAAGTGTTCTAACAACTAACTATTATGTTGCTTAAGGATTG							contig405	Solyc12g	Mitochon	GO:0016	SL2.40ch	AT5G65170.1		VQ motif	chr5:260	4.87848	4.27734	4.51627	4.82053	10.0952	9.91204
GT	Sens	Sense	0.485	Detected	-0.485	Comprom	0.000	1.108	Detected	1.285	Detected	1.197	0.136	GT	Sens	contig406	contig406	Unannota	GAAGAATTACCAATCGGGGACTTAATAGCCAAGAAAACACTGCATAGG							contig406	Solyc02g	Exoribon	GO:0003	SL2.40ch	AT5G44050.1				17.4338	6.95599	16.4707	19.6378	25.0874	27.3895
GT	Sens	Sense	0.183	Detected	-0.183	Detected	0.000	1.092	Detected	1.130	Detected	1.111	0.026	GT	Sens	contig406	contig406	Unannota	GAATCGCTTGTTGGTCGAGTTTTGATATTTGTGCTCAATAGGTCTCAA							contig406	Solyc02g	DNA poly	GO:0003	SL2.40ch	AT4G01890.1		glycosid	chr4:816	33.1802	20.1344	63.8521	73.4573	58.2404	57.7305
GT	Sens	Sense	-0.285	Comprom	0.285	Comprom	0.000	1.315	Detected	1.313	Detected	1.314	0.044	GT	Sens	contig406	contig406	Unannota	TGAGAACTTAGTCAGATGGTTCATTGGACATGATAGACAGGAACATCC							contig406	Solyc01g	Glycogen	GO:0004	SL2.40ch	AT3G45851.1				4.31608	5.00579	6.11292	4.32924	12.2223	11.784
GT	Sens	Sense	0.731	Detected	-0.731	Comprom	0.000	1.090	Detected	0.995	Detected	1.042	0.291	GT	Sens	contig407	contig407	Unannota	GGCTTCGCAGAGGTCAGTTTGTTTTTCTCACCAAACCACCCTTGTGTT							contig407	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G251	CIPK25. S	CIPK25 (	chr5:865	11.378	3.22687	8.13041	4.42488	13.6284	12.3201
GT	Sens	Sense	0.387	Comprom	-0.387	Comprom	0.000	1.270	Detected	1.714	Detected	1.492	0.079	GT	Sens	contig408	contig408	Unannota	GTCTTAAACATAGGGATATGCTCAGCATCGTAAGCACGGGGTTCAAAT							contig408	Solyc06g	Transcrip	GO:0003	SL2.40ch	AT5G12410.1				7.05107	3.22158	12.3692	4.49236	12.146	15.9581
GT	Sens	Sense	0.660	Detected	-0.660	Detected	0.000	1.007	Detected	1.309	Detected	1.158	0.229	GT	Sens	contig409	contig409	Unannota	CTCAAAGATCAAAATTGAAGGAAATAGGTACGATTTCGATATCTTGTAAA							contig409	Solyc03g	Os01g0584100 prot		SL2.40ch	AT3G19790.2				505.07	158.096	191.371	61.833	600.399	714.203
GT	Sens	Sense	0.605	Detected	-0.605	Detected	0.000	0.927	Detected	1.411	Detected	1.169	0.215	GT	Sens	contig409	contig409	Unannota	ATGAAGATAAAAATCATCAGTCAATCAAAGATCGTGGACGTGGTCAACC							contig409	Solyc03g	Os01g0584100 prot		SL2.40ch	AT3G19790.2				592.134	200.187	199.267	87.2532	691.605	934.082
GT	Sens	Sense	0.257	Detected	-0.257	Detected	0.000	1.002	Detected	1.015	Detected	1.009	0.059	GT	Sens	contig410	contig410	Unannota	ATGGCCGGTGGACCACCGAACAAACAAAATATCTTCTTCTCCCAAACC							contig410	Solyc11g	NAC dom	GO:0045	SL2.40ch	AT5G182	ANAC087	ANAC087	chr5:604	61.0887	33.4332	69.966	59.9589	95.6668	93.2189
GT	Sens	Sense	0.116	Comprom	-0.116	Detected	0.000	0.918	Detected	1.366	Detected	1.142	0.045	GT	Sens	contig410	contig410	Unannota	TTTGTAGGATGAGAGGCACCGTCATAAATTATGTGCCACTCATGCCAG							contig410	Solyc02g	CTP synt	GO:0003	SL2.40ch	AT5G45200.1		disease r	chr5:182	5.47181	3.6418	13.0867	9.94566	8.91532	11.7416
GT	Sens	Sense	0.036	Detected	-0.036	Detected	0.000	1.349	Detected	1.128	Detected	1.238	0.009	GT	Sens	contig410	contig410	Unannota	AGAAAAGCTGATTGCTGCCTCTATGATTGCCATGGTTGTTTTCTTTGCT							contig410	Solyc06g	YLP motif containin		SL2.40ch	AT5G62760.1				38.9083	28.9431	68.5304	70.3672	90.3133	74.8139
GT	Sens	Sense	-0.829	Comprom	0.829	Comprom	0.000	2.778	Detected	0.849	Detected	1.814	0.290	GT	Sens	contig411	contig411	Unannota	TTTCCAGTTCCGGCGATCGTCGGAAAGTTGAGTTTAATACGGCAACCT							contig411	Solyc03g	Receptor	GO:0005	SL2.40ch	AT3G128	PIE1. SR	PIE1 (PH	chr3:406	3.54549	8.74391	5.07819	3.58746	40.3617	10.2354
GT	Sens	Sense	0.215	Detected	-0.215	Detected	0.000	1.039	Detected	1.217	Detected	1.128	0.040	GT	Sens	contig411	contig411	Unannota	CTGTTCCATCAGCTTCCTTCAACAAGGTTTAGTGACAACATTAAAGATA							contig411	Solyc05g	Organic a	GO:0008	SL2.40ch	AT2G15420.1				105.819	61.42	113.943	121.283	175.096	191.232
GT	Sens	Sense	-0.378	Comprom	0.378	Comprom	0.000	0.957	Detected	1.424	Detected	1.191	0.116	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	306.349	404.385	512.74	381.45	722.31	963.572
GT	Sens	Sense	0.356	Detected	-0.356	Detected	0.000	1.477	Detected	1.645	Detected	1.561	0.051	GT	Sens	contig411	contig411	Unannota	TTCAAGTAGGGTACCTTGATAGGCATTCATGGGTTCCGGTCAATGAAG							contig411	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G33170.1		pentatric	chr4:159	1058.36	504.805	1029.67	973.583	2151.08	2333.28
GT	Sens	Sense	0.314	Detected	-0.314	Detected	0.000	1.281	Detected	1.308	Detected	1.294	0.054	GT	Sens	contig411	contig411	Unannota	GCGATGCCACTATCTAAATTATGGAGTTGCTTTTAGTTAAAGACTTCTA							contig411	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G33170.1		pentatric	chr4:159	1068.59	540.395	1036.08	995.257	1951.63	1919.24
GT	Sens	Sense	0.759	Detected	-0.759	Comprom	0.000	0.825	Detected	1.229	Detected	1.027	0.321	GT	Sens	contig411	contig411	Unannota	ATCAAAGGAAGCAACTTAATAACATCACATGGCTGAGTTGCTATGGAA							contig411	Solyc03g	50S ribos	GO:0003	SL2.40ch	AT4G28730.1		glutared	chr4:141	13.8491	3.77777	7.64197	11.9764	13.541	17.297
GT	Sens	Sense	-0.467	Comprom	0.467	Comprom	0.000	1.079	Detected	0.996	Detected	1.037	0.157	GT	Sens	contig412	contig412	Unannota	AGCCTTGGACGGAATTCACCGCCCGATTTGGGCTGCATTCCCAAACAA							contig412	Solyc06g	Unknown Protein (A		SL2.40ch	AT1G01480.1				448.556	669.742	705.129	726.884	1223.56	1115.12
GT	Sens	Sense	-0.557	Comprom	0.557	Comprom	0.000	1.587	Detected	1.369	Detected	1.478	0.121	GT	Sens	contig412	contig412	Unannota	GAAAACTGTGGATTACATGGGGATTTTCCTGCGGAATTAGTATGAAAATT							contig412	Solyc00g	Cysteine	GO:0004	SL2.40ch	AT4G39250.1				3.65192	6.17818	3.73409	10.5652	15.0826	12.5192
GT	Sens	Sense	0.390	Detected	-0.390	Detected	0.000	1.855	Detected	1.540	Detected	1.698	0.056	GT	Sens	contig412	contig412	Unannota	CTCTATGAACAACATCTAGTTAGTATAACTCTGTACTACCAGAGGTTTT							contig412	Solyc11g	F-box family protein		SL2.40ch	AT3G013	ATCFM2.	ATCFM2	chr3:139	18.1065	8.24754	30.411	32.3647	46.7131	36.2687
GT	Sens	Sense	-0.122	Detected	0.122	Detected	0.000	1.052	Detected	1.082	Detected	1.067	0.013	GT	Sens	contig412	contig412	Short-cha	GTTAAA	contig412	Solyc03g	Solyc03g	Short-cha	GO:0046	GO:0046	contig412	Solyc03g	Short-cha	GO:0046	SL2.40ch	AT4G23420.2		short-chi	chr4:122	15.2368	9.87384	180.013	180.028	224.888	221.731
GT	Sens	Sense	-0.242	Comprom	0.242	Comprom	0.000	0.997	Detected	1.226	Detected	1.112	0.053	GT	Sens	contig413	contig413	Unannota	TGTTGGGAATTCCAAGCACGGGTTTAATCTGGTTGTTGACATTGATTAC							contig413	Solyc11g	RNA splic	GO:0003	SL2.40ch	AT5G09880.1		RNA reco	chr5:308	6.43505	7.03792	11.8759	10.0755	14.2001	16.0607
GT	Sens	Sense	0.385	Comprom	-0.385	Comprom	0.000	2.036	Detected	1.874	Detected	1.955	0.038	GT	Sens	contig413	contig413	Unannota	GACATTCTTCCTTTTAGTTCTTTTTGGTCTTGACAAGCTAAGAATGACA							contig413	Solyc11g	Os01g0841200 prot		SL2.40ch	AT1G544	AIN1. EIN	XRN4 (E)	chr1:203	4.93077	2.25904	15.2378	15.2237	14.4688	12.4867
GT	Sens	Sense	-0.088	Detected	0.088	Detected	0.000	1.525	Detected	1.201	Detected	1.363	0.018	GT	Sens	contig414	contig414	Unannota	AAATGTTCTAAGCGGTAGTCAATGTCGCGTTCTCTACTCCGTTTTTCGT							contig414	Solyc06g	Unknown Protein (A		SL2.40ch	AT4G00890.1		proline-r	chr4:374	39.3972	34.7843	87.4673	88.8927	112.615	86.8387
GT	Sens	Sense	-0.092	Detected	0.092	Detected	0.000	1.335	Detected	0.995	Detected	1.165	0.027	GT	Sens	contig414	contig414	Unannota	GTGTGTGTGAAACCTAGGTTAGCCTTTGAACCAAAATGGGAAATACAT							contig414	Solyc06g	Unknown Protein (A		SL2.40ch	AT4G00890.1		proline-r	chr4:374	35.7181	31.732	74.9399	69.7147	89.7815	68.4619
GT	Sens	Sense	-0.850	Comprom	0.850	Comprom	0.000	0.930	Detected	1.376	Detected	1.153	0.320	GT	Sens	contig414	contig414	Unannota	ATAAGTCTTTCTTTTCTACACCCTACTCAATCTTATGTACTCTTGTGACG							contig414	Solyc02g	DNA misn	GO:0005	SL2.40ch	AT5G10650.2				3.07254	7.80725	14.1297	12.8126	9.86102	12.9705
GT	Sens	Sense	0.113	Comprom	-0.113	Comprom	0.000	1.666	Detected	1.006	Detected	1.336	0.062	GT	Sens	contig415	contig415	Unannota	ACTAAAAGAAAGAACCTTCTTGCTCTTTCTGCTTACAATATTGTTTCTT							contig415	Solyc06g	DNAJ hea	GO:0031	SL2.40ch	AT3G011	AtSS2	AtSS2 (s	chr3:624	7.17949	4.80063	6.83832	3.70011	19.6875	12.0327
GT	Sens	Sense	-0.258	Detected	0.258	Detected	0.000	1.222	Detected	0.950	Detected	1.086	0.065	GT	Sens	contig415	contig415	Unannota	CAACACCACGTAGGTGAAAGTCTACGGAACTGGGAAAGATTATCCAAG							contig415	Solyc08g	Nodule in	GO:0003	SL2.40ch	AT5G452	RRS1. AT	RRS1 (RE	chr5:183	11.385	12.7177	20.9642	25.9301	29.6743	23.7224
GT	Sens	Sense	0.110	Detected	-0.110	Detected	0.000	1.283	Detected	1.202	Detected	1.242	0.009	GT	Sens	contig416	contig416	Unannota	TAATTTGCTTTGATGCGGGTAACCAGGATCAATATCGAGCGCCTCGTT							contig416	Solyc06g	Transmem	GO:0005	SL2.40ch	AT4G31250.1		leucine-r	chr4:151	248.216	166.575	393.073	364.152	522.893	477.236
GT	Sens	Sense	-0.412	Comprom	0.412	Comprom	0.000	1.141	Detected	1.007	Detected	1.074	0.124	GT	Sens	contig416	contig416	Unannota	TTGCCCAAATACTATGTGGGTAAAGAAGTTATTTGGCAACCAAGATTGC							contig416	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G62810.1		copper a	chr1:232	4.47301	6.18949	11.7936	10.2627	12.2631	10.7881
GT	Sens	Sense	-0.409	Comprom	0.409	Comprom	0.000	1.852	Detected	1.328	Detected	1.590	0.082	GT	Sens	contig416	contig416	Unannota	GGCATTATCTCCTTTTGGAGATACTATCTTGGTCTCTGTTTTAAAAAAC							contig416	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G293	COR314-T	COR314-	chr1:102	5.39949	7.43659	12.2312	13.1644	24.1786	16.2362
GT	Sens	Sense	-0.012	Comprom	0.012	Comprom	0.000	1.242	Detected	1.937	Detected	1.590	0.045	GT	Sens	contig417	contig417	Unannota	GAGGAGTTACAATATTGGTTTTAGCTTACAAGGAACAGGTTACTTGTTA							contig417	Solyc01g	RING fing	GO:0008	SL2.40ch	AT1G20100.2				4.54061	3.61088	5.96703	5.85643	10.1245	15.8172
GT	Sens	Sense	-0.145	Comprom	0.145	Comprom	0.000	1.320	Detected	1.263	Detected	1.291	0.013	GT	Sens	contig418	contig418	Unannota	TATATAGAGCACTTGACTTGTCGCAGCAAATTTGATGCACGTTCTGAAT							contig418	Solyc01g	F-box/LRR-repeat p		SL2.40ch	AT5G52600.1				4.39881	4.20311	12.6934	13.656	11.3452	10.5266
GT	Sens	Sense	-0.075	Detected	0.075	Detected	0.000	1.640	Detected	1.077	Detected	1.358	0.043	GT	Sens	contig418	contig418	Unannota	TGGAGTTCTGGAAACCTCTTTGAGCTCTGGCCATTCTTCTGTATTTGCT							contig418	Solyc07g	HAT family dimerisa		SL2.40ch	AT3G44440.1				26.4756	22.9603	47.8069	27.1929	81.1881	53.0687
GT	Sens	Sense	0.271	Comprom	-0.271	Comprom	0.000	2.033	Detected	1.611	Detected	1.822	0.034	GT	Sens	contig418	contig418	Unannota	GCGACATCTGTTAGGTCATAATATTTGCTGAAATGTATTTCTGATGTTG							contig418	Solyc02g	Heteroge	GO:0003	SL2.40ch	AT5G60840.1		unknown	chr5:244	6.8319	3.66951	14.0523	15.8174	21.6519	15.6107
GT	Sens	Sense	-0.643	Comprom	0.643	Comprom	0.000	1.545	Detected	3.635	Detected	2.590	0.169	GT	Sens	contig419	contig419	Unannota	TGAAGCATGCAAACAAGTCCTACAATGTACACCATAATCATCATCCATA							contig419	Solyc09g	C2 domain-containi		SL2.40ch	AT3G06040.3		ribosoma	chr3:182	2.53569	4.83215	2.33656	2.59638	10.7925	44.3789
GT	Sens	Sense	-0.286	Comprom	0.286	Comprom	0.000	1.191	Detected	0.878	Detected	1.035	0.087	GT	Sens	contig419	contig419	Unannota	GCATGCATCTTCTTATCACATGCCCGAATCATCTCAAACTTGTTTTTCG							contig419	Solyc01g	Vacuolar	GO:0005	SL2.40ch	AT1G22000.1				6.42249	7.45957	14.1753	14.5836	16.7072	12.9794
GT	Sens	Sense	0.129	Detected	-0.129	Detected	0.000	0.937	Detected	1.184	Detected	1.060	0.027	GT	Sens	contig419	contig419	Unannota	GCTACTTCATCCGTATTGTCACCATTGATTAGTTTATTCGGAACGACAA							contig419	Solyc04g	Spermidi	GO:0004	SL2.40ch	AT4G08395.1				22.6043	14.7734	23.2264	28.2049	36.9747	42.3618
GT	Sens	Sense	-0.147	Detected	0.147	Detected	0.000	1.222	Detected	1.414	Detected	1.318	0.017	GT	Sens	contig419	contig419	Unannota	GCTAAGATCTTCTTGTTCAATAGCTCTTCGCTGTTGTTTGTAGATGCCC							contig419	Solyc01g	ATP-depe	GO:0005	SL2.40ch	AT1G32910.1		transfera	chr1:119	33.639	32.2418	76.4387	50.7807	81.1663	89.5189
GT	Sens	Sense	-0.119	Detected	0.119	Detected	0.000	1.405	Detected	1.699	Detected	1.552	0.014	GT	Sens	contig419	contig419	Unannota	TTCAACTTATCATTCCTTTACTCCGAGACGGCAAAATCCTTTAATTGGA							contig419	Solyc01g	ATP-depe	GO:0005	SL2.40ch	AT1G32910.1		transfera	chr1:119	114.243	105.259	351.977	268.794	306.896	363.259
GT	Sens	Sense	-0.534	Comprom	0.534	Comprom	0.000	1.487	Detected	2.293	Detected	1.890	0.106	GT	Sens	contig420	contig420	Unannota	TGGAAAATATGGAGGAAGAGAAGTAGTAGTTTGTGGGTCGAATGTCCA							contig420	Solyc07g	Zinc finge	GO:0003	SL2.40ch	AT3G256	CHUP1	CHUP1 (	chr3:935	2.42899	3.98091	3.28217	6.17336	9.20989	15.5485
GT	Sens	Sense	0.165	Detected	-0.165	Detected	0.000	1.212	Detected	1.356	Detected	1.284	0.019	GT	Sens	contig420	contig420	Unannota	CAATATGTGAGCTTCTATGAGGTCTTAGGATTATGTCCTTCGACGGA							contig420	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G06100.3				13.1198	8.16106	23.0709	22.0139	25.3264	27.0199
GT	Sens	Sense	0.218	Detected	-0.218	Detected	0.000	1.280	Detected	0.914	Detected	1.097	0.061	GT	Sens	contig420	contig420	Unannota	CCTTGGATAGTGAGATCTGCGCTTTCTAAATTTCGCATTTTCATCATCT							contig420	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G624	CDF1	CDF1 (C)	chr5:250	7.83291	4.52687	8.54683	14.9736	15.278	11.4482
GT	Sens	Sense	0.170	Detected	-0.170	Detected	0.000	1.155	Detected	1.728	Detected	1.442	0.049	GT	Sens	contig420	contig420	Unknown	TCCAAC	contig420	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig420	Solyc01g	Unknown Protein (A		SL2.40ch	AT1G06250.1		lipase cla	chr1:191	37.4368	23.1316	75.1995	54.3909	69.2784	99.4357
GT	Sens	Sense	0.124	Detected	-0.124	Detected	0.000	1.058	Detected	0.979	Detected	1.018	0.016	GT	Sens	contig421	contig421	Unannota	GGTTTTGGACGAGTCTAGTAACTTTTGCTTAGATGGAAGATCATTGAAT							contig421	Solyc09g	Ammoniu	GO:0015	SL2.40ch	AT1G643	AtGH9C2	AtGH9C2	chr1:239	57.3373	37.7596	76.9049	70.9799	102.409	93.555
GT	Sens	Sense	0.012	Detected	-0.012	Detected	0.000	1.069	Detected	1.252	Detected	1.160	0.006	GT	Sens	contig421	contig421	Unannota	TTCAACAACATTCAAAACCCGTGAACATCAAATTCTGATTACGCCTCTG							contig421	Solyc09g	Ammoniu	GO:0015	SL2.40ch	AT1G643	AtGH9C2	AtGH9C2	chr1:239	50.8638	39.0993	72.4968	74.1726	98.8497	108.376
GT	Sens	Sense	-0.035	Detected	0.035	Detected	0.000	1.002	Detected	1.361	Detected	1.182	0.023	GT	Sens	contig422	contig422	Unannota	TATTCTCCGTCATATTTCTGGGACATTGGTGTCCTTTCCGTTCAAAATC							contig422	Solyc11g	Ribonucl	GO:0006	SL2.40ch	AT5G376	UBO9	UBO9: p	chr5:149	59.6831	48.9869	116.595	99.0042	114.471	141.746
GT	Sens	Sense	-0.111	Detected	0.111	Detected	0.000	0.885	Detected	1.121	Detected	1.003	0.025	GT	Sens	contig422	contig422	Unannota	TACCTTTTACTCTGACGGATGACTGAATGAGGACACATGGCACAATCTT							contig422	Solyc11g	Ribonucl	GO:0006	SL2.40ch	AT5G376	UBO9	UBO9: p	chr5:149	71.3488	65.0206	127.696	93.7792	132.965	151.121
GT	Sens	Sense	0.687	Detected	-0.687	Comprom	0.000	1.101	Detected	0.930	Detected	1.016	0.280	GT	Sens	contig422	contig422	Unannota	GTGGTTATTTCAACTTCAATACAAGTGTGCTAGGTTGTCCTTATCAACC							contig422	Solyc03g	CYCLOIDEA-like (Fr		SL2.40ch	AT5G628	AtVEX1	AtVEX1 (	chr5:252	11.7906	3.55536	15.6224	12.827	14.6827	12.5843
GT	Sens	Sense	0.206	Detected	-0.206	Detected	0.000	0.966	Detected	1.171	Detected	1.068	0.044	GT	Sens	contig422	contig422	Unannota	TTATATTTTGTTGAGAGGGGGGAGAGGTACTAAATTAACCTTCGAAGT							contig422	Solyc01g	Calcium b	GO:0005	SL2.40ch	AT3G16600.1		SNF2 do	chr3:565	601.357	353.115	445.154	413.543	951.122	1058.45
GT	Sens	Sense	0.788	Detected	-0.788	Comprom	0.000	1.605	Detected	0.862	Detected	1.233	0.292	GT	Sens	contig423	contig423	Unannota	GGGTGAGCACATGGTGTTTTATACAATTTAAGTCTCCATCCATATATAT							contig423	Solyc04g	Beige/BEACH doma		SL2.40ch	AT5G59930.1		DC1 dom	chr5:241	13.716	3.59817	53.5496	79.1929	22.5868	13.0252
GT	Sens	Sense	0.287	Comprom	-0.287	Comprom	0.000	1.213	Detected	1.348	Detected	1.280	0.049	GT	Sens	contig424	contig424	Unannota	TTTTCGCTGCCAATTTTCCTTCTCATAACTGCTCTGCTTAGCTGCACTA							contig424	Solyc03g	E3 ubiqui	GO:0008	SL2.40ch	AT5G10290.1		leucine-r	chr5:323	6.86086	3.60187	15.0291	13.2343	12.1762	12.9114
GT	Sens	Sense	-0.626	Comprom	0.626	Comprom	0.000	1.761	Detected	1.327	Detected	1.544	0.145	GT	Sens	contig424	contig424	Unannota	GGCAAGGTTAAACCCAAGGACACAGTCCTAATGATCAACGAAGTGGGT							contig424	Solyc02g	Nuclear S	GO:0003	SL2.40ch	AT4G35785.3		nucleic a	chr4:169	2.86637	5.33586	11.5219	3.15861	14.0132	10.0097
GT	Sens	Sense	1.238	Detected	-1.238	Detected	0.000	1.807	Detected	0.905	Detected	1.356	0.412	GT	Sens	contig425	contig425	Glutared	TAAGAA	contig425	Solyc06g	Solyc06g	Glutared	GO:0045	GO:0045	contig425	Solyc06g	Glutared	GO:0045	SL2.40ch	AT3G62930.1		glutared	chr3:232	300.359	42.1938	624.579	428.992	416.398	215.157
GT	Sens	Sense	-0.176	Comprom	0.176	Comprom	0.000	1.271	Detected	1.435	Detected	1.353	0.020	GT	Sens	contig425	contig425	Unannota	ACACAGGACCTTGGAGGACAAATTCGCAGAGTATAAAGCATAGGGAT							contig425	Solyc06g	Genomic DNA chrom		SL2.40ch	AT4G04500.1		protein k	chr4:223	3.79107	3.78154	11.9922	6.76787	9.65573	10.4464
GT	Sens	Sense	0.121	Detected	-0.121	Detected	0.000	1.091	Detected	1.106	Detected	1.098	0.012	GT	Sens	contig426	contig426	Putative /	CAGGATGCTGTTGATTACCTAACATGGACCTTCATGTATAGGAGGCTG							contig426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	526.811	348.243	724.857	667.532	964.028	940.79
GT	Sens	Sense	0.057	Detected	-0.057	Detected	0.000	1.300	Detected	0.910	Detected	1.105	0.032	GT	Sens	contig426	contig426	Putative r	CTTTCAGATATATTGGGTTCTGAAGATGCATCAGGAGATATGGATTTCA							contig426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	23.4047	16.8936	31.6527	39.8259	51.7616	38.1216
GT	Sens	Sense	0.353	Detected	-0.353	Comprom	0.000	0.840	Detected	1.306	Detected	1.073	0.126	GT	Sens	contig426	contig426	AT3G627	AACTCAACCTCAGGATGTGATAGCAAAAGCTTCCTAAGCAAAGGCAATT							contig426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	13.0936	6.27819	10.2353	12.5816	17.1485	22.8715
GT	Sens	Sense	0.205	Detected	-0.205	Detected	0.000	1.255	Detected	1.286	Detected	1.271	0.025	GT	Sens	contig427	contig427	Probable	CATTCGTCTTTGTGCTGGAAAGCAGAAGACAATACAGGAACTATTTGCA							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	19.8407	11.6796	16.3863	7.54853	38.3967	37.8855

GT	Sense	Sense	0.138	Detected	-0.138	Comprom	0.000	1.198	Detected	1.029	Detected	1.113	0.020	GT Sens	contig427	contig427	FACT cor	TTGTTAAGACTGTTTCAAGCCAGCAGGATACCAACCGTAACTGTTATAT							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	13.0491	8.4232	19.0521	15.732	25.4181	21.8302
GT	Sense	Sense	-0.608	Detected	0.608	Detected	0.000	1.336	Detected	1.467	Detected	1.402	0.149	GT Sens	contig427	contig427	Putative t	TCAGTACCGGGCCTGATGTAAGGCCCGGTGACTGGTACTGCAATGTTG							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	92.301	167.6	159.396	107.966	331.898	350.851
GT	Sense	Sense	0.279	Detected	-0.279	Detected	0.000	0.893	Detected	1.236	Detected	1.064	0.083	GT Sens	contig428	contig428	O-Glycos	TGTTCAAGGACACAGTCACCTCTGATGATGAATTTGTACCCTTATTATG							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	38.0097	20.1676	38.3943	34.1027	54.3232	66.5505
GT	Sense	Sense	0.174	Detected	-0.174	Comprom	0.000	1.536	Detected	1.368	Detected	1.452	0.017	GT Sens	contig428	contig428	Zinc finge	TTTCTGATTCATCTGGGAGTGATCCCACAGTGTCAGAGTTGGTAACTG							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	11.5029	7.06318	15.6083	20.8776	27.6337	23.7331
GT	Sense	Sense	0.108	Detected	-0.108	Detected	0.000	1.656	Detected	1.199	Detected	1.427	0.030	GT Sens	contig429	contig429	Uncharac	TCTTGG	contig429	Solyc06g	Solyc06g	Uncharac	GO:0016	GO:0016	contig429	Solyc06g	Uncharac	GO:0016	SL2.40ch	AT2G272	LHW	LHW (LO	chr2:116	90.8965	61.1495	156.794	116.45	248.29	174.596
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	1.186	Detected	0.956	Detected	1.071	0.013	GT Sens	contig430	contig430	Unknown	AGGAAAATGGCAGTAAGAGCCAGAGACACTCTTTTCCTGCTGAGTGG							contig430	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	23.4515	19.3515	28.3665	27.0577	51.2371	42.1756
GT	Sense	Sense	0.140	Detected	-0.140	Detected	0.000	1.490	Detected	1.217	Detected	1.353	0.020	GT Sens	contig430	contig430	Unknown	TTGAACCGAATTCTAGGATGTATACGACTTTAATGAAAGGTTATATGAA							contig430	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	33.8432	21.7814	53.0004	58.1361	80.5792	64.3836
GT	Sense	Sense	0.297	Comprom	-0.297	Comprom	0.000	1.253	Detected	1.047	Detected	1.150	0.067	GT Sens	contig431	contig431	Nicotia ta	ACTCCTATCTTTATAAGCTGAAAGGAAACCTGCCGATTTCTCGAGCGAT							contig431	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	8.77487	4.54528	5.85745	5.7264	15.9038	13.3131
GT	Sense	Sense	0.019	Detected	-0.019	Detected	0.000	1.321	Detected	1.067	Detected	1.194	0.011	GT Sens	contig431	contig431	Nicotia ta	GCATAGAGGACACACTCCCTTGTATTATCTTGATAATCTAGAATGAATT							contig431	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	12752.8	9707.93	20388.1	23222.8	29378.7	23784.2
GT	Sense	Sense	0.484	Comprom	-0.484	Comprom	0.000	1.560	Detected	1.303	Detected	1.432	0.104	GT Sens	contig432	contig432	Nicotia ta	CCTTAAAGATAATGAGTAGAGCCTTCATTGTCTTCTTCCCTCTAGAAGA							contig432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	8.63243	3.44822	10.888	11.1889	17.004	13.7391
GT	Sense	Sense	0.186	Detected	-0.186	Detected	0.000	1.310	Detected	1.142	Detected	1.226	0.027	GT Sens	contig433	contig433	Nicotia ta	CTAGTGTTTTGCTTTTGGCCAAAACCAATGTAATCTACTGTAAAGGCCT							contig433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	204.095	123.251	343.353	223.597	415.502	357.235
GT	Sense	Sense	0.195	Detected	-0.195	Detected	0.000	1.423	Detected	0.870	Detected	1.147	0.077	GT Sens	contig434	contig434	N.tabacur	GGTTCCTTGTTTTACCACAAAGCTCTATTCTTGATCAAAATTCATAACAT							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	20.6695	12.331	49.3281	64.9418	45.2439	29.7723
GT	Sense	Sense	-1.069	Comprom	1.069	Detected	0.000	1.212	Detected	0.994	Detected	1.103	0.413	GT Sens	contig434	contig434	Nicotia ta	GGTTTCTCCTAAAAACCTAAAACTTTTCAATTTTTTCGGTGTCGATTCT							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	4.75727	16.3715	10.1796	12.213	21.6046	17.9332
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	1.114	Detected	1.043	Detected	1.079	0.012	GT Sens	contig434	contig434	Nicotia ta	GGACCTGCAAAGAATTGATCAGATCAGAGAGTATATGATCCATCATGTT							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1023.81	684.672	1687.99	1534.02	1914.75	1760.82
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	2.890	Detected	2.396	Detected	2.643	0.012	GT Sens	contig434	contig434	Chloroph	ATTAGG	contig434	Solyc07g	Solyc07g	Chloroph	GO:0016	GO:0016	contig434	Solyc07g	Chloroph	GO:0016	SL2.40ch	AT2G050	LHCB2.2.	LHCB2.2	chr2:179	1083.86	688.587	2280.88	2415.91	6769.16	4639.04
GT	Sense	Sense	-0.457	Detected	0.457	Detected	0.000	1.189	Detected	0.986	Detected	1.088	0.146	GT Sens	contig434	contig434	Nicotia ta	TCTCCGGAAACAGCTGGGAATTTTGCTTTTGGCTTGTACGATCTTGTA							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	39.814	58.6634	75.1404	101.143	116.475	97.7025
GT	Sense	Sense	-0.252	Detected	0.252	Detected	0.000	1.293	Detected	1.053	Detected	1.173	0.052	GT Sens	contig434	contig434	Mitochon	GTCTCT	contig434	Solyc08g	Solyc08g	Mitochon	GO:0016	GO:0016	contig434	Solyc08g	Mitochon	GO:0016	SL2.40ch	AT4G11440.1		binding	chr4:695	46.8368	51.8923	90.9533	72.5283	127.693	104.395
GT	Sense	Sense	0.433	Detected	-0.433	Comprom	0.000	3.024	Detected	2.140	Detected	2.582	0.053	GT Sens	contig435	contig435	Leucine-r	CTGGAA	contig435	Solyc01g	Solyc01g	Leucine-rich repeat receptor-li			contig435	Solyc01g	LRR rece	GO:0004	SL2.40ch	AT1G120	LRX1	LRX1 (LE	chr1:407	18.0733	7.74857	38.6865	42.3238	101.715	53.2389
GT	Sense	Sense	-0.131	Comprom	0.131	Comprom	0.000	2.590	Detected	2.549	Detected	2.569	0.003	GT Sens	contig445	contig445	Unknown	CTCAGC	contig445	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig445	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G32375.1				2.31151	2.16773	5.34729	2.02188	14.2442	13.3625
GT	Sense	Sense	-1.395	Comprom	1.395	Detected	0.000	1.731	Detected	2.296	Detected	2.013	0.293	GT Sens	contig452	contig452	Reverse t	CGCCTC	contig452	Solyc11g	Solyc11g	Reverse t	GO:0006	GO:0006	contig452	Solyc10g	Serine/thr	GO:0005	SL2.40ch	#N/A	#N/A	#N/A	#N/A	2.08041	11.2468	1.90295	1.89667	16.9693	24.2344
GT	Sense	Sense	0.029	Detected	-0.029	Detected	0.000	1.086	Detected	1.174	Detected	1.130	0.002	GT Sens	contig456	contig456	BHLH trai	TGATCC	contig456	Solyc09g	Solyc09g	BHLH trai	GO:0005	GO:0005	contig456	Solyc09g	BHLH trai	GO:0003	SL2.40ch	AT2G201	PIL5. PIF	PIL5 (PH	chr2:870	657.568	493.994	1194.83	1319.11	1278.3	1312
GT	Sense	Sense	-0.172	Detected	0.172	Detected	0.000	1.748	Detected	1.744	Detected	1.746	0.010	GT Sens	contig457	contig457	NHL repe	GCAATT	contig457	Solyc05g	Solyc05g	NHL repeat-containing protein			contig457	Solyc05g	NHL repeat-containi		SL2.40ch	AT1G70280.2		NHL repe	chr1:264	136.061	134.995	343.373	214.245	481.06	463.134
GT	Sense	Sense	-0.096	Detected	0.096	Detected	0.000	1.090	Detected	1.023	Detected	1.056	0.009	GT Sens	contig459	contig459	Unknown	GGTGTT	contig459	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig459	Solyc07g	Unknown Protein (A		SL2.40ch	AT4G01895.1		systemic	chr4:819	8478.82	7575.78	11941.6	14092.6	18031.9	16614.5
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	1.222	Detected	1.139	Detected	1.180	0.006	GT Sens	contig460	contig460	Formin 3	GACAGT	contig460	Solyc06g	Solyc06g	Formin 3	GO:0030	GO:0030	contig460	Solyc06g	Formin 3	GO:0030	SL2.40ch	AT3G255	AFH1. FH	AFH1 (FO	chr3:925	467.712	324.62	745.203	533.25	960.312	875.51
GT	Sense	Sense	-0.201	Comprom	0.201	Comprom	0.000	1.018	Detected	1.330	Detected	1.174	0.044	GT Sens	contig462	contig462	Cation/H+	GCATCT	contig462	Solyc08g	Solyc08g	Cation/H+	GO:0015	GO:0015	contig462	Solyc08g	Cation/H+	GO:0015	SL2.40ch	AT3G176	ATCHX19	ATCHX19	chr3:602	7.53151	7.77764	15.5723	6.13831	16.3835	19.6393
GT	Sense	Sense	0.065	Comprom	-0.065	Comprom	0.000	3.614	Detected	3.700	Detected	3.657	0.000	GT Sens	contig466	contig466	UPF0497	TTTGGT	contig466	Solyc01g	Solyc01g	UPF0497	GO:0005	GO:0005	contig466	Solyc01g	UPF0497	GO:0005	SL2.40ch	AT4G31490.1		coatome	chr4:152	4.98091	3.55761	7.13457	13.2142	54.4689	55.8113
GT	Sense	Sense	-0.604	Detected	0.604	Detected	0.000	2.269	Detected	0.977	Detected	1.623	0.208	GT Sens	contig472	contig472	Blue copp	CTTGGT	contig472	Solyc12g	Solyc12g	Blue copp	GO:0009	GO:0009	contig472	Solyc12g	Blue copp	GO:0009	SL2.40ch	AT5G45480.1		unknown	chr5:184	11.9966	21.6585	21.2288	50.7962	82.1222	32.373
GT	Sense	Sense	0.184	Detected	-0.184	Detected	0.000	1.229	Detected	0.896	Detected	1.062	0.051	GT Sens	contig474	contig474	Nodulin M	CTCCAT	contig474	Solyc01g	Solyc01g	Nodulin M	GO:0016	GO:0016	contig474	Solyc01g	Nodulin M	GO:0016	SL2.40ch	AT3G30340.1		nodulin M	chr3:119	327.203	198.1	500.011	336.169	630.62	483.371
GT	Sense	Sense	0.335	Detected	-0.335	Comprom	0.000	1.104	Detected	0.914	Detected	1.009	0.101	GT Sens	contig476	contig476	General t	GAAGAA	contig476	Solyc09g	Solyc09g	General t	GO:0003	GO:0003	contig476	Solyc09g	General t	GO:0003	SL2.40ch	AT1G19485.1		AT hook	chr1:674	18.4432	9.06642	16.558	14.792	29.3827	24.8626
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	1.750	Detected	1.332	Detected	1.541	0.027	GT Sens	contig477	contig477	Magnesiu	AAATCC	contig477	Solyc04g	Solyc04g	Magnesiu	GO:0015	GO:0015	contig477	Solyc04g	Magnesiu	GO:0019	SL2.40ch	AT5G136	GUN5. CC	GUN5 (GI	chr5:438	3768.41	2393.18	6423.75	7970.14	10673.7	7712.29
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	1.192	Detected	1.163	Detected	1.178	0.000	GT Sens	contig491	contig491	Zinc finge	GGTTCC	contig491	Solyc07g	Solyc07g	Zinc finge	GO:0008	GO:0008	contig491	Solyc07g	Zinc finge	GO:0003	SL2.40ch	AT3G52980.1		RNA reco	chr3:196	232.187	181.621	349.255	327.936	495.935	469.147
GT	Sense	Sense	0.231	Detected	-0.231	Detected	0.000	1.076	Detected	1.204	Detected	1.140	0.041	GT Sens	contig494	contig494	RNA-bind	CAGGAA	contig494	Solyc01g	Solyc01g	RNA-bind	GO:0003	GO:0003	contig494	Solyc01g	RNA-bind	GO:0003	SL2.40ch	AT1G09230.1		RNA reco	chr1:297	66.3186	37.6447	97.7746	80.1273	111.307	117.424
GT	Sense	Sense	-0.224	Detected	0.224	Detected	0.000	1.129	Detected	0.900	Detected	1.015	0.056	GT Sens	contig495	contig495	Auxin-res	GAAAAA	contig495	Solyc10g	Solyc10g	Auxin-responsive GH3-like (AH			contig495	Solyc10g	Auxin-responsive G		SL2.40ch	AT2G35960.1				3777.94	4028.02	3967.21	4440.23	9017.15	7428.3
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	1.064	Detected	0.954	Detected	1.009	0.010	GT Sens	contig508	contig508	Heat stres	ATGGAT	contig508	Solyc06g	Solyc06g	Heat stres	GO:0005	GO:0005	contig508	Solyc06g	Heat stres	GO:0005	SL2.40ch	AT5G168	HSF3. HS	HSF3 (HE	chr5:553	96.9213	84.9557	122.689	141.52	200.446	179.306
GT	Sense	Sense	0.120	Detected	-0.120	Detected	0.000	1.073	Detected	1.045	Detected	1.059	0.013	GT Sens	contig509	contig509	Ulp1 prot	AGAAAC	contig509	Solyc03g	Solyc03g	Ulp1 protease family C-termina			contig509	Solyc12g	Ulp1 protease family		SL2.40ch	AT1G14680.1		unknown	chr1:504	313.04	207.184	321.119	408.012	566.407	535.992
GT	Sense	Sense	0.470	Comprom	-0.470	Comprom	0.000	1.239	Detected	1.102	Detected	1.170	0.133	GT Sens	contig51	contig51	Unknown	CAATTA	contig51	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig51	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G02670.1		DNA repa	chr1:576	8.28331	3.37578	13.911	16.2954	13.1916	11.5794
GT	Sense	Sense	0.030	Detected	-0.030	Detected	0.000	0.989	Detected	1.171	Detected	1.080	0.008	GT Sens	contig512	contig512	Unknown	TGGATC	contig512	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig512	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G434	RPP8. HR	RPP8 (RE	chr5:174	30.8048	23.0843	60.0801	56.2006	55.9207	61.279
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	1.157	Detected	1.327	Detected	1.242	0.018	GT Sens	contig515	contig515	Beta-1%2	TTGACA	contig515	Solyc03g	Solyc03g	Beta-1%2	GO:0016	GO:0016	contig515	Solyc03g	Beta-1.3-	GO:0016	SL2.40ch	AT5G15050.1		glycosylt	chr5:487	103.51	66.1343	170.521	133.357	194.929	211.79
GT	Sense	Sense	-1.014	Comprom	1.014	Detected	0.000	3.634	Detected	2.093	Detected	2.863	0.154	GT Sens	contig515	contig515	Pectate ly	AATCTG	contig515	Solyc02g	Solyc02g	Pectate ly	GO:0016	GO:0016	contig515	Solyc02g	Pectate ly	GO:0016	SL2.40ch	AT3G24230.1		pectate l	chr3:877	3.94595	12.5759	10.086	42.9118	92.3969	30.658
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	2.270	Detected	2.139	Detected	2.205	0.001	GT Sens	contig519	contig519	Ribulose-	GCTGCA	contig519	Solyc09g	Solyc09g	Ribulose-	GO:0005	GO:0005	contig519	Solyc09g	Ribulose-	GO:0046	SL2.40ch	AT2G397	RCA	RCA (RU	chr2:165	4182.11	3195.64	10015.7	15305.4	18632.2	16434.2
GT	Sense	Sense	-0.145	Detected	0.145	Detected	0.000	1.650	Detected	0.969	Detected	1.309	0.071	GT Sens	contig523	contig523	Zinc trans	CGTGGA	contig523	Solyc02g	Solyc02g	Zinc trans	GO:0000	GO:0000	contig523	Solyc02g	Zinc trans	GO:0000	SL2.40ch	AT3G127	ZIP1	ZIP1 (ZIN	chr3:405	141.269	134.962	327.971	397.266	457.858	275.824
GT	Sense	Sense	-0.281	Detected	0.281	Detected	0.000	1.665	Detected	0.846	Detected	1.255	0.127	GT Sens	contig529	contig529	UDP-gluc	GATTTC	contig529	Solyc10g	Solyc10g	UDP-gluc	GO:0008	GO:0008	contig529	Solyc10g	UDP-gluc	GO:0008	SL2.40ch	AT1G782	AtUGT85	AtUGT85	chr1:294	10.1945	11.7663	11.1926	51.4706	36.7018	20.0857
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	1.503	Detected	1.293	Detected	1.398	0.006	GT Sens	contig532	contig532	Receptor-	AAGAGA	contig532	Solyc10g	Solyc10g	Receptor	GO:0006	GO:0006	contig532	Solyc10g	Receptor	GO:0005	SL2.40ch	AT2G01820.1		leucine-r	chr2:357	76.8992	59.0393	100.257	120.35	201.821	168.443
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	1.413	Detected	1.315	Detected	1.364	0.001	GT Sens	contig534	contig534	Nucleoso	GAAAGG	contig534	Solyc08g	Solyc08g	Nucleoso	GO:0005	GO:0005	contig534	Solyc08g	Nucleoso	GO:0003	SL2.40ch	AT2G194	NFA02. N	NAP1;2 (	chr2:843	62.9018	48.941	92.8645	89.2664	156.176	140.896
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	1.629	Detected	1.242	Detected	1.435	0.018	GT Sens	contig537	contig537	Cc-nbs-lr	TTGCTC	contig537	Solyc04g	Solyc04g	Cc-nbs-lr	GO:0005	GO:0005	contig537	Solyc04g	Lrr. resis	GO:0005	SL2.40ch	AT1G58400.1		disease r	chr1:216	292.815	216.207	785.153	793.263	822.477	607.188
GT	Sense	Sense	-0.085	Detected	0.085	Detected	0.000	1.087	Detected	0.932	Detected	1.010	0.013	GT Sens	contig544	contig544	Dihydrofl	GGGTAT	contig544	Solyc02g	Solyc02g	Dihydrofl	GO:0004	GO:0004	contig544	Solyc02g	Dihydrofl	GO:0004	SL2.40ch	AT4G16960.1		disease r	chr4:954	1404.57	1234.6	2781.86	2612.1	2956.96	2563.73
GT	Sense	Sense	0.094	Detected	-0.094	Comprom	0.000	1.509	Detected	1.371	Detected	1.440	0.006	GT Sens	contig548	contig548	Non-spec	TCTCTT	contig548	Solyc09g	Solyc09g	Non-spec	GO:0008	GO:0008	contig548	Solyc09g	Non-spec	GO:0008	SL2.40ch	AT5G53890.1		leucine-r	chr5:218	9.45617	6.49037	26.5665	35.5711	23.5608	20.6812
GT	Sense	Sense	-0.259	Detected	0.259	Detected	0.000	1.105	Detected	1.025	Detected	1.065	0.056	GT Sens	contig559	contig559	Polyaden	TGGTTT	contig559	Solyc10g	Solyc10g	Polyaden	GO:0000	GO:0000	contig559	Solyc10g	Polyaden	GO:0003	SL2.40ch	AT2G44710.1		RNA reco	chr2:184	257.354	288.182	419.159	337.604	618.995	565.367
GT	Sense	Sense	0.639	Detected	-0.639	Comprom	0.000	1.645	Detected	0.855	Detected	1.250	0.238	GT Sens	contig563	contig563	Unknown	ATCGTC	contig563	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig563	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G166	PDE120.	TIC40	chr5:545	22.3884	7.21499	16.0034	9.97765	42.0023	23.4482
GT	Sense	Sense	0.169	Detected	-0.169	Detected	0.000	1.223	Detected	0.820	Detected	1.021	0.060	GT Sens	contig565	contig565	Ferric red	CGACAA	contig565	Solyc01g	Solyc01g	Ferric red	GO:0000	GO:0000	contig565	Solyc01g	Ferric red	GO:0000	SL2.40ch	AT1G230	ATFRO3.	FRO3: fe	chr1:815	601.054	371.521	704.43	536.009	1165.65	851.187
GT	Sense	Sense	-0.155	Detected	0.155	Detected	0.000	1.548	Detected	1.117	Detected	1.332	0.037	GT Sens	contig566	contig566	Subtilisin	GAACGA	contig566	Solyc04g	Solyc04g	Subtilisin	GO:0004	GO:0004	contig566	Solyc04g	Subtilisin	GO:0004	SL2.40ch	AT5G517	ATSBT1.	ATSBT1.	chr5:210	2652.21	2568.71	3848.93	3977.55	8064.07	5776.89
GT	Sense	Sense	-0.128	Detected	0.128	Detected	0.000	1.096	Detected	0.921	Detected	1.008	0.023	GT Sens	contig569	contig569	Os02g07	ATAAAT	contig569	Solyc06g	Solyc06g	Os02g07	GO:0005	GO:0005	contig569	Solyc06g	Os02g07	GO:0005	SL2.40ch	AT3G48050.2		DNA bind	chr3:177	400.521	373.816	711.112	625.174	873.914	747.481
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	1.482	Detected	1.196	Detected	1.339	0.017	GT Sens	contig573	contig573	Vesicle-a	AGAATT	contig573	Solyc08g	Solyc08g	Vesicle-a	GO:0005	GO:0005	contig573	Solyc08g	Vesicle-a	GO:0005	SL2.40ch	AT3G606	VAP27-1	VAP (VE	chr3:224	95.6405	86.7097	221.804	232.845	268.802	212.92
GT	Sense	Sense	0.162	Detected	-0.162	Detected	0.000	1.959	Detected	1.159	Detected	1.559	0.069	GT Sens	contig576	contig576	NAC dom	CATGAA	contig576	Solyc10g	Solyc10g	NAC dom	GO:0003	GO:0003	contig576	Solyc10g	NAC dom	GO:0003	SL2.40ch	AT3G155	ATNAC2.	ATNAC2	chr3:524	64.0041	39.9602	43.9844	68.3553	207.738	115.208
GT	Sense	Sense	-0.088	Detected	0.088	Detected	0.000	0.950	Detected	1.083	Detected	1.016	0.012	GT Sens	contig577	contig577	Cellulose	TGTGGA	contig577	Solyc10g	Solyc10g	Cellulose	GO:0051	GO:0051	contig577	Solyc10g	Cellulose	GO:0051	SL2.40ch	AT5G037	ATCSLA	ATCSLA	chr5:985	220.158	194.32	391.817	373.899	422.156	447.075
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	0.820	Detected	1.189	Detected	1.005	0.042	GT Sens	contig579	contig579	Phloem p	AAATCC	contig579	Solyc02g	Solyc02g	Phloem protein 2 (AHRD V1 **-			contig579	Solyc02g	Phloem p	GO:0030	SL2.40ch	AT4G198	ATPP2-A	ATPP2-A	chr4:107	403.947	272.576	548.243	543.734	619.298	771.857
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	1.363	Detected	1.030	Detected	1.197	0.020	GT Sens	contig584	contig584	Aldehyde	TCCGTT	contig584	Solyc07g	Solyc07g	Aldehyde	GO:0055	GO:0055	contig584	Solyc07g	Aldehyde	GO:0004	SL2.40ch	AT2G242	ALDH11A	ALDH11A	chr2:103	11558.1	9640.23	19215.4	21896.4	28704.1	21988.7
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	1.658	Detected	1.140	Detected	1.399	0.037	GT Sens	contig585	contig585	Oxygen-e	AGGCAT	contig585	Solyc02g	Solyc02g	Oxygen-e	GO:0008	GO:0008	contig585	Solyc02g	Oxygen-e	GO:0008	SL2.40ch	AT5G665	PSBO-1.	PSBO1 (I	chr5:265	776.566	694.414	1496.3	1553.27	2449.14	1651.37
GT	Sense	Sense	0.083	Detected	-0.083	Detected	0.000	1.588	Detected	1.530	Detected	1.559	0.003	GT Sens	contig587	contig587	Acyl- (AH	CTACTC	contig587	Solyc11g	Solyc11g	Acyl- (AH	GO:0055	GO:0055	contig587	Solyc11g	Acyl- (AH	GO:0055	SL2.40ch	AT3G02630.1		acyl-(acy	chr3:562	209.383	145.957	395.238	281.233	555.451	515.181
GT	Sense	Sense	-0.210	Detected	0.210	Detected	0.000	1.490	Detected	1.025	Detected	1.257	0.057	GT Sens	contig595	contig595	Glycosylt	CACCTG	contig595	Solyc02g	Solyc02g	Glycosylt	GO:0016	GO:0016	contig595	Solyc02g	Glycosylt	GO:0016	SL2.40ch	AT3G507	GATL2	GATL2 (G	chr3:188	99.5476	104.048	173.193	225.53	302.064	211.266
GT	Sense	Sense	0.615	Detected	-0.615	Comprom	0.000	1.549	Detected	1.518	Detected	1.533	0.130	GT Sens	contig597	contig597	Genomic	AGCAGT	contig597	Solyc12g	Solyc12g	Genomic DNA chromosome 5			contig597	Solyc12g	Genomic DNA chror		SL2.40ch	AT5G10660.1		calmodu	chr5:337	14.9747	4.9895	6.78475	21.2915	26.7275	25.2609
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	0.956	Detected	1.069	Detected	1.012	0.003	GT Sens	contig598	contig598	Nuclear p	ATAAAC	contig598	Solyc08g	Solyc08g	Nuclear pore complex protein			contig598	Solyc08g	Nuclear pore compl		SL2.40ch	AT4G32910.1		INVOLVE	chr4:158	345.432	262.647	523.832	423.961	617.467	644.751
GT	Sense	Sense	-0.394	Detected	0.394	Detected	0.000	1.134	Detected	0.982	Detected	1.058	0.119	GT Sens	contig610	contig610	Ferredox	ATTAAG	contig610	Solyc01g	Solyc01g	Ferredoxin-like (AHRD V1 ***- (			contig610	Solyc01g	Ferredoxin-like (AH		SL2.40ch	AT1G02180.1		ferredox	chr1:413	55.4503	74.8515	95.5143	63.8327	149.382	129.846
GT	Sense	Sense	0.616	Detected	-0.616	Comprom	0.000	1.493	Detected	1.143	Detected	1.318	0.176	GT Sens	contig611	contig611	CWF19-lik	ACAGAA	contig611	Solyc05g	Solyc05g	CWF19-like protein 1 (AHRD V1			contig611	Solyc12g	CwfJ dom	GO:0008	SL2.40ch	AT4G38260.1		unknown	chr4:179	15.3485	5.10596	17.1222	24.5065	26.3425	19.95
GT	Sense	Sense	0.212	Detected	-0.212	Detected	0.000	1.186	Detected	1.668	Detected	1.427	0.047	GT Sens	contig612	contig612	Expresse	TCATGA	contig612	Solyc03g	Solyc03g	Expressed protein (Fragment)			contig612	Solyc03g	Expressed protein (		SL2.40ch	AT5G515	EXL3	EXL3 (EX	chr5:209	101.164	58.921	104.647	83.7056	185.705	250.331
GT	Sense	Sense	-0.266	Detected	0.266	Detected	0.000	1.978	Detected	2.243	Detected	2.110	0.019	GT Sens	contig614	contig614	Expansin	CTAAAT	contig614	Solyc06g	Solyc06g	Expansin	GO:0005	GO:0005	contig614	Solyc06g	Expansin	GO:0005	SL2.40ch	AT1G695	ATEXPA1	ATEXPA	chr1:261	301.888	341.107	861.636	928.996	1336.36	1549.46
GT	Sense	Sense	0.065	Detected	-0.065	Detected	0.000	1.063	Detected	1.062	Detected	1.063	0.004	GT Sens	contig615	contig615	Carboxyl	CCACAA	contig615	Solyc04g	Solyc04g	Carboxyl	GO:0008	GO:0008	contig615	Solyc04g	Carboxyl	GO:0030	SL2.40ch	AT5G66430.1		S-adeno	chr5:265	155.374	110.982	365.524	189.737	290.002	279.743
GT	Sense	Sense	-0.222	Detected	0.222	Detected	0.000	1.730	Detected	1.249	Detected	1.489	0.045	GT Sens	contig625	contig625	FAD depe	ACTTGA	contig625	Solyc01g	Solyc01g	FAD dependent oxidoreductas			contig625	Solyc01g	FAD dependent oxi		SL2.40ch	AT2G32640.1		unknown	chr2:138	132.479	140.79	311.766	315.003	478.685	331.114
GT	Sense	Sense	0.180	Comprom	-0.180	Comprom	0.000	2.093	Detected	2.273	Detected	2.183	0.008	GT Sens	contig628	contig628	F-box fam	AGATGG	contig628	Solyc08g	Solyc08g	F-box fan	GO:0004	GO:0004	contig628	Solyc08g	F-box fan	GO:0004	SL2.40ch	ATCG010	NDHF	Chloropl	chrC:110	3.84936	2.34506	49.0535	51.5367	13.5514	14.816
GT	Sense	Sense	-1.036	Comprom	1.036	Detected	0.000	3.088	Detected	1.163	Detected	2.126	0.272	GT Sens	contig628	contig628	Pollen all	GTTCGT	contig628	Solyc07g	Solyc07g	Pollen allergen Phl p 11 (AHRD			contig628	Solyc07g	Pollen allergen Phl		SL2.40ch	AT5G66560.1		phototro	chr5:265	4.96855	16.34	1.99042	32.8124	80.9926	20.5824
GT	Sense	Sense	-0.047	Comprom	0.047	Comprom	0.000	2.920	Detected	2.260	Detected	2.590	0.016	GT Sens	contig630	contig630	Syntaxin	ATTTGA	contig630	Solyc12g	Solyc12g	Syntaxin	GO:0016	GO:0016	contig630	Solyc12g	Syntaxin	GO:0016	SL2.40ch	AT1G05360.1		unknown	chr1:156	3.22753	2.69406	2.00779	4.69377	23.5816	14.4091
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	1.642	Detected	0.909	Detected	1.275	0.075	GT Sens	contig635	contig635	Cellulose	AGGAAG	contig635	Solyc07g	Solyc07g	Cellulose	GO:0016	GO:0016	contig635	Solyc07g	Cellulose	GO:0016	SL2.40ch	AT5G174	IRX3. CE	IRX3 (IRR	chr5:573	2084.56	1517.15	4713.33	3648.6	5865.54	3406.3
GT	Sense	Sense	0.422	Detected	-0.422	Detected	0.000	1.061	Detected	1.259	Detected	1.160	0.116	GT Sens	contig637	contig637	3-oxoacy	AACCCC	contig637	Solyc08g	Solyc08g	3-oxoacy	GO:0005	GO:0005	contig637	Solyc08g	3-oxoacy	GO:0005	SL2.40ch	AT5G462	KAS I	KAS I (3-	chr5:187	822.577	358.358	669.564	444.451	1196.95	1325.96
GT	Sense	Sense	-0.414	Detected	0.414	Detected	0.000	1.135	Detected	1.238	Detected	1.186	0.105	GT Sens	contig638	contig638	Protein pl	AAGGTG	contig638	Solyc02g	Solyc02g	Protein p	GO:0005	GO:0005	contig638	Solyc02g	Protein pl	GO:0005	SL2.40ch	AT2G346	AIR9	AIR9: pro	chr2:146	991.918	1376.91	2467.23	2316.34	2712.93	2811.74
GT	Sense	Sense	-0.558	Comprom	0.558	Comprom	0.000	2.480	Detected	1.447	Detected	1.964	0.123	GT Sens	contig641	contig641	Cation/H(	ATTAGG	contig641	Solyc05g	Solyc05g	Cation/H(	GO:0015	GO:0015	contig641	Solyc05g	Cation/H(	GO:0015	SL2.40ch	AT4G237	ATCHX17	ATCHX17	chr4:123	3.16699	5.36264	4.72562	7.00841	24.3053	11.4657
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	1.226	Detected	0.993	Detected	1.110	0.013	GT Sens	contig644	contig644	Os12g058	CCACAA	contig644	Solyc02g	Solyc02g	Os12g0581300 protein (Fragm			contig644	Solyc02g	Os12g0581300 prot		SL2.40ch	AT5G66740.1		unknown	chr5:266	47.0332	34.4468	71.7381	52.43	99.5406	81.7257
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	1.324	Detected	1.156	Detected	1.240	0.005	GT Sens	contig646	contig646	NAD-depe	ATGTAT	contig646	Solyc08g	Solyc08g	NAD-depe	GO:0008	GO:0008	contig646	Solyc08g	NAD-depe	GO:0008	SL2.40ch	AT1G167	HCF173	HCF173 (	chr1:572	5175.92	3856.4	7312.63	9080.27	11817.7	10159.9
GT	Sense	Sense	-0.120	Detected	0.120	Detected	0.000	1.409	Detected	1.502	Detected	1.456	0.008	GT Sens	contig648	contig648	Rhamnog	ATCAGC	contig648	Solyc04g	Solyc04g	Rhamnog	GO:0030	GO:0030	contig648	Solyc04g	Rhamnog	GO:0016	SL2.40ch	AT1G09890.1		lyase	chr1:321	23.1766	21.3831	68.0162	29.1575	62.4942	64.3545
GT	Sense	Sense	-0.481	Detected	0.481	Detected	0.000	2.355	Detected	1.193	Detected	1.774	0.143	GT Sens	contig655	contig655	GPI-anch	CGAAAT	contig655	Solyc03g	Solyc03g	GPI-anchored protein (AHRD V			contig655	Solyc03g	GPI-anchored prote		SL2.40ch	AT2G27060.1		ATP bind	chr2:115	13.451	20.4931	1.93871	51.2161	89.7864	38.7356
GT	Sense	Sense	0.508	Detected	-0.508	Detected	0.000	0.817	Detected	1.592	Detected	1.204	0.200	GT Sens	contig655	contig655	Leaf sene	AACTTA	contig655	Solyc02g	Solyc02g	Leaf senescence protein-like (			contig655	Solyc02g	Leaf senescence pr		SL2.40ch	AT3G28150.1		unknown	chr3:104	106.425	41.1111	57.79	52.1537	123.137	203.396
GT	Sense	Sense	-0.051	Comprom	0.051	Comprom	0.000	1.113	Detected	1.505	Detected	1.309	0.023	GT Sens	contig658	contig658	Rop-inter	GAAACA	contig658	Solyc03g	Solyc03g	Rop-interactive crib motif-cont			contig658	Solyc03g	Rop-interactive crib		SL2.40ch	AT5G585	RANBP1	RANBP1	chr5:236	5.34357	4.48307	3.60536	3.96226	11.1878	14.1712
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	2.012	Detected	1.773	Detected	1.893	0.004	GT Sens	contig663	contig663	Unknown	CTCTAA	contig663	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig663	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G491	MET1. MI	MET1 (M	chr5:199	155.991	118.663	332.941	500.088	580.047	474.491
GT	Sense	Sense	-0.792	Detected	0.792	Detected	0.000	1.441	Detected	1.629	Detected	1.535	0.194	GT Sens	contig663	contig663	Transcrip	CAGTTA	contig663	Solyc04g	Solyc04g	Transcrip	GO:0005	GO:0005	contig663	Solyc04g	Transcrip	GO:0030	SL2.40ch	AT1G596	ZCW32. B	ZCW32:	chr1:219	111.115	260.483	442.968	331.849	488.316	537.023
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	2.854	Detected	2.671	Detected	2.762	0.006	GT Sens	contig669	contig669	FAD-bind	CGAAGC	contig669	Solyc02g	Solyc02g	FAD-bind	GO:0009	GO:0009	contig669	Solyc02g	FAD-bind	GO:0009	SL2.40ch	AT5G44400.1		FAD-bind	chr5:178	80.1424	47.2916	106.486	49.2415	470.45	400.005
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	1.116	Detected	0.965	Detected	1.041	0.006	GT Sens	contig674	contig674	MYB tran	TCCTAG	contig674	Solyc10g	Solyc10g	MYB tran	GO:0003	GO:0003	contig674	Solyc10g	Late elon	GO:0005	SL2.40ch	AT1G010	LHY. LHY	LHY (LAT	chr1:339	376.802	283.899	638.475	696.438	749.173	651.56
GT	Sense	Sense	0.112	Detected	-0.112	Detected	0.000	2.306	Detected	2.351	Detected	2.329	0.002	GT Sens	contig678	contig678	3-oxo-5-a	CAAACA	contig678	Solyc11g	Solyc11g	3-oxo-5-a	GO:0016	GO:0016	contig678	Solyc11g	3-oxo-5-a	GO:0016	SL2.40ch	AT5G40630.1		ubiquitin	chr5:162	339.326	227.016	694.177	1079.63	1451.02	1444.62
GT	Sense	Sense	0.054	Detected	-0.054	Detected	0.000	1.624	Detected	1.425	Detected	1.524	0.005	GT Sens	contig680	contig680	Magnesiu	TTAAGA	contig680	Solyc11g	Solyc11g	Magnesiu	GO:0016	GO:0016	contig680	Solyc11g	Magnesiu	GO:0016	SL2.40ch	AT5G228	ATMGT1	ATMGT1	chr5:762	725.312	526.274	1096.16	1460.78	2012.27	1692.8
GT	Sense	Sense	-0.413	Detected	0.413	Detected	0.000	1.627	Detected	1.020	Detected	1.323	0.123	GT Sens	contig688	contig688	BHLH trai	GGAGTT	contig688	Solyc01g	Solyc01g	BHLH trai	GO:0003	GO:0003	contig688	Solyc01g	BHLH trai	GO:0003	SL2.40ch	AT4G000	UNE10	UNE10 (u	chr4:178	138.294	191.708	315.022	596.523	531.515	336.863
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	0.968	Detected	1.134	Detected	1.051	0.019	GT Sens	contig706	contig706	Ribonucl	GGTGAA	contig706	Solyc11g	Solyc11g	Ribonucl	GO:0005	GO:0005	contig706	Solyc11g	Ribonucl	GO:0006	SL2.40ch	AT3G033	DCL2	DCL2 (DI	chr3:768	40.3716	37.3526	71.3247	61.7763	80.301	86.9857
GT	Sense	Sense	-0.032	Comprom	0.032	Comprom	0.000	1.868	Detected	1.377	Detected	1.623	0.022	GT Sens	contig707	contig707	Crossove	GTTATT	contig707	Solyc01g	Solyc01g	Crossove	GO:0003	GO:0003	contig707	Solyc01g	Crossove	GO:0006	SL2.40ch	AT5G39770.1		DNA bind	chr5:159	4.14038	3.38501	12.2399	3.36336	14.4394	9.92403
GT	Sense	Sense	0.961	Detected	-0.961	Detected	0.000	2.003	Detected	1.324	Detected	1.664	0.244	GT Sens	contig709	contig709	Cytochro	ATTGGC	contig709	Solyc04g	Solyc04g	Cytochro	GO:0019	GO:0019	contig709	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT4G373	CYP81D5	CYP81D5	chr4:175	258.068	53.2513	305.337	173.881	496.729	299.46
GT	Sense	Sense	0.293	Detected	-0.293	Detected	0.000	0.840	Detected	1.305	Detected	1.072	0.103	GT Sens	contig710	contig710	MazG nuc	TATCTC	contig710	Solyc09g	Solyc09g	MazG nuc	GO:0047	GO:0047	contig710	Solyc09g	MazG nuc	GO:0047	SL2.40ch	AT3G25400.1		FUNCTIO	chr3:921	112.909	58.8301	125.818	158.332	154.193	205.456
GT	Sense	Sense	0.536	Detected	-0.536	Detected	0.000	3.735	Detected	3.938	Detected	3.836	0.020	GT Sens	contig711	contig711	Serpin (S	ATGGTA	contig711	Solyc04g	Solyc04g	Serpin (S	GO:0004	GO:0004	contig711	Solyc04g	Serpin (S	GO:0004	SL2.40ch	AT3G45220.1		serpin. p	chr3:165	119.011	44.2724	235.344	191.233	1021.17	1135.09
GT	Sense	Sense	1.484	Detected	-1.484	Comprom	0.000	0.855	Detected	1.766	Detected	1.310	0.488	GT Sens	contig711	contig711	Clathrin a	TTTTAG	contig711	Solyc12g	Solyc12g	Clathrin a	GO:0005	GO:0005	contig711	Solyc12g	Clathrin a	GO:0030	SL2.40ch	AT1G05020.1		epsin N-t	chr1:143	54.6265	5.45427	46.6651	41.4147	33.0033	59.8864
GT	Sense	Sense	-0.121	Detected	0.121	Detected	0.000	1.597	Detected	0.907	Detected	1.252	0.076	GT Sens	contig712	contig712	Genomic	TGGCAG	contig712	Solyc02g	Solyc02g	Genomic DNA chromosome 5			contig712	Solyc02g	Genomic DNA chror		SL2.40ch	AT4G31890.1		armadillo	chr4:154	171.024	158.126	268.872	334.83	525.695	314.609
GT	Sense	Sense	0.487	Detected	-0.487	Detected	0.000	1.688	Detected	1.321	Detected	1.504	0.102	GT Sens	contig717	contig717	Non-spec	TTGCTC	contig717	Solyc08g	Solyc08g	Non-spec	GO:0006	GO:0006	contig717	Solyc08g	Non-spec	GO:0005	SL2.40ch	AT5G151	PIN8	PIN8 (PIN	chr5:489	121.677	48.4459	131.995	123.868	261.47	195.695
GT	Sense	Sense	-0.086	Detected	0.086	Detected	0.000	1.139	Detected	0.905	Detected	1.022	0.020	GT Sens	contig719	contig719	Granule-b	TAAAAA	contig719	Solyc08g	Solyc08g	Granule-b	GO:0004	GO:0004	contig719	Solyc08g	Granule-b	GO:0004	SL2.40ch	AT1G32900.1		starch sy	chr1:119	2683.7	2363.55	3619.08	3938.29	5860.56	4811.98
GT	Sense	Sense	-0.592	Comprom	0.592	Comprom	0.000	1.811	Detected	2.689	Detected	2.250	0.093	GT Sens	contig721	contig721	Unknown	AGTTCG	contig721	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig721	Solyc02g	Unknown Protein (A		SL2.40ch	AT2G15240.1		UNC-50 f	chr2:661	2.49216	4.42485	6.00801	4.07494	12.3143	21.8569
GT	Sense	Sense	-0.135	Detected	0.135	Detected	0.000	1.065	Detected	1.030	Detected	1.048	0.016	GT Sens	contig725	contig725	POT fami	AATGTC	contig725	Solyc02g	Solyc02g	POT family domain containing			contig725	Solyc02g	POT family domain		SL2.40ch	AT1G61667.1		unknown	chr1:227	26.8543	25.3114	46.5888	24.2035	57.6525	54.3406
GT	Sense	Sense	-1.040	Detected	1.040	Detected	0.000	0.941	Detected	1.087	Detected	1.014	0.433	GT Sens	contig730	contig730	Cation tra	GATTAC	contig730	Solyc11g	Solyc11g	Cation transport regulator pro			contig730	Solyc11g	Cation transport reg		SL2.40ch	AT1G44790.1		ChaC-like	chr1:169	227.955	752.861	970.134	799.114	840.316	897.713
GT	Sense	Sense	1.204	Detected	-1.204	Comprom	0.000	1.850	Detected	1.115	Detected	1.482	0.360	GT Sens	contig733	contig733	Transme	ACCACC	contig733	Solyc01g	Solyc01g	Transme	GO:0015	GO:0015	contig733	Solyc01g	Transme	GO:0015	SL2.40ch	AT2G21050.1		amino ac	chr2:903	21.1676	3.11677	17.4654	9.89277	30.942	17.9524
GT	Sense	Sense	-0.143	Detected	0.143	Detected	0.000	1.835	Detected	1.320	Detected	1.577	0.033	GT Sens	contig733	contig733	Membran	TATTCA	contig733	Solyc03g	Solyc03g	Membrane protein HPP family			contig733	Solyc03g	Membrane protein H		SL2.40ch	AT3G47980.1		integral r	chr3:177	295.533	281.582	845.156	374.473	1087.42	734.796
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	2.220	Detected	1.984	Detected	2.102	0.006	GT Sens	contig735	contig735	Zinc finge	TTGCTA	contig735	Solyc02g	Solyc02g	Zinc finge	GO:0005	GO:0005	contig735	Solyc02g	Zinc finge	GO:0005	SL2.40ch	AT4G38960.1		zinc fing	chr4:181	119.939	79.8923	206.351	296.464	481.986	395.211
GT	Sense	Sense	0.152	Detected	-0.152	Detected	0.000	0.950	Detected	1.535	Detected	1.242	0.064	GT Sens	contig737	contig737	Glycosylt	TCCATA	contig737	Solyc03g	Solyc03g	Glycosyltransferase CAZy fam			contig737	Solyc03g	Glycosyltransferase		SL2.40ch	AT2G458	DTA2	DTA2 (DC	chr2:188	1150.48	728.517	935.545	759.446	1869.31	2706.74
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	2.512	Detected	2.719	Detected	2.616	0.003	GT Sens	contig737	contig737	Early ligh	TAGTGT	contig737	Solyc09g	Solyc09g	Early light-induced protein 7 (A			contig737	Solyc09g	Early ligh	GO:0016	SL2.40ch	AT5G651	ACX2. AT	ACX2 (AC	chr5:260	1898.42	1269.13	3510.17	5506.94	9356.55	10430.2
GT	Sense	Sense	-0.215	Detected	0.215	Detected	0.000	1.046	Detected	1.693	Detected	1.369	0.072	GT Sens	contig740	contig740	Integral m	CTAGCA	contig740	Solyc04g	Solyc04g	Integral membrane protein (AH			contig740	Solyc04g	Integral membrane		SL2.40ch	AT1G76800.1				357.192	376.178	282.507	532.614	799.654	1209.7
GT	Sense	Sense	-0.246	Detected	0.246	Detected	0.000	1.927	Detected	1.202	Detected	1.564	0.070	GT Sens	contig741	contig741	Alliinase	TTTGCC	contig741	Solyc03g	Solyc03g	Alliinase	GO:0016	GO:0016	contig741	Solyc03g	Alliinase	GO:0016	SL2.40ch	AT3G57350.1		FUNCTIO	chr3:212	13.7289	15.0893	29.781	22.678	57.841	33.7778
GT	Sense	Sense	0.256	Detected	-0.256	Detected	0.000	1.271	Detected	1.462	Detected	1.367	0.038	GT Sens	contig742	contig742	Acidic ch	CATCTG	contig742	Solyc05g	Solyc05g	Acidic ch	GO:0005	GO:0005	contig742	Solyc05g	Acidic ch	GO:0005	SL2.40ch	AT5G24090.1		acidic en	chr5:814	4308.36	2360.31	3162.3	5397.57	8134.53	8962.62
GT	Sense	Sense	-0.890	Detected	0.890	Detected	0.000	3.280	Detected	1.537	Detected	2.408	0.193	GT Sens	contig744	contig744	Polygalac	TTGTAG	contig744	Solyc00g	Solyc00g	Polygalac	GO:0005	GO:0005	contig744	Solyc00g	Polygalac	GO:0005	SL2.40ch	AT2G43890.1		polygala	chr2:181	12.2064	32.7611	2.2122	99.8992	205.232	59.2074
GT	Sense	Sense	-0.158	Detected	0.158	Detected	0.000	1.511	Detected	0.906	Detected	1.208	0.071	GT Sens	contig765	contig765	BES1/BZR	TAATGC	contig765	Solyc07g	Solyc07g	BES1/BZR	GO:0030	GO:0030	contig765	Solyc07g	BES1/BZR	GO:0030	SL2.40ch	AT1G78700.1		brassino	chr1:295	360.12	350.557	719.303	353.526	1070.27	679.125
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	1.249	Detected	1.131	Detected	1.190	0.004	GT Sens	contig766	contig766	Gibberelli	GGAACC	contig766	Solyc02g	Solyc02g	Gibberelli	GO:0045	GO:0045	contig766	Solyc02g	Gibberelli	GO:0045	SL2.40ch	AT1G784	ATGA2OX	ATGA2O	chr1:295	260.876	189.352	185.896	214.985	558.385	496.557
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	1.167	Detected	0.994	Detected	1.081	0.015	GT Sens	contig767	contig767	Fasciclin-	AAGTTT	contig767	Solyc12g	Solyc12g	Fasciclin-like arabinogalactan			contig767	Solyc12g	Fasciclin-like arabin		SL2.40ch	AT5G65170.1		VQ motif	chr5:260	138.71	93.8256	127.559	100.065	270.701	231.92
GT	Sense	Sense	-0.362	Detected	0.362	Detected	0.000	0.973	Detected	1.445	Detected	1.209	0.108	GT Sens	contig771	contig771	Glutathio	GCTATA	contig771	Solyc09g	Solyc09g	Glutathio	GO:0004	GO:0004	contig771	Solyc09g	Glutathio	GO:0004	SL2.40ch	AT3G092	ATGSTU	ATGSTU	chr3:284	65.2111	84.223	42.8368	63.8371	153.722	205.845
GT	Sense	Sense	0.060	Detected	-0.060	Detected	0.000	2.525	Detected	1.965	Detected	2.245	0.016	GT Sens	contig775	contig775	Chloroph	TGCTTT	contig775	Solyc12g	Solyc12g	Chloroph	GO:0016	GO:0016	contig775	Solyc12g	Chloroph	GO:0016	SL2.40ch	AT2G050	LHCB2.2.	LHCB2.2	chr2:179	87.5545	62.9802	259.853	466.568	451.611	295.903
GT	Sense	Sense	-0.533	Detected	0.533	Detected	0.000	3.380	Detected	2.565	Detected	2.972	0.047	GT Sens	contig790	contig790	Carboxyl-	CCGATG	contig790	Solyc07g	Solyc07g	Carboxyl-	GO:0005	GO:0005	contig790	Solyc07g	Carboxyl-	GO:0005	SL2.40ch	AT4G23882.1				36.2993	59.4424	246.176	191.405	511.004	280.424
GT	Sense	Sense	0.261	Detected	-0.261	Detected	0.000	1.351	Detected	1.077	Detected	1.214	0.054	GT Sens	contig792	contig792	Endo-1 4-	ATAGTC	contig792	Solyc05g	Solyc05g	Endo-1 4-	GO:0005	GO:0005	contig792	Solyc05g	Endo-1 4-	GO:0008	SL2.40ch	AT5G497	ATGH9A1	ATGH9A	chr5:201	1355.63	737.691	2067.33	1765.8	2695.4	2152.84
GT	Sense	Sense	-0.427	Detected	0.427	Detected	0.000	1.028	Detected	1.610	Detected	1.319	0.125	GT Sens	contig792	contig792	ABC tran	CTCTGT	contig792	Solyc04g	Solyc04g	ABC tran	GO:0016	GO:0016	contig792	Solyc04g	ABC tran	GO:0017	SL2.40ch	AT5G06530.3		ABC tran	chr5:199	66.1319	93.3875	179.782	136.14	169.338	244.778
GT	Sense	Sense	0.186	Detected	-0.186	Detected	0.000	2.222	Detected	1.622	Detected	1.922	0.032	GT Sens	contig798	contig798	UBA/TS-N	ATACAT	contig798	Solyc04g	Solyc04g	UBA/TS-N	GO:0005	GO:0005	contig798	Solyc04g	UBA/TS-N	GO:0005	SL2.40ch	AT1G751	JAC1	JAC1 (J-l	chr1:281	145.437	87.8258	267.127	429.128	557.303	355.029
GT	Sense	Sense	0.513	Detected	-0.513	Detected	0.000	1.052	Detected	1.324	Detected	1.188	0.154	GT Sens	contig799	contig799	Cytochro	GTTCCT	contig799	Solyc09g	Solyc09g	Cytochro	GO:0019	GO:0019	contig799	Solyc09g	Cytochro	GO:0019	SL2.40ch	AT4G133	CYP71A2	CYP71A2	chr4:775	38.6845	14.8529	36.3245	52.1404	52.5422	61.2169
GT	Sense	Sense	-0.313	Comprom	0.313	Comprom	0.000	1.227	Detected	1.047	Detected	1.137	0.073	GT Sens	contig800	contig800	F-box fam	CCATCG	contig800	Solyc02g	Solyc02g	F-box family protein (AHRD V1			contig800	Solyc02g	F-box family protein		SL2.40ch	AT3G260	ATB' DEL	ATB' DEL	chr3:951	5.24673	6.32626	14.0755	10.761	14.2519	12.1487
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	1.183	Detected	1.843	Detected	1.513	0.055	GT Sens	contig805	contig805	Gag-pol p	GAATTA	contig805	Solyc03g	Solyc03g	Gag-pol polyprotein (Fragmen			contig805	Solyc03g	Gag-pol polyprotein		SL2.40ch	AT1G76370.1				41.4857	25.809	126.154	89.7316	78.5176	119.749
GT	Sense	Sense	0.425	Detected	-0.425	Detected	0.000	1.643	Detected	1.813	Detected	1.728	0.057	GT Sens	contig808	contig808	Xyloglucan	GATCTT	contig808	Solyc01g	Solyc01g	Xyloglucan	GO:0048	GO:0048	contig808	Solyc01g	Xyloglucan	GO:0016	SL2.40ch	AT2G068	EXGT-A1	EXGT-A1	chr2:276	621.315	269.466	942.787	581.597	1350.84	1467.18
GT	Sense	Sense	0.565	Detected	-0.565	Comprom	0.000	1.050	Detected	1.073	Detected	1.061	0.201	GT Sens	contig811	contig811	Pentatric	ACCCAA	contig811	Solyc04g	Solyc04g	Pentatric	GO:0004	GO:0004	contig811	Solyc04g	Pentatric	GO:0004	SL2.40ch	AT3G28660.1		pentatric	chr3:107	12.9656	4.62775	17.9616	5.95043	16.9459	16.63
GT	Sense	Sense	-0.357	Comprom	0.357	Comprom	0.000	3.885	Detected	2.755	Detected	3.320	0.038	GT Sens	contig813	contig813	Cysteine-	ACTTTC	contig813	Solyc09g	Solyc09g	Cysteine-rich protein (AHRD V			contig813	Solyc09g	Cysteine-rich protei		SL2.40ch	AT3G03940.1		protein k	chr3:101	2.84884	3.65411	2.59996	31.1821	50.3809	22.222
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	1.134	Detected	0.933	Detected	1.034	0.010	GT Sens	contig813	contig813	Protein s	CGTCAC	contig813	Solyc06g	Solyc06g	Protein s	GO:0016	GO:0016	contig813	Solyc06g	Protein s	GO:0016	SL2.40ch	AT1G637	YDA. MAP	YDA (YO	chr1:236	260.039	193.295	372.716	352.321	519.969	436.844
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	1.289	Detected	0.912	Detected	1.100	0.029	GT Sens	contig814	contig814	Ethylene-	ATCTTC	contig814	Solyc08g	Solyc08g	Ethylene-	GO:0003	GO:0003	contig814	Solyc08g	Ethylene-	GO:0003	SL2.40ch	AT5G51190.1		AP2 dom	chr5:208	93.439	76.7543	127.181	114.037	218.716	162.576
GT	Sense	Sense	-0.243	Detected	0.243	Detected	0.000	1.289	Detected	1.560	Detected	1.424	0.036	GT Sens	contig821	contig821	Genomic	GACGAA	contig821	Solyc09g	Solyc09g	Genomic	GO:0003	GO:0003	contig821	Solyc09g	Genomic	GO:0003	SL2.40ch	AT1G48540.2		leucine-r	chr1:179	39.8658	43.6584	100.745	97.968	107.76	125.487
GT	Sense	Sense	-0.166	Comprom	0.166	Comprom	0.000	0.925	Detected	1.227	Detected	1.076	0.041	GT Sens	contig823	contig823	Acidic ch	TTAGCA	contig823	Solyc01g	Solyc01g	Acidic ch	GO:0005	GO:0005	contig823	Solyc01g	Acidic ch	GO:0005	SL2.40ch	AT3G08750.1				6.91679	6.80776	3.65194	5.471	13.7651	16.3861
GT	Sense	Sense	-0.577	Comprom	0.577	Comprom	0.000	4.749	Detected	3.370	Detected	4.059	0.046	GT Sens	contig824	contig824	Pectinest	GGAAGG	contig824	Solyc01g	Solyc01g	Pectinest	GO:0005	GO:0005	contig824	Solyc01g	Pectinest	GO:0005	SL2.40ch	AT5G07610.1		F-box fan	chr5:240	2.30712	4.01329	1.88491	33.9189	86.4633	32.0901
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	1.003	Detected	1.217	Detected	1.110	0.011	GT Sens	contig825	contig825	Undecapr	TTACGC	contig825	Solyc00g	Solyc00g	Undecapr	GO:0016	GO:0016	contig825	Solyc00g	Undecapr	GO:0016	SL2.40ch	AT5G05320.1		monooxy	chr5:157	4615.6	3879.22	5134.4	7415.54	8963.87	10034.9
GT	Sense	Sense	-0.419	Comprom	0.419	Comprom	0.000	2.918	Detected	1.712	Detected	2.315	0.088	GT Sens	contig826	contig826	Glucan sy	CTTCTC	contig826	Solyc11g	Solyc11g	Glucan sy	GO:0016	GO:0016	contig826	Solyc11g	Glucan sy	GO:0016	SL2.40ch	AT2G136	CALS5. G	CALS5 (C	chr2:569	3.59122	5.01694	3.13662	12.3366	33.8989	14.1881
GT	Sense	Sense	-0.015	Comprom	0.015	Comprom	0.000	1.119	Detected	1.344	Detected	1.232	0.008	GT Sens	contig829	contig829	Resistanc	CTAAAA	contig829	Solyc05g	Solyc05g	Resistanc	GO:0006	GO:0006	contig829	Solyc05g	Cc-nbs-lr	GO:0006	SL2.40ch	AT4G302	VEL1	Encodes	chr4:147	4.47024	3.56842	7.30288	14.4469	9.16891	10.3445
GT	Sense	Sense	-0.096	Comprom	0.096	Comprom	0.000	2.235	Detected	2.982	Detected	2.608	0.021	GT Sens	contig831	contig831	Nodulin f	ATCAAT	contig831	Solyc06g	Solyc06g	Nodulin family protein (AHRD V			contig831	Solyc06g	Nodulin family prote		SL2.40ch	AT2G28120.1		nodulin f	chr2:119	2.55517	2.28036	4.04248	4.79153	12.0063	19.4612
GT	Sense	Sense	0.224	Detected	-0.224	Detected	0.000	1.373	Detected	0.928	Detected	1.150	0.068	GT Sens	contig835	contig835	Unknown	GAATAT	contig835	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig835	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G09950.1		unknown	chr3:306	4426.81	2537.75	8170.54	6960.78	9172.35	6507.31
GT	Sense	Sense	0.186	Detected	-0.186	Detected	0.000	1.260	Detected	1.978	Detected	1.619	0.057	GT Sens	contig836	contig836	Chaperon	AATCAT	contig836	Solyc05g	Solyc05g	Chaperon	GO:0005	GO:0005	contig836	Solyc05g	Chaperon	GO:0005	SL2.40ch	AT2G040	CR88. EM	CR88: AT	chr2:128	765.029	461.77	2256.07	1937.95	1504.83	2388.72
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	1.257	Detected	1.191	Detected	1.224	0.009	GT Sens	contig837	contig837	DNA helic	CTGTGA	contig837	Solyc03g	Solyc03g	DNA helic	GO:0017	GO:0017	contig837	Solyc03g	DNA helic	GO:0043	SL2.40ch	AT5G35970.1		DNA-bind	chr5:141	2066.58	1380.61	2434.4	2595.98	4265.29	3935.51
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	1.665	Detected	1.272	Detected	1.469	0.022	GT Sens	contig837	contig837	Unknown	TTCAAA	contig837	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig837	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G25590.1		unknown	chr3:930	169.257	115.119	263.27	295.011	467.705	344.042
GT	Sense	Sense	0.689	Comprom	-0.689	Comprom	0.000	1.472	Detected	1.544	Detected	1.508	0.160	GT Sens	contig839	contig839	Pentatric	TGAGGA	contig839	Solyc10g	Solyc10g	Pentatric	GO:0005	GO:0005	contig839	Solyc10g	Pentatric	GO:0005	SL2.40ch	AT1G03560.1		pentatric	chr1:890	7.01423	2.10907	11.2613	8.51413	11.2748	11.4464
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	1.650	Detected	1.188	Detected	1.419	0.025	GT Sens	contig841	contig841	Homolog	ATAAAC	contig841	Solyc03g	Solyc03g	Homology to unknown gene (A			contig841	Solyc03g	Homology to unkno		SL2.40ch	AT3G01060.1		unknown	chr3:168	2457.57	1922.51	3195.43	4649.19	7208.16	5053.5
GT	Sense	Sense	-0.191	Detected	0.191	Detected	0.000	1.283	Detected	1.128	Detected	1.205	0.028	GT Sens	contig844	contig844	Unknown	AAGTTC	contig844	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig844	Solyc03g	Unknown Protein (A		SL2.40ch	AT1G58100.2		TCP fam	chr1:215	31.4046	32.0024	28.9455	35.7663	81.5413	70.6825
GT	Sense	Sense	0.180	Detected	-0.180	Detected	0.000	2.182	Detected	2.537	Detected	2.359	0.011	GT Sens	contig850	contig850	Plant-spe	GTGGAG	contig850	Solyc10g	Solyc10g	Plant-specific domain TIGR015			contig850	Solyc10g	Plant-specific doma		SL2.40ch	AT5G02580.1		unknown	chr5:579	21.3127	12.9764	17.3801	34.2133	79.7327	98.4833
GT	Sense	Sense	-0.203	Detected	0.203	Detected	0.000	1.270	Detected	1.203	Detected	1.237	0.027	GT Sens	contig852	contig852	IQ-domai	GGCTTC	contig852	Solyc01g	Solyc01g	IQ-domai	GO:0005	GO:0005	contig852	Solyc01g	IQ-domai	GO:0005	SL2.40ch	AT5G620	IQD23	IQD23 (IC	chr5:249	3081.88	3193.71	5742.02	4625.87	7998.78	7368.59
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	1.730	Detected	1.481	Detected	1.605	0.010	GT Sens	contig867	contig867	COL dom	AAATCA	contig867	Solyc02g	Solyc02g	COL domain class transcriptic			contig867	Solyc02g	COL domain class t		SL2.40ch	AT4G28320.1		glycosyl	chr4:140	1043.64	700.531	1654.51	2180.64	2996.81	2436.07
GT	Sense	Sense	-0.196	Detected	0.196	Detected	0.000	1.230	Detected	0.934	Detected	1.082	0.048	GT Sens	contig868	contig868	Rhodane	TAAAGT	contig868	Solyc01g	Solyc01g	Rhodane	GO:0005	GO:0005	contig868	Solyc01g	Rhodane	GO:0005	SL2.40ch	AT4G01050.1		hydroxy	chr4:455	1178.72	1209.18	1622.82	1920	2959.58	2327.02
GT	Sense	Sense	-0.065	Detected	0.065	Detected	0.000	1.812	Detected	1.666	Detected	1.739	0.003	GT Sens	contig868	contig868	Hydrolas	CTGAAA	contig868	Solyc02g	Solyc02g	Hydrolase alpha/beta fold fami			contig868	Solyc02g	Hydrolase alpha/bet		SL2.40ch	AT4G36530.2		hydrolas	chr4:172	1298.99	1110.62	2557.15	2889.4	4458.18	3888.02
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	1.881	Detected	1.546	Detected	1.714	0.018	GT Sens	contig869	contig869	Chloroph	TTCTAT	contig869	Solyc06g	Solyc06g	Chloroph	GO:0016	GO:0016	contig869	Solyc06g	Chloroph	GO:0016	SL2.40ch	AT4G103	LHCB5	LHCB5 (L	chr4:640	4313.46	2674.71	8194.9	7602.5	13221	10123.2
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	1.005	Detected	1.084	Detected	1.044	0.002	GT Sens	contig870	contig870	Unknown	GAAATC	contig870	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig870	Solyc10g	Unknown Protein (A		SL2.40ch	AT2G022	ATPSKR1	PSKR1 (F	chr2:584	184.78	141.5	224.042	162.977	342.92	349.693
GT	Sense	Sense	0.430	Detected	-0.430	Detected	0.000	1.751	Detected	1.705	Detected	1.728	0.057	GT Sens	contig871	contig871	Plant-spe	AAGAGT	contig871	Solyc04g	Solyc04g	Plant-specific domain TIGR015			contig871	Solyc12g	Casein ki	GO:0006	SL2.40ch	AT2G33230.1		flavin-co	chr2:140	1276.99	550.148	1923.2	1303.68	2982.21	2787.54
GT	Sense	Sense	-0.284	Detected	0.284	Detected	0.000	1.898	Detected	1.296	Detected	1.597	0.061	GT Sens	contig879	contig879	Boron tra	GTCCAA	contig879	Solyc06g	Solyc06g	Boron tra	GO:0080	GO:0080	contig879	Solyc06g	Boron tra	GO:0080	SL2.40ch	AT3G62270.1		anion ex	chr3:230	350.328	406.002	1036.74	732.403	1485.1	944.911
GT	Sense	Sense	0.324	Detected	-0.324	Detected	0.000	0.911	Detected	1.197	Detected	1.054	0.097	GT Sens	contig893	contig893	Isoamyl a	CGGTAA	contig893	Solyc06g	Solyc06g	Isoamyl a	GO:0016	GO:0016	contig893	Solyc06g	Isoamyl a	GO:0004	SL2.40ch	AT5G62930.1		GDSL-mo	chr5:252	60.9812	30.4388	53.2626	45.0621	85.6065	100.806
GT	Sense	Sense	0.109	Detected	-0.109	Detected	0.000	1.975	Detected	1.641	Detected	1.808	0.012	GT Sens	contig901	contig901	Hydrolas	TGTACA	contig901	Solyc08g	Solyc08g	Hydrolase alpha/beta fold fami			contig901	Solyc08g	Hydrolase alpha/bet		SL2.40ch	AT4G24140.1		hydrolas	chr4:125	82.3058	55.3335	128.637	142.741	280.438	214.768
GT	Sense	Sense	0.169	Comprom	-0.169	Comprom	0.000	1.571	Detected	1.455	Detected	1.513	0.014	GT Sens	contig902	contig902	Inositol-1	CAGTTC	contig902	Solyc12g	Solyc12g	Inositol-1	GO:0004	GO:0004	contig902	Solyc12g	Inositol-1	GO:0004	SL2.40ch	AT2G43900.1		inositol c	chr2:181	4.62942	2.86394	10.7736	4.0476	11.436	10.1879
GT	Sense	Sense	-0.099	Detected	0.099	Detected	0.000	1.046	Detected	1.117	Detected	1.081	0.009	GT Sens	contig903	contig903	Dihydrox	AAAGAA	contig903	Solyc05g	Solyc05g	Dihydrox	GO:0005	GO:0005	contig903	Solyc05g	Dihydrox	GO:0005	SL2.40ch	AT3G23940.1		dehydrat	chr3:864	195.301	175.038	264.77	224.079	403.402	409.205
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	1.215	Detected	0.984	Detected	1.100	0.069	GT Sens	contig917	contig917	MYB tran	TTATCG	contig917	Solyc01g	Solyc01g	MYB tran	GO:0003	GO:0003	contig917	Solyc01g	MYB tran	GO:0003	SL2.40ch	AT5G52660.2		myb fam	chr5:213	3744.64	1981.09	3938.82	4610	6684.1	5496.46
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	1.241	Detected	1.131	Detected	1.186	0.028	GT Sens	contig925	contig925	MATE eff	GATTAT	contig925	Solyc02g	Solyc02g	MATE eff	GO:0015	GO:0015	contig925	Solyc02g	MATE eff	GO:0015	SL2.40ch	AT1G61890.1		MATE ef	chr1:228	305.689	182.791	666.809	499.002	590.568	528.125
GT	Sense	Sense	-0.507	Detected	0.507	Detected	0.000	0.932	Detected	1.071	Detected	1.002	0.189	GT Sens	contig930	contig930	Unknown	ATTGAT	contig930	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig930	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G62640.3		proline-r	chr5:251	284.72	449.281	608.241	784.215	721.189	766.949
GT	Sense	Sense	0.290	Comprom	-0.290	Comprom	0.000	1.463	Detected	1.712	Detected	1.588	0.037	GT Sens	contig941	contig941	Unknown	CTTTCA	contig941	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)%2			contig941	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G60945.1		Encodes	chr5:245	4.37158	2.28611	4.70305	3.6777	9.21118	10.5685
GT	Sense	Sense	-0.273	Detected	0.273	Detected	0.000	1.644	Detected	1.672	Detected	1.658	0.026	GT Sens	contig941	contig941	GDSL est	AACATA	contig941	Solyc04g	Solyc04g	GDSL est	GO:0004	GO:0004	contig941	Solyc04g	GDSL est	GO:0004	SL2.40ch	AT1G539	GLIP5	GLIP5: c	chr1:201	133.063	151.806	503.692	422.657	469.598	462.008
GT	Sense	Sense	0.733	Detected	-0.733	Detected	0.000	0.900	Detected	1.130	Detected	1.015	0.305	GT Sens	contig945	contig945	Cytokinin	TGGAGG	contig945	Solyc01g	Solyc01g	Cytokinin	GO:0019	GO:0019	contig945	Solyc01g	Cytokinin	GO:0019	SL2.40ch	AT3G634	ATCKX6.	CKX6 (C	chr3:234	4693.47	1327.34	4004.3	4804.77	4922.52	5575.26
GT	Sense	Sense	-0.020	Detected	0.020	Detected	0.000	1.714	Detected	1.381	Detected	1.547	0.012	GT Sens	contig950	contig950	Thaumati	CTAGCA	contig950	Solyc01g	Solyc01g	Thaumati	GO:0005	GO:0005	contig950	Solyc01g	Thaumati	GO:0005	SL2.40ch	AT4G24180.1		FUNCTIO	chr4:125	77.0623	61.9709	171.546	134.816	239.623	183.589
GT	Sense	Sense	0.062	Detected	-0.062	Detected	0.000	1.276	Detected	1.015	Detected	1.146	0.016	GT Sens	contig961	contig961	Expresse	AATGTC	contig961	Solyc10g	Solyc10g	Expressed protein (Fragment)			contig961	Solyc10g	Expressed protein (		SL2.40ch	AT2G172	EXL5	EXL5 (EX	chr2:749	140.586	100.817	160.04	132.694	304.654	245.53
GT	Sense	Sense	0.328	Detected	-0.328	Detected	0.000	1.248	Detected	1.190	Detected	1.219	0.066	GT Sens	contig961	contig961	Non-spec	AAAGCG	contig961	Solyc08g	Solyc08g	Non-spec	GO:0006	GO:0006	contig961	Solyc08g	Non-spec	GO:0005	SL2.40ch	AT5G57710.1		heat sho	chr5:233	60.7944	30.1765	104.848	192.186	107.496	99.7179
GT	Sense	Sense	0.207	Detected	-0.207	Detected	0.000	0.955	Detected	1.057	Detected	1.006	0.042	GT Sens	contig966	contig966	Dehydrat	ATGGAT	contig966	Solyc05g	Solyc05g	Dehydration-responsive family			contig966	Solyc05g	Dehydration-respor		SL2.40ch	AT2G39750.1		dehydrat	chr2:165	1617.56	948.969	1945.45	1475.16	2537.95	2629.47
GT	Sense	Sense	-0.341	Detected	0.341	Detected	0.000	1.145	Detected	0.869	Detected	1.007	0.112	GT Sens	contig967	contig967	Gibberelli	TTTCAT	contig967	Solyc03g	Solyc03g	Gibberelli	GO:0016	GO:0016	contig967	Solyc03g	Gibberelli	GO:0016	SL2.40ch	AT4G216	ATGA3OX	GA3OX3	chr4:115	92.3864	115.927	137.136	354.384	241.845	192.906
GT	Sense	Sense	-0.265	Detected	0.265	Detected	0.000	1.075	Detected	1.135	Detected	1.105	0.053	GT Sens	contig968	contig968	Enhancer	GCCTAT	contig968	Solyc10g	Solyc10g	Enhancer	GO:0042	GO:0042	contig968	Solyc10g	Enhancer	GO:0000	SL2.40ch	AT3G133	VCS	VCS (VAI	chr3:430	344.791	388.911	632.086	632.38	815.401	820.315
GT	Sense	Sense	0.402	Detected	-0.402	Detected	0.000	1.306	Detected	0.921	Detected	1.113	0.130	GT Sens	contig969	contig969	Dihydrofl	CATTGA	contig969	Solyc05g	Solyc05g	Dihydrofl	GO:0008	GO:0008	contig969	Solyc05g	Dihydrofl	GO:0008	SL2.40ch	AT1G61980.1				139.111	62.2857	320.443	242.522	243.158	179.847
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	1.382	Detected	1.054	Detected	1.218	0.018	GT Sens	contig970	contig970	D-xylose-	ATACTC	contig970	Solyc07g	Solyc07g	D-xylose-	GO:0015	GO:0015	contig970	Solyc07g	D-xylose-	GO:0015	SL2.40ch	AT1G67300.1		hexose t	chr1:251	369.49	287.487	549.391	557.012	897.687	690.638
GT	Sense	Sense	0.085	Detected	-0.085	Detected	0.000	1.145	Detected	1.116	Detected	1.131	0.006	GT Sens	contig971	contig971	chaperon	GAATGC	contig971	Solyc11g	Solyc11g	chaperon	GO:0044	GO:0044	contig971	Solyc11g	chaperon	GO:0044	SL2.40ch	AT2G280	CPN60A.	CPN60A	chr2:119	756.468	525.554	1073.48	841.714	1473.7	1394.42
GT	Sense	Sense	-1.346	Detected	1.346	Detected	0.000	1.774	Detected	1.930	Detected	1.852	0.303	GT Sens	contig976	contig976	Lipase cl	CCATCA	contig976	Solyc08g	Solyc08g	Lipase cl	GO:0006	GO:0006	contig976	Solyc08g	Lipase cl	GO:0006	SL2.40ch	AT1G63470.1		DNA-bind	chr1:235	110.59	558.813	873.098	645.992	898.29	966.393
GT	Sense	Sense	0.089	Comprom	-0.089	Comprom	0.000	1.111	Detected	2.693	Detected	1.902	0.139	GT Sens	contig986	contig986	Unknown	TAGTAG	contig986	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig986	Solyc06g	Unknown Protein (A		SL2.40ch	AT1G48400.1		F-box fan	chr1:178	4.68673	3.2371	11.8059	7.22387	8.89031	25.7027
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	1.360	Detected	1.210	Detected	1.285	0.010	GT Sens	contig986	contig986	Kinesin-li	AAATCA	contig986	Solyc12g	Solyc12g	Kinesin-like calmodulin bindin			contig986	Solyc12g	Kinesin-like calmod		SL2.40ch	AT1G11420.1		agenet d	chr1:384	317.336	214.178	607.035	571.867	707.039	615.382
GT	Sense	Sense	-1.014	Detected	1.014	Detected	0.000	1.929	Detected	1.806	Detected	1.868	0.207	GT Sens	contig988	contig988	Ariadne-l	AAGATA	contig988	Solyc12g	Solyc12g	Ariadne-l	GO:0008	GO:0008	contig988	Solyc12g	Ariadne-l	GO:0008	SL2.40ch	AT2G160	ATARI12.	zinc fing	chr2:698	187.613	598.362	1129.01	967.696	1348.46	1195.61
GT	Sense	Sense	0.306	Detected	-0.306	Detected	0.000	1.500	Detected	1.077	Detected	1.289	0.074	GT Sens	contig989	contig989	Multidrug	TATCAG	contig989	Solyc11g	Solyc11g	Multidrug	GO:0016	GO:0016	contig989	Solyc11g	Multidrug	GO:0016	SL2.40ch	AT1G71870.1		MATE ef	chr1:270	78.6518	40.2321	199.669	76.0252	168.167	121.114
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	1.876	Detected	1.161	Detected	1.518	0.062	GT Sens	contig991	contig991	Unknown	GTTGAA	contig991	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig991	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G15020.1		unknown	chr2:649	3454.98	2119.45	5995.41	10601.8	10495	6174.31
GT	Sense	Sense	0.295	Comprom	-0.295	Comprom	0.000	3.795	Detected	1.982	Detected	2.889	0.094	GT Sens	LeIDA3 C	LeIDA3 C	Unknown	TAAAAACACAACTACAATATCAATCATTTTTGTCCTTGTGATAATAATTCAACATGCTC																4.06042	2.10782	1.84572	1.83301	42.9317	11.7922
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	2.506	Detected	2.215	Detected	2.360	0.005	GT Sens	NM_0012	NM_0012	Solanum	CAAAGAGAAGATCAACCACAAGCCCCTAAACCTAGAATTAATATTGTATCTCTTAGGTCA																1971.18	1383.12	5506.29	8274.18	9912.51	7822
GT	Sense	Sense	0.139	Detected	-0.139	Comprom	0.000	1.350	Detected	0.884	Detected	1.117	0.054	GT Sens	contig100	contig100	Heat shoc	CCCTGT	contig100	Solyc05g	Solyc05g	Heat shock protein (AHRD V1 *			contig100	Solyc05g	Heat shock protein		SL2.40ch	AT5G499	emb1441	emb1441	chr5:203	14.8155	9.55398	16.5339	21.0779	32.0507	22.4047
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	1.395	Detected	0.980	Detected	1.187	0.029	GT Sens	contig100	contig100	Heat shoc	AATGGA	contig100	Solyc05g	Solyc05g	Heat shock protein (AHRD V1 *			contig100	Solyc05g	Heat shock protein		SL2.40ch	AT5G499	emb1441	emb1441	chr5:203	21.8076	16.6933	20.803	43.7188	53.0165	38.403
GT	Sense	Sense	-0.639	Detected	0.639	Detected	0.000	1.185	Detected	1.135	Detected	1.160	0.211	GT Sens	contig102	contig102	TBC1 dor	AAGAAT	contig102	Solyc09g	Solyc09g	TBC1 dor	GO:0005	GO:0005	contig102	Solyc09g	TBC1 dor	GO:0005	SL2.40ch	AT4G13730.1		RabGAP	chr4:797	213.229	404.006	695.534	716.679	705.467	657.805
GT	Sense	Sense	-0.407	Detected	0.407	Detected	0.000	1.046	Detected	1.371	Detected	1.208	0.110	GT Sens	contig103	contig103	Unknown	TATATC	contig103	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig103	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G015	ANAC068	NTM1 (NA	chr4:670	32.3268	44.3973	54.2412	30.6705	82.6673	99.9738
GT	Sense	Sense	-0.510	Detected	0.510	Detected	0.000	1.242	Detected	1.051	Detected	1.146	0.158	GT Sens	contig106	contig106	AT hook	AATTCT	contig106	Solyc10g	Solyc10g	AT hook motif family protein (A			contig106	Solyc10g	AT hook motif family		SL2.40ch	AT3G58090.1		FUNCTIO	chr3:215	123.826	196.313	256.121	273.88	389.777	329.543
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	1.327	Detected	1.131	Detected	1.229	0.006	GT Sens	contig100	contig100	Ammoniu	ATTGAC	contig100	Solyc07g	Solyc07g	Ammoniu	GO:0016	GO:0016	contig100	Solyc07g	Ammoniu	GO:0016	SL2.40ch	AT5G582	STA1. AT	STA1 (ST	chr5:235	96.7726	77.2463	181.764	143.314	229.251	193.149
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	1.335	Detected	0.979	Detected	1.157	0.051	GT Sens	contig106	contig106	Chloroph	CCTCTT	contig106	Solyc08g	Solyc08g	Chloroph	GO:0016	GO:0016	contig106	Solyc08g	Chloroph	GO:0016	SL2.40ch	AT2G344	LHB1B1.	LHB1B1:	chr2:145	16735.1	9848.43	22765.8	18499.8	34237.4	25827.9
GT	Sense	Sense	-0.250	Detected	0.250	Detected	0.000	1.219	Detected	1.009	Detected	1.114	0.054	GT Sens	contig107	contig107	Transme	ATCGCC	contig107	Solyc07g	Solyc07g	Transmembrane protein 97 (A			contig107	Solyc07g	Transmembrane pr		SL2.40ch	AT5G186	CHR17	CHR17 (C	chr5:619	186.226	205.823	420.272	266.151	481.642	402.159
GT	Sense	Sense	-0.023	Detected	0.023	Detected	0.000	2.147	Detected	1.433	Detected	1.790	0.038	GT Sens	contig107	contig107	Unknown	AACATC	contig107	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig107	Solyc04g	Unknown Protein (A		SL2.40ch	AT4G20160.1		LOCATE	chr4:108	229.988	185.517	632.253	694.267	966.675	569.037
GT	Sense	Sense	-0.111	Comprom	0.111	Comprom	0.000	1.201	Detected	1.189	Detected	1.195	0.009	GT Sens	contig108	contig108	DNA topo	GTATAT	contig108	Solyc11g	Solyc11g	DNA topoisomerase 6 subunit			contig108	Solyc01g	Type II DN	GO:0042	SL2.40ch	AT3G207	ATTOP6E	ATTOP6	chr3:726	9.03341	8.23398	18.6336	22.6261	20.9581	20.0594
GT	Sense	Sense	-0.204	Comprom	0.204	Comprom	0.000	2.391	Detected	2.719	Detected	2.555	0.010	GT Sens	contig110	contig110	Cytochro	GTGATA	contig110	Solyc03g	Solyc03g	Cytochro	GO:0019	GO:0019	contig110	Solyc03g111990.2.1				AT4G133	CYP71A2	CYP71A2	chr4:775	2.06278	2.13929	3.6317	13.1664	11.6455	14.1152
GT	Sense	Sense	-0.232	Detected	0.232	Detected	0.000	1.893	Detected	1.845	Detected	1.869	0.015	GT Sens	contig110	contig110	Ycf2 (AHF	TTTCCT	contig110	Solyc02g	Solyc02g	Ycf2 (AHF	GO:0009	GO:0009	contig110	Solyc09g	RING fing	GO:0006	SL2.40ch	AT3G218	ATXR2. S	ATXR2 (H	chr3:768	632.41	681.499	703.323	653.855	2576.69	2406.77
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	1.282	Detected	0.957	Detected	1.120	0.023	GT Sens	contig111	contig111	Inositol-3	GCTGGT	contig111	Solyc04g	Solyc04g	Inositol-3	GO:0008	GO:0008	contig111	Solyc04g	Inositol-3	GO:0042	SL2.40ch	AT2G222	ATMIPS2	MIPS2 (M	chr2:945	551.963	396.543	632.894	764.867	1202.67	926.823
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	2.045	Detected	1.590	Detected	1.818	0.017	GT Sens	contig118	contig118	Chloroph	TCTGCC	contig118	Solyc02g	Solyc02g	Chloroph	GO:0005	GO:0005	contig118	Solyc02g	Chloroph	GO:0005	SL2.40ch	AT1G299	CAB1. AB	CAB1 (CI	chr1:104	140.957	98.4499	269.002	318.187	513.887	361.809
GT	Sense	Sense	0.309	Detected	-0.309	Detected	0.000	2.181	Detected	1.629	Detected	1.905	0.044	GT Sens	contig118	contig118	Chloroph	AAATTT	contig118	Solyc02g	Solyc02g	Chloroph	GO:0005	GO:0005	contig118	Solyc02g	Chloroph	GO:0005	SL2.40ch	AT1G299	CAB3. AB	CAB3 (CI	chr1:104	432.892	220.591	722.627	794.28	1481.42	975.223
GT	Sense	Sense	-0.299	Detected	0.299	Detected	0.000	0.888	Detected	1.139	Detected	1.014	0.089	GT Sens	contig119	contig119	Galactoki	GAAGGC	contig119	Solyc09g	Solyc09g	Galactoki	GO:0005	GO:0005	contig119	Solyc09g	Galactoki	GO:0005	SL2.40ch	AT3G10700.1		GHMP ki	chr3:334	282.343	333.933	466.824	399.003	600.679	690.186
GT	Sense	Sense	0.058	Detected	-0.058	Detected	0.000	1.618	Detected	0.877	Detected	1.248	0.080	GT Sens	contig123	contig123	1-AMINO	CCATTC	contig123	Solyc11g	Solyc11g	1-AMINO	GO:0016	GO:0016	contig123	Solyc11g	1-AMINO	GO:0016	SL2.40ch	AT3G13610.1		oxidored	chr3:444	872.459	629.069	1545.85	1983.83	2403.62	1388.23
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	1.409	Detected	1.049	Detected	1.229	0.029	GT Sens	contig123	contig123	Aquapori	AATTCT	contig123	Solyc10g	Solyc10g	Aquapori	GO:0016	GO:0016	contig123	Solyc10g	Aquapori	GO:0015	SL2.40ch	AT2G168	PIP3B. PI	PIP2;8 (P	chr2:730	293.178	268.313	531.415	783.451	787.313	592.035
GT	Sense	Sense	-0.289	Detected	0.289	Detected	0.000	1.328	Detected	1.087	Detected	1.208	0.061	GT Sens	contig124	contig124	Aquapori	GCCATG	contig124	Solyc10g	Solyc10g	Aquapori	GO:0016	GO:0016	contig124	Solyc10g	Aquapori	GO:0015	SL2.40ch	AT2G168	PIP3B. PI	PIP2;8 (P	chr2:730	626.759	731.098	1334.58	1841.75	1796.1	1467.37
GT	Sense	Sense	0.243	Detected	-0.243	Detected	0.000	1.863	Detected	2.158	Detected	2.010	0.019	GT Sens	contig125	contig125	F-box fam	TGGTGC	contig125	Solyc08g	Solyc08g	F-box family protein (AHRD V1			contig125	Solyc08g015890.1.1				AT3G47150.1		F-box far	chr3:173	54.8021	30.6051	598.703	684.718	157.401	186.459
GT	Sense	Sense	-0.086	Detected	0.086	Detected	0.000	1.279	Detected	1.167	Detected	1.223	0.007	GT Sens	contig125	contig125	UDP-gluc	AAAGTT	contig125	Solyc12g	Solyc12g	UDP-gluc	GO:0008	GO:0008	contig125	Solyc12g	UDP-gluc	GO:0008	SL2.40ch	AT2G368	DOGT1. U	DOGT1 (	chr2:154	19.8218	17.4596	47.7797	32.1526	47.6983	42.6221
GT	Sense	Sense	-0.002	Detected	0.002	Detected	0.000	1.202	Detected	0.979	Detected	1.091	0.010	GT Sens	contig127	contig127	Conserve	AGAATG	contig127	Solyc07g	Solyc07g	Conserve	GO:0016	GO:0016	contig127	Solyc07g	Conserve	GO:0016	SL2.40ch	AT1G73430.2		sec34-lik	chr1:276	303.048	237.572	550.978	452.158	652.27	539.757
GT	Sense	Sense	-0.041	Detected	0.041	Detected	0.000	1.346	Detected	0.839	Detected	1.093	0.051	GT Sens	contig127	contig127	Glucose-	TTGCCA	contig127	Solyc12g	Solyc12g	Glucose-	GO:0009	GO:0009	contig127	Solyc07g	Glucose-	GO:0008	SL2.40ch	AT5G483	ADG1. AP	ADG1 (AI	chr5:195	816.445	675.071	1217.24	985.796	1995.01	1355.1
GT	Sense	Sense	0.157	Detected	-0.157	Detected	0.000	2.155	Detected	2.149	Detected	2.152	0.005	GT Sens	contig127	contig127	Major alle	TCTTAT	contig127	Solyc09g	Solyc09g	Major alle	GO:0009	GO:0009	contig127	Solyc09g	Major alle	GO:0009	SL2.40ch	AT5G434	ETFBETA	ETFBETA	chr5:174	28.9754	18.2146	47.326	17.4701	108.146	103.943
GT	Sense	Sense	0.459	Detected	-0.459	Comprom	0.000	0.916	Detected	1.283	Detected	1.100	0.156	GT Sens	contig131	contig131	Homeobo	AGTCTC	contig131	Solyc02g	Solyc02g	Homeobo	GO:0043	GO:0043	contig131	Solyc02g	Homeobo	GO:0043	SL2.40ch	AT1G052	HDG2	HDG2 (H	chr1:151	25.7126	10.634	35.1172	40.4698	32.9806	41.0704
GT	Sense	Sense	0.247	Detected	-0.247	Detected	0.000	1.251	Detected	1.186	Detected	1.219	0.039	GT Sens	contig132	contig132	LRR rece	TGAATG	contig132	Solyc04g	Solyc04g	LRR rece	GO:0004	GO:0004	contig132	Solyc04g014200.1.1				AT4G208	FAH2. AT	FAH2 (FA	chr4:111	27.0844	15.0225	33.8586	40.9423	50.7226	46.8434
GT	Sense	Sense	0.079	Detected	-0.079	Comprom	0.000	1.363	Detected	1.029	Detected	1.196	0.023	GT Sens	contig132	contig132	Unknown	TGTAAT	contig132	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig132	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G09530.1		hydroxy	chr5:296	11.5131	8.0674	10.4081	37.2191	26.2034	20.0599
GT	Sense	Sense	-0.153	Detected	0.153	Detected	0.000	1.082	Detected	0.939	Detected	1.010	0.027	GT Sens	contig132	contig132	class I he	GAGCAA	contig132	Solyc09g	Solyc09g	class I he	GO:0051	GO:0051	contig132	Solyc09g	class I he	GO:0051	SL2.40ch	AT5G597	HSP18.2	HSP18.2	chr5:240	98.5638	95.2643	117.377	131.223	216.8	189.512
GT	Sense	Sense	0.044	Detected	-0.044	Detected	0.000	1.100	Detected	0.959	Detected	1.030	0.006	GT Sens	contig137	contig137	WD-40 re	TCCTCT	contig137	Solyc07g	Solyc07g	WD-40 re	GO:0042	GO:0042	contig137	Solyc07g	WD-40 re	GO:0042	SL2.40ch	AT1G530	SPA4	SPA4 (SP	chr1:197	4197.44	3086.1	6521.32	7368.2	8152.12	7140.47
GT	Sense	Sense	0.065	Detected	-0.065	Detected	0.000	1.152	Detected	0.985	Detected	1.069	0.010	GT Sens	contig140	contig140	Chloroph	TACCCT	contig140	Solyc11g	Solyc11g	Chloroph	GO:0055	GO:0055	contig140	Solyc11g	Chloroph	GO:0008	SL2.40ch	AT1G444	CH1. ATC	CH1 (CHL	chr1:168	279.475	199.623	382.504	410.666	554.738	477.139
GT	Sense	Sense	0.137	Detected	-0.137	Detected	0.000	1.531	Detected	1.279	Detected	1.405	0.017	GT Sens	contig140	contig140	Chloroph	TTCTTC	contig140	Solyc01g	Solyc01g	Chloroph	GO:0016	GO:0016	contig140	Solyc01g	Chloroph	GO:0016	SL2.40ch	AT1G158	LHCB6. C	LHCB6 (L	chr1:544	8669.97	5603.35	15582	16876.6	21281.4	17260.8
GT	Sense	Sense	-0.038	Detected	0.038	Detected	0.000	1.103	Detected	0.965	Detected	1.034	0.006	GT Sens	contig144	contig144	WD-40 re	AATGTT	contig144	Solyc03g	Solyc03g	WD-40 repeat protein (AHRD V			contig144	Solyc03g	WD-40 repeat protei		SL2.40ch	AT3G158	WSIP2. TI	protein b	chr3:536	681.073	561.421	1066.35	840.354	1403.69	1231.61
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	1.733	Detected	1.447	Detected	1.590	0.014	GT Sens	contig144	contig144	Naringeni	GGTATT	contig144	Solyc04g	Solyc04g	Naringeni	GO:0016	GO:0016	contig144	Solyc09g	1-aminoc	GO:0009	SL2.40ch	AT3G52140.1		tetratrico	chr3:193	117.061	109.649	245.852	276.577	398.038	315.205
GT	Sense	Sense	0.343	Detected	-0.343	Detected	0.000	0.857	Detected	1.220	Detected	1.039	0.116	GT Sens	contig147	contig147	Actin-bind	CTGAAA	contig147	Solyc05g	Solyc05g	Actin-bind	GO:0008	GO:0008	contig147	Solyc05g	Actin-bind	GO:0008	SL2.40ch	AT2G398	DAR2	DAR2 (DA	chr2:166	202.508	98.453	288.589	196.68	270.235	335.72
GT	Sense	Sense	-0.776	Comprom	0.776	Detected	0.000	1.244	Detected	0.888	Detected	1.066	0.313	GT Sens	contig150	contig150	CK25 (AH	TGAAAC	contig150	Solyc08g	Solyc08g	CK25 (AHRD V1 ***- O1W1G0_T			contig150	Solyc08g	CK25 (AHRD V1 ***- (		SL2.40ch	AT3G05900.1		neurofila	chr3:176	4.85187	11.1242	17.8449	14.0873	18.384	13.8714
GT	Sense	Sense	0.196	Detected	-0.196	Detected	0.000	1.152	Detected	1.276	Detected	1.214	0.028	GT Sens	contig150	contig150	Auxin res	CAATTA	contig150	Solyc07g	Solyc07g	Auxin res	GO:0003	GO:0003	contig150	Solyc07g	Auxin res	GO:0003	SL2.40ch	AT1G303	ARF6	ARF6 (AU	chr1:106	31.2861	18.6302	48.5397	51.1922	56.7107	59.6454
GT	Sense	Sense	0.103	Detected	-0.103	Comprom	0.000	0.960	Detected	1.685	Detected	1.323	0.072	GT Sens	contig152	contig152	Nucleopo	TTGCTT	contig152	Solyc02g	Solyc02g	Nucleoporin autopeptidase far			contig152	Solyc02g	Nucleoporin autope		SL2.40ch	AT4G10695.1		unknown	chr4:659	15.7001	10.646	22.19	21.9911	26.582	42.4223
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	1.474	Detected	0.892	Detected	1.183	0.067	GT Sens	contig154	contig154	Glycerald	AATTGC	contig154	Solyc12g	Solyc12g	Glycerald	GO:0008	GO:0008	contig154	Solyc12g	Glycerald	GO:0008	SL2.40ch	AT1G429	GAPB	GAPB (G	chr1:161	5028.84	4768.75	10171.6	10998.5	14373	9273.99
GT	Sense	Sense	0.141	Detected	-0.141	Detected	0.000	2.198	Detected	1.588	Detected	1.893	0.030	GT Sens	contig157	contig157	Chloroph	TCTGCC	contig157	Solyc02g	Solyc02g	Chloroph	GO:0005	GO:0005	contig157	Solyc02g070990.1.1				AT1G299	CAB1. AB	CAB1 (CI	chr1:104	225.309	144.844	433.448	488.831	876.096	554.013
GT	Sense	Sense	-0.066	Detected	0.066	Detected	0.000	1.360	Detected	0.816	Detected	1.088	0.060	GT Sens	contig157	contig157	Catalase	ATGCTC	contig157	Solyc01g	Solyc01g	Catalase	GO:0055	GO:0055	contig157	Solyc01g	Catalase	GO:0055	SL2.40ch	AT4G350	CAT2	CAT2 (CA	chr4:167	646.31	553.696	948.387	1182.93	1623	1074.34
GT	Sense	Sense	-0.597	Comprom	0.597	Comprom	0.000	2.914	Detected	1.758	Detected	2.336	0.107	GT Sens	contig166	contig166	Pollen all	TGCATT	contig166	Solyc06g	Solyc06g	Pollen allergen Ole e 6 (AHRD			contig166	Solyc06g	Pollen allergen Ole		SL2.40ch	AT5G19020.1		pentatric	chr5:635	5.60657	10.0274	1.81493	33.7896	59.7355	25.8707
GT	Sense	Sense	-0.538	Detected	0.538	Detected	0.000	1.982	Detected	1.346	Detected	1.664	0.117	GT Sens	contig166	contig166	Cytochro	GGCAAT	contig166	Solyc09g	Solyc09g	Cytochro	GO:0019	GO:0019	contig166	Solyc11g	Cytochro	GO:0019	SL2.40ch	AT3G533	CYP71B3	CYP71B3	chr3:197	14.6979	24.2206	45.9845	75.1286	78.8005	48.9336
GT	Sense	Sense	0.571	Detected	-0.571	Detected	0.000	1.063	Detected	1.466	Detected	1.264	0.172	GT Sens	contig166	contig166	Subtilisin	ACGAAA	contig166	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:0004	contig166	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT2G05920.1		subtilase	chr2:226	420.586	149.007	430.966	465.773	552.814	705.546
GT	Sense	Sense	-0.102	Detected	0.102	Detected	0.000	1.024	Detected	1.420	Detected	1.222	0.032	GT Sens	contig167	contig167	Gibberelli	TCAGCT	contig167	Solyc07g	Solyc07g	Gibberelli	GO:0045	GO:0045	contig167	Solyc07g	Gibberelli	GO:0045	SL2.40ch	AT2G345	ATGA2OX	ATGA2O	chr2:145	2258.79	2033.96	3857.46	4207.08	4608.04	5850.55
GT	Sense	Sense	0.514	Comprom	-0.514	Comprom	0.000	6.351	Detected	8.321	Detected	7.336	0.022	GT Sens	contig170	contig170	Gag poly	CTGCAT	contig170	Solyc00g	Solyc00g	Gag poly	GO:0008	GO:0008	contig170	Solyc11g	Kinase fa	GO:0006	SL2.40ch	AT5G286	WRKY74.	WRKY74	chr5:106	6.77264	2.59703	5.96945	10.7916	361.876	1368.44
GT	Sense	Sense	0.243	Detected	-0.243	Detected	0.000	1.283	Detected	0.922	Detected	1.103	0.068	GT Sens	contig171	contig171	Chloroph	TCTTCT	contig171	Solyc03g	Solyc03g	Chloroph	GO:0005	GO:0005	contig171	Solyc03g	Chloroph	GO:0005	SL2.40ch	AT1G299	CAB1. AB	CAB1 (CI	chr1:104	1543.79	861.12	1971.37	1406.09	2965.89	2228.85
GT	Sense	Sense	0.008	Detected	-0.008	Detected	0.000	1.400	Detected	0.898	Detected	1.149	0.045	GT Sens	contig173	contig173	Oxygen-e	AAGACA	contig173	Solyc00g	Solyc00g	Oxygen-e	GO:0019	GO:0019	contig173	Solyc02g	Oxygen-e	GO:0008	SL2.40ch	AT5G665	PSBO-1.	PSBO1 (I	chr5:265	1087.13	839.854	1829.41	1873.14	2665.67	1816.9
GT	Sense	Sense	-0.962	Detected	0.962	Detected	0.000	0.960	Detected	1.177	Detected	1.068	0.385	GT Sens	contig173	contig173	Unknown	GAATTC	contig173	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig173	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G53930.2		protein k	chr3:199	76.1653	226.021	281.757	226.413	269.734	302.683
GT	Sense	Sense	-0.093	Detected	0.093	Detected	0.000	1.200	Detected	1.124	Detected	1.162	0.007	GT Sens	contig176	contig176	Kinase fa	AAAGAA	contig176	Solyc01g	Solyc01g	Kinase family protein (AHRD V			contig176	Solyc01g	Receptor	GO:0006	SL2.40ch	AT4G02010.1		protein k	chr4:881	42.7134	37.9874	45.5871	51.5443	97.7711	89.5769
GT	Sense	Sense	1.036	Detected	-1.036	Comprom	0.000	2.595	Detected	3.213	Detected	2.904	0.115	GT Sens	contig176	contig176	Unknown	TTTGAT	contig176	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig176	Solyc08g015910.1.1				AT3G47150.1		F-box far	chr3:173	12.0896	2.24892	155.526	153.839	33.2839	49.3296
GT	Sense	Sense	0.145	Comprom	-0.145	Comprom	0.000	1.885	Detected	1.327	Detected	1.606	0.036	GT Sens	contig177	contig177	Unknown	AACTTG	contig177	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig177	Solyc01g066390.2.1				AT4G196	IRT2	IRT2: iro	chr4:107	9.11304	5.8249	7.85284	7.77646	28.4471	18.6507
GT	Sense	Sense	-1.728	Comprom	1.728	Detected	0.000	1.887	Detected	1.790	Detected	1.838	0.399	GT Sens	contig178	contig178	Equilibrat	TATGTC	contig178	Solyc02g	Solyc02g	Equilibrat	GO:0005	GO:0005	contig178	Solyc02g079330.2.1				AT4G05140.1		equilibra	chr4:265	14.5208	124.542	177.086	126.528	166.224	150.054
GT	Sense	Sense	0.236	Detected	-0.236	Comprom	0.000	2.280	Detected	2.386	Detected	2.333	0.011	GT Sens	contig179	contig179	Leucine F	TCTCAA	contig179	Solyc12g	Solyc12g	Leucine F	GO:0005	GO:0005	contig179	Solyc12g	LRR rece	GO:0016	SL2.40ch	AT4G142	RHF1A	RHF1A (F	chr4:819	19.2372	10.8392	16.182	33.6149	74.1266	76.9936
GT	Sense	Sense	-0.050	Detected	0.050	Comprom	0.000	1.221	Detected	1.171	Detected	1.196	0.002	GT Sens	contig183	contig183	SAM (And	TTTATT	contig183	Solyc06g	Solyc06g	SAM (And	GO:0030	GO:0030	contig183	Solyc02g	tRNA ade	GO:0005	SL2.40ch	AT1G33800.1		unknown	chr1:122	11.0138	9.22517	16.7999	14.065	24.8364	23.1535
GT	Sense	Sense	0.080	Detected	-0.080	Detected	0.000	0.986	Detected	1.162	Detected	1.074	0.012	GT Sens	contig184	contig184	Menaquin	TGACCT	contig184	Solyc12g	Solyc12g	Menaquin	GO:0008	GO:0008	contig184	Solyc12g	Menaquin	GO:0008	SL2.40ch	AT1G48600.1		phospho	chr1:179	326.974	228.822	748.636	402.368	572.601	624.7
GT	Sense	Sense	-0.220	Detected	0.220	Detected	0.000	1.300	Detected	0.917	Detected	1.108	0.063	GT Sens	contig185	contig185	Aquapori	TCATGT	contig185	Solyc10g	Solyc10g	Aquapori	GO:0016	GO:0016	contig185	Solyc10g	Aquapori	GO:0015	SL2.40ch	AT2G168	PIP3B. PI	PIP2;8 (P	chr2:730	427.441	453.203	798.356	1183.59	1144.99	847.814
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	1.289	Detected	0.984	Detected	1.137	0.018	GT Sens	contig186	contig186	Cytochro	GGTGAA	contig186	Solyc03g	Solyc03g	Cytochro	GO:0019	GO:0019	contig186	Solyc03g	Cytochro	GO:0019	SL2.40ch	AT4G20240.1				71.178	55.4292	120.462	181.97	162.264	126.762
GT	Sense	Sense	0.588	Comprom	-0.588	Comprom	0.000	1.392	Detected	1.902	Detected	1.647	0.124	GT Sens	contig188	contig188	Subtilisin	ATGGTA	contig188	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:0004	contig188	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT5G37920.1		unknown	chr5:150	8.39387	2.90287	12.6214	11.9066	13.6961	18.8195
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	1.154	Detected	0.985	Detected	1.070	0.010	GT Sens	contig190	contig190	Ankyrin r	ACAACA	contig190	Solyc07g	Solyc07g	Ankyrin r	GO:0008	GO:0008	contig190	Solyc07g	Ankyrin r	GO:0008	SL2.40ch	AT5G490	ATPRMT4	PRMT4A	chr5:198	28.3122	20.1604	40.8779	37.2534	56.2056	48.2585
GT	Sense	Sense	-0.055	Detected	0.055	Detected	0.000	1.167	Detected	1.316	Detected	1.241	0.006	GT Sens	contig191	contig191	F-box fam	GTGCTG	contig191	Solyc08g	Solyc08g	F-box family protein (AHRD V1			contig191	Solyc08g	F-box family protein		SL2.40ch	AT2G42270.1		U5 small	chr2:176	88.9616	75.0463	160.863	148.84	193.905	207.561
GT	Sense	Sense	0.152	Detected	-0.152	Detected	0.000	2.814	Detected	2.717	Detected	2.766	0.003	GT Sens	contig195	contig195	FAD-bind	GAGCTT	contig195	Solyc10g	Solyc10g	FAD-bind	GO:0050	GO:0050	contig195	Solyc02g	FAD-bind	GO:0009	SL2.40ch	AT5G44410.1		FAD-bind	chr5:178	138.955	87.9781	210.689	107.608	821.989	741.885
GT	Sense	Sense	0.229	Comprom	-0.229	Comprom	0.000	1.258	Detected	1.433	Detected	1.346	0.032	GT Sens	contig198	contig198	Unknown	GTTGTC	contig198	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig198	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G11580.1		UVB-resi	chr5:371	5.20327	2.96071	2.51957	9.89338	9.91978	10.8146
GT	Sense	Sense	-0.497	Detected	0.497	Detected	0.000	1.222	Detected	0.972	Detected	1.097	0.166	GT Sens	contig202	contig202	GH3 famil	TTACCA	contig202	Solyc10g	Solyc10g	GH3 famil	GO:0070	GO:0070	contig202	Solyc10g	GH3 famil	GO:0080	SL2.40ch	AT2G463	JAR1. FIN	JAR1 (JA	chr2:190	584.643	910.414	1231.01	1851.35	1798.17	1460.02
GT	Sense	Sense	-1.634	Detected	1.634	Detected	0.000	1.807	Detected	1.997	Detected	1.902	0.365	GT Sens	contig202	contig202	Ulp1 prot	AGACAT	contig202	Solyc07g	Solyc07g	Ulp1 prot	GO:0006	GO:0006	contig202	Solyc07g041690.1.1				AT3G42870.1		unknown	chr3:149	31.7767	239.199	429.158	583.055	322.409	355.172
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	1.705	Detected	1.609	Detected	1.657	0.001	GT Sens	contig202	contig202	GDSL est	CATGTA	contig202	Solyc04g	Solyc04g	GDSL esterase/lipase 1 (AHRD			contig202	Solyc04g	GDSL esterase/lipa		SL2.40ch	AT3G14820.1		carboxyl	chr3:497	303.591	235.86	888.531	705.025	922.335	832.905
GT	Sense	Sense	-0.123	Detected	0.123	Detected	0.000	1.359	Detected	0.880	Detected	1.119	0.053	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	984.693	912.427	1450.62	1063.05	2569.58	1779.81
GT	Sense	Sense	-0.341	Comprom	0.341	Comprom	0.000	1.460	Detected	1.709	Detected	1.584	0.049	GT Sens	contig205	contig205	Guanine	AGCTGC	contig205	Solyc08g	Solyc08g	Guanine	GO:0045	GO:0045	contig205	Solyc10g	WD-40 repeat family		SL2.40ch	AT5G53500.1		WD-40 re	chr5:217	5.38618	6.75906	9.91164	10.1826	17.5389	20.122
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	1.149	Detected	1.179	Detected	1.164	0.018	GT Sens	contig207	contig207	Cyclin B	GGTCCC	contig207	Solyc04g	Solyc04g	Cyclin B (AHRD V1 ***- B6V744			contig207	Solyc04g	Cyclin B (AHRD V1 *		SL2.40ch	AT1G694	AGO7. ZIP	AGO7 (AI	chr1:261	230.982	145.517	372.241	327.963	429.564	423.577

GT	Sense	Sense	-0.041	Detected	0.041	Detected	0.000	2.896	Detected	2.849	Detected	2.873	0.000	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	55.1769	45.6697	223.471	208.057	395.03	368.986
GT	Sense	Sense	-0.044	Detected	0.044	Detected	0.000	1.630	Detected	0.871	Detected	1.251	0.082	GT Sens	contig209	contig209	Flavonol	TTGTGT	contig209	Solyc11g	Solyc11g	Flavonol	GO:00164	GO:00164	contig209	Solyc11g	1-AMINOC	GO:00164	SL2.40ch	AT5G24800.1				892.594	741.851	1650.6	1981.94	2662.62	1518.44
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	1.019	Detected	1.192	Detected	1.106	0.007	GT Sens	contig213	contig213	Tubulin b	AATGGC	contig213	Solyc10g	Solyc10g	Tubulin b	GO:00058	GO:00058	contig213	Solyc10g	Tubulin b	GO:00058	SL2.40ch	AT5G122	TUB6	TUB6 (BE	chr5:396	2701.91	2032.84	3178.39	2617.96	5020.42	5464.95
GT	Sense	Sense	-0.020	Comprom	0.020	Comprom	0.000	1.742	Detected	1.399	Detected	1.570	0.012	GT Sens	contig214	contig214	Phosphat	ATTACT	contig214	Solyc06g	Solyc06g	Phosphat	GO:00038	GO:00038	contig214	Solyc06g	Phosphat	GO:00038	SL2.40ch	AT1G17710.1		phospha	chr1:609	7.16407	5.75729	13.0262	10.7223	22.7094	17.2759
GT	Sense	Sense	-0.111	Detected	0.111	Detected	0.000	1.662	Detected	1.017	Detected	1.339	0.059	GT Sens	contig215	contig215	Cytochro	GAATTA	contig215	Solyc03g	Solyc03g	Cytochro	GO:00200	GO:00200	contig215	Solyc03g	Cytochro	GO:00198	SL2.40ch	AT5G35715.1				49.5301	45.1724	85.8518	176.866	158.144	97.6838
GT	Sense	Sense	0.112	Detected	-0.112	Detected	0.000	0.927	Detected	1.336	Detected	1.132	0.040	GT Sens	contig215	contig215	Pectinest	AATGGA	contig215	Solyc07g	Solyc07g	Pectinest	GO:00305	GO:00305	contig215	Solyc07g	Pectinest	GO:00056	SL2.40ch	AT1G115	ATPMEP(	PMEPCR	chr1:388	258.456	172.947	273.312	212.939	424.83	544.701
GT	Sense	Sense	-0.244	Detected	0.244	Detected	0.000	1.021	Detected	1.128	Detected	1.075	0.050	GT Sens	contig217	contig217	Flowering	GTCGTC	contig217	Solyc01g	Solyc01g	Flowering promoting factor-lik			contig217	Solyc01g	Flowering promotin		SL2.40ch	AT2G42270.1		U5 small	chr2:176	211.175	231.398	259.226	177.926	474.12	493.116
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	1.540	Detected	1.183	Detected	1.362	0.022	GT Sens	contig219	contig219	UDP-gluc	GGATTC	contig219	Solyc04g	Solyc04g	UDP-gluc	GO:00081	GO:00081	contig219	Solyc04g	UDP-gluc	GO:00081	SL2.40ch	AT5G228	EMB1030	EMB103(	chr5:761	583.652	398.055	1131.15	1034.52	1481.23	1117.01
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	1.727	Detected	1.504	Detected	1.616	0.009	GT Sens	contig221	contig221	Response	CTGCTT	contig221	Solyc10g	Solyc10g	Response	GO:00063	GO:00063	contig221	Solyc10g	Response	GO:00063	SL2.40ch	AT3G570	ARR9. AT	ARR9 (RE	chr3:211	258.787	234.735	654.522	796.328	862.578	713.426
GT	Sense	Sense	0.405	Comprom	-0.405	Comprom	0.000	1.103	Detected	1.417	Detected	1.260	0.101	GT Sens	contig227	contig227	Steroid su	TTTCTG	contig227	Solyc05g	Solyc05g	Steroid su	GO:00081	GO:00081	contig227	Solyc05g	Steroid su	GO:00502	SL2.40ch	AT3G45070.1		sulfotran	chr3:164	6.60057	2.94243	8.58408	10.6647	10.0078	12.0044
GT	Sense	Sense	0.185	Detected	-0.185	Detected	0.000	2.322	Detected	1.718	Detected	2.020	0.029	GT Sens	contig229	contig229	Chloroph	AAATCT	contig229	Solyc02g	Solyc02g	Chloroph	GO:00161	GO:00161	contig229	Solyc02g	Chloroph	GO:00161	SL2.40ch	AT1G299	CAB1. AB	CAB1 (CI	chr1:104	451.796	273.218	856.765	934.338	1857.14	1179.04
GT	Sense	Sense	0.069	Detected	-0.069	Detected	0.000	2.299	Detected	1.494	Detected	1.896	0.043	GT Sens	contig230	contig230	1-aminoc	TCAGTT	contig230	Solyc09g	Solyc09g	1-aminoc	GO:00164	GO:00164	contig230	Solyc09g	1-aminoc	GO:00164	SL2.40ch	AT3G61400.1		2-oxoglu	chr3:227	551.224	391.6	2180.98	3875.41	2416.47	1335.01
GT	Sense	Sense	-0.005	Detected	0.005	Detected	0.000	1.299	Detected	1.088	Detected	1.194	0.008	GT Sens	contig234	contig234	Cytochro	AAGTAT	contig234	Solyc02g	Solyc02g	Cytochro	GO:00200	GO:00200	contig234	Solyc02g	Cytochro	GO:00198	SL2.40ch	AT5G249	CYP71A1	CYP71A1	chr5:859	3336.44	2624.39	4703.46	6128.01	7696.69	6419.79
GT	Sense	Sense	-0.194	Comprom	0.194	Comprom	0.000	1.444	Detected	1.110	Detected	1.277	0.038	GT Sens	contig235	contig235	Leucine-r	TGGCTT	contig235	Solyc12g	Solyc12g	Leucine-r	GO:00055	GO:00055	contig235	Solyc12g	LRR recep	GO:00046	SL2.40ch	AT1G055	SYTE. AT	NTMC2T	chr1:162	5.98092	6.11371	8.52664	22.6346	17.385	13.314
GT	Sense	Sense	-0.451	Detected	0.451	Detected	0.000	1.359	Detected	1.516	Detected	1.438	0.088	GT Sens	contig235	contig235	Subtilisin	CTACCA	contig235	Solyc08g	Solyc08g	Subtilisin	GO:00042	GO:00042	contig235	Solyc08g	Subtilisin	GO:00042	SL2.40ch	AT3G19540.1		unknown	chr3:678	145.309	212.299	203.758	181.616	476.223	512.626
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	1.712	Detected	1.396	Detected	1.554	0.010	GT Sens	contig235	contig235	Inositol-3	GATTTC	contig235	Solyc05g	Solyc05g	Inositol-3	GO:00086	GO:00086	contig235	Solyc05g	Inositol-3	GO:00428	SL2.40ch	AT2G222	ATMIPS2	MIPS2 (M	chr2:945	2450.04	1961.37	3163.82	4632.16	7592.18	5886.84
GT	Sense	Sense	-0.235	Detected	0.235	Detected	0.000	1.325	Detected	1.243	Detected	1.284	0.033	GT Sens	contig237	contig237	Dynein lig	CCAAGC	contig237	Solyc12g	Solyc12g	Dynein lig	GO:00428	GO:00428	contig237	Solyc12g	Dynein lig	GO:00428	SL2.40ch	AT1G522	ATROPGI	ROPGEF	chr1:194	152.737	165.298	480.244	256.76	420.706	383.631
GT	Sense	Sense	-0.347	Detected	0.347	Detected	0.000	1.540	Detected	1.025	Detected	1.282	0.097	GT Sens	contig237	contig237	Leucine-r	TTCCAT	contig237	Solyc12g	Solyc12g	Leucine-rich repeat receptor-li			contig237	Solyc01g	Receptor	GO:00428	SL2.40ch	AT3G04190.1				28.1615	35.634	56.9255	74.9832	97.3777	65.7534
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	1.079	Detected	1.168	Detected	1.124	0.002	GT Sens	contig238	contig238	Eukaryot	TGTGTG	contig238	Solyc01g	Solyc01g	Eukaryot	GO:00058	GO:00058	contig238	Solyc01g102570.2.1				AT3G561	EIF3C. AT	EIF3C (E	chr3:208	58.6604	47.2967	110.133	88.1128	117.631	120.752
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	1.172	Detected	1.183	Detected	1.177	0.002	GT Sens	contig239	contig239	Unknown	AATATC	contig239	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig239	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G14368.1		zinc ion I	chr4:827	28.4554	20.6125	56.6905	44.4608	57.6533	56.0913
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	1.184	Detected	1.156	Detected	1.170	0.000	GT Sens	contig245	contig245	F-box/LR	CTGAAG	contig245	Solyc07g	Solyc07g	F-box/LRR-repeat protein 13 (A			contig245	Solyc07g	F-box/LRR-repeat p		SL2.40ch	AT4G20720.1		dentin si	chr4:111	74.2441	56.7862	111.662	117.359	155.888	147.637
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	2.146	Detected	1.788	Detected	1.967	0.011	GT Sens	contig246	contig246	Unknown	GACTTG	contig246	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig246	Solyc05g024230.1.1				AT4G344	CHB3. AT	CHB3: DI	chr4:164	233.798	159.703	237.216	156.127	903.837	680.866
GT	Sense	Sense	-0.395	Detected	0.395	Detected	0.000	1.373	Detected	0.808	Detected	1.091	0.154	GT Sens	contig248	contig248	Glucose-	TGCAGA	contig248	Solyc08g	Solyc08g	Glucose-methanol-choline oxi			contig248	Solyc08g	Glucose-methanol-c		SL2.40ch	AT5G285	BIP1	BIP1: AT	chr5:105	13.8979	18.7948	47.8755	37.217	44.2561	28.8784
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	1.095	Detected	1.072	Detected	1.083	0.004	GT Sens	contig249	contig249	Auxin res	TTCACA	contig249	Solyc03g	Solyc03g	Auxin res	GO:00037	GO:00037	contig249	Solyc03g	Auxin res	GO:00037	SL2.40ch	AT5G370	ARF8	ARF8 (AU	chr5:146	756.947	653.74	1164.94	1182.68	1588.19	1508.71
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	1.927	Detected	1.516	Detected	1.722	0.019	GT Sens	contig249	contig249	Chloroph	AAATCA	contig249	Solyc02g	Solyc02g	Chloroph	GO:00055	GO:00055	contig249	Solyc02g	Chloroph	GO:00055	SL2.40ch	AT2G344	LHB1B2.	LHB1B2:	chr2:145	157.083	102.975	302.361	368.603	511.171	371.126
GT	Sense	Sense	-0.437	Detected	0.437	Detected	0.000	1.032	Detected	1.019	Detected	1.025	0.143	GT Sens	contig250	contig250	Disease r	ATCTAT	contig250	Solyc11g	Solyc11g	Disease r	GO:00055	GO:00055	contig250	Solyc11g	Cc-nbs-lr	GO:00055	SL2.40ch	AT5G10500.1		kinase in	chr5:330	46.7947	66.9909	89.2993	72.8267	120.984	115.742
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	1.490	Detected	1.234	Detected	1.362	0.012	GT Sens	contig253	contig253	Elongatio	AGTAGT	contig253	Solyc12g	Solyc12g	Elongatio	GO:00055	GO:00055	contig253	Solyc08g	Elongatio	GO:00039	SL2.40ch	AT1G627	ATSCO1.	SCO1 (SI	chr1:232	1142.71	988.18	1887.49	2418.97	3155.09	2550.54
GT	Sense	Sense	-1.099	Comprom	1.099	Detected	0.000	1.447	Detected	1.092	Detected	1.269	0.372	GT Sens	contig261	contig261	Hcr9-4E (	CCATAA	contig261	Solyc12g	Solyc12g	Hcr9-4E (AHRD V1 *-*- O50024			contig261	Solyc12g	LRR recep	GO:00163	SL2.40ch	AT3G09035.1		legume l	chr3:275	3.44402	12.3544	13.382	8.4148	18.7893	14.1901
GT	Sense	Sense	0.249	Detected	-0.249	Detected	0.000	2.510	Detected	2.717	Detected	2.614	0.010	GT Sens	contig261	contig261	Early ligh	CTAGCT	contig261	Solyc09g	Solyc09g	Early light-induced protein 7 (A			contig261	Solyc09g	Early ligh	GO:00161	SL2.40ch	AT4G146	ELIP2	ELIP2 (E	chr4:841	2457.39	1360.53	4576.69	6712.15	11008.1	12270.6
GT	Sense	Sense	-0.946	Comprom	0.946	Detected	0.000	1.716	Detected	1.991	Detected	1.853	0.192	GT Sens	contig263	contig263	Pentatric	TAGATA	contig263	Solyc11g	Solyc11g	Pentatricopeptide repeat-cont			contig263	Solyc11g	Pentatricopeptide re		SL2.40ch	AT3G49740.1		pentatric	chr3:184	4.91357	14.2532	24.8606	19.1928	29.0471	33.9431
GT	Sense	Sense	-0.021	Detected	0.021	Detected	0.000	1.034	Detected	1.039	Detected	1.037	0.000	GT Sens	contig263	contig263	Unknown	GAAAGA	contig263	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig263	Solyc05g	Unknown Protein (A		SL2.40ch	AT4G22440.1				184.017	148.054	249.359	278.492	357.325	345.99
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	1.196	Detected	0.837	Detected	1.016	0.035	GT Sens	contig267	contig267	F-box fam	GGCATA	contig267	Solyc04g	Solyc04g	F-box family protein (AHRD V1			contig267	Solyc04g	F-box family protein		SL2.40ch	AT3G05070.1		FUNCTIO	chr3:141	497.219	348.674	608.753	551.645	1008.09	758.866
GT	Sense	Sense	-0.684	Comprom	0.684	Comprom	0.000	3.562	Detected	2.886	Detected	3.224	0.052	GT Sens	contig270	contig270	FAM65A	TTGGAA	contig270	Solyc09g	Solyc09g	FAM65A protein related (AHRD			contig270	Solyc09g	FAM65A protein rela		SL2.40ch	AT4G373	YDK1. GH	BRU6: in	chr4:175	3.40407	6.86931	4.97498	4.40682	60.3787	36.4655
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	1.028	Detected	1.005	Detected	1.016	0.009	GT Sens	contig270	contig270	Hydroxyc	AGAACA	contig270	Solyc12g	Solyc12g	Hydroxyc	GO:00167	GO:00167	contig270	Solyc12g	Hydroxyc	GO:00167	SL2.40ch	AT4G15390.1		transfera	chr4:879	127.212	87.1001	180.678	158.898	226.82	215.497
GT	Sense	Sense	0.235	Comprom	-0.235	Comprom	0.000	1.793	Detected	2.344	Detected	2.069	0.029	GT Sens	contig271	contig271	Unknown	GTTAAC	contig271	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig271	Solyc08g	F-box fam	GO:00048	SL2.40ch	AT1G72660.3		developm	chr1:273	8.27512	4.66894	82.6135	91.3305	22.7631	32.2111
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	0.854	Detected	1.434	Detected	1.144	0.059	GT Sens	contig277	contig277	Cytochro	ATTCCG	contig277	Solyc03g	Solyc03g	Cytochro	GO:00200	GO:00200	contig277	Solyc03g	Cytochro	GO:00198	SL2.40ch	AT3G201	CYP705A	CYP705A	chr3:702	54.5038	40.6085	58.6259	57.9799	89.9008	129.705
GT	Sense	Sense	-0.116	Detected	0.116	Detected	0.000	1.425	Detected	1.183	Detected	1.304	0.016	GT Sens	contig279	contig279	Oxygen-e	TTCCTT	contig279	Solyc07g	Solyc07g	Oxygen-e	GO:00198	GO:00198	contig279	Solyc02g	Oxygen-e	GO:00082	SL2.40ch	AT3G508	PSBO2. P	PSBO2 (I	chr3:188	3122.32	2866.13	6214	6172.93	8488.67	6929.62
GT	Sense	Sense	-0.211	Detected	0.211	Detected	0.000	2.328	Detected	1.846	Detected	2.087	0.023	GT Sens	contig280	contig280	Chloroph	TTAGAG	contig280	Solyc12g	Solyc12g	Chloroph	GO:00160	GO:00160	contig280	Solyc12g	Chloroph	GO:00160	SL2.40ch	AT5G542	LHCB3. L	LHCB3 (L	chr5:220	243.932	255.463	750.145	928.825	1325.11	915.782
GT	Sense	Sense	0.249	Detected	-0.249	Comprom	0.000	1.353	Detected	1.349	Detected	1.351	0.032	GT Sens	contig282	contig282	Unknown	GATCTT	contig282	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig282	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G336	AGD2	AGD2 (AI	chr4:161	13.6794	7.56817	23.7928	16.1949	27.4702	26.4536
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	1.760	Detected	1.505	Detected	1.633	0.007	GT Sens	contig284	contig284	Unknown	GCTGAG	contig284	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig284	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G571	ATPAP28	PAP28 (P	chr5:231	239.404	175.809	305.805	294.947	734.35	594.189
GT	Sense	Sense	-1.830	Comprom	1.830	Detected	0.000	2.558	Detected	2.103	Detected	2.331	0.334	GT Sens	contig287	contig287	Sulfotran	ATCTTT	contig287	Solyc11g	Solyc11g	Sulfotran	GO:00081	GO:00081	contig287	Solyc11g	Sulfotran	GO:00081	SL2.40ch	AT1G470	VFB1	VFB1 (VI	chr1:172	10.692	105.672	144.883	248.258	209.231	147.331
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	1.545	Detected	1.025	Detected	1.285	0.042	GT Sens	contig288	contig288	Unknown	AAAGAC	contig288	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig288	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G09950.1		unknown	chr3:306	8384.35	5880.54	17823.8	15402.2	21659.8	14575.2
GT	Sense	Sense	0.520	Detected	-0.520	Detected	0.000	1.810	Detected	0.902	Detected	1.356	0.188	GT Sens	contig292	contig292	Acetyl co	CTACTC	contig292	Solyc05g	Solyc05g	Acetyl co	GO:00103	GO:00103	contig292	Solyc05g	Acetyl co	GO:00103	SL2.40ch	AT5G17540.1		transfera	chr5:578	1886	716.679	1825.62	2071.01	4308.06	2217.21
GT	Sense	Sense	-0.055	Detected	0.055	Detected	0.000	1.179	Detected	1.360	Detected	1.270	0.007	GT Sens	contig295	contig295	class II he	ATTTGA	contig295	Solyc08g	Solyc08g	class II he	GO:00510	GO:00510	contig295	Solyc08g	class II he	GO:00510	SL2.40ch	AT5G120	HSP17.6II	HSP17.6I	chr5:388	18.0198	15.1911	32.6136	22.801	39.604	43.3245
GT	Sense	Sense	0.280	Detected	-0.280	Detected	0.000	0.966	Detected	1.224	Detected	1.095	0.071	GT Sens	contig298	contig298	Pectinace	AGTATT	contig298	Solyc03g	Solyc03g	Pectinacetylesterase (Fragme			contig298	Solyc03g	Pectinacetylesteras		SL2.40ch	AT5G23870.1		pectinac	chr5:804	85.862	45.5421	96.2992	133.579	129.055	149.06
GT	Sense	Sense	0.007	Detected	-0.007	Detected	0.000	2.434	Detected	2.151	Detected	2.293	0.004	GT Sens	contig299	contig299	CONSTAI	GGAGTA	contig299	Solyc02g	Solyc02g	CONSTAI	GO:00037	GO:00037	contig299	Solyc02g	Tomato C	GO:00037	SL2.40ch	AT5G158	COL1. AT	COL1 (co	chr5:517	382.591	296.198	1061.23	1618.25	1922.68	1525.61
GT	Sense	Sense	0.294	Detected	-0.294	Comprom	0.000	1.321	Detected	0.898	Detected	1.109	0.092	GT Sens	contig306	contig306	Ulp1 prot	CACTTT	contig306	Solyc07g	Solyc07g	Ulp1 prot	GO:00065	GO:00065	contig306	Solyc07g	Ulp1 prot	GO:00065	SL2.40ch	AT1G42470.1		patched	chr1:159	20.7593	10.7922	27.2508	35.3432	39.5096	28.456
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	1.509	Detected	1.227	Detected	1.368	0.025	GT Sens	contig309	contig309	Chloroph	TTAATT	contig309	Solyc01g	Solyc01g	Chloroph	GO:00161	GO:00161	contig309	Solyc01g	Chloroph	GO:00161	SL2.40ch	AT1G158	LHCB6. C	LHCB6 (L	chr1:544	9055.38	5584.12	13318.8	16076.3	21394.2	16989.9
GT	Sense	Sense	-0.361	Detected	0.361	Detected	0.000	1.132	Detected	0.941	Detected	1.036	0.109	GT Sens	contig311	contig311	GH3 famil	GCAGTG	contig311	Solyc10g	Solyc10g	GH3 famil	GO:00705	GO:00705	contig311	Solyc10g	GH3 famil	GO:00801	SL2.40ch	AT2G463	JAR1. FIN	JAR1 (JA	chr2:190	673.631	868.582	1296.89	1972.95	1771.98	1498.19
GT	Sense	Sense	-0.250	Detected	0.250	Detected	0.000	1.684	Detected	0.894	Detected	1.289	0.110	GT Sens	contig312	contig312	Subtilisin	CAAGTG	contig312	Solyc08g	Solyc08g	Subtilisin	GO:00042	GO:00042	contig312	Solyc08g	Subtilisin	GO:00042	SL2.40ch	AT4G10510.1		subtilase	chr4:649	367.444	406.172	618.454	753.028	1312.09	732.597
GT	Sense	Sense	-0.330	Detected	0.330	Detected	0.000	1.355	Detected	1.204	Detected	1.280	0.063	GT Sens	contig323	contig323	Indole-3-a	AATGGG	contig323	Solyc00g	Solyc00g	Indole-3-acetic acid-amido syn			contig323	Solyc10g	GH3 famil	GO:00801	SL2.40ch	AT5G38340.1		disease r	chr5:153	231.394	285.853	457.145	680.054	695.321	604.653
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	1.232	Detected	1.221	Detected	1.227	0.006	GT Sens	contig340	contig340	Receptor	TATTAG	contig340	Solyc10g	Solyc10g	Receptor	GO:00055	GO:00055	contig340	Solyc10g	LRR recep	GO:00055	SL2.40ch	AT4G08450.1		disease r	chr4:536	275.426	189.159	311.053	215.034	566.491	543.071
GT	Sense	Sense	0.408	Detected	-0.408	Detected	0.000	0.814	Detected	1.247	Detected	1.031	0.155	GT Sens	contig355	contig355	Endogluc	TTACAA	contig355	Solyc08g	Solyc08g	Endogluc	GO:00059	GO:00059	contig355	Solyc08g	Endogluc	GO:00302	SL2.40ch	AT1G643	AtGH9C2	AtGH9C2	chr1:239	60.8762	27.0283	70.5424	34.3085	75.3734	98.2443
GT	Sense	Sense	-0.094	Comprom	0.094	Comprom	0.000	2.787	Detected	2.871	Detected	2.829	0.001	GT Sens	contig375	contig375	Leucine F	TTCTTA	contig375	Solyc12g	Solyc12g	Leucine F	GO:00055	GO:00055	contig375	Solyc12g	LRR recep	GO:00163	SL2.40ch	AT2G46915.1		unknown	chr2:192	9.21183	8.19957	12.5481	55.7702	63.3812	64.8771
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	1.387	Detected	1.133	Detected	1.260	0.025	GT Sens	contig386	contig386	Unknown	ATCGTT	contig386	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig386	Solyc06g009810.2.1				AT1G508	POLGAM	POLGAM	chr1:188	62.6129	39.1668	75.5282	61.7393	136.873	110.821
GT	Sense	Sense	0.173	Detected	-0.173	Detected	0.000	0.991	Detected	1.382	Detected	1.186	0.045	GT Sens	contig390	contig390	Digalacto	GATATT	contig390	Solyc10g	Solyc10g	Digalactosyldiacylglycerol syn			contig390	Solyc10g	Digalactosyldiacylg		SL2.40ch	AT3G116	DGD1	DGD1 (DI	chr3:368	18.9888	11.6731	26.1108	22.2622	31.2792	39.5844
GT	Sense	Sense	0.076	Comprom	-0.076	Comprom	0.000	1.964	Detected	3.102	Detected	2.533	0.048	GT Sens	contig416	contig416	Aldehyde	TCTTTC	contig416	Solyc11g	Solyc11g	Aldehyde	GO:00551	GO:00551	contig416	Solyc11g	Aldehyde	GO:00090	SL2.40ch	AT5G209	AAO1. AC	AAO1 (AI	chr5:711	3.14601	2.21174	10.8062	18.0265	10.8754	23.1168
GT	Sense	Sense	2.123	Detected	-2.123	Comprom	0.000	1.644	Detected	2.759	Detected	2.201	0.421	GT Sens	contig419	contig419	Unannota	CTCACCATTCAAATTTGTACATCATCGAATGGGAAATCTCTATCTTCTA							contig419	Solyc03g	Polyprote	GO:00065	SL2.40ch	AT5G64667.1				50.6456	2.08765	10.4512	6.49879	33.968	70.9997
GT	Sense	Sense	-0.224	Detected	0.224	Detected	0.000	1.994	Detected	1.480	Detected	1.737	0.036	GT Sens	contig429	contig429	Nicotia ta	CAAGTAAGAATCCTTCTCAAATTGTTATTTGTGCATCTTGATCATCATG							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	48.0533	51.247	111.458	125.397	208.937	141.28
GT	Sense	Sense	0.002	Detected	-0.002	Detected	0.000	1.195	Detected	0.831	Detected	1.013	0.031	GT Sens	contig441	contig441	Nodulin-li	CCGCTC	contig441	Solyc08g	Solyc08g	Nodulin-li	GO:00160	GO:00160	contig441	Solyc08g	Nodulin-li	GO:00160	SL2.40ch	AT5G45370.3		nodulin-r	chr5:183	406.507	316.669	627.683	739.121	868.006	651.354
GT	Sense	Sense	0.168	Detected	-0.168	Detected	0.000	1.954	Detected	1.858	Detected	1.906	0.008	GT Sens	contig446	contig446	Auxin-ind	CATGAT	contig446	Solyc03g	Solyc03g	Auxin-ind	GO:00055	GO:00055	contig446	Solyc03g	Auxin-ind	GO:00055	SL2.40ch	AT2G21220.1		auxin-res	chr2:908	71.1491	44.0712	142.457	125.122	229.366	207.069
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	1.248	Detected	1.261	Detected	1.254	0.006	GT Sens	contig456	contig456	ClpB cha	GAGTTA	contig456	Solyc06g	Solyc06g	ClpB cha	GO:00055	GO:00055	contig456	Solyc03g	ClpB cha	GO:00195	SL2.40ch	AT1G743	ATHSP10	ATHSP1(	chr1:279	822.129	731.823	623.454	947.106	1946.75	1896.64
GT	Sense	Sense	-0.151	Detected	0.151	Detected	0.000	1.421	Detected	0.910	Detected	1.166	0.059	GT Sens	contig461	contig461	Unknown	GGCTAC	contig461	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig461	Solyc00g	Unknown Protein (A		SL2.40ch	AT2G38160.1				13.1661	12.6922	16.9508	6.78287	36.583	24.7857
GT	Sense	Sense	-0.007	Detected	0.007	Detected	0.000	1.277	Detected	0.936	Detected	1.107	0.023	GT Sens	contig476	contig476	Tryptoph	CACGGC	contig476	Solyc10g	Solyc10g	Tryptoph	GO:00081	GO:00081	contig476	Solyc10g	Tryptoph	GO:00048	SL2.40ch	AT3G12100.2		cation ef	chr3:385	2819.85	2226.02	3199.11	4304.07	6416.6	4891.32
GT	Sense	Sense	-0.204	Detected	0.204	Detected	0.000	1.850	Detected	1.732	Detected	1.791	0.014	GT Sens	contig480	contig480	Unknown	AATAAT	contig480	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)%			contig480	Solyc12g	H-ATPase	GO:00160	SL2.40ch	AT2G13720.1				1399.45	1451.69	1685	1444.44	5430.01	4832
GT	Sense	Sense	-0.443	Comprom	0.443	Comprom	0.000	1.367	Detected	1.498	Detected	1.432	0.085	GT Sens	contig482	contig482	Helicase-l	TCTAAG	contig482	Solyc03g	Solyc03g	Helicase-like protein (AHRD V1			contig482	Solyc07g	Helicase-like protein		SL2.40ch	AT5G482	EMB1276	ACAT2 (A	chr5:195	3.18713	4.60089	8.9	6.77541	10.4408	11.0328
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	1.488	Detected	1.405	Detected	1.447	0.001	GT Sens	contig483	contig483	Metacasp	CAGAAG	contig483	Solyc01g	Solyc01g	Metacasp	GO:00057	GO:00057	contig483	Solyc01g	Metacasp	GO:00065	SL2.40ch	AT5G502	OS. OLD5	OS (QUIN	chr5:204	88.9679	68.1758	167.083	102.778	230.906	210.475
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	1.149	Detected	1.085	Detected	1.117	0.004	GT Sens	contig502	contig502	F-box/LR	AATCAT	contig502	Solyc08g	Solyc08g	F-box/LRR-repeat protein At3g			contig502	Solyc08g	F-box/LRR-repeat p		SL2.40ch	AT4G20720.1		dentin si	chr4:111	153.984	109.75	454.819	395.825	304.733	281.381
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	1.148	Detected	1.121	Detected	1.135	0.001	GT Sens	contig512	contig512	Topoisom	TTGAGA	contig512	Solyc11g	Solyc11g	Topoisomerase 6 subunit B-lik			contig512	Solyc11g	Topoisomerase 6 su		SL2.40ch	AT3G294	ATEXO70	ATEXO7(	chr3:112	34.719	28.2437	53.5356	51.8261	73.3539	69.5176
GT	Sense	Sense	-0.438	Detected	0.438	Detected	0.000	1.619	Detected	1.350	Detected	1.484	0.084	GT Sens	contig531	contig531	PHD finge	GGATGA	contig531	Solyc01g	Solyc01g	PHD finger family protein (AHR			contig531	Solyc01g	PHD finger family pr		SL2.40ch	AT3G52100.1		PHD fing	chr3:193	18.6965	26.8231	55.8783	42.6711	72.6904	58.2455
GT	Sense	Sense	0.141	Comprom	-0.141	Comprom	0.000	1.011	Detected	1.324	Detected	1.167	0.031	GT Sens	contig535	contig535	Auxin res	GCTAGC	contig535	Solyc05g	Solyc05g	Auxin res	GO:00055	GO:00055	contig535	Solyc05g	Auxin res	GO:00055	SL2.40ch	AT3G19240.1		FUNCTIO	chr3:666	10.9936	7.06378	21.4678	21.2009	18.7695	22.5075
GT	Sense	Sense	0.346	Detected	-0.346	Detected	0.000	2.198	Detected	1.667	Detected	1.932	0.047	GT Sens	contig536	contig536	Chloroph	AATTTC	contig536	Solyc02g	Solyc02g	Chloroph	GO:00055	GO:00055	contig536	Solyc02g	Chloroph	GO:00055	SL2.40ch	AT1G299	CAB3. AB	CAB3 (CI	chr1:104	347.626	168.146	621.439	626.834	1172.43	783.333
GT	Sense	Sense	-0.721	Comprom	0.721	Detected	0.000	1.477	Detected	0.933	Detected	1.205	0.258	GT Sens	contig551	contig551	Cytochro	TCAGTT	contig551	Solyc10g	Solyc10g	Cytochro	GO:00200	GO:00200	contig551	Solyc10g	cytochro	GO:00198	SL2.40ch	AT5G51900.1				8.43982	17.9302	25.9475	20.4483	36.1887	23.9717
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	1.293	Detected	1.149	Detected	1.221	0.013	GT Sens	contig60	contig60	WD-40 re	TCCCCT	contig60	Solyc12g	Solyc12g	WD-40 re	GO:00064	GO:00064	contig60	Solyc12g	WD-40 re	GO:00064	SL2.40ch	AT3G153	SPA3	SPA3 (SP	chr3:516	1211.26	800.655	2119.71	2350.46	2550.04	2228.93
GT	Sense	Sense	0.000	Detected	0.000	Detected	0.000	1.825	Detected	1.530	Detected	1.678	0.008	GT Sens	contig600	contig600	F-box fam	CTCAAG	contig600	Solyc07g	Solyc07g	F-box family protein (AHRD V1			contig600	Solyc07g	F-box family protein		SL2.40ch	AT4G20720.1		dentin si	chr4:111	62.9007	49.157	397.505	293.533	208.265	163.896
GT	Sense	Sense	-0.975	Comprom	0.975	Detected	0.000	1.015	Detected	2.354	Detected	1.685	0.290	GT Sens	contig624	contig624	Unknown	CCAAAG	contig624	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig624	Solyc00g	Unknown Protein (A		SL2.40ch	AT1G31090.1		F-box far	chr1:110	5.87173	17.7345	23.7024	13.9381	21.7971	53.2452
GT	Sense	Sense	0.669	Detected	-0.669	Comprom	0.000	2.784	Detected	2.048	Detected	2.416	0.087	GT Sens	contig629	contig629	Malonyl C	ACCATG	contig629	Solyc10g	Solyc10g	Malonyl CoA anthocyanin 5-O-			contig629	Solyc10g	Malonyl CoA anthoc		SL2.40ch	AT3G50840.1		phototro	chr3:188	14.3505	4.43432	26.8549	20.9333	58.0874	33.6663
GT	Sense	Sense	-0.049	Detected	0.049	Detected	0.000	1.138	Detected	1.004	Detected	1.071	0.006	GT Sens	contig634	contig634	RNA bind	TGCTCT	contig634	Solyc09g	Solyc09g	RNA binding protein (AHRD V1			contig634	Solyc09g	RNA binding protein		SL2.40ch	AT5G01590.1		unknown	chr5:224	159.593	133.601	214.857	198.647	339.569	298.843
GT	Sense	Sense	0.091	Detected	-0.091	Detected	0.000	2.271	Detected	1.666	Detected	1.969	0.025	GT Sens	contig660	contig660	Chloroph	AAACTC	contig660	Solyc02g	Solyc02g	Chloroph	GO:00055	GO:00055	contig660	Solyc02g070970.1.1				AT2G344	LHB1B2.	LHB1B2:	chr2:145	227.721	156.986	483.496	523.927	964.311	612.338
GT	Sense	Sense	0.242	Detected	-0.242	Detected	0.000	1.229	Detected	1.090	Detected	1.160	0.044	GT Sens	contig666	contig666	Kinesin-li	AGATAT	contig666	Solyc12g	Solyc12g	Kinesin-like calmodulin bindin			contig666	Solyc12g	Kinesin-like calmod		SL2.40ch	AT1G11420.1		agenet d	chr1:384	170.083	95.1029	258.879	279.106	315.15	276.212
GT	Sense	Sense	-1.021	Comprom	1.021	Detected	0.000	1.133	Detected	2.576	Detected	1.854	0.276	GT Sens	contig671	contig671	Cytochro	GTTCAA	contig671	Solyc10g	Solyc10g	Cytochro	GO:00200	GO:00200	contig671	Solyc10g	Cytochro	GO:00464	SL2.40ch	AT2G408	CYP98A3	CYP98A3	chr2:170	3.92301	12.6199	1.92968	1.81817	16.307	42.7961
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	1.549	Detected	1.060	Detected	1.305	0.033	GT Sens	contig725	contig725	Salicylic a	TCCTTG	contig725	Solyc09g	Solyc09g	Salicylic a	GO:00081	GO:00081	contig725	Solyc09g	Salicylic a	GO:00087	SL2.40ch	AT4G36470.1		S-adeno	chr4:172	202.465	157.099	242.325	403.955	551.672	379.455
GT	Sense	Sense	0.184	Comprom	-0.184	Comprom	0.000	2.347	Detected	2.855	Detected	2.601	0.014	GT Sens	contig731	contig731	Leucine-r	ATTAGA	contig731	Solyc12g	Solyc12g	Leucine-r	GO:00055	GO:00055	contig731	Solyc12g	LRR recep	GO:00163	SL2.40ch	AT4G142	RHF1A	RHF1A (F	chr4:819	4.27342	2.58891	6.19118	6.19868	17.8838	24.5584
GT	Sense	Sense	0.554	Comprom	-0.554	Comprom	0.000	1.230	Detected	1.100	Detected	1.165	0.172	GT Sens	contig790	contig790	Receptor	TTACAG	contig790	Solyc10g	Solyc10g	Receptor protein kinase-like (A			contig790	Solyc01g	Receptor	GO:00428	SL2.40ch	AT1G24090.1				8.95618	3.24943	14.8198	20.4175	13.3723	11.8031
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	2.352	Detected	0.972	Detected	1.662	0.139	GT Sens	contig799	contig799	Hydroxyc	TTTCCA	contig799	Solyc07g	Solyc07g	Hydroxyc	GO:00167	GO:00167	contig799	Solyc07g	Hydroxyc	GO:00167	SL2.40ch	AT5G484	ATGLR1.	ATGLR1.	chr5:196	702.884	611.882	1995.59	979.212	3538.68	1312.22
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	2.674	Detected	2.363	Detected	2.518	0.004	GT Sens	contig815	contig815	CONSTAI	TGGAAT	contig815	Solyc02g	Solyc02g	CONSTAI	GO:00037	GO:00037	contig815	Solyc02g	Tomato C	GO:00037	SL2.40ch	AT5G158	COL1. AT	COL1 (co	chr5:517	584.687	435.472	1711.06	2530.55	3402.97	2648.85
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	1.441	Detected	1.212	Detected	1.326	0.007	GT Sens	contig844	contig844	B3 domai	GTGCTT	contig844	Solyc08g	Solyc08g	B3 domai	GO:00063	GO:00063	contig844	Solyc08g	B3 domai	GO:00063	SL2.40ch	AT3G189	VRN1. RE	VRN1 (RE	chr3:654	14.7672	11.463	28.4262	22.1869	37.3215	30.759
GT	Sense	Sense	0.246	Detected	-0.246	Detected	0.000	1.139	Detected	1.035	Detected	1.087	0.050	GT Sens	contig879	contig879	Protein ki	CCATTG	contig879	Solyc07g	Solyc07g	Protein kinase family protein (			contig879	Solyc01g	Receptor-	GO:00064	SL2.40ch	AT1G09440.1		protein k	chr1:304	488.665	271.486	618.908	466.339	847.545	761.757
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	1.528	Detected	1.119	Detected	1.324	0.032	GT Sens	contig886	contig886	Cytochro	TACCAA	contig886	Solyc03g	Solyc03g	Cytochro	GO:00198	GO:00198	contig886	Solyc03g	Cytochro	GO:00198	SL2.40ch	AT3G483	CYP71A2	CYP71A2	chr3:178	1467.73	1372.83	2288.69	4501.8	4326.66	3145.96
GT	Sense	Sense	-0.131	Comprom	0.131	Comprom	0.000	1.152	Detected	1.107	Detected	1.129	0.014	GT Sens	contig889	contig889	GDSL est	CAAAAA	contig889	Solyc03g	Solyc03g	GDSL est	GO:00066	GO:00066	contig889	Solyc03g	GDSL est	GO:00040	SL2.40ch	AT3G16370.1		GDSL-m	chr3:555	7.31906	6.86023	28.5729	18.7628	16.6378	15.5759
GT	Sense	Sense	0.030	Detected	-0.030	Comprom	0.000	2.553	Detected	2.481	Detected	2.517	0.000	GT Sens	contig906	contig906	1-aminoc	GTCCAG	contig906	Solyc09g	Solyc09g	1-aminoc	GO:00164	GO:00164	contig906	Solyc09g	1-aminoc	GO:00098	SL2.40ch	AT1G06640.1		2-oxoglu	chr1:203	11.4376	8.5736	32.0604	32.8921	61.4151	56.4026
GT	Sense	Sense	-0.225	Detected	0.225	Detected	0.000	1.284	Detected	0.809	Detected	1.047	0.085	GT Sens	contig920	contig920	Photosys	TGTGTT	contig920	Solyc02g	Solyc02g	Photosys	GO:00095	GO:00095	contig920	Solyc02g	Photosys	GO:00095	SL2.40ch	AT1G313	PSAF	PSAF (ph	chr1:112	147.814	157.794	311.273	280.456	393.13	272.965
GT	Sense	Sense	-0.530	Detected	0.530	Detected	0.000	2.179	Detected	1.014	Detected	1.597	0.180	GT Sens	contig956	contig956	Subtilisin	TACCAA	contig956	Solyc08g	Solyc08g	Subtilisin	GO:00042	GO:00042	contig956	Solyc08g	Subtilisin	GO:00042	SL2.40ch	AT5G673	ARA12	ARA12: s	chr5:268	289.645	472.154	523.128	671.51	1770.13	762.252
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	2.457	Detected	1.977	Detected	2.217	0.015	GT Sens	contig959	contig959	Chloroph	AGTGAA	contig959	Solyc02g	Solyc02g	Chloroph	GO:00161	GO:00161	contig959	Solyc02g	Chloroph	GO:00161	SL2.40ch	AT2G344	LHB1B2.	LHB1B2:	chr2:145	173.365	112.697	358.878	397.379	811.217	561.411
GT	Sense	Sense	-0.471	Detected	0.471	Detected	0.000	1.483	Detected	1.560	Detected	1.522	0.084	GT Sens	contig977	contig977	GPCR-typ	TCTGTT	contig977	Solyc07g	Solyc07g	GPCR-type G protein 1 (AHRD			contig977	Solyc07g	Golgi pH	GO:00510	SL2.40ch	AT4G276	GTG2	GTG2 (G	chr4:137	247.815	371.959	598.21	603.39	897.007	913.559
GT	Sense	Sense	-0.079	Detected	0.079	Detected	0.000	1.257	Detected	1.025	Detected	1.141	0.015	GT Sens	EF667342	EF667342	SlARF8: (	CACAACTAAATACGTGCTCCAACTCATCATCACTTCCAACTTACGGGAAAGATACATTCA																503.909	439.429	957.956	835.719	1188.56	977.096

		8h_AZ_Control					8h_AZ_TAPG + TPRP vs. 8h_AZ_Control									
ProbeNar	Orientatio	Fold 8h	Flag 8h	Fold 8h	Flag 8h	Geomean	Fold 8h	Flag 8h	Fold 8h	Flag 8h	Geomean	P-value	ProbeNar	GeneNam	Systemat	Descripti
A 96 P0	Sense	-0.359	Detected	0.359	Detected	0.000	-1.434	Detected	-0.911	Detected	-1.172	0.118	A 96 P0	CHI3	NM 0012	Solanum
A 96 P01	Sense	-0.017	Detected	0.017	Detected	0.000	-2.344	Detected	-1.393	Detected	-1.869	0.059	A 96 P01	TA37200	TA37200	Rep: Path
A 96 P01	Sense	-0.610	Detected	0.610	Detected	0.000	-1.266	Detected	-1.801	Detected	-1.533	0.148	A 96 P01	cevi19	NM 0012	Solanum
A 96 P01	Sense	-0.192	Detected	0.192	Detected	0.000	-1.137	Detected	-1.312	Detected	-1.225	0.028	A 96 P01	AK31939	AK31939	Solanum
A 96 P02	Sense	-0.265	Detected	0.265	Detected	0.000	-1.792	Detected	-1.421	Detected	-1.607	0.038	A 96 P02	BI929281	BI929281	EST5491
A 96 P03	Sense	-0.223	Detected	0.223	Detected	0.000	-1.081	Detected	-1.050	Comprom	-1.065	0.041	A 96 P03	TA49945	TA49945	Rep: Cyto
A 96 P04	Sense	-0.581	Detected	0.581	Detected	0.000	-1.493	Detected	-0.855	Detected	-1.174	0.219	A 96 P04	GT16740	GT16740	M82T7el
A 96 P05	Sense	-0.335	Detected	0.335	Detected	0.000	-1.528	Detected	-0.986	Detected	-1.257	0.100	A 96 P05	BI922989	BI922989	EST5428
A 96 P06	Sense	0.609	Detected	-0.609	Detected	0.000	-1.878	Detected	-1.139	Detected	-1.508	0.169	A 96 P06	AK32951	AK32951	Solanum
A 96 P06	Sense	-0.368	Detected	0.368	Detected	0.000	-1.267	Comprom	-2.144	Comprom	-1.705	0.097	A 96 P06	ES89491	ES89491	LET084
A 96 P08	Sense	0.086	Detected	-0.086	Detected	0.000	-2.130	Detected	-1.061	Detected	-1.596	0.099	A 96 P08	AW62139	AW62139	Unknown
A 96 P08	Sense	0.191	Detected	-0.191	Detected	0.000	-0.862	Detected	-1.640	Detected	-1.251	0.102	A 96 P08	BG12915	BG12915	EST4748
A 96 P08	Sense	0.098	Detected	-0.098	Detected	0.000	-1.130	Detected	-1.067	Detected	-1.098	0.009	A 96 P08	A 96 P08	A 96 P08	Unknown
A 96 P08	Sense	-0.510	Detected	0.510	Detected	0.000	-2.043	Detected	-2.270	Detected	-2.156	0.054	A 96 P08	BW68867	BW68867	BW68867
A 96 P08	Sense	-0.261	Detected	0.261	Detected	0.000	-1.590	Detected	-1.357	Detected	-1.473	0.036	A 96 P08	ES89506	ES89506	LET086
A 96 P08	Sense	-1.127	Detected	1.127	Detected	0.000	-1.793	Detected	-1.490	Detected	-1.642	0.286	A 96 P08	TA36002	TA36002	Rep: Path
A 96 P08	Sense	0.132	Detected	-0.132	Detected	0.000	-1.136	Detected	-1.146	Detected	-1.141	0.013	A 96 P08	TA36375	TA36375	Unknown
A 96 P09	Sense	-0.182	Detected	0.182	Detected	0.000	-1.473	Detected	-0.918	Detected	-1.195	0.069	A 96 P09	AK32718	AK32718	Solanum
A 96 P09	Sense	-0.941	Detected	0.941	Detected	0.000	-1.565	Detected	-1.484	Detected	-1.524	0.247	A 96 P09	AK32681	AK32681	Solanum
A 96 P11	Sense	-0.179	Detected	0.179	Detected	0.000	-1.597	Detected	-1.792	Detected	-1.695	0.014	A 96 P11	TA53333	TA53333	Rep: Arab
A 96 P11	Sense	0.167	Detected	-0.167	Detected	0.000	-2.182	Comprom	-1.936	Comprom	-2.059	0.010	A 96 P11	TA53569	TA53569	Unknown
A 96 P11	Sense	-0.268	Detected	0.268	Detected	0.000	-1.480	Detected	-1.372	Detected	-1.426	0.035	A 96 P11	TA54138	TA54138	Rep: Clas
A 96 P11	Sense	-0.316	Detected	0.316	Detected	0.000	-0.967	Detected	-1.109	Detected	-1.038	0.085	A 96 P11	TA54838	TA54838	Rep: Chr
A 96 P13	Sense	0.046	Detected	-0.046	Detected	0.000	-1.419	Detected	-1.432	Detected	-1.425	0.001	A 96 P13	AI771618	AI771618	Unknown
A 96 P14	Sense	0.291	Detected	-0.291	Detected	0.000	-2.176	Detected	-1.572	Detected	-1.874	0.047	A 96 P14	AADC1A	NM 0012	Solanum
A 96 P16	Sense	-0.157	Detected	0.157	Detected	0.000	-1.926	Detected	-1.772	Detected	-1.849	0.009	A 96 P16	AW65032	AW65032	Unknown
A 96 P18	Sense	-0.262	Detected	0.262	Detected	0.000	-1.064	Detected	-0.988	Detected	-1.026	0.061	A 96 P18	ES89290	ES89290	LET055F
A 96 P18	Sense	-0.111	Detected	0.111	Detected	0.000	-2.098	Detected	-2.105	Detected	-2.101	0.003	A 96 P18	BG12772	BG12772	Unknown
A 96 P19	Sense	-0.441	Detected	0.441	Detected	0.000	-2.013	Detected	-0.975	Detected	-1.494	0.160	A 96 P19	BI209334	BI209334	Rep: End
A 96 P19	Sense	-0.259	Detected	0.259	Detected	0.000	-2.514	Detected	-2.035	Detected	-2.275	0.023	A 96 P19	BI422397	BI422397	Unknown
A 96 P20	Sense	0.147	Detected	-0.147	Detected	0.000	-2.357	Detected	-1.681	Detected	-2.019	0.032	A 96 P20	BI923180	BI923180	Rep: Aro
A 96 P22	Sense	-0.699	Detected	0.699	Detected	0.000	-1.476	Detected	-2.571	Detected	-2.023	0.150	A 96 P22	CK34829	CK34829	Rep: Path
A 96 P22	Sense	-0.219	Detected	0.219	Detected	0.000	-1.557	Comprom	-1.980	Comprom	-1.769	0.028	A 96 P22	AK32157	AK32157	Solanum
A 96 P22	Sense	-0.940	Detected	0.940	Detected	0.000	-1.752	Detected	-1.891	Detected	-1.821	0.193	A 96 P22	P4	NM 0012	Solanum
A 96 P23	Sense	-0.406	Detected	0.406	Detected	0.000	-0.955	Detected	-1.157	Detected	-1.056	0.128	A 96 P23	PHS1	AK32729	Solanum
A 96 P24	Sense	0.130	Detected	-0.130	Detected	0.000	-1.922	Detected	-1.011	Detected	-1.466	0.090	A 96 P24	AK32846	AK32846	Solanum
A 96 P24	Sense	-1.036	Detected	1.036	Detected	0.000	-1.317	Detected	-1.241	Detected	-1.279	0.343	A 96 P24	TA42313	TA42313	Rep: Chr
A 96 P25	Sense	-1.654	Detected	1.654	Detected	0.000	-2.453	Detected	-1.268	Detected	-1.861	0.401	A 96 P25	ES89697	ES89697	LET111
A 96 P25	Sense	-0.216	Detected	0.216	Detected	0.000	-1.248	Detected	-1.228	Detected	-1.238	0.029	A 96 P25	TC23209	TC23209	Rep: 13 k
A 96 P26	Sense	-0.344	Detected	0.344	Detected	0.000	-1.793	Detected	-0.930	Detected	-1.361	0.133	A 96 P26	ES89676	ES89676	LET108
GT Sens	Sense	0.065	Detected	-0.065	Detected	0.000	-1.911	Detected	-1.691	Detected	-1.801	0.005	GT Sens	AT1G149	AT1G149	high mob
GT Sens	Sense	0.238	Detected	-0.238	Detected	0.000	-3.561	Comprom	-4.956	Comprom	-4.258	0.029	GT Sens	AT2G438	AT2G438	putative
GT Sens	Sense	0.081	Detected	-0.081	Detected	0.000	-1.363	Detected	-1.284	Detected	-1.323	0.005	GT Sens	AT3G010	AT3G010	early nod
GT Sens	Sense	-0.699	Detected	0.699	Detected	0.000	-1.700	Comprom	-3.000	Comprom	-2.350	0.133	GT Sens	AT3G023	AT3G023	6-phosph
GT Sens	Sense	0.094	Detected	-0.094	Detected	0.000	-1.517	Detected	-0.978	Detected	-1.248	0.048	GT Sens	AT4G274	AT4G274	NAC dom
GT Sens	Sense	0.086	Detected	-0.086	Detected	0.000	-0.890	Detected	-1.167	Detected	-1.029	0.024	GT Sens	AT5G535	AT5G535	cytochro
GT Sens	Sense	0.800	Detected	-0.800	Detected	0.000	-1.410	Detected	-1.626	Detected	-1.518	0.201	GT Sens	AY55931	AY55931	Lycopers
GT Sens	Sense	-0.124	Detected	0.124	Detected	0.000	-1.678	Detected	-0.864	Detected	-1.271	0.096	GT Sens	BM41277	BM41277	RGLG2
GT Sens	Sense	-0.923	Detected	0.923	Detected	0.000	-1.927	Detected	-0.972	Detected	-1.450	0.298	GT Sens	contig10	contig10	Ubiquitin
GT Sens	Sense	-0.272	Detected	0.272	Detected	0.000	-2.051	Detected	-1.877	Detected	-1.964	0.021	GT Sens	contig101	contig101	Ethylene-
GT Sens	Sense	-0.141	Detected	0.141	Detected	0.000	-1.091	Detected	-1.165	Detected	-1.128	0.016	GT Sens	contig101	contig101	Unknown
GT Sens	Sense	-0.008	Detected	0.008	Detected	0.000	-1.552	Detected	-1.950	Detected	-1.751	0.013	GT Sens	contig102	contig102	NADH del
GT Sens	Sense	-0.834	Detected	0.834	Detected	0.000	-1.910	Detected	-1.027	Detected	-1.468	0.260	GT Sens	contig102	contig102	Unknown
GT Sens	Sense	-0.199	Detected	0.199	Detected	0.000	-1.750	Detected	-1.087	Detected	-1.418	0.067	GT Sens	contig102	contig102	Phospho
GT Sens	Sense	-0.092	Detected	0.092	Detected	0.000	-1.632	Detected	-1.571	Detected	-1.602	0.004	GT Sens	contig103	contig103	Polyprote
GT Sens	Sense	0.065	Detected	-0.065	Detected	0.000	-1.213	Detected	-1.229	Detected	-1.221	0.003	GT Sens	contig103	contig103	Unknown
GT Sens	Sense	-0.103	Detected	0.103	Detected	0.000	-1.536	Detected	-1.402	Detected	-1.469	0.007	GT Sens	contig103	contig103	Receptor-
GT Sens	Sense	-1.103	Detected	1.103	Detected	0.000	-1.239	Detected	-1.222	Detected	-1.230	0.381	GT Sens	contig103	contig103	Unknown
GT Sens	Sense	-0.375	Detected	0.375	Detected	0.000	-1.527	Detected	-1.530	Detected	-1.529	0.055	GT Sens	contig103	contig103	Major late
GT Sens	Sense	-0.411	Detected	0.411	Detected	0.000	-1.316	Detected	-0.805	Detected	-1.060	0.160	GT Sens	contig103	contig103	Aromatic
GT Sens	Sense	0.487	Detected	-0.487	Detected	0.000	-2.071	Detected	-2.037	Detected	-2.054	0.052	GT Sens	contig103	contig103	Unknown
GT Sens	Sense	-0.460	Detected	0.460	Detected	0.000	-3.657	Detected	-2.522	Detected	-3.089	0.052	GT Sens	contig104	contig104	Zinc finge
GT Sens	Sense	0.364	Detected	-0.364	Detected	0.000	-2.170	Detected	-2.470	Comprom	-2.320	0.028	GT Sens	contig104	contig104	Unknown
GT Sens	Sense	-0.809	Detected	0.809	Detected	0.000	-2.661	Comprom	-1.601	Detected	-2.131	0.158	GT Sens	contig105	contig105	Centrin (A
GT Sens	Sense	-0.229	Detected	0.229	Detected	0.000	-2.100	Detected	-0.939	Detected	-1.520	0.135	GT Sens	contig105	contig105	Cell num
GT Sens	Sense	-0.550	Detected	0.550	Detected	0.000	-1.223	Detected	-1.072	Detected	-1.147	0.175	GT Sens	contig106	contig106	Fasciclin-
GT Sens	Sense	0.180	Detected	-0.180	Detected	0.000	-1.636	Detected	-1.349	Detected	-1.493	0.023	GT Sens	contig106	contig106	Aspartyl
GT Sens	Sense	-0.330	Detected	0.330	Detected	0.000	-2.626	Detected	-2.290	Detected	-2.458	0.022	GT Sens	contig106	contig106	Cytochro
GT Sens	Sense	-0.064	Detected	0.064	Detected	0.000	-2.453	Detected	-1.258	Detected	-1.855	0.091	GT Sens	contig106	contig106	Unknown
GT Sens	Sense	-0.520	Detected	0.520	Detected	0.000	-1.282	Detected	-1.043	Detected	-1.162	0.161	GT Sens	contig106	contig106	Unknown
GT Sens	Sense	-0.281	Detected	0.281	Detected	0.000	-1.995	Comprom	-1.743	Comprom	-1.869	0.026	GT Sens	contig107	contig107	Potassiu
GT Sens	Sense	0.065	Detected	-0.065	Detected	0.000	-1.567	Detected	-1.231	Detected	-1.399	0.016	GT Sens	contig107	contig107	Alpha-hu
GT Sens	Sense	-0.148	Detected	0.148	Detected	0.000	-1.957	Detected	-1.534	Detected	-1.746	0.021	GT Sens	contig107	contig107	Short-cha
GT Sens	Sense	0.061	Detected	-0.061	Detected	0.000	-1.126	Detected	-1.617	Comprom	-1.372	0.032	GT Sens	contig107	contig107	Unknown
GT Sens	Sense	-0.739	Detected	0.739	Detected	0.000	-3.106	Detected	-2.030	Detected	-2.568	0.107	GT Sens	contig107	contig107	Inositol o
GT Sens	Sense	-0.139	Detected	0.139	Detected	0.000	-2.208	Detected	-0.935	Detected	-1.571	0.137	GT Sens	contig108	contig108	Armadillo
GT Sens	Sense	0.066	Detected	-0.066	Detected	0.000	-1.094	Detected	-1.136	Detected	-1.115	0.004	GT Sens	contig108	contig108	Unknown
GT Sens	Sense	-0.106	Detected	0.106	Detected	0.000	-1.188	Detected	-1.649	Detected	-1.419	0.031	GT Sens	contig109	contig109	UPF0497
GT Sens	Sense	0.205	Detected	-0.205	Detected	0.000	-1.636	Detected	-0.801	Detected	-1.218	0.120	GT Sens	contig109	contig109	Transcrip
GT Sens	Sense	-0.289	Detected	0.289	Detected	0.000	-2.253	Detected	-1.997	Detected	-2.125	0.021	GT Sens	contig109	contig109	Reverse t
GT Sens	Sense	-0.751	Detected	0.751	Detected	0.000	-4.532	Comprom	-2.754	Detected	-3.643	0.089	GT Sens	contig110	contig110	Pathogen
GT Sens	Sense	0.038	Detected	-0.038	Detected	0.000	-2.629	Comprom	-1.418	Detected	-2.023	0.079	GT Sens	contig110	contig110	Unknown
GT Sens	Sense	0.133	Detected	-0.133	Detected	0.000	-1.260	Detected	-1.485	Detected	-1.373	0.016	GT Sens	contig110	contig110	Unknown
GT Sens	Sense	-0.949	Detected	0.949	Detected	0.000	-3.023	Detected	-1.781	Detected	-2.402	0.168	GT Sens	contig111	contig111	Unknown
GT Sens	Sense	-0.171	Detected	0.171	Detected	0.000	-1.421	Detected	-1.023	Detected	-1.222	0.043	GT Sens	contig112	contig112	Unknown
GT Sens	Sense	-0.969	Detected	0.969	Detected	0.000	-1.443	Detected	-1.411	Detected	-1.427	0.279	GT Sens	contig112	contig112	Glycerop
GT Sens	Sense	-0.249	Detected	0.249	Detected	0.000	-3.666	Detected	-1.102	Detected	-2.384	0.209	GT Sens	contig112	contig112	ATP-bind
GT Sens	Sense	0.347	Detected	-0.347	Detected	0.000	-1.258	Detected	-1.270	Detected	-1.264	0.068	GT Sens	contig113	contig113	Apyrase
GT Sens	Sense	-0.059	Detected	0.059	Detected	0.000	-1.282	Detected	-1.150	Detected	-1.216	0.005	GT Sens	contig113	contig113	F-box pro
GT Sens	Sense	0.188	Detected	-0.188	Detected	0.000	-1.177	Detected	-1.124	Detected	-1.150	0.026	GT Sens	contig114	contig114	Nucleosi
GT Sens	Sense	-0.220	Detected	0.220	Detected	0.000	-2.678	Comprom	-1.335	Detected	-2.007	0.105	GT Sens	contig114	contig114	Unknown
GT Sens	Sense	0.119	Detected	-0.119	Detected	0.000	-1.359	Detected	-1.510	Detected	-1.434	0.009	GT Sens	contig114	contig114	Unknown
GT Sens	Sense	0.172	Detected	-0.172	Detected	0.000	-3.456	Comprom	-2.265	Comprom	-2.861	0.044	GT Sens	contig114	contig114	Unknown
GT Sens	Sense	0.202	Detected	-0.202	Detected	0.000	-1.012	Detected	-1.826	Comprom	-1.419	0.089	GT Sens	contig114	contig114	Ulp1 prot
GT Sens	Sense	0.050	Detected	-0.050	Detected	0.000	-3.671	Comprom	-2.245	Comprom	-2.958	0.054	GT Sens	contig114	contig114	Cytochro
GT Sens	Sense	0.071	Detected	-0.071	Detected	0.000	-1.072	Detected	-0.951	Detected	-1.012	0.008	GT Sens	contig114	contig114	Self-inco
GT Sens	Sense	-0.009	Detected	0.009	Detected	0.000	-1.362	Detected	-1.210	Detected	-1.286	0.003	GT Sens	contig115	contig115	Cellulose
GT Sens	Sense	0.011	Detected	-0.011	Detected	0.000	-3.229	Detected	-1.227	Detected	-2.228	0.156	GT Sens	contig115	contig115	Leucine-r
GT Sens	Sense	0.107	Detected	-0.107	Detected	0.000	-1.952	Comprom	-3.086	Comprom	-2.519	0.049	GT Sens	contig117	contig117	Genomic
GT Sens	Sense	-0.958	Detected	0.958	Detected	0.000	-3.851	Detected	-2.644	Detected	-3.247	0.103	GT Sens	contig117	contig117	Predicted
GT Sens	Sense	-0.684	Detected	0.684	Detected	0.000	-2.837	Detected	-0.953	Detected	-1.895	0.245	GT Sens	contig118	contig118	Beta-fruc
GT Sens	Sense	0.042	Detected	-0.042	Detected	0.000	-1.816	Detected	-2.355	Comprom	-2.085	0.017	GT Sens	contig118	contig118	Unknown
GT Sens	Sense	0.479	Detected	-0.479	Detected	0.000	-1.487	Detected	-1.635	Detected	-1.561	0.084	GT Sens	contig118	contig118	Unknown
GT Sens	Sense	0.050	Detected	-0.050	Detected	0.000	-1.347	Detected	-1.708	Detected	-1.528	0.015	GT Sens	contig118	contig118	Unknown
GT Sens	Sense	-0.413	Detected	0.413	Detected	0.000	-2.119	Detected	-1.601	Detected	-1.860	0.062	GT Sens	contig118	contig118	Major late
GT Sens	Sense	-0.577	Detected	0.577	Detected	0.000	-1.234	Detected	-0.849	Detected	-1.042	0.229	GT Sens	contig118	contig118	Unknown
GT Sens	Sense	-0.028	Detected	0.028	Detected	0.000	-1.782	Comprom	-1.100	Comprom	-1.441	0.052	GT Sens	contig118	contig118	NBS-codi
GT Sens	Sense	0.072	Detected	-0.072	Detected	0.000	-1.051	Comprom	-2.018	Comprom	-1.535	0.088	GT Sens	contig118	contig118	Protein B
GT Sens	Sense	-0.199	Detected	0.199	Detected	0.000	-1.505	Detected	-1.155	Detected	-1.330	0.038	GT Sens	contig118	contig118	Unknown
GT Sens	Sense	-0.054	Detected	0.054	Detected	0.000	-2.081	Detected	-1.973	Detected	-2.027	0.001	GT Sens	contig118	contig118	Integrase
GT Sens	Sense	0.216	Detected	-0.216	Detected	0.000	-0.911	Detected	-1.484	Detected	-1.198	0.079	GT Sens	contig118	contig118	Unknown
GT Sens	Sense	-0.088	Detected	0.088	Detected	0.000	-0.938	Detected	-1.237	Detected	-1.087	0.025	GT Sens	contig118	contig118	Unknown
GT Sens	Sense	0.002	Detected	-0.002	Detected	0.000	-1.555	Comprom	-2.379	Comprom	-1.967	0.041	GT Sens	contig119	contig119	Unknown
GT Sens	Sense	-0.172	Detected	0.172	Detected	0.000	-1.072	Comprom	-2.184	Comprom	-1.628	0.108	GT Sens	contig119	contig119	Genomic
GT Sens	Sense	-0.333	Detected	0.333	Detected	0.000	-1.088	Comprom	-2.299	Comprom	-1.694	0.134	GT Sens	contig119	contig119	Glycosylt
GT Sens	Sense	0.181	Detected	-0.181	Detected	0.000	-1.343	Detected	-1.336	Detected	-1.339	0.018	GT Sens	contig119	contig119	Unknown
GT Sens	Sense	0.201	Detected	-0.201	Detected	0.000	-2.160	Comprom	-2.879	Comprom	-2.520	0.026	GT Sens	contig119	contig119	Mutator-li
GT Sens	Sense	-0.044	Detected	0.044	Detected	0.000	-1.095	Detected	-1.314	Detected	-1.204	0.010	GT Sens	contig119	contig119	Unknown
GT Sens	Sense	-0.629	Detected	0.629	Detected	0.000	-1.845	Detected	-1.738	Detected	-1.791	0.105	GT Sens	contig120	contig120	Glyoxalas
GT Sens	Sense	0.238	Detected	-0.238	Detected	0.000	-0.915	Detected	-1.415	Detected	-1.165	0.078	GT Sens	contig120	contig120	Blue copp
GT Sens	Sense	0.011	Detected	-0.011	Detected	0.000	-2.182	Detected	-2.286	Detected	-2.234	0.001	GT Sens	contig120	contig120	Unknown
GT Sens	Sense	0.010	Detected	-0.010	Detected	0.000	-1.693	Detected	-1.250	Detected	-1.471	0.022	GT Sens	contig121	contig121	WRKY tra
GT Sens	Sense	0.151	Detected	-0.151	Detected	0.000	-1.375	Detected	-0.959	Detected	-1.167	0.045	GT Sens	contig121	contig121	Calmodul
GT Sens	Sense	-0.197	Detected	0.197	Detected	0.000	-2.217	Detected	-1.215	Detected	-1.716	0.086	GT Sens	contig121	contig121	PHD finge
GT Sens	Sense	-0.214	Detected	0.214	Detected	0.000	-0.964	Detected	-1.619	Detected	-1.292	0.081	GT Sens	contig121	contig121	50S ribos
GT Sens	Sense	0.153	Detected	-0.153	Detected	0.000	-2.176	Detected	-1.367	Detected	-1.771	0.055	GT Sens	contig121	contig121	RNA-bind
GT Sens	Sense	-0.410	Detected	0.410	Detected	0.000	-1.133	Detected	-1.156	Detected	-1.145	0.108	GT Sens	contig121	contig121	Rac-like
GT Sens	Sense	-0.092	Detected	0.092	Detected	0.000	-1.799	Detected	-1.863	Detected	-1.831	0.003	GT Sens	contig121	contig121	Transpos
GT Sens	Sense	0.088	Detected	-0.088	Detected	0.000	-2.730	Detected	-2.179	Detected	-2.454	0.014	GT Sens	contig121	contig121	Unknown
GT Sens	Sense	0.034	Detected	-0.034	Detected	0.000	-0.878	Detected	-1.326	Comprom	-1.102	0.040	GT Sens	contig122	contig122	Unknown
GT Sens	Sense	0.144	Detected	-0.144	Detected	0.000	-1.835	Detected	-1.977	Detected	-1.906	0.007	GT Sens	contig122	contig122	F-box fan
GT Sens	Sense	0.177	Detected	-0.177	Detected	0.000	-1.870	Detected	-1.848	Detected	-1.859	0.009	GT Sens	contig122	contig122	BTB/POZ
GT Sens	Sense	-0.619	Detected	0.619	Detected	0.000	-3.718	Detected	-1.053	Detected	-2.385	0.246	GT Sens	contig123	contig123	Alcohol d
GT Sens	Sense	0.372	Detected	-0.372	Detected	0.000	-1.266	Detected	-0.867	Detected	-1.066	0.127	GT Sens	contig123	contig123	Unknown
GT Sens	Sense	-0.219	Detected	0.219	Detected	0.000	-4.387	Detected	-1.377	Detected	-2.882	0.199	GT Sens	contig123	contig123	ABC tran
GT Sens	Sense	-0.108	Detected	0.108	Detected	0.000	-1.987	Detected	-1.070	Detected	-1.529	0.083	GT Sens	contig123	contig123	Pathogen
GT Sens	Sense	-0.339	Detected	0.339	Detected	0.000	-1.080	Detected	-1.678	Detected	-1.379	0.093	GT Sens	contig124	contig124	Legumin
GT Sens	Sense	-0.173	Detected	0.173	Detected	0.000	-1.671	Detected	-0.888	Detected	-1.279	0.096	GT Sens	contig124	contig124	Glycosyl
GT Sens	Sense	0.258	Detected	-0.258	Detected	0.000	-4.880	Detected	-2.683	Detected	-3.782	0.079	GT Sens	contig124	contig124	1-aminoc
GT Sens	Sense	-0.023	Detected	0.023	Detected	0.000	-1.978	Comprom	-2.267	Comprom	-2.123	0.005	GT Sens	contig124	contig124	Transpos
GT Sens	Sense	-0.056	Detected	0.056	Detected	0.000	-2.060	Comprom	-1.836	Comprom	-1.948	0.004	GT Sens	contig125	contig125	Macrolide
GT Sens	Sense	0.097	Detected	-0.097	Detected	0.000	-3.258	Detected	-3.572	Detected	-3.415	0.003	GT Sens	contig125	contig125	MKIAA09
GT Sens	Sense	-0.655	Detected	0.655	Detected	0.000	-4.348	Detected	-1.554	Detected	-2.951	0.196	GT Sens	contig125	contig125	Lipoxyge
GT Sens	Sense	-0.046	Detected	0.046	Detected	0.000	-1.099	Detected	-0.953	Detected	-1.026	0.007	GT Sens	contig125	contig125	Reverse t
GT Sens	Sense	-0.100	Detected	0.100	Detected	0.000	-1.622	Detected	-0.895	Detected	-1.258	0.079	GT Sens	contig126	contig126	Ankyrin r
GT Sens	Sense	-0.175	Detected	0.175	Detected	0.000	-2.294	Detected	-2.184	Detected	-2.239	0.007	GT Sens	contig126	contig126	Retroviru
GT Sens	Sense	-0.303	Detected	0.303	Detected	0.000	-1.436	Detected	-1.191	Detected	-1.313	0.057	GT Sens	contig127	contig127	Acyltrans
GT Sens	Sense	0.310	Detected	-0.310	Detected	0.000	-1.420	Detected	-1.182	Detected	-1.301	0.060	GT Sens	contig127	contig127	Os07g065
GT Sens	Sense	0.165	Detected	-0.165	Detected	0.000	-2.012	Detected	-1.224	Detected	-1.618	0.063	GT Sens	contig127	contig127	L-lactate
GT Sens	Sense	0.055	Detected	-0.055	Detected	0.000	-1.882	Comprom	-1.366	Comprom	-1.624	0.025	GT Sens	contig128	contig128	Endochiti
GT Sens	Sense	-0.850	Detected	0.850	Detected	0.000	-5.804	Comprom	-2.437	Detected	-4.120	0.161	GT Sens	contig128	contig128	Peroxida
GT Sens	Sense	0.202	Detected	-0.202	Detected	0.000	-1.543	Detected	-1.503	Detected	-1.523	0.017	GT Sens	contig129	contig129	Ulp1 prot
GT Sens	Sense	0.298	Detected	-0.298	Detected	0.000	-1.095	Detected	-1.196	Detected	-1.146	0.063	GT Sens	contig129	contig129	Harpin-in
GT Sens	Sense	-0.102	Detected	0.102	Detected	0.000	-1.139	Detected	-1.191	Detected	-1.165	0.008	GT Sens	contig129	contig129	Linalool s
GT Sens	Sense	-0.129	Detected	0.129	Detected	0.000	-1.727	Detected	-1.077	Detected	-1.402	0.057	GT Sens	contig129	contig129	Pyrimidin
GT Sens	Sense	-0.209	Detected	0.209	Detected	0.000	-2.308	Comprom	-1.308	Comprom	-1.808	0.079	GT Sens	contig129	contig129	Gag non-
GT Sens	Sense	0.140	Detected	-0.140	Detected	0.000	-1.771	Comprom	-1.631	Comprom	-1.701	0.008	GT Sens	contig130	contig130	Cathepsi
GT Sens	Sense	-0.553	Detected	0.553	Detected	0.000	-1.370	Detected	-0.841	Detected	-1.105	0.213	GT Sens	contig131	contig131	Unknown
GT Sens	Sense	-0.480	Detected	0.480	Detected	0.000	-3.235	Detected	-2.573	Detected	-2.904	0.038	GT Sens	contig131	contig131	Unknown
GT Sens	Sense	0.394	Detected	-0.394	Detected	0.000	-0.969	Detected	-1.033	Detected	-1.001	0.127	GT Sens	contig131	contig131	GDU1 (Al
GT Sens	Sense	-0.144	Detected	0.144	Detected	0.000	-1.454	Detected	-0.910	Detected	-1.182	0.062	GT Sens	contig133	contig133	Unknown
GT Sens	Sense	-0.141	Detected	0.141	Detected	0.000	-2.667	Detected	-1.268	Detected	-1.968	0.110	GT Sens	contig133	contig133	Heavy me
GT Sens	Sense	-0.422	Detected	0.422	Detected	0.000	-2.185	Detected	-1.253	Detected	-1.719	0.112	GT Sens	contig133	contig133	Major late
GT Sens	Sense	-0.393	Detected	0.393	Detected	0.000	-1.325	Detected	-1.367	Detected	-1.346	0.076	GT Sens	contig134	contig134	At4g4008
GT Sens	Sense	-0.170	Detected	0.170	Detected	0.000	-1.356	Detected	-2.087	Detected	-1.721	0.051	GT Sens	contig134	contig134	Zinc finge
GT Sens	Sense	0.010	Detected	-0.010	Detected	0.000	-2.503	Detected	-0.867	Detected	-1.685	0.176	GT Sens	contig135	contig135	Zinc-finge
GT Sens	Sense	-0.158	Detected	0.158	Detected	0.000	-2.356	Comprom	-1.707	Comprom	-2.032	0.030	GT Sens	contig135	contig135	Ring H2 fi
GT Sens	Sense	-0.650	Detected	0.650	Detected	0.000	-3.269	Detected	-2.067	Detected	-2.668	0.095	GT Sens	contig135	contig135	Unknown
GT Sens	Sense	-0.920	Detected	0.920	Detected	0.000	-1.856	Detected	-1.625	Detected	-1.741	0.201	GT Sens	contig135	contig135	Phospho
GT Sens	Sense	-0.581	Detected	0.581	Detected	0.000	-2.475	Detected	-1.996	Detected	-2.235	0.071	GT Sens	contig136	contig136	UPF0497
GT Sens	Sense	-0.440	Detected	0.440	Detected	0.000	-2.265	Detected	-0.883	Detected	-1.574	0.195	GT Sens	contig136	contig136	Alternativ
GT Sens	Sense	-0.313	Detected	0.313	Detected	0.000	-2.195	Detected	-1.092	Detected	-1.644	0.122	GT Sens	contig136	contig136	BZIP tran
GT Sens	Sense	0.159	Detected	-0.159	Detected	0.000	-1.223	Detected	-1.148	Detected	-1.185	0.019	GT Sens	contig137	contig137	Unknown
GT Sens	Sense	0.092	Detected	-0.092	Detected	0.000	-1.676	Detected	-0.993	Detected	-1.334	0.064	GT Sens	contig137	contig137	Respirato
GT Sens	Sense	-0.143	Detected	0.143	Detected	0.000	-1.669	Detected	-1.778	Detected	-1.723	0.008	GT Sens	contig137	contig137	Pol polyp
GT Sens	Sense	0.042	Detected	-0.042	Detected	0.000	-1.863	Detected	-1.142	Detected	-1.502	0.054	GT Sens	contig138	contig138	AT5G281
GT Sens	Sense	0.023	Detected	-0.023	Detected	0.000	-1.240	Detected	-1.833	Detected	-1.536	0.035	GT Sens	contig138	contig138	Nodulin N
GT Sens	Sense	-0.524	Detected	0.524	Detected	0.000	-2.112	Detected	-1.495	Detected	-1.803	0.097	GT Sens	contig138	contig138	HR7 prote
GT Sens	Sense	-0.176	Detected	0.176	Detected	0.000	-2.593	Detected	-2.852	Detected	-2.723	0.006	GT Sens	contig139	contig139	Retrotran
GT Sens	Sense	-0.058	Detected	0.058	Detected	0.000	-1.387	Detected	-1.518	Detected	-1.452	0.004	GT Sens	contig139	contig139	Unknown
GT Sens	Sense	-0.233	Detected	0.233	Detected	0.000	-1.194	Detected	-1.203	Detected	-1.199	0.036	GT Sens	contig139	contig139	Unknown
GT Sens	Sense	-0.099	Detected	0.099	Detected	0.000	-1.422	Detected	-0.841	Detected	-1.132	0.066	GT Sens	contig139	contig139	Syringoli
GT Sens	Sense	-0.309	Detected	0.309	Detected	0.000	-1.870	Detected	-1.116	Detected	-1.493	0.092	GT Sens	contig140	contig140	1-aminoc
GT Sens	Sense	-0.124	Detected	0.124	Detected	0.000	-0.867	Detected	-1.340	Detected	-1.103	0.054	GT Sens	contig140	contig140	Unknown
GT Sens	Sense	-0.624	Detected	0.624	Detected	0.000	-3.190	Comprom	-2.941	Comprom	-3.065	0.040	GT Sens	contig141	contig141	Germin-li
GT Sens	Sense	-0.206	Detected	0.206	Detected	0.000	-1.652	Detected	-1.660	Detected	-1.656	0.015	GT Sens	contig141	contig141	Unknown
GT Sens	Sense	0.110	Detected	-0.110	Detected	0.000	-2.440	Detected	-1.704	Detected	-2.072	0.033	GT Sens	contig141	contig141	F-box fan
GT Sens	Sense	-0.452	Detected	0.452	Detected	0.000	-3.824	Detected	-1.998	Detected	-2.911	0.104	GT Sens	contig141	contig141	RPW8.2 (A
GT Sens	Sense	-0.169	Detected	0.169	Detected	0.000	-1.724	Detected	-1.675	Detected	-1.699	0.010	GT Sens	contig141	contig141	Transpos
GT Sens	Sense	-0.182	Detected	0.182	Detected	0.000	-1.495	Detected	-0.912	Detected	-1.204	0.073	GT Sens	contig142	contig142	Unknown
GT Sens	Sense	-0.013	Detected	0.013	Detected	0.000	-1.385	Detected	-1.132	Detected	-1.258	0.010	GT Sens	contig142	contig142	Glycosylt
GT Sens	Sense	-0.500	Detected	0.500	Detected	0.000	-4.818	Comprom	-2.035	Detected	-3.426	0.146	GT Sens	contig143	contig143	U-box do
GT Sens	Sense	-0.190	Detected	0.190	Detected	0.000	-1.687	Detected	-1.693	Detected	-1.690	0.012	GT Sens	contig143	contig143	Unknown
GT Sens	Sense	-0.275	Detected	0.275	Detected	0.000	-2.436	Comprom	-1.826	Comprom	-2.131	0.035	GT Sens	contig143	contig143	Ulp1 prot
GT Sens	Sense	-0.177	Detected	0.177	Detected	0.000	-2.365	Detected	-1.423	Detected	-1.894	0.064	GT Sens	contig144	contig144	Alpha-hu
GT Sens	Sense	-0.405	Detected	0.405	Detected	0.000	-2.523	Detected	-1.950	Detected	-2.237	0.046	GT Sens	contig144	contig144	Cytochro
GT Sens	Sense	0.378	Detected	-0.378	Detected	0.000	-4.180	Comprom	-1.558	Detected	-2.869	0.170	GT Sens	contig145	contig145	Acyltrans
GT Sens	Sense	-0.515	Detected	0.515	Detected	0.000	-1.472	Detected	-0.890	Detected	-1.181	0.184	GT Sens	contig145	contig145	Calmodul
GT Sens	Sense	-1.062	Detected	1.062	Detected	0.000	-2.539	Comprom	-0.889	Detected	-1.714	0.331	GT Sens	contig145	contig145	Monoglyc
GT Sens	Sense	-0.386	Detected	0.386	Detected	0.000	-1.644	Comprom	-2.206	Comprom	-1.925	0.056	GT Sens	contig146	contig146	Receptor
GT Sens	Sense	0.167	Detected	-0.167	Detected	0.000	-2.135	Detected	-2.794	Comprom	-2.465	0.022	GT Sens	contig146	contig146	Unknown
GT Sens	Sense	0.051	Detected	-0.051	Detected	0.000	-1.433	Detected	-0.811	Detected	-1.122	0.070	GT Sens	contig147	contig147	Protein-m
GT Sens	Sense	-0.276	Detected	0.276	Detected	0.000	-1.542	Detected	-1.269	Detected	-1.405	0.045	GT Sens	contig147	contig147	NADH flav
GT Sens	Sense	-0.656	Detected	0.656	Detected	0.000	-5.407	Detected	-2.715	Detected	-4.061	0.113	GT Sens	contig147	contig147	Lipoxyge
GT Sens	Sense	-0.615	Detected	0.615	Detected	0.000	-1.814	Detected	-1.543	Detected	-1.679	0.117	GT Sens	contig147	contig147	Peptide tr
GT Sens	Sense	0.810	Detected	-0.810	Detected	0.000	-1.921	Comprom	-2.308	Comprom	-2.114	0.126	GT Sens	contig147	contig147	Exostosi
GT Sens	Sense	-0.505	Detected	0.505	Detected	0.000	-2.965	Comprom	-1.591	Detected	-2.278	0.116	GT Sens	contig148	contig148	Matrix me
GT Sens	Sense	-0.075	Detected	0.075	Detected	0.000	-1.339	Detected	-1.001	Detected	-1.170	0.024	GT Sens	contig149	contig149	Serine ca
GT Sens	Sense	0.320	Detected	-0.320	Detected	0.000	-1.760	Detected	-1.082	Detected	-1.421	0.093	GT Sens	contig149	contig149	Unknown
GT Sens	Sense	-0.121	Detected	0.121	Detected	0.000	-0.917	Detected	-1.325	Detected	-1.121	0.042	GT Sens	contig149	contig149	30S ribos
GT Sens	Sense	0.083	Detected	-0.083	Detected	0.000	-1.183	Detected	-0.820	Detected	-1.002	0.037	GT Sens	contig149	contig149	Mitogen-a
GT Sens	Sense	-0.537	Detected	0.537	Detected	0.000	-2.330	Detected	-0.858	Detected	-1.594	0.222	GT Sens	contig150	contig150	S-locus-s
GT Sens	Sense	0.366	Detected	-0.366	Detected	0.000	-1.253	Detected	-1.374	Detected	-1.313	0.071	GT Sens	contig150	contig150	Pre-mRN
GT Sens	Sense	-0.217	Detected	0.217	Detected	0.000	-2.616	Detected	-2.002	Detected	-2.309	0.026	GT Sens	contig150	contig150	Cys2/His
GT Sens	Sense	-0.222	Detected	0.222	Detected	0.000	-1.237	Detected	-0.840	Detected	-1.039	0.073	GT Sens	contig150	contig150	Reticulon
GT Sens	Sense	-0.076	Detected	0.076	Detected	0.000	-1.294	Detected	-1.439	Detected	-1.366	0.006	GT Sens	contig151	contig151	Unknown
GT Sens	Sense	0.034	Detected	-0.034	Detected	0.000	-1.872	Detected	-0.810	Detected	-1.341	0.128	GT Sens	contig151	contig151	cDNA clo
GT Sens	Sense	0.277	Detected	-0.277	Detected	0.000	-1.234	Detected	-1.451	Detected	-1.343	0.046	GT Sens	contig151	contig151	Unknown
GT Sens	Sense	-0.217	Detected	0.217	Detected	0.000	-1.461	Detected	-1.486	Detected	-1.474	0.021	GT Sens	contig151	contig151	Unknown
GT Sens	Sense	0.064	Detected	-0.064	Detected	0.000	-1.540	Comprom	-1.275	Comprom	-1.408	0.011	GT Sens	contig152	contig152	Unknown
GT Sens	Sense	-0.294	Detected	0.294	Detected	0.000	-2.875	Comprom	-1.690	Comprom	-2.282	0.075	GT Sens	contig153	contig153	Alpha-hu
GT Sens	Sense	-0.136	Detected	0.136	Detected	0.000	-1.154	Detected	-1.088	Detected	-1.121	0.015	GT Sens	contig153	contig153	Shikimate
GT Sens	Sense	-0.656	Detected	0.656	Detected	0.000	-3.124	Detected	-0.906	Detected	-2.015	0.258	GT Sens	contig153	contig153	Cytochro
GT Sens	Sense	-0.640	Detected	0.640	Detected	0.000	-1.375	Detected	-1.960	Comprom	-1.668	0.141	GT Sens	contig154	contig154	Rapid alk
GT Sens	Sense	0.099	Detected	-0.099	Detected	0.000	-1.589	Detected	-1.530	Detected	-1.560	0.004	GT Sens	contig154	contig154	Myb-relat
GT Sens	Sense	1.781	Detected	-1.781	Detected	0.000	-1.870	Detected	-1.577	Detected	-1.723	0.437	GT Sens	contig155	contig155	Hedgeho
GT Sens	Sense	-1.107	Detected	1.107	Detected	0.000	-3.150	Detected	-1.624	Detected	-2.387	0.218	GT Sens	contig155	contig155	EF hand
GT Sens	Sense	0.009	Detected	-0.009	Detected	0.000	-1.424	Detected	-1.777	Detected	-1.601	0.012	GT Sens	contig156	contig156	Lysine/his
GT Sens	Sense	0.128	Detected	-0.128	Detected	0.000	-3.506	Detected	-5.422	Detected	-4.464	0.044	GT Sens	contig156	contig156	Receptor-
GT Sens	Sense	-0.157	Detected	0.157	Detected	0.000	-1.231	Detected	-1.165	Detected	-1.198	0.018	GT Sens	contig156	contig156	DNA-depe
GT Sens	Sense	0.006	Detected	-0.006	Detected	0.000	-1.531	Detected	-1.374	Detected	-1.453	0.003	GT Sens	contig157	contig157	ATP synt
GT Sens	Sense	-0.159	Detected	0.159	Detected	0.000	-2.148	Detected	-2.321	Detected	-2.235	0.007	GT Sens	contig157	contig157	Transpos
GT Sens	Sense	-0.019	Detected	0.019	Detected	0.000	-1.421	Comprom	-2.610	Comprom	-2.016	0.077	GT Sens	contig157	contig157	Multidrug
GT Sens	Sense	0.072	Detected	-0.072	Detected	0.000	-0.835	Detected	-1.547	Detected	-1.191	0.082	GT Sens	contig157	contig157	Unknown
GT Sens	Sense	-0.339	Detected	0.339	Detected	0.000	-1.811	Detected	-1.026	Detected	-1.418	0.112	GT Sens	contig158	contig158	Yippee-lik
GT Sens	Sense	-0.230	Detected	0.230	Detected	0.000	-1.553	Comprom	-2.006	Comprom	-1.780	0.031	GT Sens	contig159	contig159	Mutator-li
GT Sens	Sense	-0.153	Detected	0.153	Detected	0.000	-1.091	Detected	-1.182	Detected	-1.136	0.019	GT Sens	contig159	contig159	Unknown
GT Sens	Sense	-0.381	Detected	0.381	Detected	0.000	-1.130	Detected	-1.403	Detected	-1.267	0.089	GT Sens	contig159	contig159	Unknown
GT Sens	Sense	-0.003	Detected	0.003	Detected	0.000	-2.205	Comprom	-1.173	Comprom	-1.689	0.082	GT Sens	contig159	contig159	Unknown
GT Sens	Sense	-0.497	Detected	0.497	Detected	0.000	-1.320	Detected	-0.995	Detected	-1.157	0.157	GT Sens	contig159	contig159	Thaumati
GT Sens	Sense	-0.204	Detected	0.204	Detected	0.000	-1.674	Detected	-0.952	Detected	-1.313	0.087	GT Sens	contig159	contig159	Unknown
GT Sens	Sense	0.085	Detected	-0.085	Detected	0.000	-1.057	Detected	-0.954	Detected	-1.006	0.010	GT Sens	contig161	contig161	Unknown

GT	Sense	Sense	-0.609	Detected	0.609	Detected	0.000	-2.257	Comprom	-2.495	Comprom	-2.376	0.062	GT	Sens	contig161	contig161	Hydroxyc	CCTCAG	contig161	Solyc08g	Solyc08g	Hydroxyc	GO:0016	GO:0016	contig161	Solyc08g	Hydroxyc	GO:0016	SL2.40ch	AT5G63560.1		transfera	chr5:254	10.4135	18.9294	7.87854	6.58699	3.10515	2.54079
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-1.636	Detected	-0.880	Detected	-1.258	0.080	GT	Sens	contig162	contig162	Plant-spe	CGTCGG	contig162	Solyc09g	Solyc09g	Plant-specific domain TIGR01			contig162	Solyc09g	Plant-specific doma		SL2.40ch	AT2G45590.1		protein k	chr2:187	78.8106	64.4323	51.1901	18.0897	24.2286	39.5043
GT	Sense	Sense	-0.249	Detected	0.249	Detected	0.000	-2.035	Comprom	-1.398	Comprom	-1.716	0.051	GT	Sens	contig162	contig162	LINE-type	TTAAAGT	contig162	Solyc06g	Solyc06g	LINE-type retrotransposon LIb			contig162	Solyc00g095460.1.1				AT5G519	CBF4. DR	CBF4 (C-	chr5:211	13.6827	15.1019	4.1297	13.6431	3.70818	5.56589
GT	Sense	Sense	-0.228	Detected	0.228	Detected	0.000	-1.274	Detected	-1.401	Detected	-1.337	0.030	GT	Sens	contig163	contig163	Actin rela	CCGTTC	contig163	Solyc09g	Solyc09g	Actin rela	GO:0005	GO:0005	contig163	Solyc09g	Actin rela	GO:0005	SL2.40ch	AT2G333	arpc2b	arpc2b (a	chr2:141	44.4177	47.6261	27.584	34.8514	20.0976	17.7746
GT	Sense	Sense	0.353	Detected	-0.353	Detected	0.000	-2.321	Detected	-1.624	Detected	-1.973	0.058	GT	Sens	contig163	contig163	Cysteine	AATACTT	contig163	Solyc11g	Solyc11g	Cysteine	GO:0008	GO:0008	contig163	Solyc11g	Cysteine	GO:0008	SL2.40ch	AT5G631	HDA6. AX	HDA6 (HI	chr5:253	365.041	174.86	56.3972	20.3656	53.4196	83.611
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	-1.377	Detected	-0.873	Detected	-1.125	0.100	GT	Sens	contig163	contig163	Unknown	CCATGG	contig163	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig163	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G35210.2		peptidas	chr5:134	80.3104	41.9179	49.0073	41.2949	23.6165	32.3188
GT	Sense	Sense	-0.273	Detected	0.273	Detected	0.000	-1.982	Detected	-1.104	Detected	-1.543	0.096	GT	Sens	contig163	contig163	Unknown	ACGGCA	contig163	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig163	Solyc08g	Unknown Protein (A		SL2.40ch	AT2G39170.1		unknown	chr2:163	236.064	269.3	188.277	96.0272	67.4476	119.676
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	-1.610	Detected	-1.139	Detected	-1.375	0.033	GT	Sens	contig164	contig164	MYB tran	AACAAC	contig164	Solyc08g	Solyc08g	MYB tran	GO:0045449		contig164	Solyc08g	MYB tran	GO:0003	SL2.40ch	AT1G662	MYB20. A	MYB20 (r	chr1:246	62.7907	56.7146	31.2428	41.4844	20.6637	27.64
GT	Sense	Sense	-0.389	Detected	0.389	Detected	0.000	-3.165	Detected	-2.711	Detected	-2.938	0.023	GT	Sens	contig164	contig164	WRKY tra	GATGAC	contig164	Solyc04g	Solyc04g	WRKY tra	GO:0045449		contig164	Solyc04g	WRKY tra	GO:0045	SL2.40ch	AT2G033	WRKY3	WRKY3:	chr2:101	65.3883	87.6039	24.2247	17.7078	8.91572	11.7945
GT	Sense	Sense	-0.193	Detected	0.193	Detected	0.000	-1.919	Detected	-1.924	Detected	-1.921	0.010	GT	Sens	contig164	contig164	Unknown	TTATTA	contig164	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig164	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G271	TTN7. SM	TTN7 (TI	chr2:116	4934.85	5038.93	1956.88	2327.8	1393.97	1341.03
GT	Sense	Sense	-0.473	Detected	0.473	Detected	0.000	-2.058	Detected	-1.109	Detected	-1.584	0.142	GT	Sens	contig165	contig165	Ethylene-	GCAGCT	contig165	Solyc07g	Solyc07g	Ethylene-	GO:0016	GO:0016	contig165	Solyc07g	Ethylene-	GO:0016	SL2.40ch	AT3G502	CEJ1. AT	CEJ1 (CO	chr3:186	456.725	687.299	272.705	200.604	142.227	264.947
GT	Sense	Sense	0.148	Detected	-0.148	Detected	0.000	-3.918	Detected	-3.292	Detected	-3.605	0.009	GT	Sens	contig165	contig165	Unknown	ACTGGA	contig165	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig165	Solyc12g	Aldehyde	GO:0005	SL2.40ch	AT1G29830.3		unknown	chr1:104	600.532	382.476	176.336	103.514	33.5143	49.9265
GT	Sense	Sense	-0.126	Detected	0.126	Detected	0.000	-1.397	Detected	-0.819	Detected	-1.108	0.072	GT	Sens	contig165	contig165	Major late	GGAAAA	contig165	Solyc04g	Solyc04g	Major late	GO:0009	GO:0009	contig165	Solyc04g	Major late	GO:0009	SL2.40ch	AT1G03080.1		FUNCTIO	chr1:731	1241.53	1155.51	957.365	1903.49	480.752	692.735
GT	Sense	Sense	-0.748	Detected	0.748	Detected	0.000	-1.621	Detected	-0.897	Detected	-1.259	0.269	GT	Sens	contig166	contig166	Glutared	GTAATA	contig166	Solyc02g	Solyc02g	Glutared	GO:0045	GO:0045	contig166	Solyc02g	Glutared	GO:0008	SL2.40ch	AT3G243	AMT1:3.	AMT1:3 (	chr3:880	22.0353	48.6111	25.5375	23.3533	11.2436	17.9282
GT	Sense	Sense	-0.063	Detected	0.063	Detected	0.000	-2.369	Detected	-2.092	Detected	-2.231	0.005	GT	Sens	contig166	contig166	Mutator-li	GTTGTC	contig166	Solyc05g	Solyc05g	Mutator-li	GO:0008	GO:0008	contig166	Solyc12g	Mutator-li	GO:0008	SL2.40ch	AT5G57340.1		unknown	chr5:232	59.4668	50.7122	19.8757	27.2321	11.2319	13.1436
GT	Sense	Sense	-0.294	Detected	0.294	Detected	0.000	-1.415	Detected	-0.873	Detected	-1.144	0.104	GT	Sens	contig167	contig167	Auxin res	TCATGT	contig167	Solyc06g	Solyc06g	Auxin responsive SAUR protei			contig167	Solyc06g	Auxin responsive S		SL2.40ch	AT5G50760.1		auxin-res	chr5:206	3233.32	3800.97	2487	1733.61	1389.1	1953.29
GT	Sense	Sense	0.260	Detected	-0.260	Detected	0.000	-1.509	Detected	-1.632	Detected	-1.571	0.028	GT	Sens	contig167	contig167	30S ribos	TCGCGG	contig167	Solyc12g	Solyc12g	30S ribos	GO:0005	GO:0005	contig167	Solyc12g035880.1.1				AT2G48160.1		EXPRESS	chr2:196	1347.83	734.363	887.041	693.906	369.307	327.481
GT	Sense	Sense	0.549	Detected	-0.549	Detected	0.000	-1.264	Detected	-1.761	Detected	-1.513	0.129	GT	Sens	contig168	contig168	Lipase-lik	GAGGCT	contig168	Solyc06g	Solyc06g	Lipase-lik	GO:0006	GO:0006	contig168	Solyc06g	Lipase-lik	GO:0006	SL2.40ch	AT4G16820.1		lipase cla	chr4:946	271.321	99.0596	39.9759	62.9222	72.1519	49.3447
GT	Sense	Sense	-0.221	Detected	0.221	Detected	0.000	-2.201	Comprom	-0.814	Comprom	-1.508	0.174	GT	Sens	contig168	contig168	Hydrolase	TTATCAT	contig168	Solyc06g	Solyc06g	Hydrolase alpha/beta fold fami			contig168	Solyc06g	Hydrolase	GO:0016	SL2.40ch	AT5G24740.1		INVOLVE	chr5:847	11.3536	12.0501	3.24795	3.05335	2.68815	6.78839
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	-1.312	Detected	-1.542	Detected	-1.427	0.069	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	50.8002	66.9998	38.3303	63.3709	24.8417	20.4387
GT	Sense	Sense	0.233	Detected	-0.233	Detected	0.000	-2.197	Detected	-1.998	Detected	-2.097	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	2046.35	1158.63	1321.49	861.735	355.031	393.203
GT	Sense	Sense	-0.820	Detected	0.820	Detected	0.000	-3.129	Comprom	-1.525	Comprom	-2.327	0.180	GT	Sens	contig170	contig170	Unknown	TTTTGCA	contig170	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)%:			contig170	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G62280.1		unknown	chr5:250	11.2856	27.4886	13.5064	8.15582	2.12712	6.2455
GT	Sense	Sense	-0.038	Detected	0.038	Detected	0.000	-1.666	Detected	-0.819	Detected	-1.242	0.100	GT	Sens	contig172	contig172	Plant-spe	AGGATA	contig172	Solyc06g	Solyc06g	Plant-specific domain TIGR01			contig172	Solyc06g	Plant-specific doma		SL2.40ch	AT4G36230.1		unknown	chr4:171	360.302	296.945	160.05	121.782	108.944	189.22
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-1.802	Detected	-1.294	Detected	-1.548	0.030	GT	Sens	contig172	contig172	Ethylene-	ATTTGAT	contig172	Solyc08g	Solyc08g	Ethylene-	GO:0016	GO:0016	contig172	Solyc08g	Ethylene-	GO:0016	SL2.40ch	AT5G52020.1		AP2 dom	chr5:211	200.593	181.798	141.541	74.5662	57.8916	79.4382

GT	Sens	Sense	-0.309	Detected	0.309	Detected	0.000	-2.068	Detected	-1.660	Detected	-1.864	0.037	GT	Sens	contig241	contig241	Stearoyl-	GTGCAC	contig241	Solyc06g	Solyc06g	Stearoyl-	GO:00047	GO:00047	contig241	Solyc06g	Stearoyl-	GO:00047	SL2.40ch	AT1G43800.1		acyl-(acy	chr1:165	1578.2	1892.94	962.645	2628.23	435.55	557.943
GT	Sens	Sense	-0.081	Detected	0.081	Detected	0.000	-1.621	Detected	-1.692	Detected	-1.657	0.003	GT	Sens	contig241	contig241	cDNA clo	TCTGAT	contig241	Solyc10g	Solyc10g	cDNA clone J013057C16 full in			contig241	Solyc10g	cDNA clone J01305		SL2.40ch	AT3G20730.1		pentatric	chr3:724	3987.74	3489.69	4707.62	4159.48	1281.63	1178.07
GT	Sens	Sense	-0.058	Detected	0.058	Detected	0.000	-1.178	Detected	-1.139	Detected	-1.159	0.003	GT	Sens	contig242	contig242	Receptor	AGTCCA	contig242	Solyc03g	Solyc03g	Receptor	GO:0005529		contig242	Solyc03g	Receptor	GO:00055	SL2.40ch	AT5G609	RLK1	RLK1 (RE	chr5:244	5851.7	4956.45	3575.66	2494.78	2515.79	2494.42
GT	Sens	Sense	-0.205	Detected	0.205	Detected	0.000	-2.960	Comprom	-1.110	Detected	-2.035	0.165	GT	Sens	contig242	contig242	Fatty acid	GGTGTC	contig242	Solyc12g	Solyc12g	Fatty acid	GO:00055	GO:00055	contig242	Solyc12g	Fatty acid	GO:00055	SL2.40ch	AT3G121	FAD2	FAD2 (FA	chr3:386	21.645	22.4854	5.20491	1.87935	2.99645	10.429
GT	Sens	Sense	-0.499	Detected	0.499	Detected	0.000	-1.190	Detected	-0.874	Detected	-1.032	0.188	GT	Sens	contig243	contig243	Unknown	GCTCAG	contig243	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig243	Solyc12g	Unknown Protein (A		SL2.40ch	AT4G20790.1		leucine-r	chr4:111	4181.63	6532.12	5066.76	2177.85	2420.31	2909.32
GT	Sens	Sense	-0.183	Detected	0.183	Detected	0.000	-2.336	Detected	-0.986	Detected	-1.661	0.141	GT	Sens	contig243	contig243	CXE carb	CATGAG	contig243	Solyc07g	Solyc07g	CXE carb	GO:0004	GO:0004	contig243	Solyc07g	CXE carb	GO:0004	SL2.40ch	AT4G01760.1		DC1 dom	chr4:759	1730.47	1742.76	833.376	309.273	363.538	894.772
GT	Sens	Sense	-0.109	Detected	0.109	Detected	0.000	-1.866	Detected	-1.548	Detected	-1.707	0.012	GT	Sens	contig243	contig243	SEC14-lik	ATGTTC	contig243	Solyc11g	Solyc11g	SEC14-lik	GO:0005	GO:0005	contig243	Solyc03g	Diphosph	GO:00084	SL2.40ch	#N/A	#N/A	#N/A	#N/A	2968.05	2697.86	1845.22	1177.78	820.627	987.448
GT	Sens	Sense	-0.040	Detected	0.040	Detected	0.000	-2.754	Detected	-1.550	Detected	-2.152	0.070	GT	Sens	contig243	contig243	Beta-ocin	GGAACT	contig243	Solyc05g	Solyc05g	Beta-ocin	GO:00050	GO:00050	contig243	Solyc06g	Sister chromatid co		SL2.40ch	#N/A	#N/A	#N/A	#N/A	17795	14697	9239.37	2814.3	2534.49	5633.53
GT	Sens	Sense	0.279	Detected	-0.279	Detected	0.000	-3.255	Comprom	-1.283	Detected	-2.269	0.157	GT	Sens	contig244	contig244	HAT famil	CAAGAG	contig244	Solyc11g	Solyc11g	HAT famil	GO:0003	GO:0003	contig244	Solyc11g	HAT famil	GO:0003	SL2.40ch	AT2G42450.1		lipase cla	chr2:176	52.2247	27.7364	17.9432	28.2437	4.21389	15.9632
GT	Sens	Sense	-0.299	Detected	0.299	Detected	0.000	-5.109	Detected	-1.191	Detected	-3.150	0.253	GT	Sens	contig244	contig244	Calmodul	AAGTTA	contig244	Solyc07g	Solyc07g	Calmodulin-binding protein (A			contig244	Solyc07g	Calmodul	GO:00055	SL2.40ch	AT2G26190.1		calmodu	chr2:111	1445.95	1710.56	344.903	66.5951	48.1705	703.053
GT	Sens	Sense	-0.095	Detected	0.095	Detected	0.000	-2.355	Detected	-2.423	Detected	-2.389	0.002	GT	Sens	contig244	contig244	Gag/pol p	AGGATT	contig244	Solyc10g	Solyc10g	Gag/pol polyprotein (AHRD V1			contig244	Solyc10g	Gag/pol polyprotein		SL2.40ch	AT3G10840.1		hydrolas	chr3:339	93.436	83.3287	25.3612	32.9795	18.2313	16.7866
GT	Sens	Sense	-0.412	Detected	0.412	Detected	0.000	-1.897	Comprom	-1.802	Comprom	-1.850	0.047	GT	Sens	contig244	contig244	Reverse t	AATAAT	contig244	Solyc12g	Solyc12g	Reverse t	GO:00062	GO:00062	contig244	Solyc12g	Genomic DNA chror		SL2.40ch	AT2G154	UGT73B5	UGT73B5	chr2:675	13.8849	19.2168	14.0306	15.4695	4.63629	4.77856
GT	Sens	Sense	-0.133	Detected	0.133	Detected	0.000	-1.129	Detected	-0.927	Detected	-1.028	0.025	GT	Sens	contig244	contig244	ATP synt	CGACAT	contig244	Solyc12g	Solyc12g	ATP synthase subunit beta ch			contig244	Solyc12g	ATP synthase subu		SL2.40ch	ATCG004	ATPB	chloropla	chrC:526	88.6732	83.2959	53.5372	59.1864	41.528	46.1066
GT	Sens	Sense	-0.834	Detected	0.834	Detected	0.000	-3.762	Detected	-2.394	Detected	-3.078	0.104	GT	Sens	contig244	contig244	WRKY tra	AGAAAG	contig244	Solyc04g	Solyc04g	WRKY tra	GO:0045449		contig244	Solyc04g	WRKY tra	GO:00454	SL2.40ch	AT5G648	WRKY51.	WRKY51	chr5:259	148.172	368.126	103.701	60.4761	18.1899	45.3241
GT	Sens	Sense	-0.459	Detected	0.459	Detected	0.000	-1.992	Detected	-1.515	Detected	-1.753	0.077	GT	Sens	contig244	contig244	CM0216.2	GTATCA	contig244	Solyc04g	Solyc04g	CM0216.210.nc protein (AHRD			contig244	Solyc04g	CM0216.210.nc prot		SL2.40ch	AT1G76240.1		unknowr	chr1:286	261.419	385.986	140.193	98.4372	84.4049	113.427
GT	Sens	Sense	0.221	Detected	-0.221	Detected	0.000	-4.717	Comprom	-2.646	Comprom	-3.682	0.074	GT	Sens	contig245	contig245	Transmer	CCATAT	contig245	Solyc05g	Solyc05g	Transmer	GO:00048	GO:00048	contig245	Solyc05g	Transmer	GO:00055	SL2.40ch	AT2G24170.1		endomer	chr2:102	59.0632	33.964	11.8664	2.04987	1.79919	7.30164
GT	Sens	Sense	-0.508	Detected	0.508	Detected	0.000	-1.621	Detected	-0.801	Detected	-1.211	0.205	GT	Sens	contig245	contig245	Zinc finge	CAGAAA	contig245	Solyc08g	Solyc08g	Zinc finge	GO:00037	GO:00037	contig245	Solyc08g	Zinc finge	GO:00055	SL2.40ch	AT2G245	FZF	FZF: tran	chr2:104	524.821	829.528	473.601	296.666	226.755	386.431
GT	Sens	Sense	-0.433	Detected	0.433	Detected	0.000	-1.366	Detected	-0.947	Detected	-1.156	0.138	GT	Sens	contig245	contig245	Xylogluca	CAGTCC	contig245	Solyc08g	Solyc08g	Xylogluca	GO:00059	GO:00059	contig245	Solyc08g	Xylogluca	GO:00167	SL2.40ch	AT1G321	XTR4. XT	XTR4 (XY	chr1:115	93.0537	132.587	68.0683	50.3709	45.5575	58.7761
GT	Sens	Sense	-0.118	Detected	0.118	Detected	0.000	-3.152	Detected	-1.401	Detected	-2.276	0.123	GT	Sens	contig245	contig245	Long cell	AAGAGC	contig245	Solyc01g	Solyc01g	Long cell-linked locus protein			contig245	Solyc01g	Long cell-linked loc		SL2.40ch	AT4G16790.1		hydroxy	chr4:945	280.729	258.409	112.661	43.9065	32.0196	104.091
GT	Sens	Sense	0.064	Detected	-0.064	Detected	0.000	-2.710	Detected	-1.867	Detected	-2.289	0.033	GT	Sens	contig246	contig246	Lipid tran	AAAGAG	contig246	Solyc03g	Solyc03g	Lipid tran	GO:00068	GO:00068	contig246	Solyc03g	Lipid tran	GO:00068	SL2.40ch	AT1G780	SULTR1:	SULTR1:	chr1:293	833.701	596.156	232.078	757.4	113.844	197.214
GT	Sens	Sense	-0.874	Detected	0.874	Detected	0.000	-3.324	Comprom	-2.076	Detected	-2.700	0.128	GT	Sens	contig246	contig246	Unknown	GTTCAC	contig246	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig246	Solyc04g	Unknown Protein (A		SL2.40ch	AT4G02810.1		unknowr	chr4:125	35.8923	94.21	18.9524	10.3223	6.13591	14.0693
GT	Sens	Sense	-0.805	Detected	0.805	Detected	0.000	-6.258	Detected	-1.703	Detected	-3.981	0.241	GT	Sens	contig247	contig247	Cytochro	CAAGCA	contig247	Solyc04g	Solyc04g	Cytochro	GO:00198	GO:00198	contig247	Solyc04g	cytochro	GO:00198	SL2.40ch	AT4G153	CYP705A	CYP705A	chr4:876	481.662	1148.91	303.339	9.09022	10.2692	233.097
GT	Sens	Sense	-0.729	Detected	0.729	Detected	0.000	-5.090	Detected	-2.516	Detected	-3.803	0.124	GT	Sens	contig247	contig247	MYB tran	TTTGGT	contig247	Solyc05g	Solyc05g	MYB tran	GO:00037	GO:00037	contig247	Solyc05g	MYB tran	GO:00037	SL2.40ch	AT3G243	MYB305.	MYB305	chr3:881	1568.17	3368.16	1185.25	294.064	71.3137	410.089
GT	Sens	Sense	0.275	Detected	-0.275	Detected	0.000	-1.004	Detected	-1.106	Detected	-1.055	0.064	GT	Sens	contig247	contig247	Hypotheti	GGATAT	contig247	Solyc11g	Solyc11g	Hypothetical chloroplast RF1 (			contig247	Solyc11g	Hypothetical chloro		SL2.40ch	ATCG011	YCF1.2	hypothet	chrC:123	417.409	222.794	377.151	292.409	160.726	144.584
GT	Sens	Sense	0.258	Detected	-0.258	Detected	0.000	-1.031	Detected	-0.993	Detected	-1.012	0.060	GT	Sens	contig247	contig247	WRKY tra	AACCAG	contig247	Solyc08g	Solyc08g	WRKY tra	GO:00037	GO:00037	contig247	Solyc08g	WRKY tra	GO:00037	SL2.40ch	AT5G241	WRKY30.	WRKY30	chr5:815	4621.5	2526.02	2383.2	1027.55	1766.65	1751.09
GT	Sens	Sense	-0.272	Detected	0.272	Detected	0.000	-1.335	Comprom	-2.147	Comprom	-1.741	0.071	GT	Sens	contig247	contig247	Calmodul	GAGTGT	contig247	Solyc11g	Solyc11g	Calmodul	GO:00055	GO:00055	contig247	Solyc11g	Calmodul	GO:00055	SL2.40ch	AT1G76640.1		calmodu	chr1:287	18.8765	21.5069	5.62006	7.4666	8.44063	4.64246
GT	Sens	Sense	0.080	Detected	-0.080	Detected	0.000	-1.991	Comprom	-1.908	Comprom	-1.949	0.002	GT	Sens	contig248	contig248	Unknown	TTGATG	contig248	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig248	Solyc05g	Unknown Protein (A		SL2.40ch	AT1G51880.1		leucine-r	chr1:192	16.0627	11.2342	25.5507	9.67863	3.57175	3.65274
GT	Sens	Sense	0.057	Detected	-0.057	Detected	0.000	-1.445	Detected	-1.654	Detected	-1.549	0.006	GT	Sens	contig248	contig248	Delta-6 de	GTGTGT	contig248	Solyc10g	Solyc10g	Delta-6 desaturase (AHRD V1 *			contig248	Solyc10g	Delta-6 desaturase		SL2.40ch	AT3G52700.1		unknowr	chr3:195	81.1492	58.6451	63.1261	68.983	26.786	22.366
GT	Sens	Sense	-0.619	Detected	0.619	Detected	0.000	-3.811	Detected	-0.983	Detected	-2.397	0.261	GT	Sens	contig249	contig249	Inosine-u	AAGACT	contig249	Solyc01g	Solyc01g	Inosine-u	GO:00167	GO:00167	contig249	Solyc01g	Inosine-u	GO:00167	SL2.40ch	AT5G18860.1		inosine-u	chr5:629	109.961	202.65	49.4553	9.84779	11.2407	77.0533
GT	Sens	Sense	-1.037	Detected	1.037	Detected	0.000	-1.317	Detected	-1.359	Detected	-1.338	0.326	GT	Sens	contig249	contig249	Gibberell	GTTATT	contig249	Solyc09g	Solyc09g	Gibberell	GO:00040	GO:00040	contig249	Solyc09g	Gibberell	GO:00040	SL2.40ch	AT5G37350.2		RIO1 fam	chr5:147	122.95	404.458	115.19	116.474	94.6205	88.6765
GT	Sens	Sense	-0.368	Detected	0.368	Detected	0.000	-2.795	Comprom	-1.063	Detected	-1.929	0.177	GT	Sens	contig249	contig249	RNase H f	AACATT	contig249	Solyc07g	Solyc07g	RNase H f	GO:00030	GO:00030	contig249	Solyc07g	RNase H f	GO:00030	SL2.40ch	AT4G37210.1		tetratrico	chr4:175	45.5674	59.289	20.1911	5.21414	7.91772	25.3774
GT	Sens	Sense	-0.387	Detected	0.387	Detected	0.000	-1.206	Detected	-0.983	Detected	-1.094	0.113	GT	Sens	contig249	contig249	Cellulose	TGTGCT	contig249	Solyc02g	Solyc02g	Cellulose	GO:00167	GO:00167	contig249	Solyc02g	Cellulose	GO:00167	SL2.40ch	AT4G187	CESA8. IF	IRX1 (IRR	chr4:103	296.025	395.821	296.116	386.511	156.842	176.68
GT	Sens	Sense	-0.614	Detected	0.614	Detected	0.000	-2.970	Comprom	-1.242	Detected	-2.106	0.185	GT	Sens	contig249	contig249	C4-dicarb	CTCAGT	contig249	Solyc06g	Solyc06g	C4-dicarb	GO:00160	GO:00160	contig249	Solyc06g	C4-dicarb	GO:00052	SL2.40ch	AT5G240	SLAH3	SLAH3 (S	chr5:811	40.6716	74.5133	22.5466	14.2557	7.42316	23.7443
GT	Sens	Sense	0.734	Detected	-0.734	Detected	0.000	-1.998	Comprom	-1.918	Comprom	-1.958	0.117	GT	Sens	contig249	contig249	Ripening-	TCACCT	contig249	Solyc11g	Solyc11g	Ripening-related protein 3 (AH			contig249	Solyc11g	Ripening-related pr		SL2.40ch	AT5G08230.1		PWWP d	chr5:264	41.5306	11.7425	4.07743	5.40453	5.84351	5.96119
GT	Sens	Sense	0.290	Detected	-0.290	Detected	0.000	-2.736	Detected	-1.140	Detected	-1.938	0.150	GT	Sens	contig250	contig250	Unknown	GAAAAA	contig250	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig250	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G30320.1		unknowr	chr3:119	140.137	73.2328	103.277	77.4737	16.0685	46.8989
GT	Sens	Sense	0.549	Detected	-0.549	Detected	0.000	-4.750	Comprom	-2.163	Detected	-3.456	0.133	GT	Sens	contig250	contig250	Ethylene	GTAAAA	contig250	Solyc03g	Solyc03g	Ethylene	GO:00037	GO:00037	contig250	Solyc03g	Ethylene	GO:00165	SL2.40ch	AT3G232	ERF1. AT	ERF1 (ET	chr3:829	85.0682	31.0453	47.0225	7.8926	2.01806	11.7113
GT	Sens	Sense	-0.045	Detected	0.045	Detected	0.000	-2.331	Detected	-0.857	Detected	-1.594	0.164	GT	Sens	contig251	contig251	Alpha-1 4	GATGGA	contig251	Solyc10g	Solyc10g	Alpha-1 4	GO:00057	GO:00057	contig251	Solyc10g	Alpha-1 4	GO:00057	SL2.40ch	AT5G448	CHR4	CHR4 (CI	chr5:180	1410.9	1174.03	870.087	259.463	270.324	725.001
GT	Sens	Sense	0.028	Detected	-0.028	Detected	0.000	-1.619	Detected	-1.552	Detected	-1.585	0.001	GT	Sens	contig252	contig252	Unknown	TAGCAC	contig252	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig252	Solyc00g	Unknown Protein (A		SL2.40ch	AT2G17787.1				75.9441	57.1213	31.5479	46.2297	22.666	22.921
GT	Sens	Sense	1.280	Detected	-1.280	Detected	0.000	-1.745	Detected	-2.392	Detected	-2.068	0.258	GT	Sens	contig252	contig252	1-AMINO	GAAAGT	contig252	Solyc11g	Solyc11g	1-AMINO(	GO:00164	GO:00164	contig252	Solyc11g	1-AMINO(	GO:00164	SL2.40ch	AT3G12900.1		oxidored	chr3:410	237.658	31.5184	36.9916	49.1233	27.2894	16.83
GT	Sens	Sense	-0.451	Detected	0.451	Detected	0.000	-2.404	Detected	-1.996	Detected	-2.200	0.047	GT	Sens	contig252	contig252	Alpha-hu	GTGTGG	contig252	Solyc06g	Solyc06g	Alpha-hu	GO:00080	GO:00080	contig252	Solyc06g	Sesquiterpene synt		SL2.40ch	AT4G19180.1		nucleosi	chr4:104	358.787	523.851	198.888	622.646	86.5956	110.87
GT	Sens	Sense	0.213	Detected	-0.213	Detected	0.000	-3.856	Detected	-0.961	Detected	-2.408	0.242	GT	Sens	contig252	contig252	Glycosylt	CAAAGG	contig252	Solyc05g	Solyc05g	Glycosylt	GO:00065	GO:00065	contig252	Solyc05g	Glycosylt	GO:00167	SL2.40ch	AT3G57880.1		C2 doma	chr3:214	2858.87	1662.95	518.059	137.765	159.152	1143.12
GT	Sens	Sense	-0.427	Detected	0.427	Detected	0.000	-1.246	Detected	-0.862	Detected	-1.054	0.153	GT	Sens	contig252	contig252	Unknown	GTCAGT	contig252	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig252	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G16680.1		RNA heli	chr4:938	17.5203	24.745	18.7306	12.4092	9.27578	11.6876
GT	Sens	Sense	-0.152	Detected	0.152	Detected	0.000	-1.031	Detected	-1.152	Detected	-1.092	0.022	GT	Sens	contig252	contig252	Receptor	AAATAT	contig252	Solyc11g	Solyc11g	Receptor	GO:00064	GO:00064	contig252	Solyc11g	Receptor	GO:00046	SL2.40ch	AT1G56510.1				31.7878	30.6857	21.1557	21.7227	16.1522	14.3402
GT	Sens	Sense	-0.173	Detected	0.173	Detected	0.000	-1.970	Detected	-2.168	Detected	-2.069	0.009	GT	Sens	contig252	contig252	Gag-Pol p	CATGTT	contig252	Solyc11g	Solyc11g	Gag-Pol polyprotein (AHRD V1			contig252	Solyc05g	Nucleore	GO:00047	SL2.40ch	AT2G28940.2		protein k	chr2:124	378.166	375.921	128.223	147.616	101.683	85.6033
GT	Sens	Sense	-0.149	Detected	0.149	Detected	0.000	-1.684	Comprom	-0.805	Detected	-1.244	0.116	GT	Sens	contig253	contig253	Ring H2 fi	CAGAAG	contig253	Solyc07g	Solyc07g	Ring H2 fi	GO:00082	GO:00082	contig253	Solyc07g	Ring H2 fi	GO:00082	SL2.40ch	AT5G17600.1		zinc fing	chr5:580	23.065	22.1685	20.9916	13.6041	7.43854	13.2081
GT	Sens	Sense	-0.219	Detected	0.219	Detected	0.000	-1.430	Detected	-0.962	Detected	-1.196	0.065	GT	Sens	contig253	contig253	LRR rece	ATGAGA	contig253	Solyc06g	Solyc06g	LRR rece	GO:00046	GO:00046	contig253	Solyc06g	Receptor	GO:00046	SL2.40ch	AT5G45840.1		leucine-r	chr5:185	3078.31	3260	1968.61	1283	1242.81	1659.79
GT	Sens	Sense	-0.642	Detected	0.642	Detected	0.000	-2.921	Comprom	-3.061	Comprom	-2.991	0.044	GT	Sens	contig254	contig254	Beta-gala	GTGAGC	contig254	Solyc07g	Solyc07g	Beta-gala	GO:00055	GO:00055	contig254	Solyc07g	Beta-gala	GO:00045	SL2.40ch	AT1G317	BGAL15	BGAL15	chr1:113	14.2908	27.2136	11.8903	1.88313	2.75192	2.41078
GT	Sens	Sense	-0.736	Detected	0.736	Detected	0.000	-1.718	Detected	-1.977	Detected	-1.848	0.132	GT	Sens	contig254	contig254	Amino ac	ATGAGT	contig254	Solyc09g	Solyc09g	Amino ac	GO:00151	GO:00151	contig254	Solyc09g	Amino ac	GO:00151	SL2.40ch	AT4G32970.1		unknowr	chr4:159	33.9968	73.6804	45.1587	6.66377	16.0732	12.9729
GT	Sens	Sense	-0.157	Detected	0.157	Detected	0.000	-1.949	Detected	-1.784	Detected	-1.866	0.009	GT	Sens	contig255	contig255	Mutator-l	TAAATA	contig255	Solyc01g	Solyc01g	Mutator-like transposase (AHF			contig255	Solyc01g	Mutator-l	GO:00082	SL2.40ch	AT4G163	SPK1	SPK1 (SF	chr4:922	89.0714	86.5307	33.1949	44.6808	24.0372	26.0191
GT	Sens	Sense	-0.075	Detected	0.075	Detected	0.000	-2.125	Comprom	-1.723	Comprom	-1.924	0.012	GT	Sens	contig255	contig255	Non-LTR	TAAACT	contig255	Solyc07g	Solyc07g	Non-LTR reverse transcriptase			contig255	Solyc11g	Zinc finger CCHC-ty		SL2.40ch	AT5G04670.1		FUNCTIC	chr5:133	17.8752	15.4975	13.0547	10.9877	4.03219	5.14258
GT	Sens	Sense	-0.720	Detected	0.720	Detected	0.000	-3.513	Detected	-1.942	Detected	-2.727	0.125	GT	Sens	contig255	contig255	Late emb	ATTGAT	contig255	Solyc01g	Solyc01g	Late emb	GO:00092	GO:00092	contig255	Solyc01g	Late emb	GO:00092	SL2.40ch	AT5G07310.1		AP2 dom	chr5:230	3423.61	7264.6	2151.74	435.388	461.827	1324.13
GT	Sens	Sense	-0.672	Detected	0.672	Detected	0.000	-5.482	Detected	-1.160	Detected	-3.321	0.280	GT	Sens	contig255	contig255	Fucosyltr	TACAAG	contig255	Solyc06g	Solyc06g	Fucosyltr	GO:00048	GO:00048	contig255	Solyc06g	Fucosyltr	GO:00084	SL2.40ch	AT1G141	FUT8	FUT8 (FU	chr1:482	425.11	843.472	331.292	42.3793	14.1584	273.365
GT	Sens	Sense	0.132	Detected	-0.132	Detected	0.000	-1.392	Comprom	-1.549	Comprom	-1.471	0.011	GT	Sens	contig256	contig256	Nucleolar	GGCTTT	contig256	Solyc07g	Solyc07g	Nucleolar GTP-binding protein			contig256	Solyc07g	Nucleolar GTP-bind		SL2.40ch	AT4G25360.2		INVOLVE	chr4:129	19.3631	12.6029	10.0905	5.25875	6.28918	5.44541
GT	Sens	Sense	-0.314	Detected	0.314	Detected	0.000	-1.569	Detected	-0.802	Detected	-1.185	0.139	GT	Sens	contig256	contig256	SRC2 hor	ATATCA	contig256	Solyc01g	Solyc01g	SRC2 hor	GO:00055	GO:00055	contig256	Solyc01g	SRC2 hor	GO:00055	SL2.40ch	AT5G45660.1		unknowr	chr5:185	5830.56	7046.17	2688.29	1389.83	2283.29	3750.97
GT	Sens	Sense	-0.203	Detected	0.203	Detected	0.000	-2.007	Detected	-2.236	Comprom	-2.121	0.012	GT	Sens	contig256	contig256	Decarbox	GAGAAA	contig256	Solyc08g	Solyc08g	Decarbox	GO:00197	GO:00197	contig256	Solyc08g	Decarbox	GO:00301	SL2.40ch	AT5G020	LSN. PNY	RPL (REF	chr5:395	42.6403	44.1708	13.5742	42.315	11.4081	9.40272
GT	Sens	Sense	-0.019	Detected	0.019	Detected	0.000	-1.594	Detected	-1.011	Detected	-1.302	0.047	GT	Sens	contig256	contig256	Unknown	TTCGCA	contig256	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig256	Solyc03g	Unknown Protein (A		SL2.40ch	AT1G73130.1		unknowr	chr1:274	38.4111	30.8066	32.1503	13.6128	12.0414	17.4185
GT	Sens	Sense	-0.001	Detected	0.001	Detected	0.000	-2.518	Comprom	-2.188	Comprom	-2.353	0.005	GT	Sens	contig257	contig257	Unknown	TAGACA	contig257	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig257	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G46070.1		GTP bind	chr5:186	43.8062	34.2697	11.506	13.9786	7.15042	8.6731
GT	Sens	Sense	-0.174	Detected	0.174	Detected	0.000	-1.332	Comprom	-2.070	Comprom	-1.701	0.053	GT	Sens	contig257	contig257	Self-prun	AGAGAA	contig257	Solyc11g	Solyc11g	Self-pruning interacting protei			contig257	Solyc11g	Self-pruning interac		SL2.40ch	AT2G43570.1		chitinase	chr2:180	16.2167	16.1315	4.41098	10.7193	6.78803	3.92998
GT	Sens	Sense	-0.053	Detected	0.053	Detected	0.000	-1.049	Detected	-1.191	Detected	-1.120	0.006	GT	Sens	contig258	contig258	Reverse t	CTATTA	contig258	Solyc11g	Solyc11g	Reverse t	GO:00062	GO:00062	contig258	Solyc02g	Glucan endo-1 3-be		SL2.40ch	AT3G617	ATX3	SDG14 (S	chr3:228	46.2783	38.9267	39.5537	28.3621	21.6843	18.9699
GT	Sens	Sense	0.053	Detected	-0.053	Detected	0.000	-1.154	Detected	-0.972	Detected	-1.063	0.010	GT	Sens	contig259	contig259	HAT famil	ATGTTG	contig259	Solyc07g	Solyc07g	HAT family dimerisation doma			contig259	Solyc04g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	483.993	351.373	433.51	325.405	195.831	214.457
GT	Sens	Sense	-0.645	Detected	0.645	Detected	0.000	-4.486	Detected	-2.469	Detected	-3.478	0.101	GT	Sens	contig260	contig260	Calmodul	TCGGAT	contig260	Solyc06g	Solyc06g	Calmodul	GO:00055	GO:00055	contig260	Solyc06g	Calmodul	GO:00055	SL2.40ch	AT1G76640.1		calmodu	chr1:287	1674.52	3199.13	1116.43	235.322	109.137	426.598
GT	Sens	Sense	0.315	Detected	-0.315	Detected	0.000	-2.481	Comprom	-1.310	Detected	-1.895	0.104	GT	Sens	contig260	contig260	Mutator-l	GTGCAC	contig260	Solyc10g	Solyc10g	Mutator-like transposase (AHF			contig260	Solyc08g	Mutator-l	GO:00082	SL2.40ch	AT3G51120.1		DNA bind	chr3:189	38.0233	19.2174	20.2915	14.8355	5.11894	11.1253
GT	Sens	Sense	-0.107	Detected	0.107	Detected	0.000	-1.326	Detected	-1.132	Detected	-1.229	0.014	GT	Sens	contig260	contig260	F-box prc	AACAGT	contig260	Solyc01g	Solyc01g	F-box prc	GO:00302	GO:00302	contig260	Solyc01g	F-box prc	GO:00302	SL2.40ch	AT5G59000.1		zinc fing	chr5:238	2420.42	2194.75	1505.69	1010.14	971.621	1073.23
GT	Sens	Sense	0.298	Detected	-0.298	Detected	0.000	-1.438	Detected	-0.941	Detected	-1.189	0.092	GT	Sens	contig260	contig260	CCR4-NO	CTCCCC	contig260	Solyc06g	Solyc06g	CCR4-NO	GO:00056	GO:00056	contig260	Solyc06g	CCR4-NO	GO:00001	SL2.40ch	AT5G22250.1		CCR4-NO	chr5:736	32306.8	16714.2	23384.1	11486.4	9063.36	12354.3
GT	Sens	Sense	-1.289	Detected	1.289	Detected	0.000	-1.350	Detected	-1.363	Detected	-1.357	0.403	GT	Sens	contig261	contig261	Leucine-r	CAAACA	contig261	Solyc05g	Solyc05g	Leucine-r	GO:00163	GO:00163	contig261	Solyc05g	LRR rece	GO:00163	SL2.40ch	AT3G21220.1				12.7951	59.702	12.7427	16.4213	11.4596	10.9626
GT	Sens	Sense	0.007	Detected	-0.007	Detected	0.000	-1.304	Detected	-1.099	Detected	-1.201	0.007	GT	Sens	contig261	contig261	Methyl-ac	TGGGTG	contig261	Solyc02g	Solyc02g	Methyl-ac	GO:00160	GO:00160	contig261	Solyc02g	Methyl-ac	GO:00160	SL2.40ch	AT5G49290.1		protein b	chr5:199	69.3064	53.6814	44.1771	62.1291	26.1151	29.0524
GT	Sens	Sense	0.005	Detected	-0.005	Detected	0.000	-1.150	Comprom	-1.706	Comprom	-1.428	0.036	GT	Sens	contig261	contig261	Transpos	GGAGTC	contig261	Solyc05g	Solyc05g	Transposon protein-like (AHRI			contig261	Solyc05g	Transposon protein		SL2.40ch	AT2G27200.1		GTP-bind	chr2:116	18.9795	14.7375	9.76233	13.6695	7.96594	5.2317
GT	Sens	Sense	-0.082	Detected	0.082	Detected	0.000	-1.929	Detected	-1.704	Detected	-1.816	0.006	GT	Sens	contig261	contig261	Retrotran	TAAGAA	contig261	Solyc07g	Solyc07g	Retrotransposon gag protein (			contig261	Solyc04g	Retrotransposon ga		SL2.40ch	AT2G17420.1				62.9523	55.1067	35.4023	45.4018	16.3513	18.4492
GT	Sens	Sense	-0.339	Detected	0.339	Detected	0.000	-1.336	Detected	-1.501	Detected	-1.418	0.055	GT	Sens	contig261	contig261	Cellulose	TGTTTT	contig261	Solyc11g	Solyc11g	Cellulose	GO:00517	GO:00517	contig261	Solyc11g	Cellulose	GO:00517	SL2.40ch	AT5G227	ATCSLAC	ATCSLAC	chr5:755	140.641	175.816	108.867	91.6328	65.833	56.7053
GT	Sens	Sense	0.025	Detected	-0.025	Detected	0.000	-0.916	Detected	-1.125	Detected	-1.020	0.011	GT	Sens	contig262	contig262	Solute ca	AATCTC	contig262	Solyc08g	Solyc08g	Solute ca	GO:00160	GO:00160	contig262	Solyc08g080300.1.1				AT1G112	STP1. AT	STP1 (SU	chr1:377	23.5454	17.7871	14.5821	15.3534	11.4661	9.57231
GT	Sens	Sense	-0.451	Detected	0.451	Detected	0.000	-2.159	Detected	-1.436	Detected	-1.798	0.090	GT	Sens	contig262	contig262	Unknown	TGCACA	contig262	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig262	Solyc03g	Unknown Protein (A		SL2.40ch	AT2G35610.1		FUNCTIC	chr2:149	282.825	412.824	231.212	55.2877	80.849	128.865
GT	Sens	Sense	0.046	Detected	-0.046	Detected	0.000	-1.886	Detected	-1.981	Detected	-1.933	0.001	GT	Sens	contig263	contig263	Cinnamyl	AGACAT	contig263	Solyc05g	Solyc05g	Cinnamyl alcohol dehydrogen			contig263	Solyc11g	Alcohol d	GO:00081	SL2.40ch	AT1G02330.1		FUNCTIC	chr1:462	121.583	89.1045	42.9394	50.777	29.7669	26.8992
GT	Sens	Sense	-0.109	Detected	0.109	Detected	0.000	-1.048	Detected	-1.055	Detected	-1.052	0.011	GT	Sens	contig263	contig263	Receptor	CAACAG	contig263	Solyc07g	Solyc07g	Receptor	GO:00055	GO:00055	contig263	Solyc07g	Receptor	GO:00055	SL2.40ch	AT4G323	SD2-5	SD2-5 (S	chr4:155	235.315	213.861	187.546	174	114.635	110.185
GT	Sens	Sense	0.240	Detected	-0.240	Detected	0.000	-1.399	Detected	-1.138	Detected	-1.268	0.044	GT	Sens	contig263	contig263	Unknown	ACTCAT	contig263	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig263	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G16385.1		unknowr	chr2:709	59.9173	33.5573	35.2856	52.3787	17.9752	20.792
GT	Sens	Sense	-0.076	Detected	0.076	Detected	0.000	-1.236	Detected	-1.683	Detected	-1.460	0.025	GT	Sens	contig263	contig263	DNA-direc	ATAAAT	contig263	Solyc12g	Solyc12g	DNA-direc	GO:0006350		contig263	Solyc12g	DNA-direc	GO:00063	SL2.40ch	ATCG001	RPOB	Chloropl	chrC:231	494.317	429.199	246.857	260.34	206.603	146.39
GT	Sens	Sense	-0.226	Detected	0.226	Detected	0.000	-1.309	Detected	-0.901	Detected	-1.105	0.068	GT	Sens	contig263	contig263	Alcohol a	GTTGAG	contig263	Solyc11g	Solyc11g	Alcohol a	GO:00167	GO:00167	contig263	Solyc11g	Alcohol a	GO:00167	SL2.40ch	AT1G77830.1		zinc fing	chr1:292	44.8151	47.9283	24.5396	53.1604	19.7725	25.3258
GT	Sens	Sense	0.225	Detected	-0.225	Detected	0.000	-1.969	Detected	-2.339	Detected	-2.154	0.018	GT	Sens	contig264	contig264	Hypotheti	AAGTTG	contig264	Solyc10g	Solyc10g	Hypothetical chloroplast RF1 (			contig264	Solyc10g	Hypothetical chloro		SL2.40ch	AT4G04790.1		FUNCTIC	chr4:243	108.35	61.9981	84.6526	74.7765	22.1187	16.5266
GT	Sens	Sense	0.101	Detected	-0.101	Detected	0.000	-1.433	Detected	-1.397	Detected	-1.415	0.005	GT	Sens	contig264	contig264	Methyl bi	ATACTT	contig264	Solyc11g	Solyc11g	Methyl bi	GO:00030	GO:00030	contig264	Solyc11g	Methyl bi	GO:00056	SL2.40ch	AT4G38520.2		protein p	chr4:180	297.564	202.296	199.481	107.834	96.051	95.0696
GT	Sens	Sense	-0.175	Detected	0.175	Detected	0.000	-2.425	Detected	-2.121	Detected	-2.273	0.010	GT	Sens	contig264	contig264	Decarbox	TTGTTA	contig264	Solyc08g	Solyc08g	Decarbox	GO:00197	GO:00197	contig264	Solyc08g068640.2.1				AT5G408	AtUK/UPI	AtUK/UPI	chr5:163	202.566	201.919	138.426	178.701	39.7996	47.4546
GT	Sens	Sense	-0.133	Detected	0.133	Detected	0.000	-1.322	Detected	-1.186	Detected	-1.254	0.014	GT	Sens	contig264	contig264	UDP-D-gl	ATGAGC	contig264	Solyc06g	Solyc06g	UDP-D-gl	GO:00090	GO:00090	contig264	Solyc06g	UDP-D-gl	GO:00039	SL2.40ch	AT5G39320.1		UDP-gluc	chr5:157	161.561	151.944	44.0769	52.6966	66.2116	70.2843
GT	Sens	Sense	-0.139	Detected	0.139	Detected	0.000	-1.482	Detected	-0.983	Detected	-1.233	0.050	GT	Sens	contig264	contig264	Unknown	ATAGGT	contig264	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig264	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G624	CP12-2. C	CP12-2: i	chr3:230	572.691	542.876	361.564	181.3	210.982	287.782
GT	Sens	Sense	-0.255	Detected	0.255	Detected	0.000	-0.928	Detected	-1.233	Detected	-1.080	0.068	GT	Sens	contig265	contig265	LRR rece	CTTGAG	contig265	Solyc07g	Solyc07g	LRR rece	GO:00055	GO:00055	contig265	Solyc07g	Receptor	GO:00055	SL2.40ch	AT1G34420.1		leucine-r	chr1:125	74.5264	82.9357	29.9285	40.856	43.6627	34.1378
GT	Sens	Sense	0.444	Detected	-0.444	Detected	0.000	-1.248	Detected	-1.083	Detected	-1.165	0.123	GT	Sens	contig265	contig265	Unknown	CGTGGA	contig265	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig265	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G11385.1		DC1 dom	chr3:356	37.5013	15.8345	29.2775	24.8456	10.8454	11.7392
GT	Sens	Sense	-0.061	Detected	0.061	Detected	0.000	-3.026	Comprom	-2.844	Comprom	-2.935	0.001	GT	Sens	contig265	contig265	Aldehyde	ACTTGG	contig265	Solyc01g	Solyc01g	Aldehyde	GO:00515	GO:00515	contig265	Solyc01g	Aldehyde	GO:00515	SL2.40ch	AT1G544	AIN1. EIN	XRN4 (EX	chr1:203	18.8838	16.0603	12.4677	29.6794	2.25902	2.475
GT	Sens	Sense	-1.661	Detected	1.661	Detected	0.000	-5.194	Comprom	-5.089	Comprom	-5.142	0.091	GT	Sens	contig265	contig265	Phenylala	AAGGGC	contig265	Solyc03g	Solyc03g	Phenylala	GO:00038	GO:00038	contig265	Solyc03g	Phenylala	GO:00090	SL2.40ch	AT2G370	pal1. ATP	pal1 (Phe	chr2:155	23.828	186.35	2.56967	2.78633	1.92418	1.99703
GT	Sens	Sense	-0.488	Detected	0.488	Detected	0.000	-1.118	Detected	-1.333	Detected	-1.225	0.134	GT	Sens	contig265	contig265	Os03g029	GGAGGC	contig265	Solyc09g	Solyc09g	Os03g0291800 protein (Fragm			contig265	Solyc09g	Os03g0291800 prot		SL2.40ch	AT2G38320.1		unknowr	chr2:160	27.3905	42.0866	15.5776	39.9976	16.5353	13.7545
GT	Sens	Sense	-0.384	Detected	0.384	Detected	0.000	-1.894	Detected	-1.171	Detected	-1.532	0.101	GT	Sens	contig266	contig266	Arf-GAP w	TATTGC	contig266	Solyc03g	Solyc03g	Arf-GAP w	GO:00323	GO:00323	contig266	Solyc03g	Arf-GAP w	GO:00323	SL2.40ch	AT5G543	AGD5	AGD5 (AI	chr5:220	376.219	500.652	194.524	127.77	123.431	196.693
GT	Sens	Sense	-0.163	Detected	0.163	Detected	0.000	-1.638	Detected	-0.931	Detected	-1.284	0.081	GT	Sens	contig266	contig266	Undecapr	GCAATT	contig266	Solyc06g	Solyc06g	Undecapr	GO:00455	GO:00455	contig266	Solyc06g	Undecapr	GO:00455	SL2.40ch	AT5G58770.1		dehydrod	chr5:237	141.983	139.108	107.739	268.537	47.734	75.2326
GT	Sens	Sense	-0.118	Detected	0.118	Detected	0.000	-2.263	Detected	-1.008	Detected	-1.635	0.125	GT	Sens	contig266	contig266	Plastid-ta	GTTGCT	contig266	Solyc04g	Solyc04g	Plastid-targeted protein 3 (AHF			contig266	Solyc04g	Plastid-targeted pro		SL2.40ch	AT3G53040.1		late embi	chr3:196	4122.06	3796.42	2451.75	876.4	871.208	2007.13
GT	Sens	Sense	-0.064	Detected	0.064	Detected	0.000	-3.082	Comprom	-2.777	Comprom	-2.929	0.003	GT	Sens	contig266	contig266	MuDR far	AGTATG	contig266	Solyc08g	Solyc08g	MuDR family transposase con			contig266	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	33.645	28.7334	33.6587	15.657	3.88051	4.62948
GT	Sens	Sense	0.335	Detected	-0.335	Detected	0.000	-1.999	Comprom	-1.038	Detected	-1.519	0.122	GT	Sens	contig266	contig266	Reverse t	ATATGA	contig266	Solyc06g	Solyc06g	Reverse t	GO:00062	GO:00062	contig266	Solyc03g013430.1.1				AT1G10370.1				33.3717	16.3877	25.3487	30.6501	6.18375	11.6185
GT	Sens	Sense	0.117	Detected	-0.117	Detected	0.000	-1.332	Detected	-1.298	Detected	-1.315	0.008	GT	Sens	contig266	contig266	Transpos	ATCTCG	contig266	Solyc10g	Solyc10g	Transpos	GO:00150	GO:00150	contig266	Solyc10g	Transpos	GO:00030	SL2.40ch	AT1G116	CYP51G1	CYP51G1	chr1:393	54.1322	35.9651	22.6225	17.7191	18.5208	18.304
GT	Sens	Sense	-0.221	Detected	0.221	Detected	0.000	-3.770	Detected	-1.910	Detected	-2.840	0.097	GT	Sens	contig267	contig267	CHP-rich	GTCCAA	contig267	Solyc02g	Solyc02g	CHP-rich	GO:00082	GO:00082	contig267	Solyc02g	CHP-rich	GO:00230	SL2.40ch	AT3G256	CHUP1	CHUP1 (C	chr3:935	888.213	942.64	253.68	108.561	70.8962	248.358
GT	Sens	Sense	0.161	Detected	-0.161	Detected	0.000	-1.591	Detected	-1.520	Detected	-1.556	0.011	GT	Sens	contig267	contig267	Receptor	AGTATG	contig267	Solyc10g	Solyc10g	Receptor	GO:00311	GO:00311	contig267	Solyc10g	Receptor	GO:00064	SL2.40ch	AT1G56140.1				1336.17	835.591	878.556	642.086	370.667	375.807
GT	Sens	Sense	-0.599	Detected	0.599	Detected	0.000	-1.156	Detected	-1.157	Detected	-1.156	0.193	GT	Sens	contig267	contig267	Solute ca	ACAAAA	contig267	Solyc11g	Solyc11g	Solute carrier family 35 membe			contig267	Solyc11g	Solute carrier family		SL2.40ch	AT2G28315.1		LOCATE	chr2:120	91.1542	163.384	99.9149	116.267	57.8887	55.8481
GT	Sens	Sense	-0.018	Detected	0.018	Detected	0.000	-1.173	Detected	-0.860	Detected	-1.017	0.023	GT	Sens	contig268	contig268	NAC dom	CTTTAA	contig268	Solyc06g	Solyc06g	NAC dom	GO:0045449		contig268	Solyc06g	NAC dom	GO:00454	SL2.40ch	AT5G245	ANAC091	TIP (TCV	chr5:841	4103.97	3288.27	2520.08	1595.6	1721.92	2064.83
GT	Sens	Sense	-0.123	Detected	0.123	Detected	0.000	-1.424	Detected	-1.183	Detected	-1.303	0.017	GT	Sens	contig268	contig268	Fatty acy	AGATTG	contig268	Solyc06g	Solyc06g	Fatty acy	GO:00080	GO:00080	contig268	Solyc06g	Fatty acy	GO:00080	SL2.40ch	AT3G445	FAR8	FAR8 (FA	chr3:161	220.158	203.956	119.07	258.342	83.4839	95.2493
GT	Sens	Sense	-0.062	Detected	0.062	Detected	0.000	-2.997	Detected	-0.842	Detected	-1.919	0.217	GT	Sens	contig269	contig269	Ethylene-	TTGAGT	contig269	Solyc08g	Solyc08g	Ethylene-	GO:00037	GO:00037	contig269	Solyc08g	Ethylene-	GO:00165	SL2.40ch	AT4G175	ATERF-1	ATERF-1	chr4:975	7972.68	6791.9	5770.41	2283.25	974.474	4188.64
GT	Sens	Sense	0.359	Detected	-0.359	Detected	0.000	-1.180	Detected	-0.842	Detected	-1.011	0.126	GT	Sens	contig270	contig270	Calmodul	GCAACC	contig270	Solyc03g	Solyc03g	Calmodul	GO:00055	GO:00055	contig270	Solyc03g	Calmodul	GO:00055	SL2.40ch	AT2G331	ATCSLD1	ATCSLD	chr2:140	67.9906	32.2979	32.8472	27.0062	21.8586	26.6703
GT	Sens	Sense	-0.106	Detected	0.106	Detected	0.000	-1.145	Detected	-1.087	Detected	-1.116	0.009	GT	Sens	contig270	contig270	Abscisic	TCCACT	contig270	Solyc09g	Solyc09g	Abscisic	GO:00428	GO:00428	contig270	Solyc09g	Abscisic	GO:00428	SL2.40ch	AT2G38310.1		unknowr	chr2:160	32.3007	29.225	16.9788	39.2106	14.6831	14.7591
GT	Sens	Sense	0.013	Detected	-0.013	Detected	0.000	-2.197	Detected	-1.915	Detected	-2.056	0.005	GT	Sens	contig271	contig271	Unknown	TGGGAT	contig271	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig271	Solyc04g026120.1.1				AT2G36470.1		unknowr	chr2:152	176.893	135.811	76.3654	64.3054	35.7249	41.9399
GT	Sens	Sense	-1.359	Detected	1.359	Detected	0.000	-6.236	Comprom	-2.263	Detected	-4.250	0.220	GT	Sens	contig271	contig271	Pre-mRNA	GGGAAA	contig271	Solyc10g	Solyc10g	Pre-mRNA splicing factor CLF			contig271	Solyc03g	Kunitz-typ	GO:00048	SL2.40ch	AT5G112	ATGLR2.	ATGLR2.	chr5:357	58.8802	302.929	104.814	11.1488	1.87209	28.3947
GT	Sens	Sense	-0.774	Detected	0.774	Detected	0.000	-1.045	Detected	-0.969	Detected	-1.007	0.323	GT	Sens	contig272	contig272	HAD-sup	TTGAGG	contig272	Solyc07g	Solyc07g	HAD-sup	GO:00085	GO:00085	contig272	Solyc07g	HAD-sup	GO:00039	SL2.40ch	AT3G12900.1		oxidored	chr3:410	571.152	1305.62	781.512	375.982	442.189	450.203
GT	Sens	Sense	-0.214	Detected	0.214	Detected	0.000	-2.475	Detected	-1.493	Detected	-1.984	0.066	GT	Sens	contig272	contig272	Cell divis	GATGGC	contig272	Solyc02g	Solyc02g	Cell divis	GO:00055	GO:00055	contig272	Solyc02g	Cell divis	GO:00420	SL2.40ch	AT3G509	BCS1	BCS1 (C	chr3:189	1218.82	1281.46	796.442	292.051	237.522	452.917
GT	Sens	Sense	0.272	Detected	-0.272	Detected	0.000	-2.816	Comprom	-3.715	Comprom	-3.265	0.025	GT	Sens	contig272	contig272	Gag-Pol p	GAGCAA	contig272	Solyc04g	Solyc04g	Gag-Pol p	GO:00030	GO:00030	contig272	Solyc04g011970.1.1				AT3G022	BIG. DOC	BIG (BIG	chr3:431	45.6537	24.4692	20.3497	15.3596	5.01748	2.59755
GT	Sens	Sense	-0.027	Detected	0.027	Detected	0.000	-1.999	Comprom	-0.820	Detected	-1.410	0.139	GT	Sens	contig272	contig272	Lipoxyge	CACGAC	contig272	Solyc09g	Solyc09g	Lipoxyge	GO:00161	GO:00161	contig272	Solyc09g	Lipoxyge	GO:00161	SL2.40ch	AT1G550	LOX1	LOX1: lic	chr1:205	22.8616	18.5399	22.7795	6.25643	5.44341	11.8972
GT	Sens	Sense	0.570	Detected	-0.570	Detected	0.000	-3.798	Comprom	-3.576	Comprom	-3.687	0.024	GT	Sens	contig272	contig272	Signal rec	CTTGTG	contig272	Solyc02g	Solyc02g	Signal recognition particle pro			contig272	Solyc02g	Signal rec	GO:00050	SL2.40ch	AT3G090	DEX1	DEX1 (DE	chr3:278	47.098	16.6983	18.1813	29.2943	2.13117	2.39982
GT	Sens	Sense	-0.200	Detected	0.200	Detected	0.000	-1.730	Detected	-1.003	Detected	-1.366	0.081	GT	Sens	contig272	contig272	Potassiu	TGGAGC	contig272	Solyc12g	Solyc12g	Potassiu	GO:00160	GO:00160	contig272	Solyc12g	Potassiu	GO:00160	SL2.40ch	AT2G266	AKT1. AT	AKT1 (AF	chr2:113	1049.31	1081.96	659.029	480.967	339.573	542.352
GT	Sens	Sense	0.052	Detected	-0.052	Detected	0.000	-1.433	Detected	-0.922	Detected	-1.178	0.046	GT	Sens	contig273	contig273	Unknown	AGCTTT	contig273	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig273	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G08570.1		pyruvate	chr5:277	79.8371	58.0264	44.8432	48.0286	26.6343	36.6519
GT	Sens	Sense	0.266	Detected	-0.266	Detected	0.000	-1.948	Detected	-1.130	Detected	-1.539	0.088	GT	Sens	contig273	contig273	Auxin res	AATTCT	contig273	Solyc06g	Solyc06g	Auxin res	GO:00056	GO:00056	contig273	Solyc06g	Auxin res	GO:00037	SL2.40ch	AT1G155	IAA5. AT	IAA5 (IND	chr1:536	58.3976	31.5745	13.617	11.8212	11.761	20.0202
GT	Sens	Sense	-0.278	Detected	0.278	Detected	0.000	-1.795	Detected	-0.898	Detected	-1.347	0.125	GT	Sens	contig273	contig273	Unknown	CTACAA	contig273	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig273	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G23890.1		LOCATE	chr5:805	1550.13	1781.52	1398.34	607.914	506.095	909.698
GT	Sens	Sense	-0.189	Detected	0.189	Detected	0.000	-1.973	Detected	-2.246	Detected	-2.109	0.012	GT	Sens	contig273	contig273	Integrase	GACTAC	contig273	Solyc10g	Solyc10g	Integrase core domain contair			contig273	Solyc08g	WD-repea	GO:00428	SL2.40ch	AT5G05350.1		unknowr	chr5:158	449.045	456.441	161.301	191.891	121.863	97.4027
GT	Sens	Sense	-0.342	Detected	0.342	Detected	0.000	-3.651	Detected	-1.483	Detected	-2.567	0.152	GT	Sens	contig274	contig274	Acyltrans	TTGATG	contig274	Solyc05g	Solyc05g	Acyltrans	GO:00167	GO:00167	contig274	Solyc05g	Acyltrans	GO:00167	SL2.40ch	AT2G20340.1		tyrosine	chr2:877	620.995	779.341	335.169	83.1417	58.5302	253.91
GT	Sens	Sense	0.147	Detected	-0.147	Detected	0.000	-0.840	Detected	-1.273	Detected	-1.056	0.056	GT	Sens	contig274	contig274	Unknown	ACTTTG	contig274	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig274	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G52530.2		dentin si	chr5:213	29.0404	18.5126	36.0826	35.5519	13.6921	9.79067
GT	Sens	Sense	0.079	Detected	-0.079	Detected	0.000	-1.527	Detected	-1.609	Detected	-1.568	0.003	GT	Sens	contig274	contig274	Tir-nbs-lr	ACTACC	contig274	Solyc01g	Solyc01g	Tir-nbs-lr	GO:00312	GO:00312	contig274	Solyc01g102920.2.1				AT2G29310.1		tropinon	chr2:125	525.757	368.351	193.282	200.826	161.416	147.211
GT	Sens	Sense	-0.335	Detected	0.335	Detected	0.000	-2.428	Detected	-0.915	Detected	-1.671	0.181	GT	Sens	contig274	contig274	Myb-like	CTTCAC	contig274	Solyc12g	Solyc12g	Myb-like	GO:0045449		contig274	Solyc12g	Myb-like	GO:00454	SL2.40ch	AT4G04580.1		myb fam	chr4:229	2848.59	3541.83	2137.68	811.173	623.972	1718.7
GT	Sens	Sense	-0.775	Detected	0.775	Detected	0.000	-6.896	Detected	-1.338	Detected	-4.117	0.290	GT	Sens	contig275	contig275	Cytochro	CAGGAA	contig275	Solyc07g	Solyc07g	Cytochro	GO:00198	GO:00198	contig275	Solyc07g	Cytochro	GO:00198	SL2.40ch	AT3G610	CYP76C7	CYP76C7	chr3:225	4645.52	10630.3	3554.59	131.083	62.3798	2836.08
GT	Sens	Sense	-0.174	Detected	0.174	Detected	0.000	-2.444	Detected	-2.499	Detected	-2.472	0.005	GT	Sens	contig275	contig275	Unknown	AAGTTG	contig275	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig275	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G09770.1		meprin a	chr4:615	453.35	450.731	164.432	158.245	87.791	81.5842
GT	Sens	Sense	0.152	Detected	-0.152	Detected	0.000	-2.390	Detected	-1.425	Detected	-1.907	0.064	GT	Sens	contig275	contig275	Major alle	GAGGGT	contig275	Solyc12g	Solyc12g	Major alle	GO:00090	GO:00090	contig275	Solyc12g	Major alle	GO:00090	SL2.40ch	AT1G76770.1		heat sho	chr1:288	3775.41	2389.93	1535.14	656.11	605.655	1141.58
GT	Sens	Sense	-1.555	Detected	1.555	Detected	0.000	-3.603	Detected	-2.806	Detected	-3.204	0.184	GT	Sens	contig275	contig275	Unknown	TTCAAG	contig275	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig275	Solyc06g	Unknown Protein (A		SL2.40ch	AT1G687	AGP19. A	AGP19 (A	chr1:258	103.256	697.293	41.3105	4.22869	23.3433	39.1481
GT	Sens	Sense	0.077	Detected	-0.077	Detected	0.000	-1.315	Detected	-1.013	Detected	-1.164	0.021	GT	Sens	contig275	contig275	WRKY tra	ATCAAT	contig275	Solyc08g	Solyc08g	WRKY tra	GO:00037	GO:00037	contig275	Solyc08g	WRKY tra	GO:00037	SL2.40ch	AT1G808	WRKY40.	WRKY40	chr1:303	109.702	77.0654	60.6335	86.2239	39.052	46.489
GT	Sens	Sense	-0.033	Detected	0.033	Detected	0.000	-3.020	Comprom	-2.870	Comprom	-2.945	0.001	GT	Sens	contig275	contig275	NAC dom	TCCATC	contig275	Solyc11g	Solyc11g	NAC dom	GO:0045449		contig275	Solyc11g	NAC dom	GO:00454	SL2.40ch	AT1G627	VND5. AN	ANAC026	chr1:232	19.2414	15.741	4.21803	2.8668	2.26707	2.42824
GT	Sens	Sense	-0.249	Detected	0.249	Detected	0.000	-2.056	Detected	-1.537	Detected	-1.797	0.038	GT	Sens	contig275	contig275	Transfera	GTTGTA	contig275	Solyc02g	Solyc02g	Transfera	GO:00167	GO:00167	contig275	Solyc02g	Transfera	GO:00167	SL2.40ch	AT4G29250.1		transfera	chr4:144	503.713	556.305	382.878	885.992	134.503	186.065
GT	Sens	Sense	-0.082	Detected	0.082	Detected	0.000	-1.942	Detected	-1.421	Detected	-1.681	0.025	GT	Sens	contig276	contig276	Unknown	GTCTCG	contig276	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig276	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G036	SBE2.2	SBE2.2 (S	chr5:931	70.896	62.0882	34.9931	39.6204	18.2428	25.2901
GT	Sens	Sense	-0.136	Detected	0.136	Detected	0.000	-1.291	Detected	-0.837	Detected	-1.064	0.057	GT	Sens	contig276	contig276	Patatin-lil	AAGAAG	contig276	Solyc02g	Solyc02g	Patatin-lil	GO:00066	GO:00066	contig276	Solyc02g	Patatin-lil	GO:00046	SL2.40ch	AT2G265	PLP2. PL	PLA2A (F	chr2:112	41623.5	39287.2	29224.4	14039	17461.7	23098.4
GT	Sens	Sense	0.146	Detected	-0.146	Detected	0.000	-1.573	Detected	-1.132	Detected	-1.353	0.036	GT	Sens	contig277	contig277	Cytokinin	ATCATA	contig277	Solyc01g	Solyc01g	Cytokinin riboside 5%26apos%			contig277	Solyc01g	Cytokinin riboside 5		SL2.40ch	AT5G03270.1		unknowr	chr5:781	857.18	547.247	735.988	301.677	243.332	318.778
GT	Sens	Sense	-0.373	Detected	0.373	Detected	0.000	-2.140	Detected	-1.790	Detected	-1.965	0.041	GT	Sens	contig277	contig277	Fatty acy	GATGGT	contig277	Solyc09g	Solyc09g	Fatty acy	GO:00160	GO:00160	contig277	Solyc09g	Fatty acy	GO:00160	SL2.40ch	AT3G567	FAR6	FAR6 (FA	chr3:209	280.171	367.138	206.041	643.106	76.9284	94.6392
GT	Sens	Sense	-0.206	Detected	0.206	Detected	0.000	-2.463	Comprom	-1.572	Comprom	-2.018	0.054	GT	Sens	contig277	contig277	Unknown	GGGCAT	contig277	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig277	Solyc08g	Unknown Protein (A		SL2.40ch	AT4G162	FCA	FCA: RN	chr4:920	16.9566	17.6416	10.8081	6.15378	3.31582	5.93461
GT	Sens	Sense	-0.206	Detected	0.206	Detected	0.000	-2.702	Detected	-1.350	Detected	-2.026	0.103	GT	Sens	contig277	contig277	Sigma fac	TTAATA	contig277	Solyc01g	Solyc01g	Sigma factor binding protein 1			contig277	Solyc01g	Sigma factor bindin		SL2.40ch	AT4G10480.2		nascent	chr4:647	2456.82	2553.79	1087.65	745.248	406.935	1002.73
GT	Sens	Sense	-0.270	Detected	0.270	Detected	0.000	-1.435	Detected	-0.860	Detected	-1.148	0.101	GT	Sens	contig277	contig277	ATP bind	AATACA	contig277	Solyc04g	Solyc04g	ATP bind	GO:00055	GO:00055	contig277	Solyc04g	ATP bind	GO:00055	SL2.40ch	AT4G356	CONNEXI	CONNEX	chr4:168	664.044	754.463	326.348	217.468	276.572	397.982
GT	Sens	Sense	-0.246	Detected	0.246	Detected	0.000	-1.786	Detected	-1.279	Detected	-1.532	0.049	GT	Sens	contig278	contig278	Avr9/Cf-9	CGCGGA	contig278	Solyc08g	Solyc08g	Avr9/Cf-9 rapidly elicited prote			contig278	Solyc08g	Avr9/Cf-9 rapidly ele		SL2.40ch	AT4G178	UBP20	UBP20 (U	chr4:993	2083.35	2288.87	1207.49	843.796	669.251	918.424
GT	Sens	Sense	-0.275	Detected	0.275	Detected	0.000	-1.320	Detected	-0.818	Detected	-1.069	0.103	GT	Sens	contig278	contig278	Late emb	CCCTCT	contig278	Solyc01g	Solyc01g	Late emb	GO:00092	GO:00092	contig278	Solyc01g	Late emb	GO:00092	SL2.40ch	AT4G21060.1		galactos	chr4:112	14389.2	16462.3	11796.7	5674.69	6514.82	8906.76
GT	Sens	Sense	0.029	Detected	-0.029	Detected	0.000	-1.092	Detected	-1.591	Comprom	-1.342	0.033	GT	Sens	contig279	contig279	Transcrip	CAGAAA	contig279	Solyc12g	Solyc12g	Transcription factor (Fragmen			contig279	Solyc12g	Transcription factor		SL2.40ch	AT5G12980.1				25.2193	18.9469	15.9014	16.4586	10.8353	7.40187
GT	Sens	Sense	0.322	Detected	-0.322	Detected	0.000	-1.608	Detected	-1.394	Detected	-1.501	0.048	GT	Sens	contig279	contig279	F-box fan	AAATGC	contig279	Solyc02g	Solyc02g	F-box family protein (AHRD V1			contig279	Solyc02g	F-box family protein		SL2.40ch	AT4G08280.1		FUNCTIC	chr4:523	80.135	40.0643	63.7378	18.6531	19.6479	21.9964
GT	Sens	Sense	-0.137	Detected	0.137	Detected	0.000	-1.106	Detected	-1.032	Detected	-1.069	0.017	GT	Sens	contig280	contig280	Carboxyl-	TTGTTA	contig280	Solyc11g	Solyc11g	Carboxyl-terminal peptidase (/			contig280	Solyc04g	Transcrip	GO:00056	SL2.40ch	AT4G050	NDB2	NDB2 (N/	chr4:257	131.267	124.075	104.824	67.3337	62.6409	63.6938
GT	Sens	Sense	-0.076	Detected	0.076	Detected	0.000	-1.344	Detected	-0.889	Detected	-1.117	0.043	GT	Sens	contig280	contig280	Unknown	AATTGG	contig280	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)%			contig280	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G27220.1		protein t	chr5:957	73.9703	64.2405	64.1415	54.4971	28.6986	37.9803
GT	Sens	Sense	-0.467	Detected	0.467	Detected	0.000	-2.309	Detected	-1.211	Detected	-1.760	0.135	GT	Sens	contig280	contig280	Unknown	TTGTTT	contig280	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig280	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G11000.1		unknowr	chr5:347	1052.13	1572.06	879.538	384.323	274.281	566.665
GT	Sens	Sense	-0.158	Detected	0.158	Detected	0.000	-1.112	Detected	-1.124	Detected	-1.118	0.019	GT	Sens	contig280	contig280	Paired an	AAGAGA	contig280	Solyc04g	Solyc04g	Paired an	GO:00056	GO:00056	contig280	Solyc01g	Rapid alk	GO:00048	SL2.40ch	AT2G36325.1		hydrolas	chr2:152	123.55	120.214	76.5939	74.4399	59.5784	57.0618
GT	Sens	Sense	-0.422	Detected	0.422	Detected	0.000	-2.024	Detected	-1.526	Detected	-1.775	0.068	GT	Sens	contig280	contig280	S-adenos	GAAGTT	contig280	Solyc00g	Solyc00g	S-adenos	GO:00081	GO:00081	contig280	Solyc00g	S-adenos	GO:00087	SL2.40ch	AT5G37990.1		S-adenos	chr5:151	161.162	226.07	114.56	202.17	49.6064	67.6085
GT	Sens	Sense	-0.134	Detected	0.134	Detected	0.000	-1.914	Detected	-2.164	Detected	-2.039	0.008	GT	Sens	contig280	contig280	Reverse t	TCCAGG	contig280	Solyc10g	Solyc10g	Reverse transcriptase (Fragm			contig280	Solyc03g	Transpos	GO:00030	SL2.40ch	AT5G61780.1				433.126	407.916	148.995	165.864	117.898	95.6975
GT	Sens	Sense	-0.398	Detected	0.398	Detected	0.000	-2.214	Detected	-1.282	Detected	-1.748	0.104	GT	Sens	contig281	contig281	(R)-limon	CCTTAT	contig281	Solyc01g	Solyc01g	(R)-limon	GO:00168	GO:00168	contig281	Solyc01g	(R)-limon	GO:00168	SL2.40ch	AT3G25810.1		myrcene	chr3:943	129.361	175.593	98.356	249.712	34.3431	63.2173
GT	Sens	Sense	-0.293	Detected	0.293	Detected	0.000	-2.643	Comprom	-1.709	Comprom	-2.176	0.059	GT	Sens	contig281	contig281	Oligopep	CAACTA	contig281	Solyc02g	Solyc02g	Oligopep	GO:00151	GO:00151	contig281	Solyc02g	Oligopep	GO:00151	SL2.40ch	AT5G535	YSL3. AT	YSL3 (YE	chr5:217	10.2771	12.0553	4.47381	3.05769	1.88297	3.47493
GT	Sens	Sense	-0.164	Detected	0.164	Detected	0.000	-3.874	Detected	-0.998	Detected	-2.436	0.234	GT	Sens	contig281	contig281	Legumin	AGTTGG	contig281	Solyc01g	Solyc01g	Legumin	GO:00082	GO:00082	contig281	Solyc01g	Legumin	GO:00082	SL2.40ch	AT3G52700.1		unknowr	chr3:195	26.9298	26.4186	13.5384	2.13663	1.92251	13.6311
GT	Sens	Sense	-0.170	Detected	0.170	Detected	0.000	-0.940	Detected	-1.447	Detected	-1.193	0.060	GT	Sens	contig282	contig282	Light-dep	GCTATT	contig282	Solyc04g	Solyc04g	Light-dependent short hypocc			contig282	Solyc04g	Light-dependent sh		SL2.40ch	AT3G045	LSH2	LSH2 (LI	chr3:121	379.323	375.531	303.688	426.674	207.978	141.268
GT	Sens	Sense	0.240	Detected	-0.240	Detected	0.000	-1.612	Detected	-1.595	Detected	-1.604	0.022	GT	Sens	contig282	contig282	FAD-bind	TTCAGA	contig282	Solyc02g	Solyc02g	FAD-bind	GO:00050	GO:00050	contig282	Solyc02g	FAD-bind	GO:00551	SL2.40ch	AT4G20860.1		FAD-bind	chr4:111	95.1218	53.3055	38.4172	17.7664	24.6155	24.0496
GT	Sens	Sense	-0.029	Detected	0.029	Detected	0.000	-2.628	Comprom	-1.525	Comprom	-2.076	0.064	GT	Sens	contig282	contig282	Unknown	ATCTTC	contig282	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig282	Solyc05g	Unknown Protein (A		SL2.40ch	AT4G38770.1				17.0684	13.8931	11.3083	6.09566	2.63343	5.45955
GT	Sens	Sense	-0.026	Detected	0.026	Detected	0.000	-1.605	Detected	-1.027	Detected	-1.316	0.045	GT	Sens	contig282	contig282	Heat shoc	CATGAT	contig282	Solyc01g	Solyc01g	Heat shoc	GO:00055	GO:00055	contig282	Solyc01g	Heat shoc	GO:00055	SL2.40ch	AT5G285	BIP1	BIP1: AT	chr5:105	44.6494	36.1962	18.3901	14.5702	13.9633	20.1234
GT	Sens	Sense	-1.995	Detected	1.995	Detected	0.000	-1.694	Detected	-1.778	Detected	-1.736	0.476	GT	Sens	contig283	contig283	Pentatric	GGAAAC	contig283	Solyc11g	Solyc11g	Pentatricopeptide repeat-conta			contig283	Solyc11g	Pentatricopeptide re		SL2.40ch	AT3G13880.1		pentatric	chr3:457	10.2554	127.434	16.3174	11.218	11.8084	10.7545
GT	Sens	Sense	0.391	Detected	-0.391	Detected	0.000	-1.138	Detected	-1.438	Detected	-1.288	0.091	GT	Sens	contig283	contig283	Squamos	ATAAAG	contig283	Solyc07g	Solyc07g	Squamos	GO:00056	GO:00056	contig283	Solyc07g	Squamos	GO:00056	SL2.40ch	AT2G338	SPL3	SPL3 (SC	chr2:143	75.3513	34.255	32.0547	24.8881	24.3986	19.1316
GT	Sens	Sense	-0.035	Detected	0.035	Detected	0.000	-1.837	Detected	-0.953	Detected	-1.395	0.088	GT	Sens	contig283	contig283	Unknown	ACATTT	contig283	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig283	Solyc09g	Mutator-like transpc		SL2.40ch	AT1G597	ARF1	ARF1 (AU	chr1:219	60.9429	50.019	36.5604	37.443	16.3362	29.095
GT	Sens	Sense	-0.533	Detected	0.533	Detected	0.000	-1.448	Detected	-2.275	Detected	-1.862	0.110	GT	Sens	contig283	contig283	DNA-direc	CAGATA	contig283	Solyc01g	Solyc01g	DNA-direc	GO:0006350		contig283	Solyc01g	DNA-direc	GO:00063	SL2.40ch	ATCG007	RPOA	RNA poly	chrC:775	48.3253	79.0798	90.561	90.8972	23.9404	13.0346
GT	Sens	Sense	0.056	Detected	-0.056	Detected	0.000	-0.946	Detected	-1.086	Detected	-1.016	0.008	GT	Sens	contig283	contig283	Unknown	GAGGTG	contig283	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig283	Solyc00g005170.1.1				AT4G00755.2		F-box far	chr4:325	66.4986	48.0838	53.4222	52.5964	31.0221	27.1734
GT	Sens	Sense	-0.195	Detected	0.195	Detected	0.000	-2.461	Detected	-1.594	Detected	-2.027	0.051	GT	Sens	contig283	contig283	Ribosom	TCATAG	contig283	Solyc09g	Solyc09g	Ribosom	GO:00081	GO:00081	contig283	Solyc09g	Ribosom	GO:00089	SL2.40ch	AT2G32020.1		GCN5-rel	chr2:136	2017.9	2066.76	1107.82	374.614	391.958	690.338
GT	Sens	Sense	-0.489	Detected	0.489	Detected	0.000	-3.045	Comprom	-2.107	Comprom	-2.576	0.063	GT	Sens	contig284	contig284	Ethylene-	ACGTTT	contig284	Solyc11g	Solyc11g	Ethylene-	GO:00063	GO:00063	contig284	Solyc11g	Ethylene-	GO:00030	SL2.40ch	AT2G40340.1		AP2 dom	chr2:168	25.1943	38.792	12.8621	10.282	4.00192	7.40302
GT	Sens	Sense	-1.005	Detected	1.005	Detected	0.000	-2.484	Detected	-2.041	Detected	-2.263	0.159	GT	Sens	contig284	contig284	Germin-li	TTGAGC	contig284	Solyc10g	Solyc10g	Germin-li	GO:00048	GO:00048	contig284	Solyc10g	Germin-li	GO:00457	SL2.40ch	AT4G19910.1		Toll-Inter	chr4:107	40.5471	127.63	77.5905	17.3239	13.5905	17.8324
GT	Sens	Sense	-0.274	Detected	0.274	Detected	0.000	-1.558	Detected	-0.881	Detected	-1.219	0.107	GT	Sens	contig284	contig284	BHLH trai	AAACAA	contig284	Solyc03g	Solyc03g	BHLH trai	GO:00056	GO:00056	contig284	Solyc03g	BHLH trai	GO:00056	SL2.40ch	AT1G61660.2		basic hel	chr1:227	27.1593	31.0212	13.9798	10.9393	10.4172	16.0852
GT	Sens	Sense	-0.200	Detected	0.200	Detected	0.000	-0.928	Detected	-3.010	Comprom	-1.969	0.204	GT	Sens	contig284	contig284	Unknown	TTATGA	contig284	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig284	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G66170.2		FUNCTIC	chr5:264	17.5179	18.0602	4.11526	4.87074	9.87776	2.25337
GT	Sens	Sense	-0.004	Detected	0.004	Detected	0.000	-2.058	Detected	-1.089	Detected	-1.574	0.083	GT	Sens	contig284	contig284	Beta-gala	TTCCAT	contig284	Solyc11g	Solyc11g	Beta-gala	GO:00055	GO:00055	contig284	Solyc11g	Beta-gala	GO:00055	SL2.40ch	AT2G328	BGAL9	BGAL9 (I	chr2:139	128.664	101.075	33.0413	42.4034	28.9371	54.6977
GT	Sens	Sense	0.074	Detected	-0.074	Detected	0.000	-1.556	Detected	-0.825	Detected	-1.191	0.086	GT	Sens	contig285	contig285	GAI-like p	AAGTTG	contig285	Solyc01g	Solyc01g	GAI-like p	GO:00037	GO:00037	contig285	Solyc01g	GAI-like p	GO:00037	SL2.40ch	AT1G744	FUT3. AT	FUT3 (FU	chr1:279	44.0712	31.0841	25.4228	5.31341	13.299	21.3136
GT	Sens	Sense	0.046	Detected	-0.046	Detected	0.000	-2.433	Comprom	-1.974	Comprom	-2.204	0.011	GT	Sens	contig285	contig285	Unknown	TGAAAT	contig285	Solyc02g	Solyc02g	Unknown	GO:00160	GO:00160	contig285	Solyc03g	SPFH domain/band		SL2.40ch	AT5G22550.2		unknowr	chr5:748	39.6373	29.056	26.9482	41.8758	6.63961	8.8132
GT	Sens	Sense	0.152	Detected	-0.152	Detected	0.000	-1.214	Detected	-1.830	Comprom	-1.522	0.047	GT	Sens	contig285	contig285	SUPERM	TTTCAA	contig285	Solyc10g	Solyc10g	SUPERM	GO:00056	GO:00056	contig285	Solyc06g	Tubulin b	GO:00052	SL2.40ch	AT5G12410.1				29.9404	18.9443	16.023	16.4796	10.8483	6.83257
GT	Sens	Sense	-0.167	Detected	0.167	Detected	0.000	-1.917	Comprom	-1.390	Comprom	-1.653	0.034	GT	Sens	contig285	contig285	Unknown	GATCGA	contig285	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig285	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G171	ENH1	ENH1 (en	chr5:564	13.5489	13.3447	10.7062	6.06447	3.76435	5.23592
GT	Sens	Sense	-0.251	Detected	0.251	Detected	0.000	-1.339	Detected	-0.881	Detected	-1.110	0.082	GT	Sens	contig286	contig286	Receptor	CTGATA	contig286	Solyc09g	Solyc09g	Receptor	GO:00163	GO:00163	contig286	Solyc09g	Receptor	GO:00163	SL2.40ch	AT5G59260.1		lectin pro	chr5:239	1103.23	1221.22	482.514	386.323	484.846	642.879
GT	Sens	Sense	-0.015	Detected	0.015	Detected	0.000	-1.766	Detected	-0.970	Detected	-1.368	0.075	GT	Sens	contig286	contig286	Aspartic p	TTTCCA	contig286	Solyc07g	Solyc07g	Aspartic p	GO:00065	GO:00065	contig286	Solyc07g	Aspartic p	GO:00030	SL2.40ch	AT2G42980.1		aspartyl	chr2:178	2255.4	1800.66	1194.76	536.145	626.02	1049.99
GT	Sens	Sense	-0.045	Detected	0.045	Detected	0.000	-1.588	Detected	-1.587	Detected	-1.588	0.001	GT	Sens	contig286	contig286	Pol polyp	TGACCA	contig286	Solyc10g	Solyc10g	Pol polyp	GO:00030	GO:00030	contig286	Solyc10g	Pol polyp	GO:00030	SL2.40ch	AT3G073	ATCSLC0	ATCSLC0	chr3:233	93.2455	77.5329	40.9293	56.1014	29.8941	28.8731
GT	Sens	Sense	-0.131	Detected	0.131	Detected	0.000	-1.063	Detected	-1.367	Detected	-1.215	0.026	GT	Sens	contig287	contig287	NADH del	TATATA	contig287	Solyc01g	Solyc01g	NADH del	GO:00055	GO:00055	contig287	Solyc01g	NADH del	GO:00055	SL2.40ch	ATCG010	NDHF	Chloropl	chrC:110	338.678	317.617	214.758	229.76	165.945	129.765
GT	Sens	Sense	-0.093	Detected	0.093	Detected	0.000	-1.331	Detected	-1.619	Detected	-1.475	0.013	GT	Sens	contig287	contig287	Unknown	AATAGA	contig287	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig287	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G48960.1		5' nucleo	chr5:198	804.824	715.943	278.034	338.616	318.987	252.234
GT	Sens	Sense	-0.264	Detected	0.264	Detected	0.000	-1.647	Detected	-1.312	Comprom	-1.479	0.042	GT	Sens	contig288	contig288	TIR-NBS-	CTGAGG	contig288	Solyc01g	Solyc01g	TIR-NBS-	GO:00048	GO:00048	contig288	Solyc01g	Tir-nbs-lr	GO:00301	SL2.40ch	AT3G44670.2		ATP bind	chr3:162	13.2608	14.9563	10.0654	7.52326	4.75366	5.78848
GT	Sens	Sense	-0.104	Detected	0.104	Detected	0.000	-0.961	Detected	-1.264	Detected	-1.113	0.026	GT	Sens	contig288	contig288	Unknown	ACCAGC	contig288	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig288	Solyc04g	Unknown Protein (A		SL2.40ch	AT2G44020.1		mitochor	chr2:182	77.9246	70.3337	51.8847	43.9002	40.1914	31.4425
GT	Sens	Sense	-0.136	Detected	0.136	Detected	0.000	-0.876	Detected	-1.549	Detected	-1.212	0.079	GT	Sens	contig289	contig289	NAD(P)H-	AAATTG	contig289	Solyc08g	Solyc08g	NAD(P)H-quinone oxidoreduct			contig289	Solyc08g	NAD(P)H-quinone o		SL2.40ch	AT3G01210.1		nucleic a	chr3:721	617.221	582.654	406.404	405.487	345.341	209.153
GT	Sens	Sense	-0.292	Detected	0.292	Detected	0.000	-1.220	Detected	-1.043	Detected	-1.132	0.066	GT	Sens	contig289	contig289	Endo-1 4	GGTGAA	contig289	Solyc01g	Solyc01g	Endo-1 4	GO:00055	GO:00055	contig289	Solyc01g	Endo-1 4	GO:00055	SL2.40ch	AT4G38300.1		glycosyl	chr4:179	453.048	530.812	434.669	487.213	222.411	242.77
GT	Sens	Sense	-0.669	Detected	0.669	Detected	0.000	-3.627	Detected	-0.945	Detected	-2.286	0.267	GT	Sens	contig289	contig289	Geranylg	CTACTT	contig289	Solyc07g	Solyc07g	Geranylg	GO:00082	GO:00082	contig289	Solyc07g	Geranylg	GO:00043	SL2.40ch	AT2G36710.1		pectines	chr2:153	1197.18	2365.17	1153.56	110.265	143.954	891.726
GT	Sens	Sense	0.107	Detected	-0.107	Detected	0.000	-1.208	Detected	-0.837	Detected	-1.022	0.041	GT	Sens	contig289	contig289	VO motif	GCTGGA	contig289	Solyc04g	Solyc04g	VO motif family protein expres			contig289	Solyc04g	VO motif family prot		SL2.40ch	AT1G75150.1		unknowr	chr1:282	4002.45	2698.65	2404.96	1562.02	1503.56	1877.33
GT	Sens	Sense	-0.471	Detected	0.471	Detected	0.000	-1.197	Detected	-1.284	Detected	-1.241	0.120	GT	Sens	contig290	contig290	Expresse	GTTGAG	contig290	Solyc01g	Solyc01g	Expressed protein (Fragment)			contig290	Solyc01g	Expressed protein (		SL2.40ch	AT1G09610.1		unknowr	chr1:311	114.842	172.425	77.9225	170.915	64.859	58.9457
GT	Sens	Sense	-0.003	Detected	0.003	Detected	0.000	-1.983	Detected	-1.508	Detected	-1.746	0.018	GT	Sens	contig290	contig290	Unknown	AGAGGA	contig290	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig290	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G61240.1		protein b	chr5:246	39.9567	31.3506	18.4422	24.8664	9.45901	12.6973
GT	Sens	Sense	0.186	Detected	-0.186	Detected	0.000	-1.473	Detected	-1.541	Detected	-1.507	0.015	GT	Sens	contig290	contig290	Unknown	CATTTA	contig290	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig290	Solyc10g	Transport protein p		SL2.40ch	AT5G439	MYA2. AT	MYA2 (AI	chr5:176	371.553	224.303	299.416	249.931	109.899	101.259
GT	Sens	Sense	0.013	Detected	-0.013	Detected	0.000	-2.895	Detected	-1.106	Detected	-2.001	0.155	GT	Sens	contig291	contig291	Unknown	TCATTG	contig291	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig291	Solyc05g	Unknown Protein (A		SL2.40ch	AT2G05360.1		FUNCTIC	chr2:195	1732.8	1329.71	1155.72	267.24	215.628	719.564
GT	Sens	Sense	-0.239	Detected	0.239	Detected	0.000	-1.439	Comprom	-2.303	Comprom	-1.871	0.063	GT	Sens	contig291	contig291	Unknown	AAATTG	contig291	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig291	Solyc10g	Unknown Protein (A		SL2.40ch	AT2G16890.2				11.7156	12.7598	10.0129	3.66101	4.76501	2.52818
GT	Sens	Sense	-0.261	Detected	0.261	Detected	0.000	-2.732	Detected	-1.014	Detected	-1.873	0.172	GT	Sens	contig292	contig292	Calmodul	AACAAG	contig292	Solyc12g	Solyc12g	Calmodulin-binding protein (A			contig292	Solyc12g	Calmodulin-binding		SL2.40ch	AT2G26190.1		calmodu	chr2:111	1794.47	2012.78	1209.07	481.262	302.419	960.088
GT	Sens	Sense	-0.285	Detected	0.285	Detected	0.000	-2.010	Detected	-0.842	Detected	-1.426	0.160	GT	Sens	contig293	contig293	Receptor	AACAGG	contig293	Solyc11g	Solyc11g	Receptor	GO:00055	GO:00055	contig293	Solyc11g	LRR rece	GO:00055	SL2.40ch	AT5G05030.1		unknowr	chr5:148	469.545	544.945	388.59	170.915	132.686	287.95
GT	Sens	Sense	-0.317	Detected	0.317	Detected	0.000	-2.189	Detected	-1.677	Detected	-1.933	0.042	GT	Sens	contig293	contig293	Major late	CCAAAT	contig293	Solyc07g	Solyc07g	Major late	GO:00090	GO:00090	contig293	Solyc07g	Major late	GO:00090	SL2.40ch	AT5G46770.1		unknowr	chr5:189	2310.49	2801.82	1224.28	3341.47	589.633	811.673
GT	Sens	Sense	0.443	Detected	-0.443	Detected	0.000	-1.046	Detected	-0.973	Detected	-1.009	0.151	GT	Sens	contig293	contig293	Transcrip	AACTCA	contig293	Solyc05g	Solyc05g	Transcrip	GO:00056	GO:00056	contig293	Solyc05g	Transcrip	GO:00055	SL2.40ch	AT1G242	SEP3. AG	SEP3 (SE	chr1:859	391.225	165.389	199.317	328.62	130.239	132.226
GT	Sens	Sense	-0.536	Detected	0.536	Detected	0.000	-3.610	Detected	-1.909	Detected	-2.759	0.111	GT	Sens	contig293	contig293	Vesicular	TCTAAT	contig293	Solyc09g	Solyc09g	Vesicular	GO:00053	GO:00053	contig293	Solyc09g	Vesicular	GO:00053	SL2.40ch	AT2G380	PHT4:2	PHT4:2 (I	chr2:159	780.149	1282.46	150.334	73.1772	86.6082	271.694
GT	Sens	Sense	-0.210	Detected	0.210	Detected	0.000	-3.590	Comprom	-1.941	Comprom	-2.766	0.083	GT	Sens	contig293	contig293	Ulp1 prot	GAAAGA	contig293	Solyc10g	Solyc10g	Ulp1 protease family C-termina			contig293	Solyc10g	Ulp1 protease family		SL2.40ch	AT3G44440.1				20.2186	21.1336	17.295	9.28512	1.81421	5.49252
GT	Sens	Sense	-0.918	Detected	0.918	Detected	0.000	-2.097	Comprom	-3.171	Comprom	-2.634	0.132	GT	Sens	contig293	contig293	Potassiu	AAGGGA	contig293	Solyc03g	Solyc03g	Potassiu	GO:00096	GO:00096	contig293	Solyc03g	Potassiu	GO:00096	SL2.40ch	AT2G381	AUX1. WA	AUX1 (AL	chr2:159	13.8266	38.5915	7.95906	11.9131	5.70716	2.61761
GT	Sens	Sense	0.089	Detected	-0.089	Detected	0.000	-1.350	Detected	-1.529	Detected	-1.440	0.008	GT	Sens	contig293	contig293	Potassiu	ATAAAG	contig293	Solyc08g	Solyc08g	Potassiu	GO:00305	GO:00305	contig293	Solyc08g	Potassiu	GO:00052	SL2.40ch	AT1G58390.1		disease r	chr1:216	545.71	376.792	530.552	405.554	188.022	160.291
GT	Sens	Sense	-0.121	Detected	0.121	Detected	0.000	-1.143	Detected	-2.132	Comprom	-1.637	0.085	GT	Sens	contig294	contig294	Nucleore	TTATAC	contig294	Solyc05g	Solyc05g	Nucleore	GO:00047	GO:00047	contig294	Solyc05g	Nucleore	GO:00047	SL2.40ch	AT5G196	ATSBT6.	S1P (SIT	chr5:664	21.9887	20.3265	14.6254	16.7821	10.1206	4.92064
GT	Sens	Sense	0.448	Detected	-0.448	Detected	0.000	-1.634	Detected	-1.671	Detected	-1.652	0.067	GT	Sens	contig294	contig294	Unknown	CTTGGT	contig294	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig294	Solyc04g	Unknown Protein (A		SL2.40ch	AT2G41330.1		glutared	chr2:172	419.386	176.039	155.059	282.1	92.5143	87.0813
GT	Sens	Sense	-0.144	Detected	0.144	Detected	0.000	-1.404	Detected	-1.834	Detected	-1.619	0.025	GT	Sens	contig294	contig294	F-box prc	CTTGGA	contig294	Solyc01g	Solyc01g	F-box prc	GO:00302	GO:00302	contig294	Solyc01g	F-box prc	GO:00302	SL2.40ch	AT2G023	AtPP2-B7	AtPP2-B7	chr2:610	8208.96	7831.17	5688.25	4356.29	3200.98	2294.37
GT	Sens	Sense	-0.009	Detected	0.009	Detected	0.000	-1.490	Detected	-1.465	Detected	-1.477	0.000	GT	Sens	contig294	contig294	Unknown	AATAAA	contig294	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig294	Solyc05g	UDP-gluc	GO:00150	SL2.40ch	AT1G05370.1		FUNCTIC	chr1:156	286.598	226.874	300.985	310.675	95.924	94.2671
GT	Sens	Sense	-0.690	Detected	0.690	Detected	0.000	-2.984	Detected	-1.298	Detected	-2.141	0.188	GT	Sens	contig294	contig294	ATP-bind	AATGAC	contig294	Solyc09g	Solyc09g	ATP-bind	GO:00171	GO:00171	contig294	Solyc09g	ATP-bind	GO:00420	SL2.40ch	AT2G299	PDR3. AT	PDR3 (PL	chr2:127	3722.61	7572.03	1409.19	444.304	709.255	2203.05
GT	Sens	Sense	-0.312	Detected	0.312	Detected	0.000	-1.223	Detected	-0.876	Detected	-1.050	0.099	GT	Sens	contig294	contig294	Glucose-	AGGCCT	contig294	Solyc09g	Solyc09g	Glucose-	GO:00055	GO:00055	contig294	Solyc09g	Glucose-	GO:00160	SL2.40ch	AT1G03990.1		alcohol c	chr1:102	785.678	946.535	587.108	1318.41	390.359	479.334
GT	Sens	Sense	-0.141	Detected	0.141	Detected	0.000	-2.111	Detected	-2.362	Detected	-2.237	0.007	GT	Sens	contig295	contig295	Unknown	ACTAGA	contig295	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig295	Solyc00g	Unknown Protein (A		SL2.40ch	AT1G12000.1		pyropho	chr1:405	76.6485	72.8533	46.1204	48.0427	18.2818	14.8307
GT	Sens	Sense	-0.403	Detected	0.403	Detected	0.000	-1.354	Detected	-1.198	Detected	-1.276	0.090	GT	Sens	contig295	contig295	Unknown	TGACAC	contig295	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig295	Solyc01g	Unknown Protein (A		SL2.40ch	AT1G084	BSL2	kelch rep	chr1:264	237.428	324.659	199.197	257.978	114.756	123.516
GT	Sens	Sense	-0.122	Detected	0.122	Detected	0.000	-2.656	Detected	-1.302	Detected	-1.979	0.103	GT	Sens	contig296	contig296	Glutared	GAAAAT	contig296	Solyc10g	Solyc10g	Glutared	GO:00454	GO:00454	contig296	Solyc10g	Glutared	GO:00454	SL2.40ch	AT1G03850.2		glutared	chr1:977	487.76	451.657	199.685	87.0383	78.7286	194.237
GT	Sens	Sense	-0.111	Detected	0.111	Detected	0.000	-1.387	Detected	-1.642	Detected	-1.515	0.012	GT	Sens	contig296	contig296	Gag-Pol p	TATTAA	contig296	Solyc04g	Solyc04g	Gag-Pol polyprotein (AHRD V1			contig296	Solyc04g	Gag-Pol polyprotein		SL2.40ch	AT3G05345.1		heat sho	chr3:152	380.11	346.618	212.891	195.039	146.673	118.671
GT	Sens	Sense	-0.079	Detected	0.079	Detected	0.000	-1.152	Detected	-1.123	Detected	-1.137	0.005	GT	Sens	contig296	contig296	Unknown	ATTAAA	contig296	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig296	Solyc08g	Unknown Protein (A		SL2.40ch	AT4G252	RIN2	RIN2 (RP	chr4:129	66.3971	57.8989	48.8367	41.5081	29.4938	29.0415
GT	Sens	Sense	0.250	Detected	-0.250	Detected	0.000	-1.168	Detected	-1.205	Detected	-1.187	0.042	GT	Sens	contig296	contig296	Receptor	AAACCA	contig296	Solyc07g	Solyc07g	Receptor	GO:00064	GO:00064	contig296	Solyc07g064130.1.1				AT4G22890.5				44.8919	24.8046	19.981	16.4195	15.6917	14.7687
GT	Sens	Sense	0.089	Detected	-0.089	Detected	0.000	-1.980	Detected	-2.063	Detected	-2.022	0.002	GT	Sens	contig296	contig296	Pol polyp	TTCTGA	contig296	Solyc00g	Solyc00g	Pol polyp	GO:00062	GO:00062	contig296	Solyc00g	Pol polyp	GO:00062	SL2.40ch	AT4G099	EMB1691	EMB1691	chr4:624	75.0104	51.8178	27.6045	38.9217	16.7018	15.2207
GT	Sens	Sense	0.242	Detected	-0.242	Detected	0.000	-2.501	Detected	-2.332	Detected	-2.417	0.011	GT	Sens	contig296	contig296	Monooxy	GGGGAA	contig296	Solyc09g	Solyc09g	Monooxy	GO:00551	GO:00551	contig296	Solyc09g	Monooxy	GO:00551	SL2.40ch	AT3G14170.1		unknowr	chr3:469	2814.44	1572.15	1206.52	835.801	392.621	426.384
GT	Sens	Sense	-0.165	Detected	0.165	Detected	0.000	-1.612	Comprom	-1.266	Comprom	-1.439	0.026	GT	Sens	contig297	contig297	Ulp1 prot	ACTACC	contig297	Solyc06g	Solyc06g	Ulp1 protease family C-termina			contig297	Solyc06g	Ulp1 protease family		SL2.40ch	AT5G44180.1		homeobo	chr5:177	12.3179	12.0961	11.1453	14.9221	4.22058	5.18046
GT	Sens	Sense	0.142	Detected	-0.142	Detected	0.000	-1.214	Detected	-1.108	Detected	-1.161	0.017	GT	Sens	contig297	contig297	Unknown	ACGGCT	contig297	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig297	Solyc06g048800.1.1				AT1G324	EMB2733	ESP3 (EN	chr1:117	405.202	260.251	202.109	222.255	147.968	153.693
GT	Sens	Sense	-0.715	Detected	0.715	Detected	0.000	-4.019	Detected	-1.658	Detected	-2.838	0.176	GT	Sens	contig297	contig297	Calmodul	CTTTCT	contig297	Solyc02g	Solyc02g	Calmodul	GO:00055	GO:00055	contig297	Solyc02g	Calmodul	GO:00055	SL2.40ch	AT3G59120.1		DC1 dom	chr3:218	3613.67	7615.46	2580.4	488.573	342.052	1696.22
GT	Sens	Sense	-0.289	Detected	0.289	Detected	0.000	-1.277	Detected	-1.041	Detected	-1.159	0.066	GT	Sens	contig298	contig298	Serine/thr	ATCAGT	contig298	Solyc02g	Solyc02g	Serine/thr	GO:00047	GO:00047	contig298	Solyc02g	RLK. Rec	GO:00047	SL2.40ch	AT2G356	FEI2	FEI2 (FEI	chr2:149	31.6533	36.9419	22.5639	12.6298	14.9083	16.9516
GT	Sens	Sense	0.130	Detected	-0.130	Detected	0.000	-1.434	Detected	-0.857	Detected	-1.145	0.069	GT	Sens	contig298	contig298	Receptor	GTTAAG	contig298	Solyc09g	Solyc09g	Receptor	GO:0005529		contig298	Solyc09g	Receptor	GO:00048	SL2.40ch	AT4G04490.1		protein k	chr4:223	3791.24	2474.94	2040.68	1573.67	1198.32	1725.68
GT	Sens	Sense	-0.164	Detected	0.164	Detected	0.000	-0.901	Detected	-1.694	Detected	-1.298	0.094	GT	Sens	contig298	contig298	Cytochro	GTTATC	contig298	Solyc08g	Solyc08g	Cytochro	GO:00160	GO:00160	contig298	Solyc08g	Cytochro	GO:00058	SL2.40ch	ATMG005	RPL2	encodes	chrM:15	250.867	246.176	172.134	206.908	140.653	78.3671
GT	Sens	Sense	0.139	Detected	-0.139	Detected	0.000	-1.900	Comprom	-1.740	Comprom	-1.820	0.008	GT	Sens	contig298	contig298	Unknown	AATGGT	contig298	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig298	Solyc08g	Helicase-	GO:00054	SL2.40ch	AT1G76140.2		serine-ty	chr1:285	19.8612	12.8077	15.0158	16.2006	4.51793	4.87124
GT	Sens	Sense	-0.452	Detected	0.452	Detected	0.000	-1.918	Detected	-1.370	Detected	-1.644	0.090	GT	Sens	contig299	contig299	Unknown	CTTCCA	contig299	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)%			contig299	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G054	DDB1A	DDB1A (I	chr4:274	1019.88	1492.53	834.757	2283.42	345.14	487.15
GT	Sens	Sense	-0.139	Detected	0.139	Detected	0.000	-1.241	Detected	-0.842	Detected	-1.041	0.051	GT	Sens	contig299	contig299	Cell numl	CTGTTT	contig299	Solyc01g	Solyc01g	Cell number regulator 10 (AHR			contig299	Solyc01g	Cell number regulat		SL2.40ch	AT3G18470.1		unknowr	chr3:633	83229.5	78918.9	69104.4	34543.7	36250.3	46143.6
GT	Sens	Sense	-0.475	Detected	0.475	Detected	0.000	-0.958	Detected	-1.206	Detected	-1.082	0.158	GT	Sens	contig299	contig299	UPA23 (A	TATGGT	contig299	Solyc06g	Solyc06g	UPA23 (AHRD V1 ***- C8YZB5			contig299	Solyc06g	UPA23 (AHRD V1 ***		SL2.40ch	AT1G35830.1		VO motif	chr1:133	195.212	294.728	148.712	59.2617	130.495	106.085
GT	Sens	Sense	-0.350	Detected	0.350	Detected	0.000	-2.077	Detected	-1.195	Detected	-1.636	0.101	GT	Sens	contig299	contig299	Unknown	GAGTCC	contig299	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig299	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G540	AT-HSFA	AT-HSFA	chr5:219	598.525	759.86	357.561	181.823	168.973	300.478
GT	Sens	Sense	-0.044	Detected	0.044	Detected	0.000	-0.822	Detected	-1.391	Detected	-1.107	0.061	GT	Sens	contig299	contig299	1-aminoc	TATTCA	contig299	Solyc06g	Solyc06g	1-aminoc	GO:00164	GO:00164	contig299	Solyc06g	1-aminoc	GO:00454	SL2.40ch	AT1G293	UNE1	UNE1 (ur	chr1:102	68.9971	57.3134	39.4164	44.4234	37.5892	24.4621
GT	Sens	Sense	-0.331	Detected	0.331	Detected	0.000	-4.533	Detected	-1.179	Detected	-2.856	0.237	GT	Sens	contig300	contig300	ABC tran	TGATAT	contig300	Solyc03g	Solyc03g	ABC transporter family proteir			contig300	Solyc03g	ABC transporter fan		SL2.40ch	AT5G19130.2		GPI trans	chr5:641	2973.48	3679.62	1579.79	135.819	150.956	1491.14
GT	Sens	Sense	-0.097	Detected	0.097	Detected	0.000	-2.675	Detected	-1.416	Detected	-2.046	0.085	GT	Sens	contig300	contig300	Unknown	CTCATG	contig300	Solyc10g	Solyc10g	Unknown Protein (AHRD V1):O			contig300	Solyc11g068390.1.1				AT3G28770.1		unknowr	chr3:107	108.652	97.1965	47.2343	43.3276	17.0081	39.2821
GT	Sens	Sense	-0.090	Detected	0.090	Detected	0.000	-1.539	Detected	-1.080	Detected	-1.310	0.034	GT	Sens	contig300	contig300	Os03g081	AGTATA	contig300	Solyc10g	Solyc10g	Os03g0816700 protein (Fragm			contig300	Solyc10g	Os03g0816700 prot		SL2.40ch	AT3G12020.1		kinesin r	chr3:382	6525.35	5781.55	4124.58	2218.1	2233.37	2964.52
GT	Sens	Sense	-0.030	Detected	0.030	Detected	0.000	-1.295	Detected	-1.243	Detected	-1.269	0.001	GT	Sens	contig300	contig300	Unknown	TTAAGT	contig300	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig300	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G324	PKp3	PKp3 (pl	chr1:117	29.575	24.114	14.5461	10.6932	11.4985	11.5138
GT	Sens	Sense	0.227	Detected	-0.227	Detected	0.000	-1.140	Detected	-0.988	Detected	-1.064	0.047	GT	Sens	contig300	contig300	Unknown	GTATTT	contig300	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig300	Solyc10g036650.1.1				AT4G31100.1		wall-ass	chr4:151	1653.86	943.339	1444.26	989.344	598.889	642.683
GT	Sens	Sense	-0.139	Detected	0.139	Detected	0.000	-2.009	Detected	-0.968	Detected	-1.489	0.110	GT	Sens	contig301	contig301	Unknown	TAAATT	contig301	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig301	Solyc02g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	14125.6	13392.2	11192.5	3069.13	3611.38	7172.92
GT	Sens	Sense	-0.498	Detected	0.498	Detected	0.000	-2.345	Detected	-1.052	Detected	-1.698	0.173	GT	Sens	contig301	contig301	F-box fan	GGTATT	contig301	Solyc11g	Solyc11g	F-box family protein (AHRD V1			contig301	Solyc11g	F-box family protein		SL2.40ch	AT3G57180.1		GTP bind	chr3:211	49.5108	77.1816	39.5363	16.9358	12.8626	30.4256
GT	Sens	Sense	-0.367	Detected	0.367	Detected	0.000	-0.892	Detected	-1.515	Detected	-1.203	0.130	GT	Sens	contig301	contig301	Galactosy	CTTTTA	contig301	Solyc09g	Solyc09g	Galactosy	GO:00150	GO:00150	contig301	Solyc09g	Galactosy	GO:00150	SL2.40ch	AT2G370	IRX9	IRX9 (IRF	chr2:155	67.073	87.1685	54.0804	79.808	43.5506	27.3002
GT	Sens	Sense	0.035	Detected	-0.035	Detected	0.000	-1.841	Comprom	-1.872	Comprom	-1.856	0.000	GT	Sens	contig301	contig301	Expansin	GATCAC	contig301	Solyc07g	Solyc07g	Expansin	GO:00051	GO:00051	contig301	Solyc07g	Expansin	GO:00051	SL2.40ch	AT4G016	ATEXPA1	ATEXPA1	chr4:700	15.2409	11.3492	12.8637	5.91464	3.88108	3.6651
GT	Sens	Sense	-0.274	Detected	0.274	Detected	0.000	-2.393	Detected	-1.014	Detected	-1.704	0.149	GT	Sens	contig302	contig302	Genomic	CTTCAA	contig302	Solyc11g	Solyc11g	Genomic DNA chromosome 5			contig302	Solyc11g	Genomic DNA chror		SL2.40ch	AT3G273	SDH2-1	SDH2-1:	chr3:101	56.1311	64.1805	37.0631	8.12579	12.0732	30.3254
GT	Sens	Sense	-0.063	Detected	0.063	Detected	0.000	-2.267	Detected	-1.247	Detected	-1.757	0.076	GT	Sens	contig302	contig302	Prephena	AAAGTT	contig302	Solyc09g	Solyc09g	Prephena	GO:00081	GO:00081	contig302	Solyc09g	Prephena	GO:00081	SL2.40ch	AT5G34930.1		arogenat	chr5:132	9226.03	7865.26	6450.12	1481.76	1870.26	3663.11
GT	Sens	Sense	0.165	Detected	-0.165	Detected	0.000	-3.566	Detected	-1.379	Detected	-2.472	0.155	GT	Sens	contig302	contig302	U-box do	GGGGGA	contig302	Solyc06g	Solyc06g	U-box do	GO:00054	GO:00054	contig302	Solyc06g	U-box do	GO:00048	SL2.40ch	AT2G40860.1		protein k	chr2:170	6266.07	3896.61	3372.23	1085.04	440.928	1938.93
GT	Sens	Sense	-0.036	Detected	0.036	Detected	0.000	-1.530	Detected	-0.948	Detected	-1.239	0.052	GT	Sens	contig302	contig302	Uncharac	TTGACG	contig302	Solyc01g	Solyc01g	Uncharacterized GPI-anchored			contig302	Solyc01g	Uncharacterized GP		SL2.40ch	AT5G462	CUL4. AT	CUL4 (CU	chr5:187	305.544	250.949	247.705	132.475	101.327	146.469
GT	Sens	Sense	-0.193	Detected	0.193	Detected	0.000	-1.876	Comprom	-1.431	Comprom	-1.653	0.030	GT	Sens	contig302	contig302	Unknown	ATGCGC	contig302	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig302	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G25415.1		unknowr	chr5:883	15.4209	15.7439	13.3093	8.2864	4.48627	5.8968
GT	Sens	Sense	0.186	Detected	-0.186	Detected	0.000	-1.087	Detected	-0.928	Detected	-1.008	0.038	GT	Sens	contig303	contig303	Serine/thr	GTCTGA	contig303	Solyc09g	Solyc09g	Serine/thr	GO:00199	GO:00199	contig303	Solyc09g	Serine/thr	GO:00082	SL2.40ch	AT3G098	ATB' BET	ATB' BET	chr3:302	1167.36	704.977	933.461	692.321	451.275	486.521
GT	Sens	Sense	-0.137	Detected	0.137	Detected	0.000	-2.146	Detected	-2.222	Detected	-2.184	0.004	GT	Sens	contig304	contig304	Pol polyp	TGTTTT	contig304	Solyc05g	Solyc05g	Pol polyp	GO:00062	GO:00062	contig304	Solyc05g	Pol polyp	GO:00030	SL2.40ch	AT5G45720.1		ATP bind	chr5:185	658.235	622.518	247.576	265.857	152.843	140.017
GT	Sens	Sense	0.499	Detected	-0.499	Detected	0.000	-1.705	Detected	-1.272	Detected	-1.488	0.112	GT	Sens	contig304	contig304	Myb-relat	GACGGA	contig304	Solyc03g	Solyc03g	Myb-relat	GO:00037	GO:00037	contig304	Solyc03g	Myb-relat	GO:00055	SL2.40ch	AT3G232	MYB15. A	MYB15 (I	chr3:830	1336.83	523.273	608.786	346.883	271.205	353.459
GT	Sens	Sense	0.203	Detected	-0.203	Detected	0.000	-2.524	Detected	-1.050	Detected	-1.787	0.144	GT	Sens	contig304	contig304	WRKY-lik	TTCAAG	contig304	Solyc09g	Solyc09g	WRKY-lik	GO:00037	GO:00037	contig304	Solyc09g	WRKY-lik	GO:00055	SL2.40ch	AT5G562	WRKY2. A	WRKY2:	chr5:227	11420.1	6736.66	4714.72	2031.05	1611.59	4320.96
GT	Sens	Sense	-0.144	Detected	0.144	Detected	0.000	-1.929	Detected	-1.886	Detected	-1.907	0.006	GT	Sens	contig304	contig304	Polyprote	ATGCAG	contig304	Solyc04g	Solyc04g	Polyprotein (AHRD V1 ***- O9X			contig304	Solyc04g	Polyprotein (AHRD V		SL2.40ch	AT5G38100.1				122.673	117.027	64.8874	75.5646	33.2612	33.0883
GT	Sens	Sense	-0.013	Detected	0.013	Detected	0.000	-1.007	Detected	-1.613	Detected	-1.310	0.050	GT	Sens	contig305	contig305	Unknown	ATGACT	contig305	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig305	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G387	EMB2765	EMB2765	chr2:162	942.034	749.497	481.555	472.724	441.898	280.218
GT	Sens	Sense	-0.674	Detected	0.674	Detected	0.000	-2.383	Detected	-1.770	Detected	-2.077	0.107	GT	Sens	contig305	contig305	ATP-bind	TTATTT	contig305	Solyc12g	Solyc12g	ATP-bind	GO:00171	GO:00171	contig305	Solyc12g	ATP-bind	GO:00160	SL2.40ch	AT2G299	PDR3. AT	PDR3 (PL	chr2:127	141.167	280.881	112.31	28.0588	40.3348	59.5529
GT	Sens	Sense	-0.244	Detected	0.244	Detected	0.000	-1.068	Detected	-1.929	Comprom	-1.499	0.094	GT	Sens	contig305	contig305	Protein F	GATGGC	contig305	Solyc05g	Solyc05g	Protein FAR1-RELATED SEQU			contig305	Solyc05g	Protein FAR1-RELA		SL2.40ch	AT3G602	EIF4G. CI	EIF4G (E	chr3:222	18.3608	20.1174	6.08624	15.3582	9.69034	5.14817
GT	Sens	Sense	-0.365	Detected	0.365	Detected	0.000	-1.261	Detected	-1.279	Detected	-1.270	0.074	GT	Sens	contig305	contig305	Auxin-rec	TAGAAG	contig305	Solyc11g	Solyc11g	Auxin-regulated protein (AHRD			contig305	Solyc11g	Auxin-regulated pro		SL2.40ch	AT5G10150.1		unknowr	chr5:318	68.5255	88.8034	47.0092	17.5199	34.4076	32.8037
GT	Sens	Sense	-0.137	Detected	0.137	Detected	0.000	-2.299	Detected	-0.899	Detected	-1.599	0.154	GT	Sens	contig306	contig306	Unknown	AACTTA	contig306	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig306	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G010	WRKY58.	WRKY58	chr3:255	469.341	443.395	195.681	157.095	97.9728	249.644
GT	Sens	Sense	-0.225	Detected	0.225	Detected	0.000	-1.081	Detected	-0.960	Detected	-1.020	0.049	GT	Sens	contig306	contig306	Uncharac	ACGAAA	contig306	Solyc12g	Solyc12g	Uncharacterized 8.8 kDa prote			contig306	Solyc12g	Uncharacterized 8.8		SL2.40ch	ATCG001	RPOC1	RNA poly	chrC:202	102.383	109.369	83.4222	82.1796	52.8513	55.5213
GT	Sens	Sense	0.168	Detected	-0.168	Detected	0.000	-1.753	Comprom	-1.380	Comprom	-1.567	0.025	GT	Sens	contig306	contig306	Ulp1 prot	CTTGAA	contig306	Solyc03g	Solyc03g	Ulp1 protease family C-termina			contig306	Solyc03g	Ulp1 pept	GO:00065	SL2.40ch	AT3G26140.1		glycosyl	chr3:955	20.0326	12.4049	9.50264	7.31322	4.94132	6.17969
GT	Sens	Sense	-0.421	Detected	0.421	Detected	0.000	-1.473	Detected	-1.235	Detected	-1.354	0.090	GT	Sens	contig306	contig306	Dirigent p	GGGAGT	contig306	Solyc08g	Solyc08g	Dirigent protein (AHRD V1 ***- (			contig306	Solyc08g	Dirigent protein (AH		SL2.40ch	AT4G11190.1		disease r	chr4:682	104.661	146.648	53.7769	107.779	47.1567	53.7089
GT	Sens	Sense	-0.409	Detected	0.409	Detected	0.000	-1.914	Detected	-1.677	Detected	-1.796	0.052	GT	Sens	contig307	contig307	Undecapr	GCTTAC	contig307	Solyc08g	Solyc08g	Undecapr	GO:00455	GO:00455	contig307	Solyc08g	Undecapr	GO:00455	SL2.40ch	AT5G58770.1		dehydrod	chr5:237	2980.51	4106.41	1669.11	4073.88	980.831	1116.54
GT	Sens	Sense	-0.212	Detected	0.212	Detected	0.000	-2.238	Comprom	-2.027	Comprom	-2.132	0.012	GT	Sens	contig307	contig307	Unknown	GCAAAC	contig307	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig307	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G215	ENDO4	ENDO4 (	chr4:114	23.3004	24.4234	15.4576	12.5081	5.34421	5.97296
GT	Sens	Sense	-0.106	Detected	0.106	Detected	0.000	-3.704	Detected	-2.989	Detected	-3.347	0.012	GT	Sens	contig308	contig308	Heat stres	GATGAA	contig308	Solyc04g	Solyc04g	Heat stres	GO:00056	GO:00056	contig308	Solyc04g	Heat stres	GO:00030	SL2.40ch	AT2G416	AT-HSFB	AT-HSFB	chr2:173	319.004	288.976	148.066	79.5024	24.6249	39.0158
GT	Sens	Sense	-0.668	Detected	0.668	Detected	0.000	-1.851	Detected	-1.509	Detected	-1.680	0.135	GT	Sens	contig309	contig309	IST1 hom	AACAGA	contig309	Solyc05g	Solyc05g	IST1 homolog (AHRD V1 *--- IST			contig309	Solyc05g	IST1 homolog (AHR		SL2.40ch	AT1G13340.1		unknowr	chr1:456	192.761	380.529	91.4052	116.635	79.3683	97.1143
GT	Sens	Sense	-1.140	Detected	1.140	Detected	0.000	-2.883	Detected	-0.875	Detected	-1.879	0.342	GT	Sens	contig309	contig309	Seed mat	TTGCAG	contig309	Solyc10g	Solyc10g	Seed mat	GO:00097	GO:00097	contig309	Solyc10g	Seed mat	GO:00097	SL2.40ch	AT3G021	LNG2	LNG2 (LC	chr3:396	445.64	1690.88	88.1442	1385.32	124.349	482.86

GT	Sense	Sense	-0.424	Detected	0.424	Detected	0.000	-2.375	Detected	-1.962	Detected	-2.169	0.044	GT	Sens
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	-1.341	Detected	-1.365	Detected	-1.353	0.001	GT	Sens
GT	Sense	Sense	-0.768	Detected	0.768	Detected	0.000	-1.273	Detected	-1.132	Detected	-1.202	0.259	GT	Sens
GT	Sense	Sense	-0.306	Detected	0.306	Detected	0.000	-1.442	Detected	-1.221	Detected	-1.331	0.055	GT	Sens
GT	Sense	Sense	-0.207	Detected	0.207	Detected	0.000	-2.545	Detected	-0.816	Detected	-1.680	0.199	GT	Sens
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.405	Detected	-2.801	Comprom	-2.103	0.095	GT	Sens
GT	Sense	Sense	0.306	Detected	-0.306	Detected	0.000	-1.752	Detected	-1.267	Detected	-1.510	0.061	GT	Sens
GT	Sense	Sense	-0.196	Detected	0.196	Detected	0.000	-1.111	Detected	-1.177	Detected	-1.144	0.029	GT	Sens
GT	Sense	Sense	-0.260	Detected	0.260	Detected	0.000	-3.754	Detected	-1.459	Detected	-2.606	0.157	GT	Sens
GT	Sense	Sense	-1.313	Detected	1.313	Detected	0.000	-5.287	Detected	-0.847	Detected	-3.067	0.356	GT	Sens
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-1.355	Detected	-0.940	Detected	-1.148	0.037	GT	Sens
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-1.726	Detected	-0.979	Detected	-1.352	0.071	GT	Sens
GT	Sense	Sense	0.271	Detected	-0.271	Detected	0.000	-1.967	Detected	-1.470	Detected	-1.719	0.043	GT	Sens
GT	Sense	Sense	-0.125	Detected	0.125	Detected	0.000	-1.518	Detected	-1.066	Detected	-1.292	0.038	GT	Sens
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	-1.360	Detected	-0.958	Detected	-1.159	0.036	GT	Sens
GT	Sense	Sense	-0.175	Detected	0.175	Detected	0.000	-1.292	Detected	-0.841	Detected	-1.067	0.065	GT	Sens
GT	Sense	Sense	-0.207	Detected	0.207	Detected	0.000	-1.481	Detected	-1.476	Detected	-1.478	0.019	GT	Sens
GT	Sense	Sense	-0.085	Detected	0.085	Detected	0.000	-1.283	Comprom	-1.903	Comprom	-1.593	0.038	GT	Sens
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	-1.021	Detected	-1.285	Detected	-1.153	0.013	GT	Sens
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-1.274	Detected	-1.286	Detected	-1.280	0.012	GT	Sens
GT	Sense	Sense	-0.320	Detected	0.320	Detected	0.000	-1.159	Comprom	-1.416	Comprom	-1.287	0.065	GT	Sens
GT	Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-2.777	Comprom	-1.809	Comprom	-2.293	0.044	GT	Sens
GT	Sense	Sense	-0.057	Detected	0.057	Detected	0.000	-1.704	Detected	-0.856	Detected	-1.280	0.096	GT	Sens
GT	Sense	Sense	-0.233	Detected	0.233	Detected	0.000	-0.844	Detected	-1.228	Detected	-1.036	0.076	GT	Sens
GT	Sense	Sense	-0.209	Detected	0.209	Detected	0.000	-1.369	Comprom	-1.918	Comprom	-1.644	0.041	GT	Sens
GT	Sense	Sense	-0.856	Detected	0.856	Detected	0.000	-3.302	Comprom	-3.082	Comprom	-3.192	0.066	GT	Sens
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	-1.454	Comprom	-1.832	Comprom	-1.643	0.014	GT	Sens
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-1.186	Detected	-1.043	Detected	-1.115	0.005	GT	Sens
GT	Sense	Sense	-0.297	Detected	0.297	Detected	0.000	-0.991	Detected	-1.460	Detected	-1.225	0.083	GT	Sens
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	-1.430	Detected	-1.429	Detected	-1.429	0.006	GT	Sens
GT	Sense	Sense	-0.169	Detected	0.169	Detected	0.000	-1.763	Detected	-1.804	Detected	-1.783	0.009	GT	Sens
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-0.929	Comprom	-1.451	Comprom	-1.190	0.047	GT	Sens
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-1.476	Detected	-2.114	Detected	-1.795	0.030	GT	Sens
GT	Sense	Sense	-0.145	Detected	0.145	Detected	0.000	-1.845	Comprom	-1.267	Comprom	-1.556	0.041	GT	Sens
GT	Sense	Sense	-0.126	Detected	0.126	Detected	0.000	-1.224	Detected	-1.544	Detected	-1.384	0.021	GT	Sens
GT	Sense	Sense	0.674	Detected	-0.674	Detected	0.000	-1.901	Comprom	-1.568	Comprom	-1.735	0.130	GT	Sens
GT	Sense	Sense	-0.224	Detected	0.224	Detected	0.000	-2.153	Detected	-2.148	Detected	-2.150	0.011	GT	Sens
GT	Sense	Sense	-0.380	Detected	0.380	Detected	0.000	-1.330	Detected	-0.859	Detected	-1.095	0.134	GT	Sens
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-2.903	Comprom	-3.039	Comprom	-2.971	0.001	GT	Sens
GT	Sense	Sense	-0.468	Detected	0.468	Detected	0.000	-1.842	Detected	-1.198	Detected	-1.520	0.116	GT	Sens
GT	Sense	Sense	-0.562	Detected	0.562	Detected	0.000	-1.609	Detected	-1.027	Detected	-1.318	0.173	GT	Sens
GT	Sense	Sense	-0.353	Detected	0.353	Detected	0.000	-1.537	Comprom	-2.080	Comprom	-1.808	0.056	GT	Sens
GT	Sense	Sense	0.000	Detected	0.000	Detected	0.000	-0.847	Detected	-1.430	Detected	-1.138	0.060	GT	Sens
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.686	Comprom	-2.203	Comprom	-1.944	0.018	GT	Sens
GT	Sense	Sense	0.208	Detected	-0.208	Detected	0.000	-2.221	Comprom	-0.889	Detected	-1.555	0.156	GT	Sens
GT	Sense	Sense	0.300	Detected	-0.300	Detected	0.000	-1.146	Detected	-1.787	Detected	-1.467	0.079	GT	Sens
GT	Sense	Sense	-0.189	Detected	0.189	Detected	0.000	-2.304	Detected	-2.149	Detected	-2.227	0.008	GT	Sens
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	-2.425	Detected	-2.309	Detected	-2.367	0.004	GT	Sens
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.129	Detected	-1.239	Detected	-1.184	0.004	GT	Sens
GT	Sense	Sense	-0.659	Detected	0.659	Detected	0.000	-1.799	Detected	-1.572	Detected	-1.686	0.128	GT	Sens
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	-1.098	Detected	-1.169	Detected	-1.134	0.023	GT	Sens
GT	Sense	Sense	-0.204	Detected	0.204	Detected	0.000	-1.719	Detected	-1.336	Detected	-1.528	0.032	GT	Sens
GT	Sense	Sense	-0.390	Detected	0.390	Detected	0.000	-1.633	Detected	-1.213	Detected	-1.423	0.085	GT	Sens
GT	Sense	Sense	-0.016	Detected	0.016	Detected	0.000	-1.060	Detected	-2.919	Comprom	-1.990	0.166	GT	Sens
GT	Sense	Sense	-0.041	Detected	0.041	Detected	0.000	-1.614	Detected	-1.207	Detected	-1.411	0.021	GT	Sens
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	-1.799	Detected	-1.463	Detected	-1.631	0.011	GT	Sens
GT	Sense	Sense	0.481	Detected	-0.481	Detected	0.000	-1.593	Detected	-0.821	Detected	-1.207	0.190	GT	Sens
GT	Sense	Sense	-0.090	Detected	0.090	Detected	0.000	-1.988	Detected	-1.767	Detected	-1.877	0.006	GT	Sens
GT	Sense	Sense	-0.389	Detected	0.389	Detected	0.000	-1.158	Detected	-0.862	Detected	-1.010	0.136	GT	Sens
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-1.403	Comprom	-1.759	Comprom	-1.581	0.021	GT	Sens
GT	Sense	Sense	-0.121	Detected	0.121	Detected	0.000	-1.537	Comprom	-1.233	Comprom	-1.385	0.019	GT	Sens
GT	Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-1.093	Detected	-1.209	Detected	-1.151	0.003	GT	Sens
GT	Sense	Sense	-0.041	Detected	0.041	Detected	0.000	-2.744	Detected	-2.474	Detected	-2.609	0.003	GT	Sens
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-1.320	Detected	-1.820	Detected	-1.570	0.025	GT	Sens
GT	Sense	Sense	-0.057	Detected	0.057	Detected	0.000	-4.434	Comprom	-3.930	Comprom	-4.182	0.004	GT	Sens
GT	Sense	Sense	0.432	Detected	-0.432	Detected	0.000	-3.583	Comprom	-3.442	Comprom	-3.513	0.015	GT	Sens
GT	Sense	Sense	-3.060	Detected	3.060	Detected	0.000	-3.146	Detected	-1.541	Detected	-2.344	0.536	GT	Sens
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-0.907	Comprom	-2.720	Comprom	-1.814	0.185	GT	Sens
GT	Sense	Sense	0.580	Detected	-0.580	Detected	0.000	-1.458	Detected	-2.482	Comprom	-1.970	0.126	GT	Sens
GT	Sense	Sense	0.683	Detected	-0.683	Detected	0.000	-1.832	Comprom	-2.155	Comprom	-1.994	0.105	GT	Sens
GT	Sense	Sense	0.111	Detected	-0.111	Detected	0.000	-1.608	Detected	-2.982	Comprom	-2.295	0.081	GT	Sens
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.719	Detected	-1.239	Detected	-1.479	0.033	GT	Sens
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-3.348	Comprom	-1.072	Detected	-2.210	0.192	GT	Sens
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-1.221	Detected	-1.713	Detected	-1.467	0.029	GT	Sens
GT	Sense	Sense	-0.137	Detected	0.137	Detected	0.000	-0.995	Detected	-1.441	Detected	-1.218	0.043	GT	Sens
GT	Sense	Sense	-0.591	Detected	0.591	Detected	0.000	-2.271	Comprom	-1.978	Comprom	-2.125	0.073	GT	Sens
GT	Sense	Sense	-0.193	Detected	0.193	Detected	0.000	-1.032	Detected	-1.147	Detected	-1.090	0.032	GT	Sens
GT	Sense	Sense	0.017	Detected	-0.017	Detected	0.000	-2.994	Comprom	-1.860	Comprom	-2.427	0.051	GT	Sens
GT	Sense	Sense	-0.364	Detected	0.364	Detected	0.000	-2.232	Comprom	-1.204	Detected	-1.718	0.112	GT	Sens
GT	Sense	Sense	-0.588	Detected	0.588	Detected	0.000	-1.392	Detected	-1.285	Detected	-1.338	0.152	GT	Sens
GT	Sense	Sense	-0.632	Detected	0.632	Detected	0.000	-1.344	Detected	-1.376	Detected	-1.360	0.164	GT	Sens
GT	Sense	Sense	-0.506	Detected	0.506	Detected	0.000	-4.333	Comprom	-3.817	Comprom	-4.075	0.019	GT	Sens
GT	Sense	Sense	-0.920	Detected	0.920	Detected	0.000	-0.975	Detected	-1.077	Detected	-1.026	0.381	GT	Sens
GT	Sense	Sense	0.253	Detected	-0.253	Detected	0.000	-1.122	Detected	-0.941	Detected	-1.032	0.061	GT	Sens
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-1.441	Detected	-1.233	Detected	-1.337	0.006	GT	Sens
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-1.231	Detected	-0.914	Detected	-1.073	0.023	GT	Sens
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-1.802	Detected	-1.164	Detected	-1.483	0.048	GT	Sens
GT	Sense	Sense	-0.145	Detected	0.145	Detected	0.000	-2.594	Comprom	-0.885	Comprom	-1.740	0.183	GT	Sens
GT	Sense	Sense	-0.397	Detected	0.397	Detected	0.000	-0.872	Detected	-1.499	Comprom	-1.185	0.144	GT	Sens
GT	Sense	Sense	-0.065	Detected	0.065	Detected	0.000	-1.200	Detected	-1.005	Detected	-1.102	0.011	GT	Sens
GT	Sense	Sense	-0.465	Detected	0.465	Detected	0.000	-1.172	Detected	-0.868	Detected	-1.020	0.172	GT	Sens
GT	Sense	Sense	-0.450	Detected	0.450	Detected	0.000	-0.927	Detected	-1.981	Detected	-1.454	0.171	GT	Sens
GT	Sense	Sense	0.108	Detected	-0.108	Detected	0.000	-1.310	Detected	-1.154	Detected	-1.232	0.011	GT	Sens
GT	Sense	Sense	-0.021	Detected	0.021	Detected	0.000	-1.170	Detected	-1.498	Detected	-1.334	0.015	GT	Sens
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.101	Detected	-1.638	Detected	-1.369	0.037	GT	Sens
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-1.313	Detected	-1.012	Detected	-1.162	0.023	GT	Sens
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	-1.370	Comprom	-1.388	Comprom	-1.379	0.009	GT	Sens
GT	Sense	Sense	-0.732	Detected	0.732	Detected	0.000	-1.516	Detected	-1.083	Detected	-1.299	0.231	GT	Sens
GT	Sense	Sense	-0.069	Detected	0.069	Detected	0.000	-2.031	Detected	-0.845	Detected	-1.438	0.138	GT	Sens
GT	Sense	Sense	-0.452	Detected	0.452	Detected	0.000	-2.852	Detected	-1.470	Detected	-2.161	0.120	GT	Sens
GT	Sense	Sense	-0.422	Detected	0.422	Detected	0.000	-3.268	Detected	-1.849	Detected	-2.559	0.090	GT	Sens
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	-0.906	Detected	-1.785	Comprom	-1.346	0.097	GT	Sens
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	-1.681	Comprom	-1.337	Comprom	-1.509	0.018	GT	Sens
GT	Sense	Sense	0.248	Detected	-0.248	Detected	0.000	-3.142	Comprom	-2.726	Comprom	-2.934	0.012	GT	Sens
GT	Sense	Sense	-0.324	Detected	0.324	Detected	0.000	-1.771	Comprom	-1.441	Comprom	-1.606	0.048	GT	Sens
GT	Sense	Sense	-0.245	Detected	0.245	Detected	0.000	-1.251	Comprom	-1.506	Comprom	-1.378	0.038	GT	Sens
GT	Sense	Sense	0.019	Detected	-0.019	Detected	0.000	-1.163	Detected	-1.062	Detected	-1.113	0.002	GT	Sens
GT	Sense	Sense	-0.277	Detected	0.277	Detected	0.000	-1.093	Detected	-0.952	Detected	-1.023	0.070	GT	Sens
GT	Sense	Sense	-0.693	Detected	0.693	Detected	0.000	-4.206	Comprom	-2.235	Comprom	-3.220	0.116	GT	Sens
GT	Sense	Sense	-0.068	Detected	0.068	Detected	0.000	-2.352	Detected	-2.327	Detected	-2.340	0.001	GT	Sens
GT	Sense	Sense	-0.010	Detected	0.010	Detected	0.000	-2.283	Detected	-2.186	Detected	-2.235	0.000	GT	Sens
GT	Sense	Sense	0.232	Detected	-0.232	Detected	0.000	-1.289	Detected	-1.403	Detected	-1.346	0.030	GT	Sens
GT	Sense	Sense	0.436	Detected	-0.436	Detected	0.000	-1.988	Comprom	-2.390	Comprom	-2.189	0.045	GT	Sens
GT	Sense	Sense	-0.156	Detected	0.156	Detected	0.000	-2.309	Comprom	-1.079	Comprom	-1.694	0.116	GT	Sens
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-1.107	Detected	-1.021	Detected	-1.064	0.019	GT	Sens
GT	Sense	Sense	0.446	Detected	-0.446	Detected	0.000	-1.713	Detected	-1.478	Detected	-1.595	0.074	GT	Sens
GT	Sense	Sense	-0.476	Detected	0.476	Detected	0.000	-2.239	Detected	-1.519	Detected	-1.879	0.088	GT	Sens
GT	Sense	Sense	-0.291	Detected	0.291	Detected	0.000	-1.559	Detected	-0.976	Detected	-1.268	0.091	GT	Sens
GT	Sense	Sense	-0.349	Detected	0.349	Detected	0.000	-1.028	Detected	-1.111	Detected	-1.070	0.093	GT	Sens
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-0.848	Detected	-1.715	Comprom	-1.281	0.101	GT	Sens
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	-1.409	Detected	-1.170	Detected	-1.289	0.009	GT	Sens
GT	Sense	Sense	-0.066	Detected	0.066	Detected	0.000	-1.574	Detected	-1.438	Detected	-1.506	0.004	GT	Sens
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	-1.225	Detected	-1.401	Detected	-1.313	0.024	GT	Sens
GT	Sense	Sense	-0.115	Detected	0.115	Detected	0.000	-1.145	Detected	-1.234	Detected	-1.189	0.011	GT	Sens
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	-1.324	Detected	-1.146	Detected	-1.235	0.005	GT	Sens
GT	Sense	Sense	-0.177	Detected	0.177	Detected	0.000	-1.307	Detected	-0.967	Detected	-1.137	0.044	GT	Sens
GT	Sense	Sense	-0.174	Detected	0.174	Detected	0.000	-1.853	Detected	-2.010	Detected	-1.932	0.010	GT	Sens
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-2.398	Detected	-2.208	Detected	-2.303	0.002	GT	Sens
GT	Sense	Sense	0.210	Detected	-0.210	Detected	0.000	-0.931	Detected	-1.103	Detected	-1.017	0.046	GT	Sens
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-2.531	Comprom	-3.432	Comprom	-2.982	0.022	GT	Sens
GT	Sense	Sense	-0.273	Detected	0.273	Detected	0.000	-1.590	Comprom	-0.999	Comprom	-1.294	0.085	GT	Sens
GT	Sense	Sense	-0.206	Detected	0.206	Detected	0.000	-1.900	Comprom	-0.832	Comprom	-1.366	0.140	GT	Sens
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-2.405	Detected	-2.723	Detected	-2.564	0.005	GT	Sens
GT	Sense	Sense	-0.166	Detected	0.166	Detected	0.000	-1.977	Detected	-1.812	Detected	-1.895	0.009	GT	Sens
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-1.025	Detected	-1.027	Detected	-1.026	0.003	GT	Sens
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	-1.205	Detected	-0.914	Detected	-1.060	0.018	GT	Sens
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-1.645	Detected	-2.039	Detected	-1.842	0.013	GT	Sens
GT	Sense	Sense	-0.103	Detected	0.103	Detected	0.000	-2.210	Detected	-2.220	Detected	-2.215	0.002	GT	Sens
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-1.964	Detected	-1.946	Detected	-1.955	0.000	GT	Sens
GT	Sense	Sense	-0.149	Detected	0.149	Detected	0.000	-2.135	Detected	-2.119	Detected	-2.127	0.005	GT	Sens
GT	Sense	Sense	-0.210	Detected	0.210	Detected	0.000	-1.243	Detected	-1.101	Detected	-1.172	0.034	GT	Sens
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.300	Detected	-1.185	Detected	-1.243	0.007	GT	Sens
GT	Sense	Sense	-0.307	Detected	0.307	Detected	0.000	-1.055	Detected	-1.224	Detected	-1.140	0.070	GT	Sens
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.235	Detected	-0.900	Detected	-1.067	0.024	GT	Sens
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	-1.780	Detected	-2.008	Detected	-1.894	0.006	GT	Sens
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	-1.988	Detected	-1.900	Detected	-1.944	0.001	GT	Sens
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	-3.007	Comprom	-2.936	Comprom	-2.972	0.001	GT	Sens
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	-4.115	Comprom	-3.194	Comprom	-3.655	0.016	GT	Sens
GT	Sense	Sense	-0.587	Detected	0.587	Detected	0.000	-4.988	Comprom	-5.100	Comprom	-5.044	0.013	GT	Sens
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-1.268	Detected	-0.813	Detected	-1.040	0.049	GT	Sens
GT	Sense	Sense	0.414	Detected	-0.414	Detected	0.000	-1.084	Detected	-1.134	Detected	-1.109	0.116	GT	Sens
GT	Sense	Sense	0.188	Detected	-0.188	Detected	0.000	-1.194	Detected	-0.849	Detected	-1.022	0.057	GT	Sens
GT	Sense	Sense	-0.416	Detected	0.416	Detected	0.000	-1.947	Detected	-1.184	Detected	-1.565	0.109	GT	Sens
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	-1.145	Detected	-1.193	Detected	-1.169	0.025	GT	Sens
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-2.468	Comprom	-1.269	Detected	-1.869	0.091	GT	Sens
GT	Sense	Sense	-0.141	Detected	0.141	Detected	0.000	-2.573	Detected	-1.991	Detected	-2.282	0.020	GT	Sens
GT	Sense	Sense	-0.066	Detected	0.066	Detected	0.000	-1.099	Comprom	-0.911	Comprom	-1.005	0.013	GT	Sens
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-1.570	Detected	-2.098	Detected	-1.834	0.023	GT	Sens
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	-1.624	Detected	-2.178	Detected	-1.901	0.021	GT	Sens
GT	Sense	Sense	-1.380	Detected	1.380	Detected	0.000	-2.128	Comprom	-2.144	Comprom	-2.136	0.262	GT	Sens
GT	Sense	Sense	-0.579	Detected	0.579	Detected	0.000	-1.316	Detected	-0.918	Detected	-1.117	0.209	GT	Sens
GT	Sense	Sense	-0.496	Detected	0.496	Detected	0.000	-1.567	Detected	-1.078	Detected	-1.323	0.139	GT	Sens
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-1.780	Comprom	-1.663	Comprom	-1.722	0.004	GT	Sens
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-2.250	Detected	-2.472	Detected	-2.361	0.002	GT	Sens
GT	Sense	Sense	-0.161	Detected	0.161	Detected	0.000	-2.140	Detected	-2.244	Detected	-2.192	0.006	GT	Sens
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-1.961	Detected	-2.075	Detected	-2.018	0.004	GT	Sens
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-1.250	Detected	-0.834	Detected	-1.042	0.039	GT	Sens
GT	Sense	Sense	-0.396	Detected	0.396	Detected	0.000	-1.389	Comprom	-0.826	Comprom	-1.108	0.150	GT	Sens
GT	Sense	Sense	0.281	Detected	-0.281	Detected	0.000	-1.298	Detected	-1.204	Detected	-1.251	0.048	GT	Sens
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-1.005	Detected	-1.115	Detected	-1.060	0.011	GT	Sens
GT	Sense	Sense	-0.651	Detected	0.651	Detected	0.000	-1.435	Detected	-1.559	Detected	-1.497	0.149	GT	Sens
GT	Sense	Sense	-0.345	Detected	0.345	Detected	0.000	-1.216	Detected	-0.924	Detected	-1.070	0.104	GT	Sens
GT	Sense	Sense	-0.214	Detected	0.214	Detected	0.000	-1.801	Comprom	-2.184	Comprom	-1.992	0.020	GT	Sens
GT	Sense	Sense	-0.136	Detected	0.136	Detected	0.000	-0.976	Detected	-1.471	Detected	-1.224	0.049	GT	Sens
GT	Sense	Sense	-0.338	Detected	0.338	Detected	0.000	-1.972	Detected	-0.904	Detected	-1.438	0.151	GT	Sens
GT	Sense	Sense	-0.374	Detected	0.374	Detected	0.000	-1.849	Detected	-1.100	Detected	-1.475	0.108	GT	Sens
GT	Sense	Sense	0.206	Detected	-0.206	Detected	0.000	-1.066	Detected	-3.081	Comprom	-2.074	0.181	GT	Sens
GT	Sense	Sense	-0.643	Detected	0.643	Detected	0.000	-1.137	Detected	-1.127	Detected	-1.132	0.220	GT	Sens
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-3.725	Detected	-3.574	Detected	-3.650	0.001	GT	Sens
GT	Sense	Sense	-0.232	Detected	0.232	Detected	0.000	-1.596	Comprom	-1.856	Comprom	-1.726	0.023	GT	Sens
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.993	Comprom	-2.443	Comprom	-2.218	0.010	GT	Sens
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-2.464	Detected	-2.420	Detected	-2.442	0.000	GT	Sens
GT	Sense	Sense	-0.023	Detected	0.023	Detected	0.000	-2.350	Detected	-2.509	Detected	-2.430	0.001	GT	Sens
GT	Sense	Sense	-0.235	Detected	0.235	Detected	0.000	-1.224	Detected	-0.934	Detected	-1.079	0.060	GT	Sens
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-1.150	Detected	-1.022	Detected	-1.086	0.005	GT	Sens
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-1.813	Detected	-1.726	Detected	-1.770	0.001	GT	Sens
GT	Sense	Sense	-0.115	Detected	0.115	Detected	0.000	-1.543	Comprom	-2.042	Comprom	-1.793	0.023	GT	Sens
GT	Sense	Sense	-0.009	Detected	0.009	Detected	0.000	-1.266	Detected	-1.173	Detected	-1.219	0.001	GT	Sens
GT	Sense	Sense	-0.346	Detected	0.346	Detected	0.000	-0.964	Detected	-1.119	Detected	-1.041	0.099	GT	Sens
GT	Sense	Sense	0.402	Detected	-0.402	Detected	0.000	-1.419	Detected	-1.527	Detected	-1.473	0.068	GT	Sens
GT	Sense	Sense	-0.193	Detected	0.193	Detected	0.000	-2.920	Comprom	-1.918	Comprom	-2.419	0.046	GT	Sens
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-1.837	Detected	-1.210	Detected	-1.523	0.040	GT	Sens
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-2.581	Detected	-1.415	Detected	-1.998	0.076	GT	Sens
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.219	Detected	-1.283	Detected	-1.251	0.001	GT	Sens
GT	Sense	Sense	1.173	Detected	-1.173	Detected	0.000	-1.064	Detected	-1.106	Detected	-1.085	0.452	GT	Sens
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.803	Detected	-1.232	Detected	-1.518	0.034	GT	Sens
GT	Sense	Sense	0.187	Detected	-0.187	Detected	0.000	-1.724	Detected	-1.325	Detected	-1.525	0.031	GT	Sens
GT	Sense	Sense	-0.604	Detected	0.604	Detected	0.000	-1.087	Detected	-1.168	Detected	-1.127	0.203	GT	Sens
GT	Sense	Sense	-0.239	Detected	0.239	Detected	0.000	-1.168	Comprom	-1.320	Comprom	-1.244	0.038	GT	Sens
GT	Sense	Sense	-0.608	Detected	0.608	Detected	0.000	-1.134	Detected	-2.070	Comprom	-1.602	0.172	GT	Sens
GT	Sense	Sense	-0.128	Detected	0.128	Detected	0.000	-2.593	Detected	-2.537	Detected	-2.565	0.003	GT	Sens
GT	Sense	Sense	-0.515	Detected	0.515	Detected	0.000	-2.507	Detected	-2.040	Detected	-2.274	0.057	GT	Sens
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.333	Detected	-1.151	Detected	-1.242	0.005	GT	Sens
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	-1.749	Detected	-1.418	Detected	-1.583	0.017	GT	Sens
GT	Sense	Sense	-0.197	Detected	0.197	Detected	0.000	-1.876	Detected	-1.679	Detected	-1.778	0.015	GT	Sens
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-2.262	Detected	-2.327	Detected	-2.295	0.004	GT	Sens
GT	Sense	Sense	0.215	Detected	-0.215	Detected	0.000	-1.205	Detected	-1.061	Detected	-1.133	0.038	GT	Sens
GT	Sense	Sense	-0.472	Detected	0.472	Detected	0.000	-2.041	Comprom	-2.788	Comprom	-2.415	0.057	GT	Sens
GT	Sense	Sense	-0.174	Detected	0.174	Detected	0.000	-0.849	Detected	-1.389	Detected	-1.119	0.073	GT	Sens
GT	Sense	Sense	0.008	Detected	-0.008	Detected	0.000	-2.280	Detected	-2.129	Detected	-2.204	0.001	GT	Sens
GT	Sense	Sense	-0.126	Detected	0.126	Detected	0.000	-2.092	Detected	-2.192	Detected	-2.142	0.004	GT	Sens
GT	Sense	Sense	0.749	Detected	-0.749	Detected	0.000	-1.124	Detected	-0.979	Detected	-1.052	0.297	GT	Sens
GT	Sense	Sense	-0.386	Detected	0.386	Detected	0.000	-2.034	Detected	-1.266	Detected	-1.650	0.094	GT	Sens
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	-2.337	Detected	-1.590	Detected	-1.963	0.066	GT	Sens
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-1.292	Comprom	-1.030	Comprom	-1.161	0.031	GT	Sens
GT	Sense	Sense	-0.159	Detected	0.159	Detected	0.000	-1.526	Detected	-0.851	Detected	-1.189	0.086	GT	Sens
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-1.060	Detected	-1.146	Detected	-1.103	0.002	GT	Sens
GT	Sense	Sense	-0.416	Detected	0.416	Detected	0.000	-1.983	Comprom	-1.365	Comprom	-1.674	0.084	GT	Sens
GT	Sense	Sense	-0.080	Detected	0.080	Detected	0.000	-0.946	Comprom	-1.181	Comprom	-1.063	0.017	GT	Sens
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	-2.281	Detected	-2.631	Detected	-2.456	0.007	GT	Sens
GT	Sense	Sense	-0.147	Detected	0.147	Detected	0.000	-2.273	Detected	-2.299	Detected	-2.286	0.004	GT	Sens
GT	Sense	Sense	0.213	Detected	-0.213	Detected	0.000	-1.344	Detected	-1.184	Detected	-1.264	0.031	GT	Sens
GT	Sense	Sense	-0.197	Detected	0.197	Detected	0.000	-1.430	Detected	-1.510	Detected	-1.470	0.018	GT	Sens
GT	Sense	Sense	-0.226	Detected	0.226	Detected	0.000	-0.900	Comprom	-1.703	Comprom	-1.301	0.106	GT	Sens
GT	Sense	Sense	-0.190	Detected	0.190	Detected	0.000	-2.067	Detected	-1.406	Detected	-1.737	0.045	GT	Sens
GT	Sense	Sense	-0.228	Detected	0.228	Detected	0.000	-1.792	Detected	-1.274	Detected	-1.533	0.047	GT	Sens
GT	Sense	Sense	-0.121	Detected	0.121	Detected	0.000	-1.923	Comprom	-2.030	Comprom	-1.976	0.004	GT	Sens
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-2.017	Comprom	-1.357	Comprom	-1.687	0.040	GT	Sens
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.702	Detected	-0.957	Detected	-1.330	0.071	GT	Sens
GT	Sense	Sense	-0.256	Detected	0.256	Detected	0.000	-1.242	Comprom	-2.012	Comprom	-1.627	0.072	GT	Sens
GT	Sense	Sense	-0.084	Detected	0.084	Detected	0.000	-1.779	Comprom	-1.112	Comprom	-1.445	0.052	GT	Sens
GT	Sense	Sense	-0.650	Detected	0.650	Detected	0.000	-2.810	Comprom	-2.141	Comprom	-2.475	0.077	GT	Sens
GT	Sense	Sense	-0.005	Detected	0.005	Detected	0.000	-1.011	Detected	-1.202	Detected	-1.107	0.007	GT	Sens
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.401	Detected	-1.104	Detected	-1.253	0.015	GT	Sens
GT	Sense	Sense	-0.212	Detected	0.212	Detected	0.000	-1.417	Detected	-1.042	Detected	-1.229	0.049	GT	Sens
GT	Sense	Sense	-0.531	Detected	0.531	Detected	0.000	-1.545	Comprom	-1.348	Comprom	-1.446	0.116	GT	Sens
GT	Sense	Sense	0.234	Detected	-0.234	Detected	0.000	-1.465	Detected	-0.919	Detected	-1.192	0.080	GT	Sens
GT	Sense	Sense	-0.267	Detected	0.267	Detected	0.000	-0.950	Detected	-1.133	Detected	-1.042	0.066	GT	Sens
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	-1.594	Detected	-0.895	Detected	-1.245	0.071	GT	Sens
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	-0.867	Detected	-1.356	Comprom	-1.111	0.054	GT	Sens
GT	Sense	Sense	-0.287	Detected	0.287	Detected	0.000	-1.181	Detected	-0.967	Detected	-1.074	0.073	GT	Sens
GT	Sense	Sense	-0.403	Detected	0.403	Detected	0.000	-0.878	Detected	-2.121	Comprom	-1.500	0.180	GT	Sens
GT	Sense	Sense	-0.133	Detected	0.133	Detected	0.000	-1.909	Detected	-1.616	Detected	-1.762	0.012	GT	Sens
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-1.807	Detected	-1.616	Detected	-1.711	0.006	GT	Sens

GT	Sense	Sense	-0.057	Detected	0.057	Detected	0.000	-1.780	Comprom	-1.751	Comprom	-1.765	0.001	GT	Sens
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-1.995	Comprom	-0.818	Detected	-1.407	0.142	GT	Sens
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-1.466	Comprom	-2.578	Comprom	-2.022	0.071	GT	Sens
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.394	Detected	-1.337	Detected	-1.366	0.002	GT	Sens
GT	Sense	Sense	-0.254	Detected	0.254	Detected	0.000	-1.385	Detected	-0.966	Detected	-1.175	0.070	GT	Sens
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.989	Detected	-1.689	Detected	-1.839	0.007	GT	Sens
GT	Sense	Sense	0.856	Detected	-0.856	Detected	0.000	-1.297	Detected	-1.357	Detected	-1.327	0.261	GT	Sens
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.718	Detected	-2.572	Detected	-2.145	0.041	GT	Sens
GT	Sense	Sense	0.103	Detected	-0.103	Detected	0.000	-1.765	Detected	-2.077	Detected	-1.921	0.009	GT	Sens
GT	Sense	Sense	0.942	Detected	-0.942	Detected	0.000	-1.716	Detected	-3.224	Comprom	-2.470	0.177	GT	Sens
GT	Sense	Sense	-0.295	Detected	0.295	Detected	0.000	-1.799	Detected	-0.943	Detected	-1.371	0.119	GT	Sens
GT	Sense	Sense	0.699	Detected	-0.699	Detected	0.000	-1.219	Detected	-1.231	Detected	-1.225	0.222	GT	Sens
GT	Sense	Sense	-0.025	Detected	0.025	Detected	0.000	-1.548	Detected	-1.192	Detected	-1.370	0.017	GT	Sens
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	-1.488	Detected	-1.759	Detected	-1.624	0.012	GT	Sens
GT	Sense	Sense	-0.110	Detected	0.110	Detected	0.000	-1.542	Comprom	-1.082	Comprom	-1.312	0.036	GT	Sens
GT	Sense	Sense	-0.376	Detected	0.376	Detected	0.000	-2.920	Comprom	-2.243	Comprom	-2.581	0.036	GT	Sens
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-1.397	Comprom	-1.514	Comprom	-1.455	0.004	GT	Sens
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-1.344	Comprom	-1.447	Comprom	-1.396	0.002	GT	Sens
GT	Sense	Sense	0.424	Detected	-0.424	Detected	0.000	-1.453	Detected	-1.004	Detected	-1.228	0.125	GT	Sens
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	-1.818	Comprom	-2.230	Comprom	-2.024	0.013	GT	Sens
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-1.623	Detected	-1.347	Detected	-1.485	0.013	GT	Sens
GT	Sense	Sense	-0.406	Detected	0.406	Detected	0.000	-1.266	Detected	-0.933	Detected	-1.100	0.129	GT	Sens
GT	Sense	Sense	-1.850	Detected	1.850	Detected	0.000	-3.919	Comprom	-3.097	Detected	-3.508	0.205	GT	Sens
GT	Sense	Sense	0.052	Detected	-0.052	Detected	0.000	-2.459	Detected	-2.358	Detected	-2.409	0.001	GT	Sens
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	-1.365	Detected	-1.606	Detected	-1.485	0.007	GT	Sens
GT	Sense	Sense	0.140	Detected	-0.140	Detected	0.000	-1.528	Detected	-0.875	Detected	-1.202	0.077	GT	Sens
GT	Sense	Sense	0.382	Detected	-0.382	Detected	0.000	-2.423	Detected	-1.626	Detected	-2.025	0.067	GT	Sens
GT	Sense	Sense	0.232	Detected	-0.232	Detected	0.000	-2.107	Detected	-1.551	Detected	-1.829	0.037	GT	Sens
GT	Sense	Sense	-0.168	Detected	0.168	Detected	0.000	-2.390	Comprom	-1.887	Comprom	-2.139	0.019	GT	Sens
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-2.165	Detected	-1.103	Detected	-1.634	0.097	GT	Sens
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	-2.276	Detected	-1.132	Detected	-1.704	0.098	GT	Sens
GT	Sense	Sense	-0.195	Detected	0.195	Detected	0.000	-2.104	Comprom	-1.154	Comprom	-1.629	0.087	GT	Sens
GT	Sense	Sense	-0.260	Detected	0.260	Detected	0.000	-1.551	Comprom	-1.263	Comprom	-1.407	0.042	GT	Sens
GT	Sense	Sense	-0.157	Detected	0.157	Detected	0.000	-1.464	Comprom	-1.944	Comprom	-1.704	0.027	GT	Sens
GT	Sense	Sense	0.868	Detected	-0.868	Detected	0.000	-1.474	Detected	-1.206	Detected	-1.340	0.267	GT	Sens
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-1.388	Detected	-0.840	Detected	-1.114	0.073	GT	Sens
GT	Sense	Sense	0.069	Detected	-0.069	Detected	0.000	-1.407	Detected	-1.370	Detected	-1.389	0.003	GT	Sens
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	-1.179	Detected	-0.906	Detected	-1.042	0.041	GT	Sens
GT	Sense	Sense	-0.289	Detected	0.289	Detected	0.000	-1.190	Detected	-0.984	Detected	-1.087	0.071	GT	Sens
GT	Sense	Sense	-0.099	Detected	0.099	Detected	0.000	-1.671	Comprom	-1.160	Comprom	-1.415	0.036	GT	Sens
GT	Sense	Sense	-0.715	Detected	0.715	Detected	0.000	-1.031	Detected	-1.351	Detected	-1.191	0.245	GT	Sens
GT	Sense	Sense	-0.310	Detected	0.310	Detected	0.000	-1.419	Comprom	-1.410	Comprom	-1.414	0.045	GT	Sens
GT	Sense	Sense	-0.379	Detected	0.379	Detected	0.000	-2.915	Comprom	-3.426	Comprom	-3.170	0.020	GT	Sens
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	-1.662	Comprom	-2.286	Comprom	-1.974	0.029	GT	Sens
GT	Sense	Sense	1.112	Detected	-1.112	Detected	0.000	-2.154	Comprom	-2.194	Comprom	-2.174	0.190	GT	Sens
GT	Sense	Sense	1.400	Detected	-1.400	Detected	0.000	-1.651	Detected	-1.568	Detected	-1.609	0.369	GT	Sens
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.897	Detected	-1.418	Detected	-1.657	0.022	GT	Sens
GT	Sense	Sense	-0.780	Detected	0.780	Detected	0.000	-2.531	Detected	-0.991	Detected	-1.761	0.249	GT	Sens
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	-1.903	Comprom	-1.701	Comprom	-1.802	0.003	GT	Sens
GT	Sense	Sense	-0.021	Detected	0.021	Detected	0.000	-1.339	Detected	-1.720	Detected	-1.529	0.015	GT	Sens
GT	Sense	Sense	0.214	Detected	-0.214	Detected	0.000	-1.091	Detected	-1.021	Detected	-1.056	0.040	GT	Sens
GT	Sense	Sense	0.207	Detected	-0.207	Detected	0.000	-1.066	Detected	-0.999	Detected	-1.032	0.039	GT	Sens
GT	Sense	Sense	-0.014	Detected	0.014	Detected	0.000	-3.006	Comprom	-2.471	Comprom	-2.738	0.009	GT	Sens
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	-1.508	Detected	-0.986	Detected	-1.247	0.042	GT	Sens
GT	Sense	Sense	-0.198	Detected	0.198	Detected	0.000	-1.420	Detected	-0.862	Detected	-1.141	0.079	GT	Sens
GT	Sense	Sense	-0.315	Detected	0.315	Detected	0.000	-2.149	Comprom	-2.454	Comprom	-2.302	0.022	GT	Sens
GT	Sense	Sense	-0.124	Detected	0.124	Detected	0.000	-1.113	Detected	-1.036	Detected	-1.075	0.014	GT	Sens
GT	Sense	Sense	-0.153	Detected	0.153	Detected	0.000	-1.149	Detected	-1.490	Detected	-1.320	0.029	GT	Sens
GT	Sense	Sense	0.201	Detected	-0.201	Detected	0.000	-1.724	Detected	-2.308	Detected	-2.016	0.029	GT	Sens
GT	Sense	Sense	0.167	Detected	-0.167	Detected	0.000	-1.767	Detected	-2.362	Detected	-2.065	0.026	GT	Sens
GT	Sense	Sense	-0.091	Detected	0.091	Detected	0.000	-1.625	Detected	-0.898	Detected	-1.261	0.078	GT	Sens
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-2.840	Detected	-1.244	Detected	-2.042	0.126	GT	Sens
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	-1.813	Comprom	-2.525	Comprom	-2.169	0.029	GT	Sens
GT	Sense	Sense	0.022	Detected	-0.022	Detected	0.000	-1.311	Detected	-0.976	Detected	-1.144	0.021	GT	Sens
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-1.271	Detected	-1.212	Detected	-1.242	0.002	GT	Sens
GT	Sense	Sense	0.039	Detected	-0.039	Detected	0.000	-1.579	Detected	-1.608	Detected	-1.593	0.001	GT	Sens
GT	Sense	Sense	-0.690	Detected	0.690	Detected	0.000	-1.060	Detected	-1.115	Detected	-1.087	0.256	GT	Sens
GT	Sense	Sense	-0.051	Detected	0.051	Detected	0.000	-1.360	Detected	-1.244	Detected	-1.302	0.004	GT	Sens
GT	Sense	Sense	-0.133	Detected	0.133	Detected	0.000	-1.186	Detected	-1.175	Detected	-1.181	0.012	GT	Sens
GT	Sense	Sense	-0.753	Detected	0.753	Detected	0.000	-0.832	Detected	-1.212	Detected	-1.022	0.319	GT	Sens
GT	Sense	Sense	0.200	Detected	-0.200	Detected	0.000	-1.987	Comprom	-2.567	Comprom	-2.277	0.023	GT	Sens
GT	Sense	Sense	-0.745	Detected	0.745	Detected	0.000	-1.250	Detected	-2.851	Comprom	-2.051	0.202	GT	Sens
GT	Sense	Sense	0.031	Detected	-0.031	Detected	0.000	-1.237	Detected	-1.104	Detected	-1.170	0.004	GT	Sens
GT	Sense	Sense	-0.243	Detected	0.243	Detected	0.000	-2.195	Comprom	-2.630	Comprom	-2.413	0.018	GT	Sens
GT	Sense	Sense	-0.183	Detected	0.183	Detected	0.000	-1.504	Comprom	-1.136	Comprom	-1.320	0.037	GT	Sens
GT	Sense	Sense	-0.243	Detected	0.243	Detected	0.000	-1.271	Comprom	-1.239	Comprom	-1.255	0.036	GT	Sens
GT	Sense	Sense	-0.425	Detected	0.425	Detected	0.000	-1.992	Detected	-1.247	Detected	-1.619	0.103	GT	Sens
GT	Sense	Sense	0.075	Detected	-0.075	Detected	0.000	-0.868	Detected	-1.267	Detected	-1.068	0.037	GT	Sens
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-1.641	Comprom	-1.344	Comprom	-1.492	0.018	GT	Sens
GT	Sense	Sense	-0.357	Detected	0.357	Detected	0.000	-1.244	Detected	-0.837	Detected	-1.041	0.127	GT	Sens
GT	Sense	Sense	-0.160	Detected	0.160	Detected	0.000	-1.227	Comprom	-1.537	Comprom	-1.382	0.025	GT	Sens
GT	Sense	Sense	0.762	Detected	-0.762	Detected	0.000	-1.760	Detected	-2.062	Comprom	-1.911	0.133	GT	Sens
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	-1.134	Detected	-1.506	Detected	-1.320	0.025	GT	Sens
GT	Sense	Sense	0.328	Detected	-0.328	Detected	0.000	-1.437	Detected	-2.099	Detected	-1.768	0.063	GT	Sens
GT	Sense	Sense	-0.651	Detected	0.651	Detected	0.000	-1.157	Detected	-0.862	Detected	-1.010	0.270	GT	Sens
GT	Sense	Sense	-0.599	Detected	0.599	Detected	0.000	-1.579	Detected	-0.808	Detected	-1.193	0.236	GT	Sens
GT	Sense	Sense	-0.033	Detected	0.033	Detected	0.000	-0.900	Detected	-1.220	Detected	-1.060	0.023	GT	Sens
GT	Sense	Sense	-0.053	Detected	0.053	Detected	0.000	-1.084	Comprom	-1.748	Comprom	-1.416	0.052	GT	Sens
GT	Sense	Sense	-0.215	Detected	0.215	Detected	0.000	-3.134	Detected	-0.996	Detected	-2.065	0.199	GT	Sens
GT	Sense	Sense	-0.291	Detected	0.291	Detected	0.000	-2.642	Detected	-0.985	Detected	-1.814	0.175	GT	Sens
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-1.870	Comprom	-1.052	Comprom	-1.461	0.070	GT	Sens
GT	Sense	Sense	-0.173	Detected	0.173	Detected	0.000	-1.522	Comprom	-1.283	Comprom	-1.403	0.022	GT	Sens
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-1.221	Detected	-0.925	Detected	-1.073	0.020	GT	Sens
GT	Sense	Sense	0.182	Detected	-0.182	Detected	0.000	-1.345	Comprom	-2.173	Comprom	-1.759	0.060	GT	Sens
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	-1.469	Detected	-0.841	Detected	-1.155	0.067	GT	Sens
GT	Sense	Sense	0.292	Detected	-0.292	Detected	0.000	-1.260	Comprom	-1.437	Comprom	-1.348	0.048	GT	Sens
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.427	Detected	-1.150	Detected	-1.288	0.012	GT	Sens
GT	Sense	Sense	-0.108	Detected	0.108	Detected	0.000	-3.877	Comprom	-1.965	Comprom	-2.921	0.094	GT	Sens
GT	Sense	Sense	-0.602	Detected	0.602	Detected	0.000	-2.557	Detected	-1.429	Detected	-1.993	0.137	GT	Sens
GT	Sense	Sense	-0.120	Detected	0.120	Detected	0.000	-2.365	Comprom	-1.180	Detected	-1.773	0.099	GT	Sens
GT	Sense	Sense	-0.317	Detected	0.317	Detected	0.000	-1.542	Comprom	-0.904	Comprom	-1.223	0.113	GT	Sens
GT	Sense	Sense	-0.294	Detected	0.294	Detected	0.000	-1.634	Comprom	-1.042	Detected	-1.338	0.085	GT	Sens
GT	Sense	Sense	-0.254	Detected	0.254	Detected	0.000	-1.475	Comprom	-1.701	Comprom	-1.588	0.029	GT	Sens
GT	Sense	Sense	-0.380	Detected	0.380	Detected	0.000	-1.915	Detected	-0.942	Detected	-1.428	0.147	GT	Sens
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-1.572	Detected	-1.868	Detected	-1.720	0.011	GT	Sens
GT	Sense	Sense	-0.219	Detected	0.219	Detected	0.000	-1.451	Detected	-1.853	Detected	-1.652	0.031	GT	Sens
GT	Sense	Sense	-0.579	Detected	0.579	Detected	0.000	-1.610	Comprom	-0.856	Detected	-1.233	0.216	GT	Sens
GT	Sense	Sense	-0.197	Detected	0.197	Detected	0.000	-1.280	Comprom	-1.268	Comprom	-1.274	0.023	GT	Sens
GT	Sense	Sense	-0.155	Detected	0.155	Detected	0.000	-2.248	Detected	-2.645	Detected	-2.446	0.010	GT	Sens
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	-2.689	Detected	-2.344	Detected	-2.516	0.010	GT	Sens
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	-1.674	Detected	-1.679	Detected	-1.677	0.000	GT	Sens
GT	Sense	Sense	-0.278	Detected	0.278	Detected	0.000	-2.596	Detected	-1.702	Detected	-2.149	0.055	GT	Sens
GT	Sense	Sense	-0.298	Detected	0.298	Detected	0.000	-2.132	Detected	-1.634	Detected	-1.883	0.040	GT	Sens
GT	Sense	Sense	-0.221	Detected	0.221	Detected	0.000	-1.543	Detected	-0.880	Detected	-1.211	0.093	GT	Sens
GT	Sense	Sense	-0.308	Detected	0.308	Detected	0.000	-1.009	Detected	-1.027	Detected	-1.018	0.081	GT	Sens
GT	Sense	Sense	0.060	Detected	-0.060	Detected	0.000	-1.255	Detected	-1.765	Detected	-1.510	0.029	GT	Sens
GT	Sense	Sense	0.226	Detected	-0.226	Detected	0.000	-1.841	Detected	-0.978	Detected	-1.409	0.102	GT	Sens
GT	Sense	Sense	0.255	Detected	-0.255	Detected	0.000	-2.133	Detected	-1.161	Detected	-1.647	0.095	GT	Sens
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-1.942	Comprom	-1.440	Comprom	-1.691	0.023	GT	Sens
GT	Sense	Sense	-0.892	Detected	0.892	Detected	0.000	-2.399	Detected	-1.010	Detected	-1.705	0.271	GT	Sens
GT	Sense	Sense	-0.768	Detected	0.768	Detected	0.000	-2.418	Detected	-1.285	Detected	-1.851	0.192	GT	Sens
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.311	Detected	-1.144	Detected	-1.228	0.007	GT	Sens
GT	Sense	Sense	-0.143	Detected	0.143	Detected	0.000	-1.705	Detected	-1.739	Detected	-1.722	0.007	GT	Sens
GT	Sense	Sense	-0.125	Detected	0.125	Detected	0.000	-1.625	Detected	-1.484	Detected	-1.555	0.008	GT	Sens
GT	Sense	Sense	-0.067	Detected	0.067	Detected	0.000	-2.299	Comprom	-2.454	Comprom	-2.376	0.002	GT	Sens
GT	Sense	Sense	0.170	Detected	-0.170	Detected	0.000	-1.749	Detected	-1.596	Detected	-1.672	0.012	GT	Sens
GT	Sense	Sense	-0.509	Detected	0.509	Detected	0.000	-1.476	Comprom	-1.405	Comprom	-1.440	0.106	GT	Sens
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-1.393	Detected	-1.143	Detected	-1.268	0.010	GT	Sens
GT	Sense	Sense	0.335	Detected	-0.335	Detected	0.000	-1.948	Detected	-2.154	Comprom	-2.051	0.028	GT	Sens
GT	Sense	Sense	-0.067	Detected	0.067	Detected	0.000	-1.279	Detected	-1.497	Detected	-1.388	0.008	GT	Sens
GT	Sense	Sense	-0.929	Detected	0.929	Detected	0.000	-1.273	Detected	-1.020	Detected	-1.147	0.346	GT	Sens
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	-1.383	Comprom	-1.053	Comprom	-1.218	0.027	GT	Sens
GT	Sense	Sense	-0.014	Detected	0.014	Detected	0.000	-2.071	Comprom	-3.108	Comprom	-2.589	0.038	GT	Sens
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	-2.546	Detected	-4.370	Comprom	-3.458	0.063	GT	Sens
GT	Sense	Sense	-0.927	Detected	0.927	Detected	0.000	-0.887	Detected	-1.318	Detected	-1.102	0.367	GT	Sens
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-1.477	Detected	-1.387	Detected	-1.432	0.004	GT	Sens
GT	Sense	Sense	-0.009	Detected	0.009	Detected	0.000	-1.256	Comprom	-0.960	Comprom	-1.108	0.017	GT	Sens
GT	Sense	Sense	-0.276	Detected	0.276	Detected	0.000	-1.181	Detected	-0.835	Detected	-1.008	0.091	GT	Sens
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-1.270	Detected	-1.215	Detected	-1.243	0.004	GT	Sens
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	-1.168	Comprom	-1.613	Comprom	-1.391	0.033	GT	Sens
GT	Sense	Sense	-0.956	Detected	0.956	Detected	0.000	-1.920	Detected	-1.804	Detected	-1.862	0.191	GT	Sens
GT	Sense	Sense	-1.175	Detected	1.175	Detected	0.000	-2.245	Detected	-2.220	Detected	-2.232	0.198	GT	Sens
GT	Sense	Sense	-0.050	Detected	0.050	Detected	0.000	-2.274	Comprom	-1.670	Comprom	-1.972	0.023	GT	Sens
GT	Sense	Sense	-0.174	Detected	0.174	Detected	0.000	-2.075	Detected	-0.914	Detected	-1.495	0.132	GT	Sens
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-1.689	Detected	-1.334	Detected	-1.511	0.015	GT	Sens
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	-1.128	Detected	-1.477	Comprom	-1.303	0.023	GT	Sens
GT	Sense	Sense	-0.283	Detected	0.283	Detected	0.000	-1.568	Comprom	-1.798	Comprom	-1.683	0.031	GT	Sens
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	-0.947	Detected	-1.548	Comprom	-1.248	0.062	GT	Sens
GT	Sense	Sense	-0.297	Detected	0.297	Detected	0.000	-1.205	Detected	-0.885	Detected	-1.045	0.091	GT	Sens
GT	Sense	Sense	0.213	Detected	-0.213	Detected	0.000	-1.606	Comprom	-1.360	Comprom	-1.483	0.026	GT	Sens
GT	Sense	Sense	-0.203	Detected	0.203	Detected	0.000	-1.216	Detected	-0.805	Detected	-1.010	0.073	GT	Sens
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.181	Detected	-1.042	Detected	-1.111	0.008	GT	Sens
GT	Sense	Sense	-0.291	Detected	0.291	Detected	0.000	-1.520	Detected	-0.854	Detected	-1.187	0.115	GT	Sens
GT	Sense	Sense	-0.336	Detected	0.336	Detected	0.000	-2.839	Comprom	-2.390	Comprom	-2.615	0.023	GT	Sens
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	-1.734	Comprom	-0.916	Detected	-1.325	0.084	GT	Sens
GT	Sense	Sense	-1.201	Detected	1.201	Detected	0.000	-1.841	Detected	-1.554	Detected	-1.698	0.296	GT	Sens
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-1.172	Detected	-1.421	Detected	-1.296	0.012	GT	Sens
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-1.067	Detected	-1.357	Detected	-1.212	0.014	GT	Sens
GT	Sense	Sense	-0.166	Detected	0.166	Detected	0.000	-1.710	Comprom	-1.832	Comprom	-1.771	0.010	GT	Sens
GT	Sense	Sense	-0.181	Detected	0.181	Detected	0.000	-1.207	Detected	-0.957	Detected	-1.082	0.039	GT	Sens
GT	Sense	Sense	-0.753	Detected	0.753	Detected	0.000	-1.447	Comprom	-1.730	Comprom	-1.588	0.174	GT	Sens
GT	Sense	Sense	0.294	Detected	-0.294	Detected	0.000	-0.829	Detected	-1.618	Comprom	-1.223	0.131	GT	Sens
GT	Sense	Sense	-0.355	Detected	0.355	Detected	0.000	-2.037	Detected	-1.527	Detected	-1.782	0.055	GT	Sens
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-1.324	Detected	-1.301	Detected	-1.312	0.008	GT	Sens
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	-1.352	Detected	-1.363	Detected	-1.358	0.009	GT	Sens
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	-1.142	Detected	-1.063	Detected	-1.103	0.023	GT	Sens
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-1.090	Detected	-1.066	Detected	-1.078	0.007	GT	Sens
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	-1.332	Detected	-1.097	Detected	-1.215	0.010	GT	Sens
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-1.300	Comprom	-0.873	Comprom	-1.086	0.037	GT	Sens
GT	Sense	Sense	-0.321	Detected	0.321	Detected	0.000	-1.000	Comprom	-1.303	Comprom	-1.151	0.083	GT	Sens
GT	Sense	Sense	-0.339	Detected	0.339	Detected	0.000	-1.394	Detected	-1.803	Comprom	-1.598	0.056	GT	Sens
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	-1.321	Detected	-1.298	Detected	-1.309	0.005	GT	Sens
GT	Sense	Sense	-0.713	Detected	0.713	Detected	0.000	-0.981	Detected	-1.149	Comprom	-1.065	0.276	GT	Sens
GT	Sense	Sense	-0.990	Detected	0.990	Detected	0.000	-4.515	Comprom	-1.953	Detected	-3.234	0.184	GT	Sens
GT	Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-1.351	Comprom	-2.647	Comprom	-1.999	0.091	GT	Sens
GT	Sense	Sense	0.091	Detected	-0.091	Detected	0.000	-1.336	Detected	-1.518	Detected	-1.427	0.008	GT	Sens
GT	Sense	Sense	-0.305	Detected	0.305	Detected	0.000	-1.040	Detected	-1.296	Detected	-1.168	0.072	GT	Sens
GT	Sense	Sense	-0.130	Detected	0.130	Detected	0.000	-1.616	Detected	-1.531	Detected	-1.573	0.007	GT	Sens
GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	-1.947	Detected	-1.407	Detected	-1.677	0.029	GT	Sens
GT	Sense	Sense	-0.289	Detected	0.289	Detected	0.000	-1.352	Detected	-0.955	Detected	-1.154	0.081	GT	Sens
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.062	Detected	-0.951	Detected	-1.006	0.006	GT	Sens
GT	Sense	Sense	-0.069	Detected	0.069	Detected	0.000	-2.499	Detected	-1.697	Detected	-2.098	0.036	GT	Sens
GT	Sense	Sense	-0.421	Detected	0.421	Detected	0.000	-2.848	Comprom	-1.227	Detected	-2.037	0.155	GT	Sens
GT	Sense	Sense	0.229	Detected	-0.229	Detected	0.000	-1.681	Comprom	-2.091	Comprom	-1.886	0.026	GT	Sens
GT	Sense	Sense	0.056	Detected	-0.056	Detected	0.000	-1.609	Detected	-1.102	Detected	-1.355	0.035	GT	Sens
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-2.809	Detected	-2.814	Detected	-2.812	0.001	GT	Sens
GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-2.074	Detected	-2.417	Detected	-2.245	0.011	GT	Sens
GT	Sense	Sense	-0.046	Detected	0.046	Detected	0.000	-1.227	Comprom	-2.195	Comprom	-1.711	0.072	GT	Sens
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.169	Detected	-0.967	Detected	-1.068	0.011	GT	Sens
GT	Sense	Sense	-0.180	Detected	0.180	Detected	0.000	-1.720	Detected	-1.398	Detected	-1.559	0.023	GT	Sens
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-1.240	Detected	-1.128	Detected	-1.184	0.005	GT	Sens
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-1.264	Detected	-1.675	Detected	-1.469	0.022	GT	Sens
GT	Sense	Sense	-0.653	Detected	0.653	Detected	0.000	-3.109	Comprom	-2.676	Comprom	-2.892	0.052	GT	Sens
GT	Sense	Sense	-0.172	Detected	0.172	Detected	0.000	-2.506	Comprom	-1.792	Comprom	-2.149	0.032	GT	Sens
GT	Sense	Sense	-0.216	Detected	0.216	Detected	0.000	-0.893	Detected	-1.196	Detected	-1.045	0.058	GT	Sens
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	-1.207	Detected	-1.647	Detected	-1.427	0.025	GT	Sens
GT	Sense	Sense	-0.461	Detected	0.461	Detected	0.000	-1.518	Comprom	-2.118	Comprom	-1.818	0.081	GT	Sens
GT	Sense	Sense	0.191	Detected	-0.191	Detected	0.000	-1.536	Detected	-0.849	Detected	-1.193	0.094	GT	Sens
GT	Sense	Sense	0.305	Detected	-0.305	Detected	0.000	-2.289	Comprom	-2.422	Comprom	-2.355	0.017	GT	Sens
GT	Sense	Sense	-0.373	Detected	0.373	Detected	0.000	-2.641	Comprom	-2.340	Comprom	-2.491	0.025	GT	Sens
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.553	Detected	-1.050	Detected	-1.302	0.035	GT	Sens
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-1.254	Detected	-0.883	Detected	-1.068	0.033	GT	Sens
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-1.776	Detected	-1.472	Detected	-1.624	0.009	GT	Sens
GT	Sense	Sense	-0.545	Detected	0.545	Detected	0.000	-1.816	Comprom	-2.375	Comprom	-2.095	0.076	GT	Sens
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	-1.101	Detected	-1.552	Comprom	-1.326	0.042	GT	Sens
GT	Sense	Sense	-0.125	Detected	0.125	Detected	0.000	-1.062	Detected	-1.315	Detected	-1.188	0.022	GT	Sens
GT	Sense	Sense	-0.068	Detected	0.068	Detected	0.000	-1.391	Detected	-1.837	Comprom	-1.614	0.020	GT	Sens
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-1.237	Detected	-0.859	Detected	-1.048	0.035	GT	Sens
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-1.636	Comprom	-1.381	Comprom	-1.508	0.016	GT	Sens
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.087	Detected	-0.926	Detected	-1.006	0.010	GT	Sens
GT	Sense	Sense	-0.046	Detected	0.046	Detected	0.000	-1.393	Detected	-1.156	Detected	-1.275	0.010	GT	Sens
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-0.923	Detected	-1.536	Detected	-1.229	0.064	GT	Sens
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	-1.058	Detected	-1.509	Detected	-1.284	0.031	GT	Sens
GT	Sense	Sense	-0.208	Detected	0.208	Detected	0.000	-1.080	Comprom	-1.176	Comprom	-1.128	0.034	GT	Sens
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	-1.928	Comprom	-2.663	Comprom	-2.295	0.025	GT	Sens
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	-2.072	Comprom	-0.943	Detected	-1.508	0.117	GT	Sens
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-0.928	Detected	-1.200	Detected	-1.064	0.018	GT	Sens
GT	Sense	Sense	0.086	Detected	-0.086	Detected	0.000	-0.989	Detected	-1.023	Detected	-1.006	0.008	GT	Sens
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-1.410	Comprom	-1.451	Comprom	-1.430	0.001	GT	Sens
GT	Sense	Sense	0.108	Detected	-0.108	Detected	0.000	-1.808	Detected	-1.247	Detected	-1.527	0.037	GT	Sens
GT	Sense	Sense	0.037	Detected	-0.037	Detected	0.000	-1.795	Detected	-1.314	Detected	-1.554	0.024	GT	Sens
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	-2.071	Comprom	-2.269	Comprom	-2.170	0.006	GT	Sens
GT	Sense	Sense	-0.005	Detected	0.005	Detected	0.000	-1.075	Detected	-0.982	Detected	-1.029	0.002	GT	Sens
GT	Sense	Sense	-0.282	Detected	0.282	Detected	0.000	-1.051	Detected	-1.304	Detected	-1.177	0.063	GT	Sens
GT	Sense	Sense	-0.520	Detected	0.520	Detected	0.000	-1.539	Comprom	-1.015	Comprom	-1.277	0.160	GT	Sens
GT	Sense	Sense	0.091	Detected	-0.091	Detected	0.000	-1.358	Comprom	-2.058	Comprom	-1.708	0.042	GT	Sens
GT	Sense	Sense	-0.153	Detected	0.153	Detected	0.000	-2.153	Detected	-0.882	Detected	-1.518	0.146	GT	Sens
GT	Sense	Sense	-0.150	Detected	0.150	Detected	0.000	-2.295	Detected	-1.041	Detected	-1.668	0.123	GT	Sens
GT	Sense	Sense	-0.227	Detected	0.227	Detected	0.000	-1.276	Detected	-1.190	Detected	-1.233	0.033	GT	Sens
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	-1.919	Detected	-1.876	Detected	-1.898	0.002	GT	Sens
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	-2.102	Detected	-2.151	Detected	-2.126	0.004	GT	Sens
GT	Sense	Sense	-0.061	Detected	0.061	Detected	0.000	-0.954	Detected	-1.079	Detected	-1.016	0.007	GT	Sens
GT	Sense	Sense	-0.912	Detected	0.912	Detected	0.000	-3.338	Detected	-2.095	Detected	-2.716	0.133	GT	Sens
GT	Sense	Sense	-0.265	Detected	0.265	Detected	0.000	-1.440	Detected	-0.881	Detected	-1.161	0.095	GT	Sens
GT	Sense	Sense	-0.223	Detected	0.223	Detected	0.000	-1.150	Comprom	-1.364	Comprom	-1.257	0.037	GT	Sens
GT	Sense	Sense	-0.440	Detected	0.440	Detected	0.000	-0.958	Detected	-1.404	Detected	-1.181	0.139	GT	Sens
GT	Sense	Sense	-0.149	Detected	0.149	Detected	0.000	-1.318	Comprom	-1.013	Comprom	-1.165	0.032	GT	Sens
GT	Sense	Sense	0.548	Detected	-0.548	Detected	0.000	-0.881	Detected	-1.129	Comprom	-1.005	0.216	GT	Sens
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-1.254	Detected	-1.672	Detected	-1.463	0.026	GT	Sens
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.581	Detected	-0.963	Detected	-1.272	0.055	GT	Sens
GT	Sense	Sense	-0.116	Detected	0.116	Detected	0.000	-1.638	Detected	-1.122	Detected	-1.380	0.040	GT	Sens
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-1.600	Detected	-0.955	Detected	-1.278	0.059	GT	Sens
GT	Sense	Sense	0.327	Detected	-0.327	Detected	0.000	-1.393	Detected	-1.089	Detected	-1.241	0.075	GT	Sens
GT	Sense	Sense	-0.137	Detected	0.137	Detected	0.000	-5.920	Comprom	-6.202	Comprom	-6.061	0.001	GT	Sens

GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-5.538	Comprom	-5.146	Comprom	-5.342	0.002	GT Sens	contig39	contig39	Unannota	GGCAATTAAAAAGGCTACATAATACAATTCAAAGAGGTAGGTTTCTCAT	contig39	Solvc10g	Unknown	GO:0016	SL2.40ch	AT3G138	AtIDD11	AtIDD11	chr3:454	103.409	95.2694	2.79726	3.2251	2.25771	2.86122
GT	Sense	Sense	0.170	Detected	-0.170	Detected	0.000	-1.271	Detected	-1.108	Detected	-1.189	0.024	GT Sens	contig40	contig40	Unannota	TTGGGGTTCTCATAGCTTCTCAGTCCTCCAACTGTTGTAGAGTAGAAA	contig40	Solvc01g	Asparagine synthet		SL2.40ch	AT5G19140.2				1501.2	926.454	1102.24	1083.08	516.469	558.371
GT	Sense	Sense	0.346	Detected	-0.346	Detected	0.000	-1.307	Detected	-0.968	Detected	-1.138	0.098	GT Sens	contig40	contig40	Unannota	ATATTCATTTATTATTTGACCTGAATTACAATGTCTCCACATAATTATTT	contig40	Solvc01g	Unknown Protein (A		SL2.40ch	AT4G04670.1		Met-10+	chr4:236	172.703	83.5236	128.276	68.5612	51.2879	62.6492
GT	Sense	Sense	0.379	Detected	-0.379	Detected	0.000	-1.388	Detected	-1.095	Detected	-1.242	0.093	GT Sens	contig40	contig40	Unannota	TTAAATTGAAAATTTAACTTCAAACTTGTTTTGTGGTATTGTTACGCAG	contig40	Solvc01g	Unknown Protein (A		SL2.40ch	AT4G04670.1		Met-10+	chr4:236	182.497	84.3026	117.035	68.081	50.0826	59.2508
GT	Sense	Sense	-0.471	Detected	0.471	Detected	0.000	-1.209	Comprom	-1.204	Comprom	-1.206	0.124	GT Sens	contig40	contig40	Unannota	GGGATGGCTGCAGATTCAGCTAACTCTTAACAAAAACTAATCAAAGTAA	contig40	Solvc12g	Inositol 1	GO:0004	SL2.40ch	AT5G38310.1		unknown	chr5:153	12.3711	18.5668	5.09388	6.81754	6.9303	6.71204
GT	Sense	Sense	0.110	Detected	-0.110	Detected	0.000	-1.311	Detected	-0.991	Detected	-1.151	0.027	GT Sens	contig40	contig40	Unannota	GAGGATTCTCTTCAAATGGGTTATGCTTGAATAGGTTGAGATTGAACC	contig40	Solvc01g034170.1.1				AT5G56452.2				44.997	30.1999	34.8737	33.7433	15.7001	18.9221
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-1.822	Detected	-0.890	Detected	-1.356	0.103	GT Sens	contig40	contig40	Unannota	GAATTTGGAGATTCAAACACATCATATGAAGTGGGCTGGTTATCATCTT	contig40	Solvc11g	Membrane bound O		SL2.40ch	AT3G58980.1				253.347	219.181	144.321	73.5412	70.4265	129.772
GT	Sense	Sense	0.111	Detected	-0.111	Detected	0.000	-2.039	Detected	-0.960	Detected	-1.500	0.113	GT Sens	contig40	contig40	Unannota	AGTCGAGACATCTTGAAGCGAGCTAGTCTTGTAAGTTGTAAGGTGCAT	contig40	Solvc11g	Membrane bound O		SL2.40ch	AT3G58980.1				466.654	312.76	228.359	111.133	98.2139	200.358
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-2.199	Comprom	-1.971	Comprom	-2.085	0.005	GT Sens	contig40	contig40	Unannota	CCTGTCTTCTTTCTAGGTAAAAGCCAAAAGATAATGCTTTAGTCTCAGG	contig40	Solvc09g	Unknown Protein (A		SL2.40ch	AT5G18980.1		binding	chr5:633	18.1198	12.4975	16.9018	11.0022	3.46299	3.91776
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	-2.019	Comprom	-1.863	Comprom	-1.941	0.002	GT Sens	contig40	contig40	Unannota	CAAACGTATTCATTACCCCACTGTACTTGAAGCTTTTTATTCAGTGTAC	contig40	Solvc12g	Pentatricopeptide re		SL2.40ch	AT3G61900.1				20.4884	15.2717	13.9154	12.8912	4.61135	4.96258
GT	Sense	Sense	-0.231	Detected	0.231	Detected	0.000	-1.770	Comprom	-1.322	Comprom	-1.546	0.041	GT Sens	contig40	contig40	Unannota	GCCAACCTTCACAATTCACAAATCAAACTTTCTCTTATATGACTTGCTC	contig40	Solvc12g	Pentatricopeptide re		SL2.40ch	AT3G61900.1				13.2555	14.2648	13.5779	15.1731	4.26001	5.61168
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	-1.728	Detected	-1.057	Detected	-1.393	0.060	GT Sens	contig40	contig40	Unannota	AGTTTAGTTAATCAAGTAAAAGAACTTCTTTTTTAAGGCGATTAATAAT	contig40	Solvc08g	Blight-associated p		SL2.40ch	AT5G41120.1		esterase	chr5:164	171.649	113.196	88.1443	40.7038	44.4577	68.3786
GT	Sense	Sense	-0.375	Detected	0.375	Detected	0.000	-1.022	Detected	-0.988	Detected	-1.005	0.116	GT Sens	contig40	contig40	Unannota	TTTTATTCATAGCAATCTGGCGGAAAATTACAGCAATCATATCACAGAG	contig40	Solvc09g	Dymeclin	GO:0005	SL2.40ch	AT5G57000.1				30.9921	40.7352	27.6931	20.9664	18.4959	18.2735
GT	Sense	Sense	-0.489	Detected	0.489	Detected	0.000	-3.838	Detected	-2.714	Detected	-3.276	0.048	GT Sens	contig40	contig40	Unannota	TTTGTACTAAGTTATATAAACAATGAAATAGATACTTTTTCTTCTTCTAA	contig40	Solvc03g	Xylogluca	GO:00167	SL2.40ch	AT5G50540.1		unknown	chr5:205	706.1	1086.83	402.154	82.4848	64.7431	136.226
GT	Sense	Sense	-0.658	Detected	0.658	Detected	0.000	-3.276	Detected	-2.028	Detected	-2.652	0.100	GT Sens	contig40	contig40	Unannota	TGGGCTAGTTTTATCCAAAAGTGAACAGCCCAAAGCCTAAAAAATAAGA	contig40	Solvc03g	Xylogluca	GO:00167	SL2.40ch	AT5G50540.1		unknown	chr5:205	309.655	602.83	164.78	39.068	47.1285	108.07
GT	Sense	Sense	-0.178	Detected	0.178	Detected	0.000	-1.467	Detected	-0.979	Detected	-1.223	0.056	GT Sens	contig40	contig40	Unannota	CCTCTATTTCACTAGTTTCTTATTGCTCCGATAGTTTGAACAGATGCAT	contig40	Solvc11g	Unknown Protein (A		SL2.40ch	AT3G21130.1				81.5627	81.6159	118.937	76.3688	31.1968	42.2385
GT	Sense	Sense	-0.118	Detected	0.118	Detected	0.000	-1.478	Detected	-1.031	Detected	-1.254	0.038	GT Sens	contig40	contig40	Unannota	CATGCTATTAGTCATTTTTCTACCTTGCAATGAGCATTGCTTTGGCTTT	contig40	Solvc11g	Unknown Protein (A		SL2.40ch	AT3G21130.1				72.7709	66.9599	93.4204	61.234	26.482	34.8648
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-1.174	Comprom	-0.950	Comprom	-1.062	0.018	GT Sens	contig40	contig40	Unannota	ACGAAGATCAAATGGCTCAGAATCACAGGGAAATATAGGTCACAAACCT	contig40	Solvc03g	Unknown Protein (A		SL2.40ch	AT3G52700.1		unknown	chr3:195	17.8135	15.8597	15.4464	10.28	7.87384	8.87694
GT	Sense	Sense	-0.065	Detected	0.065	Detected	0.000	-1.676	Detected	-1.942	Detected	-1.809	0.007	GT Sens	contig40	contig40	Unannota	CTTTTGGTCAAAATATAAATAGGGGTTGAAAGAAAAGAATCTTTCGATT	contig40	Solvc12g	Beta-1,3-	GO:00167	SL2.40ch	AT5G59930.1		DC1 dom	chr5:241	56.4393	48.2891	41.3715	35.7211	17.2723	13.8585
GT	Sense	Sense	-0.257	Detected	0.257	Detected	0.000	-1.536	Detected	-1.029	Detected	-1.283	0.071	GT Sens	contig401	contig401	Unannota	CTGTGACTGTCGATTTTCTCTAGTGATATTCTAAATCGTTATATGTGTT	contig401	Solvc07g	Unknown Protein (A		SL2.40ch	AT5G61140.1		DEAD bo	chr5:245	216.29	241.453	198.763	151.853	83.2733	114.248
GT	Sense	Sense	-0.439	Detected	0.439	Detected	0.000	-1.368	Detected	-1.049	Detected	-1.208	0.122	GT Sens	contig401	contig401	Unannota	GTCCATAAATACAGAAACCTAAGGCACACACCAGGTTGAAACAAAATCA	contig401	Solvc10g	Ubiquitin	GO:0043	SL2.40ch	AT1G653	UBO13	UBO13:	chr1:242	21.8346	31.3646	12.4467	8.13653	10.7164	12.9041
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-2.191	Comprom	-1.121	Detected	-1.656	0.091	GT Sens	contig401	contig401	Unannota	GCCCTTTCTGATTCAAAACCAGACCCAAACACAACAAATAACACAATTA	contig401	Solvc10g	Ubiquitin	GO:0043	SL2.40ch	AT1G653	UBO13	UBO13:	chr1:242	30.0387	21.746	12.1583	16.8039	5.91507	11.9871
GT	Sense	Sense	-0.668	Detected	0.668	Detected	0.000	-2.316	Detected	-1.409	Detected	-1.862	0.147	GT Sens	contig401	contig401	Unannota	TAAACCCTGGACACCAGAGTTCAAATTCCAGCAGAGCCATCTATTCCTC	contig401	Solvc11g	Glutamyl-	GO:0016	SL2.40ch	AT4G04650.1				74.5969	147.181	152.865	56.5562	22.2417	40.2639
GT	Sense	Sense	-0.609	Detected	0.609	Detected	0.000	-2.769	Detected	-1.258	Detected	-2.014	0.174	GT Sens	contig401	contig401	Unannota	AAGAGAAAAGTTGTAACTAGACTGCATCCAACAGTGGCCAAGTGGTCA	contig401	Solvc11g	Glutamyl-	GO:0016	SL2.40ch	AT4G04650.1				71.8232	130.625	137.187	43.1408	15.0167	41.3112
GT	Sense	Sense	-0.149	Detected	0.149	Detected	0.000	-1.787	Detected	-1.659	Detected	-1.723	0.009	GT Sens	contig401	contig401	Unannota	GGTTCCTTTCACCCATTGGGTTTTCTAGTTTTCAGCCAGATTCTTAATT	contig401	Solvc08g	Transpos	GO:0003	SL2.40ch	AT4G183	DEG5, DE	DEG5 (D	chr4:101	368.836	354.492	217.673	227.868	110.711	116.84
GT	Sense	Sense	-0.607	Detected	0.607	Detected	0.000	-3.395	Comprom	-2.285	Comprom	-2.840	0.075	GT Sens	contig401	contig401	Unannota	CGGGATTTCTCAATGATGCCATGCTTTTTGCTTTTCAATTGTTTACTAA	contig401	Solvc05g	Transcriptional acti		SL2.40ch	AT5G53850.1		haloacid	chr5:218	14.1414	25.645	5.22499	6.10306	1.91305	3.98825
GT	Sense	Sense	-0.568	Detected	0.568	Detected	0.000	-2.264	Comprom	-1.330	Comprom	-1.797	0.134	GT Sens	contig401	contig401	Unannota	GTGAAACTGCTCCTTGTGATATCTGACGAAGCATTTTAATCTTTGATTG	contig401	Solvc05g	Transcriptional acti		SL2.40ch	AT5G53850.1		haloacid	chr5:218	9.96397	17.1084	5.92902	2.34605	2.87343	5.2973

GT	Sens	Sense	-0.036	Detected	0.036	Detected	0.000	-1.783	Detected	-1.429	Detected	-1.606	0.012	GT	Sens
GT	Sens	Sense	-0.783	Detected	0.783	Detected	0.000	-1.593	Comprom	-2.611	Comprom	-2.102	0.153	GT	Sens
GT	Sens	Sense	-0.689	Detected	0.689	Detected	0.000	-1.609	Detected	-1.057	Detected	-1.333	0.214	GT	Sens
GT	Sens	Sense	-0.167	Detected	0.167	Detected	0.000	-1.230	Detected	-1.234	Detected	-1.232	0.018	GT	Sens
GT	Sens	Sense	-0.158	Detected	0.158	Detected	0.000	-1.440	Detected	-1.298	Detected	-1.369	0.016	GT	Sens
GT	Sens	Sense	0.009	Detected	-0.009	Detected	0.000	-2.169	Detected	-2.848	Comprom	-2.509	0.018	GT	Sens
GT	Sens	Sense	-0.009	Detected	0.009	Detected	0.000	-0.871	Detected	-1.310	Comprom	-1.091	0.038	GT	Sens
GT	Sens	Sense	-0.180	Detected	0.180	Detected	0.000	-1.974	Detected	-0.884	Detected	-1.429	0.131	GT	Sens
GT	Sens	Sense	-0.808	Detected	0.808	Detected	0.000	-1.493	Detected	-1.633	Detected	-1.563	0.194	GT	Sens
GT	Sens	Sense	-0.171	Detected	0.171	Detected	0.000	-1.502	Detected	-0.829	Detected	-1.166	0.091	GT	Sens
GT	Sens	Sense	0.143	Detected	-0.143	Detected	0.000	-1.126	Detected	-1.141	Detected	-1.134	0.016	GT	Sens
GT	Sens	Sense	-0.069	Detected	0.069	Detected	0.000	-2.223	Comprom	-2.349	Comprom	-2.286	0.002	GT	Sens
GT	Sens	Sense	-0.092	Detected	0.092	Detected	0.000	-1.882	Detected	-1.921	Detected	-1.901	0.002	GT	Sens
GT	Sens	Sense	-0.106	Detected	0.106	Detected	0.000	-1.041	Detected	-1.069	Detected	-1.055	0.010	GT	Sens
GT	Sens	Sense	-0.161	Detected	0.161	Detected	0.000	-1.452	Detected	-1.499	Detected	-1.475	0.012	GT	Sens
GT	Sens	Sense	-0.759	Detected	0.759	Detected	0.000	-1.813	Detected	-0.877	Detected	-1.345	0.270	GT	Sens
GT	Sens	Sense	1.230	Detected	-1.230	Detected	0.000	-3.717	Detected	-3.024	Detected	-3.371	0.119	GT	Sens
GT	Sens	Sense	0.065	Detected	-0.065	Detected	0.000	-1.844	Detected	-1.329	Detected	-1.587	0.027	GT	Sens
GT	Sens	Sense	-0.227	Detected	0.227	Detected	0.000	-2.391	Detected	-0.853	Detected	-1.622	0.180	GT	Sens
GT	Sens	Sense	-0.221	Detected	0.221	Detected	0.000	-1.500	Comprom	-1.775	Comprom	-1.637	0.024	GT	Sens
GT	Sens	Sense	-0.562	Detected	0.562	Detected	0.000	-1.639	Detected	-1.341	Detected	-1.490	0.124	GT	Sens
GT	Sens	Sense	-0.062	Detected	0.062	Detected	0.000	-1.058	Detected	-1.025	Detected	-1.042	0.004	GT	Sens
GT	Sens	Sense	-0.550	Detected	0.550	Detected	0.000	-1.289	Detected	-0.851	Detected	-1.070	0.212	GT	Sens
GT	Sens	Sense	-0.124	Detected	0.124	Detected	0.000	-1.720	Detected	-1.585	Detected	-1.653	0.007	GT	Sens
GT	Sens	Sense	-0.242	Detected	0.242	Detected	0.000	-2.712	Detected	-1.188	Detected	-1.950	0.135	GT	Sens
GT	Sens	Sense	0.118	Detected	-0.118	Detected	0.000	-2.052	Detected	-1.851	Detected	-1.952	0.006	GT	Sens
GT	Sens	Sense	-0.799	Detected	0.799	Detected	0.000	-2.726	Detected	-1.094	Detected	-1.910	0.237	GT	Sens
GT	Sens	Sense	-0.121	Detected	0.121	Detected	0.000	-1.772	Detected	-1.870	Detected	-1.821	0.005	GT	Sens
GT	Sens	Sense	-0.088	Detected	0.088	Detected	0.000	-1.287	Detected	-1.409	Detected	-1.348	0.006	GT	Sens
GT	Sens	Sense	-0.361	Detected	0.361	Detected	0.000	-3.186	Detected	-1.750	Detected	-2.468	0.092	GT	Sens
GT	Sens	Sense	-0.040	Detected	0.040	Detected	0.000	-2.792	Comprom	-1.791	Comprom	-2.291	0.045	GT	Sens
GT	Sens	Sense	0.007	Detected	-0.007	Detected	0.000	-1.137	Detected	-0.926	Detected	-1.031	0.010	GT	Sens
GT	Sens	Sense	-0.225	Detected	0.225	Detected	0.000	-0.834	Detected	-1.555	Detected	-1.194	0.107	GT	Sens
GT	Sens	Sense	-0.738	Detected	0.738	Detected	0.000	-2.936	Detected	-1.391	Detected	-2.163	0.180	GT	Sens
GT	Sens	Sense	-0.911	Detected	0.911	Detected	0.000	-2.827	Detected	-0.919	Detected	-1.873	0.292	GT	Sens
GT	Sens	Sense	-0.821	Detected	0.821	Detected	0.000	-5.899	Comprom	-1.171	Detected	-3.535	0.293	GT	Sens
GT	Sens	Sense	0.077	Detected	-0.077	Detected	0.000	-1.568	Detected	-1.518	Detected	-1.543	0.003	GT	Sens
GT	Sens	Sense	0.068	Detected	-0.068	Detected	0.000	-0.804	Detected	-2.075	Comprom	-1.439	0.153	GT	Sens
GT	Sens	Sense	0.047	Detected	-0.047	Detected	0.000	-1.051	Detected	-1.046	Detected	-1.049	0.002	GT	Sens
GT	Sens	Sense	-0.208	Detected	0.208	Detected	0.000	-1.889	Detected	-2.211	Detected	-2.050	0.016	GT	Sens
GT	Sens	Sense	-0.555	Detected	0.555	Detected	0.000	-1.280	Detected	-0.806	Detected	-1.043	0.226	GT	Sens
GT	Sens	Sense	-0.351	Detected	0.351	Detected	0.000	-2.084	Detected	-1.136	Detected	-1.610	0.112	GT	Sens
GT	Sens	Sense	0.064	Detected	-0.064	Detected	0.000	-1.610	Comprom	-1.935	Comprom	-1.772	0.010	GT	Sens
GT	Sens	Sense	-0.666	Detected	0.666	Detected	0.000	-1.427	Detected	-1.371	Detected	-1.399	0.171	GT	Sens
GT	Sens	Sense	-0.316	Detected	0.316	Detected	0.000	-1.867	Detected	-1.285	Detected	-1.576	0.067	GT	Sens
GT	Sens	Sense	-0.637	Detected	0.637	Detected	0.000	-5.076	Detected	-1.656	Detected	-3.366	0.206	GT	Sens
GT	Sens	Sense	-0.165	Detected	0.165	Detected	0.000	-1.206	Detected	-1.191	Detected	-1.198	0.019	GT	Sens
GT	Sens	Sense	-0.204	Detected	0.204	Detected	0.000	-1.381	Detected	-1.191	Detected	-1.286	0.029	GT	Sens
GT	Sens	Sense	-0.345	Detected	0.345	Detected	0.000	-3.085	Comprom	-1.669	Comprom	-2.377	0.095	GT	Sens
GT	Sens	Sense	0.002	Detected	-0.002	Detected	0.000	-2.012	Comprom	-3.717	Comprom	-2.865	0.078	GT	Sens
GT	Sens	Sense	0.027	Detected	-0.027	Detected	0.000	-1.432	Detected	-0.852	Detected	-1.142	0.059	GT	Sens
GT	Sens	Sense	-0.527	Detected	0.527	Detected	0.000	-1.804	Detected	-1.237	Detected	-1.520	0.126	GT	Sens
GT	Sens	Sense	-0.015	Detected	0.015	Detected	0.000	-1.238	Detected	-1.450	Detected	-1.344	0.006	GT	Sens
GT	Sens	Sense	-0.868	Detected	0.868	Detected	0.000	-2.476	Detected	-1.012	Detected	-1.744	0.265	GT	Sens
GT	Sens	Sense	-0.016	Detected	0.016	Detected	0.000	-1.653	Comprom	-2.082	Comprom	-1.868	0.013	GT	Sens
GT	Sens	Sense	-0.154	Detected	0.154	Detected	0.000	-1.201	Detected	-1.397	Detected	-1.299	0.019	GT	Sens
GT	Sens	Sense	-0.107	Detected	0.107	Detected	0.000	-1.116	Detected	-1.025	Detected	-1.070	0.012	GT	Sens
GT	Sens	Sense	-0.409	Detected	0.409	Detected	0.000	-1.618	Detected	-1.538	Detected	-1.578	0.062	GT	Sens
GT	Sens	Sense	-0.512	Detected	0.512	Detected	0.000	-1.558	Detected	-1.042	Detected	-1.300	0.151	GT	Sens
GT	Sens	Sense	-0.518	Detected	0.518	Detected	0.000	-1.301	Detected	-1.628	Detected	-1.464	0.115	GT	Sens
GT	Sens	Sense	-0.234	Detected	0.234	Detected	0.000	-1.187	Comprom	-1.082	Comprom	-1.135	0.042	GT	Sens
GT	Sens	Sense	-0.213	Detected	0.213	Detected	0.000	-1.065	Detected	-0.963	Detected	-1.014	0.044	GT	Sens
GT	Sens	Sense	0.039	Detected	-0.039	Detected	0.000	-1.717	Detected	-1.110	Detected	-1.414	0.044	GT	Sens
GT	Sens	Sense	-0.047	Detected	0.047	Detected	0.000	-1.974	Detected	-1.972	Detected	-1.973	0.001	GT	Sens
GT	Sens	Sense	-0.301	Detected	0.301	Detected	0.000	-1.678	Detected	-1.279	Detected	-1.478	0.055	GT	Sens
GT	Sens	Sense	-0.058	Detected	0.058	Detected	0.000	-1.154	Detected	-1.097	Detected	-1.126	0.003	GT	Sens
GT	Sens	Sense	-0.713	Detected	0.713	Detected	0.000	-2.270	Comprom	-1.621	Comprom	-1.946	0.131	GT	Sens
GT	Sens	Sense	0.138	Detected	-0.138	Detected	0.000	-1.801	Detected	-1.356	Detected	-1.578	0.026	GT	Sens
GT	Sens	Sense	-0.076	Detected	0.076	Detected	0.000	-1.427	Detected	-0.946	Detected	-1.187	0.042	GT	Sens
GT	Sens	Sense	-0.827	Detected	0.827	Detected	0.000	-5.760	Detected	-0.976	Detected	-3.368	0.315	GT	Sens
GT	Sens	Sense	0.055	Detected	-0.055	Detected	0.000	-1.056	Detected	-1.372	Detected	-1.214	0.018	GT	Sens
GT	Sens	Sense	-1.097	Detected	1.097	Detected	0.000	-0.958	Detected	-2.093	Comprom	-1.526	0.342	GT	Sens
GT	Sens	Sense	-0.048	Detected	0.048	Detected	0.000	-0.884	Detected	-1.349	Detected	-1.116	0.042	GT	Sens
GT	Sens	Sense	-0.161	Detected	0.161	Detected	0.000	-2.856	Detected	-2.569	Detected	-2.712	0.006	GT	Sens
GT	Sens	Sense	-0.248	Detected	0.248	Detected	0.000	-1.389	Detected	-1.218	Detected	-1.304	0.038	GT	Sens
GT	Sens	Sense	0.224	Detected	-0.224	Detected	0.000	-1.245	Detected	-0.969	Detected	-1.107	0.052	GT	Sens
GT	Sens	Sense	-0.562	Detected	0.562	Detected	0.000	-2.074	Detected	-2.381	Detected	-2.228	0.062	GT	Sens
GT	Sens	Sense	-0.553	Detected	0.553	Detected	0.000	-3.667	Comprom	-1.228	Detected	-2.447	0.209	GT	Sens
GT	Sens	Sense	-0.278	Detected	0.278	Detected	0.000	-2.041	Comprom	-0.898	Detected	-1.470	0.147	GT	Sens
GT	Sens	Sense	-0.147	Detected	0.147	Detected	0.000	-2.262	Detected	-2.076	Detected	-2.169	0.006	GT	Sens
GT	Sens	Sense	-0.149	Detected	0.149	Detected	0.000	-1.129	Detected	-1.234	Detected	-1.181	0.017	GT	Sens
GT	Sens	Sense	-0.714	Detected	0.714	Detected	0.000	-1.508	Detected	-1.559	Detected	-1.533	0.165	GT	Sens
GT	Sens	Sense	-0.188	Detected	0.188	Detected	0.000	-5.057	Comprom	-4.893	Comprom	-4.975	0.002	GT	Sens
GT	Sens	Sense	0.398	Detected	-0.398	Detected	0.000	-0.982	Detected	-1.120	Detected	-1.051	0.121	GT	Sens
GT	Sens	Sense	-0.689	Detected	0.689	Detected	0.000	-2.030	Detected	-0.832	Detected	-1.431	0.258	GT	Sens
GT	Sens	Sense	-0.150	Detected	0.150	Detected	0.000	-1.398	Detected	-1.098	Detected	-1.248	0.028	GT	Sens
GT	Sens	Sense	-0.242	Detected	0.242	Detected	0.000	-2.875	Comprom	-2.714	Comprom	-2.795	0.008	GT	Sens
GT	Sens	Sense	-1.145	Detected	1.145	Detected	0.000	-1.989	Detected	-1.726	Detected	-1.857	0.248	GT	Sens
GT	Sens	Sense	-0.236	Detected	0.236	Detected	0.000	-1.251	Detected	-0.855	Detected	-1.053	0.076	GT	Sens
GT	Sens	Sense	-0.359	Detected	0.359	Detected	0.000	-1.593	Detected	-1.059	Detected	-1.326	0.098	GT	Sens
GT	Sens	Sense	-0.054	Detected	0.054	Detected	0.000	-1.426	Detected	-1.326	Detected	-1.376	0.003	GT	Sens
GT	Sens	Sense	-0.288	Detected	0.288	Detected	0.000	-3.757	Comprom	-2.966	Comprom	-3.362	0.020	GT	Sens
GT	Sens	Sense	-0.511	Detected	0.511	Detected	0.000	-1.606	Comprom	-0.962	Detected	-1.284	0.168	GT	Sens
GT	Sens	Sense	-0.069	Detected	0.069	Detected	0.000	-1.826	Detected	-2.589	Comprom	-2.207	0.030	GT	Sens
GT	Sens	Sense	-0.266	Detected	0.266	Detected	0.000	-1.022	Detected	-1.828	Detected	-1.425	0.098	GT	Sens
GT	Sens	Sense	-0.261	Detected	0.261	Detected	0.000	-2.580	Comprom	-1.870	Comprom	-2.225	0.037	GT	Sens
GT	Sens	Sense	-0.213	Detected	0.213	Detected	0.000	-1.021	Comprom	-1.397	Comprom	-1.209	0.051	GT	Sens
GT	Sens	Sense	-0.436	Detected	0.436	Detected	0.000	-2.464	Detected	-1.313	Detected	-1.889	0.120	GT	Sens
GT	Sens	Sense	-0.122	Detected	0.122	Detected	0.000	-2.252	Detected	-2.537	Detected	-2.395	0.006	GT	Sens
GT	Sens	Sense	0.305	Detected	-0.305	Detected	0.000	-1.367	Detected	-1.547	Detected	-1.457	0.044	GT	Sens
GT	Sens	Sense	0.408	Detected	-0.408	Detected	0.000	-6.060	Comprom	-1.315	Detected	-3.687	0.265	GT	Sens
GT	Sens	Sense	-0.357	Detected	0.357	Detected	0.000	-2.429	Detected	-1.636	Detected	-2.032	0.062	GT	Sens
GT	Sens	Sense	-0.098	Detected	0.098	Detected	0.000	-1.799	Detected	-1.397	Detected	-1.598	0.019	GT	Sens
GT	Sens	Sense	0.039	Detected	-0.039	Detected	0.000	-2.696	Detected	-2.289	Detected	-2.492	0.007	GT	Sens
GT	Sens	Sense	-0.213	Detected	0.213	Detected	0.000	-2.668	Detected	-2.653	Detected	-2.661	0.006	GT	Sens
GT	Sens	Sense	-0.432	Detected	0.432	Detected	0.000	-2.422	Comprom	-1.769	Comprom	-2.095	0.061	GT	Sens
GT	Sens	Sense	-0.205	Detected	0.205	Detected	0.000	-1.453	Detected	-1.400	Detected	-1.426	0.020	GT	Sens
GT	Sens	Sense	-0.884	Detected	0.884	Detected	0.000	-3.044	Comprom	-1.349	Detected	-2.197	0.215	GT	Sens
GT	Sens	Sense	-0.588	Detected	0.588	Detected	0.000	-4.271	Comprom	-1.268	Detected	-2.769	0.228	GT	Sens
GT	Sens	Sense	-0.124	Detected	0.124	Detected	0.000	-0.989	Detected	-1.150	Detected	-1.069	0.018	GT	Sens
GT	Sens	Sense	-0.281	Detected	0.281	Detected	0.000	-1.620	Detected	-0.808	Detected	-1.214	0.133	GT	Sens
GT	Sens	Sense	-0.105	Detected	0.105	Detected	0.000	-2.295	Detected	-2.085	Detected	-2.190	0.005	GT	Sens
GT	Sens	Sense	-0.296	Detected	0.296	Detected	0.000	-2.195	Comprom	-1.608	Comprom	-1.902	0.045	GT	Sens
GT	Sens	Sense	-0.656	Detected	0.656	Detected	0.000	-1.636	Detected	-1.467	Detected	-1.551	0.144	GT	Sens
GT	Sens	Sense	-0.212	Detected	0.212	Detected	0.000	-1.745	Detected	-1.626	Detected	-1.686	0.017	GT	Sens
GT	Sens	Sense	0.290	Detected	-0.290	Detected	0.000	-1.316	Detected	-1.030	Detected	-1.173	0.068	GT	Sens
GT	Sens	Sense	-1.098	Detected	1.098	Detected	0.000	-3.289	Detected	-0.977	Detected	-2.133	0.313	GT	Sens
GT	Sens	Sense	0.279	Detected	-0.279	Detected	0.000	-2.993	Detected	-2.755	Detected	-2.874	0.011	GT	Sens
GT	Sens	Sense	-0.668	Detected	0.668	Detected	0.000	-4.692	Comprom	-2.867	Detected	-3.780	0.079	GT	Sens
GT	Sens	Sense	0.152	Detected	-0.152	Detected	0.000	-1.393	Detected	-0.996	Detected	-1.194	0.041	GT	Sens
GT	Sens	Sense	0.185	Detected	-0.185	Detected	0.000	-1.203	Detected	-1.444	Detected	-1.323	0.027	GT	Sens
GT	Sens	Sense	-0.298	Detected	0.298	Detected	0.000	-1.226	Comprom	-1.311	Comprom	-1.269	0.052	GT	Sens
GT	Sens	Sense	0.352	Detected	-0.352	Detected	0.000	-0.927	Detected	-1.302	Detected	-1.115	0.108	GT	Sens
GT	Sens	Sense	0.166	Detected	-0.166	Detected	0.000	-0.942	Detected	-1.110	Detected	-1.026	0.031	GT	Sens
GT	Sens	Sense	-0.807	Detected	0.807	Detected	0.000	-3.229	Detected	-1.550	Detected	-2.389	0.177	GT	Sens
GT	Sens	Sense	0.051	Detected	-0.051	Detected	0.000	-1.115	Detected	-1.087	Detected	-1.101	0.002	GT	Sens
GT	Sens	Sense	-0.106	Detected	0.106	Detected	0.000	-1.072	Detected	-0.938	Detected	-1.005	0.015	GT	Sens
GT	Sens	Sense	0.021	Detected	-0.021	Detected	0.000	-3.414	Comprom	-3.283	Comprom	-3.348	0.000	GT	Sens
GT	Sens	Sense	-0.867	Detected	0.867	Detected	0.000	-5.143	Detected	-0.978	Detected	-3.060	0.308	GT	Sens
GT	Sens	Sense	-0.576	Detected	0.576	Detected	0.000	-1.581	Detected	-0.990	Detected	-1.286	0.185	GT	Sens
GT	Sens	Sense	0.223	Detected	-0.223	Detected	0.000	-2.156	Comprom	-3.305	Comprom	-2.730	0.047	GT	Sens
GT	Sens	Sense	0.072	Detected	-0.072	Detected	0.000	-2.470	Detected	-2.850	Detected	-2.660	0.006	GT	Sens
GT	Sens	Sense	-0.076	Detected	0.076	Detected	0.000	-1.148	Detected	-1.110	Detected	-1.129	0.005	GT	Sens
GT	Sens	Sense	-0.367	Detected	0.367	Detected	0.000	-0.864	Detected	-1.515	Detected	-1.189	0.136	GT	Sens
GT	Sens	Sense	-0.150	Detected	0.150	Detected	0.000	-2.027	Detected	-1.253	Detected	-1.640	0.059	GT	Sens
GT	Sens	Sense	-0.472	Detected	0.472	Detected	0.000	-2.017	Detected	-1.367	Detected	-1.692	0.098	GT	Sens
GT	Sens	Sense	-1.016	Detected	1.016	Detected	0.000	-3.476	Comprom	-3.243	Comprom	-3.360	0.081	GT	Sens
GT	Sens	Sense	-0.339	Detected	0.339	Detected	0.000	-1.289	Detected	-1.132	Detected	-1.210	0.074	GT	Sens
GT	Sens	Sense	0.166	Detected	-0.166	Detected	0.000	-2.862	Comprom	-2.406	Comprom	-2.634	0.011	GT	Sens
GT	Sens	Sense	-0.207	Detected	0.207	Detected	0.000	-1.551	Detected	-1.062	Detected	-1.306	0.055	GT	Sens
GT	Sens	Sense	-0.252	Detected	0.252	Detected	0.000	-2.064	Detected	-0.950	Detected	-1.507	0.133	GT	Sens
GT	Sens	Sense	-0.613	Detected	0.613	Detected	0.000	-2.471	Detected	-1.249	Detected	-1.860	0.165	GT	Sens
GT	Sens	Sense	-0.079	Detected	0.079	Detected	0.000	-1.211	Detected	-1.180	Detected	-1.195	0.004	GT	Sens
GT	Sens	Sense	-0.583	Detected	0.583	Detected	0.000	-1.163	Detected	-1.022	Detected	-1.093	0.204	GT	Sens
GT	Sens	Sense	-0.127	Detected	0.127	Detected	0.000	-1.830	Detected	-1.366	Detected	-1.598	0.026	GT	Sens
GT	Sens	Sense	-0.348	Detected	0.348	Detected	0.000	-1.876	Comprom	-1.004	Comprom	-1.440	0.123	GT	Sens
GT	Sens	Sense	-1.036	Detected	1.036	Detected	0.000	-2.614	Detected	-1.108	Detected	-1.861	0.283	GT	Sens
GT	Sens	Sense	-0.073	Detected	0.073	Detected	0.000	-0.854	Detected	-1.194	Detected	-1.024	0.031	GT	Sens
GT	Sens	Sense	-0.065	Detected	0.065	Detected	0.000	-1.329	Detected	-0.947	Detected	-1.138	0.030	GT	Sens
GT	Sens	Sense	0.002	Detected	-0.002	Detected	0.000	-1.273	Comprom	-0.921	Comprom	-1.097	0.025	GT	Sens
GT	Sens	Sense	-0.097	Detected	0.097	Detected	0.000	-1.698	Detected	-1.914	Detected	-1.806	0.006	GT	Sens
GT	Sens	Sense	-0.078	Detected	0.078	Detected	0.000	-1.783	Detected	-1.825	Detected	-1.804	0.002	GT	Sens
GT	Sens	Sense	-0.087	Detected	0.087	Detected	0.000	-1.149	Detected	-1.274	Detected	-1.211	0.008	GT	Sens
GT	Sens	Sense	-0.283	Detected	0.283	Detected	0.000	-2.049	Comprom	-0.931	Comprom	-1.490	0.140	GT	Sens
GT	Sens	Sense	-1.656	Detected	1.656	Detected	0.000	-6.776	Comprom	-1.821	Detected	-4.299	0.286	GT	Sens
GT	Sens	Sense	-0.045	Detected	0.045	Detected	0.000	-1.512	Detected	-1.373	Detected	-1.442	0.003	GT	Sens
GT	Sens	Sense	-0.110	Detected	0.110	Detected	0.000	-1.865	Detected	-1.870	Detected	-1.867	0.003	GT	Sens
GT	Sens	Sense	-0.096	Detected	0.096	Detected	0.000	-2.209	Detected	-1.193	Detected	-1.701	0.081	GT	Sens
GT	Sens	Sense	-0.083	Detected	0.083	Detected	0.000	-1.527	Detected	-0.812	Detected	-1.170	0.086	GT	Sens
GT	Sens	Sense	-0.170	Detected	0.170	Detected	0.000	-1.676	Detected	-1.776	Detected	-1.726	0.010	GT	Sens
GT	Sens	Sense	-0.364	Detected	0.364	Detected	0.000	-1.646	Detected	-1.463	Detected	-1.554	0.054	GT	Sens
GT	Sens	Sense	-0.168	Detected	0.168	Detected	0.000	-1.718	Detected	-1.975	Detected	-1.846	0.013	GT	Sens
GT	Sens	Sense	0.047	Detected	-0.047	Detected	0.000	-0.837	Detected	-1.219	Detected	-1.028	0.035	GT	Sens
GT	Sens	Sense	-0.335	Detected	0.335	Detected	0.000	-1.845	Detected	-0.859	Detected	-1.352	0.151	GT	Sens
GT	Sens	Sense	-0.119	Detected	0.119	Detected	0.000	-1.228	Detected	-0.916	Detected	-1.072	0.032	GT	Sens
GT	Sens	Sense	0.018	Detected	-0.018	Detected	0.000	-1.081	Detected	-1.866	Detected	-1.473	0.064	GT	Sens
GT	Sens	Sense	0.196	Detected	-0.196	Detected	0.000	-1.690	Detected	-0.912	Detected	-1.301	0.096	GT	Sens
GT	Sens	Sense	0.309	Detected	-0.309	Detected	0.000	-1.680	Detected	-1.648	Detected	-1.664	0.033	GT	Sens
GT	Sens	Sense	-0.015	Detected	0.015	Detected	0.000	-1.242	Detected	-1.205	Detected	-1.224	0.000	GT	Sens
GT	Sens	Sense	-0.288	Detected	0.288	Detected	0.000	-1.386	Detected	-1.956	Detected	-1.671	0.054	GT	Sens
GT	Sens	Sense	0.198	Detected	-0.198	Detected	0.000	-1.469	Detected	-1.677	Detected	-1.573	0.020	GT	Sens
GT	Sens	Sense	0.214	Detected	-0.214	Detected	0.000	-1.735	Detected	-1.485	Detected	-1.610	0.023	GT	Sens
GT	Sens	Sense	-0.047	Detected	0.047	Detected	0.000	-1.772	Detected	-2.308	Detected	-2.040	0.017	GT	Sens
GT	Sens	Sense	0.089	Detected	-0.089	Detected	0.000	-1.017	Detected	-1.414	Detected	-1.215	0.031	GT	Sens
GT	Sens	Sense	-0.112	Detected	0.112	Detected	0.000	-0.915	Detected	-1.344	Detected	-1.130	0.043	GT	Sens
GT	Sens	Sense	-0.710	Detected	0.710	Detected	0.000	-2.815	Detected	-1.163	Detected	-1.989	0.209	GT	Sens
GT	Sens	Sense	-0.094	Detected	0.094	Detected	0.000	-1.272	Comprom	-1.077	Detected	-1.174	0.013	GT	Sens
GT	Sens	Sense	-0.106	Detected	0.106	Detected	0.000	-1.824	Detected	-1.925	Detected	-1.875	0.004	GT	Sens
GT	Sens	Sense	0.127	Detected	-0.127	Detected	0.000	-1.488	Detected	-1.368	Detected	-1.428	0.010	GT	Sens
GT	Sens	Sense	0.156	Detected	-0.156	Detected	0.000	-1.240	Detected	-1.054	Detected	-1.147	0.024	GT	Sens
GT	Sens	Sense	-0.636	Detected	0.636	Detected	0.000	-1.822	Comprom	-1.296	Detected	-1.559	0.152	GT	Sens
GT	Sens	Sense	-0.491	Detected	0.491	Detected	0.000	-3.171	Detected	-0.882	Detected	-2.026	0.245	GT	Sens
GT	Sens	Sense	-0.108	Detected	0.108	Detected	0.000	-0.886	Detected	-1.649	Detected	-1.267	0.086	GT	Sens
GT	Sens	Sense	-0.417	Detected	0.417	Detected	0.000	-2.091	Detected	-1.698	Detected	-1.895	0.055	GT	Sens
GT	Sens	Sense	-0.282	Detected	0.282	Detected	0.000	-2.053	Detected	-0.964	Detected	-1.508	0.133	GT	Sens
GT	Sens	Sense	0.219	Detected	-0.219	Detected	0.000	-1.382	Detected	-1.476	Detected	-1.429	0.024	GT	Sens
GT	Sens	Sense	-0.172	Detected	0.172	Detected	0.000	-3.279	Detected	-1.681	Detected	-2.480	0.094	GT	Sens
GT	Sens	Sense	-0.100	Detected	0.100	Detected	0.000	-1.296	Detected	-0.990	Detected	-1.143	0.025	GT	Sens
GT	Sens	Sense	-0.168	Detected	0.168	Detected	0.000	-2.012	Detected	-0.977	Detected	-1.494	0.111	GT	Sens
GT	Sens	Sense	-0.124	Detected	0.124	Detected	0.000	-1.731	Comprom	-1.900	Comprom	-1.815	0.007	GT	Sens
GT	Sens	Sense	-0.526	Detected	0.526	Detected	0.000	-1.322	Detected	-1.249	Detected	-1.286	0.135	GT	Sens
GT	Sens	Sense	0.001	Detected	-0.001	Detected	0.000	-1.396	Detected	-0.827	Detected	-1.112	0.060	GT	Sens
GT	Sens	Sense	-0.141	Detected	0.141	Detected	0.000	-2.573	Detected	-2.970	Detected	-2.772	0.008	GT	Sens
GT	Sens	Sense	0.144	Detected	-0.144	Detected	0.000	-1.143	Detected	-1.026	Detected	-1.084	0.020	GT	Sens
GT	Sens	Sense	-0.232	Detected	0.232	Detected	0.000	-1.667	Detected	-1.702	Detected	-1.685	0.019	GT	Sens
GT	Sens	Sense	0.004	Detected	-0.004	Detected	0.000	-1.863	Detected	-1.856	Detected	-1.859	0.000	GT	Sens
GT	Sens	Sense	-0.285	Detected	0.285	Detected	0.000	-2.107	Detected	-2.171	Detected	-2.139	0.018	GT	Sens
GT	Sens	Sense	0.126	Detected	-0.126	Detected	0.000	-1.576	Detected	-0.884	Detected	-1.230	0.079	GT	Sens
GT	Sens	Sense	0.187	Detected	-0.187	Detected	0.000	-1.477	Comprom	-0.990	Detected	-1.234	0.057	GT	Sens
GT	Sens	Sense	0.332	Detected	-0.332	Detected	0.000	-1.295	Detected	-2.164	Detected	-1.730	0.087	GT	Sens
GT	Sens	Sense	-0.470	Detected	0.470	Detected	0.000	-1.848	Detected	-0.850	Detected	-1.349	0.188	GT	Sens
GT	Sens	Sense	0.161	Detected	-0.161	Detected	0.000	-1.060	Detected	-1.212	Comprom	-1.136	0.024	GT	Sens
GT	Sens	Sense	-0.208	Detected	0.208	Detected	0.000	-1.897	Detected	-1.811	Detected	-1.854	0.013	GT	Sens
GT	Sens	Sense	-0.050	Detected	0.050	Detected	0.000	-3.436	Detected	-2.533	Detected	-2.984	0.022	GT	Sens
GT	Sens	Sense	-0.246	Detected	0.246	Detected	0.000	-2.175	Detected	-2.289	Detected	-2.232	0.013	GT	Sens
GT	Sens	Sense	-0.954	Detected	0.954	Detected	0.000	-5.050	Detected	-2.761	Detected	-3.905	0.120	GT	Sens
GT	Sens	Sense	-0.191	Detected	0.191	Detected	0.000	-1.849	Detected	-2.157	Detected	-2.003	0.015	GT	Sens
GT	Sens	Sense	0.053	Detected	-0.053	Detected	0.000	-1.346	Detected	-1.134	Detected	-1.240	0.009	GT	Sens
GT	Sens	Sense	-0.188	Detected	0.188	Detected	0.000	-3.337	Detected	-1.223	Detected	-2.280	0.168	GT	Sens
GT	Sens	Sense	-0.218	Detected	0.218	Detected	0.000	-2.032	Detected	-2.102	Detected	-2.067	0.011	GT	Sens
GT	Sens	Sense	-0.089	Detected	0.089	Detected	0.000	-1.357	Detected	-1.424	Detected	-1.391	0.005	GT	Sens
GT	Sens	Sense	-0.139	Detected	0.139	Detected	0.000	-1.868	Detected	-2.667	Detected	-2.268	0.033	GT	Sens
GT	Sens	Sense	-0.146	Detected	0.146	Detected	0.000	-1.184	Detected	-1.146	Detected	-1.165	0.016	GT	Sens
GT	Sens	Sense	-0.259	Detected	0.259	Detected	0.000	-1.884	Detected	-1.320	Detected	-1.602	0.053	GT	Sens
GT	Sens	Sense	-0.088	Detected	0.088	Detected	0.000	-1.955	Detected	-2.104	Detected	-2.029	0.003	GT	Sens
GT	Sens	Sense	-0.193	Detected	0.193	Detected	0.000	-1.577	Detected	-2.068	Detected	-1.823	0.028	GT	Sens
GT	Sens	Sense	-0.073	Detected	0.073	Detected	0.000	-0.958	Detected	-1.485	Comprom	-1.221	0.047	GT	Sens
GT	Sens	Sense	-0.260	Detected	0.260	Detected	0.000	-1.140	Detected	-1.061	Detected	-1.101	0.053	GT	Sens
GT	Sens	Sense	-0.021	Detected	0.021	Detected	0.000	-1.806	Detected	-2.349	Detected	-2.077	0.017	GT	Sens
GT	Sens	Sense	-0.136	Detected	0.136	Detected	0.000	-1.461	Detected	-2.181	Comprom	-1.821	0.042	GT	Sens
GT	Sens	Sense	-0.094	Detected	0.094	Detected	0.000	-2.051	Detected	-2.109	Detected	-2.080	0.002	GT	Sens
GT	Sens	Sense	-0.101	Detected	0.101	Detected	0.000	-1.905	Comprom	-2.010	Comprom	-1.957	0.003	GT	Sens
GT	Sens	Sense	-0.269	Detected	0.269	Detected	0.000	-1.515	Comprom	-2.170	Comprom	-1.842	0.049	GT	Sens
GT	Sens	Sense	-0.071	Detected	0.071	Detected	0.000	-0.924	Detected	-1.524	Detected	-1.224	0.058	GT	Sens
GT	Sens	Sense	-0.362	Detected	0.362	Detected	0.000	-1.621	Detected	-1.310	Detected	-1.466	0.065	GT	Sens
GT	Sens	Sense	0.209	Detected	-0.209	Detected	0.000	-1.139	Detected	-0.956	Detected	-1.048	0.044	GT	Sens
GT	Sens	Sense	-0.170	Detected	0.170	Detected	0.000	-1.231	Detected	-1.415	Detected	-1.323	0.021	GT	Sens
GT	Sens	Sense	-0.540	Detected	0.540	Detected	0.000	-1.893	Detected	-1.314	Detected	-1.603	0.120	GT	Sens
GT	Sens	Sense	0.089	Detected	-0.089	Detected	0.000	-1.915	Detected	-1.831	Detected	-1.873	0.003	GT	Sens
GT	Sens	Sense	-0.055	Detected	0.055	Detected	0.000	-1.740	Detected	-2.401	Detected	-2.071	0.025	GT	Sens
GT	Sens	Sense	-0.082	Detected	0.082	Detected	0.000	-3.374	Detected	-1.508	Detected	-2.441	0.121	GT	Sens
GT	Sens	Sense	-0.197	Detected	0.197	Detected	0.000	-2.935	Detected	-3.006	Detected	-2.971	0.005	GT	Sens
GT	Sens	Sense	-0.229	Detected	0.229	Detected	0.000	-0.877	Detected	-1.718	Detected	-1.297	0.114	GT	Sens
GT	Sens	Sense	-0.014	Detected	0.014	Detected	0.000	-1.034	Detected	-1.224	Detected	-1.129	0.007	GT	Sens
GT	Sens	Sense	-0.213	Detected	0.213	Detected	0.000	-1.944	Detected	-2.169	Detected	-2.056	0.013	GT	Sens
GT	Sens	Sense	-0.008	Detected	0.008	Detected	0.000	-1.739	Comprom	-1.825	Comprom	-1.782	0.001	GT	Sens
GT	Sens	Sense	-0.399	Detected	0.399	Detected	0.000	-1.100	Comprom	-2.274	Comprom	-1.687	0.141	GT	Sens
GT	Sens	Sense	1.898	Detected	-1.898	Detected	0.000	-2.296	Detected	-2.349	Detected	-2.323	0.346	GT	Sens
GT	Sens	Sense	-0.634	Detected	0.634	Detected	0.000	-3.283	Detected	-2.186	Detected	-2.734	0.083	GT	Sens
GT	Sens	Sense	-0.112	Detected	0.112	Detected	0.000	-2.227	Detected	-2.499	Detected	-2.363	0.006	GT	Sens
GT	Sens	Sense	-0.106	Detected	0.106	Detected	0.000	-2.646	Detected	-2.599	Detected	-2.623	0.002	GT	Sens
GT	Sens	Sense	-0.152	Detected	0.152	Detected	0.000	-2.043	Detected	-2.239	Detected	-2.141	0.007	GT	Sens
GT	Sens	Sense	0.198	Detected	-0.198	Detected	0.000	-1.473	Detected	-1.338	Detected	-1.405	0.021	GT	Sens
GT	Sens	Sense	-0.444	Detected	0.444	Detected	0.000	-1.435	Detected	-1.328	Detected	-1.381	0.091	GT	Sens

GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	-1.709	Detected	-1.844	Detected	-1.777	0.007
GT	Sense	Sense	0.267	Detected	-0.267	Detected	0.000	-1.445	Detected	-1.705	Detected	-1.575	0.034
GT	Sense	Sense	0.078	Detected	-0.078	Detected	0.000	-0.935	Detected	-1.686	Detected	-1.311	0.076
GT	Sense	Sense	-0.641	Detected	0.641	Detected	0.000	-2.429	Detected	-0.847	Detected	-1.638	0.249
GT	Sense	Sense	-0.247	Detected	0.247	Detected	0.000	-1.760	Detected	-1.879	Detected	-1.819	0.019
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-2.300	Detected	-2.185	Detected	-2.242	0.001
GT	Sense	Sense	-0.209	Detected	0.209	Detected	0.000	-1.182	Comprom	-1.659	Comprom	-1.421	0.046
GT	Sense	Sense	-0.091	Detected	0.091	Detected	0.000	-2.519	Comprom	-1.729	Detected	-2.124	0.035
GT	Sense	Sense	-0.413	Detected	0.413	Detected	0.000	-1.473	Detected	-1.972	Comprom	-1.723	0.070
GT	Sense	Sense	-0.189	Detected	0.189	Detected	0.000	-1.621	Detected	-1.777	Detected	-1.699	0.014
GT	Sense	Sense	-0.068	Detected	0.068	Detected	0.000	-2.507	Comprom	-2.114	Comprom	-2.310	0.008
GT	Sense	Sense	-0.079	Detected	0.079	Detected	0.000	-1.235	Detected	-1.635	Detected	-1.435	0.022
GT	Sense	Sense	-0.261	Detected	0.261	Detected	0.000	-2.195	Detected	-2.375	Detected	-2.285	0.014
GT	Sense	Sense	0.320	Detected	-0.320	Detected	0.000	-1.488	Comprom	-0.803	Detected	-1.145	0.134
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-2.194	Comprom	-1.868	Comprom	-2.031	0.007
GT	Sense	Sense	-0.492	Detected	0.492	Detected	0.000	-1.127	Detected	-0.971	Detected	-1.049	0.170
GT	Sense	Sense	-0.226	Detected	0.226	Detected	0.000	-1.808	Detected	-1.226	Detected	-1.517	0.054
GT	Sense	Sense	-0.018	Detected	0.018	Detected	0.000	-2.287	Comprom	-2.215	Comprom	-2.251	0.000
GT	Sense	Sense	-0.155	Detected	0.155	Detected	0.000	-2.104	Detected	-2.143	Detected	-2.123	0.005
GT	Sense	Sense	0.028	Detected	-0.028	Detected	0.000	-1.272	Detected	-1.037	Detected	-1.155	0.011
GT	Sense	Sense	-0.234	Detected	0.234	Detected	0.000	-4.246	Detected	-1.913	Detected	-3.079	0.123
GT	Sense	Sense	0.008	Detected	-0.008	Detected	0.000	-1.067	Detected	-1.051	Detected	-1.059	0.000
GT	Sense	Sense	-0.448	Detected	0.448	Detected	0.000	-1.616	Detected	-1.790	Detected	-1.703	0.065
GT	Sense	Sense	0.244	Detected	-0.244	Detected	0.000	-1.324	Detected	-1.747	Detected	-1.535	0.042
GT	Sense	Sense	1.454	Detected	-1.454	Detected	0.000	-0.844	Detected	-2.477	Comprom	-1.661	0.424
GT	Sense	Sense	-0.246	Detected	0.246	Detected	0.000	-1.209	Comprom	-1.145	Comprom	-1.177	0.042
GT	Sense	Sense	-0.260	Detected	0.260	Detected	0.000	-2.609	Detected	-0.823	Detected	-1.716	0.206
GT	Sense	Sense	-0.316	Detected	0.316	Detected	0.000	-1.417	Detected	-0.950	Detected	-1.184	0.095
GT	Sense	Sense	-0.081	Detected	0.081	Detected	0.000	-1.501	Detected	-0.882	Detected	-1.191	0.065
GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	-2.660	Detected	-2.673	Detected	-2.666	0.002
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-1.214	Detected	-0.882	Detected	-1.048	0.032
GT	Sense	Sense	0.087	Detected	-0.087	Detected	0.000	-1.336	Detected	-1.087	Detected	-1.212	0.015
GT	Sense	Sense	-0.191	Detected	0.191	Detected	0.000	-2.205	Detected	-2.340	Detected	-2.273	0.008
GT	Sense	Sense	-0.148	Detected	0.148	Detected	0.000	-1.606	Detected	-1.365	Detected	-1.485	0.016
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-1.671	Detected	-1.653	Comprom	-1.662	0.003
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-3.252	Detected	-2.242	Detected	-2.747	0.032
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-3.516	Detected	-1.367	Detected	-2.442	0.153
GT	Sense	Sense	-0.216	Detected	0.216	Detected	0.000	-2.053	Detected	-1.115	Detected	-1.584	0.092
GT	Sense	Sense	-0.233	Detected	0.233	Detected	0.000	-2.172	Detected	-2.255	Detected	-2.214	0.011
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	-1.241	Detected	-1.178	Detected	-1.209	0.018
GT	Sense	Sense	-0.160	Detected	0.160	Detected	0.000	-1.747	Detected	-1.950	Detected	-1.849	0.010
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-1.378	Detected	-1.116	Detected	-1.247	0.013
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	-1.107	Detected	-1.220	Detected	-1.163	0.032
GT	Sense	Sense	-0.386	Detected	0.386	Detected	0.000	-1.334	Detected	-0.931	Detected	-1.133	0.122
GT	Sense	Sense	-0.100	Detected	0.100	Detected	0.000	-1.217	Detected	-1.794	Detected	-1.506	0.039
GT	Sense	Sense	-0.008	Detected	0.008	Detected	0.000	-1.163	Detected	-1.538	Detected	-1.350	0.019
GT	Sense	Sense	-0.172	Detected	0.172	Detected	0.000	-1.579	Detected	-1.609	Detected	-1.594	0.012
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	-2.041	Comprom	-1.911	Comprom	-1.976	0.004
GT	Sense	Sense	0.065	Detected	-0.065	Detected	0.000	-1.284	Comprom	-1.091	Comprom	-1.187	0.009
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	-0.899	Detected	-1.426	Detected	-1.163	0.066
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	-1.365	Detected	-1.889	Comprom	-1.627	0.032
GT	Sense	Sense	0.152	Detected	-0.152	Detected	0.000	-2.326	Detected	-1.414	Detected	-1.870	0.060
GT	Sense	Sense	-0.103	Detected	0.103	Detected	0.000	-1.347	Detected	-1.472	Detected	-1.410	0.007
GT	Sense	Sense	-0.177	Detected	0.177	Detected	0.000	-1.354	Detected	-1.115	Detected	-1.235	0.029
GT	Sense	Sense	-0.273	Detected	0.273	Detected	0.000	-2.153	Detected	-2.282	Detected	-2.218	0.016
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	-1.920	Detected	-2.128	Detected	-2.024	0.003
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-1.118	Detected	-2.379	Detected	-1.748	0.112
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-1.483	Detected	-1.893	Detected	-1.688	0.019
GT	Sense	Sense	-0.333	Detected	0.333	Detected	0.000	-1.535	Detected	-1.505	Detected	-1.520	0.045
GT	Sense	Sense	0.066	Detected	-0.066	Detected	0.000	-1.418	Detected	-1.011	Detected	-1.215	0.030
GT	Sense	Sense	-0.098	Detected	0.098	Detected	0.000	-2.231	Detected	-1.201	Detected	-1.716	0.082
GT	Sense	Sense	-0.507	Detected	0.507	Detected	0.000	-1.564	Detected	-1.999	Detected	-1.782	0.084
GT	Sense	Sense	0.030	Detected	-0.030	Detected	0.000	-1.645	Detected	-2.735	Comprom	-2.190	0.057
GT	Sense	Sense	-0.573	Detected	0.573	Detected	0.000	-2.054	Comprom	-1.543	Comprom	-1.798	0.103
GT	Sense	Sense	-0.374	Detected	0.374	Detected	0.000	-1.538	Comprom	-1.212	Comprom	-1.375	0.078
GT	Sense	Sense	-0.127	Detected	0.127	Detected	0.000	-0.934	Detected	-2.108	Comprom	-1.521	0.127
GT	Sense	Sense	-0.099	Detected	0.099	Detected	0.000	-3.497	Comprom	-2.400	Comprom	-2.948	0.034
GT	Sense	Sense	0.147	Detected	-0.147	Detected	0.000	-1.826	Detected	-1.516	Detected	-1.671	0.016
GT	Sense	Sense	-0.160	Detected	0.160	Detected	0.000	-1.990	Detected	-2.089	Detected	-2.039	0.007
GT	Sense	Sense	-0.463	Detected	0.463	Detected	0.000	-3.359	Detected	-2.332	Detected	-2.845	0.054
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	-2.212	Detected	-2.129	Detected	-2.170	0.001
GT	Sense	Sense	-0.288	Detected	0.288	Detected	0.000	-1.348	Detected	-0.822	Detected	-1.085	0.109
GT	Sense	Sense	-0.041	Detected	0.041	Detected	0.000	-2.818	Comprom	-2.189	Comprom	-2.503	0.016
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	-1.860	Detected	-1.086	Detected	-1.473	0.069
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	-1.158	Detected	-1.395	Detected	-1.277	0.019
GT	Sense	Sense	-0.183	Detected	0.183	Detected	0.000	-1.147	Detected	-1.515	Detected	-1.331	0.036
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-1.986	Detected	-1.785	Detected	-1.886	0.004
GT	Sense	Sense	-0.190	Detected	0.190	Detected	0.000	-2.489	Detected	-2.146	Detected	-2.317	0.012
GT	Sense	Sense	-0.227	Detected	0.227	Detected	0.000	-1.490	Detected	-1.258	Detected	-1.374	0.033
GT	Sense	Sense	0.818	Detected	-0.818	Detected	0.000	-1.509	Detected	-1.462	Detected	-1.485	0.211
GT	Sense	Sense	-0.228	Detected	0.228	Detected	0.000	-2.303	Detected	-1.286	Detected	-1.795	0.085
GT	Sense	Sense	-0.050	Detected	0.050	Detected	0.000	-1.368	Detected	-2.000	Detected	-1.684	0.034
GT	Sense	Sense	0.131	Detected	-0.131	Detected	0.000	-2.187	Detected	-1.475	Detected	-1.831	0.040
GT	Sense	Sense	-0.418	Detected	0.418	Detected	0.000	-3.131	Detected	-1.516	Detected	-2.324	0.125
GT	Sense	Sense	-0.169	Detected	0.169	Detected	0.000	-1.903	Detected	-2.068	Detected	-1.986	0.009
GT	Sense	Sense	-0.481	Detected	0.481	Detected	0.000	-1.640	Detected	-1.105	Detected	-1.373	0.130
GT	Sense	Sense	0.454	Detected	-0.454	Detected	0.000	-1.119	Detected	-1.534	Comprom	-1.327	0.117
GT	Sense	Sense	-0.245	Detected	0.245	Detected	0.000	-2.207	Detected	-2.362	Detected	-2.285	0.012
GT	Sense	Sense	-0.358	Detected	0.358	Detected	0.000	-1.886	Comprom	-0.867	Detected	-1.377	0.157
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	-2.324	Detected	-2.394	Detected	-2.359	0.003
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	-1.495	Detected	-1.663	Detected	-1.579	0.010
GT	Sense	Sense	-0.920	Detected	0.920	Detected	0.000	-0.952	Detected	-1.071	Detected	-1.012	0.387
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-2.105	Comprom	-3.234	Comprom	-2.669	0.042
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	-2.019	Comprom	-1.587	Comprom	-1.803	0.015
GT	Sense	Sense	-0.174	Detected	0.174	Detected	0.000	-1.194	Detected	-1.757	Detected	-1.475	0.047
GT	Sense	Sense	-0.081	Detected	0.081	Detected	0.000	-2.538	Detected	-2.767	Detected	-2.652	0.003
GT	Sense	Sense	-0.382	Detected	0.382	Detected	0.000	-3.281	Comprom	-2.742	Comprom	-3.011	0.023
GT	Sense	Sense	-0.476	Detected	0.476	Detected	0.000	-1.935	Detected	-1.162	Detected	-1.549	0.128
GT	Sense	Sense	-0.032	Detected	0.032	Detected	0.000	-1.252	Detected	-1.086	Detected	-1.169	0.006
GT	Sense	Sense	0.355	Detected	-0.355	Detected	0.000	-2.327	Comprom	-3.096	Comprom	-2.712	0.035
GT	Sense	Sense	-0.157	Detected	0.157	Detected	0.000	-1.611	Detected	-1.825	Detected	-1.718	0.012
GT	Sense	Sense	-0.229	Detected	0.229	Detected	0.000	-2.201	Detected	-2.341	Detected	-2.271	0.011
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	-1.851	Comprom	-1.419	Detected	-1.635	0.017
GT	Sense	Sense	0.212	Detected	-0.212	Detected	0.000	-2.249	Comprom	-0.808	Detected	-1.528	0.179
GT	Sense	Sense	-0.096	Detected	0.096	Detected	0.000	-2.403	Detected	-2.314	Detected	-2.359	0.002
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-1.049	Detected	-1.083	Detected	-1.066	0.020
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	-1.898	Detected	-1.885	Detected	-1.892	0.005
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	-1.012	Detected	-1.243	Comprom	-1.128	0.011
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-2.094	Detected	-1.162	Detected	-1.628	0.075
GT	Sense	Sense	-0.366	Detected	0.366	Detected	0.000	-2.330	Detected	-1.668	Detected	-1.999	0.056
GT	Sense	Sense	-0.161	Detected	0.161	Detected	0.000	-0.969	Detected	-2.000	Detected	-1.484	0.111
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-4.571	Detected	-2.397	Detected	-3.484	0.086
GT	Sense	Sense	-0.533	Detected	0.533	Detected	0.000	-1.010	Detected	-1.451	Detected	-1.230	0.166
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-1.708	Detected	-1.442	Detected	-1.575	0.008
GT	Sense	Sense	-0.110	Detected	0.110	Detected	0.000	-1.102	Detected	-1.431	Detected	-1.266	0.024
GT	Sense	Sense	-0.440	Detected	0.440	Detected	0.000	-1.787	Detected	-1.217	Detected	-1.502	0.103
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	-2.245	Detected	-1.957	Detected	-2.101	0.005
GT	Sense	Sense	-0.252	Detected	0.252	Detected	0.000	-1.086	Detected	-1.206	Detected	-1.146	0.047
GT	Sense	Sense	-0.582	Detected	0.582	Detected	0.000	-2.307	Detected	-2.326	Detected	-2.317	0.058
GT	Sense	Sense	0.218	Detected	-0.218	Detected	0.000	-2.811	Detected	-2.663	Detected	-2.737	0.007
GT	Sense	Sense	-0.177	Detected	0.177	Detected	0.000	-2.294	Detected	-2.212	Detected	-2.253	0.006
GT	Sense	Sense	-0.085	Detected	0.085	Detected	0.000	-1.998	Detected	-1.661	Detected	-1.829	0.011
GT	Sense	Sense	-0.108	Detected	0.108	Detected	0.000	-1.664	Detected	-1.655	Detected	-1.659	0.004
GT	Sense	Sense	0.235	Detected	-0.235	Detected	0.000	-3.160	Comprom	-1.405	Comprom	-2.282	0.129
GT	Sense	Sense	-0.509	Detected	0.509	Detected	0.000	-2.188	Detected	-1.647	Detected	-1.918	0.080
GT	Sense	Sense	-0.116	Detected	0.116	Detected	0.000	-0.944	Detected	-1.172	Detected	-1.058	0.023
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	-1.424	Detected	-1.252	Detected	-1.338	0.006
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.078	Detected	-1.223	Comprom	-1.150	0.004
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-2.757	Detected	-2.188	Detected	-2.472	0.013
GT	Sense	Sense	-0.006	Detected	0.006	Detected	0.000	-1.298	Detected	-1.280	Detected	-1.289	0.000
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	-1.178	Detected	-1.074	Detected	-1.126	0.002
GT	Sense	Sense	-0.221	Detected	0.221	Detected	0.000	-1.566	Detected	-1.587	Detected	-1.576	0.019
GT	Sense	Sense	-1.103	Detected	1.103	Detected	0.000	-2.661	Detected	-1.850	Detected	-2.255	0.195
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-1.075	Detected	-0.929	Detected	-1.002	0.012
GT	Sense	Sense	-0.196	Detected	0.196	Detected	0.000	-1.282	Detected	-1.554	Detected	-1.418	0.027
GT	Sense	Sense	-0.031	Detected	0.031	Detected	0.000	-1.516	Detected	-1.386	Detected	-1.451	0.002
GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-1.796	Detected	-1.935	Detected	-1.865	0.009
GT	Sense	Sense	-0.197	Detected	0.197	Detected	0.000	-1.805	Detected	-1.790	Detected	-1.797	0.012
GT	Sense	Sense	0.217	Detected	-0.217	Detected	0.000	-0.979	Detected	-1.532	Detected	-1.255	0.070
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	-2.214	Detected	-2.330	Detected	-2.272	0.001
GT	Sense	Sense	-0.166	Detected	0.166	Detected	0.000	-1.336	Detected	-1.350	Detected	-1.343	0.015
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-1.293	Detected	-0.969	Detected	-1.131	0.020
GT	Sense	Sense	-0.279	Detected	0.279	Detected	0.000	-2.424	Detected	-1.542	Detected	-1.983	0.063
GT	Sense	Sense	-0.211	Detected	0.211	Detected	0.000	-0.968	Detected	-1.412	Detected	-1.190	0.060
GT	Sense	Sense	0.217	Detected	-0.217	Detected	0.000	-1.297	Detected	-1.326	Detected	-1.311	0.026
GT	Sense	Sense	-0.179	Detected	0.179	Detected	0.000	-1.107	Detected	-1.146	Detected	-1.126	0.025
GT	Sense	Sense	-0.299	Detected	0.299	Detected	0.000	-1.358	Detected	-0.827	Detected	-1.093	0.112
GT	Sense	Sense	-0.462	Detected	0.462	Detected	0.000	-2.396	Detected	-1.656	Detected	-2.026	0.076
GT	Sense	Sense	0.315	Detected	-0.315	Detected	0.000	-3.112	Comprom	-2.929	Comprom	-3.021	0.012
GT	Sense	Sense	0.248	Detected	-0.248	Detected	0.000	-1.842	Detected	-1.845	Detected	-1.844	0.018
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-1.302	Detected	-1.015	Detected	-1.159	0.023
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-0.998	Detected	-1.005	Detected	-1.002	0.002
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	-1.143	Detected	-1.845	Detected	-1.494	0.052
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	-2.085	Detected	-1.003	Detected	-1.544	0.104
GT	Sense	Sense	-0.214	Detected	0.214	Detected	0.000	-1.288	Detected	-0.871	Detected	-1.080	0.069
GT	Sense	Sense	-0.299	Detected	0.299	Detected	0.000	-2.801	Detected	-1.562	Detected	-2.181	0.087
GT	Sense	Sense	-0.511	Detected	0.511	Detected	0.000	-2.344	Detected	-1.512	Detected	-1.928	0.100
GT	Sense	Sense	-0.090	Detected	0.090	Detected	0.000	-1.987	Detected	-1.958	Detected	-1.972	0.002
GT	Sense	Sense	-0.447	Detected	0.447	Detected	0.000	-1.624	Detected	-1.942	Detected	-1.783	0.064
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-0.804	Detected	-1.433	Detected	-1.118	0.085
GT	Sense	Sense	-0.322	Detected	0.322	Detected	0.000	-1.177	Detected	-1.220	Detected	-1.199	0.066
GT	Sense	Sense	0.016	Detected	-0.016	Detected	0.000	-1.212	Detected	-1.332	Detected	-1.272	0.002
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	-1.455	Detected	-1.240	Detected	-1.348	0.010
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	-1.071	Detected	-2.077	Detected	-1.574	0.101
GT	Sense	Sense	0.182	Detected	-0.182	Detected	0.000	-1.554	Detected	-1.373	Detected	-1.464	0.019
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-2.027	Detected	-2.002	Detected	-2.014	0.002
GT	Sense	Sense	0.192	Detected	-0.192	Detected	0.000	-0.821	Detected	-2.965	Comprom	-1.893	0.224
GT	Sense	Sense	-0.079	Detected	0.079	Detected	0.000	-2.112	Detected	-2.289	Detected	-2.200	0.003
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	-1.515	Detected	-1.196	Detected	-1.356	0.032
GT	Sense	Sense	0.442	Detected	-0.442	Detected	0.000	-1.272	Detected	-1.370	Detected	-1.321	0.097
GT	Sense	Sense	-0.125	Detected	0.125	Detected	0.000	-1.630	Comprom	-2.488	Comprom	-2.059	0.044
GT	Sense	Sense	-0.260	Detected	0.260	Detected	0.000	-1.617	Detected	-1.821	Detected	-1.719	0.025
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-1.875	Comprom	-0.953	Comprom	-1.414	0.092
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-1.372	Comprom	-1.759	Comprom	-1.566	0.020
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.833	Comprom	-2.218	Comprom	-2.025	0.009
GT	Sense	Sense	-0.161	Detected	0.161	Detected	0.000	-0.876	Detected	-3.168	Comprom	-2.022	0.223
GT	Sense	Sense	-0.497	Detected	0.497	Detected	0.000	-0.952	Detected	-1.304	Detected	-1.128	0.166
GT	Sense	Sense	-0.216	Detected	0.216	Detected	0.000	-2.572	Detected	-2.823	Detected	-2.698	0.008
GT	Sense	Sense	-0.153	Detected	0.153	Detected	0.000	-2.462	Detected	-1.040	Detected	-1.751	0.138
GT	Sense	Sense	-0.248	Detected	0.248	Detected	0.000	-2.110	Detected	-2.285	Detected	-2.198	0.014
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.965	Comprom	-1.773	Comprom	-1.869	0.003
GT	Sense	Sense	-0.822	Detected	0.822	Detected	0.000	-2.943	Comprom	-3.315	Comprom	-3.129	0.065
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	-1.188	Detected	-1.588	Detected	-1.388	0.021
GT	Sense	Sense	-0.111	Detected	0.111	Detected	0.000	-4.747	Comprom	-1.772	Detected	-3.259	0.160
GT	Sense	Sense	-0.419	Detected	0.419	Detected	0.000	-1.698	Detected	-1.174	Detected	-1.436	0.101
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	-2.593	Detected	-2.749	Detected	-2.671	0.005
GT	Sense	Sense	0.083	Detected	-0.083	Detected	0.000	-1.561	Detected	-1.512	Detected	-1.536	0.003
GT	Sense	Sense	-0.258	Detected	0.258	Detected	0.000	-1.376	Detected	-0.848	Detected	-1.112	0.095
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	-1.264	Detected	-1.504	Detected	-1.384	0.008
GT	Sense	Sense	-0.193	Detected	0.193	Detected	0.000	-3.538	Comprom	-3.394	Comprom	-3.466	0.004
GT	Sense	Sense	-0.238	Detected	0.238	Detected	0.000	-1.235	Detected	-1.423	Detected	-1.329	0.035
GT	Sense	Sense	-0.066	Detected	0.066	Detected	0.000	-1.216	Detected	-1.544	Detected	-1.380	0.016
GT	Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-1.307	Detected	-1.264	Detected	-1.286	0.003
GT	Sense	Sense	-0.222	Detected	0.222	Detected	0.000	-1.209	Detected	-1.825	Detected	-1.517	0.057
GT	Sense	Sense	0.044	Detected	-0.044	Detected	0.000	-1.904	Detected	-2.449	Detected	-2.177	0.016
GT	Sense	Sense	-0.239	Detected	0.239	Detected	0.000	-1.989	Detected	-2.053	Detected	-2.021	0.014
GT	Sense	Sense	-0.249	Detected	0.249	Detected	0.000	-2.829	Detected	-2.477	Detected	-2.653	0.013
GT	Sense	Sense	-0.391	Detected	0.391	Detected	0.000	-1.551	Detected	-1.072	Detected	-1.311	0.104
GT	Sense	Sense	-0.233	Detected	0.233	Detected	0.000	-2.193	Detected	-1.812	Detected	-2.002	0.022
GT	Sense	Sense	-0.264	Detected	0.264	Detected	0.000	-2.011	Detected	-2.158	Detected	-2.084	0.017
GT	Sense	Sense	-0.006	Detected	0.006	Detected	0.000	-2.212	Detected	-1.430	Detected	-1.821	0.043
GT	Sense	Sense	-0.490	Detected	0.490	Detected	0.000	-2.177	Comprom	-2.779	Comprom	-2.478	0.050
GT	Sense	Sense	-0.010	Detected	0.010	Detected	0.000	-1.447	Detected	-0.877	Detected	-1.162	0.055
GT	Sense	Sense	-0.151	Detected	0.151	Detected	0.000	-2.318	Detected	-2.336	Detected	-2.327	0.004
GT	Sense	Sense	-0.093	Detected	0.093	Detected	0.000	-2.901	Detected	-3.786	Comprom	-3.344	0.018
GT	Sense	Sense	0.407	Detected	-0.407	Detected	0.000	-0.965	Detected	-2.074	Comprom	-1.520	0.158
GT	Sense	Sense	-0.069	Detected	0.069	Detected	0.000	-1.991	Detected	-2.259	Comprom	-2.125	0.005
GT	Sense	Sense	-0.328	Detected	0.328	Detected	0.000	-1.287	Detected	-1.582	Detected	-1.435	0.058
GT	Sense	Sense	-0.145	Detected	0.145	Detected	0.000	-1.268	Detected	-1.491	Detected	-1.380	0.017
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	-1.349	Detected	-0.970	Detected	-1.160	0.035
GT	Sense	Sense	-0.176	Detected	0.176	Detected	0.000	-2.458	Detected	-2.218	Detected	-2.338	0.008
GT	Sense	Sense	-0.232	Detected	0.232	Detected	0.000	-2.427	Detected	-2.656	Detected	-2.542	0.010
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	-1.972	Detected	-1.613	Detected	-1.792	0.019
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	-2.119	Detected	-1.507	Detected	-1.813	0.030
GT	Sense	Sense	-0.144	Detected	0.144	Detected	0.000	-2.143	Comprom	-1.778	Comprom	-1.961	0.014
GT	Sense	Sense	-0.655	Detected	0.655	Detected	0.000	-1.595	Detected	-1.880	Detected	-1.738	0.122
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	-2.805	Detected	-1.452	Detected	-2.129	0.088
GT	Sense	Sense	-0.169	Detected	0.169	Detected	0.000	-1.666	Detected	-1.239	Detected	-1.453	0.033
GT	Sense	Sense	-0.050	Detected	0.050	Detected	0.000	-1.622	Detected	-0.929	Detected	-1.276	0.068
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	-1.521	Detected	-3.670	Comprom	-2.596	0.137
GT	Sense	Sense	0.148	Detected	-0.148	Detected	0.000	-0.953	Detected	-1.666	Detected	-1.309	0.077
GT	Sense	Sense	-0.572	Detected	0.572	Detected	0.000	-4.946	Detected	-1.530	Detected	-3.238	0.214
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-2.262	Detected	-1.792	Detected	-2.027	0.016
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	-1.581	Detected	-1.261	Detected	-1.421	0.019
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-2.110	Comprom	-2.397	Comprom	-2.253	0.004
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	-1.303	Detected	-2.054	Detected	-1.679	0.047
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	-1.347	Detected	-1.663	Comprom	-1.505	0.024
GT	Sense	Sense	-0.012	Detected	0.012	Detected	0.000	-1.643	Detected	-0.915	Detected	-1.279	0.072
GT	Sense	Sense	-0.725	Detected	0.725	Detected	0.000	-1.682	Detected	-1.290	Detected	-1.486	0.187
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	-1.669	Detected	-1.597	Detected	-1.633	0.011
GT	Sense	Sense	-0.187	Detected	0.187	Detected	0.000	-2.002	Detected	-2.052	Detected	-2.027	0.009
GT	Sense	Sense	0.044	Detected	-0.044	Detected	0.000	-3.632	Detected	-1.363	Detected	-2.497	0.159
GT	Sense	Sense	-0.320	Detected	0.320	Detected	0.000	-1.174	Detected	-0.933	Detected	-1.054	0.091
GT	Sense	Sense	-0.136	Detected	0.136	Detected	0.000	-2.618	Detected	-1.559	Detected	-2.089	0.062
GT	Sense	Sense	-0.043	Detected	0.043	Detected	0.000	-2.462	Detected	-2.759	Detected	-2.610	0.004
GT	Sense	Sense	-0.217	Detected	0.217	Detected	0.000	-1.588	Comprom	-1.428	Comprom	-1.508	0.023
GT	Sense	Sense	-0.368	Detected	0.368	Detected	0.000	-2.007	Comprom	-0.905	Detected	-1.456	0.159
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.879	Detected	-2.154	Detected	-2.017	0.005
GT	Sense	Sense	-0.147	Detected	0.147	Detected	0.000	-1.866	Detected	-1.974	Detected	-1.920	0.007
GT	Sense	Sense	-0.204	Detected	0.204	Detected	0.000	-2.084	Detected	-1.708	Detected	-1.896	0.021
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-1.929	Detected	-1.213	Detected	-1.571	0.049
GT	Sense	Sense	-0.487	Detected	0.487	Detected	0.000	-3.246	Detected	-2.114	Detected	-2.680	0.070
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-2.667	Detected	-3.082	Detected	-2.875	0.006
GT	Sense	Sense	0.308	Detected	-0.308	Detected	0.000	-2.069	Detected	-1.643	Detected	-1.856	0.038

GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	-1.813	Detected	-1.860	Detected	-1.836	0.000	457.451	372.066	229.921	206.471	124.112	115.96
GT	Sense	Sense	-0.230	Detected	0.230	Detected	0.000	-1.863	Detected	-2.135	Detected	-1.999	0.017	486.674	523.144	155.73	200.295	146.637	117.235
GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	-1.329	Detected	-0.928	Detected	-1.128	0.038	72.5214	65.5699	46.4621	52.2479	29.0099	36.9913
GT	Sense	Sense	-0.323	Detected	0.323	Detected	0.000	-1.667	Comprom	-1.126	Comprom	-1.397	0.080	16.2677	19.9101	7.6776	10.28	5.99019	8.41217
GT	Sense	Sense	0.383	Detected	-0.383	Detected	0.000	-1.223	Detected	-1.244	Detected	-1.233	0.085	1696.71	779.644	1138.91	1193.54	520.723	495.48
GT	Sense	Sense	-0.186	Detected	0.186	Detected	0.000	-1.482	Detected	-1.598	Detected	-1.540	0.016	48.9254	49.51	24.7828	24.1074	18.6236	16.5846
GT	Sense	Sense	-0.404	Detected	0.404	Detected	0.000	-1.243	Comprom	-2.952	Comprom	-2.098	0.157	12.4817	17.0918	12.2697	3.77185	6.52138	1.92603
GT	Sense	Sense	-0.212	Detected	0.212	Detected	0.000	-2.578	Detected	-2.617	Detected	-2.598	0.007	593.561	622.57	194.755	231.819	107.598	101.089
GT	Sense	Sense	-0.108	Detected	0.108	Detected	0.000	-1.501	Detected	-1.707	Detected	-1.604	0.009	495.87	450.205	227.39	253.931	176.372	147.702
GT	Sense	Sense	-0.084	Detected	0.084	Detected	0.000	-1.735	Detected	-1.431	Detected	-1.583	0.012	208.008	182.784	157.053	114.758	61.9071	73.7998
GT	Sense	Sense	0.234	Detected	-0.234	Detected	0.000	-1.006	Detected	-1.190	Detected	-1.098	0.049	14198.8	8025.91	15819.8	13933.6	5616.1	4775.12
GT	Sense	Sense	0.202	Detected	-0.202	Detected	0.000	-2.083	Comprom	-2.159	Comprom	-2.121	0.009	29.9099	17.6584	13.3629	13.4411	5.73233	5.25188
GT	Sense	Sense	-0.070	Detected	0.070	Detected	0.000	-1.035	Detected	-1.035	Detected	-1.035	0.005	455.156	392.021	446.133	377.112	217.852	210.294
GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-0.969	Detected	-1.619	Detected	-1.294	0.071	58.3383	57.1358	36.4738	31.7466	31.1689	19.1764
GT	Sense	Sense	-0.150	Detected	0.150	Detected	0.000	-1.698	Detected	-2.011	Comprom	-1.854	0.013	32.2691	31.063	6.21273	14.7863	10.3112	8.01644
GT	Sense	Sense	0.528	Detected	-0.528	Detected	0.000	-0.962	Detected	-1.117	Detected	-1.040	0.191	86.2932	32.4211	28.6891	32.7993	28.6873	24.8789
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-0.888	Detected	-1.797	Detected	-1.343	0.102	52.4137	35.9949	38.8145	39.3824	24.8053	12.7508
GT	Sense	Sense	-0.110	Detected	0.110	Detected	0.000	-1.140	Detected	-0.956	Detected	-1.048	0.018	40.1195	36.5373	33.3941	25.9563	18.3648	20.1446
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-2.561	Detected	-2.717	Detected	-2.639	0.004	2241.62	2162.64	559.16	657.172	394.335	341.696
GT	Sense	Sense	-0.225	Detected	0.225	Detected	0.000	-2.346	Detected	-2.503	Detected	-2.425	0.010	3920.82	4186.01	1102.05	1394.63	841.95	729.021
GT	Sense	Sense	0.002	Detected	-0.002	Detected	0.000	-1.199	Detected	-1.445	Detected	-1.322	0.009	64.2402	50.048	27.2035	26.0711	26.1079	21.2464
GT	Sense	Sense	-0.452	Detected	0.452	Detected	0.000	-1.936	Detected	-2.043	Detected	-1.989	0.049	90.4993	132.335	86.5053	142.52	30.2165	27.1049
GT	Sense	Sense	-0.499	Detected	0.499	Detected	0.000	-4.418	Detected	-1.456	Detected	-2.937	0.201	731.641	1142.37	469.031	72.9044	45.1835	339.922
GT	Sense	Sense	0.359	Detected	-0.359	Detected	0.000	-1.338	Detected	-1.215	Detected	-1.277	0.073	15471.1	7349.66	8473.76	5476.74	4456.69	4687.67
GT	Sense	Sense	-0.130	Detected	0.130	Detected	0.000	-2.406	Detected	-2.602	Detected	-2.504	0.004	7161.78	6703.45	1734.18	2191.21	1382.05	1164.69
GT	Sense	Sense	0.100	Detected	-0.100	Detected	0.000	-1.114	Detected	-1.174	Detected	-1.144	0.008	116.659	79.4184	51.949	41.6667	47.001	43.5361
GT	Sense	Sense	-0.359	Detected	0.359	Detected	0.000	-1.773	Detected	-1.903	Detected	-1.838	0.037	286.602	368.337	126.53	136.076	100.48	88.6215
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-2.102	Detected	-2.124	Detected	-2.113	0.002	1898.09	1689.11	713.62	815.39	440.744	418.998
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-2.802	Detected	-1.813	Detected	-2.308	0.045	120.466	82.2085	52.7499	33.6281	15.0758	28.9042
GT	Sense	Sense	-1.068	Detected	1.068	Detected	0.000	-3.295	Detected	-1.577	Detected	-2.436	0.217	658.087	2260.45	351.633	82.3817	131.331	417.192
GT	Sense	Sense	0.232	Detected	-0.232	Detected	0.000	-1.323	Detected	-1.227	Detected	-1.275	0.033	157.37	89.2244	62.118	45.6941	50.0479	51.6551
GT	Sense	Sense	-0.158	Detected	0.158	Detected	0.000	-0.883	Detected	-1.761	Detected	-1.322	0.105	129.577	126.007	73.1789	57.2833	73.2154	38.4595
GT	Sense	Sense	-0.207	Detected	0.207	Detected	0.000	-1.142	Detected	-1.531	Detected	-1.337	0.042	543.067	565.576	364.826	392.114	265.365	195.656
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-1.788	Detected	-0.802	Detected	-1.295	0.125	15411.8	10212.9	8822.7	4441.69	3839.64	7342.33
GT	Sense	Sense	0.106	Detected	-0.106	Detected	0.000	-1.020	Detected	-1.049	Detected	-1.034	0.011	51.4411	34.7065	24.9819	30.4219	22.0211	20.8401
GT	Sense	Sense	-0.211	Detected	0.211	Detected	0.000	-4.343	Comprom	-1.948	Comprom	-3.145	0.123	35.6078	37.2942	10.4305	1.94204	1.89833	9.63661
GT	Sense	Sense	-0.219	Detected	0.219	Detected	0.000	-2.143	Detected	-2.308	Detected	-2.225	0.011	6048.26	6401.77	1823.26	2086	1488.65	1282.48
GT	Sense	Sense	-0.052	Detected	0.052	Detected	0.000	-1.625	Detected	-2.371	Detected	-1.998	0.034	70.8321	59.5193	24.6343	38.2048	22.2471	12.8048
GT	Sense	Sense	0.245	Detected	-0.245	Detected	0.000	-1.329	Detected	-1.381	Detected	-1.355	0.031	43.8038	24.3937	23.7137	23.4117	13.7544	12.8033
GT	Sense	Sense	-0.199	Detected	0.199	Detected	0.000	-2.255	Detected	-2.527	Detected	-2.391	0.010	4375.6	4504.25	1283.52	1506.65	983.047	785.955
GT	Sense	Sense	-0.264	Detected	0.264	Detected	0.000	-1.173	Comprom	-0.916	Comprom	-1.044	0.071	17.7475	19.9998	6.47669	22.8324	8.82905	10.1899
GT	Sense	Sense	-0.250	Detected	0.250	Detected	0.000	-1.436	Detected	-0.977	Detected	-1.206	0.071	17501.8	19355.3	13848	6069.98	7190.08	9544.05
GT	Sense	Sense	-0.170	Detected	0.170	Detected	0.000	-1.534	Detected	-1.846	Detected	-1.690	0.018	510.392	504.967	315.132	263.75	185.33	144.039
GT	Sense	Sense	-0.106	Detected	0.106	Detected	0.000	-3.506	Comprom	-3.834	Comprom	-3.670	0.003	55.4236	50.1984	21.5302	22.1319	4.90849	3.77379
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-2.522	Detected	-2.443	Detected	-2.483	0.002	1410.13	1261.05	530.482	578.925	245.387	250.156
GT	Sense	Sense	0.126	Detected	-0.126	Detected	0.000	-1.438	Detected	-1.286	Detected	-1.362	0.012	84.3953	55.3574	42.5608	38.9189	26.661	28.6046
GT	Sense	Sense	-0.103	Detected	0.103	Detected	0.000	-2.951	Detected	-2.899	Detected	-2.925	0.001	385.49	347.749	102.804	127.355	50.05	50.0986
GT	Sense	Sense	-0.227	Detected	0.227	Detected	0.000	-2.067	Detected	-1.705	Detected	-1.886	0.023	74.1829	79.3872	26.5201	33.0654	19.3494	24.019
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	-2.818	Comprom	-1.991	Detected	-2.404	0.029	42.5043	35.8201	24.2804	12.503	5.84887	10.0165
GT	Sense	Sense	0.060	Detected	-0.060	Detected	0.000	-1.426	Detected	-1.357	Detected	-1.391	0.002	271.528	195.325	217.9	112.122	90.574	91.7559
GT	Sense	Sense	-0.162	Detected	0.162	Detected	0.000	-1.746	Detected	-1.456	Detected	-1.601	0.018	61.872	60.5004	41.0367	42.6834	19.2774	22.7499
GT	Sense	Sense	-0.157	Detected	0.157	Detected	0.000	-2.387	Detected	-2.540	Detected	-2.464	0.005	3553.95	3451.18	1041.66	1170.94	707.541	614.397
GT	Sense	Sense	-0.172	Detected	0.172	Detected	0.000	-1.977	Detected	-2.162	Detected	-2.069	0.009	2111.24	2094.93	823.305	872.699	564.487	479.584
GT	Sense	Sense	-0.330	Detected	0.330	Detected	0.000	-0.943	Detected	-1.137	Detected	-1.040	0.094	40.5896	50.1191	33.1461	42.476	24.7894	20.93
GT	Sense	Sense	-0.291	Detected	0.291	Detected	0.000	-3.544	Detected	-1.477	Detected	-2.510	0.144	389.666	456.135	247.306	26.0239	38.2081	154.521
GT	Sense	Sense	-0.224	Detected	0.224	Detected	0.000	-0.976	Detected	-1.257	Detected	-1.116	0.052	73.2883	78.1544	37.6417	47.2747	40.6695	32.3156
GT	Sense	Sense	0.048	Detected	-0.048	Detected	0.000	-1.283	Detected	-0.852	Detected	-1.067	0.040	67.9979	49.702	49.4062	56.0867	25.2541	32.856
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	-1.880	Detected	-2.578	Comprom	-2.229	0.028	48.4918	30.5302	18.6871	20.5703	11.0448	6.57586
GT	Sense	Sense	-0.297	Detected	0.297	Detected	0.000	-2.557	Detected	-0.846	Detected	-1.701	0.201	197.612	233.222	97.5665	28.2935	38.5534	121.89
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-2.356	Detected	-2.500	Detected	-2.428	0.001	758.952	634.015	202.356	250.252	143.204	125.11
GT	Sense	Sense	-0.180	Detected	0.180	Detected	0.000	-1.436	Detected	-1.371	Detected	-1.404	0.017	2065.4	2072.97	1160.23	846.302	808.247	816.182
GT	Sense	Sense	-0.142	Detected	0.142	Detected	0.000	-1.849	Detected	-1.878	Detected	-1.864	0.006	3792.98	3611.08	1682.13	1894.54	1085.51	1027.18
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-1.842	Detected	-1.873	Detected	-1.857	0.007	7082.83	6835.19	2736.38	3162.51	2051.72	1938.51
GT	Sense	Sense	-0.343	Detected	0.343	Detected	0.000	-1.588	Detected	-0.870	Detected	-1.229	0.132	29177.7	36685.3	19180.6	14248	11504.4	18263.1
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	-1.923	Comprom	-1.574	Comprom	-1.749	0.052	18.3032	24.1329	8.31088	6.78881	5.85599	7.2019
GT	Sense	Sense	-0.417	Detected	0.417	Detected	0.000	-1.675	Comprom	-1.489	Comprom	-1.582	0.066	12.7545	17.7806	11.0288	2.1714	4.98473	5.47518
GT	Sense	Sense	-0.170	Detected	0.170	Detected	0.000	-1.137	Detected	-1.152	Detected	-1.145	0.021	10359.7	10247	6326.02	7264.03	4951.14	4730.5
GT	Sense	Sense	0.339	Detected	-0.339	Detected	0.000	-0.898	Detected	-1.244	Detected	-1.071	0.107	109.308	53.3759	48.1412	63.3476	43.3275	32.8949
GT	Sense	Sense	0.409	Detected	-0.409	Detected	0.000	-2.043	Comprom	-1.525	Comprom	-1.784	0.066	27.789	12.3271	23.5629	21.7399	4.74664	6.56124
GT	Sense	Sense	-0.532	Detected	0.532	Detected	0.000	-4.295	Comprom	-1.147	Detected	-2.721	0.243	72.7403	118.899	27.3492	15.2479	5.00617	42.8582
GT	Sense	Sense	-0.295	Detected	0.295	Detected	0.000	-0.862	Detected	-1.163	Detected	-1.013	0.093	54.1486	63.7406	46.6474	44.2832	34.1636	26.7679
GT	Sense	Sense	-0.185	Detected	0.185	Detected	0.000	-1.265	Detected	-1.469	Detected	-1.367	0.023	25693.1	25948.6	11937.8	13739.8	11354.7	9514.22
GT	Sense	Sense	-0.102	Detected	0.102	Detected	0.000	-1.136	Detected	-1.327	Detected	-1.232	0.013	644.978	581.089	286.136	352.949	294.301	249.07
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	-1.697	Detected	-1.705	Detected	-1.701	0.006	4992.2	4678.63	2637.77	3025.42	1574.86	1512.11
GT	Sense	Sense	-0.352	Detected	0.352	Detected	0.000	-1.325	Detected	-0.860	Detected	-1.093	0.122	96.0398	122.301	96.6067	47.825	45.7155	60.9243
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-2.596	Detected	-2.762	Detected	-2.679	0.004	3568.86	3441.91	935.985	1060.79	612.677	527.339
GT	Sense	Sense	-0.164	Detected	0.164	Detected	0.000	-1.777	Detected	-1.171	Detected	-1.474	0.051	2055.79	2016.91	1095.63	1901.46	627.947	922.825
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-2.614	Detected	-1.300	Detected	-1.957	0.098	25437.6	22072.4	11330.3	3882.63	4089.41	9816.32
GT	Sense	Sense	-0.136	Detected	0.136	Detected	0.000	-2.347	Detected	-2.429	Detected	-2.388	0.004	3513.24	3316.61	923.014	1056.82	708.961	646.835
GT	Sense	Sense	-0.128	Detected	0.128	Detected	0.000	-2.128	Detected	-2.574	Detected	-2.351	0.012	912.208	851.861	257.01	307.947	213.151	151.035
GT	Sense	Sense	0.098	Detected	-0.098	Detected	0.000	-1.617	Detected	-1.087	Detected	-1.352	0.041	10363.1	7074.51	5523.61	2518.83	2949.95	4112.11
GT	Sense	Sense	-0.179	Detected	0.179	Detected	0.000	-1.362	Detected	-1.464	Detected	-1.413	0.017	33598.7	33646.2	17107.9	18709.9	13825.8	12438.4
GT	Sense	Sense	-0.184	Detected	0.184	Detected	0.000	-2.474	Detected	-2.394	Detected	-2.434	0.006	129.425	130.513	27.3858	35.739	24.7249	25.2316
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	-1.302	Detected	-2.099	Detected	-1.701	0.061	54.5263	55.342	30.1378	33.6955	23.5459	13.0826
GT	Sense	Sense	0.173	Detected	-0.173	Detected	0.000	-1.263	Detected	-1.065	Detected	-1.164	0.028	3162.21	1943.53	2086.94	2482.99	1091.68	1209.17
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	-1.552	Detected	-1.576	Detected	-1.564	0.001	57.7359	47.4628	25.0694	22.1091	18.8614	17.9114
GT	Sense	Sense	-0.675	Detected	0.675	Detected	0.000	-2.344	Detected	-1.596	Detected	-1.970	0.125	95.187	189.54	45.6036	48.4048	27.9573	45.3292
GT	Sense	Sense	-0.537	Detected	0.537	Detected	0.000	-1.518	Detected	-0.995	Detected	-1.256	0.170	114.171	187.898	100.748	184.246	54.0642	75.0014
GT	Sense	Sense	-0.169	Detected	0.169	Detected	0.000	-2.480	Detected	-2.408	Detected	-2.444	0.005	71.1308	70.2492	81.5778	83.6902	13.3932	13.5882
GT	Sense	Sense	-0.126	Detected	0.126	Detected	0.000	-2.746	Detected	-2.204	Detected	-2.475	0.014	76.2885	71.025	19.3267	31.1125	11.5929	16.2976
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.160	Detected	-1.189	Detected	-1.174	0.003	378.383	322.396	261.819	277.427	165.237	156.319
GT	Sense	Sense	-0.500	Detected	0.500	Detected	0.000	-1.383	Detected	-1.056	Detected	-1.219	0.146	55.8316	87.3007	31.6531	30.1869	28.3003	34.256
GT	Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-1.102	Detected	-1.205	Detected	-1.154	0.007	158.882	111.363	128.629	108.006	65.5019	58.8537
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-1.305	Detected	-2.361	Comprom	-1.833	0.078	30.1278	19.807	16.9184	16.4256	10.4485	4.85155
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.067	Detected	-1.101	Detected	-1.084	0.001	256.016	193.016	269.21	241.605	112.12	105.739
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.261	Detected	-0.938	Detected	-1.099	0.023	927.16	680.538	868.266	1167.34	350.294	423.184
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	-2.153	Detected	-1.841	Detected	-1.997	0.009	197.892	181.188	70.662	82.3558	44.9954	53.9285
GT	Sense	Sense	0.060	Detected	-0.060	Detected	0.000	-1.040	Detected	-1.283	Detected	-1.161	0.013	289.203	207.939	371.699	419.379	126.084	102.821
GT	Sense	Sense	-0.031	Detected	0.031	Detected	0.000	-1.419	Comprom	-2.084	Comprom	-1.751	0.034	23.2624	18.9773	10.5484	16.9569	8.3051	5.05727
GT	Sense	Sense	0.274	Detected	-0.274	Detected	0.000	-3.201	Comprom	-2.900	Comprom	-3.051	0.010	87.0497	46.5407	20.6306	24.4334	7.31366	8.70164
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	-2.071	Detected	-1.921	Detected	-1.996	0.003	657.811	569.694	246.597	345.637	154.006	164.943
GT	Sense	Sense	0.136	Detected	-0.136	Detected	0.000	-3.437	Comprom	-1.749	Detected	-2.593	0.094	62.1329	40.2029	27.5168	49.5188	4.87796	15.1766
GT	Sense	Sense	-0.306	Detected	0.306	Detected	0.000	-1.157	Detected	-2.792	Detected	-1.974	0.152	301.197	359.675	72.2779	75.0555	156.033	48.5041
GT	Sense	Sense	-0.442	Detected	0.442	Detected	0.000	-1.218	Detected	-0.803	Detected	-1.011	0.175	57.8077	83.4447	47.1382	66.0824	31.5544	40.6071
GT	Sense	Sense	0.474	Detected	-0.474	Detected	0.000	-0.989	Detected	-1.832	Comprom	-1.411	0.156	47.6386	19.3102	23.5114	23.7589	16.151	8.69148
GT	Sense	Sense	-0.700	Detected	0.700	Detected	0.000	-1.749	Detected	-1.012	Detected	-1.381	0.223	1110.31	2290.07	386.055	213.063	501.229	806.864
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	-2.194	Detected	-1.623	Detected	-1.909	0.022	141.029	112.564	73.3583	52.9224	29.0927	41.7332
GT	Sense	Sense	-0.287	Detected	0.287	Detected	0.000	-2.030	Comprom	-1.984	Comprom	-2.007	0.020	27.2366	31.6874	4.27725	5.60345	7.60248	7.57495
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	-1.971	Detected	-2.095	Detected	-2.033	0.001	384.872	307.233	141.858	143.252	92.7183	82.1545
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.184	Detected	-1.568	Detected	-1.376	0.022	820.634	709.07	336.796	388.82	354.86	262.529
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.184	Detected	-1.863	Detected	-1.524	0.048	408.18	347.5	174.309	193.765	175.206	105.605
GT	Sense	Sense	-0.101	Detected	0.101	Detected	0.000	-2.377	Detected	-2.604	Detected	-2.491	0.004	393.951	353.977	107.832	123.783	75.9687	62.6548
GT	Sense	Sense	-0.207	Detected	0.207	Detected	0.000	-2.036	Detected	-0.832	Detected	-1.434	0.153	166.785	173.655	130.96	71.7771	43.8631	97.569
GT	Sense	Sense	0.247	Detected	-0.247	Detected	0.000	-1.900	Detected	-1.365	Detected	-1.633	0.046	3837.97	2129.54	1405.15	747.307	809.47	1132.13
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	-1.025	Detected	-1.908	Comprom	-1.466	0.080	32.4287	23.8708	27.2082	32.1704	14.4463	7.5669
GT	Sense	Sense	-0.873	Detected	0.873	Detected	0.000	-4.096	Detected	-1.804	Detected	-2.950	0.177	683.565	1792.78	455.855	37.4143	68.4223	323.439
GT	Sense	Sense	-0.111	Detected	0.111	Detected	0.000	-2.157	Detected	-2.116	Detected	-2.136	0.003	888.768	810.588	357.995	403.931	201.142	199.812
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	-2.381	Comprom	-1.457	Detected	-1.919	0.053	34.83	26.3465	23.9523	34.0679	6.14591	11.2554
GT	Sense	Sense	-0.178	Detected	0.178	Detected	0.000	-2.250	Detected	-2.512	Detected	-2.381	0.009	1207.44	1207.94	459.83	553.324	268.325	215.977
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	-2.372	Comprom	-2.181	Comprom	-2.277	0.007	45.7583	28.4925	21.8217	27.5784	7.3707	8.12544
GT	Sense	Sense	-0.200	Detected	0.200	Detected	0.000	-2.191	Detected	-2.362	Detected	-2.276	0.009	3206.14	3309.09	987.334	1177.56	754.062	646.693
GT	Sense	Sense	-0.195	Detected	0.195	Detected	0.000	-1.988	Detected	-2.019	Detected	-2.004	0.009	2589.57	2653.72	1158.28	1355.25	698.21	660.133
GT	Sense	Sense	-0.239	Detected	0.239	Detected	0.000	-1.410	Detected	-1.791	Detected	-1.601	0.035	1229.99	1338.8	658.808	742.362	510.385	378.295
GT	Sense	Sense	-0.009	Detected	0.009	Detected	0.000	-2.291	Comprom	-3.194	Comprom	-2.743	0.026	39.8903	31.583	9.34578	10.9804	7.66319	3.95787
GT	Sense	Sense	0.218	Detected	-0.218	Detected	0.000	-1.356	Detected	-1.395	Detected	-1.376	0.024	92.7693	53.566	41.5247	50.0831	29.0978	27.3458
GT	Sense	Sense	0.373	Detected	-0.373	Detected	0.000	-1.722	Detected	-2.006	Detected	-1.864	0.043	5551.2	2585.59	4406.53	3693.05	1213.61	962.229
GT	Sense	Sense	0.198	Detected	-0.198	Detected	0.000	-1.537	Detected	-1.740	Comprom	-1.638	0.018	39.287	23.3521	9.80168	18.5244	11.035	9.24931
GT	Sense	Sense	-0.192	Detected	0.192	Detected	0.000	-1.779	Comprom	-1.170	Comprom	-1.474	0.055	17.1246	17.461	20.2778	17.5263	5.32651	7.84101
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	-2.110	Detected	-1.358	Detected	-1.734	0.045	160.755	113.74	33.9524	15.5671	33.099	53.8139
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-1.803	Comprom	-2.148	Comprom	-1.975	0.008	33.6428	28.063	16.5839	17.4118	9.30486	7.07589
GT	Sense	Sense	0.261	Detected	-0.261	Detected	0.000	-2.401	Comprom	-1.741	Comprom	-2.071	0.039	29.114	15.8446	13.9145	13.4522	4.2974	6.55528
GT	Sense	Sense	-0.109	Detected	0.109	Detected	0.000	-1.118	Detected	-1.126	Detected	-1.122	0.009	85.4918	77.6726	58.5306	65.8726	39.6685	38.0951
GT	Sense	Sense	0.211	Detected	-0.211	Detected	0.000	-1.313	Detected	-0.802	Detected	-1.058	0.086	35.0265	20.4344	22.227	12.6051	11.3795	15.6525
GT	Sense	Sense	-0.270	Detected	0.270	Detected	0.000	-1.206	Detected	-1.328	Detected	-1.267	0.044	2501.81	2841.5	1436.2	1885.32	1221.43	1083.4
GT	Sense	Sense	-0.177	Detected	0.177	Detected	0.000	-1.461	Detected	-1.119	Detected	-1.290	0.034	1023.37	1021.84	750.799	571.138	392.551	480.511
GT	Sense	Sense	-0.789	Detected	0.789	Detected	0.000	-3.183	Comprom	-2.033	Detected	-2.608	0.116	38.9544	90.9111	14.2263	8.97117	6.92563	14.8331
GT	Sense	Sense	-0.123	Detected	0.123	Detected	0.000	-1.755	Comprom	-1.944	Comprom	-1.850	0.007	16.8355	15.5973	5.56395	11.8372	5.07276	4.29762
GT	Sense	Sense	-0.227	Detected	0.227	Detected	0.000	-1.518	Detected	-1.212	Detected	-1.365	0.038	46.6928	49.9619	42.0396	17.9232	17.8283	21.2806
GT	Sense	Sense	0.019	Detected	-0.019	Detected	0.000	-0.957	Detected	-1.553	Detected	-1.255	0.052	368.028	280.012	198.451	201.864	174.709	111.648
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-0.976	Detected	-1.060	Detected	-1.018	0.002	1277.42	978.121	535.702	630.851	600.716	546.873
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-2.407	Detected	-1.734	Detected	-2.070	0.027	1361.52	1212.69	715.59	789.07	256.036	394.273
GT	Sense	Sense	-0.120	Detected	0.120	Detected	0.000	-2.419	Detected	-2.420	Detected	-2.419	0.002	2376.03	2193.42	742.989	841.669	451.232	435.226
GT	Sense	Sense	-0.610	Detected	0.610	Detected	0.000	-2.573	Detected	-0.836	Detected	-1.705	0.249	8270.83	15058.2	3835.23	1895.97	1982.26	6377.95
GT	Sense	Sense	-0.173	Detected	0.173	Detected	0.000	-2.519	Detected	-2.691	Detected	-2.605	0.005	1226.25	1218.88	293.917	371.744	225.412	193.224
GT	Sense	Sense	0.116	Detected	-0.116	Detected	0.000	-1.536	Detected	-2.155	Detected	-1.846	0.031	192.205	127.924	76.8368	82.2301	57.1493	35.9142
GT	Sense	Sense	-0.153	Detected	0.153	Detected	0.000	-2.147	Detected	-2.244	Detected	-2.195	0.005	2071.08	2001.18	860.155	948.343	485.914	438.544
GT	Sense	Sense	-0.196	Detected	0.196	Detected	0.000	-1.189	Detected	-2.046	Detected	-1.617	0.075	181.261	185.92	111.488	88.7007	85.1232	45.3594
GT	Sense	Sense	-0.194	Detected	0.194	Detected	0.000	-2.541	Detected	-1.075	Detected	-1.808	0.140	14780.7	15109.2	7344.09	2998.98	2713.21	7239.36
GT	Sense	Sense	-0.083	Detected	0.083	Detected	0.000	-1.259	Detected	-1.265	Detected	-1.262	0.004	695.066	609.948	392.58	416.295	287.541	276.531
GT	Sense	Sense	-1.683	Detected	1.683	Detected	0.000	-2.659	Detected	-0.802	Detected	-1.731	0.463	24.6173	198.405	9.86505	9.09377	11.6939	40.8974
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	-1.520	Detected	-1.421	Detected	-1.470	0.013	8588.73	8436.06	6511.3	2692.33	3136.77	3244.63
GT	Sense	Sense	-0.162	Detected	0.162	Detected	0.000	-1.120	Detected	-2.056	Detected	-1.588	0.085	169.954	166.258	72.1132	85.7384	81.742	41.2444
GT	Sense	Sense	0.051	Detected	-0.051	Detected	0.000	-1.110	Detected	-1.009	Detected	-1.059	0.005	139.063	101.25	111.082	94.8749	58.1117	60.1798
GT	Sense	Sense	-0.304	Detected	0.304	Detected	0.000	-1.974	Detected	-1.024	Detected	-1.499	0.117	11434.7	13626.9	6740.98	8936.52	3358.79	6262.28
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-2.118	Detected	-2.283	Detected	-2.200	0.003	2433.79	2175.95	779.757	793.673	560.298	482.607
GT	Sense	Sense	-0.154	Detected	0.154	Detected	0.000	-1.112	Detected	-1.136	Detected	-1.124	0.018	66.2825	64.1086	47.0161	58.61	31.8712	30.2696
GT	Sense	Sense	-0.174	Detected	0.174	Detected	0.000	-1.672	Detected	-1.602	Detected	-1.637	0.012	5676.1	5647.66	2567.09	2796.99	1877.37	1902.6
GT	Sense	Sense	-0.188	Detected	0.188	Detected	0.000	-1.896	Detected	-1.961	Detected	-1.928	0.010	1603.06	1626.94	510.308	623.535	458.564	423.294
GT	Sense	Sense	-0.958	Detected	0.958	Detected	0.000	-2.381	Comprom	-1.678	Detected	-2.029	0.185	23.6323	69.6693	9.65486	10.0494	8.23494	12.9424
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	-1.055	Detected	-1.202	Detected	-1.129	0.009	95.0526	66.4084	56.0662	74.1252	40.4143	35.2269
GT	Sense	Sense	-0.148	Detected	0.148	Detected	0.000	-1.495	Detected	-1.157	Detected	-1.326	0.028	192.996	185.216	132.003	291.355	70.8991	86.5313
GT	Sense	Sense	-0.221	Detected	0.221	Detected	0.000	-2.881	Comprom	-2.746	Comprom	-2.813	0.007	12.13	12.8843	4.38584	1.87631	1.79356	1.90169
GT	Sense	Sense	-0.066	Detected	0.066	Detected	0.000	-2.695	Detected	-2.464	Detected	-2.579	0.003	7342.16	6288.98	1371.64	1339.69	1109.35	1257.05
GT	Sense	Sense	-0.352	Detected	0.352	Detected	0.000	-1.822	Detected	-1.027	Detected	-1.424	0.115	921.209	1172.29	620.029	278.702	310.719	520.185
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	-1.742	Comprom	-3.245	Comprom	-2.493	0.083	22.1833	13.9663	8.15884	12.5143	5.56136	1.89437
GT	Sense	Sense	-0.177	Detected	0.177	Detected	0.000	-0.978	Detected	-1.436	Detected	-1.207	0.053	569.825	569.642	394.532	411.556	305.788	214.871
GT	Sense	Sense	-0.226	Detected	0.226	Detected	0.000	-1.050	Detected	-0.973	Detected	-1.012	0.048	3896.24	4165.77	2913.83	3327.09	2056.66	2093.77
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-1.475	Detected	-1.481	Detected	-1.478	0.000	395.74	303.482	212.696	233.261	131.762	126.634
GT	Sense	Sense	-0.376	Detected	0.376	Detected	0.000	-1.954	Detected	-1.418	Detected	-1.686	0.067	1716.26	2257.89	1280.38	2767.33	536.784	751.781
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	-1.636	Detected	-0.982	Detected	-1.309	0.059	153.104	109.522	78.2644	34.7127	44.0195	66.8881
GT	Sense	Sense	0.009	Detected	-0.009	Detected	0.000	-0.868	Detected	-1.250	Detected	-1.059	0.031	194.893	150.486	119.434	113.281	99.1703	73.4855
GT	Sense	Sense	-0.220	Detected	0.220	Detected	0.000	-1.227	Detected	-1.987	Detected	-1.607	0.067	340.79	361.132	164.657	162.22	158.336	90.3269
GT	Sense	Sense	-0.752	Detected	0.752	Detected	0.000	-2.199	Comprom	-2.090	Comprom	-2.145	0.105	11.5575	25.6402	13.4333	7.25385	3.96142	4.1253
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	-1.842	Detected	-1.884	Detected	-1.863	0.004	52.261	47.7288	24.2603	22.4727	14.7278	13.8024
GT	Sense	Sense	-0.077	Detected	0.077	Detected	0.000	-2.004	Detected	-2.368	Detected	-2.186	0.008	231.439	201.398	76.3212	92.1254	56.9023	42.6813
GT	Sense	Sense	0.846	Detected	-0.846	Detected	0.000	-2.289	Detected	-2.738	Detected	-2.513	0.103	248.87	60.2064	89.5288	74.1595	26.4792	18.7244
GT	Sense	Sense	0.268	Detected	-0.268	Detected	0.000	-3.620	Comprom	-2.743	Comprom	-3.181	0.025	49.5788	26.7164	20.6817	18.8736	3.12863	5.54698
GT	Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.932	Detected	-2.379	Detected	-2.155	0.011	80.3927	64.933	28.7094	31.1714	20.0132	14.1759
GT	Sense	Sense	-0.285	Detected	0.285	Detected	0.000	-2.006	Detected	-2.193	Detected	-2.099	0.020	5996.82	6955.98	2010.22	2449.4	1698.96	1441.58
GT	Sense	Sense	-0.063	Detected	0.063	Detected	0.000	-2.843	Detected	-2.680	Detected	-2.762	0.001	693.181	591.587	217.021	242.628	94.3299	101.931
GT	Sense	Sense	-0.435	Detected	0.435	Detected	0.000	-1.172	Detected	-0.968	Detected	-1.070	0.139	647.426	925.302	516.889	398.676	363.032	403.843
GT	Sense	Sense	-0.304	Detected	0.304	Detected	0.000	-3.196	Comprom	-1.468	Detected	-2.332	0.126	46.7973	55.7379	22.8875	17.8299	5.89178	18.8414
GT	Sense	Sense	-0.193	Detected	0.193	Detected	0.000	-2.113	Detected	-2.208	Detected	-2.161	0.008	8894.95	9089.1	3113.95	3433.45	2196.02	1986.24
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	-3.207	Detected	-2.879	Detected	-3.043	0.007	1375.25	811.68	601.521	553.957	120.96	146.568
GT	Sense	Sense	-0.585	Detected	0.585	Detected	0.000	-1.597	Detected	-1.153	Detected	-1.375	0.159	77.8724	137.037	81.1069	129.828	36.1019	47.3989
GT	Sense	Sense	0.397	Detected	-0.397	Detected	0.000	-1.831	Comprom	-1.595	Comprom	-1.713	0.054	30.5963	13.784	2.4988	7.02486	6.10002	6.93724
GT	Sense	Sense	-0.553	Detected	0.553	Detected	0.000	-2.456	Detected	-0.885	Detected	-1.671	0.224	436.429	734.443	248.898	189.55	109.043	312.787
GT	Sense	Sense	-0.104	Detected	0.104	Detected	0.000	-3.495	Detected	-2.005	Detected	-2.750	0.067	133642	120623	92728.1	54447.3	11897.5	32265.4
GT	Sense	Sense	-0.046	Detected	0.046	Detected	0.000	-3.781	Detected	-2.142	Detected	-2.961	0.069	92117.7	76797.1	61644.5	28902.1	6465.75	19448.7

GO ID	GO ACCESSION	GO Term	p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
9396	GO:0016168	chlorophyll binding	**0.00**	12	2.169982	46	0.13284431
22409	GO:0046906	tetrapyrrole binding	**0.00**	33	5.96745	596	1.7212002
9266	GO:0016020	membrane	**0.00**	93	16.81736	3741	10.803708
3872	GO:0005506	iron ion binding	**0.00**	22	3.9783	563	1.6258988
11931	GO:0020037	heme binding	**0.00**	21	3.7974684	550	1.5883559
3827	GO:0005372	water transmembrane trans	**0.00**	7	1.2658228	81	0.23392151
8652	GO:0015250	water channel activity	**0.00**	7	1.2658228	81	0.23392151
4927	GO:0006833	water transport	**0.00**	7	1.2658228	81	0.23392151
18429	GO:0042044	fluid transport	**0.00**	7	1.2658228	81	0.23392151
2868	GO:0004062	aryl sulfotransferase activity	**0.00**	3	0.5424955	15	0.043318797
5702	GO:0008146	sulfotransferase activity	**0.00**	5	0.9041591	54	0.15594767
2986	GO:0004252	serine-type endopeptidase a	**0.00**	8	1.4466546	144	0.41586044
13082	GO:0030599	pectinesterase activity	**0.00**	9	1.6274865	178	0.5140497
9832	GO:0016782	transferase activity, transfe	**0.01**	5	0.9041591	74	0.21370606
6613	GO:0009250	glucan biosynthetic process	**0.01**	2	0.36166364	8	0.023103358
5766	GO:0008236	serine-type peptidase activi	**0.01**	9	1.6274865	214	0.6180149
10103	GO:0017171	serine hydrolase activity	**0.01**	9	1.6274865	220	0.63534236
4215	GO:0005975	carbohydrate metabolic pro	**0.01**	26	4.7016273	990	2.8590407
11776	GO:0019825	oxygen binding	**0.01**	13	2.3508136	389	1.1234008
6216	GO:0008810	cellulase activity	**0.01**	3	0.5424955	30	0.086637594
11827	GO:0019898|GO:0030396	extrinsic to membrane	**0.01**	3	0.5424955	30	0.086637594
3156	GO:0004497	monooxygenase activity	**0.02**	7	1.2658228	172	0.49672222
16081	GO:0033692	cellular polysaccharide bios	**0.02**	2	0.36166364	15	0.043318797
206	GO:0000271	polysaccharide biosynthetic	**0.03**	2	0.36166364	16	0.046206716
12533	GO:0022838	substrate-specific channel a	**0.03**	8	1.4466546	221	0.63823026
9771	GO:0016709	oxidoreductase activity, act	**0.03**	4	0.7233273	71	0.2050423
4909	GO:0006810|GO:0015457|	transport	**0.03**	49	8.86076	2315	6.6855345
25529	GO:0051234	establishment of localizatio	**0.03**	49	8.86076	2315	6.6855345
25476	GO:0051179	localization	**0.03**	49	8.86076	2319	6.697086
31498	GO:0080123	jasmonate-amino synthetas	**0.03**	2	0.36166364	17	0.049094636
8660	GO:0015267|GO:0015249|	channel activity	**0.03**	8	1.4466546	226	0.6526699
12515	GO:0022803	passive transmembrane tra	**0.03**	8	1.4466546	226	0.6526699
3013	GO:0004328|GO:0034566	formamidase activity	**0.03**	1	0.18083182	2	0.00577584
4429	GO:0006223	uracil salvage	**0.03**	1	0.18083182	2	0.00577584
4907	GO:0006808	regulation of nitrogen utiliza	**0.03**	1	0.18083182	2	0.00577584
6080	GO:0008655	pyrimidine-containing comp	**0.03**	1	0.18083182	2	0.00577584
6828	GO:0009540	zeaxanthin epoxidase [over	**0.03**	1	0.18083182	2	0.00577584
7504	GO:0010277|GO:0046407	chlorophyllide a oxygenase	**0.03**	1	0.18083182	2	0.00577584
7532	GO:0010307	acetylglutamate kinase regu	**0.03**	1	0.18083182	2	0.00577584
8612	GO:0015204|GO:0015287	urea transmembrane transp	**0.03**	1	0.18083182	2	0.00577584
9106	GO:0015840	urea transport	**0.03**	1	0.18083182	2	0.00577584
9766	GO:0016703	oxidoreductase activity, act	**0.03**	1	0.18083182	2	0.00577584
11797	GO:0019860	uracil metabolic process	**0.03**	1	0.18083182	2	0.00577584
14849	GO:0032441	pheophorbide a oxygenase	**0.03**	1	0.18083182	2	0.00577584
19204	GO:0042887	amide transmembrane tran	**0.03**	1	0.18083182	2	0.00577584
19407	GO:0043100	pyrimidine base salvage	**0.03**	1	0.18083182	2	0.00577584
23921	GO:0048529	magnesium-protoporphyrin	**0.03**	1	0.18083182	2	0.00577584
30280	GO:0071918	urea transmembrane transp	**0.03**	1	0.18083182	2	0.00577584
31514	GO:0080139	borate efflux transmembran	**0.03**	1	0.18083182	2	0.00577584
3723	GO:0005215|GO:0005478	transporter activity	**0.03**	40	7.233273	1844	5.325324
12547	GO:0022857|GO:0005386|	transmembrane transporter	**0.04**	33	5.96745	1483	4.282785
3877	GO:0005516	calmodulin binding	**0.04**	8	1.4466546	236	0.6815491
26931	GO:0055085	transmembrane transport	**0.04**	34	6.148282	1548	4.4705
9767	GO:0016705	oxidoreductase activity, act	**0.04**	10	1.8083183	329	0.95012563
9784	GO:0016723	oxidoreductase activity, oxi	**0.04**	2	0.36166364	20	0.0577584
225	GO:0000293	ferric-chelate reductase act	**0.04**	2	0.36166364	20	0.0577584
28930	GO:0070566	adenylyltransferase activity	**0.04**	3	0.5424955	48	0.13862015
7074	GO:0009815	1-aminocyclopropane-1-car	**0.04**	3	0.5424955	49	0.14150807
31421	GO:0080044	quercetin 7-O-glucosyltrans	**0.04**	3	0.5424955	49	0.14150807
7166	GO:0009914	hormone transport	**0.05**	3	0.5424955	50	0.14439599
27891	GO:0060918	auxin transport	**0.05**	3	0.5424955	50	0.14439599
31536	GO:0080161	auxin transmembrane trans	**0.05**	3	0.5424955	50	0.14439599
12574	GO:0022892	substrate-specific transport	**0.05**	32	5.786618	1463	4.2250266
3134	GO:0004474	malate synthase activity	**0.05**	1	0.18083182	3	0.00866376
4319	GO:0006081	cellular aldehyde metabolic	**0.05**	1	0.18083182	3	0.00866376
4330	GO:0006097	glyoxylate cycle	**0.05**	1	0.18083182	3	0.00866376
21936	GO:0046409	p-coumarate 3-hydroxylase	**0.05**	1	0.18083182	3	0.00866376
22011	GO:0046487	glyoxylate metabolic proces	**0.05**	1	0.18083182	3	0.00866376
24613	GO:0050294	steroid sulfotransferase act	**0.05**	1	0.18083182	3	0.00866376
4954	GO:0006869	lipid transport	**0.05**	7	1.2658228	208	0.6006873
8085	GO:0010876	lipid localization	**0.05**	7	1.2658228	208	0.6006873
26845	GO:0052689	carboxylic ester hydrolase a	**0.05**	14	2.5316455	538	1.5537009
4311	GO:0006073	cellular glucan metabolic pr	0.06	2	0.36166364	24	0.06931008
20293	GO:0044042	glucan metabolic process	0.06	2	0.36166364	24	0.06931008
2969	GO:0004167|GO:0048059	dopachrome isomerase act	0.06	1	0.18083182	4	0.011551679
3057	GO:0004373	glycogen (starch) synthase	0.06	1	0.18083182	4	0.011551679
3320	GO:0004697|GO:0004701	protein kinase C activity	0.06	1	0.18083182	4	0.011551679
3452	GO:0004845	uracil phosphoribosyltransf	0.06	1	0.18083182	4	0.011551679
3834	GO:0005395	eye pigment precursor tran	0.06	1	0.18083182	4	0.011551679
4218	GO:0005978	glycogen biosynthetic proce	0.06	1	0.18083182	4	0.011551679
4413	GO:0006206	pyrimidine base metabolic	0.06	1	0.18083182	4	0.011551679
5942	GO:0008456	alpha-N-acetylgalactosamir	0.06	1	0.18083182	4	0.011551679
7538	GO:0010313	phytochrome binding	0.06	1	0.18083182	4	0.011551679
8637	GO:0015231	5-formyltetrahydrofolate tra	0.06	1	0.18083182	4	0.011551679
9147	GO:0015885	5-formyltetrahydrofolate tra	0.06	1	0.18083182	4	0.011551679
9351	GO:0016119	carotene metabolic process	0.06	1	0.18083182	4	0.011551679
9352	GO:0016120	carotene biosynthetic proce	0.06	1	0.18083182	4	0.011551679
9790	GO:0016730	oxidoreductase activity, act	0.06	1	0.18083182	4	0.011551679
9819	GO:0016767	geranylgeranyl-diphosphate	0.06	1	0.18083182	4	0.011551679
11857	GO:0019932	second-messenger-mediate	0.06	1	0.18083182	4	0.011551679
17811	GO:0035445	borate transmembrane tran	0.06	1	0.18083182	4	0.011551679
18575	GO:0042214	terpene metabolic process	0.06	1	0.18083182	4	0.011551679
18729	GO:0042380	hydroxymethylbutenyl pyro	0.06	1	0.18083182	4	0.011551679
21791	GO:0046246	terpene biosynthetic proces	0.06	1	0.18083182	4	0.011551679
22222	GO:0046713	borate transport	0.06	1	0.18083182	4	0.011551679
22224	GO:0046715	borate transmembrane tran	0.06	1	0.18083182	4	0.011551679
22366	GO:0046863|GO:0018236	ribulose-1,5-bisphosphate c	0.06	1	0.18083182	4	0.011551679
22408	GO:0046905	phytoene synthase activity	0.06	1	0.18083182	4	0.011551679
23493	GO:0048015	phosphatidylinositol-mediat	0.06	1	0.18083182	4	0.011551679
23495	GO:0048017	inositol lipid-mediated signa	0.06	1	0.18083182	4	0.011551679
25055	GO:0050750	low-density lipoprotein parti	0.06	1	0.18083182	4	0.011551679
28689	GO:0070325	lipoprotein particle receptor	0.06	1	0.18083182	4	0.011551679
8673	GO:0015291|GO:0015290|	secondary active transmem	0.06	11	1.98915	407	1.1753833
8028	GO:0010817	regulation of hormone level	0.07	3	0.5424955	58	0.16749935
12573	GO:0022891	substrate-specific transmen	0.07	27	4.882459	1241	3.5839086
9541	GO:0016413	O-acetyltransferase activity	0.07	2	0.36166364	27	0.077973835
25379	GO:0051082	unfolded protein binding	0.07	4	0.7233273	98	0.28301615
2975	GO:0004175|GO:0016809	endopeptidase activity	0.07	9	1.6274865	320	0.9241344
6940	GO:0009672	auxin:hydrogen symporter a	0.07	2	0.36166364	28	0.080861755
8863	GO:0015562	efflux transmembrane trans	0.07	2	0.36166364	28	0.080861755
11210	GO:0019207	kinase regulator activity	0.08	3	0.5424955	62	0.17905103
2962	GO:0004160	dihydroxy-acid dehydratase	0.08	1	0.18083182	5	0.0144396
5989	GO:0008517	folic acid transporter activit	0.08	1	0.18083182	5	0.0144396
9146	GO:0015884	folic acid transport	0.08	1	0.18083182	5	0.0144396
2870	GO:0004064	arylesterase activity	0.08	2	0.36166364	30	0.086637594
20514	GO:0044264	cellular polysaccharide met	0.09	2	0.36166364	31	0.08952551
19253	GO:0042936	dipeptide transporter activit	0.09	4	0.7233273	105	0.3032316
19255	GO:0042938	dipeptide transport	0.09	4	0.7233273	105	0.3032316
3845	GO:0005452	inorganic anion exchanger a	0.09	1	0.18083182	6	0.01732752
3940	GO:0005615	extracellular space	0.09	1	0.18083182	6	0.01732752
4118	GO:0005852	eukaryotic translation initiat	0.09	1	0.18083182	6	0.01732752
5559	GO:0007602	phototransduction	0.09	1	0.18083182	6	0.01732752
5775	GO:0008251	tRNA-specific adenosine de	0.09	1	0.18083182	6	0.01732752

6868	GO:0009585	red, far-red light phototrans	0.09	1	0.18083182	6	0.01732752	
7135	GO:0009883	red or far-red light photorec	0.09	1	0.18083182	6	0.01732752	
7255	GO:0010017	red or far-red light signaling	0.09	1	0.18083182	6	0.01732752	
9248	GO:0015994	chlorophyll metabolic proce	0.09	1	0.18083182	6	0.01732752	
9249	GO:0015995	chlorophyll biosynthetic pro	0.09	1	0.18083182	6	0.01732752	
10045	GO:0017091	AU-rich element binding	0.09	1	0.18083182	6	0.01732752	
19203	GO:0042886	amide transport	0.09	1	0.18083182	6	0.01732752	
22188	GO:0046677	response to antibiotic	0.09	1	0.18083182	6	0.01732752	
29853	GO:0071489	cellular response to red or f	0.09	1	0.18083182	6	0.01732752	
5	GO:0000007	low-affinity zinc ion transm	0.09	1	0.18083182	6	0.01732752	
19125	GO:0042802	identical protein binding	0.10	16	2.893309	697	2.01288	
2632	GO:0003682	chromatin binding	0.10	2	0.36166364	33	0.09530135	
9722	GO:0016641	oxidoreductase activity, act	0.10	3	0.5424955	69	0.19926646	
8517	GO:0015103	inorganic anion transmemb	0.10	5	0.9041591	154	0.44473964	
6004	GO:0008536	Ran GTPase binding	0.10	2	0.36166364	34	0.09818927	
3021	GO:0004337	geranyltranstransferase act	0.11	1	0.18083182	7	0.020215439	
19401	GO:0043094	cellular metabolic compour	0.11	1	0.18083182	7	0.020215439	
21107	GO:0045505	dynein intermediate chain b	0.11	1	0.18083182	7	0.020215439	
21146	GO:0045544	gibberellin 20-oxidase activ	0.11	2	0.36166364	35	0.10107719	
11202	GO:0019199	transmembrane receptor pr	0.11	12	2.169982	504	1.4555116	
8739	GO:0015385|GO:0015502	sodium:hydrogen antiporter	0.11	2	0.36166364	36	0.10396511	
9185	GO:0015925	galactosidase activity	0.11	2	0.36166364	36	0.10396511	
12626	GO:0030029	actin filament-based proces	0.11	2	0.36166364	36	0.10396511	
12633	GO:0030036	actin cytoskeleton organiza	0.11	2	0.36166364	36	0.10396511	
2816	GO:0004000	adenosine deaminase activ	0.12	1	0.18083182	8	0.023103358	
3803	GO:0005344|GO:0015033	oxygen transporter activity	0.12	1	0.18083182	8	0.023103358	
4961	GO:0006879	cellular iron ion homeostas	0.12	1	0.18083182	8	0.023103358	
7843	GO:0010628	positive regulation of gene	0.12	1	0.18083182	8	0.023103358	
8940	GO:0015669	gas transport	0.12	1	0.18083182	8	0.023103358	
8942	GO:0015671	oxygen transport	0.12	1	0.18083182	8	0.023103358	
11196	GO:0019187	beta-1,4-mannosyltransfera	0.12	1	0.18083182	8	0.023103358	
13262	GO:0030795|GO:0045546	jasmonate O-methyltransfe	0.12	1	0.18083182	8	0.023103358	
21461	GO:0045893|GO:0043193|	positive regulation of transc	0.12	1	0.18083182	8	0.023103358	
22702	GO:0047209	coniferyl-alcohol glucosyltra	0.12	1	0.18083182	8	0.023103358	
26035	GO:0051753	mannan synthase activity	0.12	1	0.18083182	8	0.023103358	
26918	GO:0055072	iron ion homeostasis	0.12	1	0.18083182	8	0.023103358	
5066	GO:0007010	cytoskeleton organization	0.12	2	0.36166364	38	0.10974095	
9637	GO:0016538|GO:0003751|	cyclin-dependent protein ki	0.12	2	0.36166364	38	0.10974095	
22479	GO:0046983	protein dimerization activity	0.13	12	2.169982	517	1.4930545	
3475	GO:0004871|GO:0005062|	signal transducer activity	0.13	17	3.074141	787	2.2727928	
27063	GO:0060089	molecular transducer activi	0.13	17	3.074141	787	2.2727928	
19126	GO:0042803	protein homodimerization a	0.13	7	1.2658228	265	0.7652988	
2837	GO:0004028	3-chloroallyl aldehyde dehy	0.13	1	0.18083182	9	0.025991278	
5735	GO:0008198	ferrous iron binding	0.13	1	0.18083182	9	0.025991278	
7225	GO:0009978	allene oxide synthase activi	0.13	1	0.18083182	9	0.025991278	
9769	GO:0016707	gibberellin 3-beta-dioxygen	0.13	1	0.18083182	9	0.025991278	
19342	GO:0043027	caspase inhibitor activity	0.13	1	0.18083182	9	0.025991278	
19343	GO:0043028	caspase regulator activity	0.13	1	0.18083182	9	0.025991278	
19458	GO:0043154|GO:0001719	negative regulation of casp	0.13	1	0.18083182	9	0.025991278	
19579	GO:0043281|GO:0043026	regulation of caspase activi	0.13	1	0.18083182	9	0.025991278	
21104	GO:0045502	dynein binding	0.13	1	0.18083182	9	0.025991278	
28365	GO:0065008	regulation of biological qua	0.14	8	1.4466546	316	0.9125827	
17617	GO:0035251	UDP-glucosyltransferase a	0.14	6	1.084991	218	0.62956655	
18674	GO:0042325	regulation of phosphorylatio	0.14	3	0.5424955	81	0.23392151	
22049	GO:0046527	glucosyltransferase activity	0.14	7	1.2658228	270	0.77973837	
5019	GO:0006952|GO:0002217|	defense response	0.14	6	1.084991	221	0.63823026	
8675	GO:0015293	symporter activity	0.14	5	0.9041591	173	0.49961013	
3203	GO:0004557	alpha-galactosidase activity	0.15	1	0.18083182	10	0.0288792	
6275	GO:0008878	glucose-1-phosphate aden	0.15	1	0.18083182	10	0.0288792	
6479	GO:0009112	nucleobase metabolic proc	0.15	1	0.18083182	10	0.0288792	
8651	GO:0015248	sterol transporter activity	0.15	1	0.18083182	10	0.0288792	
9178	GO:0015918	sterol transport	0.15	1	0.18083182	10	0.0288792	
10072	GO:0017127	cholesterol transporter acti	0.15	1	0.18083182	10	0.0288792	
12859	GO:0030301	cholesterol transport	0.15	1	0.18083182	10	0.0288792	
19443	GO:0043139	5'-3' DNA helicase activity	0.15	1	0.18083182	10	0.0288792	
19445	GO:0043141|GO:0008722	ATP-dependent 5'-3' DNA h	0.15	1	0.18083182	10	0.0288792	
26069	GO:0051787	misfolded protein binding	0.15	1	0.18083182	10	0.0288792	
29578	GO:0071214	cellular response to abiotic	0.15	1	0.18083182	10	0.0288792	
29842	GO:0071478	cellular response to radiatio	0.15	1	0.18083182	10	0.0288792	
29846	GO:0071482	cellular response to light sti	0.15	1	0.18083182	10	0.0288792	
25095	GO:0050790	regulation of catalytic activi	0.15	11	1.98915	480	1.3862015	
25998	GO:0051716	cellular response to stimulu	0.15	23	4.159132	1138	3.2864528	
9768	GO:0016706	oxidoreductase activity, act	0.15	5	0.9041591	175	0.505386	
25195	GO:0050896|GO:0051869	response to stimulus	0.15	36	6.509946	1881	5.432177	
8967	GO:0015698	inorganic anion transport	0.15	5	0.9041591	176	0.5082739	
28378	GO:0070011	peptidase activity, acting o	0.15	12	2.169982	537	1.550813	
11222	GO:0019220	regulation of phosphate me	0.15	3	0.5424955	85	0.24547319	
25471	GO:0051174	regulation of phosphorus m	0.15	3	0.5424955	85	0.24547319	
28366	GO:0065009	regulation of molecular fun	0.16	11	1.98915	484	1.3977532	
3904	GO:0005576	extracellular region	0.16	5	0.9041591	178	0.5140497	
31431	GO:0080054	low affinity nitrate transmer	0.16	2	0.36166364	45	0.1299564	
3416	GO:0004806	triglyceride lipase activity	0.16	1	0.18083182	11	0.03176712	
11152	GO:0019139|GO:0046420	cytokinin dehydrogenase a	0.16	1	0.18083182	11	0.03176712	
9719	GO:0016638	oxidoreductase activity, act	0.17	3	0.5424955	89	0.25702485	
2843	GO:0004034	aldose 1-epimerase activity	0.18	1	0.18083182	12	0.03465504	
3049	GO:0004365	glyceraldehyde-3-phosphat	0.18	1	0.18083182	12	0.03465504	
3386	GO:0004773	steryl-sulfatase activity	0.18	1	0.18083182	12	0.03465504	
4217	GO:0005977	glycogen metabolic process	0.18	1	0.18083182	12	0.03465504	
4344	GO:0006112	energy reserve metabolic p	0.18	1	0.18083182	12	0.03465504	
5965	GO:0008484	sulfuric ester hydrolase acti	0.18	1	0.18083182	12	0.03465504	
6336	GO:0008943	glyceraldehyde-3-phosphat	0.18	1	0.18083182	12	0.03465504	
6826	GO:0009538	photosystem I reaction cen	0.18	1	0.18083182	12	0.03465504	
6864	GO:0009581	detection of external stimul	0.18	1	0.18083182	12	0.03465504	
6865	GO:0009582	detection of abiotic stimulus	0.18	1	0.18083182	12	0.03465504	
6866	GO:0009583	detection of light stimulus	0.18	1	0.18083182	12	0.03465504	
8748	GO:0015398	high affinity secondary activ	0.18	1	0.18083182	12	0.03465504	
9775	GO:0016713	oxidoreductase activity, act	0.18	1	0.18083182	12	0.03465504	
10743	GO:0018685|GO:0008393	alkane 1-monooxygenase a	0.18	1	0.18083182	12	0.03465504	
20615	GO:0044421	extracellular region part	0.18	1	0.18083182	12	0.03465504	
21503	GO:0045935	positive regulation of nucle	0.18	1	0.18083182	12	0.03465504	
25470	GO:0051173	positive regulation of nitrog	0.18	1	0.18083182	12	0.03465504	
25546	GO:0051254	positive regulation of RNA	0.18	1	0.18083182	12	0.03465504	
25890	GO:0051606	detection of stimulus	0.18	1	0.18083182	12	0.03465504	
2976	GO:0004176|GO:0004280	ATP-dependent peptidase a	0.18	2	0.36166364	48	0.13862015	
4942	GO:0006855	drug transmembrane trans	0.18	4	0.7233273	139	0.40142086	
8607	GO:0015197|GO:0015637	peptide transporter activity	0.18	4	0.7233273	139	0.40142086	
8608	GO:0015198	oligopeptide transporter act	0.18	4	0.7233273	139	0.40142086	
8642	GO:0015238|GO:0015239|	drug transmembrane trans	0.18	4	0.7233273	139	0.40142086	
9154	GO:0015893	drug transport	0.18	4	0.7233273	139	0.40142086	
18832	GO:0042493|GO:0017035	response to drug	0.18	4	0.7233273	139	0.40142086	
3844	GO:0005451	monovalent cation:hydroge	0.18	2	0.36166364	49	0.14150807	
8909	GO:0015630	microtubule cytoskeleton	0.18	2	0.36166364	49	0.14150807	
3002	GO:0004315	3-oxoacyl-[acyl-carrier-prot	0.19	1	0.18083182	13	0.037542958	
7551	GO:0010327	acetyl CoA:(Z)-3-hexen-1-o	0.19	1	0.18083182	13	0.037542958	
8149	GO:0010941	regulation of cell death	0.19	1	0.18083182	13	0.037542958	
13443	GO:0030984	kininogen binding	0.19	1	0.18083182	13	0.037542958	
19298	GO:0042981	regulation of apoptosis	0.19	1	0.18083182	13	0.037542958	
19381	GO:0043067|GO:0043070	regulation of programmed	0.19	1	0.18083182	13	0.037542958	
4944	GO:0006857	oligopeptide transport	0.19	4	0.7233273	141	0.4071967	
8676	GO:0015294	solute:cation symporter act	0.19	4	0.7233273	141	0.4071967	
9099	GO:0015833	peptide transport	0.19	4	0.7233273	141	0.4071967	
4216	GO:0005976	polysaccharide metabolic p	0.19	2	0.36166364	50	0.14439599	
9783	GO:0016722	oxidoreductase activity, oxi	0.19	2	0.36166364	50	0.14439599	
9993	GO:0017016	Ras GTPase binding	0.19	2	0.36166364	50	0.14439599	
3476	GO:0004872|GO:0019041	receptor activity	0.19	14	2.5316455	672	1.9406822	
28364	GO:0065007	biological regulation	0.20	77	13.92405	4376	12.637537	
5763	GO:0008233	peptidase activity	0.20	12	2.169982	565	1.6316746	

12794	GO:0030234	enzyme regulator activity	0.20	9	1.6274865	403	1.1638317	
5981	GO:0008509	anion transmembrane trans	0.20	6	1.084991	245	0.70754033	
5195	GO:0007165|GO:0023033	signal transduction	0.20	19	3.4358046	961	2.775291	
12602	GO:0023052|GO:0023046	signaling	0.20	19	3.4358046	961	2.775291	
3629	GO:0005087	Ran guanyl-nucleotide exch	0.20	1	0.18083182	14	0.040430877	
11238	GO:0019239	deaminase activity	0.20	1	0.18083182	14	0.040430877	
4917	GO:0006820|GO:0006822	anion transport	0.20	6	1.084991	247	0.7133162	
25626	GO:0051336	regulation of hydrolase acti	0.21	5	0.9041591	196	0.5660323	
3490	GO:0004888|GO:0004926	transmembrane receptor ac	0.21	12	2.169982	571	1.6490022	
9600	GO:0016491	oxidoreductase activity	0.21	32	5.786618	1724	4.9787736	
6810	GO:0009522	photosystem I	0.21	1	0.18083182	15	0.043318797	
9340	GO:0016108	tetraterpenoid metabolic pro	0.21	1	0.18083182	15	0.043318797	
9341	GO:0016109	tetraterpenoid biosynthetic	0.21	1	0.18083182	15	0.043318797	
9348	GO:0016116	carotenoid metabolic proce	0.21	1	0.18083182	15	0.043318797	
9349	GO:0016117	carotenoid biosynthetic pro	0.21	1	0.18083182	15	0.043318797	
10079	GO:0017134	fibroblast growth factor bind	0.21	1	0.18083182	15	0.043318797	
4478	GO:0006281	DNA repair	0.22	4	0.7233273	149	0.43030006	
5037	GO:0006974|GO:0034984	response to DNA damage s	0.22	4	0.7233273	149	0.43030006	
13697	GO:0031267	small GTPase binding	0.23	2	0.36166364	56	0.16172351	
7133	GO:0009881	photoreceptor activity	0.23	1	0.18083182	16	0.046206716	
7178	GO:0009927	histidine phosphotransfer k	0.23	1	0.18083182	16	0.046206716	
7521	GO:0010295	(+)-abscisic acid 8'-hydroxy	0.23	1	0.18083182	16	0.046206716	
9189	GO:0015929	hexosaminidase activity	0.23	1	0.18083182	16	0.046206716	
9386	GO:0016157	sucrose synthase activity	0.23	1	0.18083182	16	0.046206716	
9898	GO:0016863	intramolecular oxidoreducta	0.23	1	0.18083182	16	0.046206716	
18757	GO:0042409	caffeoyl-CoA O-methyltrans	0.23	1	0.18083182	16	0.046206716	
30066	GO:0071702	organic substance transpor	0.23	11	1.98915	529	1.5277096	
3307	GO:0004675	transmembrane receptor pr	0.24	8	1.4466546	367	1.0598665	
4913	GO:0006814|GO:0006834|	sodium ion transport	0.24	2	0.36166364	58	0.16749935	
8499	GO:0015081|GO:0022816	sodium ion transmembrane	0.24	2	0.36166364	58	0.16749935	
11820	GO:0019887	protein kinase regulator act	0.24	2	0.36166364	58	0.16749935	
18086	GO:0035725	sodium ion transmembrane	0.24	2	0.36166364	58	0.16749935	
29800	GO:0071436	sodium ion export	0.24	2	0.36166364	58	0.16749935	
4135	GO:0005875	microtubule associated con	0.24	1	0.18083182	17	0.049094636	
4957	GO:0006875	cellular metal ion homeosta	0.24	1	0.18083182	17	0.049094636	
12610	GO:0030003	cellular cation homeostasis	0.24	1	0.18083182	17	0.049094636	
26912	GO:0055065	metal ion homeostasis	0.24	1	0.18083182	17	0.049094636	
26926	GO:0055080	cation homeostasis	0.24	1	0.18083182	17	0.049094636	
2831	GO:0004022	alcohol dehydrogenase (NA	0.24	2	0.36166364	59	0.17038727	
3942	GO:0005618	cell wall	0.24	3	0.5424955	107	0.30900744	
5704	GO:0008150|GO:0000004|	biological_process	0.25	363	65.64195	22215	64.155136	
25319	GO:0051020	GTPase binding	0.25	2	0.36166364	60	0.17327519	
2630	GO:0003680	AT DNA binding	0.25	1	0.18083182	18	0.051982556	
3963	GO:0005643|GO:0005644	nuclear pore	0.25	1	0.18083182	18	0.051982556	
4134	GO:0005874	microtubule	0.25	1	0.18083182	18	0.051982556	
4225	GO:0005985	sucrose metabolic process	0.25	1	0.18083182	18	0.051982556	
4252	GO:0006014	D-ribose metabolic process	0.25	1	0.18083182	18	0.051982556	
5792	GO:0008271	secondary active sulfate tra	0.25	1	0.18083182	18	0.051982556	
7773	GO:0010557	positive regulation of macro	0.25	1	0.18083182	18	0.051982556	
8662	GO:0015271	outward rectifier potassium	0.25	1	0.18083182	18	0.051982556	
8736	GO:0015381	high affinity sulfate transme	0.25	1	0.18083182	18	0.051982556	
12887	GO:0030332	cyclin binding	0.25	1	0.18083182	18	0.051982556	
22431	GO:0046930	pore complex	0.25	1	0.18083182	18	0.051982556	
22917	GO:0047429	nucleoside-triphosphate dip	0.25	1	0.18083182	18	0.051982556	
8494	GO:0015075	ion transmembrane transpo	0.25	16	2.893309	827	2.3883097	
8526	GO:0015112	nitrate transmembrane tran	0.25	2	0.36166364	61	0.1761631	
8975	GO:0015706|GO:0006872	nitrate transport	0.25	2	0.36166364	61	0.1761631	
25098	GO:0050794|GO:0051244	regulation of cellular proces	0.26	69	12.477396	3987	11.514136	
7690	GO:0010466	negative regulation of pepti	0.26	3	0.5424955	110	0.31767118	
12946	GO:0030414	peptidase inhibitor activity	0.26	3	0.5424955	110	0.31767118	
25636	GO:0051346	negative regulation of hydro	0.26	3	0.5424955	110	0.31767118	
5732	GO:0008194	UDP-glycosyltransferase ac	0.26	7	1.2658228	322	0.9299102	
16603	GO:0034220	ion transmembrane transpo	0.26	16	2.893309	833	2.4056373	
12868	GO:0030312	external encapsulating stru	0.26	3	0.5424955	111	0.3205591	
12985	GO:0030488	tRNA methylation	0.26	1	0.18083182	19	0.054870475	
26711	GO:0052547	regulation of peptidase acti	0.27	3	0.5424955	112	0.32344702	
28100	GO:0061134	peptidase regulator activity	0.27	3	0.5424955	112	0.32344702	
17016	GO:0034637	cellular carbohydrate biosy	0.27	2	0.36166364	63	0.18193895	
8943	GO:0015672	monovalent inorganic catio	0.27	8	1.4466546	383	1.1060733	
25094	GO:0050789|GO:0050791	regulation of biological proc	0.27	74	13.381556	4315	12.461374	
9293	GO:0016051|GO:0006093	carbohydrate biosynthetic p	0.27	2	0.36166364	64	0.18482687	
25820	GO:0051536	iron-sulfur cluster binding	0.27	2	0.36166364	64	0.18482687	
25824	GO:0051540	metal cluster binding	0.27	2	0.36166364	64	0.18482687	
4910	GO:0006811	ion transport	0.28	18	3.254973	959	2.769515	
3798	GO:0005337	nucleoside transmembrane	0.28	1	0.18083182	20	0.0577584	
3956	GO:0005635|GO:0005636	nuclear envelope	0.28	1	0.18083182	20	0.0577584	
5991	GO:0008519	ammonium transmembrane	0.28	1	0.18083182	20	0.0577584	
8965	GO:0015696	ammonium transport	0.28	1	0.18083182	20	0.0577584	
9122	GO:0015858	nucleoside transport	0.28	1	0.18083182	20	0.0577584	
9856	GO:0016814	hydrolase activity, acting or	0.28	1	0.18083182	20	0.0577584	
25477	GO:0051180	vitamin transport	0.28	1	0.18083182	20	0.0577584	
25480	GO:0051183	vitamin transporter activity	0.28	1	0.18083182	20	0.0577584	
30844	GO:0072488	ammonium transmembrane	0.28	1	0.18083182	20	0.0577584	
9811	GO:0016757|GO:0016932	transferase activity, transfe	0.28	14	2.5316455	729	2.1052935	
9812	GO:0016758	transferase activity, transfe	0.28	10	1.8083183	501	1.4468478	
3129	GO:0004467	long-chain fatty acid-CoA li	0.29	1	0.18083182	21	0.060646318	
3364	GO:0004745	retinol dehydrogenase activ	0.29	1	0.18083182	21	0.060646318	
3474	GO:0004869|GO:0004870	cysteine-type endopeptidas	0.29	1	0.18083182	21	0.060646318	
4955	GO:0006873	cellular ion homeostasis	0.29	1	0.18083182	21	0.060646318	
12999	GO:0030506	ankyrin binding	0.29	1	0.18083182	21	0.060646318	
25104	GO:0050801	ion homeostasis	0.29	1	0.18083182	21	0.060646318	
26928	GO:0055082	cellular chemical homeosta	0.29	1	0.18083182	21	0.060646318	
24966	GO:0050660	flavin adenine dinucleotide	0.29	3	0.5424955	118	0.34077454	
2662	GO:0003746|GO:0008182|	translation elongation facto	0.30	1	0.18083182	22	0.06353424	
3831	GO:0005385	zinc ion transmembrane tra	0.30	1	0.18083182	22	0.06353424	
4574	GO:0006414|GO:0006442|	translational elongation	0.30	1	0.18083182	22	0.06353424	
4882	GO:0006778	porphyrin metabolic proces	0.30	1	0.18083182	22	0.06353424	
4883	GO:0006779	porphyrin biosynthetic proc	0.30	1	0.18083182	22	0.06353424	
4924	GO:0006829	zinc ion transport	0.30	1	0.18083182	22	0.06353424	
7143	GO:0009891	positive regulation of biosyr	0.30	1	0.18083182	22	0.06353424	
13758	GO:0031328	positive regulation of cellula	0.30	1	0.18083182	22	0.06353424	
18524	GO:0042162	telomeric DNA binding	0.30	1	0.18083182	22	0.06353424	
21152	GO:0045551	cinnamyl-alcohol dehydrog	0.30	1	0.18083182	22	0.06353424	
29941	GO:0071577	zinc ion transmembrane tra	0.30	1	0.18083182	22	0.06353424	
15949	GO:0033554	cellular response to stress	0.30	4	0.7233273	173	0.49961013	
21710	GO:0046148	pigment biosynthetic proce	0.30	2	0.36166364	69	0.19926646	
15524	GO:0033124	regulation of GTP catabolic	0.31	2	0.36166364	70	0.20215438	
19394	GO:0043087	regulation of GTPase activi	0.31	2	0.36166364	70	0.20215438	
2633	GO:0003684	damaged DNA binding	0.31	1	0.18083182	23	0.06642216	
7527	GO:0010302	2-oxoglutarate-dependent d	0.31	1	0.18083182	23	0.06642216	
22414	GO:0046912	transferase activity, transfe	0.31	1	0.18083182	23	0.06642216	
9845	GO:0016798	hydrolase activity, acting or	0.31	8	1.4466546	401	1.1580559	
26959	GO:0055114	oxidation-reduction process	0.32	43	7.7757688	2490	7.1909204	
11695	GO:0019725	cellular homeostasis	0.32	5	0.9041591	234	0.67577326	
8559	GO:0015146	pentose transmembrane tra	0.32	1	0.18083182	24	0.06931008	
8561	GO:0015148	D-xylose transmembrane tr	0.32	1	0.18083182	24	0.06931008	
8829	GO:0015519	D-xylose:hydrogen symport	0.32	1	0.18083182	24	0.06931008	
9019	GO:0015750	pentose transport	0.32	1	0.18083182	24	0.06931008	
9022	GO:0015753	D-xylose transport	0.32	1	0.18083182	24	0.06931008	
4916	GO:0006818	hydrogen transport	0.32	6	1.084991	292	0.84327257	
9246	GO:0015992	proton transport	0.32	6	1.084991	292	0.84327257	
9703	GO:0016620	oxidoreductase activity, act	0.33	2	0.36166364	73	0.21081814	
18786	GO:0042440	pigment metabolic process	0.33	2	0.36166364	73	0.21081814	
3884	GO:0005524	ATP binding	0.33	10	1.8083183	524	1.51327	
11828	GO:0019899	enzyme binding	0.33	5	0.9041591	237	0.684437	
9817	GO:0016763	transferase activity, transfe	0.33	2	0.36166364	74	0.21370606	
973	GO:0001653	peptide receptor activity	0.33	1	0.18083182	25	0.072197996	

9876	GO:0016837	carbon-oxygen lyase activit	0.33	1	0.18083182	25	0.072197996	
13054	GO:0030570	pectate lyase activity	0.33	1	0.18083182	25	0.072197996	
24256	GO:0048878	chemical homeostasis	0.33	1	0.18083182	25	0.072197996	
31493	GO:0080118	brassinosteroid sulfotransfe	0.33	1	0.18083182	25	0.072197996	
18925	GO:0042592	homeostatic process	0.33	5	0.9041591	238	0.68732494	
8810	GO:0015491	cation:cation antiporter acti	0.34	2	0.36166364	75	0.21659398	
3210	GO:0004565	beta-galactosidase activity	0.34	1	0.18083182	26	0.075085916	
5978	GO:0008506	sucrose:hydrogen symporte	0.34	1	0.18083182	26	0.075085916	
5987	GO:0008515|GO:0019188	sucrose transmembrane tra	0.34	1	0.18083182	26	0.075085916	
6907	GO:0009639	response to red or far red li	0.34	1	0.18083182	26	0.075085916	
7000	GO:0009734	auxin mediated signaling pa	0.34	1	0.18083182	26	0.075085916	
7540	GO:0010315	auxin efflux	0.34	1	0.18083182	26	0.075085916	
7553	GO:0010329	auxin efflux transmembrane	0.34	1	0.18083182	26	0.075085916	
8516	GO:0015101	organic cation transmembra	0.34	1	0.18083182	26	0.075085916	
8530	GO:0015116	sulfate transmembrane tran	0.34	1	0.18083182	26	0.075085916	
8567	GO:0015154	disaccharide transmembrar	0.34	1	0.18083182	26	0.075085916	
8964	GO:0015695	organic cation transport	0.34	1	0.18083182	26	0.075085916	
9035	GO:0015766	disaccharide transport	0.34	1	0.18083182	26	0.075085916	
9039	GO:0015770	sucrose transport	0.34	1	0.18083182	26	0.075085916	
9744	GO:0016671	oxidoreductase activity, act	0.34	1	0.18083182	26	0.075085916	
29729	GO:0071365	cellular response to auxin s	0.34	1	0.18083182	26	0.075085916	
126	GO:0000160	two-component signal trans	0.34	1	0.18083182	26	0.075085916	
18000	GO:0035639	purine ribonucleoside tripho	0.35	14	2.5316455	769	2.2208104	
4562	GO:0006400|GO:0016549	tRNA modification	0.35	1	0.18083182	27	0.077973835	
8919	GO:0015645	fatty acid ligase activity	0.35	1	0.18083182	27	0.077973835	
9346	GO:0016114	terpenoid biosynthetic proc	0.35	1	0.18083182	27	0.077973835	
25481	GO:0051184	cofactor transporter activity	0.35	1	0.18083182	27	0.077973835	
19393	GO:0043086	negative regulation of catal	0.35	4	0.7233273	188	0.54292893	
20342	GO:0044092	negative regulation of mole	0.35	4	0.7233273	188	0.54292893	
5840	GO:0008324	cation transmembrane tran	0.36	10	1.8083183	538	1.5537009	
2833	GO:0004024	alcohol dehydrogenase acti	0.36	1	0.18083182	28	0.080861755	
5793	GO:0008272|GO:0006870	sulfate transport	0.36	1	0.18083182	28	0.080861755	
6079	GO:0008654	phospholipid biosynthetic p	0.36	1	0.18083182	28	0.080861755	
6809	GO:0009521|GO:0030090	photosystem	0.36	1	0.18083182	28	0.080861755	
7145	GO:0009893	positive regulation of metab	0.36	1	0.18083182	28	0.080861755	
7819	GO:0010604	positive regulation of macro	0.36	1	0.18083182	28	0.080861755	
9238	GO:0015980	energy derivation by oxidati	0.36	1	0.18083182	28	0.080861755	
13634	GO:0031177	phosphopantetheine bindin	0.36	1	0.18083182	28	0.080861755	
13755	GO:0031325	positive regulation of cellula	0.36	1	0.18083182	28	0.080861755	
20512	GO:0044262|GO:0006092	cellular carbohydrate metab	0.36	5	0.9041591	248	0.7162041	
4358	GO:0006140	regulation of nucleotide me	0.37	2	0.36166364	80	0.2310336	
7146	GO:0009894	regulation of catabolic proc	0.37	2	0.36166364	80	0.2310336	
9875	GO:0016836	hydro-lyase activity	0.37	2	0.36166364	80	0.2310336	
13278	GO:0030811	regulation of nucleotide cat	0.37	2	0.36166364	80	0.2310336	
13759	GO:0031329	regulation of cellular catabo	0.37	2	0.36166364	80	0.2310336	
15521	GO:0033121	regulation of purine nucleot	0.37	2	0.36166364	80	0.2310336	
4911	GO:0006812|GO:0006819|	cation transport	0.37	12	2.169982	662	1.9118029	
4841	GO:0006721	terpenoid metabolic proces	0.37	1	0.18083182	29	0.083749674	
4641	GO:0006508	proteolysis	0.37	17	3.074141	965	2.7868426	
9869	GO:0016829	lyase activity	0.38	9	1.6274865	488	1.4093049	
12516	GO:0022804	active transmembrane trans	0.38	14	2.5316455	787	2.2727928	
3200	GO:0004553|GO:0016800	hydrolase activity, hydrolyz	0.38	6	1.084991	312	0.90103096	
2774	GO:0003950	NAD+ ADP-ribosyltransfera	0.38	1	0.18083182	30	0.086637594	
8683	GO:0015301|GO:0015380|	anion:anion antiporter activ	0.38	1	0.18083182	30	0.086637594	
15414	GO:0033013	tetrapyrrole metabolic proce	0.38	1	0.18083182	30	0.086637594	
15415	GO:0033014	tetrapyrrole biosynthetic pro	0.38	1	0.18083182	30	0.086637594	
23	GO:0000030	mannosyltransferase activit	0.38	1	0.18083182	30	0.086637594	
3787	GO:0005319	lipid transporter activity	0.38	2	0.36166364	83	0.23969735	
16738	GO:0034357	photosynthetic membrane	0.38	2	0.36166364	83	0.23969735	
13041	GO:0030554	adenyl nucleotide binding	0.38	10	1.8083183	550	1.5883559	
14965	GO:0032559	adenyl ribonucleotide bindir	0.38	10	1.8083183	550	1.5883559	
5018	GO:0006950	response to stress	0.39	11	1.98915	611	1.764519	
4912	GO:0006813|GO:0015458	potassium ion transport	0.39	2	0.36166364	84	0.24258527	
30168	GO:0071804	cellular potassium ion trans	0.39	2	0.36166364	84	0.24258527	
30169	GO:0071805	potassium ion transmembra	0.39	2	0.36166364	84	0.24258527	
12608	GO:0030001	metal ion transport	0.39	7	1.2658228	374	1.080082	
14959	GO:0032553	ribonucleotide binding	0.39	14	2.5316455	795	2.2958963	
14961	GO:0032555	purine ribonucleotide bindir	0.39	14	2.5316455	795	2.2958963	
14422	GO:0032012	regulation of ARF protein si	0.39	1	0.18083182	31	0.08952551	
14720	GO:0032312	regulation of ARF GTPase	0.39	1	0.18083182	31	0.08952551	
25478	GO:0051181	cofactor transport	0.39	1	0.18083182	31	0.08952551	
5624	GO:0008047	enzyme activator activity	0.39	2	0.36166364	85	0.24547319	
10033	GO:0017076	purine nucleotide binding	0.40	14	2.5316455	797	2.3016722	
3717	GO:0005199	structural constituent of cel	0.40	1	0.18083182	32	0.09241343	
3785	GO:0005315|GO:0005317	inorganic phosphate transm	0.40	1	0.18083182	32	0.09241343	
6942	GO:0009674	potassium:sodium symport	0.40	1	0.18083182	32	0.09241343	
9041	GO:0015772	oligosaccharide transport	0.40	1	0.18083182	32	0.09241343	
12522	GO:0022820	potassium ion symporter ac	0.40	1	0.18083182	32	0.09241343	
23914	GO:0048522|GO:0051242	positive regulation of cellula	0.40	1	0.18083182	32	0.09241343	
20624	GO:0044430	cytoskeletal part	0.41	2	0.36166364	88	0.25413695	
119	GO:0000151	ubiquitin ligase complex	0.41	2	0.36166364	88	0.25413695	
4493	GO:0006298|GO:0006300	mismatch repair	0.41	1	0.18083182	33	0.09530135	
3749	GO:0005249	voltage-gated potassium ch	0.42	1	0.18083182	34	0.09818927	
11831	GO:0019902	phosphatase binding	0.42	1	0.18083182	34	0.09818927	
11832	GO:0019903	protein phosphatase bindin	0.42	1	0.18083182	34	0.09818927	
9829	GO:0016779	nucleotidyltransferase activ	0.42	3	0.5424955	148	0.42741212	
20630	GO:0044436	thylakoid part	0.42	2	0.36166364	90	0.2599128	
18582	GO:0042221	response to chemical stimu	0.43	6	1.084991	328	0.94723773	
16785	GO:0034404	nucleobase, nucleoside and	0.43	2	0.36166364	92	0.26568863	
17033	GO:0034654	nucleobase, nucleoside, nu	0.43	2	0.36166364	92	0.26568863	
21058	GO:0045454|GO:0030503|	cell redox homeostasis	0.44	4	0.7233273	211	0.6093511	
8679	GO:0015297	antiporter activity	0.44	3	0.5424955	152	0.4389638	
8682	GO:0015300	solute:solute antiporter acti	0.44	3	0.5424955	152	0.4389638	
11314	GO:0019321	pentose metabolic process	0.44	1	0.18083182	36	0.10396511	
22376	GO:0046873	metal ion transmembrane t	0.44	4	0.7233273	213	0.6151269	
3808	GO:0005351|GO:0005403	sugar:hydrogen symporter	0.44	2	0.36166364	94	0.27146447	
3835	GO:0005402	cation:sugar symporter acti	0.44	2	0.36166364	94	0.27146447	
6863	GO:0009579	thylakoid	0.44	2	0.36166364	94	0.27146447	
13656	GO:0031224	intrinsic to membrane	0.44	20	3.6166365	1193	3.4452884	
15436	GO:0033036	macromolecule localization	0.45	7	1.2658228	397	1.1465042	
3758	GO:0005267	potassium channel activity	0.45	1	0.18083182	37	0.10685303	
3472	GO:0004866	endopeptidase inhibitor acti	0.45	2	0.36166364	95	0.27435237	
8159	GO:0010951	negative regulation of endo	0.45	2	0.36166364	95	0.27435237	
26712	GO:0052548	regulation of endopeptidase	0.45	2	0.36166364	95	0.27435237	
28101	GO:0061135	endopeptidase regulator ac	0.45	2	0.36166364	95	0.27435237	
12538	GO:0022843	voltage-gated cation chann	0.46	1	0.18083182	38	0.10974095	
3464	GO:0004857	enzyme inhibitor activity	0.46	3	0.5424955	157	0.4534034	
8677	GO:0015295	solute:hydrogen symporter	0.47	2	0.36166364	98	0.28301615	
8681	GO:0015299	solute:hydrogen antiporter	0.47	2	0.36166364	98	0.28301615	
30883	GO:0072527	pyrimidine-containing comp	0.47	1	0.18083182	39	0.11262887	
868	GO:0001510	RNA methylation	0.47	1	0.18083182	39	0.11262887	
19831	GO:0043565	sequence-specific DNA bin	0.47	3	0.5424955	159	0.45917925	
4755	GO:0006629	lipid metabolic process	0.47	10	1.8083183	590	1.7038727	
6882	GO:0009605	response to external stimul	0.47	1	0.18083182	40	0.1155168	
7021	GO:0009755	hormone-mediated signalin	0.47	1	0.18083182	40	0.1155168	
15271	GO:0032870	cellular response to hormo	0.47	1	0.18083182	40	0.1155168	
23910	GO:0048518|GO:0043119	positive regulation of biolog	0.47	1	0.18083182	40	0.1155168	
16430	GO:0034046	poly(G) RNA binding	0.48	2	0.36166364	100	0.28879198	
14667	GO:0032259	methylation	0.48	5	0.9041591	285	0.8230572	
3638	GO:0005096	GTPase activator activity	0.48	1	0.18083182	41	0.118404716	
19813	GO:0043547	positive regulation of GTPa	0.48	1	0.18083182	41	0.118404716	
5874	GO:0008374	O-acyltransferase activity	0.49	2	0.36166364	102	0.29456782	
9837	GO:0016788	hydrolase activity, acting or	0.49	25	4.520796	1534	4.430069	
8461	GO:0015020|GO:0003981	glucuronosyltransferase act	0.49	1	0.18083182	42	0.121292636	
13884	GO:0031461	cullin-RING ubiquitin ligase	0.49	1	0.18083182	42	0.121292636	
9267	GO:0016021	integral to membrane	0.50	18	3.254973	1103	3.1853757	
19392	GO:0043085	positive regulation of cataly	0.50	2	0.36166364	104	0.30034366	

20343	GO:0044093	positive regulation of molec	0.50	2	0.36166364	104	0.30034366	
13531	GO:0031072	heat shock protein binding	0.50	4	0.7233273	230	0.6642216	
11224	GO:0019222	regulation of metabolic proc	0.51	50	9.041592	3115	8.995871	
9753	GO:0016682	oxidoreductase activity, act	0.51	1	0.18083182	44	0.12706847	
29859	GO:0071495	cellular response to endoge	0.51	1	0.18083182	44	0.12706847	
3630	GO:0005088	Ras guanyl-nucleotide exch	0.52	1	0.18083182	45	0.1299564	
5692	GO:0008134	transcription factor binding	0.52	1	0.18083182	45	0.1299564	
9893	GO:0016857	racemase and epimerase a	0.52	1	0.18083182	45	0.1299564	
14726	GO:0032318	regulation of Ras GTPase a	0.52	1	0.18083182	45	0.1299564	
22096	GO:0046578	regulation of Ras protein si	0.52	1	0.18083182	45	0.1299564	
25355	GO:0051056	regulation of small GTPase	0.52	1	0.18083182	45	0.1299564	
2636	GO:0003690	double-stranded DNA bindi	0.52	1	0.18083182	46	0.13284431	
6999	GO:0009733	response to auxin stimulus	0.52	1	0.18083182	46	0.13284431	
9795	GO:0016740	transferase activity	0.53	60	10.84991	3764	10.870131	
8497	GO:0015079|GO:0022817	potassium ion transmembra	0.53	1	0.18083182	47	0.13573223	
8680	GO:0015298	solute:cation antiporter acti	0.54	2	0.36166364	112	0.32344702	
29081	GO:0070717	poly-purine tract binding	0.54	2	0.36166364	112	0.32344702	
13753	GO:0031323	regulation of cellular metab	0.54	44	7.9566	2770	7.999538	
9933	GO:0016903	oxidoreductase activity, act	0.54	2	0.36166364	113	0.32633495	
9800	GO:0016746	transferase activity, transfe	0.54	8	1.4466546	498	1.438184	
3756	GO:0005261|GO:0015281|	cation channel activity	0.55	1	0.18083182	49	0.14150807	
9725	GO:0016645	oxidoreductase activity, act	0.55	1	0.18083182	49	0.14150807	
11784	GO:0019838	growth factor binding	0.55	1	0.18083182	49	0.14150807	
6166	GO:0008757	S-adenosylmethionine-depe	0.55	3	0.5424955	180	0.5198256	
9535	GO:0016407	acetyltransferase activity	0.55	2	0.36166364	115	0.3321108	
3885	GO:0005525	GTP binding	0.55	4	0.7233273	245	0.70754033	
11032	GO:0019001	guanyl nucleotide binding	0.55	4	0.7233273	245	0.70754033	
14967	GO:0032561	guanyl ribonucleotide bindi	0.55	4	0.7233273	245	0.70754033	
29674	GO:0071310	cellular response to organic	0.55	1	0.18083182	50	0.14439599	
3903	GO:0005575|GO:0008372	cellular_component	0.56	135	24.412296	8515	24.590637	
20619	GO:0044425	membrane part	0.56	24	4.339964	1523	4.398302	
3293	GO:0004659	prenyltransferase activity	0.56	1	0.18083182	51	0.14728391	
7213	GO:0009966|GO:0035466	regulation of signal transdu	0.56	1	0.18083182	51	0.14728391	
12601	GO:0023051	regulation of signaling	0.56	1	0.18083182	51	0.14728391	
25416	GO:0051119	sugar transmembrane trans	0.56	2	0.36166364	118	0.34077454	
4915	GO:0006817	phosphate transport	0.57	1	0.18083182	52	0.15017183	
8528	GO:0015114	phosphate transmembrane	0.57	1	0.18083182	52	0.15017183	
17801	GO:0035435	phosphate transmembrane	0.57	1	0.18083182	52	0.15017183	
9818	GO:0016765|GO:0016766	transferase activity, transfe	0.57	3	0.5424955	185	0.53426516	
12805	GO:0030246	carbohydrate binding	0.57	4	0.7233273	251	0.7248679	
3946	GO:0005623	cell	0.57	130	23.508137	8227	23.758917	
20657	GO:0044464	cell part	0.57	130	23.508137	8227	23.758917	
9750	GO:0016679	oxidoreductase activity, act	0.57	1	0.18083182	53	0.15305975	
25635	GO:0051345	positive regulation of hydro	0.57	1	0.18083182	53	0.15305975	
2657	GO:0003727|GO:0003728	single-stranded RNA bindin	0.58	3	0.5424955	188	0.54292893	
17918	GO:0035556|GO:0007242|	intracellular signal transduc	0.58	1	0.18083182	54	0.15594767	
29251	GO:0070887	cellular response to chemic	0.58	1	0.18083182	54	0.15594767	
2628	GO:0003677	DNA binding	0.58	19	3.4358046	1224	3.534814	
4951	GO:0006865|GO:0006866	amino acid transport	0.59	2	0.36166364	123	0.35521415	
24968	GO:0050662	coenzyme binding	0.59	3	0.5424955	191	0.5515927	
5809	GO:0008289	lipid binding	0.59	4	0.7233273	258	0.74508333	
9801	GO:0016747	transferase activity, transfe	0.59	7	1.2658228	456	1.3168914	
4224	GO:0005984	disaccharide metabolic pro	0.59	1	0.18083182	56	0.16172351	
9369	GO:0016137	glycoside metabolic proces	0.59	1	0.18083182	56	0.16172351	
9883	GO:0016846	carbon-sulfur lyase activity	0.59	1	0.18083182	56	0.16172351	
4849	GO:0006730|GO:0019753|	one-carbon metabolic proce	0.59	5	0.9041591	325	0.93857396	
4121	GO:0005856	cytoskeleton	0.60	2	0.36166364	126	0.3638779	
5715	GO:0008171	O-methyltransferase activit	0.60	1	0.18083182	57	0.16461143	
9813	GO:0016759	cellulose synthase activity	0.60	1	0.18083182	57	0.16461143	
23973	GO:0048583	regulation of response to st	0.60	1	0.18083182	57	0.16461143	
3323	GO:0004702	receptor signaling protein s	0.61	1	0.18083182	58	0.16749935	
5819	GO:0008299|GO:0009241	isoprenoid biosynthetic pro	0.61	1	0.18083182	58	0.16749935	
6665	GO:0009311	oligosaccharide metabolic	0.61	1	0.18083182	58	0.16749935	
8558	GO:0015145	monosaccharide transmem	0.61	1	0.18083182	58	0.16749935	
9018	GO:0015749	monosaccharide transport	0.61	1	0.18083182	58	0.16749935	
3333	GO:0004712	protein serine/threonine/tyr	0.61	1	0.18083182	59	0.17038727	
18981	GO:0042651	thylakoid membrane	0.61	1	0.18083182	59	0.17038727	
30700	GO:0072341	modified amino acid bindin	0.61	1	0.18083182	59	0.17038727	
12572	GO:0022890|GO:0015082	inorganic cation transmem	0.61	5	0.9041591	332	0.9587894	
3340	GO:0004721	phosphoprotein phosphatas	0.62	3	0.5424955	199	0.57469606	
2980	GO:0004185	serine-type carboxypeptidas	0.62	1	0.18083182	60	0.17327519	
4840	GO:0006720|GO:0016096	isoprenoid metabolic proce	0.62	1	0.18083182	60	0.17327519	
28375	GO:0070008	serine-type exopeptidase a	0.62	1	0.18083182	60	0.17327519	
2818	GO:0004003	ATP-dependent DNA helica	0.63	1	0.18083182	61	0.1761631	
4768	GO:0006644	phospholipid metabolic pro	0.63	1	0.18083182	61	0.1761631	
9874	GO:0016835	carbon-oxygen lyase activit	0.63	3	0.5424955	202	0.5833598	
30069	GO:0071705	nitrogen compound transpo	0.63	3	0.5424955	202	0.5833598	
3876	GO:0005515|GO:0045308	protein binding	0.63	108	19.529837	6933	20.021948	
2978	GO:0004180	carboxypeptidase activity	0.63	1	0.18083182	62	0.17905103	
6018	GO:0008559|GO:0005226|	xenobiotic-transporting ATP	0.63	1	0.18083182	62	0.17905103	
19225	GO:0042908	xenobiotic transport	0.63	1	0.18083182	62	0.17905103	
19227	GO:0042910	xenobiotic transporter activ	0.63	1	0.18083182	62	0.17905103	
11221	GO:0019219	regulation of nucleobase, n	0.63	41	7.414105	2675	7.7251854	
25468	GO:0051171	regulation of nitrogen comp	0.63	41	7.414105	2675	7.7251854	
9852	GO:0016810	hydrolase activity, acting or	0.63	2	0.36166364	134	0.38698125	
9103	GO:0015837	amine transport	0.64	2	0.36166364	135	0.38986918	
3103	GO:0004437	inositol or phosphatidylinos	0.64	1	0.18083182	64	0.18482687	
22416	GO:0046915	transition metal ion transm	0.64	1	0.18083182	64	0.18482687	
11616	GO:0019637	organophosphate metaboli	0.65	1	0.18083182	65	0.18771479	
2626	GO:0003674|GO:0005554	molecular_function	0.65	386	69.80109	24394	70.447914	
9836	GO:0016787	hydrolase activity	0.65	57	10.307414	3723	10.751725	
3473	GO:0004867	serine-type endopeptidase	0.65	1	0.18083182	66	0.1906027	
4561	GO:0006399	tRNA metabolic process	0.65	1	0.18083182	66	0.1906027	
5615	GO:0008033	tRNA processing	0.65	1	0.18083182	66	0.1906027	
9890	GO:0016854	racemase and epimerase a	0.65	1	0.18083182	66	0.1906027	
11829	GO:0019900	kinase binding	0.65	1	0.18083182	66	0.1906027	
3895	GO:0005543	phospholipid binding	0.66	2	0.36166364	140	0.40430877	
2629	GO:0003678|GO:0003679	DNA helicase activity	0.66	1	0.18083182	67	0.19349062	
6046	GO:0008610	lipid biosynthetic process	0.66	2	0.36166364	141	0.4071967	
13164	GO:0030695	GTPase regulator activity	0.66	2	0.36166364	142	0.4100846	
31465	GO:0080090	regulation of primary metab	0.66	41	7.414105	2710	7.826263	
2999	GO:0004312	fatty acid synthase activity	0.67	1	0.18083182	68	0.19637854	
18742	GO:0042393	histone binding	0.67	1	0.18083182	68	0.19637854	
32	GO:0000041	transition metal ion transpo	0.67	1	0.18083182	68	0.19637854	
8495	GO:0015077	monovalent inorganic catio	0.67	3	0.5424955	214	0.6180149	
8557	GO:0015144	carbohydrate transmembra	0.67	2	0.36166364	143	0.41297254	
16602	GO:0034219	carbohydrate transmembra	0.67	2	0.36166364	143	0.41297254	
3620	GO:0005057	receptor signaling protein a	0.67	1	0.18083182	69	0.19926646	
4530	GO:0006355|GO:0032583|	regulation of transcription,	0.67	39	7.052441	2591	7.4826	
25544	GO:0051252	regulation of RNA metaboli	0.68	39	7.052441	2593	7.488376	
5726	GO:0008187	poly-pyrimidine tract bindin	0.68	1	0.18083182	70	0.20215438	
5788	GO:0008266	poly(U) RNA binding	0.68	1	0.18083182	70	0.20215438	
9191	GO:0015931	nucleobase, nucleoside, nu	0.68	1	0.18083182	70	0.20215438	
9192	GO:0015932	nucleobase, nucleoside, nu	0.68	1	0.18083182	70	0.20215438	
9853	GO:0016811	hydrolase activity, acting or	0.68	1	0.18083182	70	0.20215438	
23522	GO:0048046	apoplast	0.68	1	0.18083182	70	0.20215438	
3873	GO:0005507	copper ion binding	0.68	2	0.36166364	146	0.42163628	
6071	GO:0008643|GO:0006861|	carbohydrate transport	0.68	2	0.36166364	147	0.42452422	
3744	GO:0005244	voltage-gated ion channel a	0.69	1	0.18083182	72	0.20793022	
9740	GO:0016667	oxidoreductase activity, act	0.69	1	0.18083182	72	0.20793022	
9764	GO:0016701	oxidoreductase activity, act	0.69	1	0.18083182	72	0.20793022	
12528	GO:0022832	voltage-gated channel activ	0.69	1	0.18083182	72	0.20793022	
15280	GO:0032879	regulation of localization	0.69	1	0.18083182	72	0.20793022	
17141	GO:0034762	regulation of transmembran	0.69	1	0.18083182	72	0.20793022	
17144	GO:0034765	regulation of ion transmem	0.69	1	0.18083182	72	0.20793022	
19568	GO:0043269	regulation of ion transport	0.69	1	0.18083182	72	0.20793022	
25348	GO:0051049	regulation of transport	0.69	1	0.18083182	72	0.20793022	

7141	GO:0009889	regulation of biosynthetic p	0.69	39	7.052441	2605	7.523031	
7772	GO:0010556	regulation of macromolecul	0.69	39	7.052441	2605	7.523031	
13756	GO:0031326	regulation of cellular biosyn	0.69	39	7.052441	2605	7.523031	
32213	GO:2000112	regulation of cellular macro	0.69	39	7.052441	2605	7.523031	
27562	GO:0060589	nucleoside-triphosphatase	0.70	2	0.36166364	152	0.4389638	
3627	GO:0005085|GO:0008433|	guanyl-nucleotide exchange	0.70	1	0.18083182	75	0.21659398	
4990	GO:0006915|GO:0008632	apoptosis	0.70	3	0.5424955	227	0.6555578	
5663	GO:0008094|GO:0004011	DNA-dependent ATPase ac	0.71	1	0.18083182	76	0.2194819	
6424	GO:0009055|GO:0009053|	electron carrier activity	0.71	2	0.36166364	154	0.44473964	
5604	GO:0008017	microtubule binding	0.71	1	0.18083182	77	0.22236982	
6529	GO:0009165	nucleotide biosynthetic proc	0.71	1	0.18083182	77	0.22236982	
7692	GO:0010468	regulation of gene expressi	0.71	39	7.052441	2635	7.6096687	
9114	GO:0015849	organic acid transport	0.71	2	0.36166364	156	0.45051548	
22443	GO:0046942	carboxylic acid transport	0.71	2	0.36166364	156	0.45051548	
9909	GO:0016877	ligase activity, forming carb	0.72	1	0.18083182	78	0.22525774	
19832	GO:0043566	structure-specific DNA bind	0.72	1	0.18083182	78	0.22525774	
30865	GO:0072509	divalent inorganic cation tra	0.72	1	0.18083182	78	0.22525774	
3888	GO:0005529	sugar binding	0.72	2	0.36166364	158	0.45629135	
9682	GO:0016597	amino acid binding	0.72	1	0.18083182	80	0.2310336	
19479	GO:0043176	amine binding	0.72	1	0.18083182	80	0.2310336	
8496	GO:0015078	hydrogen ion transmembra	0.73	2	0.36166364	160	0.4620672	
6668	GO:0009314	response to radiation	0.73	1	0.18083182	81	0.23392151	
6751	GO:0009416	response to light stimulus	0.73	1	0.18083182	81	0.23392151	
15189	GO:0032787	monocarboxylic acid metab	0.73	1	0.18083182	81	0.23392151	
6991	GO:0009725	response to hormone stimu	0.73	1	0.18083182	82	0.23680943	
29202	GO:0070838	divalent metal ion transport	0.73	1	0.18083182	82	0.23680943	
9839	GO:0016791|GO:0016302	phosphatase activity	0.73	5	0.9041591	383	1.1060733	
27228	GO:0060255	regulation of macromolecul	0.73	39	7.052441	2660	7.6818666	
5756	GO:0008219	cell death	0.74	3	0.5424955	239	0.69021285	
8209	GO:0012501|GO:0016244	programmed cell death	0.74	3	0.5424955	239	0.69021285	
9462	GO:0016265	death	0.74	3	0.5424955	239	0.69021285	
5055	GO:0006996	organelle organization	0.74	2	0.36166364	164	0.47361887	
3048	GO:0004364	glutathione transferase acti	0.74	1	0.18083182	84	0.24258527	
4327	GO:0006091	generation of precursor me	0.74	1	0.18083182	84	0.24258527	
30867	GO:0072511	divalent inorganic cation tra	0.74	1	0.18083182	84	0.24258527	
131	GO:0000166	nucleotide binding	0.74	17	3.074141	1213	3.5030468	
2643	GO:0003700|GO:0000130	sequence-specific DNA bin	0.75	20	3.6166365	1417	4.0921826	
716	GO:0001071	nucleic acid binding transcr	0.75	20	3.6166365	1417	4.0921826	
5712	GO:0008168|GO:0004480	methyltransferase activity	0.75	3	0.5424955	244	0.7046524	
5768	GO:0008238	exopeptidase activity	0.75	1	0.18083182	86	0.24836111	
6985	GO:0009719	response to endogenous st	0.75	1	0.18083182	86	0.24836111	
12734	GO:0030163	protein catabolic process	0.75	1	0.18083182	86	0.24836111	
3341	GO:0004722|GO:0000158|	protein serine/threonine pho	0.76	2	0.36166364	171	0.4938343	
21331	GO:0045735	nutrient reservoir activity	0.76	1	0.18083182	89	0.25702485	
2982	GO:0004197	cysteine-type endopeptidas	0.77	1	0.18083182	90	0.2599128	
4605	GO:0006457|GO:0007022|	protein folding	0.77	2	0.36166364	173	0.49961013	
3644	GO:0005102	receptor binding	0.77	1	0.18083182	91	0.2628007	
6784	GO:0009451|GO:0016547	RNA modification	0.77	1	0.18083182	91	0.2628007	
5693	GO:0008135	translation factor activity, n	0.77	1	0.18083182	92	0.26568863	
2674	GO:0003824	catalytic activity	0.77	164	29.65642	10750	31.045137	
11712	GO:0019748	secondary metabolic proce	0.78	1	0.18083182	95	0.27435237	
18633	GO:0042277	peptide binding	0.78	1	0.18083182	95	0.27435237	
30306	GO:0071944	cell periphery	0.78	3	0.5424955	259	0.74797124	
9796	GO:0016741	transferase activity, transfe	0.79	3	0.5424955	261	0.7537471	
9823	GO:0016772	transferase activity, transfe	0.79	27	4.882459	1932	5.579461	
5610	GO:0008026	ATP-dependent helicase ac	0.79	2	0.36166364	183	0.52848935	
28401	GO:0070035	purine NTP-dependent helic	0.79	2	0.36166364	183	0.52848935	
13829	GO:0031406	carboxylic acid binding	0.79	1	0.18083182	98	0.28301615	
20505	GO:0044255	cellular lipid metabolic proc	0.79	2	0.36166364	184	0.53137726	
9486	GO:0016298	lipase activity	0.80	2	0.36166364	185	0.53426516	
3999	GO:0005694	chromosome	0.80	1	0.18083182	99	0.28590405	
16851	GO:0034470	ncRNA processing	0.80	1	0.18083182	99	0.28590405	
17039	GO:0034660	ncRNA metabolic process	0.80	1	0.18083182	99	0.28590405	
9488	GO:0016301	kinase activity	0.80	24	4.339964	1740	5.0249805	
3304	GO:0004672|GO:0050222	protein kinase activity	0.80	18	3.254973	1333	3.8495972	
9699	GO:0016616	oxidoreductase activity, act	0.80	3	0.5424955	266	0.7681867	
7271	GO:0010033	response to organic substa	0.80	1	0.18083182	100	0.28879198	
4459	GO:0006259|GO:0055132	DNA metabolic process	0.80	6	1.084991	493	1.4237444	
5705	GO:0008152	metabolic process	0.80	269	48.64376	17432	50.34222	
3306	GO:0004674|GO:0004695|	protein serine/threonine kin	0.80	14	2.5316455	1062	3.0669708	
3068	GO:0004386	helicase activity	0.81	2	0.36166364	189	0.54581684	
9494	GO:0016311	dephosphorylation	0.81	5	0.9041591	425	1.227366	
30206	GO:0071842	cellular component organiz	0.82	2	0.36166364	193	0.5573685	
2897	GO:0004091|GO:0004302|	carboxylesterase activity	0.82	2	0.36166364	194	0.5602564	
6426	GO:0009057|GO:0043285	macromolecule catabolic pr	0.82	1	0.18083182	106	0.3061195	
2653	GO:0003723	RNA binding	0.82	10	1.8083183	797	2.3016722	
8910	GO:0015631	tubulin binding	0.82	1	0.18083182	107	0.30900744	
3178	GO:0004519	endonuclease activity	0.82	4	0.7233273	356	1.0280994	
3626	GO:0005083	small GTPase regulator act	0.83	1	0.18083182	111	0.3205591	
19686	GO:0043414	macromolecule methylation	0.84	1	0.18083182	113	0.32633495	
18912	GO:0042578	phosphoric ester hydrolase	0.84	5	0.9041591	444	1.2822365	
22478	GO:0046982	protein heterodimerization a	0.84	1	0.18083182	114	0.32922286	
4612	GO:0006468	protein phosphorylation	0.84	30	5.424955	2205	6.367863	
9697	GO:0016614	oxidoreductase activity, act	0.85	3	0.5424955	293	0.84616053	
2521	GO:0003333	amino acid transmembrane	0.85	1	0.18083182	118	0.34077454	
8584	GO:0015171|GO:0015359	amino acid transmembrane	0.85	1	0.18083182	118	0.34077454	
18956	GO:0042626	ATPase activity, coupled to	0.85	2	0.36166364	211	0.6093511	
9861	GO:0016820	hydrolase activity, acting or	0.85	2	0.36166364	212	0.612239	
9493	GO:0016310	phosphorylation	0.86	34	6.148282	2504	7.2313514	
18953	GO:0042623	ATPase activity, coupled	0.86	6	1.084991	537	1.550813	
6884	GO:0009607	response to biotic stimulus	0.86	1	0.18083182	122	0.3523262	
12532	GO:0022836	gated channel activity	0.86	1	0.18083182	122	0.3523262	
25485	GO:0051188	cofactor biosynthetic proces	0.86	1	0.18083182	123	0.35521415	
3863	GO:0005488	binding	0.86	210	37.97468	13903	40.15075	
4236	GO:0005996	monosaccharide metabolic	0.87	1	0.18083182	125	0.36099	
3761	GO:0005275|GO:0005279	amine transmembrane tran	0.87	1	0.18083182	126	0.3638779	
9913	GO:0016881	acid-amino acid ligase activ	0.87	4	0.7233273	391	1.1291766	
22415	GO:0046914	transition metal ion binding	0.87	35	6.329114	2599	7.5057034	
4526	GO:0006351|GO:0006350|	transcription, DNA-depende	0.88	20	3.6166365	1575	4.548474	
15176	GO:0032774	RNA biosynthetic process	0.88	20	3.6166365	1575	4.548474	
2758	GO:0003924	GTPase activity	0.88	1	0.18083182	132	0.3812054	
4394	GO:0006184	GTP catabolic process	0.88	1	0.18083182	132	0.3812054	
21605	GO:0046039	GTP metabolic process	0.88	1	0.18083182	132	0.3812054	
4408	GO:0006200	ATP catabolic process	0.89	7	1.2658228	641	1.8511566	
9918	GO:0016887|GO:0004002	ATPase activity	0.89	7	1.2658228	641	1.8511566	
21600	GO:0046034	ATP metabolic process	0.89	7	1.2658228	641	1.8511566	
3801	GO:0005342	organic acid transmembran	0.89	1	0.18083182	136	0.3927571	
22444	GO:0046943	carboxylic acid transmembr	0.89	1	0.18083182	136	0.3927571	
19758	GO:0043492	ATPase activity, coupled to	0.89	2	0.36166364	235	0.67866117	
3724	GO:0005216	ion channel activity	0.90	1	0.18083182	140	0.40430877	
23515	GO:0048037	cofactor binding	0.90	3	0.5424955	327	0.94434977	
5909	GO:0008415	acyltransferase activity	0.90	3	0.5424955	330	0.95301354	
4897	GO:0006793	phosphorus metabolic proc	0.90	39	7.052441	2925	8.4471655	
4900	GO:0006796	phosphate metabolic proce	0.90	39	7.052441	2925	8.4471655	
4304	GO:0006066	alcohol metabolic process	0.90	1	0.18083182	143	0.41297254	
9895	GO:0016860	intramolecular oxidoreducta	0.91	1	0.18083182	146	0.42163628	
6824	GO:0009536	plastid	0.91	2	0.36166364	247	0.7133162	
5661	GO:0008092	cytoskeletal protein binding	0.91	2	0.36166364	249	0.719092	
3177	GO:0004518	nuclease activity	0.91	4	0.7233273	427	1.2331418	
9824	GO:0016773	phosphotransferase activity	0.91	18	3.254973	1493	4.311664	
8749	GO:0015399	primary active transmembra	0.92	2	0.36166364	260	0.75085914	
8753	GO:0015405	P-P-bond-hydrolysis-driven	0.92	2	0.36166364	260	0.75085914	
9285	GO:0016043	cellular component organiz	0.92	2	0.36166364	261	0.7537471	
5764	GO:0008234|GO:0004220	cysteine-type peptidase act	0.93	1	0.18083182	163	0.47073093	
4405	GO:0006195	purine nucleotide catabolic	0.93	8	1.4466546	773	2.232362	
6508	GO:0009143	nucleoside triphosphate cat	0.93	8	1.4466546	773	2.232362	
6509	GO:0009144	purine nucleoside triphosph	0.93	8	1.4466546	773	2.232362	

6511	GO:0009146	purine nucleoside triphosph	0.93	8	1.4466546	773	2.232362	
6519	GO:0009154	purine ribonucleotide catab	0.93	8	1.4466546	773	2.232362	
6530	GO:0009166	nucleotide catabolic proces	0.93	8	1.4466546	773	2.232362	
6567	GO:0009203	ribonucleoside triphosphate	0.93	8	1.4466546	773	2.232362	
6569	GO:0009205	purine ribonucleoside tripho	0.93	8	1.4466546	773	2.232362	
6571	GO:0009207	purine ribonucleoside tripho	0.93	8	1.4466546	773	2.232362	
6624	GO:0009261	ribonucleotide catabolic pro	0.93	8	1.4466546	773	2.232362	
17034	GO:0034655	nucleobase, nucleoside, nu	0.93	8	1.4466546	773	2.232362	
17035	GO:0034656	nucleobase, nucleoside and	0.93	8	1.4466546	773	2.232362	
22209	GO:0046700	heterocycle catabolic proce	0.93	8	1.4466546	773	2.232362	
30879	GO:0072523	purine-containing compoun	0.93	8	1.4466546	773	2.232362	
25483	GO:0051186	cofactor metabolic process	0.93	1	0.18083182	164	0.47361887	
2627	GO:0003676	nucleic acid binding	0.93	31	5.605787	2453	7.0840673	
20520	GO:0044270	cellular nitrogen compound	0.93	8	1.4466546	777	2.2439137	
4476	GO:0006278	RNA-dependent DNA replic	0.93	1	0.18083182	166	0.4793947	
20521	GO:0044271	cellular nitrogen compound	0.93	3	0.5424955	367	1.0598665	
9911	GO:0016879	ligase activity, forming carb	0.93	4	0.7233273	456	1.3168914	
6899	GO:0009628	response to abiotic stimulus	0.94	1	0.18083182	170	0.49094638	
26932	GO:0055086	nucleobase, nucleoside and	0.94	10	1.8083183	944	2.7261963	
6563	GO:0009199	ribonucleoside triphosphate	0.94	8	1.4466546	790	2.2814567	
6515	GO:0009150	purine ribonucleotide metab	0.94	8	1.4466546	791	2.2843447	
3874	GO:0005509	calcium ion binding	0.94	2	0.36166364	279	0.8057296	
11522	GO:0019538|GO:0006411	protein metabolic process	0.94	55	9.94575	4134	11.938661	
6506	GO:0009141	nucleoside triphosphate me	0.94	8	1.4466546	796	2.2987843	
9579	GO:0016462	pyrophosphatase activity	0.94	10	1.8083183	954	2.7550755	
9859	GO:0016818	hydrolase activity, acting or	0.94	10	1.8083183	956	2.7608514	
10058	GO:0017111	nucleoside-triphosphatase	0.94	9	1.6274865	878	2.5355935	
11787	GO:0019842	vitamin binding	0.94	1	0.18083182	177	0.5111618	
20622	GO:0044428	nuclear part	0.94	1	0.18083182	178	0.5140497	
30205	GO:0071841	cellular component organiz	0.94	2	0.36166364	285	0.8230572	
9858	GO:0016817	hydrolase activity, acting or	0.94	10	1.8083183	959	2.769515	
17024	GO:0034645|GO:0034961	cellular macromolecule bio	0.94	24	4.339964	1999	5.7729516	
4572	GO:0006412|GO:0006416|	translation	0.95	1	0.18083182	180	0.5198256	
6428	GO:0009059|GO:0043284	macromolecule biosynthetic	0.95	24	4.339964	2003	5.7845035	
4373	GO:0006163	purine nucleotide metabolic	0.95	8	1.4466546	810	2.339215	
6622	GO:0009259|GO:0009121	ribonucleotide metabolic pr	0.95	8	1.4466546	812	2.344991	
4844	GO:0006725	cellular aromatic compound	0.95	1	0.18083182	185	0.53426516	
30877	GO:0072521	purine-containing compoun	0.95	8	1.4466546	827	2.3883097	
4867	GO:0006753	nucleoside phosphate meta	0.96	9	1.6274865	914	2.6395588	
6484	GO:0009117	nucleotide metabolic proces	0.96	9	1.6274865	914	2.6395588	
9889	GO:0016853	isomerase activity	0.96	2	0.36166364	306	0.8837035	
10244	GO:0018130	heterocycle biosynthetic pro	0.96	1	0.18083182	199	0.57469606	
22375	GO:0046872	metal ion binding	0.96	37	6.690778	2985	8.6204405	
14380	GO:0031967	organelle envelope	0.96	1	0.18083182	201	0.5804719	
19470	GO:0043167	ion binding	0.96	37	6.690778	2997	8.655096	
19472	GO:0043169	cation binding	0.96	37	6.690778	2997	8.655096	
9906	GO:0016874	ligase activity	0.96	5	0.9041591	597	1.7240882	
14387	GO:0031975	envelope	0.96	1	0.18083182	205	0.59202355	
22007	GO:0046483	heterocycle metabolic proce	0.96	11	1.98915	1094	3.1593843	
20532	GO:0044282	small molecule catabolic pr	0.96	8	1.4466546	854	2.4662836	
9308	GO:0016070	RNA metabolic process	0.96	21	3.7974684	1855	5.3570914	
3449	GO:0004842|GO:0004840|	ubiquitin-protein ligase acti	0.97	2	0.36166364	326	0.94146186	
20488	GO:0044238	primary metabolic process	0.97	128	23.146473	9167	26.47356	
9654	GO:0016567	protein ubiquitination	0.97	2	0.36166364	332	0.9587894	
14854	GO:0032446	protein modification by sma	0.97	2	0.36166364	332	0.9587894	
29011	GO:0070647	protein modification by sma	0.97	2	0.36166364	332	0.9587894	
4558	GO:0006396|GO:0006394	RNA processing	0.97	1	0.18083182	219	0.63245445	
11747	GO:0019787|GO:0008639|	small conjugating protein li	0.97	2	0.36166364	339	0.9790048	
31895	GO:0090304	nucleic acid metabolic proc	0.97	27	4.882459	2340	6.7577324	
4460	GO:0006260|GO:0055133	DNA replication	0.97	1	0.18083182	224	0.64689404	
7691	GO:0010467	gene expression	0.97	22	3.9783	1974	5.7007537	
20498	GO:0044248	cellular catabolic process	0.98	8	1.4466546	894	2.5818002	
6796	GO:0009507	chloroplast	0.98	1	0.18083182	229	0.6613336	
20533	GO:0044283	small molecule biosynthetic	0.98	2	0.36166364	347	1.0021082	
8211	GO:0012505	endomembrane system	0.98	1	0.18083182	242	0.6988766	
30204	GO:0071840	cellular component organiz	0.98	2	0.36166364	362	1.045427	
4609	GO:0006464	protein modification proces	0.98	32	5.786618	2781	8.031305	
19533	GO:0043234	protein complex	0.98	7	1.2658228	848	2.448956	
6427	GO:0009058	biosynthetic process	0.98	32	5.786618	2796	8.074624	
19684	GO:0043412	macromolecule modificatio	0.99	33	5.96745	2900	8.374968	
3716	GO:0005198	structural molecule activity	0.99	2	0.36166364	393	1.1349525	
6425	GO:0009056	catabolic process	0.99	9	1.6274865	1051	3.0352037	
20499	GO:0044249	cellular biosynthetic proces	0.99	29	5.244123	2635	7.6096687	
19473	GO:0043170|GO:0043283	macromolecule metabolic p	0.99	84	15.189874	6553	18.92454	
3955	GO:0005634	nucleus	0.99	13	2.3508136	1433	4.138389	
4357	GO:0006139|GO:0055134	nucleobase, nucleoside, nu	0.99	37	6.690778	3285	9.486816	
20517	GO:0044267	cellular protein metabolic p	0.99	36	6.509946	3225	9.313541	
20531	GO:0044281	small molecule metabolic p	0.99	17	3.074141	1788	5.1636004	
4320	GO:0006082	organic acid metabolic proc	1.00	1	0.18083182	369	1.0656425	
11716	GO:0019752	carboxylic acid metabolic p	1.00	1	0.18083182	369	1.0656425	
19707	GO:0043436	oxoacid metabolic process	1.00	1	0.18083182	369	1.0656425	
7229	GO:0009987|GO:0008151|	cellular process	1.00	140	25.316456	10601	30.614838	
18541	GO:0042180	cellular ketone metabolic pr	1.00	1	0.18083182	375	1.0829699	
20510	GO:0044260|GO:0034960	cellular macromolecule me	1.00	65	11.754068	5577	16.105928	
17020	GO:0034641	cellular nitrogen compound	1.00	38	6.871609	3678	10.621769	
20640	GO:0044446	intracellular organelle part	1.00	3	0.5424955	710	2.0504231	
20616	GO:0044422	organelle part	1.00	3	0.5424955	712	2.0561988	
4906	GO:0006807	nitrogen compound metabo	1.00	38	6.871609	3725	10.757502	
19527	GO:0043228	non-membrane-bounded or	1.00	4	0.7233273	923	2.66555	
19531	GO:0043232	intracellular non-membrane	1.00	4	0.7233273	923	2.66555	
20487	GO:0044237	cellular metabolic process	1.00	94	16.998192	8185	23.637625	
19526	GO:0043227	membrane-bounded organe	1.00	15	2.7124774	2142	6.185924	
19530	GO:0043231	intracellular membrane-bou	1.00	15	2.7124774	2142	6.185924	
4109	GO:0005840|GO:0033279	ribosome	1.00	1	0.18083182	682	1.9695613	
5791	GO:0008270	zinc ion binding	1.00	11	1.98915	1880	5.4292893	
15392	GO:0032991	macromolecular complex	1.00	8	1.4466546	1616	4.666878	
13018	GO:0030529	ribonucleoprotein complex	1.00	1	0.18083182	741	2.1399486	
19525	GO:0043226	organelle	1.00	19	3.4358046	3013	8.701303	
19528	GO:0043229	intracellular organelle	1.00	19	3.4358046	3013	8.701303	
3945	GO:0005622	intracellular	1.00	37	6.690778	4751	13.720507	
20618	GO:0044424	intracellular part	1.00	27	4.882459	3853	11.127155	
4027	GO:0005737	cytoplasm	1.00	7	1.2658228	2001	5.7787275	
20638	GO:0044444	cytoplasmic part	1.00	4	0.7233273	1644	4.7477403	

GO ID	GO ACCESSION	GO Term	p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
4476	GO:0006278	RNA-dependent DNA re	**0.00**	38	5.322129	166	0.4793947
4459	GO:0006259|GO:00551	DNA metabolic process	**0.00**	59	8.263306	493	1.4237444
4460	GO:0006260|GO:00551	DNA replication	**0.00**	38	5.322129	224	0.64689404
8493	GO:0015074	DNA integration	**0.00**	21	2.9411764	47	0.13573223
31895	GO:0090304	nucleic acid metabolic p	**0.00**	94	13.165266	2340	6.7577324
31393	GO:0080016	(-)-E-beta-caryophyllene	**0.00**	9	1.2605042	25	0.072197996
31394	GO:0080017	alpha-humulene syntha	**0.00**	9	1.2605042	25	0.072197996
7558	GO:0010334	sesquiterpene synthase	**0.00**	9	1.2605042	29	0.083749674
7222	GO:0009975	cyclase activity	**0.00**	9	1.2605042	31	0.08952551
7557	GO:0010333	terpene synthase activit	**0.00**	11	1.5406163	57	0.16461143
9877	GO:0016838	carbon-oxygen lyase ac	**0.00**	12	1.6806723	77	0.22236982
4357	GO:0006139|GO:00551	nucleobase, nucleoside	**0.00**	111	15.546219	3285	9.486816
17024	GO:0034645|GO:00349	cellular macromolecule	**0.00**	73	10.22409	1999	5.7729516
6428	GO:0009059|GO:00432	macromolecule biosynth	**0.00**	73	10.22409	2003	5.7845035
17020	GO:0034641	cellular nitrogen compou	**0.00**	114	15.966387	3678	10.621769
4906	GO:0006807	nitrogen compound met	**0.00**	114	15.966387	3725	10.757502
6884	GO:0009607	response to biotic stimu	**0.00**	11	1.5406163	122	0.3523262
23522	GO:0048046	apoplast	**0.00**	8	1.1204482	70	0.20215438
5705	GO:0008152	metabolic process	**0.00**	408	57.142857	17432	50.34222
9869	GO:0016829	lyase activity	**0.00**	23	3.2212884	488	1.4093049
22375	GO:0046872	metal ion binding	**0.00**	89	12.464986	2985	8.6204405
9874	GO:0016835	carbon-oxygen lyase ac	**0.00**	13	1.8207283	202	0.5833598
19470	GO:0043167	ion binding	**0.00**	89	12.464986	2997	8.655096
19472	GO:0043169	cation binding	**0.00**	89	12.464986	2997	8.655096
20499	GO:0044249	cellular biosynthetic pro	**0.00**	80	11.204482	2635	7.6096687
3009	GO:0004322	ferroxidase activity	**0.00**	5	0.70028013	30	0.086637594
9785	GO:0016724	oxidoreductase activity,	**0.00**	5	0.70028013	30	0.086637594
6427	GO:0009058	biosynthetic process	**0.00**	83	11.62465	2796	8.074624
26959	GO:0055114	oxidation-reduction proc	**0.00**	75	10.504202	2490	7.1909204
2864	GO:0004058|GO:00164	aromatic-L-amino-acid d	**0.00**	3	0.42016807	9	0.025991278
3874	GO:0005509	calcium ion binding	**0.00**	15	2.1008403	279	0.8057296
3904	GO:0005576	extracellular region	**0.00**	11	1.5406163	178	0.5140497
3386	GO:0004773	steryl-sulfatase activity	**0.00**	3	0.42016807	12	0.03465504
5965	GO:0008484	sulfuric ester hydrolase	**0.00**	3	0.42016807	12	0.03465504
9816	GO:0016762	xyloglucan:xyloglucosyl	**0.00**	4	0.5602241	27	0.077973835
5704	GO:0008150|GO:00000	biological_process	**0.00**	494	69.187675	22215	64.155136
3473	GO:0004867	serine-type endopeptida	**0.00**	6	0.84033614	66	0.1906027
5791	GO:0008270	zinc ion binding	**0.00**	57	7.9831934	1880	5.4292893
14101	GO:0031683	G-protein beta/gamma-s	**0.00**	3	0.42016807	15	0.043318797
9783	GO:0016722	oxidoreductase activity,	**0.00**	5	0.70028013	50	0.14439599
18757	GO:0042409	caffeoyl-CoA O-methyltr	**0.00**	3	0.42016807	16	0.046206716
25837	GO:0051553	flavone biosynthetic pro	**0.00**	4	0.5602241	32	0.09241343
25838	GO:0051554	flavonol metabolic proce	**0.00**	4	0.5602241	32	0.09241343
25839	GO:0051555	flavonol biosynthetic pro	**0.00**	4	0.5602241	32	0.09241343
21041	GO:0045431	flavonol synthase activit	**0.00**	4	0.5602241	32	0.09241343
25836	GO:0051552	flavone metabolic proce	**0.00**	4	0.5602241	32	0.09241343
19707	GO:0043436	oxoacid metabolic proce	**0.00**	16	2.2408965	369	1.0656425
4320	GO:0006082	organic acid metabolic p	**0.00**	16	2.2408965	369	1.0656425
11716	GO:0019752	carboxylic acid metaboli	**0.00**	16	2.2408965	369	1.0656425
22415	GO:0046914	transition metal ion bind	**0.00**	73	10.22409	2599	7.5057034
5702	GO:0008146	sulfotransferase activity	**0.01**	5	0.70028013	54	0.15594767
18541	GO:0042180	cellular ketone metaboli	**0.01**	16	2.2408965	375	1.0829699
3888	GO:0005529	sugar binding	**0.01**	9	1.2605042	158	0.45629135
7072	GO:0009813	flavonoid biosynthetic p	**0.01**	4	0.5602241	40	0.1155168
13038	GO:0030551	cyclic nucleotide binding	**0.01**	3	0.42016807	22	0.06353424
3256	GO:0004616	phosphogluconate dehy	**0.01**	2	0.28011206	8	0.023103358
7071	GO:0009812	flavonoid metabolic proc	**0.01**	4	0.5602241	44	0.12706847
3472	GO:0004866	endopeptidase inhibitor	**0.01**	6	0.84033614	95	0.27435237
8159	GO:0010951	negative regulation of e	**0.01**	6	0.84033614	95	0.27435237
26712	GO:0052548	regulation of endopeptic	**0.01**	6	0.84033614	95	0.27435237
28101	GO:0061135	endopeptidase regulato	**0.01**	6	0.84033614	95	0.27435237
12805	GO:0030246	carbohydrate binding	**0.02**	11	1.5406163	251	0.7248679
6632	GO:0009269	response to desiccation	**0.02**	2	0.28011206	10	0.0288792
21148	GO:0045547	dehydrodolichyl diphosp	**0.02**	2	0.28011206	10	0.0288792
6750	GO:0009415	response to water	**0.02**	4	0.5602241	49	0.14150807
9832	GO:0016782	transferase activity, tran	**0.02**	5	0.70028013	74	0.21370606
9767	GO:0016705	oxidoreductase activity,	**0.02**	13	1.8207283	329	0.95012563
19473	GO:0043170|GO:00432	macromolecule metabol	**0.02**	157	21.988796	6553	18.92454
6965	GO:0009699	phenylpropanoid biosyn	**0.02**	4	0.5602241	52	0.15017183
7690	GO:0010466	negative regulation of p	**0.03**	6	0.84033614	110	0.31767118
12946	GO:0030414	peptidase inhibitor activ	**0.03**	6	0.84033614	110	0.31767118
25636	GO:0051346	negative regulation of h	**0.03**	6	0.84033614	110	0.31767118
26711	GO:0052547	regulation of peptidase	**0.03**	6	0.84033614	112	0.32344702
28100	GO:0061134	peptidase regulator acti	**0.03**	6	0.84033614	112	0.32344702
5715	GO:0008171	O-methyltransferase act	**0.03**	4	0.5602241	57	0.16461143
9871	GO:0016831	carboxy-lyase activity	**0.03**	6	0.84033614	115	0.3321108
11776	GO:0019825	oxygen binding	**0.03**	14	1.9607843	389	1.1234008
31408	GO:0080031	methyl salicylate esteras	**0.03**	2	0.28011206	14	0.040430877
6964	GO:0009698	phenylpropanoid metab	**0.04**	4	0.5602241	60	0.17327519
14811	GO:0032403	protein complex binding	**0.04**	4	0.5602241	60	0.17327519
9393	GO:0016165	lipoxygenase activity	**0.04**	3	0.42016807	36	0.10396511
6018	GO:0008559|GO:00052	xenobiotic-transporting	**0.04**	4	0.5602241	62	0.17905103
19225	GO:0042908	xenobiotic transport	**0.04**	4	0.5602241	62	0.17905103
19227	GO:0042910	xenobiotic transporter a	**0.04**	4	0.5602241	62	0.17905103
4699	GO:0006570	tyrosine metabolic proce	**0.04**	1	0.14005603	2	0.00577584
4700	GO:0006571	tyrosine biosynthetic pro	**0.04**	1	0.14005603	2	0.00577584
9419	GO:0016206	catechol O-methyltransf	**0.04**	1	0.14005603	2	0.00577584
3382	GO:0004768|GO:00162	stearoyl-CoA 9-desatura	**0.04**	2	0.28011206	16	0.046206716
9427	GO:0016215	CoA desaturase activity	**0.04**	2	0.28011206	16	0.046206716
31396	GO:0080019	fatty-acyl-CoA reductase	**0.04**	2	0.28011206	16	0.046206716
6749	GO:0009414	response to water depri	**0.04**	3	0.42016807	38	0.10974095
21710	GO:0046148	pigment biosynthetic pro	**0.05**	4	0.5602241	69	0.19926646
9812	GO:0016758	transferase activity, tran	0.06	16	2.2408965	501	1.4468478
13651	GO:0031219	levanase activity	0.06	1	0.14005603	3	0.00866376
9764	GO:0016701	oxidoreductase activity,	0.06	4	0.5602241	72	0.20793022
9753	GO:0016682	oxidoreductase activity,	0.06	3	0.42016807	44	0.12706847
18786	GO:0042440	pigment metabolic proce	0.06	4	0.5602241	73	0.21081814
8666	GO:0015276	ligand-gated ion channe	0.07	3	0.42016807	45	0.1299564
12530	GO:0022834	ligand-gated channel ac	0.07	3	0.42016807	45	0.1299564
23518	GO:0048040	UDP-glucuronate decar	0.07	2	0.28011206	21	0.060646318
3129	GO:0004467	long-chain fatty acid-Co	0.07	2	0.28011206	21	0.060646318

20510	GO:0044260|GO:00349	cellular macromolecule	0.07	130	18.207283	5577	16.105928
9768	GO:0016706	oxidoreductase activity,	0.07	7	0.98039216	175	0.505386
18956	GO:0042626	ATPase activity, couple	0.07	8	1.1204482	211	0.6093511
9861	GO:0016820	hydrolase activity, actin	0.07	8	1.1204482	212	0.612239
24858	GO:0050551	myrcene synthase activ	0.07	2	0.28011206	22	0.06353424
11787	GO:0019842	vitamin binding	0.07	7	0.98039216	177	0.5111618
23515	GO:0048037	cofactor binding	0.08	11	1.5406163	327	0.94434977
9811	GO:0016757|GO:00169	transferase activity, tran	0.08	21	2.9411764	729	2.1052935
3291	GO:0004657	proline dehydrogenase	0.08	1	0.14005603	4	0.011551679
3834	GO:0005395	eye pigment precursor t	0.08	1	0.14005603	4	0.011551679
4325	GO:0006089	lactate metabolic proces	0.08	1	0.14005603	4	0.011551679
4345	GO:0006113	fermentation	0.08	1	0.14005603	4	0.011551679
6422	GO:0009051	pentose-phosphate shu	0.08	1	0.14005603	4	0.011551679
8459	GO:0015018	galactosylgalactosylxylo	0.08	1	0.14005603	4	0.011551679
11632	GO:0019656	glucose catabolic proce	0.08	1	0.14005603	4	0.011551679
11635	GO:0019659	glucose catabolic proce	0.08	1	0.14005603	4	0.011551679
11638	GO:0019662	non-glycolytic fermentat	0.08	1	0.14005603	4	0.011551679
16391	GO:0034007	S-linalool synthase activ	0.08	1	0.14005603	4	0.011551679
22893	GO:0047405	pyrimidine-5'-nucleotide	0.08	1	0.14005603	4	0.011551679
24433	GO:0050113	inositol oxygenase activ	0.08	1	0.14005603	4	0.011551679
2753	GO:0003919	FMN adenylyltransferas	0.08	1	0.14005603	4	0.011551679
9779	GO:0016717	oxidoreductase activity,	0.09	2	0.28011206	24	0.06931008
31407	GO:0080030	methyl indole-3-acetate	0.09	2	0.28011206	24	0.06931008
3293	GO:0004659	prenyltransferase activit	0.09	3	0.42016807	51	0.14728391
9482	GO:0016291|GO:00087	acyl-CoA thioesterase a	0.09	2	0.28011206	25	0.072197996
31493	GO:0080118	brassinosteroid sulfotra	0.09	2	0.28011206	25	0.072197996
9750	GO:0016679	oxidoreductase activity,	0.10	3	0.42016807	53	0.15305975
5978	GO:0008506	sucrose:hydrogen symp	0.10	2	0.28011206	26	0.075085916
5987	GO:0008515|GO:00191	sucrose transmembrane	0.10	2	0.28011206	26	0.075085916
8567	GO:0015154	disaccharide transmemb	0.10	2	0.28011206	26	0.075085916
9035	GO:0015766	disaccharide transport	0.10	2	0.28011206	26	0.075085916
9039	GO:0015770	sucrose transport	0.10	2	0.28011206	26	0.075085916
17147	GO:0034768	(E)-beta-ocimene synth	0.10	2	0.28011206	26	0.075085916
4641	GO:0006508	proteolysis	0.10	26	3.6414566	965	2.7868426
8919	GO:0015645	fatty acid ligase activity	0.11	2	0.28011206	27	0.077973835
3464	GO:0004857	enzyme inhibitor activity	0.11	6	0.84033614	157	0.4534034
119	GO:0000151	ubiquitin ligase complex	0.11	4	0.5602241	88	0.25413695
3260	GO:0004620	phospholipase activity	0.11	5	0.70028013	123	0.35521415
25626	GO:0051336	regulation of hydrolase	0.11	7	0.98039216	196	0.5660323
9813	GO:0016759	cellulose synthase activ	0.11	3	0.42016807	57	0.16461143
19758	GO:0043492	ATPase activity, couple	0.11	8	1.1204482	235	0.67866117
9870	GO:0016830	carbon-carbon lyase act	0.12	6	0.84033614	161	0.4649551
3376	GO:0004758	serine C-palmitoyltransf	0.12	1	0.14005603	6	0.01732752
3845	GO:0005452	inorganic anion exchan	0.12	1	0.14005603	6	0.01732752
4375	GO:0006165	nucleoside diphosphate	0.12	1	0.14005603	6	0.01732752
5966	GO:0008486	diphosphoinositol-polyp	0.12	1	0.14005603	6	0.01732752
6000	GO:0008531	riboflavin kinase activity	0.12	1	0.14005603	6	0.01732752
9572	GO:0016454	C-palmitoyltransferase	0.12	1	0.14005603	6	0.01732752
9772	GO:0016710	trans-cinnamate 4-mon	0.12	1	0.14005603	6	0.01732752
11899	GO:0019992	diacylglycerol binding	0.12	1	0.14005603	6	0.01732752
19761	GO:0043495	protein anchor	0.12	1	0.14005603	6	0.01732752
3073	GO:0004397	histidine ammonia-lyase	0.12	1	0.14005603	6	0.01732752
3197	GO:0004550	nucleoside diphosphate	0.12	1	0.14005603	6	0.01732752
12741	GO:0030170	pyridoxal phosphate bin	0.12	5	0.70028013	126	0.3638779
28643	GO:0070279	vitamin B6 binding	0.12	5	0.70028013	126	0.3638779
2870	GO:0004064	arylesterase activity	0.13	2	0.28011206	30	0.086637594
28375	GO:0070008	serine-type exopeptidas	0.13	3	0.42016807	60	0.17327519
2980	GO:0004185	serine-type carboxypep	0.13	3	0.42016807	60	0.17327519
11712	GO:0019748	secondary metabolic pr	0.13	4	0.5602241	95	0.27435237
3255	GO:0004615|GO:00089	phosphomannomutase	0.14	1	0.14005603	7	0.020215439
16115	GO:0033729	anthocyanidin reductase	0.14	1	0.14005603	7	0.020215439
21149	GO:0045548	phenylalanine ammonia	0.14	1	0.14005603	7	0.020215439
2945	GO:0004143	diacylglycerol kinase ac	0.14	1	0.14005603	7	0.020215439
2978	GO:0004180	carboxypeptidase activit	0.14	3	0.42016807	62	0.17905103
6942	GO:0009674	potassium:sodium symp	0.14	2	0.28011206	32	0.09241343
9041	GO:0015772	oligosaccharide transpo	0.14	2	0.28011206	32	0.09241343
12522	GO:0022820	potassium ion symporte	0.14	2	0.28011206	32	0.09241343
9600	GO:0016491	oxidoreductase activity	0.15	42	5.882353	1724	4.9787736
3356	GO:0004737	pyruvate decarboxylase	0.15	1	0.14005603	8	0.023103358
3402	GO:0004791	thioredoxin-disulfide red	0.15	1	0.14005603	8	0.023103358
5953	GO:0008471	laccase activity	0.15	1	0.14005603	8	0.023103358
6378	GO:0008999	ribosomal-protein-alanin	0.15	1	0.14005603	8	0.023103358
6497	GO:0009132	nucleoside diphosphate	0.15	1	0.14005603	8	0.023103358
7003	GO:0009737	response to abscisic ac	0.15	1	0.14005603	8	0.023103358
7168	GO:0009916	alternative oxidase activ	0.15	1	0.14005603	8	0.023103358
9680	GO:0016595	glutamate binding	0.15	1	0.14005603	8	0.023103358
11196	GO:0019187	beta-1,4-mannosyltrans	0.15	1	0.14005603	8	0.023103358
18639	GO:0042284	sphingolipid delta-4 des	0.15	1	0.14005603	8	0.023103358
26035	GO:0051753	mannan synthase activi	0.15	1	0.14005603	8	0.023103358
2988	GO:0004300|GO:00165	enoyl-CoA hydratase ac	0.15	1	0.14005603	8	0.023103358
9765	GO:0016702	oxidoreductase activity,	0.16	3	0.42016807	66	0.1906027
11829	GO:0019900	kinase binding	0.16	3	0.42016807	66	0.1906027
4942	GO:0006855	drug transmembrane tra	0.16	5	0.70028013	139	0.40142086
8642	GO:0015238|GO:00152	drug transmembrane tra	0.16	5	0.70028013	139	0.40142086
9154	GO:0015893	drug transport	0.16	5	0.70028013	139	0.40142086
18832	GO:0042493|GO:00170	response to drug	0.16	5	0.70028013	139	0.40142086
9480	GO:0016289	CoA hydrolase activity	0.16	2	0.28011206	35	0.10107719
11931	GO:0020037	heme binding	0.17	15	2.1008403	550	1.5883559
8749	GO:0015399	primary active transmen	0.17	8	1.1204482	260	0.75085914
8753	GO:0015405	P-P-bond-hydrolysis-dri	0.17	8	1.1204482	260	0.75085914
4079	GO:0005795|GO:00169	Golgi stack	0.17	1	0.14005603	9	0.025991278
20488	GO:0044238	primary metabolic proce	0.18	200	28.011204	9167	26.47356
9486	GO:0016298	lipase activity	0.18	6	0.84033614	185	0.53426516
9818	GO:0016765|GO:00167	transferase activity, tran	0.18	6	0.84033614	185	0.53426516
5911	GO:0008417	fucosyltransferase activ	0.19	1	0.14005603	10	0.0288792
6464	GO:0009095	aromatic amino acid fan	0.19	1	0.14005603	10	0.0288792
8727	GO:0015369	calcium:hydrogen antip	0.19	1	0.14005603	10	0.0288792
9741	GO:0016668|GO:00166	oxidoreductase activity,	0.19	1	0.14005603	10	0.0288792
23116	GO:0047631	ADP-ribose diphosphat	0.19	1	0.14005603	10	0.0288792
2797	GO:0003979	UDP-glucose 6-dehydro	0.19	1	0.14005603	10	0.0288792
4530	GO:0006355|GO:00325	regulation of transcripti	0.19	60	8.403361	2591	7.4826
3872	GO:0005506	iron ion binding	0.19	15	2.1008403	563	1.6258988
25544	GO:0051252	regulation of RNA meta	0.19	60	8.403361	2593	7.488376
20487	GO:0044237	cellular metabolic proce	0.19	179	25.070028	8185	23.637625
19393	GO:0043086	negative regulation of c	0.19	6	0.84033614	188	0.54292893
20342	GO:0044092	negative regulation of m	0.19	6	0.84033614	188	0.54292893
11426	GO:0019438	aromatic compound bio	0.20	5	0.70028013	149	0.43030006

25510	GO:0051213	dioxygenase activity	0.20	3	0.42016807	75	0.21659398
7141	GO:0009889	regulation of biosyntheti	0.20	60	8.403361	2605	7.523031
7772	GO:0010556	regulation of macromole	0.20	60	8.403361	2605	7.523031
13756	GO:0031326	regulation of cellular bio	0.20	60	8.403361	2605	7.523031
32213	GO:2000112	regulation of cellular ma	0.20	60	8.403361	2605	7.523031
24968	GO:0050662	coenzyme binding	0.20	6	0.84033614	191	0.5515927
6288	GO:0008891	glycolate oxidase activit	0.20	1	0.14005603	11	0.03176712
11152	GO:0019139|GO:00464	cytokinin dehydrogenas	0.20	1	0.14005603	11	0.03176712
24696	GO:0050378	UDP-glucuronate 4-epin	0.20	1	0.14005603	11	0.03176712
2791	GO:0003973	(S)-2-hydroxy-acid oxida	0.20	1	0.14005603	11	0.03176712
9845	GO:0016798	hydrolase activity, acting	0.21	11	1.5406163	401	1.1580559
8461	GO:0015020|GO:00039	glucuronosyltransferase	0.21	2	0.28011206	42	0.121292636
3877	GO:0005516	calmodulin binding	0.22	7	0.98039216	236	0.6815491
9909	GO:0016877	ligase activity, forming c	0.22	3	0.42016807	78	0.22525774
25436	GO:0051139	metal ion:hydrogen anti	0.22	1	0.14005603	12	0.03465504
31380	GO:0080002	UDP-glucose:4-aminobe	0.22	1	0.14005603	12	0.03465504
11221	GO:0019219	regulation of nucleobase	0.22	61	8.543417	2675	7.7251854
25468	GO:0051171	regulation of nitrogen co	0.22	61	8.543417	2675	7.7251854
7692	GO:0010468	regulation of gene expre	0.23	60	8.403361	2635	7.6096687
9682	GO:0016597	amino acid binding	0.23	3	0.42016807	80	0.2310336
19479	GO:0043176	amine binding	0.23	3	0.42016807	80	0.2310336
13443	GO:0030984	kininogen binding	0.24	1	0.14005603	13	0.037542958
18582	GO:0042221	response to chemical st	0.24	9	1.2605042	328	0.94723773
12532	GO:0022836	gated channel activity	0.24	4	0.5602241	122	0.3523262
4912	GO:0006813|GO:00154	potassium ion transport	0.25	3	0.42016807	84	0.24258527
30168	GO:0071804	cellular potassium ion tr	0.25	3	0.42016807	84	0.24258527
30169	GO:0071805	potassium ion transmen	0.25	3	0.42016807	84	0.24258527
3048	GO:0004364	glutathione transferase	0.25	3	0.42016807	84	0.24258527
27228	GO:0060255	regulation of macromole	0.25	60	8.403361	2660	7.6818666
22409	GO:0046906	tetrapyrrole binding	0.25	15	2.1008403	596	1.7212002
8497	GO:0015079|GO:00228	potassium ion transmen	0.25	2	0.28011206	47	0.13573223
4670	GO:0006541	glutamine metabolic pro	0.25	1	0.14005603	14	0.040430877
6423	GO:0009052	pentose-phosphate shu	0.25	1	0.14005603	14	0.040430877
9399	GO:0016174	NAD(P)H oxidase activit	0.25	1	0.14005603	14	0.040430877
9879	GO:0016841	ammonia-lyase activity	0.25	1	0.14005603	14	0.040430877
11157	GO:0019144	ADP-sugar diphosphata	0.25	1	0.14005603	14	0.040430877
24970	GO:0050664	oxidoreductase activity,	0.25	1	0.14005603	14	0.040430877
2998	GO:0004311	farnesyltranstransferase	0.25	1	0.14005603	14	0.040430877
31465	GO:0080090	regulation of primary me	0.25	61	8.543417	2710	7.826263
9422	GO:0016209	antioxidant activity	0.25	5	0.70028013	165	0.47650677
5768	GO:0008238	exopeptidase activity	0.26	3	0.42016807	86	0.24836111
7074	GO:0009815	1-aminocyclopropane-1	0.27	2	0.28011206	49	0.14150807
8909	GO:0015630	microtubule cytoskeleto	0.27	2	0.28011206	49	0.14150807
9725	GO:0016645	oxidoreductase activity,	0.27	2	0.28011206	49	0.14150807
3209	GO:0004564	beta-fructofuranosidase	0.27	1	0.14005603	15	0.043318797
9536	GO:0016408	C-acyltransferase activit	0.27	1	0.14005603	15	0.043318797
2868	GO:0004062	aryl sulfotransferase act	0.27	1	0.14005603	15	0.043318797
21331	GO:0045735	nutrient reservoir activity	0.28	3	0.42016807	89	0.25702485
3334	GO:0004713|GO:00047	protein tyrosine kinase a	0.28	1	0.14005603	16	0.046206716
3742	GO:0005242	inward rectifier potassiu	0.28	1	0.14005603	16	0.046206716
7521	GO:0010295	(+)-abscisic acid 8'-hydr	0.28	1	0.14005603	16	0.046206716
9878	GO:0016840	carbon-nitrogen lyase a	0.28	1	0.14005603	16	0.046206716
13435	GO:0030976	thiamine pyrophosphate	0.28	1	0.14005603	16	0.046206716
4135	GO:0005875	microtubule associated	0.30	1	0.14005603	17	0.049094636
4446	GO:0006241	CTP biosynthetic proces	0.30	1	0.14005603	17	0.049094636
6507	GO:0009142	nucleoside triphosphate	0.30	1	0.14005603	17	0.049094636
6513	GO:0009148	pyrimidine nucleoside tr	0.30	1	0.14005603	17	0.049094636
6565	GO:0009201	ribonucleoside triphosph	0.30	1	0.14005603	17	0.049094636
6572	GO:0009208	pyrimidine ribonucleosid	0.30	1	0.14005603	17	0.049094636
6573	GO:0009209	pyrimidine ribonucleosid	0.30	1	0.14005603	17	0.049094636
9930	GO:0016899	oxidoreductase activity,	0.30	1	0.14005603	17	0.049094636
18738	GO:0042389	omega-3 fatty acid desa	0.30	1	0.14005603	17	0.049094636
21602	GO:0046036|GO:00062	CTP metabolic process	0.30	1	0.14005603	17	0.049094636
3242	GO:0004601|GO:00166	peroxidase activity	0.30	4	0.5602241	135	0.38986918
9754	GO:0016684	oxidoreductase activity,	0.30	4	0.5602241	135	0.38986918
12533	GO:0022838	substrate-specific chann	0.31	6	0.84033614	221	0.63823026
17918	GO:0035556|GO:00072	intracellular signal trans	0.31	2	0.28011206	54	0.15594767
3239	GO:0004596	peptide alpha-N-acetyltr	0.31	1	0.14005603	18	0.051982556
4134	GO:0005874	microtubule	0.31	1	0.14005603	18	0.051982556
5776	GO:0008252	nucleotidase activity	0.31	1	0.14005603	18	0.051982556
10899	GO:0018858	benzoate-CoA ligase ac	0.31	1	0.14005603	18	0.051982556
16595	GO:0034212	peptide N-acetyltransfer	0.31	1	0.14005603	18	0.051982556
13753	GO:0031323	regulation of cellular me	0.31	61	8.543417	2770	7.999538
26845	GO:0052689	carboxylic ester hydrola	0.32	13	1.8207283	538	1.5537009
8660	GO:0015267|GO:00152	channel activity	0.32	6	0.84033614	226	0.6526699
12515	GO:0022803	passive transmembrane	0.32	6	0.84033614	226	0.6526699
19887	GO:0043621	protein self-association	0.33	1	0.14005603	19	0.054870475
3724	GO:0005216	ion channel activity	0.33	4	0.5602241	140	0.40430877
13829	GO:0031406	carboxylic acid binding	0.33	3	0.42016807	98	0.28301615
4844	GO:0006725	cellular aromatic compo	0.33	5	0.70028013	185	0.53426516
3323	GO:0004702	receptor signaling prote	0.34	2	0.28011206	58	0.16749935
3328	GO:0004707|GO:00083	MAP kinase activity	0.34	1	0.14005603	20	0.0577584
6201	GO:0008794	arsenate reductase (glu	0.34	1	0.14005603	20	0.0577584
8726	GO:0015368	calcium:cation antiporte	0.34	1	0.14005603	20	0.0577584
13086	GO:0030611	arsenate reductase acti	0.34	1	0.14005603	20	0.0577584
13088	GO:0030613	oxidoreductase activity,	0.34	1	0.14005603	20	0.0577584
13089	GO:0030614	oxidoreductase activity,	0.34	1	0.14005603	20	0.0577584
30700	GO:0072341	modified amino acid bin	0.34	2	0.28011206	59	0.17038727
4526	GO:0006351|GO:00063	transcription, DNA-depe	0.35	35	4.901961	1575	4.548474
15176	GO:0032774	RNA biosynthetic proces	0.35	35	4.901961	1575	4.548474
4420	GO:0006213	pyrimidine nucleoside m	0.35	1	0.14005603	21	0.060646318
6582	GO:0009218	pyrimidine ribonucleotid	0.35	1	0.14005603	21	0.060646318
6584	GO:0009220	pyrimidine ribonucleotid	0.35	1	0.14005603	21	0.060646318
9902	GO:0016868|GO:00167	intramolecular transfera	0.35	1	0.14005603	21	0.060646318
21697	GO:0046131	pyrimidine ribonucleosid	0.35	1	0.14005603	21	0.060646318
8526	GO:0015112	nitrate transmembrane t	0.36	2	0.28011206	61	0.1761631
8975	GO:0015706|GO:00068	nitrate transport	0.36	2	0.28011206	61	0.1761631
12516	GO:0022804	active transmembrane t	0.36	18	2.5210085	787	2.2727928
8489	GO:0015066	alpha-amylase inhibitor	0.37	1	0.14005603	22	0.06353424
10032	GO:0017075	syntaxin-1 binding	0.37	1	0.14005603	22	0.06353424
11224	GO:0019222	regulation of metabolic	0.38	67	9.383754	3115	8.995871
6512	GO:0009147	pyrimidine nucleoside tr	0.38	1	0.14005603	23	0.06642216
7052	GO:0009790|GO:00097	embryo development	0.38	1	0.14005603	23	0.06642216
9806	GO:0016752	sinapoyltransferase acti	0.38	1	0.14005603	23	0.06642216
9807	GO:0016753	O-sinapoyltransferase a	0.38	1	0.14005603	23	0.06642216
9808	GO:0016754	sinapoylglucose-malate	0.38	1	0.14005603	23	0.06642216
9710	GO:0016628	oxidoreductase activity,	0.39	2	0.28011206	65	0.18771479

9838	GO:0016790	thiolester hydrolase acti	0.39	2	0.28011206	65	0.18771479
6424	GO:0009055|GO:00090	electron carrier activity	0.39	4	0.5602241	154	0.44473964
3213	GO:0004568	chitinase activity	0.39	1	0.14005603	24	0.06931008
3262	GO:0004622|GO:00451	lysophospholipase activ	0.39	1	0.14005603	24	0.06931008
6248	GO:0008843	endochitinase activity	0.39	1	0.14005603	24	0.06931008
13657	GO:0031225	anchored to membrane	0.39	1	0.14005603	24	0.06931008
22440	GO:0046939	nucleotide phosphorylat	0.39	1	0.14005603	24	0.06931008
25578	GO:0051287|GO:00512	NAD binding	0.39	1	0.14005603	24	0.06931008
6824	GO:0009536	plastid	0.40	6	0.84033614	247	0.7133162
4331	GO:0006098	pentose-phosphate shu	0.41	1	0.14005603	25	0.072197996
4855	GO:0006739	NADP metabolic proces	0.41	1	0.14005603	25	0.072197996
4856	GO:0006740	NADPH regeneration	0.41	1	0.14005603	25	0.072197996
9846	GO:0016799	hydrolase activity, hydro	0.41	1	0.14005603	25	0.072197996
21145	GO:0045543	gibberellin 2-beta-dioxy	0.41	1	0.14005603	25	0.072197996
125	GO:0000159	protein phosphatase typ	0.41	1	0.14005603	25	0.072197996
3620	GO:0005057	receptor signaling prote	0.42	2	0.28011206	69	0.19926646
9722	GO:0016641	oxidoreductase activity,	0.42	2	0.28011206	69	0.19926646
3210	GO:0004565	beta-galactosidase activ	0.42	1	0.14005603	26	0.075085916
4030	GO:0005741	mitochondrial outer mer	0.42	1	0.14005603	26	0.075085916
9421	GO:0016208	AMP binding	0.42	1	0.14005603	26	0.075085916
20625	GO:0044431	Golgi apparatus part	0.42	1	0.14005603	26	0.075085916
3725	GO:0005217	intracellular ligand-gate	0.43	1	0.14005603	27	0.077973835
6433	GO:0009064	glutamine family amino	0.43	1	0.14005603	27	0.077973835
9771	GO:0016709	oxidoreductase activity,	0.43	2	0.28011206	71	0.2050423
3744	GO:0005244	voltage-gated ion chann	0.44	2	0.28011206	72	0.20793022
12528	GO:0022832	voltage-gated channel a	0.44	2	0.28011206	72	0.20793022
15280	GO:0032879	regulation of localization	0.44	2	0.28011206	72	0.20793022
17141	GO:0034762	regulation of transmemb	0.44	2	0.28011206	72	0.20793022
17144	GO:0034765	regulation of ion transm	0.44	2	0.28011206	72	0.20793022
19568	GO:0043269	regulation of ion transpo	0.44	2	0.28011206	72	0.20793022
25348	GO:0051049	regulation of transport	0.44	2	0.28011206	72	0.20793022
24966	GO:0050660	flavin adenine dinucleot	0.44	3	0.42016807	118	0.34077454
3284	GO:0004650	polygalacturonase activ	0.44	1	0.14005603	28	0.080861755
9238	GO:0015980	energy derivation by oxi	0.44	1	0.14005603	28	0.080861755
9827	GO:0016776	phosphotransferase act	0.44	1	0.14005603	28	0.080861755
13634	GO:0031177	phosphopantetheine bin	0.44	1	0.14005603	28	0.080861755
139	GO:0000175	3'-5'-exoribonuclease ac	0.44	1	0.14005603	28	0.080861755
2833	GO:0004024	alcohol dehydrogenase	0.44	1	0.14005603	28	0.080861755
25195	GO:0050896|GO:00518	response to stimulus	0.44	40	5.602241	1881	5.432177
9703	GO:0016620	oxidoreductase activity,	0.45	2	0.28011206	73	0.21081814
20531	GO:0044281	small molecule metaboli	0.45	38	5.322129	1788	5.1636004
5766	GO:0008236	serine-type peptidase ac	0.45	5	0.70028013	214	0.6180149
4427	GO:0006221	pyrimidine nucleotide bi	0.45	1	0.14005603	29	0.083749674
11834	GO:0019905	syntaxin binding	0.45	1	0.14005603	29	0.083749674
20887	GO:0045263	proton-transporting ATP	0.45	1	0.14005603	29	0.083749674
3310	GO:0004679	AMP-activated protein k	0.46	1	0.14005603	30	0.086637594
8683	GO:0015301|GO:00153	anion:anion antiporter a	0.46	1	0.14005603	30	0.086637594
23	GO:0000030	mannosyltransferase ac	0.46	1	0.14005603	30	0.086637594
2774	GO:0003950	NAD+ ADP-ribosyltrans	0.46	1	0.14005603	30	0.086637594
6899	GO:0009628	response to abiotic stim	0.47	4	0.5602241	170	0.49094638
11202	GO:0019199	transmembrane recepto	0.47	11	1.5406163	504	1.4555116
716	GO:0001071	nucleic acid binding tran	0.47	30	4.2016807	1417	4.0921826
2643	GO:0003700|GO:00001	sequence-specific DNA	0.47	30	4.2016807	1417	4.0921826
4078	GO:0005794	Golgi apparatus	0.48	1	0.14005603	31	0.08952551
14422	GO:0032012	regulation of ARF protei	0.48	1	0.14005603	31	0.08952551
14720	GO:0032312	regulation of ARF GTPa	0.48	1	0.14005603	31	0.08952551
19590	GO:0043295	glutathione binding	0.48	1	0.14005603	31	0.08952551
22019	GO:0046496	nicotinamide nucleotide	0.48	1	0.14005603	31	0.08952551
30884	GO:0072528	pyrimidine-containing co	0.48	1	0.14005603	31	0.08952551
10103	GO:0017171	serine hydrolase activity	0.48	5	0.70028013	220	0.63534236
8675	GO:0015293	symporter activity	0.48	4	0.5602241	173	0.49961013
4121	GO:0005856	cytoskeleton	0.48	3	0.42016807	126	0.3638779
22049	GO:0046527	glucosyltransferase acti	0.48	6	0.84033614	270	0.77973837
3265	GO:0004630	phospholipase D activity	0.49	1	0.14005603	32	0.09241343
3717	GO:0005199	structural constituent of	0.49	1	0.14005603	32	0.09241343
3785	GO:0005315|GO:00053	inorganic phosphate tra	0.49	1	0.14005603	32	0.09241343
4510	GO:0006323	DNA packaging	0.49	1	0.14005603	32	0.09241343
4514	GO:0006334	nucleosome assembly	0.49	1	0.14005603	32	0.09241343
9537	GO:0016409	palmitoyltransferase act	0.49	1	0.14005603	32	0.09241343
9927	GO:0016896	exoribonuclease activity	0.49	1	0.14005603	32	0.09241343
13920	GO:0031497	chromatin assembly	0.49	1	0.14005603	32	0.09241343
14381	GO:0031968	organelle outer membra	0.49	1	0.14005603	32	0.09241343
17107	GO:0034728	nucleosome organizatio	0.49	1	0.14005603	32	0.09241343
28361	GO:0065004	protein-DNA complex as	0.49	1	0.14005603	32	0.09241343
29467	GO:0071103	DNA conformation chan	0.49	1	0.14005603	32	0.09241343
30188	GO:0071824	protein-DNA complex su	0.49	1	0.14005603	32	0.09241343
3190	GO:0004532	exoribonuclease activity	0.49	1	0.14005603	32	0.09241343
3827	GO:0005372	water transmembrane tr	0.50	2	0.28011206	81	0.23392151
4927	GO:0006833	water transport	0.50	2	0.28011206	81	0.23392151
8652	GO:0015250	water channel activity	0.50	2	0.28011206	81	0.23392151
15189	GO:0032787	monocarboxylic acid me	0.50	2	0.28011206	81	0.23392151
18429	GO:0042044	fluid transport	0.50	2	0.28011206	81	0.23392151
4849	GO:0006730|GO:00197	one-carbon metabolic p	0.51	7	0.98039216	325	0.93857396
3749	GO:0005249	voltage-gated potassium	0.51	1	0.14005603	34	0.09818927
5270	GO:0007264	small GTPase mediated	0.51	1	0.14005603	34	0.09818927
5827	GO:0008308|GO:00228	voltage-gated anion cha	0.51	1	0.14005603	34	0.09818927
6486	GO:0009119	ribonucleoside metaboli	0.51	1	0.14005603	34	0.09818927
11208	GO:0019205	nucleobase, nucleoside	0.51	1	0.14005603	34	0.09818927
11831	GO:0019902	phosphatase binding	0.51	1	0.14005603	34	0.09818927
11832	GO:0019903	protein phosphatase bin	0.51	1	0.14005603	34	0.09818927
20321	GO:0044070	regulation of anion trans	0.51	1	0.14005603	34	0.09818927
6166	GO:0008757	S-adenosylmethionine-c	0.51	4	0.5602241	180	0.5198256
6796	GO:0009507	chloroplast	0.51	5	0.70028013	229	0.6613336
3490	GO:0004888|GO:00049	transmembrane recepto	0.51	12	1.6806723	571	1.6490022
4426	GO:0006220	pyrimidine nucleotide m	0.52	1	0.14005603	35	0.10107719
6355	GO:0008970	phospholipase A1 activi	0.52	1	0.14005603	35	0.10107719
21146	GO:0045544	gibberellin 20-oxidase a	0.52	1	0.14005603	35	0.10107719
23199	GO:0047714	galactolipase activity	0.52	1	0.14005603	35	0.10107719
4513	GO:0006333	chromatin assembly or c	0.53	1	0.14005603	36	0.10396511
5902	GO:0008408	3'-5' exonuclease activit	0.53	1	0.14005603	36	0.10396511
9185	GO:0015925	galactosidase activity	0.53	1	0.14005603	36	0.10396511
11314	GO:0019321	pentose metabolic proce	0.53	1	0.14005603	36	0.10396511
3758	GO:0005267	potassium channel activ	0.54	1	0.14005603	37	0.10685303
9193	GO:0015934	large ribosomal subunit	0.54	1	0.14005603	37	0.10685303
11355	GO:0019362	pyridine nucleotide meta	0.54	1	0.14005603	37	0.10685303
30880	GO:0072524	pyridine-containing com	0.54	1	0.14005603	37	0.10685303
20624	GO:0044430	cytoskeletal part	0.54	2	0.28011206	88	0.25413695

8501	GO:0015085	calcium ion transmembr	0.55	1	0.14005603	38	0.10974095
12538	GO:0022843	voltage-gated cation ch	0.55	1	0.14005603	38	0.10974095
117	GO:0000149	SNARE binding	0.55	1	0.14005603	38	0.10974095
2628	GO:0003677	DNA binding	0.55	25	3.5014005	1224	3.534814
9719	GO:0016638	oxidoreductase activity,	0.55	2	0.28011206	89	0.25702485
6623	GO:0009260	ribonucleotide biosynthe	0.56	1	0.14005603	39	0.11262887
30883	GO:0072527	pyrimidine-containing co	0.56	1	0.14005603	39	0.11262887
4408	GO:0006200	ATP catabolic process	0.56	13	1.8207283	641	1.8511566
9918	GO:0016887|GO:00040	ATPase activity	0.56	13	1.8207283	641	1.8511566
21600	GO:0046034	ATP metabolic process	0.56	13	1.8207283	641	1.8511566
9697	GO:0016614	oxidoreductase activity,	0.56	6	0.84033614	293	0.84616053
4058	GO:0005773	vacuole	0.57	1	0.14005603	40	0.1155168
5891	GO:0008395|GO:00083	steroid hydroxylase acti	0.57	1	0.14005603	40	0.1155168
9843	GO:0016796	exonuclease activity, ac	0.57	1	0.14005603	40	0.1155168
11804	GO:0019867	outer membrane	0.57	1	0.14005603	40	0.1155168
5712	GO:0008168|GO:00044	methyltransferase activi	0.57	5	0.70028013	244	0.7046524
2897	GO:0004091|GO:00043	carboxylesterase activity	0.57	4	0.5602241	194	0.5602564
5981	GO:0008509	anion transmembrane tr	0.57	5	0.70028013	245	0.70754033
4851	GO:0006733	oxidoreduction coenzym	0.57	1	0.14005603	41	0.118404716
25098	GO:0050794|GO:00512	regulation of cellular pro	0.57	81	11.344538	3987	11.514136
4917	GO:0006820|GO:00068	anion transport	0.58	5	0.70028013	247	0.7133162
3808	GO:0005351|GO:00054	sugar:hydrogen sympor	0.58	2	0.28011206	94	0.27146447
3835	GO:0005402	cation:sugar symporter	0.58	2	0.28011206	94	0.27146447
3753	GO:0005253	anion channel activity	0.58	1	0.14005603	42	0.121292636
4756	GO:0006631	fatty acid metabolic proc	0.58	1	0.14005603	42	0.121292636
9801	GO:0016747	transferase activity, tran	0.60	9	1.2605042	456	1.3168914
4914	GO:0006816	calcium ion transport	0.60	1	0.14005603	44	0.12706847
6822	GO:0009534	chloroplast thylakoid	0.60	1	0.14005603	44	0.12706847
6823	GO:0009535	chloroplast thylakoid me	0.60	1	0.14005603	44	0.12706847
14388	GO:0031976	plastid thylakoid	0.60	1	0.14005603	44	0.12706847
14395	GO:0031984	organelle subcompartm	0.60	1	0.14005603	44	0.12706847
26883	GO:0055035	plastid thylakoid membr	0.60	1	0.14005603	44	0.12706847
28952	GO:0070588	calcium ion transmembr	0.60	1	0.14005603	44	0.12706847
8677	GO:0015295	solute:hydrogen sympor	0.60	2	0.28011206	98	0.28301615
8681	GO:0015299	solute:hydrogen antipor	0.60	2	0.28011206	98	0.28301615
8673	GO:0015291|GO:00152	secondary active transm	0.60	8	1.1204482	407	1.1753833
25094	GO:0050789|GO:00507	regulation of biological	0.61	87	12.184874	4315	12.461374
9893	GO:0016857	racemase and epimeras	0.61	1	0.14005603	45	0.1299564
14726	GO:0032318	regulation of Ras GTPa	0.61	1	0.14005603	45	0.1299564
17001	GO:0034622	cellular macromolecular	0.61	1	0.14005603	45	0.1299564
22096	GO:0046578	regulation of Ras protei	0.61	1	0.14005603	45	0.1299564
25355	GO:0051056	regulation of small GTP	0.61	1	0.14005603	45	0.1299564
28360	GO:0065003	macromolecular comple	0.61	1	0.14005603	45	0.1299564
8679	GO:0015297	antiporter activity	0.61	3	0.42016807	152	0.4389638
8682	GO:0015300	solute:solute antiporter	0.61	3	0.42016807	152	0.4389638
4073	GO:0005789	endoplasmic reticulum	0.62	1	0.14005603	46	0.13284431
18536	GO:0042175	nuclear outer membrane	0.62	1	0.14005603	46	0.13284431
20626	GO:0044432	endoplasmic reticulum	0.62	1	0.14005603	46	0.13284431
8517	GO:0015103	inorganic anion transme	0.62	3	0.42016807	154	0.44473964
5280	GO:0007275	multicellular organismal	0.62	2	0.28011206	101	0.2916799
5807	GO:0008287	protein serine/threonine	0.62	1	0.14005603	47	0.13573223
6442	GO:0009073|GO:00160	aromatic amino acid fan	0.62	1	0.14005603	47	0.13573223
21943	GO:0046417	chorismate metabolic pr	0.62	1	0.14005603	47	0.13573223
9796	GO:0016741	transferase activity, tran	0.63	5	0.70028013	261	0.7537471
14591	GO:0032183	SUMO binding	0.63	1	0.14005603	48	0.13862015
28930	GO:0070566	adenylyltransferase acti	0.63	1	0.14005603	48	0.13862015
9709	GO:0016627	oxidoreductase activity,	0.64	2	0.28011206	104	0.30034366
19831	GO:0043565	sequence-specific DNA	0.64	3	0.42016807	159	0.45917925
3756	GO:0005261|GO:00152	cation channel activity	0.64	1	0.14005603	49	0.14150807
6483	GO:0009116	nucleoside metabolic pr	0.64	1	0.14005603	49	0.14150807
11830	GO:0019901	protein kinase binding	0.64	1	0.14005603	49	0.14150807
31421	GO:0080044	quercetin 7-O-glucosyltr	0.64	1	0.14005603	49	0.14150807
19126	GO:0042803	protein homodimerizatio	0.64	5	0.70028013	265	0.7652988
14909	GO:0032501|GO:00508	multicellular organismal	0.64	2	0.28011206	105	0.3032316
2668	GO:0003779	actin binding	0.64	2	0.28011206	105	0.3032316
9795	GO:0016740	transferase activity	0.64	75	10.504202	3764	10.870131
8495	GO:0015077	monovalent inorganic ca	0.65	4	0.5602241	214	0.6180149
5096	GO:0007047	cellular cell wall organiz	0.65	1	0.14005603	50	0.14439599
6932	GO:0009664	plant-type cell wall orga	0.65	1	0.14005603	50	0.14439599
19914	GO:0043648	dicarboxylic acid metab	0.65	1	0.14005603	50	0.14439599
20857	GO:0045229	external encapsulating	0.65	1	0.14005603	50	0.14439599
30033	GO:0071669	plant-type cell wall orga	0.65	1	0.14005603	50	0.14439599
3185	GO:0004527|GO:00088	exonuclease activity	0.65	1	0.14005603	50	0.14439599
7213	GO:0009966|GO:00354	regulation of signal tran	0.65	1	0.14005603	51	0.14728391
9975	GO:0016998	cell wall macromolecule	0.65	1	0.14005603	51	0.14728391
12492	GO:0022607	cellular component asse	0.65	1	0.14005603	51	0.14728391
12601	GO:0023051	regulation of signaling	0.65	1	0.14005603	51	0.14728391
30208	GO:0071844	cellular component asse	0.65	1	0.14005603	51	0.14728391
3099	GO:0004428	inositol or phosphatidyli	0.65	1	0.14005603	51	0.14728391
28364	GO:0065007	biological regulation	0.66	87	12.184874	4376	12.637537
4915	GO:0006817	phosphate transport	0.66	1	0.14005603	52	0.15017183
8528	GO:0015114	phosphate transmembra	0.66	1	0.14005603	52	0.15017183
17801	GO:0035435	phosphate transmembra	0.66	1	0.14005603	52	0.15017183
20287	GO:0044036	cell wall macromolecule	0.66	1	0.14005603	52	0.15017183
6563	GO:0009199	ribonucleoside triphosph	0.66	15	2.1008403	790	2.2814567
29246	GO:0070882	cellular cell wall organiz	0.67	1	0.14005603	53	0.15305975
18953	GO:0042623	ATPase activity, couple	0.67	10	1.4005603	537	1.550813
6506	GO:0009141	nucleoside triphosphate	0.67	15	2.1008403	796	2.2987843
8680	GO:0015298	solute:cation antiporter	0.67	2	0.28011206	112	0.32344702
9730	GO:0016651	oxidoreductase activity,	0.67	2	0.28011206	112	0.32344702
29918	GO:0071554	cell wall organization or	0.67	2	0.28011206	112	0.32344702
8943	GO:0015672	monovalent inorganic ca	0.68	7	0.98039216	383	1.1060733
9933	GO:0016903	oxidoreductase activity,	0.68	2	0.28011206	113	0.32633495
9533	GO:0016405	CoA-ligase activity	0.68	1	0.14005603	55	0.15883559
15576	GO:0033177	proton-transporting two-	0.69	1	0.14005603	56	0.16172351
3156	GO:0004497	monooxygenase activity	0.69	3	0.42016807	172	0.49672222
6441	GO:0009072	aromatic amino acid fan	0.70	1	0.14005603	57	0.16461143
9910	GO:0016878	acid-thiol ligase activity	0.70	1	0.14005603	57	0.16461143
23973	GO:0048583	regulation of response t	0.70	1	0.14005603	57	0.16461143
9800	GO:0016746	transferase activity, tran	0.70	9	1.2605042	498	1.438184
5819	GO:0008299|GO:00092	isoprenoid biosynthetic	0.70	1	0.14005603	58	0.16749935
29919	GO:0071555	cell wall organization	0.70	1	0.14005603	58	0.16749935
14667	GO:0032259	methylation	0.70	5	0.70028013	285	0.8230572
8584	GO:0015171|GO:00153	amino acid transmembra	0.70	2	0.28011206	118	0.34077454
25416	GO:0051119	sugar transmembrane tr	0.70	2	0.28011206	118	0.34077454
2521	GO:0003333	amino acid transmembra	0.70	2	0.28011206	118	0.34077454
6622	GO:0009259|GO:00091	ribonucleotide metabolic	0.70	15	2.1008403	812	2.344991

8967	GO:0015698	inorganic anion transpo	0.71	3	0.42016807	176	0.5082739
9900	GO:0016866	intramolecular transfera	0.71	1	0.14005603	59	0.17038727
18981	GO:0042651	thylakoid membrane	0.71	1	0.14005603	59	0.17038727
2831	GO:0004022	alcohol dehydrogenase	0.71	1	0.14005603	59	0.17038727
13082	GO:0030599	pectinesterase activity	0.71	3	0.42016807	178	0.5140497
4840	GO:0006720|GO:00160	isoprenoid metabolic pro	0.71	1	0.14005603	60	0.17327519
5652	GO:0008081|GO:00044	phosphoric diester hydro	0.71	1	0.14005603	60	0.17327519
14910	GO:0032502	developmental process	0.72	2	0.28011206	121	0.3494383
2818	GO:0004003	ATP-dependent DNA he	0.72	1	0.14005603	61	0.1761631
11828	GO:0019899	enzyme binding	0.72	4	0.5602241	237	0.684437
4951	GO:0006865|GO:00068	amino acid transport	0.72	2	0.28011206	123	0.35521415
17000	GO:0034621	cellular macromolecular	0.73	1	0.14005603	62	0.17905103
20186	GO:0043933|GO:00346	macromolecular comple	0.73	1	0.14005603	62	0.17905103
20883	GO:0045259|GO:00452	proton-transporting ATP	0.73	1	0.14005603	62	0.17905103
4405	GO:0006195	purine nucleotide catab	0.73	14	1.9607843	773	2.232362
6508	GO:0009143	nucleoside triphosphate	0.73	14	1.9607843	773	2.232362
6509	GO:0009144	purine nucleoside tripho	0.73	14	1.9607843	773	2.232362
6511	GO:0009146	purine nucleoside tripho	0.73	14	1.9607843	773	2.232362
6519	GO:0009154	purine ribonucleotide ca	0.73	14	1.9607843	773	2.232362
6530	GO:0009166	nucleotide catabolic pro	0.73	14	1.9607843	773	2.232362
6567	GO:0009203	ribonucleoside triphosph	0.73	14	1.9607843	773	2.232362
6569	GO:0009205	purine ribonucleoside tri	0.73	14	1.9607843	773	2.232362
6571	GO:0009207	purine ribonucleoside tri	0.73	14	1.9607843	773	2.232362
6624	GO:0009261	ribonucleotide catabolic	0.73	14	1.9607843	773	2.232362
17034	GO:0034655	nucleobase, nucleoside	0.73	14	1.9607843	773	2.232362
17035	GO:0034656	nucleobase, nucleoside	0.73	14	1.9607843	773	2.232362
22209	GO:0046700	heterocycle catabolic pr	0.73	14	1.9607843	773	2.232362
30879	GO:0072523	purine-containing comp	0.73	14	1.9607843	773	2.232362
9308	GO:0016070	RNA metabolic process	0.73	35	4.901961	1855	5.3570914
20520	GO:0044270	cellular nitrogen compo	0.73	14	1.9607843	777	2.2439137
3476	GO:0004872|GO:00190	receptor activity	0.73	12	1.6806723	672	1.9406822
3761	GO:0005275|GO:00052	amine transmembrane t	0.74	2	0.28011206	126	0.3638779
25820	GO:0051536	iron-sulfur cluster bindin	0.74	1	0.14005603	64	0.18482687
25824	GO:0051540	metal cluster binding	0.74	1	0.14005603	64	0.18482687
22007	GO:0046483	heterocycle metabolic p	0.74	20	2.8011205	1094	3.1593843
25314	GO:0051015	actin filament binding	0.74	1	0.14005603	65	0.18771479
9890	GO:0016854	racemase and epimeras	0.75	1	0.14005603	66	0.1906027
3475	GO:0004871|GO:00050	signal transducer activit	0.75	14	1.9607843	787	2.2727928
27063	GO:0060089	molecular transducer ac	0.75	14	1.9607843	787	2.2727928
5651	GO:0008080	N-acetyltransferase acti	0.75	1	0.14005603	67	0.19349062
2629	GO:0003678|GO:00036	DNA helicase activity	0.75	1	0.14005603	67	0.19349062
6515	GO:0009150	purine ribonucleotide me	0.76	14	1.9607843	791	2.2843447
31420	GO:0080043	quercetin 3-O-glucosyltr	0.76	1	0.14005603	69	0.19926646
9579	GO:0016462	pyrophosphatase activit	0.76	17	2.3809524	954	2.7550755
9859	GO:0016818	hydrolase activity, actin	0.77	17	2.3809524	956	2.7608514
5726	GO:0008187	poly-pyrimidine tract bin	0.77	1	0.14005603	70	0.20215438
5788	GO:0008266	poly(U) RNA binding	0.77	1	0.14005603	70	0.20215438
15524	GO:0033124	regulation of GTP catab	0.77	1	0.14005603	70	0.20215438
19394	GO:0043087	regulation of GTPase ac	0.77	1	0.14005603	70	0.20215438
9103	GO:0015837	amine transport	0.77	2	0.28011206	135	0.38986918
3307	GO:0004675	transmembrane recepto	0.77	6	0.84033614	367	1.0598665
9858	GO:0016817	hydrolase activity, actin	0.77	17	2.3809524	959	2.769515
20532	GO:0044282	small molecule cataboli	0.77	15	2.1008403	854	2.4662836
3801	GO:0005342	organic acid transmemb	0.77	2	0.28011206	136	0.3927571
22444	GO:0046943	carboxylic acid transme	0.77	2	0.28011206	136	0.3927571
19125	GO:0042802	identical protein binding	0.78	12	1.6806723	697	2.01288
9740	GO:0016667	oxidoreductase activity,	0.78	1	0.14005603	72	0.20793022
5809	GO:0008289	lipid binding	0.78	4	0.5602241	258	0.74508333
4867	GO:0006753	nucleoside phosphate m	0.78	16	2.2408965	914	2.6395588
6484	GO:0009117	nucleotide metabolic pro	0.78	16	2.2408965	914	2.6395588
4247	GO:0006007	glucose catabolic proce	0.78	1	0.14005603	73	0.21081814
11313	GO:0019320	hexose catabolic proces	0.78	1	0.14005603	73	0.21081814
20525	GO:0044275	cellular carbohydrate ca	0.78	1	0.14005603	73	0.21081814
21726	GO:0046164	alcohol catabolic proces	0.78	1	0.14005603	73	0.21081814
21894	GO:0046365	monosaccharide catabo	0.78	1	0.14005603	73	0.21081814
8607	GO:0015197|GO:00156	peptide transporter activ	0.78	2	0.28011206	139	0.40142086
8608	GO:0015198	oligopeptide transporter	0.78	2	0.28011206	139	0.40142086
4373	GO:0006163	purine nucleotide metab	0.78	14	1.9607843	810	2.339215
3311	GO:0004683|GO:00046	calmodulin-dependent p	0.79	1	0.14005603	74	0.21370606
9817	GO:0016763	transferase activity, tran	0.79	1	0.14005603	74	0.21370606
20628	GO:0044434	chloroplast part	0.79	1	0.14005603	74	0.21370606
20629	GO:0044435	plastid part	0.79	1	0.14005603	74	0.21370606
3895	GO:0005543	phospholipid binding	0.79	2	0.28011206	140	0.40430877
4944	GO:0006857	oligopeptide transport	0.79	2	0.28011206	141	0.4071967
8676	GO:0015294	solute:cation symporter	0.79	2	0.28011206	141	0.4071967
9099	GO:0015833	peptide transport	0.79	2	0.28011206	141	0.4071967
8810	GO:0015491	cation:cation antiporter	0.79	1	0.14005603	75	0.21659398
5663	GO:0008094|GO:00040	DNA-dependent ATPas	0.80	1	0.14005603	76	0.2194819
5732	GO:0008194	UDP-glycosyltransferase	0.80	5	0.70028013	322	0.9299102
8557	GO:0015144	carbohydrate transmem	0.80	2	0.28011206	143	0.41297254
16602	GO:0034219	carbohydrate transmem	0.80	2	0.28011206	143	0.41297254
6529	GO:0009165	nucleotide biosynthetic	0.80	1	0.14005603	77	0.22236982
9538	GO:0016410	N-acyltransferase activit	0.80	1	0.14005603	77	0.22236982
2986	GO:0004252	serine-type endopeptida	0.80	2	0.28011206	144	0.41586044
9699	GO:0016616	oxidoreductase activity,	0.80	4	0.5602241	266	0.7681867
30865	GO:0072509	divalent inorganic cation	0.80	1	0.14005603	78	0.22525774
10058	GO:0017111	nucleoside-triphosphata	0.80	15	2.1008403	878	2.5355935
4954	GO:0006869	lipid transport	0.81	3	0.42016807	208	0.6006873
8085	GO:0010876	lipid localization	0.81	3	0.42016807	208	0.6006873
3873	GO:0005507	copper ion binding	0.81	2	0.28011206	146	0.42163628
8494	GO:0015075	ion transmembrane tran	0.81	14	1.9607843	827	2.3883097
30877	GO:0072521	purine-containing comp	0.81	14	1.9607843	827	2.3883097
6071	GO:0008643|GO:00068	carbohydrate transport	0.81	2	0.28011206	147	0.42452422
4215	GO:0005975	carbohydrate metabolic	0.81	17	2.3809524	990	2.8590407
4358	GO:0006140	regulation of nucleotide	0.81	1	0.14005603	80	0.2310336
7146	GO:0009894	regulation of catabolic p	0.81	1	0.14005603	80	0.2310336
9875	GO:0016836	hydro-lyase activity	0.81	1	0.14005603	80	0.2310336
13278	GO:0030811	regulation of nucleotide	0.81	1	0.14005603	80	0.2310336
13759	GO:0031329	regulation of cellular cat	0.81	1	0.14005603	80	0.2310336
15521	GO:0033121	regulation of purine nuc	0.81	1	0.14005603	80	0.2310336
16603	GO:0034220	ion transmembrane tran	0.82	14	1.9607843	833	2.4056373
22376	GO:0046873	metal ion transmembran	0.82	3	0.42016807	213	0.6151269
6991	GO:0009725	response to hormone st	0.82	1	0.14005603	82	0.23680943
29202	GO:0070838	divalent metal ion trans	0.82	1	0.14005603	82	0.23680943
26932	GO:0055086	nucleobase, nucleoside	0.82	16	2.2408965	944	2.7261963
4029	GO:0005740	mitochondrial envelope	0.82	2	0.28011206	151	0.4360759
16738	GO:0034357	photosynthetic membra	0.82	1	0.14005603	83	0.23969735

4327	GO:0006091	generation of precursor	0.83	1	0.14005603	84	0.24258527
30867	GO:0072511	divalent inorganic cation	0.83	1	0.14005603	84	0.24258527
12547	GO:0022857|GO:00053	transmembrane transpo	0.83	26	3.6414566	1483	4.282785
17617	GO:0035251	UDP-glucosyltransferas	0.83	3	0.42016807	218	0.62956655
6985	GO:0009719	response to endogenou	0.83	1	0.14005603	86	0.24836111
9114	GO:0015849	organic acid transport	0.83	2	0.28011206	156	0.45051548
22443	GO:0046942	carboxylic acid transpor	0.83	2	0.28011206	156	0.45051548
4246	GO:0006006	glucose metabolic proce	0.84	1	0.14005603	87	0.25124902
7229	GO:0009987|GO:00081	cellular process	0.84	207	28.991596	10601	30.614838
26931	GO:0055085	transmembrane transpo	0.84	27	3.7815125	1548	4.4705
12794	GO:0030234	enzyme regulator activit	0.84	6	0.84033614	403	1.1638317
5195	GO:0007165|GO:00230	signal transduction	0.84	16	2.2408965	961	2.775291
12602	GO:0023052|GO:00230	signaling	0.84	16	2.2408965	961	2.775291
7691	GO:0010467	gene expression	0.84	35	4.901961	1974	5.7007537
8496	GO:0015078	hydrogen ion transmem	0.84	2	0.28011206	160	0.4620672
14590	GO:0032182	small conjugating protei	0.85	1	0.14005603	90	0.2599128
20630	GO:0044436	thylakoid part	0.85	1	0.14005603	90	0.2599128
2982	GO:0004197	cysteine-type endopepti	0.85	1	0.14005603	90	0.2599128
4990	GO:0006915|GO:00086	apoptosis	0.85	3	0.42016807	227	0.6555578
3644	GO:0005102	receptor binding	0.85	1	0.14005603	91	0.2628007
9294	GO:0016052|GO:00060	carbohydrate catabolic	0.85	1	0.14005603	91	0.2628007
5764	GO:0008234|GO:00042	cysteine-type peptidase	0.85	2	0.28011206	163	0.47073093
16785	GO:0034404	nucleobase, nucleoside	0.85	1	0.14005603	92	0.26568863
17033	GO:0034654	nucleobase, nucleoside	0.85	1	0.14005603	92	0.26568863
4916	GO:0006818	hydrogen transport	0.85	4	0.5602241	292	0.84327257
9246	GO:0015992	proton transport	0.85	4	0.5602241	292	0.84327257
20336	GO:0044085	cellular component biog	0.86	1	0.14005603	93	0.26857653
20623	GO:0044429	mitochondrial part	0.86	2	0.28011206	165	0.47650677
6863	GO:0009579	thylakoid	0.86	1	0.14005603	94	0.27146447
18633	GO:0042277	peptide binding	0.86	1	0.14005603	95	0.27435237
25095	GO:0050790	regulation of catalytic ac	0.87	7	0.98039216	480	1.3862015
5756	GO:0008219	cell death	0.87	3	0.42016807	239	0.69021285
8209	GO:0012501|GO:00162	programmed cell death	0.87	3	0.42016807	239	0.69021285
9462	GO:0016265	death	0.87	3	0.42016807	239	0.69021285
28366	GO:0065009	regulation of molecular	0.87	7	0.98039216	484	1.3977532
7271	GO:0010033	response to organic sub	0.88	1	0.14005603	100	0.28879198
4067	GO:0005783	endoplasmic reticulum	0.88	2	0.28011206	174	0.50249803
2674	GO:0003824	catalytic activity	0.88	208	29.131653	10750	31.045137
8211	GO:0012505	endomembrane system	0.88	3	0.42016807	242	0.6988766
11311	GO:0019318	hexose metabolic proce	0.88	1	0.14005603	101	0.2916799
5874	GO:0008374	O-acyltransferase activi	0.88	1	0.14005603	102	0.29456782
20498	GO:0044248	cellular catabolic proces	0.88	14	1.9607843	894	2.5818002
3306	GO:0004674|GO:00046	protein serine/threonine	0.89	17	2.3809524	1062	3.0669708
12608	GO:0030001	metal ion transport	0.89	5	0.70028013	374	1.080082
3200	GO:0004553|GO:00168	hydrolase activity, hydro	0.89	4	0.5602241	312	0.90103096
19253	GO:0042936	dipeptide transporter ac	0.89	1	0.14005603	105	0.3032316
19255	GO:0042938	dipeptide transport	0.89	1	0.14005603	105	0.3032316
3195	GO:0004540	ribonuclease activity	0.89	1	0.14005603	106	0.3061195
4910	GO:0006811	ion transport	0.89	15	2.1008403	959	2.769515
3942	GO:0005618	cell wall	0.89	1	0.14005603	107	0.30900744
20505	GO:0044255	cellular lipid metabolic p	0.90	2	0.28011206	184	0.53137726
12868	GO:0030312	external encapsulating	0.90	1	0.14005603	111	0.3205591
4512	GO:0006325	chromatin organization	0.90	1	0.14005603	112	0.32344702
25568	GO:0051276|GO:00070	chromosome organizati	0.90	1	0.14005603	112	0.32344702
4850	GO:0006732|GO:00067	coenzyme metabolic pro	0.91	1	0.14005603	113	0.32633495
3449	GO:0004842|GO:00048	ubiquitin-protein ligase	0.91	4	0.5602241	326	0.94146186
14379	GO:0031966	mitochondrial membran	0.91	1	0.14005603	114	0.32922286
22478	GO:0046982	protein heterodimerizati	0.91	1	0.14005603	114	0.32922286
9535	GO:0016407	acetyltransferase activit	0.91	1	0.14005603	115	0.3321108
22479	GO:0046983	protein dimerization acti	0.91	7	0.98039216	517	1.4930545
9654	GO:0016567	protein ubiquitination	0.91	4	0.5602241	332	0.9587894
12572	GO:0022890|GO:00150	inorganic cation transme	0.91	4	0.5602241	332	0.9587894
14854	GO:0032446	protein modification by	0.91	4	0.5602241	332	0.9587894
29011	GO:0070647	protein modification by	0.91	4	0.5602241	332	0.9587894
3955	GO:0005634	nucleus	0.91	23	3.2212884	1433	4.138389
4144	GO:0005886|GO:00059	plasma membrane	0.92	1	0.14005603	120	0.34655038
6425	GO:0009056	catabolic process	0.92	16	2.2408965	1051	3.0352037
11747	GO:0019787|GO:00086	small conjugating protei	0.92	4	0.5602241	339	0.9790048
14380	GO:0031967	organelle envelope	0.92	2	0.28011206	201	0.5804719
30066	GO:0071702	organic substance trans	0.92	7	0.98039216	529	1.5277096
4755	GO:0006629	lipid metabolic process	0.92	8	1.1204482	590	1.7038727
30069	GO:0071705	nitrogen compound tran	0.92	2	0.28011206	202	0.5833598
14387	GO:0031975	envelope	0.93	2	0.28011206	205	0.59202355
4236	GO:0005996	monosaccharide metab	0.93	1	0.14005603	125	0.36099
4649	GO:0006520|GO:00065	cellular amino acid meta	0.93	3	0.42016807	277	0.7999538
634	GO:0000988	protein binding transcrip	0.93	1	0.14005603	126	0.3638779
635	GO:0000989	transcription factor bindi	0.93	1	0.14005603	126	0.3638779
2648	GO:0003712	transcription cofactor ac	0.93	1	0.14005603	126	0.3638779
28378	GO:0070011	peptidase activity, acting	0.93	7	0.98039216	537	1.550813
5840	GO:0008324	cation transmembrane t	0.93	7	0.98039216	538	1.5537009
9583	GO:0016469	proton-transporting two-	0.93	1	0.14005603	127	0.36676583
21058	GO:0045454|GO:00305	cell redox homeostasis	0.93	2	0.28011206	211	0.6093511
4394	GO:0006184	GTP catabolic process	0.94	1	0.14005603	132	0.3812054
21605	GO:0046039	GTP metabolic process	0.94	1	0.14005603	132	0.3812054
2758	GO:0003924	GTPase activity	0.94	1	0.14005603	132	0.3812054
9837	GO:0016788	hydrolase activity, acting	0.94	24	3.3613446	1534	4.430069
4028	GO:0005739	mitochondrion	0.94	2	0.28011206	219	0.63245445
13547	GO:0031090	organelle membrane	0.95	2	0.28011206	224	0.64689404
6046	GO:0008610	lipid biosynthetic proces	0.95	1	0.14005603	141	0.4071967
5763	GO:0008233	peptidase activity	0.95	7	0.98039216	565	1.6316746
4304	GO:0006066	alcohol metabolic proce	0.95	1	0.14005603	143	0.41297254
20356	GO:0044106	cellular amine metabolic	0.95	3	0.42016807	303	0.8750397
9488	GO:0016301	kinase activity	0.95	27	3.7815125	1740	5.0249805
9829	GO:0016779	nucleotidyltransferase a	0.95	1	0.14005603	148	0.42741212
11695	GO:0019725	cellular homeostasis	0.96	2	0.28011206	234	0.67577326
12573	GO:0022891	substrate-specific trans	0.96	18	2.5210085	1241	3.5839086
18925	GO:0042592	homeostatic process	0.96	2	0.28011206	238	0.68732494
6662	GO:0009308	amine metabolic proces	0.96	3	0.42016807	314	0.9068068
25998	GO:0051716	cellular response to stin	0.96	16	2.2408965	1138	3.2864528
9913	GO:0016881	acid-amino acid ligase a	0.96	4	0.5602241	391	1.1291766
2975	GO:0004175|GO:00168	endopeptidase activity	0.96	3	0.42016807	320	0.9241344
3716	GO:0005198	structural molecule activ	0.96	4	0.5602241	393	1.1349525
2660	GO:0003735|GO:00037	structural constituent of	0.96	2	0.28011206	246	0.7104283
9906	GO:0016874	ligase activity	0.96	7	0.98039216	597	1.7240882
4911	GO:0006812|GO:00068	cation transport	0.96	8	1.1204482	662	1.9118029
5661	GO:0008092	cytoskeletal protein bind	0.97	2	0.28011206	249	0.719092
3723	GO:0005215|GO:00054	transporter activity	0.97	28	3.9215686	1844	5.325324

3304	GO:0004672|GO:00502	protein kinase activity	0.97	19	2.6610644	1333	3.8495972
5055	GO:0006996	organelle organization	0.97	1	0.14005603	164	0.47361887
25483	GO:0051186	cofactor metabolic proc	0.97	1	0.14005603	164	0.47361887
5909	GO:0008415	acyltransferase activity	0.97	3	0.42016807	330	0.95301354
5018	GO:0006950	response to stress	0.97	7	0.98039216	611	1.764519
6077	GO:0008652	cellular amino acid bios	0.97	1	0.14005603	169	0.48805845
19526	GO:0043227	membrane-bounded org	0.97	33	4.6218486	2142	6.185924
19530	GO:0043231	intracellular membrane-	0.97	33	4.6218486	2142	6.185924
30306	GO:0071944	cell periphery	0.97	2	0.28011206	259	0.74797124
9285	GO:0016043	cellular component orga	0.97	2	0.28011206	261	0.7537471
13656	GO:0031224	intrinsic to membrane	0.98	16	2.2408965	1193	3.4452884
6663	GO:0009309	amine biosynthetic proc	0.98	1	0.14005603	181	0.5227135
9824	GO:0016773	phosphotransferase act	0.98	21	2.9411764	1493	4.311664
5610	GO:0008026	ATP-dependent helicas	0.98	1	0.14005603	183	0.52848935
28401	GO:0070035	purine NTP-dependent	0.98	1	0.14005603	183	0.52848935
9836	GO:0016787	hydrolase activity	0.98	61	8.543417	3723	10.751725
2657	GO:0003727|GO:00037	single-stranded RNA bi	0.98	1	0.14005603	188	0.54292893
30204	GO:0071840	cellular component orga	0.98	3	0.42016807	362	1.045427
3068	GO:0004386	helicase activity	0.98	1	0.14005603	189	0.54581684
30205	GO:0071841	cellular component orga	0.98	2	0.28011206	285	0.8230572
30206	GO:0071842	cellular component orga	0.98	1	0.14005603	193	0.5573685
9267	GO:0016021	integral to membrane	0.98	14	1.9607843	1103	3.1853757
10244	GO:0018130	heterocycle biosyntheti	0.98	1	0.14005603	199	0.57469606
9911	GO:0016879	ligase activity, forming	0.99	4	0.5602241	456	1.3168914
9889	GO:0016853	isomerase activity	0.99	2	0.28011206	306	0.8837035
9295	GO:0016053	organic acid biosyntheti	0.99	1	0.14005603	211	0.6093511
21922	GO:0046394	carboxylic acid biosynth	0.99	1	0.14005603	211	0.6093511
4612	GO:0006468	protein phosphorylation	0.99	32	4.481793	2205	6.367863
15436	GO:0033036	macromolecule localizat	0.99	3	0.42016807	397	1.1465042
9493	GO:0016310	phosphorylation	0.99	37	5.1820726	2504	7.2313514
9823	GO:0016772	transferase activity, tran	0.99	27	3.7815125	1932	5.579461
28365	GO:0065008	regulation of biological	0.99	2	0.28011206	316	0.9125827
2627	GO:0003676	nucleic acid binding	0.99	36	5.042017	2453	7.0840673
12574	GO:0022892	substrate-specific trans	0.99	19	2.6610644	1463	4.2250266
5019	GO:0006952|GO:00022	defense response	0.99	1	0.14005603	221	0.63823026
20640	GO:0044446	intracellular organelle p	0.99	7	0.98039216	710	2.0504231
20616	GO:0044422	organelle part	0.99	7	0.98039216	712	2.0561988
13531	GO:0031072	heat shock protein bindi	0.99	1	0.14005603	230	0.6642216
4909	GO:0006810|GO:00154	transport	0.99	33	4.6218486	2315	6.6855345
25529	GO:0051234	establishment of localiz	0.99	33	4.6218486	2315	6.6855345
25476	GO:0051179	localization	0.99	33	4.6218486	2319	6.697086
20533	GO:0044283	small molecule biosynth	0.99	2	0.28011206	347	1.0021082
20512	GO:0044262|GO:00060	cellular carbohydrate m	0.99	1	0.14005603	248	0.7162041
20521	GO:0044271	cellular nitrogen compo	1.00	2	0.28011206	367	1.0598665
19533	GO:0043234	protein complex	1.00	8	1.1204482	848	2.448956
20619	GO:0044425	membrane part	1.00	18	2.5210085	1523	4.398302
11522	GO:0019538|GO:00064	protein metabolic proce	1.00	62	8.683474	4134	11.938661
4109	GO:0005840|GO:00332	ribosome	1.00	5	0.70028013	682	1.9695613
19527	GO:0043228	non-membrane-bounde	1.00	8	1.1204482	923	2.66555
19531	GO:0043232	intracellular non-membr	1.00	8	1.1204482	923	2.66555
19525	GO:0043226	organelle	1.00	41	5.7422967	3013	8.701303
19528	GO:0043229	intracellular organelle	1.00	41	5.7422967	3013	8.701303
18912	GO:0042578	phosphoric ester hydrol	1.00	2	0.28011206	444	1.2822365
13041	GO:0030554	adenyl nucleotide bindi	1.00	3	0.42016807	550	1.5883559
14965	GO:0032559	adenyl ribonucleotide bi	1.00	3	0.42016807	550	1.5883559
4609	GO:0006464	protein modification pro	1.00	36	5.042017	2781	8.031305
13018	GO:0030529	ribonucleoprotein compl	1.00	5	0.70028013	741	2.1399486
4897	GO:0006793	phosphorus metabolic p	1.00	38	5.322129	2925	8.4471655
4900	GO:0006796	phosphate metabolic pr	1.00	38	5.322129	2925	8.4471655
9839	GO:0016791|GO:00163	phosphatase activity	1.00	1	0.14005603	383	1.1060733
3884	GO:0005524	ATP binding	1.00	2	0.28011206	524	1.51327
19684	GO:0043412	macromolecule modifica	1.00	36	5.042017	2900	8.374968
9494	GO:0016311	dephosphorylation	1.00	1	0.14005603	425	1.227366
3177	GO:0004518	nuclease activity	1.00	1	0.14005603	427	1.2331418
3863	GO:0005488	binding	1.00	240	33.613445	13903	40.15075
20618	GO:0044424	intracellular part	1.00	50	7.002801	3853	11.127155
20638	GO:0044444	cytoplasmic part	1.00	15	2.1008403	1644	4.7477403
131	GO:0000166	nucleotide binding	1.00	9	1.2605042	1213	3.5030468
9266	GO:0016020	membrane	1.00	46	6.442577	3741	10.803708
15392	GO:0032991	macromolecular comple	1.00	13	1.8207283	1616	4.666878
3945	GO:0005622	intracellular	1.00	62	8.683474	4751	13.720507
4027	GO:0005737	cytoplasm	1.00	18	2.5210085	2001	5.7787275
14959	GO:0032553	ribonucleotide binding	1.00	3	0.42016807	795	2.2958963
14961	GO:0032555	purine ribonucleotide bi	1.00	3	0.42016807	795	2.2958963
10033	GO:0017076	purine nucleotide bindi	1.00	3	0.42016807	797	2.3016722
20517	GO:0044267	cellular protein metaboli	1.00	36	5.042017	3225	9.313541
18000	GO:0035639	purine ribonucleoside tri	1.00	2	0.28011206	769	2.2208104
2626	GO:0003674|GO:00055	molecular_function	1.00	446	62.464985	24394	70.447914
3903	GO:0005575|GO:00083	cellular_component	1.00	119	16.666666	8515	24.590637
2653	GO:0003723	RNA binding	1.00	1	0.14005603	797	2.3016722
3876	GO:0005515|GO:00453	protein binding	1.00	87	12.184874	6933	20.021948
3946	GO:0005623	cell	1.00	108	15.12605	8227	23.758917
20657	GO:0044464	cell part	1.00	108	15.12605	8227	23.758917