Table S5. Differentially regulated genes (up and down regulated) in the control compared with THyPRP silenced plants in FAZ at 12 h along with their expression values, fold changes, annotations, GO ids and terms.

Worksheet 2 & 3

Set4					
Line	Array	Details	Time	Treated vs. Con	Set
Control – New Yorker	254331010026_1_3	12h_7_AZ	12h	Control	Set 4
Control – New Yorker	254331010026_1_4	12h_8_AZ	12h		
TAPG + TPRP	254331010035_1_3	12h_43_AZ	12h	Treated	
TAPG + TPRP	254331010035_1_4	12h_44_AZ	12h		

Note:

Fold change expression values are provided as logbase 2

Flagging Criteria:

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

Detected: If the gProcessedSignal value is above background intensity

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

Cut off used to filter up and down regulated genes

Upregulated

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

Downregulated

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

Differentially Regulated Probes

Sample	Up	Down
4h_TPRP_ AZ vs. 4h_Control_AZ_Sense	1415	1392
4h_TPRP_ AZ vs. 4h_Control_AZ_Antisense	536	872

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.

		12h_AZ_Control					12h_AZ_TAPG + TPRP vs. 12h_AZ_Control					
ProbeNar	Orientatic	Fold 12h	Flag 12h	Fold 12h	Flag 12h	Geomean	Fold 12h	Flag 12h	Fold 12h	Flag 12h	Geomean	P-value
A 96 P00	Sense	0.582	Detected	-0.582	Detected	0.000	0.959	Detected	1.109	Detected	1.034	0.220
A 96 P01	Sense	0.515	Detected	-0.515	Detected	0.000	1.430	Detected	1.692	Detected	1.561	0.099
A 96 P01	Sense	-0.074	Detected	0.074	Detected	0.000	0.958	Detected	1.371	Detected	1.165	0.034
A 96 P01	Sense	0.282	Detected	-0.282	Detected	0.000	1.399	Detected	2.101	Detected	1.750	0.060
A 96 P01	Sense	0.177	Detected	-0.177	Detected	0.000	1.101	Detected	1.779	Detected	1.440	0.064
A 96 P01	Sense	0.873	Detected	-0.873	Detected	0.000	1.144	Detected	1.277	Detected	1.210	0.301
A 96 P01	Sense	0.572	Detected	-0.572	Detected	0.000	0.932	Detected	1.399	Detected	1.166	0.200
A 96 P01	Sense	0.460	Detected	-0.460	Detected	0.000	1.542	Detected	2.015	Detected	1.778	0.075
A 96 P01	Sense	0.379	Detected	-0.379	Detected	0.000	1.376	Detected	1.338	Detected	1.357	0.070
A 96 P01	Sense	2.042	Detected	-2.042	Detected	0.000	2.647	Detected	2.240	Detected	2.444	0.356
A 96 P01	Sense	0.806	Detected	-0.806	Detected	0.000	1.475	Detected	1.303	Detected	1.389	0.229
A 96 P01	Sense	1.208	Detected	-1.208	Detected	0.000	2.935	Detected	1.360	Detected	2.148	0.275
A 96 P01	Sense	0.563	Detected	-0.563	Detected	0.000	1.001	Detected	1.592	Detected	1.297	0.178
A 96 P02	Sense	0.653	Detected	-0.653	Comprom	0.000	0.882	Detected	1.526	Detected	1.204	0.240
A 96 P02	Sense	0.257	Detected	-0.257	Detected	0.000	0.952	Detected	1.164	Detected	1.058	0.063
A 96 P02	Sense	0.444	Detected	-0.444	Detected	0.000	1.524	Detected	1.988	Detected	1.756	0.073
A 96 P02	Sense	-0.418	Comprom	0.418	Comprom	0.000	1.049	Detected	1.401	Detected	1.225	0.114
A 96 P02	Sense	1.388	Detected	-1.388	Comprom	0.000	1.293	Detected	1.433	Detected	1.363	0.430
A 96 P02	Sense	0.732	Detected	-0.732	Detected	0.000	1.226	Detected	1.622	Detected	1.424	0.201
A 96 P03	Sense	1.522	Detected	-1.522	Comprom	0.000	1.909	Detected	2.312	Detected	2.110	0.303
A 96 P03	Sense	-0.243	Comprom	0.243	Comprom	0.000	1.810	Detected	1.881	Detected	1.846	0.017
A 96 P03	Sense	0.382	Detected	-0.382	Detected	0.000	1.036	Detected	1.398	Detected	1.217	0.102
A 96 P03	Sense	0.559	Detected	-0.559	Detected	0.000	1.354	Detected	2.145	Detected	1.750	0.125
A 96 P03	Sense	0.259	Detected	-0.259	Detected	0.000	0.976	Detected	1.266	Detected	1.121	0.063
A 96 P04	Sense	0.239	Detected	-0.239	Detected	0.000	1.229	Detected	1.313	Detected	1.271	0.035
A 96 P04	Sense	0.461	Comprom	-0.461	Comprom	0.000	1.321	Detected	1.516	Detected	1.418	0.095
A 96 P05	Sense	0.608	Detected	-0.608	Detected	0.000	2.446	Detected	1.186	Detected	1.816	0.174
A 96 P05	Sense	0.471	Detected	-0.471	Detected	0.000	1.154	Detected	1.919	Detected	1.537	0.127
A 96 P05	Sense	0.222	Detected	-0.222	Detected	0.000	1.069	Detected	1.105	Detected	1.087	0.039
A 96 P05	Sense	0.586	Detected	-0.586	Detected	0.000	1.194	Detected	1.564	Detected	1.379	0.154
A 96 P06	Sense	0.857	Detected	-0.857	Detected	0.000	1.180	Detected	0.894	Detected	1.037	0.355
A 96 P06	Sense	0.450	Detected	-0.450	Detected	0.000	0.937	Detected	1.215	Detected	1.076	0.150
A 96 P06	Sense	0.728	Detected	-0.728	Detected	0.000	0.952	Detected	1.332	Detected	1.142	0.268
A 96 P06	Sense	0.054	Detected	-0.054	Detected	0.000	1.128	Detected	1.596	Detected	1.362	0.030
A 96 P06	Sense	0.611	Detected	-0.611	Detected	0.000	0.811	Detected	1.832	Detected	1.321	0.239
A 96 P06	Sense	1.275	Detected	-1.275	Detected	0.000	1.172	Detected	2.253	Detected	1.712	0.342
A 96 P07	Sense	1.386	Detected	-1.386	Comprom	0.000	2.598	Detected	2.746	Detected	2.672	0.194
A 96 P07	Sense	0.779	Detected	-0.779	Detected	0.000	1.155	Detected	1.660	Detected	1.407	0.228
A 96 P07	Sense	0.355	Detected	-0.355	Detected	0.000	1.588	Detected	2.260	Detected	1.924	0.059
A 96 P07	Sense	0.858	Detected	-0.858	Detected	0.000	1.660	Detected	1.740	Detected	1.700	0.186
A 96 P07	Sense	1.315	Detected	-1.315	Comprom	0.000	2.124	Detected	1.438	Detected	1.781	0.320
A 96 P08	Sense	0.591	Detected	-0.591	Detected	0.000	0.831	Detected	1.384	Detected	1.108	0.232
A 96 P08	Sense	2.246	Detected	-2.246	Comprom	0.000	2.929	Detected	2.609	Detected	2.769	0.344
A 96 P08	Sense	0.645	Detected	-0.645	Detected	0.000	1.037	Detected	1.349	Detected	1.193	0.214
A 96 P08	Sense	0.434	Detected	-0.434	Detected	0.000	0.963	Detected	1.563	Detected	1.263	0.139
A 96 P08	Sense	0.314	Detected	-0.314	Detected	0.000	1.162	Detected	1.374	Detected	1.268	0.062
A 96 P08	Sense	0.448	Detected	-0.448	Detected	0.000	0.894	Detected	1.618	Detected	1.256	0.161
A 96 P08	Sense	0.188	Detected	-0.188	Detected	0.000	0.848	Detected	1.644	Detected	1.246	0.105
A 96 P08	Sense	1.563	Detected	-1.563	Detected	0.000	1.034	Detected	2.112	Detected	1.573	0.442
A 96 P08	Sense	0.575	Detected	-0.575	Detected	0.000	1.060	Detected	1.893	Detected	1.476	0.173
A 96 P08	Sense	1.208	Detected	-1.208	Detected	0.000	2.043	Detected	1.019	Detected	1.531	0.364
A 96 P08	Sense	0.544	Detected	-0.544	Detected	0.000	0.823	Detected	1.365	Detected	1.094	0.214
A 96 P09	Sense	0.762	Detected	-0.762	Detected	0.000	1.757	Detected	1.866	Detected	1.811	0.141
A 96 P09	Sense	1.024	Detected	-1.024	Detected	0.000	2.080	Detected	2.176	Detected	2.128	0.174
A 96 P09	Sense	0.104	Detected	-0.104	Detected	0.000	0.887	Detected	1.319	Detected	1.103	0.044
A 96 P09	Sense	0.643	Detected	-0.643	Detected	0.000	1.291	Detected	1.520	Detected	1.405	0.165
A 96 P09	Sense	0.314	Detected	-0.314	Detected	0.000	1.086	Detected	1.280	Detected	1.183	0.069
A 96 P09	Sense	0.445	Detected	-0.445	Detected	0.000	1.207	Detected	1.514	Detected	1.360	0.102
A 96 P09	Sense	1.637	Detected	-1.637	Comprom	0.000	1.703	Detected	2.703	Detected	2.203	0.327
A 96 P10	Sense	1.091	Detected	-1.091	Detected	0.000	1.661	Detected	0.876	Detected	1.268	0.388
A 96 P10	Sense	0.218	Detected	-0.218	Detected	0.000	0.885	Detected	1.462	Detected	1.174	0.083
A 96 P11	Sense	0.613	Detected	-0.613	Detected	0.000	1.646	Detected	1.511	Detected	1.579	0.125
A 96 P11	Sense	0.079	Detected	-0.079	Detected	0.000	1.510	Detected	1.530	Detected	1.520	0.003
A 96 P11	Sense	0.038	Comprom	-0.038	Comprom	0.000	1.175	Detected	1.188	Detected	1.182	0.001
A 96 P11	Sense	0.521	Detected	-0.521	Detected	0.000	1.390	Detected	1.414	Detected	1.402	0.115
A 96 P11	Sense	0.213	Detected	-0.213	Detected	0.000	0.913	Detected	1.551	Detected	1.232	0.085
A 96 P11	Sense	0.521	Detected	-0.521	Detected	0.000	0.825	Detected	1.485	Detected	1.155	0.202
A 96 P12	Sense	0.466	Detected	-0.466	Detected	0.000	1.441	Detected	1.707	Detected	1.574	0.083
A 96 P12	Sense	0.648	Detected	-0.648	Detected	0.000	1.118	Detected	1.188	Detected	1.153	0.218
A 96 P12	Sense	0.781	Detected	-0.781	Detected	0.000	1.318	Detected	2.130	Detected	1.724	0.189
A 96 P12	Sense	-0.451	Detected	0.451	Detected	0.000	1.092	Detected	1.514	Detected	1.303	0.120
A 96 P12	Sense	1.003	Detected	-1.003	Detected	0.000	0.963	Detected	1.370	Detected	1.167	0.372
A 96 P12	Sense	0.913	Detected	-0.913	Detected	0.000	0.902	Detected	1.470	Detected	1.186	0.341
A 96 P12	Sense	0.863	Detected	-0.863	Detected	0.000	1.667	Detected	1.585	Detected	1.626	0.200
A 96 P13	Sense	1.068	Detected	-1.068	Detected	0.000	0.860	Detected	1.888	Detected	1.374	0.366
A 96 P13	Sense	0.940	Detected	-0.940	Detected	0.000	1.074	Detected	1.715	Detected	1.394	0.295
A 96 P13	Sense	0.960	Detected	-0.960	Detected	0.000	1.156	Detected	1.699	Detected	1.427	0.289
A 96 P13	Sense	0.664	Detected	-0.664	Detected	0.000	0.971	Detected	1.173	Detected	1.072	0.252
A 96 P13	Sense	0.570	Detected	-0.570	Detected	0.000	1.285	Detected	1.814	Detected	1.550	0.133
A 96 P13	Sense	0.774	Detected	-0.774	Detected	0.000	1.060	Detected	1.624	Detected	1.342	0.245
A 96 P13	Sense	0.364	Detected	-0.364	Detected	0.000	1.025	Detected	1.609	Detected	1.317	0.106
A 96 P13	Sense	0.307	Detected	-0.307	Detected	0.000	1.222	Detected	1.363	Detected	1.293	0.054
A 96 P13	Sense	0.881	Detected	-0.881	Comprom	0.000	1.219	Detected	1.354	Detected	1.286	0.283
A 96 P14	Sense	1.224	Detected	-1.224	Detected	0.000	2.033	Detected	1.033	Detected	1.533	0.366
A 96 P14	Sense	1.055	Detected	-1.055	Detected	0.000	1.934	Detected	2.006	Detected	1.970	0.203
A 96 P14	Sense	1.676	Detected	-1.676	Detected	0.000	1.187	Detected	2.347	Detected	1.767	0.424
A 96 P14	Sense	0.132	Detected	-0.132	Detected	0.000	0.904	Detected	1.457	Detected	1.181	0.061
A 96 P15	Sense	0.692	Detected	-0.692	Detected	0.000	1.038	Detected	1.012	Detected	1.025	0.277
A 96 P15	Sense	0.697	Detected	-0.697	Detected	0.000	0.973	Detected	1.060	Detected	1.016	0.283
A 96 P15	Sense	0.318	Detected	-0.318	Detected	0.000	0.987	Detected	1.228	Detected	1.108	0.083
A 96 P15	Sense	0.814	Detected	-0.814	Detected	0.000	1.631	Detected	1.601	Detected	1.616	0.186
A 96 P15	Sense	0.254	Detected	-0.254	Detected	0.000	1.128	Detected	1.290	Detected	1.209	0.045
A 96 P16	Sense	0.452	Detected	-0.452	Detected	0.000	0.911	Detected	1.437	Detected	1.174	0.154
A 96 P16	Sense	2.419	Detected	-2.419	Detected	0.000	3.301	Detected	2.976	Detected	3.139	0.325
A 96 P16	Sense	0.792	Detected	-0.792	Detected	0.000	0.950	Detected	1.544	Detected	1.247	0.279
A 96 P16	Sense	0.260	Detected	-0.260	Detected	0.000	2.830	Detected	1.214	Detected	2.022	0.140
A 96 P17	Sense	0.961	Detected	-0.961	Detected	0.000	0.961	Detected	1.459	Detected	1.210	0.347
A 96 P17	Sense	0.149	Detected	-0.149	Detected	0.000	1.010	Detected	1.069	Detected	1.040	0.021
A 96 P17	Sense	0.191	Detected	-0.191	Detected	0.000	0.870	Detected	1.200	Detected	1.035	0.055
A 96 P17	Sense	0.654	Detected	-0.654	Detected	0.000	1.145	Detected	1.075	Detected	1.110	0.232
A 96 P17	Sense	1.645	Detected	-1.645	Detected	0.000	1.057	Detected	2.153	Detected	1.605	0.452
A 96 P17	Sense	0.568	Detected	-0.568	Detected	0.000	1.145	Detected	1.136	Detected	1.141	0.183
A 96 P17	Sense	0.231	Detected	-0.231	Detected	0.000	0.880	Detected	1.317	Detected	1.099	0.075
A 96 P17	Sense	0.441	Detected	-0.441	Detected	0.000	1.115	Detected	1.283	Detected	1.199	0.116
A 96 P17	Sense	0.668	Detected	-0.668	Detected	0.000	1.006	Detected	2.370	Detected	1.688	0.219
A 96 P18	Sense	0.317	Detected	-0.317	Detected	0.000	1.036	Detected	1.840	Detected	1.438	0.107
A 96 P18	Sense	0.693	Detected	-0.693	Detected	0.000	1.058	Detected	1.040	Detected	1.049	0.269
A 96 P19	Sense	0.469	Detected	-0.469	Detected	0.000	1.062	Detected	1.381	Detected	1.221	0.133
A 96 P19	Sense	0.532	Detected	-0.532	Detected	0.000	1.481	Detected	2.455	Detected	1.968	0.112
A 96 P19	Sense	0.241	Detected	-0.241	Detected	0.000	0.866	Detected	1.718	Detected	1.292	0.119
A 96 P19	Sense	0.580	Detected	-0.580	Detected	0.000	0.805	Detected	1.305	Detected	1.055	0.237
A 96 P19	Sense	0.496	Detected	-0.496	Detected	0.000	1.082	Detected	1.257	Detected	1.169	0.146
A 96 P19	Sense	-0.280	Comprom	0.280	Detected	0.000	0.900	Detected	1.237	Detected	1.069	0.082
A 96 P19	Sense	-0.020	Detected	0.020	Detected	0.000	0.810	Detected	1.197	Detected	1.003	0.036
A 96 P20	Sense	1.099	Detected	-1.099	Detected	0.000	1.380	Detected	1.351	Detected	1.366	0.340
A 96 P20	Sense	0.145	Detected	-0.145	Detected	0.000	1.349	Detected	1.534	Detected	1.441	0.014
A 96 P20	Sense	0.738	Detected	-0.738	Detected	0.000	1.136	Detected	1.585	Detected	1.360	0.220
A 96 P20	Sense	0.686	Detected	-0.686	Detected	0.000	1.207	Detected	1.745	Detected	1.476	0.183
A 96 P20	Sense	0.196	Detected	-0.196	Comprom	0.000	1.059	Detected	1.667	Detected	1.363	0.064
A 96 P20	Sense	0.166	Detected	-0.166	Detected	0.000	0.879	Detected	1.382	Detected	1.131	0.064
A 96 P20	Sense	0.728	Detected	-0.728	Detected	0.000	0.909	Detected	1.201	Detected	1.055	0.291
A 96 P20	Sense	0.974	Detected	-0.974	Comprom	0.000	1.214	Detected	1.964	Detected	1.589	0.267
A 96 P20	Sense	1.319	Detected	-1.319	Comprom	0.000	0.840	Detected	1.599	Detected	1.220	0.468
A 96 P21	Sense	0.264	Detected	-0.264	Detected	0.000	1.166	Detected	0.925	Detected	1.045	0.069
A 96 P21	Sense	0.454	Detected	-0.454	Detected	0.000	1.205	Detected	1.571	Detected	1.388	0.105
A 96 P21	Sense	1.073	Detected	-1.073	Comprom	0.000	1.420	Detected	1.903	Detected	1.661	0.270
A 96 P21	Sense	0.586	Detected	-0.586	Detected	0.000	1.262	Detected	1.657	Detected	1.459	0.142
A 96 P21	Sense	0.277	Detected	-0.277	Detected	0.000	0.918	Detected	1.783	Detected	1.351	0.119
A 96 P22	Sense	0.267	Detected	-0.267	Detected	0.000	1.129	Detected	1.190	Detected	1.160	0.050
A 96 P22	Sense	0.713	Detected	-0.713	Detected	0.000	0.825	Detected	1.934	Detected	1.379	0.266
A 96 P22	Sense	0.354	Detected	-0.354	Detected	0.000	1.085	Detected	1.337	Detected	1.211	0.084
A 96 P22	Sense	0.306	Detected	-0.306	Detected	0.000	0.928	Detected	1.371	Detected	1.150	0.093
A 96 P22	Sense	0.295	Detected	-0.295	Detected	0.000	1.417	Detected	1.611	Detected	1.514	0.040
A 96 P22	Sense	0.616	Detected	-0.616	Detected	0.000	1.482	Detected	1.902	Detected	1.692	0.121
A 96 P23	Sense	0.730	Detected	-0.730	Detected	0.000	1.385	Detected	1.464	Detected	1.424	0.191
A 96 P23	Sense	0.377	Detected	-0.377	Detected	0.000	1.126	Detected	1.154	Detected	1.140	0.094
A 96 P23	Sense	0.166	Detected	-0.166	Detected	0.000	1.032	Detected	1.509	Detected	1.271	0.048
A 96 P23	Sense	0.366	Detected	-0.366	Detected	0.000	1.570	Detected	2.209	Detected	1.890	0.060
A 96 P23	Sense	1.315	Detected	-1.315	Comprom	0.000	1.764	Detected	2.266	Detected	2.015	0.271
A 96 P23	Sense	0.696	Detected	-0.696	Detected	0.000	1.524	Detected	1.271	Detected	1.398	0.187
A 96 P23	Sense	0.817	Detected	-0.817	Detected	0.000	0.858	Detected	1.595	Detected	1.227	0.304
A 96 P24	Sense	0.577	Detected	-0.577	Detected	0.000	1.049	Detected	1.751	Detected	1.400	0.174
A 96 P24	Sense	0.776	Detected	-0.776	Detected	0.000	1.172	Detected	1.672	Detected	1.422	0.223
A 96 P24	Sense	0.745	Detected	-0.745	Detected	0.000	1.001	Detected	1.259	Detected	1.130	0.274
A 96 P24	Sense	0.530	Detected	-0.530	Detected	0.000	2.174	Detected	1.027	Detected	1.601	0.177
A 96 P24	Sense	0.583	Detected	-0.583	Detected	0.000	1.561	Detected	1.636	Detected	1.598	0.112
A 96 P24	Sense	0.379	Detected	-0.379	Detected	0.000	0.835	Detected	1.669	Detected	1.252	0.156
A 96 P25	Sense	0.251	Detected	-0.251	Detected	0.000	1.189	Detected	1.873	Detected	1.531	0.069
A 96 P25	Sense	0.339	Detected	-0.339	Detected	0.000	1.051	Detected	1.825	Detected	1.438	0.108
A 96 P25	Sense	1.197	Detected	-1.197	Detected	0.000	1.714	Detected	0.826	Detected	1.270	0.425
A 96 P25	Sense	0.168	Detected	-0.168	Detected	0.000	0.895	Detected	1.401	Detected	1.148	0.063
A 96 P25	Sense	0.344	Detected	-0.344	Detected	0.000	1.360	Detected	1.247	Detected	1.303	0.065
A 96 P25	Sense	0.503	Detected	-0.503	Detected	0.000	2.466	Detected	1.203	Detected	1.835	0.151
A 96 P26	Sense	0.493	Detected	-0.493	Detected	0.000	0.843	Detected	2.033	Detected	1.438	0.204
GT Sense	Sense	0.781	Detected	-0.781	Detected	0.000	1.282	Detected	2.540	Detected	1.911	0.197
GT Sense	Sense	-0.981	Comprom	0.981	Detected	0.000	1.177	Detected	0.850	Detected	1.014	0.415
GT Sense	Sense	0.628	Detected	-0.628	Detected	0.000	0.954	Detected	1.476	Detected	1.215	0.216
GT Sense	Sense	0.223	Detected	-0.223	Detected	0.000	1.867	Detected	1.334	Detected	1.601	0.044
GT Sense	Sense	-0.182	Detected	0.182	Detected	0.000	1.200	Detected	1.039	Detected	1.119	0.030
GT Sense	Sense	0.674	Comprom	-0.674	Comprom	0.000	1.427	Detected	1.448	Detected	1.438	0.167
GT Sense	Sense	0.044	Detected	-0.044	Detected	0.000	1.239	Detected	1.343	Detected	1.291	0.003
GT Sense	Sense	0.445	Detected	-0.445	Detected	0.000	0.823	Detected	1.280	Detected	1.052	0.170
GT Sense	Sense	0.609	Detected	-0.609	Detected	0.000	0.819	Detected	1.199	Detected	1.009	0.255
GT Sense	Sense	0.529	Comprom	-0.529	Comprom	0.000	1.421	Detected	1.143	Detected	1.282	0.144
GT Sense	Sense	0.510	Detected	-0.510	Detected	0.000	1.695	Detected	2.096	Detected	1.895	0.074
GT Sense	Sense	0.529	Detected	-0.529	Detected	0.000	1.678	Detected	2.339	Detected	2.009	0.084
GT Sense	Sense	0.145	Detected	-0.145	Detected	0.000	1.076	Detected	1.271	Detected	1.173	0.021
GT Sense	Sense	0.151	Detected	-0.151	Detected	0.000	0.943	Detected	1.167	Detected	1.055	0.030
GT Sense	Sense	0.274	Detected	-0.274	Detected	0.000	1.169	Detected	2.417	Detected	1.793	0.119
GT Sense	Sense	0.123	Detected	-0.123	Detected	0.000	1.324	Detected	1.895	Detected	1.609	0.035
GT Sense	Sense	0.394	Detected	-0.394	Detected	0.000	1.143	Detected	1.242	Detected	1.192	0.095
GT Sense	Sense	0.326	Detected	-0.326	Detected	0.000	1.192	Detected	1.604	Detected	1.398	0.068
GT Sense	Sense	0.178	Comprom	-0.178	Comprom	0.000	1.880	Detected	2.022	Detected	1.951	0.010
GT Sense	Sense	-0.020	Detected	0.020	Detected	0.000	1.383	Detected	1.639	Detected	1.511	0.007
GT Sense	Sense	0.316	Detected	-0.316	Detected	0.000	1.960	Detected	1.366	Detected	1.663	0.062
GT Sense	Sense	0.678	Detected	-0.678	Comprom	0.000	2.160	Detected	2.070	Detected	2.115	0.090
GT Sense	Sense	0.312	Detected	-0.312	Detected	0.000	1.444	Detected	1.718	Detected	1.581	0.044
GT Sense	Sense	0.440	Detected	-0.440	Detected	0.000	1.441	Detected	1.082	Detected	1.261	0.118
GT Sense	Sense	0.144	Detected	-0.144	Detected	0.000	1.253	Detected	1.333	Detected	1.293	0.013
GT Sense	Sense	0.094	Detected	-0.094	Detected	0.000	0.879	Detected	1.743	Detected	1.311	0.097
GT Sense	Sense	0.498	Detected	-0.498	Detected	0.000	0.831	Detected	1.197	Detected	1.014	0.196
GT Sense	Sense	0.970	Detected	-0.970	Comprom	0.000	1.310	Detected	1.316	Detected	1.313	0.308
GT Sense	Sense	0.348	Detected	-0.348	Detected	0.000	0.860	Detected	1.415	Detected	1.138	0.125
GT Sense	Sense	-0.798	Comprom	0.798	Detected	0.000	1.446	Detected	1.962	Detected	1.704	0.179
GT Sense	Sense	0.083	Detected	-0.083	Detected	0.000	0.995	Detected	1.327	Detected	1.161	0.025
GT Sense	Sense	0.952	Detected	-0.952	Detected	0.000	2.174	Detected	1.480	Detected	1.827	0.213
GT Sense	Sense	0.413	Detected	-0.413	Detected	0.000	0.927	Detected	1.248	Detected	1.088	0.134
GT Sense	Sense	0.649	Detected	-0.649	Detected	0.000	1.581	Detected	1.346	Detected	1.464	0.157
GT Sense	Sense	-0.144	Detected	0.144	Detected	0.000	1.693	Detected	1.261	Detected	1.477	0.029
GT Sense	Sense	-1.489	Detected	1.489	Detected	0.000	1.364	Detected	1.683	Detected	1.523	0.416
GT Sense	Sense	0.287	Comprom	-0.287	Comprom	0.000	1.092	Detected	1.281	Detected	1.186	0.059
GT Sense	Sense	0.408	Detected	-0.408	Comprom	0.000	1.482	Detected	1.676	Detected	1.579	0.064
GT Sense	Sense	0.171	Detected	-0.171	Detected	0.000	1.178	Detected	0.979	Detected	1.079	0.032
GT Sense	Sense	0.415	Detected	-0.415	Detected	0.000	0.868	Detected	1.184	Detected	1.026	0.147
GT Sense	Sense	-0.123	Detected	0.123	Detected	0.000	1.028	Detected	1.360	Detected	1.194	0.029
GT Sense	Sense	0.622	Detected	-0.622	Detected	0.000	1.114	Detected	1.079	Detected	1.096	0.220
GT Sense	Sense	0.178	Comprom	-0.178	Comprom	0.000	1.471	Detected	2.855	Detected	2.163	0.094
GT Sense	Sense	0.485	Detected	-0.485	Detected	0.000	1.627	Detected	1.046	Detected	1.337	0.142
GT Sense	Sense	0.027	Detected	-0.027	Detected	0.000	1.325	Detected	1.355	Detected	1.340	0.001
GT Sense	Sense	0.235	Comprom	-0.235	Comprom	0.000	0.974	Detected	1.277	Detected	1.125	0.057
GT Sense	Sense	0.490	Detected	-0.490	Detected	0.000	0.947	Detected	1.110	Detected	1.029	0.174
GT Sense	Sense	0.699	Comprom	-0.699	Comprom	0.000	1.609	Detected	1.566	Detected	1.588	0.151
GT Sense	Sense	0.019	Detected	-0.019	Detected	0.000	1.026	Detected	1.814	Detected	1.420	0.069
GT Sense	Sense	0.812	Detected	-0.812	Comprom	0.000	1.167	Detected	1.301	Detected	1.234	0.269
GT Sense	Sense	0.831	Detected	-0.831	Detected	0.000	1.275	Detected	1.209	Detected	1.242	0.274
GT Sense	Sense	1.552	Detected	-1.552	Detected	0.000	2.750	Detected	1.105	Detected	1.927	0.387
GT Sense	Sense	-0.111	Detected	0.111	Detected	0.000	1.212	Detected	1.873	Detected	1.543	0.048
GT Sense	Sense	0.532	Detected	-0.532	Detected	0.000	1.471	Detected	1.207	Detected	1.339	0.135
GT Sense	Sense	0.652	Detected	-0.652	Detected	0.000	1.038	Detected	1.481	Detected	1.260	0.209
GT Sense	Sense	0.237	Detected	-0.237	Detected	0.000	0.980	Detected	1.726	Detected	1.353	0.092
GT Sense	Sense	0.094	Detected	-0.094	Comprom	0.000	1.445	Detected	1.754	Detected	1.600	0.013
GT Sense	Sense	0.836	Detected	-0.836	Detected	0.000	0.926	Detected	1.124	Detected	1.025	0.347
GT Sense	Sense	-0.322	Comprom	0.322	Comprom	0.000	1.452	Detected	1.726	Detected	1.589	0.045
GT Sense	Sense	0.286	Detected	-0.286	Detected	0.000	0.863	Detected	1.208	Detected	1.036	0.090
GT Sense	Sense	0.571	Detected	-0.571	Detected	0.000	1.331	Detected	1.474	Detected	1.402	0.135
GT Sense	Sense	0.595	Detected	-0.595	Detected	0.000	1.579	Detected	1.684	Detected	1.632	0.112
GT Sense	Sense	0.431	Detected	-0.431	Detected	0.000	1.106	Detected	1.158	Detected	1.132	0.120
GT Sense	Sense	-0.132	Comprom	0.132	Comprom	0.000	2.885	Detected	2.623	Detected	2.754	0.005
GT Sense	Sense	0.589	Detected	-0.589	Comprom	0.000	2.064	Detected	1.513	Detected	1.788	0.111
GT Sense	Sense	0.033	Detected	-0.033	Detected	0.000	1.010	Detected	1.365	Detected	1.188	0.022
GT Sense	Sense	0.494	Comprom	-0.494	Comprom	0.000	1.873	Detected	1.876	Detected	1.874	0.063
GT Sense	Sense	-0.238	Detected	0.238	Detected	0.000	1.728	Detected	2.449	Detected	2.088	0.040
GT Sense	Sense	0.370	Detected	-0.370	Detected	0.000	1.283	Detected	1.701	Detected	1.492	0.072
GT Sense	Sense	1.547	Detected	-1.547	Comprom	0.000	1.743	Detected	1.273	Detected	1.508	0.437
GT Sense	Sense	0.491	Detected	-0.491	Detected	0.000	0.962	Detected	1.531	Detected	1.247	0.159
GT Sense	Sense	-0.161	Detected	0.161	Detected	0.000	1.269	Detected	0.884	Detected	1.076	0.050
GT Sense	Sense	1.403	Detected	-1.403	Detected	0.000	2.272	Detected	3.483	Detected	2.877	0.200
GT Sense	Sense	0.248	Detected	-0.248	Detected	0.000	0.951	Detected	1.880	Detected	1.415	0.115
GT Sense	Sense	0.376	Detected	-0.376	Detected	0.000	1.729	Detected	2.099	Detected	1.914	0.045
GT Sense	Sense	0.332	Detected	-0.332	Detected	0.000	0.992	Detected	1.323	Detected	1.158	0.089
GT Sense	Sense	0.932	Detected	-0.932	Comprom	0.000	2.377	Detected	2.007	Detected	2.192	0.147
GT Sense	Sense	-0.686	Comprom	0.686	Detected	0.000	0.973	Detected	1.867	Detected	1.420	0.225
GT Sense	Sense	0.514	Detected	-0.514	Detected	0.000	1.398	Detected	1.065	Detected	1.232	0.150
GT Sense	Sense	0.494	Detected	-0.494	Detected	0.000	1.242	Detected	1.380	Detected	1.311	0.119
GT Sense	Sense	0.060	Detected	-0.060	Detected	0.000	1.788	Detected	2.160	Detected	1.974	0.010
GT Sense	Sense	-0.076	Detected	0.076	Detected	0.000	1.055	Detected	1.298	Detected	1.177	0.015
GT Sense	Sense	-0.120	Detected	0.120	Detected	0.000	0.942	Detected	1.087	Detected	1.014	0.018
GT Sense	Sense	0.477	Detected	-0.477	Detected	0.000	1.274	Detected	1.122	Detected	1.198	0.131
GT Sense	Sense	1.750	Detected	-1.750	Detected	0.000	2.320	Detected	1.401	Detected	1.860	0.412
GT Sense	Sense	-0.092	Detected	0.092	Detected	0.000	1.076	Detected	0.927	Detected	1.001	0.014
GT Sense	Sense	0.977	Detected	-0.977	Comprom	0.000	1.220	Detected	1.194	Detected	1.207	0.342
GT Sense	Sense	0.495	Detected	-0.495	Detected	0.000	0.811	Detected	1.479	Detected	1.145	0.195

GT	Sense	Sense	0.069	Comprom	-0.069	Comprom	0.000	0.897	Detected	1.271	Detected	1.084	0.032	GT	Sens
GT	Sense	Sense	1.393	Detected	-1.393	Detected	0.000	2.077	Detected	2.252	Detected	2.164	0.261	GT	Sens
GT	Sense	Sense	0.567	Detected	-0.567	Detected	0.000	1.400	Detected	1.144	Detected	1.272	0.160	GT	Sens
GT	Sense	Sense	0.348	Detected	-0.348	Detected	0.000	0.844	Detected	1.311	Detected	1.078	0.124	GT	Sens
GT	Sense	Sense	1.495	Detected	-1.495	Comprom	0.000	1.712	Detected	2.388	Detected	2.050	0.313	GT	Sens
GT	Sense	Sense	1.160	Detected	-1.160	Detected	0.000	1.879	Detected	1.762	Detected	1.821	0.258	GT	Sens
GT	Sense	Sense	0.373	Detected	-0.373	Detected	0.000	1.045	Detected	1.950	Detected	1.497	0.125	GT	Sens
GT	Sense	Sense	0.359	Detected	-0.359	Detected	0.000	1.441	Detected	1.437	Detected	1.439	0.057	GT	Sens
GT	Sense	Sense	0.495	Detected	-0.495	Detected	0.000	0.920	Detected	1.262	Detected	1.091	0.173	GT	Sens
GT	Sense	Sense	0.575	Detected	-0.575	Detected	0.000	1.318	Detected	1.097	Detected	1.207	0.175	GT	Sens
GT	Sense	Sense	0.201	Detected	-0.201	Detected	0.000	0.822	Detected	1.291	Detected	1.057	0.076	GT	Sens
GT	Sense	Sense	-0.149	Comprom	0.149	Comprom	0.000	2.167	Detected	2.284	Detected	2.226	0.005	GT	Sens
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	1.053	Detected	1.177	Detected	1.115	0.017	GT	Sens
GT	Sense	Sense	0.204	Detected	-0.204	Detected	0.000	1.191	Detected	1.262	Detected	1.227	0.027	GT	Sens
GT	Sense	Sense	0.259	Detected	-0.259	Detected	0.000	1.064	Detected	0.970	Detected	1.017	0.061	GT	Sens
GT	Sense	Sense	0.658	Detected	-0.658	Detected	0.000	1.463	Detected	1.821	Detected	1.642	0.138	GT	Sens
GT	Sense	Sense	0.056	Comprom	-0.056	Comprom	0.000	1.419	Detected	1.087	Detected	1.253	0.019	GT	Sens
GT	Sense	Sense	0.882	Detected	-0.882	Detected	0.000	1.083	Detected	1.353	Detected	1.218	0.305	GT	Sens
GT	Sense	Sense	0.159	Detected	-0.159	Detected	0.000	0.970	Detected	1.272	Detected	1.121	0.036	GT	Sens
GT	Sense	Sense	0.503	Detected	-0.503	Detected	0.000	1.379	Detected	1.410	Detected	1.394	0.109	GT	Sens
GT	Sense	Sense	1.139	Detected	-1.139	Detected	0.000	1.361	Detected	1.739	Detected	1.550	0.311	GT	Sens
GT	Sense	Sense	1.024	Detected	-1.024	Detected	0.000	0.884	Detected	1.239	Detected	1.062	0.414	GT	Sens
GT	Sense	Sense	0.646	Detected	-0.646	Detected	0.000	1.801	Detected	2.052	Detected	1.926	0.100	GT	Sens
GT	Sense	Sense	0.975	Detected	-0.975	Detected	0.000	1.659	Detected	1.044	Detected	1.351	0.317	GT	Sens
GT	Sense	Sense	-0.522	Comprom	0.522	Comprom	0.000	1.924	Detected	1.705	Detected	1.815	0.077	GT	Sens
GT	Sense	Sense	0.237	Detected	-0.237	Detected	0.000	0.842	Detected	1.179	Detected	1.010	0.074	GT	Sens
GT	Sense	Sense	0.885	Detected	-0.885	Detected	0.000	1.873	Detected	1.984	Detected	1.928	0.162	GT	Sens
GT	Sense	Sense	0.378	Detected	-0.378	Detected	0.000	0.802	Detected	1.263	Detected	1.033	0.145	GT	Sens
GT	Sense	Sense	0.357	Comprom	-0.357	Comprom	0.000	1.920	Detected	1.109	Detected	1.514	0.107	GT	Sens
GT	Sense	Sense	1.015	Detected	-1.015	Detected	0.000	2.219	Detected	1.777	Detected	1.998	0.194	GT	Sens
GT	Sense	Sense	1.191	Detected	-1.191	Comprom	0.000	1.725	Detected	1.575	Detected	1.650	0.301	GT	Sens
GT	Sense	Sense	0.548	Detected	-0.548	Detected	0.000	1.053	Detected	1.120	Detected	1.087	0.186	GT	Sens
GT	Sense	Sense	0.332	Comprom	-0.332	Comprom	0.000	4.117	Detected	4.020	Detected	4.069	0.007	GT	Sens
GT	Sense	Sense	0.245	Detected	-0.245	Detected	0.000	1.504	Detected	1.659	Detected	1.581	0.025	GT	Sens
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	1.835	Detected	1.285	Detected	1.560	0.032	GT	Sens
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	0.803	Detected	1.250	Detected	1.026	0.051	GT	Sens
GT	Sense	Sense	0.742	Detected	-0.742	Detected	0.000	1.490	Detected	0.976	Detected	1.233	0.257	GT	Sens
GT	Sense	Sense	0.433	Detected	-0.433	Detected	0.000	1.099	Detected	1.423	Detected	1.261	0.112	GT	Sens
GT	Sense	Sense	0.109	Detected	-0.109	Detected	0.000	1.127	Detected	1.320	Detected	1.223	0.014	GT	Sens
GT	Sense	Sense	-0.029	Detected	0.029	Detected	0.000	1.085	Detected	2.054	Detected	1.569	0.084	GT	Sens
GT	Sense	Sense	0.114	Comprom	-0.114	Comprom	0.000	1.544	Detected	1.706	Detected	1.625	0.007	GT	Sens
GT	Sense	Sense	0.380	Detected	-0.380	Detected	0.000	0.869	Detected	1.212	Detected	1.040	0.130	GT	Sens
GT	Sense	Sense	1.343	Detected	-1.343	Comprom	0.000	2.580	Detected	2.670	Detected	2.625	0.190	GT	Sens
GT	Sense	Sense	-0.628	Detected	0.628	Detected	0.000	2.217	Detected	2.180	Detected	2.198	0.073	GT	Sens
GT	Sense	Sense	0.343	Detected	-0.343	Detected	0.000	1.333	Detected	1.492	Detected	1.413	0.057	GT	Sens
GT	Sense	Sense	-0.925	Comprom	0.925	Comprom	0.000	1.792	Detected	2.465	Detected	2.129	0.163	GT	Sens
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	0.986	Detected	1.098	Detected	1.042	0.003	GT	Sens
GT	Sense	Sense	0.542	Detected	-0.542	Detected	0.000	1.131	Detected	1.212	Detected	1.172	0.164	GT	Sens
GT	Sense	Sense	0.777	Detected	-0.777	Detected	0.000	0.846	Detected	2.081	Detected	1.463	0.278	GT	Sens
GT	Sense	Sense	-0.044	Detected	0.044	Detected	0.000	1.061	Detected	0.946	Detected	1.004	0.005	GT	Sens
GT	Sense	Sense	0.457	Detected	-0.457	Detected	0.000	1.187	Detected	1.081	Detected	1.134	0.133	GT	Sens
GT	Sense	Sense	0.352	Detected	-0.352	Detected	0.000	1.498	Detected	1.598	Detected	1.548	0.049	GT	Sens
GT	Sense	Sense	0.329	Detected	-0.329	Detected	0.000	1.073	Detected	1.134	Detected	1.104	0.079	GT	Sens
GT	Sense	Sense	0.949	Detected	-0.949	Detected	0.000	2.021	Detected	0.809	Detected	1.415	0.336	GT	Sens
GT	Sense	Sense	0.180	Detected	-0.180	Detected	0.000	1.020	Detected	1.632	Detected	1.326	0.065	GT	Sens
GT	Sense	Sense	0.129	Detected	-0.129	Detected	0.000	0.956	Detected	1.085	Detected	1.021	0.019	GT	Sens
GT	Sense	Sense	0.556	Detected	-0.556	Detected	0.000	1.211	Detected	1.096	Detected	1.153	0.175	GT	Sens
GT	Sense	Sense	-0.583	Detected	0.583	Detected	0.000	1.598	Detected	1.304	Detected	1.451	0.137	GT	Sens
GT	Sense	Sense	0.302	Detected	-0.302	Detected	0.000	1.120	Detected	1.191	Detected	1.155	0.063	GT	Sens
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	0.831	Detected	1.581	Detected	1.206	0.093	GT	Sens
GT	Sense	Sense	0.479	Detected	-0.479	Detected	0.000	1.119	Detected	0.955	Detected	1.037	0.166	GT	Sens
GT	Sense	Sense	0.745	Detected	-0.745	Detected	0.000	1.222	Detected	1.785	Detected	1.503	0.200	GT	Sens
GT	Sense	Sense	0.853	Detected	-0.853	Detected	0.000	1.752	Detected	1.844	Detected	1.798	0.170	GT	Sens
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	0.884	Detected	1.275	Detected	1.080	0.041	GT	Sens
GT	Sense	Sense	0.221	Detected	-0.221	Detected	0.000	1.191	Detected	1.082	Detected	1.136	0.038	GT	Sens
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	0.914	Detected	1.863	Detected	1.389	0.100	GT	Sens
GT	Sense	Sense	-0.092	Detected	0.092	Detected	0.000	1.236	Detected	1.248	Detected	1.242	0.005	GT	Sens
GT	Sense	Sense	0.367	Detected	-0.367	Detected	0.000	1.317	Detected	1.429	Detected	1.373	0.066	GT	Sens
GT	Sense	Sense	-0.023	Detected	0.023	Detected	0.000	0.886	Detected	1.166	Detected	1.026	0.019	GT	Sens
GT	Sense	Sense	0.296	Comprom	-0.296	Comprom	0.000	3.048	Detected	2.120	Detected	2.584	0.042	GT	Sens
GT	Sense	Sense	0.155	Detected	-0.155	Detected	0.000	1.067	Detected	1.574	Detected	1.321	0.047	GT	Sens
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	1.415	Detected	1.636	Detected	1.526	0.037	GT	Sens
GT	Sense	Sense	0.310	Detected	-0.310	Detected	0.000	1.042	Detected	1.407	Detected	1.225	0.077	GT	Sens
GT	Sense	Sense	0.601	Detected	-0.601	Detected	0.000	1.289	Detected	1.446	Detected	1.368	0.153	GT	Sens
GT	Sense	Sense	0.178	Detected	-0.178	Detected	0.000	0.875	Detected	1.479	Detected	1.177	0.078	GT	Sens
GT	Sense	Sense	1.245	Detected	-1.245	Detected	0.000	1.759	Detected	3.923	Detected	2.841	0.227	GT	Sens
GT	Sense	Sense	0.150	Detected	-0.150	Detected	0.000	1.294	Detected	1.559	Detected	1.427	0.019	GT	Sens
GT	Sense	Sense	0.512	Detected	-0.512	Detected	0.000	1.014	Detected	1.128	Detected	1.071	0.173	GT	Sens
GT	Sense	Sense	0.303	Detected	-0.303	Detected	0.000	1.492	Detected	1.514	Detected	1.503	0.038	GT	Sens
GT	Sense	Sense	0.323	Detected	-0.323	Detected	0.000	1.077	Detected	1.207	Detected	1.142	0.074	GT	Sens
GT	Sense	Sense	0.621	Detected	-0.621	Detected	0.000	0.998	Detected	1.097	Detected	1.047	0.235	GT	Sens
GT	Sense	Sense	0.617	Detected	-0.617	Detected	0.000	1.045	Detected	1.231	Detected	1.138	0.210	GT	Sens
GT	Sense	Sense	0.222	Detected	-0.222	Detected	0.000	1.031	Detected	1.179	Detected	1.105	0.042	GT	Sens
GT	Sense	Sense	-0.298	Comprom	0.298	Comprom	0.000	1.220	Detected	1.906	Detected	1.563	0.075	GT	Sens
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	1.570	Detected	2.308	Detected	1.939	0.034	GT	Sens
GT	Sense	Sense	0.445	Detected	-0.445	Detected	0.000	1.122	Detected	1.257	Detected	1.189	0.118	GT	Sens
GT	Sense	Sense	0.954	Detected	-0.954	Comprom	0.000	2.124	Detected	1.198	Detected	1.661	0.258	GT	Sens
GT	Sense	Sense	-1.118	Comprom	1.118	Detected	0.000	1.135	Detected	1.216	Detected	1.175	0.404	GT	Sens
GT	Sense	Sense	0.399	Comprom	-0.399	Comprom	0.000	1.329	Detected	1.706	Detected	1.517	0.075	GT	Sens
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	0.819	Detected	1.188	Detected	1.004	0.046	GT	Sens
GT	Sense	Sense	0.216	Detected	-0.216	Detected	0.000	1.176	Detected	1.361	Detected	1.268	0.033	GT	Sens
GT	Sense	Sense	0.017	Detected	-0.017	Detected	0.000	1.692	Detected	1.843	Detected	1.767	0.002	GT	Sens
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	1.061	Detected	1.087	Detected	1.074	0.018	GT	Sens
GT	Sense	Sense	0.874	Detected	-0.874	Detected	0.000	1.602	Detected	1.720	Detected	1.661	0.198	GT	Sens
GT	Sense	Sense	0.232	Detected	-0.232	Detected	0.000	1.161	Detected	1.267	Detected	1.214	0.036	GT	Sens
GT	Sense	Sense	0.075	Detected	-0.075	Detected	0.000	1.326	Detected	1.930	Detected	1.628	0.035	GT	Sens
GT	Sense	Sense	0.640	Detected	-0.640	Detected	0.000	1.687	Detected	2.065	Detected	1.876	0.107	GT	Sens
GT	Sense	Sense	1.104	Detected	-1.104	Comprom	0.000	1.602	Detected	1.006	Detected	1.304	0.372	GT	Sens
GT	Sense	Sense	1.233	Detected	-1.233	Detected	0.000	1.902	Detected	2.509	Detected	2.206	0.225	GT	Sens
GT	Sense	Sense	0.664	Detected	-0.664	Detected	0.000	0.921	Detected	1.233	Detected	1.077	0.255	GT	Sens
GT	Sense	Sense	0.325	Detected	-0.325	Detected	0.000	1.170	Detected	1.451	Detected	1.311	0.066	GT	Sens
GT	Sense	Sense	0.521	Detected	-0.521	Detected	0.000	0.927	Detected	1.207	Detected	1.067	0.186	GT	Sens
GT	Sense	Sense	0.523	Detected	-0.523	Detected	0.000	0.907	Detected	1.134	Detected	1.021	0.197	GT	Sens
GT	Sense	Sense	0.202	Detected	-0.202	Detected	0.000	1.509	Detected	1.789	Detected	1.649	0.022	GT	Sens
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	1.082	Detected	0.930	Detected	1.006	0.010	GT	Sens
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	0.930	Detected	1.585	Detected	1.258	0.063	GT	Sens
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	1.101	Detected	1.159	Detected	1.130	0.001	GT	Sens
GT	Sense	Sense	0.803	Detected	-0.803	Detected	0.000	1.730	Detected	1.931	Detected	1.830	0.152	GT	Sens
GT	Sense	Sense	0.475	Detected	-0.475	Detected	0.000	0.859	Detected	1.341	Detected	1.100	0.175	GT	Sens
GT	Sense	Sense	0.414	Detected	-0.414	Detected	0.000	0.854	Detected	1.248	Detected	1.051	0.149	GT	Sens
GT	Sense	Sense	0.944	Detected	-0.944	Detected	0.000	1.639	Detected	1.371	Detected	1.505	0.255	GT	Sens
GT	Sense	Sense	0.386	Detected	-0.386	Detected	0.000	1.042	Detected	1.667	Detected	1.355	0.112	GT	Sens
GT	Sense	Sense	0.411	Detected	-0.411	Detected	0.000	1.302	Detected	1.762	Detected	1.532	0.083	GT	Sens
GT	Sense	Sense	0.687	Detected	-0.687	Detected	0.000	1.098	Detected	1.502	Detected	1.300	0.211	GT	Sens
GT	Sense	Sense	0.168	Detected	-0.168	Detected	0.000	2.420	Detected	2.766	Detected	2.593	0.009	GT	Sens
GT	Sense	Sense	0.385	Detected	-0.385	Detected	0.000	1.160	Detected	1.015	Detected	1.088	0.109	GT	Sens
GT	Sense	Sense	0.490	Detected	-0.490	Detected	0.000	0.884	Detected	1.253	Detected	1.068	0.178	GT	Sens
GT	Sense	Sense	0.561	Detected	-0.561	Comprom	0.000	1.101	Detected	0.900	Detected	1.001	0.221	GT	Sens
GT	Sense	Sense	0.435	Detected	-0.435	Detected	0.000	1.020	Detected	1.467	Detected	1.244	0.126	GT	Sens
GT	Sense	Sense	1.113	Detected	-1.113	Detected	0.000	0.838	Detected	1.277	Detected	1.057	0.450	GT	Sens
GT	Sense	Sense	0.581	Detected	-0.581	Detected	0.000	1.798	Detected	1.574	Detected	1.686	0.104	GT	Sens
GT	Sense	Sense	-0.158	Detected	0.158	Detected	0.000	1.083	Detected	1.388	Detected	1.236	0.030	GT	Sens
GT	Sense	Sense	0.601	Detected	-0.601	Detected	0.000	0.929	Detected	1.110	Detected	1.019	0.235	GT	Sens
GT	Sense	Sense	0.321	Detected	-0.321	Detected	0.000	1.341	Detected	1.383	Detected	1.362	0.051	GT	Sens
GT	Sense	Sense	-0.282	Comprom	0.282	Comprom	0.000	1.312	Detected	1.117	Detected	1.214	0.055	GT	Sens
GT	Sense	Sense	1.011	Detected	-1.011	Detected	0.000	2.445	Detected	1.212	Detected	1.829	0.263	GT	Sens
GT	Sense	Sense	0.667	Detected	-0.667	Detected	0.000	1.862	Detected	1.891	Detected	1.877	0.107	GT	Sens
GT	Sense	Sense	1.114	Detected	-1.114	Comprom	0.000	1.553	Detected	1.171	Detected	1.362	0.351	GT	Sens
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	2.932	Detected	0.820	Detected	1.876	0.220	GT	Sens
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	1.782	Detected	2.379	Detected	2.080	0.024	GT	Sens
GT	Sense	Sense	0.720	Detected	-0.720	Detected	0.000	1.180	Detected	2.080	Detected	1.630	0.195	GT	Sens
GT	Sense	Sense	1.025	Detected	-1.025	Detected	0.000	1.046	Detected	1.557	Detected	1.302	0.343	GT	Sens
GT	Sense	Sense	0.408	Detected	-0.408	Detected	0.000	0.908	Detected	1.216	Detected	1.062	0.135	GT	Sens
GT	Sense	Sense	0.264	Comprom	-0.264	Comprom	0.000	2.406	Detected	1.983	Detected	2.194	0.023	GT	Sens
GT	Sense	Sense	0.030	Detected	-0.030	Detected	0.000	1.201	Detected	0.840	Detected	1.020	0.031	GT	Sens
GT	Sense	Sense	1.536	Detected	-1.536	Comprom	0.000	2.321	Detected	4.408	Detected	3.365	0.212	GT	Sens
GT	Sense	Sense	0.234	Detected	-0.234	Detected	0.000	0.969	Detected	1.269	Detected	1.119	0.057	GT	Sens
GT	Sense	Sense	0.451	Detected	-0.451	Detected	0.000	0.944	Detected	1.872	Detected	1.408	0.162	GT	Sens
GT	Sense	Sense	0.278	Detected	-0.278	Detected	0.000	1.322	Detected	1.465	Detected	1.393	0.040	GT	Sens
GT	Sense	Sense	0.057	Detected	-0.057	Detected	0.000	1.267	Detected	1.336	Detected	1.301	0.003	GT	Sens
GT	Sense	Sense	0.905	Detected	-0.905	Detected	0.000	1.433	Detected	1.949	Detected	1.691	0.214	GT	Sens
GT	Sense	Sense	0.446	Detected	-0.446	Detected	0.000	0.886	Detected	1.269	Detected	1.077	0.157	GT	Sens
GT	Sense	Sense	0.918	Detected	-0.918	Detected	0.000	0.841	Detected	1.423	Detected	1.132	0.361	GT	Sens
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	1.118	Detected	1.029	Detected	1.074	0.017	GT	Sens
GT	Sense	Sense	0.130	Detected	-0.130	Detected	0.000	1.448	Detected	1.637	Detected	1.543	0.011	GT	Sens
GT	Sense	Sense	0.021	Comprom	-0.021	Comprom	0.000	1.065	Detected	1.507	Detected	1.286	0.029	GT	Sens
GT	Sense	Sense	0.476	Comprom	-0.476	Comprom	0.000	1.003	Detected	1.230	Detected	1.116	0.150	GT	Sens
GT	Sense	Sense	0.885	Detected	-0.885	Detected	0.000	1.026	Detected	2.145	Detected	1.586	0.269	GT	Sens
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	1.123	Detected	0.982	Detected	1.052	0.014	GT	Sens
GT	Sense	Sense	-0.787	Comprom	0.787	Detected	0.000	1.681	Detected	1.083	Detected	1.382	0.242	GT	Sens
GT	Sense	Sense	-0.946	Comprom	0.946	Comprom	0.000	1.573	Detected	1.328	Detected	1.451	0.268	GT	Sens
GT	Sense	Sense	0.319	Detected	-0.319	Detected	0.000	1.046	Detected	1.791	Detected	1.419	0.102	GT	Sens
GT	Sense	Sense	2.106	Detected	-2.106	Comprom	0.000	1.846	Detected	1.057	Detected	1.451	0.568	GT	Sens
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	1.359	Detected	1.254	Detected	1.306	0.003	GT	Sens
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	1.139	Detected	1.265	Detected	1.202	0.023	GT	Sens
GT	Sense	Sense	0.673	Detected	-0.673	Detected	0.000	1.252	Detected	1.190	Detected	1.221	0.211	GT	Sens
GT	Sense	Sense	0.372	Comprom	-0.372	Comprom	0.000	2.827	Detected	3.910	Detected	3.368	0.036	GT	Sens
GT	Sense	Sense	0.493	Detected	-0.493	Detected	0.000	1.119	Detected	1.121	Detected	1.120	0.151	GT	Sens
GT	Sense	Sense	-0.627	Comprom	0.627	Comprom	0.000	3.167	Detected	1.979	Detected	2.573	0.097	GT	Sens
GT	Sense	Sense	0.493	Comprom	-0.493	Comprom	0.000	1.309	Detected	1.289	Detected	1.299	0.119	GT	Sens
GT	Sense	Sense	0.825	Detected	-0.825	Detected	0.000	1.172	Detected	2.161	Detected	1.667	0.225	GT	Sens
GT	Sense	Sense	0.400	Detected	-0.400	Detected	0.000	0.961	Detected	1.183	Detected	1.072	0.123	GT	Sens
GT	Sense	Sense	1.366	Detected	-1.366	Comprom	0.000	1.108	Detected	1.811	Detected	1.460	0.410	GT	Sens
GT	Sense	Sense	0.204	Detected	-0.204	Comprom	0.000	1.902	Detected	1.193	Detected	1.548	0.063	GT	Sens
GT	Sense	Sense	1.028	Detected	-1.028	Detected	0.000	2.611	Detected	1.675	Detected	2.143	0.198	GT	Sens
GT	Sense	Sense	0.239	Detected	-0.239	Detected	0.000	1.482	Detected	1.448	Detected	1.465	0.026	GT	Sens
GT	Sense	Sense	-0.258	Comprom	0.258	Comprom	0.000	1.627	Detected	2.259	Detected	1.943	0.041	GT	Sens
GT	Sense	Sense	0.893	Detected	-0.893	Detected	0.000	1.734	Detected	2.267	Detected	2.000	0.165	GT	Sens
GT	Sense	Sense	0.556	Detected	-0.556	Detected	0.000	1.224	Detected	1.263	Detected	1.244	0.155	GT	Sens
GT	Sense	Sense	0.572	Detected	-0.572	Detected	0.000	1.095	Detected	1.054	Detected	1.075	0.201	GT	Sens
GT	Sense	Sense	0.213	Detected	-0.213	Detected	0.000	1.185	Detected	1.399	Detected	1.292	0.033	GT	Sens
GT	Sense	Sense	0.506	Detected	-0.506	Detected	0.000	1.251	Detected	2.346	Detected	1.798	0.137	GT	Sens
GT	Sense	Sense	0.245	Detected	-0.245	Detected	0.000	1.185	Detected	1.123	Detected	1.154	0.043	GT	Sens
GT	Sense	Sense	1.245	Detected	-1.245	Detected	0.000	1.474	Detected	3.407	Detected	2.440	0.262	GT	Sens
GT	Sense	Sense	0.535	Detected	-0.535	Detected	0.000	0.994	Detected	1.515	Detected	1.254	0.169	GT	Sens
GT	Sense	Sense	0.360	Detected	-0.360	Detected	0.000	0.979	Detected	1.406	Detected	1.192	0.104	GT	Sens
GT	Sense	Sense	0.340	Detected	-0.340	Detected	0.000	1.391	Detected	1.322	Detected	1.357	0.058	GT	Sens
GT	Sense	Sense	0.654	Detected	-0.654	Detected	0.000	1.076	Detected	0.956	Detected	1.016	0.262	GT	Sens
GT	Sense	Sense	1.269	Detected	-1.269	Comprom	0.000	3.744	Detected	2.908	Detected	3.326	0.130	GT	Sens
GT	Sense	Sense	0.283	Detected	-0.283	Detected	0.000	0.882	Detected	1.284	Detected	1.083	0.089	GT	Sens
GT	Sense	Sense	0.362	Detected	-0.362	Detected	0.000	0.871	Detected	1.537	Detected	1.204	0.134	GT	Sens
GT	Sense	Sense	0.777	Detected	-0.777	Detected	0.000	2.380	Detected	1.572	Detected	1.976	0.153	GT	Sens
GT	Sense	Sense	-0.070	Detected	0.070	Detected	0.000	1.073	Detected	1.438	Detected	1.255	0.023	GT	Sens
GT	Sense	Sense	0.191	Detected	-0.191	Detected	0.000	1.537	Detected	1.374	Detected	1.455	0.020	GT	Sens
GT	Sense	Sense	1.135	Detected	-1.135	Comprom	0.000	1.450	Detected	2.243	Detected	1.846	0.264	GT	Sens
GT	Sense	Sense	0.147	Detected	-0.147	Detected	0.000	0.847	Detected	1.279	Detected	1.063	0.055	GT	Sens
GT	Sense	Sense	0.294	Detected	-0.294	Detected	0.000	1.214	Detected	1.607	Detected	1.411	0.057	GT	Sens
GT	Sense	Sense	0.380	Comprom	-0.380	Comprom	0.000	1.851	Detected	2.001	Detected	1.926	0.038	GT	Sens
GT	Sense	Sense	0.425	Detected	-0.425	Detected	0.000	0.860	Detected	1.279	Detected	1.069	0.153	GT	Sens
GT	Sense	Sense	0.472	Detected	-0.472	Detected	0.000	1.077	Detected	1.179	Detected	1.128	0.141	GT	Sens
GT	Sense	Sense	0.301	Detected	-0.301	Detected	0.000	1.056	Detected	1.117	Detected	1.087	0.070	GT	Sens
GT	Sense	Sense	0.320	Detected	-0.320	Detected	0.000	0.834	Detected	1.598	Detected	1.216	0.135	GT	Sens
GT	Sense	Sense	0.578	Comprom	-0.578	Comprom	0.000	1.710	Detected	1.534	Detected	1.622	0.109	GT	Sens
GT	Sense	Sense	0.057	Detected	-0.057	Detected	0.000	1.117	Detected	1.404	Detected	1.260	0.015	GT	Sens
GT	Sense	Sense	0.357	Detected	-0.357	Detected	0.000	1.039	Detected	1.155	Detected	1.097	0.094	GT	Sens
GT	Sense	Sense	0.483	Detected	-0.483	Detected	0.000	0.895	Detected	1.145	Detected	1.020	0.177	GT	Sens
GT	Sense	Sense	1.172	Detected	-1.172	Comprom	0.000	1.223	Detected	1.211	Detected	1.217	0.408	GT	Sens
GT	Sense	Sense	0.338	Detected	-0.338	Detected	0.000	1.181	Detected	1.161	Detected	1.171	0.074	GT	Sens
GT	Sense	Sense	-0.367	Comprom	0.367	Comprom	0.000	1.430	Detected	1.398	Detected	1.414	0.061	GT	Sens
GT	Sense	Sense	-0.327	Detected	0.327	Detected	0.000	1.213	Detected	1.551	Detected	1.382	0.064	GT	Sens
GT	Sense	Sense	0.526	Detected	-0.526	Detected	0.000	1.067	Detected	1.282	Detected	1.174	0.160	GT	Sens
GT	Sense	Sense	0.274	Detected	-0.274	Detected	0.000	1.379	Detected	1.128	Detected	1.254	0.053	GT	Sens
GT	Sense	Sense	0.972	Detected	-0.972	Detected	0.000	1.357	Detected	2.147	Detected	1.752	0.237	GT	Sens
GT	Sense	Sense	0.704	Detected	-0.704	Comprom	0.000	1.200	Detected	1.080	Detected	1.140	0.248	GT	Sens
GT	Sense	Sense	0.500	Detected	-0.500	Detected	0.000	1.229	Detected	2.044	Detected	1.637	0.127	GT	Sens
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	0.948	Detected	1.103	Detected	1.026	0.009	GT	Sens
GT	Sense	Sense	0.225	Detected	-0.225	Detected	0.000	1.172	Detected	1.211	Detected	1.192	0.034	GT	Sens
GT	Sense	Sense	0.986	Detected	-0.986	Comprom	0.000	0.829	Detected	1.202	Detected	1.015	0.418	GT	Sens
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	1.703	Detected	1.203	Detected	1.453	0.035	GT	Sens
GT	Sense	Sense	0.561	Detected	-0.561	Detected	0.000	0.961	Detected	1.307	Detected	1.134	0.193	GT	Sens
GT	Sense	Sense	0.176	Comprom	-0.176	Comprom	0.000	1.472	Detected	1.015	Detected	1.244	0.050	GT	Sens
GT	Sense	Sense	0.822	Comprom	-0.822	Comprom	0.000	1.535	Detected	1.775	Detected	1.655	0.185	GT	Sens
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	1.031	Detected	1.463	Detected	1.247	0.044	GT	Sens
GT	Sense	Sense	1.157	Detected	-1.157	Comprom	0.000	0.868	Detected	3.092	Detected	1.980	0.343	GT	Sens
GT	Sense	Sense	0.773	Detected	-0.773	Comprom	0.000	1.594	Detected	1.126	Detected	1.360	0.234	GT	Sens
GT	Sense	Sense	0.491	Detected	-0.491	Detected	0.000	1.904	Detected	1.653	Detected	1.779	0.072	GT	Sens
GT	Sense	Sense	0.821	Detected	-0.821	Detected	0.000	1.651	Detected	2.743	Detected	2.197	0.156	GT	Sens
GT	Sense	Sense	1.479	Detected	-1.479	Detected	0.000	2.239	Detected	1.349	Detected	1.794	0.365	GT	Sens
GT	Sense	Sense	0.815	Comprom	-0.815	Comprom	0.000	1.540	Detected	1.440	Detected	1.490	0.209	GT	Sens
GT	Sense	Sense	0.951	Detected	-0.951	Comprom	0.000	1.142	Detected	1.277	Detected	1.209	0.332	GT	Sens
GT	Sense	Sense	0.834	Detected	-0.834	Detected	0.000	2.072	Detected	1.668	Detected	1.870	0.161	GT	Sens
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	1.328	Detected	1.598	Detected	1.463	0.009	GT	Sens
GT	Sense	Sense	0.706	Detected	-0.706	Detected	0.000	1.021	Detected	1.158	Detected	1.090	0.264	GT	Sens
GT	Sense	Sense	-0.352	Detected	0.352	Detected	0.000	1.108	Detected	1.007	Detected	1.058	0.097	GT	Sens
GT	Sense	Sense	0.786	Detected	-0.786	Detected	0.000	1.410	Detected	1.125	Detected	1.268	0.253	GT	Sens
GT	Sense	Sense	0.747	Detected	-0.747	Detected	0.000	1.010	Detected	2.141	Detected	1.575	0.234	GT	Sens
GT	Sense	Sense	1.634	Detected	-1.634	Detected	0.000	2.955	Detected	3.193	Detected	3.074	0.201	GT	Sens
GT	Sense	Sense	-0.209	Comprom	0.209	Detected	0.000	1.506	Detected	1.095	Detected	1.301	0.047	GT	Sens
GT	Sense	Sense	-0.018	Detected	0.018	Detected	0.000	1.750	Detected	1.149	Detected	1.450	0.041	GT	Sens
GT	Sense	Sense	-0.109	Detected	0.109	Detected	0.000	1.160	Detected	2.085	Detected	1.623	0.076	GT	Sens
GT	Sense	Sense	0.573	Detected	-0.573	Detected	0.000	0.873	Detected	1.169	Detected	1.021	0.227	GT	Sens
GT	Sense	Sense	0.495	Detected	-0.495	Detected	0.000	0.928	Detected	1.766	Detected	1.347	0.173	GT	Sens
GT	Sense	Sense	1.085	Detected	-1.085	Detected	0.000	2.802	Detected	1.330	Detected	2.066	0.256	GT	Sens
GT	Sense	Sense	0.424	Detected	-0.424	Detected	0.000	1.591	Detected	1.414	Detected	1.503	0.074	GT	Sens
GT	Sense	Sense	0.561	Detected	-0.561	Detected	0.000	1.160	Detected	0.855	Detected	1.007	0.225	GT	Sens
GT	Sense	Sense	0.608	Detected	-0.608	Detected	0.000	1.145	Detected	1.352	Detected	1.248	0.180	GT	Sens
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	1.165	Detected	0.891	Detected	1.028	0.017	GT	Sens
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	0.962	Detected	1.354	Detected	1.158	0.035	GT	Sens
GT	Sense	Sense	0.529	Comprom	-0.529	Comprom	0.000	1.596	Detected	1.099	Detected	1.348	0.147	GT	Sens
GT	Sense	Sense	0.031	Detected	-0.031	Detected	0.000	1.239	Detected	1.311	Detected	1.275	0.001	GT	Sens
GT	Sense	Sense	0.283	Detected	-0.283	Detected	0.000	1.203	Detected	0.868	Detected	1.036	0.088	GT	Sens
GT	Sense	Sense	-0.035	Detected	0.035	Detected	0.000	1.308	Detected	1.630	Detected	1.469	0.012	GT	Sens
GT	Sense	Sense	0.268	Detected	-0.268	Detected	0.000	0.964	Detected	1.258	Detected	1.111	0.068	GT	Sens
GT	Sense	Sense	0.353	Detected	-0.353	Detected	0.000	1.031	Detected	1.214	Detected	1.123	0.091	GT	Sens

GT	Sens	Sense	1.227	Detected	-1.227	Detected	0.000	2.187	Detected	1.931	Detected	2.059	0.237	GT	Sens	contig21	contig21	UDP-gluc	TTGGAA	contig21	Solyc01g	Solyc01g	UDP-gluc	GO:0008	GO:0008	contig21	Solyc01g	UDP-gluc	GO:0015	SL2.40ch	AT1G782	AtUGT85	AtUGT85	chr1:294	2724.74	453.428	1631.81	5086.84	4833.35	4263.03
GT	Sens	Sense	0.527	Detected	-0.527	Detected	0.000	0.890	Detected	1.162	Detected	1.026	0.200	GT	Sens	contig21	contig21	ATP-depe	ATACAA	contig21	Solyc05g	Solyc05g	ATP-depe	GO:0005	GO:0005	contig21	Solyc05g	ATP-depe	GO:0004	SL2.40ch	AT2G01440.1		ATP bind	chr2:193	65.1122	28.6008	21.937	101.7	76.371	97.1518
GT	Sens	Sense	-0.331	Detected	0.331	Detected	0.000	1.250	Detected	1.638	Detected	1.444	0.064	GT	Sens	contig22	contig22	Cell cycle	TTGCAT	contig22	Solyc02g	Solyc02g	Cell cycle	GO:0005	GO:0005	contig22	Solyc02g	Cell cycle	GO:0005	SL2.40ch	AT1G54320.1		LEM3 (lig	chr1:202	39.2347	56.6113	55.5261	86.4736	107.009	147.584
GT	Sens	Sense	-0.245	Comprom	0.245	Comprom	0.000	2.214	Detected	4.765	Detected	3.489	0.115	GT	Sens	contig22	contig22	Cold sho	TATTAG	contig22	Solyc01g	Solyc01g	Cold sho	GO:0005	GO:0005	contig22	Solyc01g	Cold sho	GO:0030	SL2.40ch	AT5G59950.4		RNA and	chr5:241	2.29948	2.94469	2.11661	13.1874	11.5239	71.163
GT	Sens	Sense	0.317	Detected	-0.317	Detected	0.000	0.868	Detected	1.263	Detected	1.066	0.104	GT	Sens	contig22	contig22	Phenylala	ATTGCA	contig22	Solyc10g	Solyc10g	Phenylala	GO:0003	GO:0003	contig22	Solyc10g	Phenylala	GO:0009	SL2.40ch	AT2G370	pal1. ATP	pal1 (Phe	chr2:155	14264.5	8384.13	11511.3	23793.1	19055.7	26409.8
GT	Sens	Sense	0.467	Detected	-0.467	Detected	0.000	1.375	Detected	1.079	Detected	1.227	0.129	GT	Sens	contig22	contig22	GDSL est	GAAGCT	contig22	Solyc02g	Solyc02g	GDSL est	GO:0006	GO:0006	contig22	Solyc02g	GDSL est	GO:0006	SL2.40ch	AT1G31550.2				94.9648	45.3254	51.6577	172.422	162.421	139.445
GT	Sens	Sense	0.188	Detected	-0.188	Detected	0.000	1.021	Detected	1.412	Detected	1.216	0.046	GT	Sens	contig22	contig22	LRR rece	AACGAA	contig22	Solyc11g	Solyc11g	LRR rece	GO:0004	GO:0004	contig22	Solyc11g	RLK. Rec	GO:0004	SL2.40ch	AT5G37450.1		leucine-r	chr5:148	164.805	115.826	112.227	104.827	267.685	369.778
GT	Sens	Sense	0.221	Detected	-0.221	Detected	0.000	0.976	Detected	1.429	Detected	1.202	0.063	GT	Sens	contig22	contig22	GDSL est	GGGCAT	contig22	Solyc05g	Solyc05g	GDSL est	GO:0006	GO:0006	contig22	Solyc05g	GDSL est	GO:0004	SL2.40ch	AT3G05180.1		GDSL-m	chr3:146	2017.63	1353.36	1431.47	3588.05	3103.87	4474.86
GT	Sens	Sense	0.794	Detected	-0.794	Detected	0.000	1.774	Detected	1.693	Detected	1.733	0.161	GT	Sens	contig22	contig22	Pyruvate	TATTAT	contig22	Solyc11g	Solyc11g	Pyruvate	GO:0006	GO:0006	contig22	Solyc11g	Pyruvate	GO:0004	SL2.40ch	AT3G52990.2		pyruvate	chr3:196	521.481	158.073	171.476	675.322	937.265	933.942
GT	Sens	Sense	0.438	Detected	-0.438	Detected	0.000	1.232	Detected	1.233	Detected	1.233	0.106	GT	Sens	contig22	contig22	BZIP tran	AATCTT	contig22	Solyc05g	Solyc05g	BZIP tran	GO:0003	GO:0003	contig22	Solyc05g	BZIP tran	GO:0005	SL2.40ch	AT1G686	PAN	PAN (PEI	chr1:257	90.0462	44.7373	39.7121	142.134	142.341	150.127
GT	Sens	Sense	0.745	Detected	-0.745	Detected	0.000	1.764	Detected	2.280	Detected	2.022	0.124	GT	Sens	contig22	contig22	Ring H2 fi	AATCAT	contig22	Solyc04g	Solyc04g	Ring H2 fi	GO:0008	GO:0008	contig22	Solyc04g	Ring H2 fi	GO:0008	SL2.40ch	AT5G10380.1				186.604	60.5255	42.2372	174.462	344.571	519.282
GT	Sens	Sense	-0.190	Comprom	0.190	Comprom	0.000	0.983	Detected	1.453	Detected	1.218	0.056	GT	Sens	contig22	contig22	Major late	GATATA	contig22	Solyc09g	Solyc09g	Major late	GO:0009	GO:0009	contig22	Solyc09g	Major late	GO:0009	SL2.40ch	AT1G708	MLP28	MLP28 (M	chr1:267	5.31383	6.30746	7.0859	10.6568	10.929	15.9406
GT	Sens	Sense	0.994	Detected	-0.994	Comprom	0.000	1.061	Detected	0.986	Detected	1.024	0.411	GT	Sens	contig22	contig22	Patatin-lik	AATTTAT	contig22	Solyc08g	Solyc08g	Patatin-lik	GO:0045	GO:0045	contig22	Solyc08g	Patatin-lik	GO:0045	SL2.40ch	AT3G549	PLP7. PL	PLA IIIA (	chr3:203	22.946	5.27608	25.2851	13.3727	21.9141	21.9312
GT	Sens	Sense	0.413	Detected	-0.413	Detected	0.000	0.898	Detected	1.462	Detected	1.180	0.142	GT	Sens	contig22	contig22	RING fing	AGCACA	contig22	Solyc05g	Solyc05g	RING fing	GO:0008	GO:0008	contig22	Solyc05g	RING fing	GO:0008	SL2.40ch	AT5G28320.1		unknown	chr5:103	519.381	267.259	450.415	504.251	662.977	1032.73
GT	Sens	Sense	0.330	Detected	-0.330	Detected	0.000	0.945	Detected	1.087	Detected	1.016	0.095	GT	Sens	contig22	contig22	Aquapori	GAGGTG	contig22	Solyc08g	Solyc08g	Aquapori	GO:0016	GO:0016	contig22	Solyc08g	Aquapori	GO:0015	SL2.40ch	AT2G258	TIP4:1	TIP4:1 (t	chr2:110	8732.99	5041.66	6077.98	22702.2	12192.9	14183.1
GT	Sens	Sense	0.716	Detected	-0.716	Comprom	0.000	1.017	Detected	1.040	Detected	1.029	0.287	GT	Sens	contig22	contig22	Protein A	AATTCC	contig22	Solyc12g	Solyc12g	Protein ABIL1 (AHRD V1 *--- B6			contig22	Solyc12g	Protein ABIL1 (AHRI		SL2.40ch	AT5G523	COR78. L	LTI78 (L	chr5:212	16.1556	5.45895	19.3453	31.537	18.1485	19.4236
GT	Sens	Sense	0.288	Detected	-0.288	Detected	0.000	0.950	Detected	1.407	Detected	1.179	0.085	GT	Sens	contig22	contig22	Pentatric	ATGAAAT	contig22	Solyc03g	Solyc03g	Pentatricopeptide repeat-cont			contig22	Solyc03g	Pentatricopeptide re		SL2.40ch	AT5G40400.1		FUNCTIO	chr5:161	29.7656	18.2029	25.8139	46.6018	42.9379	62.1124
GT	Sens	Sense	0.656	Detected	-0.656	Detected	0.000	1.592	Detected	1.735	Detected	1.663	0.128	GT	Sens	contig22	contig22	heat shoc	AAGATG	contig22	Solyc11g	Solyc11g	heat shoc	GO:0005	GO:0005	contig22	Solyc11g	heat shoc	GO:0005	SL2.40ch	AT3G125	HSP70	HSP70 (h	chr3:399	8811.89	3235.15	5264.26	11115.7	15364.2	17874.3
GT	Sens	Sense	0.511	Detected	-0.511	Detected	0.000	1.214	Detected	1.257	Detected	1.236	0.137	GT	Sens	contig22	contig22	Argonaut	GAAGTT	contig22	Solyc01g	Solyc01g	Argonaut	GO:0003	GO:0003	contig22	Solyc01g	Argonaut	GO:0019	SL2.40ch	AT2G270	AGO4. O	AGO4 (A	chr2:115	6302.94	2830.29	3218.43	9154.85	9357.13	10154.4
GT	Sens	Sense	-0.077	Comprom	0.077	Comprom	0.000	1.562	Detected	1.240	Detected	1.401	0.016	GT	Sens	contig22	contig22	Unknown	ATGCGA	contig22	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig22	Solyc10g076620.1.1				AT3G12990.2				5.19837	5.27358	7.0273	12.349	14.7626	12.4368
GT	Sens	Sense	0.401	Detected	-0.401	Detected	0.000	1.102	Detected	1.698	Detected	1.400	0.107	GT	Sens	contig22	contig22	Cupin 2 c	CCTATT	contig22	Solyc08g	Solyc08g	Cupin 2 c	GO:0003	GO:0003	contig22	Solyc08g	Cupin 2 c	GO:0003	SL2.40ch	AT4G170	UGLYAH	UGLYAH	chr4:958	38.5238	20.1543	33.7316	88.85	57.1132	90.9386
GT	Sens	Sense	0.168	Detected	-0.168	Detected	0.000	0.922	Detected	1.081	Detected	1.001	0.033	GT	Sens	contig22	contig22	Abhydrol	TCTGAA	contig22	Solyc02g	Solyc02g	Abhydrolase domain-containir			contig22	Solyc02g	Abhydrolase domai		SL2.40ch	AT5G38220.3		hydrolas	chr5:152	1667.19	1203.35	1353.49	1922.77	2562.67	3013.77
GT	Sens	Sense	1.100	Detected	-1.100	Comprom	0.000	1.288	Detected	1.341	Detected	1.315	0.355	GT	Sens	contig22	contig22	Nodulin-li	ATTTTCT	contig22	Solyc01g	Solyc01g	Nodulin-li	GO:0009	GO:0009	contig22	Solyc01g	Nodulin-li	GO:0009	SL2.40ch	AT4G19450.1		nodulin-	chr4:106	16.9383	3.36288	5.09627	18.6288	17.5952	19.2384
GT	Sens	Sense	0.128	Detected	-0.128	Detected	0.000	1.012	Detected	1.105	Detected	1.059	0.016	GT	Sens	contig22	contig22	Seed mat	AACAGA	contig22	Solyc04g	Solyc04g	Seed maturation protein PM23			contig22	Solyc04g	Seed maturation pr		SL2.40ch	AT1G63610.2		unknown	chr1:235	275.476	210.371	200.06	578.104	463.481	520.98
GT	Sens	Sense	0.252	Detected	-0.252	Detected	0.000	0.979	Detected	1.122	Detected	1.051	0.057	GT	Sens	contig22	contig22	Aldo/keto	TGAGCA	contig22	Solyc07g	Solyc07g	Aldo/keto	GO:0055	GO:0055	contig22	Solyc07g	Aldo/keto	GO:0055	SL2.40ch	AT1G06690.1		aldo/keto	chr1:204	11151.4	7165.06	7560.86	15965.6	16820.8	19578.2
GT	Sens	Sense	1.422	Detected	-1.422	Detected	0.000	2.983	Detected	2.246	Detected	2.614	0.217	GT	Sens	contig22	contig22	Hydroxyc	TAAAAA	contig22	Solyc07g	Solyc07g	Hydroxyc	GO:0016	GO:0016	contig22	Solyc07g	Hydroxyc	GO:0016	SL2.40ch	AT5G484	ATGLR1.	ATGLR1.	chr5:196	90.7863	11.5339	90.2994	885.15	244.251	154.372
GT	Sens	Sense	0.176	Detected	-0.176	Detected	0.000	1.489	Detected	1.826	Detected	1.657	0.021	GT	Sens	contig22	contig22	Maltose e	ATTTTTC	contig22	Solyc04g	Solyc04g	Maltose excess protein 1-like%			contig22	Solyc04g	Maltose e	GO:0005	SL2.40ch	AT5G175	RCP1. ME	RCP1 (R	chr5:577	565.34	403.642	588.927	1404.17	1280.06	1703.98
GT	Sens	Sense	-0.601	Comprom	0.601	Detected	0.000	1.405	Detected	2.345	Detected	1.875	0.133	GT	Sens	contig22	contig22	Nodulin-li	CCTGAA	contig22	Solyc03g	Solyc03g	Nodulin-li	GO:0016	GO:0016	contig22	Solyc03g	Nodulin-li	GO:0016	SL2.40ch	AT1G48780.1		unknown	chr1:180	5.33571	11.1853	13.9	24.4584	19.5304	39.4969
GT	Sens	Sense	0.861	Detected	-0.861	Detected	0.000	1.797	Detected	0.840	Detected	1.319	0.313	GT	Sens	contig22	contig22	MtN3-like	TTAACT	contig22	Solyc06g	Solyc06g	MtN3-like	GO:0016	GO:0016	contig22	Solyc06g	MtN3-like	GO:0016	SL2.40ch	AT2G39060.1		nodulin M	chr2:163	127.919	35.3442	63.9487	145.866	223.064	121.111
GT	Sens	Sense	0.471	Detected	-0.471	Detected	0.000	1.351	Detected	2.116	Detected	1.734	0.104	GT	Sens	contig22	contig22	Glycine-r	CGTCGG	contig22	Solyc01g	Solyc01g	Glycine-r	GO:0008	GO:0008	contig22	Solyc01g	Glycine-r	GO:0008	SL2.40ch	AT2G216	ATGRP7.	CCR2 (C	chr2:926	680.346	322.694	232.314	438.116	1141.03	2043.8
GT	Sens	Sense	0.637	Detected	-0.637	Detected	0.000	1.434	Detected	1.292	Detected	1.363	0.167	GT	Sens	contig22	contig22	Ascorbat	TTCCTA	contig22	Solyc09g	Solyc09g	Ascorbat	GO:0004	GO:0004	contig22	Solyc09g	Ascorbat	GO:0004	SL2.40ch	AT3G096	APX2. AP	APX2 (A	chr3:295	670.87	253.038	463.173	777.34	1063.16	1015.25
GT	Sens	Sense	0.417	Detected	-0.417	Detected	0.000	0.808	Detected	1.248	Detected	1.028	0.161	GT	Sens	contig22	contig22	Receptor	ATGTGG	contig22	Solyc02g	Solyc02g	Receptor protein kinase-like p			contig22	Solyc02g	Receptor protein kir		SL2.40ch	AT4G17080.1		FUNCTIO	chr4:960	110.336	56.4519	52.3398	127.7	131.895	188.627
GT	Sens	Sense	-0.254	Detected	0.254	Detected	0.000	1.725	Detected	1.643	Detected	1.684	0.023	GT	Sens	contig22	contig22	Histidine	TCAATT	contig22	Solyc08g	Solyc08g	Histidine	GO:0009	GO:0009	contig22	Solyc08g	Histidine	GO:0009	SL2.40ch	AT2G269	CIPK3	CIPK3 (C	chr2:115	13.5596	17.5912	23.8742	29.9905	48.7352	48.5141
GT	Sens	Sense	-0.206	Detected	0.206	Detected	0.000	1.443	Detected	1.923	Detected	1.683	0.034	GT	Sens	contig22	contig22	Chloroph	ATCCAC	contig22	Solyc05g	Solyc05g	Chloroph	GO:0016	GO:0016	contig22	Solyc05g	Chloroph	GO:0016	SL2.40ch	AT3G548	LHCA1	LHCA1:	chr3:203	29.6566	35.9653	76.5057	117.626	84.7611	124.629
GT	Sens	Sense	0.774	Detected	-0.774	Detected	0.000	1.674	Detected	1.663	Detected	1.669	0.164	GT	Sens	contig22	contig22	Glucan sy	GTGGCA	contig22	Solyc01g	Solyc01g	Glucan sy	GO:0016	GO:0016	contig22	Solyc01g	Glucan sy	GO:0016	SL2.40ch	AT1G055	CALS1. G	CALS1 (	chr1:164	511.533	159.402	224.899	843.054	870.155	909.737
GT	Sens	Sense	0.747	Detected	-0.747	Detected	0.000	1.289	Detected	0.809	Detected	1.049	0.313	GT	Sens	contig22	contig22	Polygalac	TCCATC	contig22	Solyc10g	Solyc10g	Polygalac	GO:0005	GO:0005	contig22	Solyc10g047590.1.1				AT5G45440.1				51.9838	16.8283	33.3991	140.01	69.0155	52.1349
GT	Sens	Sense	-0.404	Comprom	0.404	Comprom	0.000	1.452	Detected	1.154	Detected	1.303	0.094	GT	Sens	contig23	contig23	Os06g02	ATCCTT	contig23	Solyc07g	Solyc07g	Os06g0207500 protein (Fragm			contig23	Solyc07g	Os06g0207500 prot		SL2.40ch	AT2G30900.1		unknown	chr2:131	5.70411	9.10089	11.1181	19.7152	18.8219	16.1277
GT	Sens	Sense	0.270	Detected	-0.270	Detected	0.000	0.920	Detected	1.421	Detected	1.171	0.086	GT	Sens	contig23	contig23	ATP-depe	TTGGTG	contig23	Solyc12g	Solyc12g	ATP-depe	GO:0005	GO:0005	contig23	Solyc12g	ATP-depe	GO:0008	SL2.40ch	AT3G223	PMH1. AT	PMH1 (P	chr3:788	629.073	394.314	478.273	1259.1	900.06	1341.44
GT	Sens	Sense	0.367	Detected	-0.367	Detected	0.000	0.970	Detected	1.303	Detected	1.136	0.106	GT	Sens	contig23	contig23	Pentatric	CTCTTT	contig23	Solyc03g	Solyc03g	Pentatricopeptide repeat-cont			contig23	Solyc03g	Pentatricopeptide re		SL2.40ch	AT1G748	PTAC2	PTAC2 (	chr1:281	83.3358	45.6697	67.2715	206.346	115.407	153.085
GT	Sens	Sense	0.264	Detected	-0.264	Detected	0.000	0.987	Detected	1.556	Detected	1.271	0.082	GT	Sens	contig23	contig23	Elongatio	GGTGGA	contig23	Solyc10g	Solyc10g	Elongatio	GO:0005	GO:0005	contig23	Solyc10g	Elongatio	GO:0006	SL2.40ch	AT2G441	ASHH3. S	ASHH3 (	chr2:182	268.037	169.497	307.98	749.364	403.463	630.311
GT	Sens	Sense	0.111	Detected	-0.111	Detected	0.000	0.992	Detected	1.171	Detected	1.082	0.017	GT	Sens	contig23	contig23	Cytochro	AATCTG	contig23	Solyc02g	Solyc02g	Cytochro	GO:0019	GO:0019	contig23	Solyc02g	Cytochro	GO:0019	SL2.40ch	AT1G116	CYP77B1	CYP77B	chr1:390	628.955	491.404	675.751	1668.71	1055.86	1259.23
GT	Sens	Sense	-1.048	Comprom	1.048	Detected	0.000	0.872	Detected	1.506	Detected	1.189	0.391	GT	Sens	contig23	contig23	Aldose 1-	TGGATT	contig23	Solyc10g	Solyc10g	Aldose 1-	GO:0005	GO:0005	contig23	Solyc10g	Aldose 1-	GO:0047	SL2.40ch	AT3G61610.1		aldose 1	chr3:227	4.38757	17.0959	8.45879	16.5335	15.1322	24.7419
GT	Sens	Sense	0.275	Detected	-0.275	Detected	0.000	0.888	Detected	1.181	Detected	1.035	0.080	GT	Sens	contig23	contig23	Universal	TTCTAG	contig23	Solyc01g	Solyc01g	Universal	GO:0006	GO:0006	contig23	Solyc01g	Universal	GO:0006	SL2.40ch	AT3G58450.2		universa	chr3:216	1334.27	830.693	1649.9	3210.61	1860.49	2401.09
GT	Sens	Sense	0.462	Detected	-0.462	Detected	0.000	0.861	Detected	1.535	Detected	1.198	0.171	GT	Sens	contig23	contig23	Ethylene	TTCCAAT	contig23	Solyc01g	Solyc01g	Ethylene	GO:0003	GO:0003	contig23	Solyc01g	Ethylene	GO:0003	SL2.40ch	AT3G167	RAP2.3. A	ATEBP (	chr3:570	12068	5798.78	8229.49	14935.9	14506.9	24392.7
GT	Sens	Sense	0.269	Detected	-0.269	Detected	0.000	0.950	Detected	1.553	Detected	1.252	0.090	GT	Sens	contig23	contig23	Homeobo	GGAGTA	contig23	Solyc02g	Solyc02g	Homeobo	GO:0006	GO:0006	contig23	Solyc02g	Homeobo	GO:0005	SL2.40ch	AT5G41840.1		F-box fa	chr5:167	658.155	413.124	1500.86	2047.6	962.081	1539.46
GT	Sens	Sense	1.419	Detected	-1.419	Comprom	0.000	2.598	Detected	2.789	Detected	2.694	0.199	GT	Sens	contig23	contig23	Solute ca	TATGTG	contig23	Solyc05g	Solyc05g	Solute ca	GO:0008	GO:0008	contig23	Solyc05g	Solute ca	GO:0008	SL2.40ch	AT3G16180.1		proton-d	chr3:548	16.9532	2.16107	17.0714	129.926	34.9918	42.0863
GT	Sens	Sense	0.034	Detected	-0.034	Detected	0.000	0.824	Detected	1.436	Detected	1.130	0.067	GT	Sens	contig23	contig23	Receptor	ATAGGT	contig23	Solyc09g	Solyc09g	Receptor	GO:0005	GO:0005	contig23	Solyc09g	Receptor-	GO:0005	SL2.40ch	AT1G79680.1		wall-ass	chr1:299	378.068	328.664	331.475	686.139	595.676	959.583
GT	Sens	Sense	0.670	Detected	-0.670	Comprom	0.000	0.801	Detected	1.570	Detected	1.186	0.265	GT	Sens	contig23	contig23	Reverse t	ATCTAA	contig23	Solyc00g	Solyc00g	Reverse t	GO:0006	GO:0006	contig23	Solyc00g	Nucleolar	GO:0005	SL2.40ch	AT5G438	ZLL. PNH	ZLL (ZW	chr5:176	11.3181	4.07635	4.18531	14.508	11.3012	20.2911
GT	Sens	Sense	0.125	Detected	-0.125	Detected	0.000	0.958	Detected	1.271	Detected	1.115	0.031	GT	Sens	contig23	contig23	Beta-gala	ATGTGT	contig23	Solyc02g	Solyc02g	Beta-gala	GO:0005	GO:0005	contig23	Solyc02g	Beta-gala	GO:0004	SL2.40ch	AT2G328	BGAL9	BGAL9 (	chr2:139	128.344	98.4468	115.269	353.264	208.508	272.91
GT	Sens	Sense	0.232	Detected	-0.232	Detected	0.000	0.990	Detected	1.020	Detected	1.005	0.050	GT	Sens	contig23	contig23	Phosphat	TTTCTC	contig23	Solyc09g	Solyc09g	Phosphat	GO:0004	GO:0004	contig23	Solyc09g	Phosphat	GO:0004	SL2.40ch	AT5G58560.1		phospha	chr5:236	1682.2	1111.11	895.985	2562.3	2592.97	2789.22
GT	Sens	Sense	0.742	Detected	-0.742	Detected	0.000	0.834	Detected	1.558	Detected	1.196	0.285	GT	Sens	contig23	contig23	Phospho	GAAACA	contig23	Solyc02g	Solyc02g	Phospho	GO:0009	GO:0009	contig23	Solyc02g	Phospho	GO:0009	SL2.40ch	AT4G046	APR1. AP	APR1 (A	chr4:232	566.888	184.753	503.981	863.945	550.694	958.933
GT	Sens	Sense	-0.519	Comprom	0.519	Detected	0.000	1.109	Detected	1.302	Detected	1.205	0.150	GT	Sens	contig23	contig23	Amino ac	GCCTAT	contig23	Solyc05g	Solyc05g	Amino ac	GO:0015	GO:0015	contig23	Solyc05g	Amino ac	GO:0015	SL2.40ch	AT5G14860.1		transfera	chr5:480	6.6037	12.3608	3.60096	3.75784	18.6007	22.4094
GT	Sens	Sense	0.639	Detected	-0.639	Detected	0.000	0.893	Detected	1.167	Detected	1.030	0.255	GT	Sens	contig23	contig23	WD-repea	TAAACG	contig23	Solyc08g	Solyc08g	WD-repea	GO:0016	GO:0016	contig23	Solyc08g	WD-repea	GO:0042	SL2.40ch	AT3G158	WSIP2. T	protein b	chr3:536	67.6825	25.4595	29.0358	88.697	73.62	93.793
GT	Sens	Sense	-0.834	Comprom	0.834	Comprom	0.000	1.129	Detected	1.024	Detected	1.077	0.327	GT	Sens	contig23	contig23	Unknown	ATTCCC	contig23	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig23	Solyc04g	Unknown Protein (A		SL2.40ch	AT4G22285.1		ubiquitin	chr4:117	2.97147	8.60937	5.76275	13.7263	10.5598	10.3505

GT	Sense	Sense	0.851	Detected	-0.851	Detected	0.000	1.084	Detected	1.411	Detected	1.247	0.287	GT	Sens	contig301	contig301	Dihydrofl	AAGGAT	contig301	Solyc04g	Solyc04g	Dihydrofl	GO:0008	GO:0008	contig301	Solyc04g	Dihydrofl	GO:0044	SL2.40ch	AT5G14700.1		cinnamo	chr5:474	223.791	62.6933	67.1177	250.028	239.777	316.765
GT	Sense	Sense	1.589	Detected	-1.589	Detected	0.000	1.053	Detected	2.820	Detected	1.937	0.398	GT	Sens	contig302	contig302	U-box do	GGGGGA	contig302	Solyc06g	Solyc06g	U-box do	GO:0005	GO:0005	contig302	Solyc06g	U-box do	GO:0004	SL2.40ch	AT2G40860.1		protein k	chr2:170	1679.09	169.119	725.643	821.962	1055.81	3785.5
GT	Sense	Sense	0.426	Comprom	-0.426	Comprom	0.000	1.243	Detected	1.101	Detected	1.172	0.113	GT	Sens	contig302	contig302	Condens	GAAGAC	contig302	Solyc03g	Solyc03g	Condens	GO:0005	GO:0005	contig302	Solyc03g	Condensi	GO:0005	SL2.40ch	AT1G64960.1		binding	chr1:241	9.48226	4.79094	5.43567	20.6178	15.2336	14.5477
GT	Sense	Sense	0.973	Detected	-0.973	Detected	0.000	1.547	Detected	3.210	Detected	2.378	0.204	GT	Sens	contig302	contig302	Peroxida	TCCGAT	contig302	Solyc07g	Solyc07g	Peroxida	GO:0005	GO:0005	contig302	Solyc07g	Peroxida	GO:0004	SL2.40ch	AT4G11290.1		peroxida	chr4:686	63.3136	14.9752	28.8212	132.195	85.8804	286.541
GT	Sense	Sense	0.897	Detected	-0.897	Detected	0.000	1.294	Detected	2.005	Detected	1.649	0.230	GT	Sens	contig303	contig303	Ring H2 fi	GAAGAT	contig303	Solyc06g	Solyc06g	Ring H2 fi	GO:0008	GO:0008	contig303	Solyc06g	Ring H2 fi	GO:0008	SL2.40ch	AT3G167	ATL2	ATL2: pr	chr3:569	646.534	169.939	331.22	436.8	776.104	1338.04
GT	Sense	Sense	-0.374	Comprom	0.374	Comprom	0.000	1.788	Detected	1.644	Detected	1.716	0.046	GT	Sens	contig303	contig303	Short-cha	TTCTGG	contig303	Solyc11g	Solyc11g	Short-cha	GO:0008	GO:0008	contig303	Solyc11g	Short-cha	GO:0008	SL2.40ch	AT1G17830.1		unknown	chr1:613	5.02672	7.69509	3.07727	22.2121	20.5125	19.5574
GT	Sense	Sense	0.190	Detected	-0.190	Detected	0.000	1.580	Detected	1.473	Detected	1.527	0.016	GT	Sens	contig303	contig303	Unknown	GTTAGA	contig303	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig303	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G48200.1		unknown	chr3:178	692.248	484.673	531.213	1778.41	1653.25	1617.95
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	0.982	Detected	1.250	Detected	1.116	0.018	GT	Sens	contig304	contig304	Chloropla	CTGGAA	contig304	Solyc02g	Solyc02g	Chloropla	GO:0003	GO:0003	contig304	Solyc02g	Chloropla	GO:0003	SL2.40ch	AT5G161	CRS1, AT	CRS1 (AT	chr5:527	24.4855	20.3262	13.6307	55.1992	42.0597	53.3668
GT	Sense	Sense	0.964	Detected	-0.964	Detected	0.000	0.838	Detected	2.382	Detected	1.610	0.322	GT	Sens	contig304	contig304	WRKY-lik	TTCAAG	contig304	Solyc09g	Solyc09g	WRKY-lik	GO:0003	GO:0003	contig304	Solyc09g	WRKY-lik	GO:0005	SL2.40ch	AT5G562	WRKY2, A	WRKY2:	chr5:227	3490.43	836.807	1944.07	2033.76	2917.61	8964.97
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	2.000	Detected	2.330	Detected	2.165	0.006	GT	Sens	contig305	contig305	At5g2428	AGATTG	contig305	Solyc03g	Solyc03g	At5g24280-like protein (Fragm			contig305	Solyc03g	At5g24280-like prote		SL2.40ch	AT2G16485.1		DNA bind	chr2:713	41.8366	40.0747	48.1672	77.817	156.365	207.07
GT	Sense	Sense	0.404	Comprom	-0.404	Comprom	0.000	2.678	Detected	2.225	Detected	2.451	0.034	GT	Sens	contig305	contig305	Ethylene-	GCTATG	contig305	Solyc06g	Solyc06g	Ethylene-	GO:0006	GO:0006	contig305	Solyc06g	Ethylene-	GO:0003	SL2.40ch	AT2G40340.1		AP2 dom	chr2:168	4.30837	2.24407	2.13606	8.06121	18.9952	14.6199
GT	Sense	Sense	-0.742	Comprom	0.742	Detected	0.000	1.440	Detected	0.956	Detected	1.198	0.264	GT	Sens	contig305	contig305	Phospho	AGTACA	contig305	Solyc10g	Solyc10g	Phosphol	GO:0004	GO:0004	contig305	Solyc10g	Phosphol	GO:0004	SL2.40ch	AT4G118	PLDGAM	PLDGAM	chr4:711	4.35481	11.1064	4.45692	11.1726	18.0219	13.5743
GT	Sense	Sense	0.414	Detected	-0.414	Detected	0.000	1.179	Detected	1.169	Detected	1.174	0.105	GT	Sens	contig306	contig306	Calmodul	AATTGG	contig306	Solyc10g	Solyc10g	Calmodulin binding protein (Al			contig306	Solyc10g	Calmodulin binding		SL2.40ch	AT3G52870.1		calmodu	chr3:195	3215.61	1651.6	2444.13	6590.9	4981.36	5212.12
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	1.028	Detected	0.993	Detected	1.011	0.038	GT	Sens	contig306	contig306	Leucine-r	TGCCGG	contig306	Solyc02g	Solyc02g	Leucine-r	GO:0005	GO:0005	contig306	Solyc02g	LRR rece	GO:0004	SL2.40ch	AT1G02890.2		AAA-type	chr1:645	27396.8	18845.9	16748.4	36300.7	44251.2	45490.2
GT	Sense	Sense	-0.533	Comprom	0.533	Detected	0.000	1.440	Detected	1.775	Detected	1.608	0.103	GT	Sens	contig307	contig307	Nucleopo	TTCAAT	contig307	Solyc11g	Solyc11g	Nucleoporin NUP188 homolog			contig307	Solyc11g	Nucleoporin NUP18		SL2.40ch	AT4G38760.1		unknown	chr4:180	5.68936	10.8599	5.65673	8.64563	20.361	27.0653
GT	Sense	Sense	0.312	Detected	-0.312	Detected	0.000	1.051	Detected	1.452	Detected	1.252	0.078	GT	Sens	contig307	contig307	Protein re	GAAATA	contig307	Solyc07g	Solyc07g	Protein re	GO:0006	GO:0006	contig307	Solyc07g	Protein re	GO:0003	SL2.40ch	AT1G79050.1		DNA repa	chr1:297	555.478	328.697	246.236	744.681	845.521	1176.32
GT	Sense	Sense	0.412	Detected	-0.412	Detected	0.000	2.539	Detected	2.858	Detected	2.698	0.026	GT	Sens	contig309	contig309	Unknown	TTCAACA	contig309	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig309	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G08695.1		nucleic a	chr5:282	42.0609	21.6698	35.6405	131.182	167.492	220.241
GT	Sense	Sense	0.496	Detected	-0.496	Detected	0.000	0.852	Detected	1.527	Detected	1.190	0.186	GT	Sens	contig309	contig309	Receptor	GGTATG	contig309	Solyc05g	Solyc05g	Receptor	GO:0005	GO:0005	contig309	Solyc05g	Receptor	GO:0005	SL2.40ch	AT3G55550.1		lectin pro	chr3:206	1016.5	466.2	962.856	1842.1	1186.55	1995.98
GT	Sense	Sense	0.190	Detected	-0.190	Detected	0.000	3.126	Detected	3.513	Detected	3.320	0.007	GT	Sens	contig309	contig309	Pentatric	TATCCA	contig309	Solyc02g	Solyc02g	Pentatricopeptide repeat-cont			contig309	Solyc02g	Pentatricopeptide re		SL2.40ch	AT2G35130.1		pentatric	chr2:148	16.1904	11.3457	47.6252	81.9175	112.973	155.7
GT	Sense	Sense	0.944	Detected	-0.944	Comprom	0.000	1.210	Detected	2.266	Detected	1.738	0.249	GT	Sens	contig310	contig310	Os01g068	TCTCAA	contig310	Solyc03g	Solyc03g	Os01g0686000 protein (Fragm			contig310	Solyc03g	Os01g0686000 prot		SL2.40ch	AT3G50800.1		unknown	chr3:188	16.5774	4.08132	35.7824	14.9199	18.1646	39.7893
GT	Sense	Sense	0.481	Detected	-0.481	Detected	0.000	0.819	Detected	1.258	Detected	1.038	0.189	GT	Sens	contig310	contig310	DsRNA-bi	ATGGGG	contig310	Solyc02g	Solyc02g	DsRNA-bi	GO:0005	GO:0005	contig310	Solyc02g	DsRNA-bi	GO:0005	SL2.40ch	AT1G31670.1		copper a	chr1:113	372.746	174.405	204.961	571.925	429.457	613.425
GT	Sense	Sense	-0.060	Detected	0.060	Detected	0.000	1.631	Detected	1.889	Detected	1.760	0.007	GT	Sens	contig310	contig310	NBS-LRR	ATTGCA	contig310	Solyc08g	Solyc08g	NBS-LRR	GO:0005	GO:0005	contig310	Solyc08g	Cc-nbs-lr	GO:0005	SL2.40ch	AT5G397	EMB2745	EMB2745	chr5:158	23.8292	23.6249	21.9284	27.9014	70.1449	88.4321
GT	Sense	Sense	0.483	Detected	-0.483	Detected	0.000	1.225	Detected	1.286	Detected	1.255	0.122	GT	Sens	contig311	contig311	Caffeoyl-	CCGATC	contig311	Solyc08g	Solyc08g	Caffeoyl-(	GO:0042	GO:0042	contig311	Solyc08g	Caffeoyl-(	GO:0042	SL2.40ch	AT3G61990.1		O-methyl	chr3:229	61.1766	28.5397	33.6757	113.795	93.2736	102.472
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	1.009	Detected	1.015	Detected	1.012	0.016	GT	Sens	contig311	contig311	Glucose-	TTGTTA	contig311	Solyc07g	Solyc07g	Glucose-(	GO:0004	GO:0004	contig311	Solyc07g	Glucose-(	GO:0004	SL2.40ch	AT5G357	G6PD1	G6PD1 ((	chr5:139	766.841	585.664	654.12	1273.54	1288.08	1362.38
GT	Sense	Sense	0.315	Comprom	-0.315	Comprom	0.000	1.223	Detected	1.948	Detected	1.586	0.081	GT	Sens	contig311	contig311	Protein-ty	TGTTCT	contig311	Solyc03g	Solyc03g	Protein-ty	GO:0004	GO:0004	contig311	Solyc03g	Protein-ty	GO:0004	SL2.40ch	AT2G41970.1		protein k	chr2:175	8.459	4.98217	5.85673	54.0201	14.469	25.1997
GT	Sense	Sense	1.788	Detected	-1.788	Comprom	0.000	2.307	Detected	2.007	Detected	2.157	0.352	GT	Sens	contig312	contig312	Laccase-	AAATGT	contig312	Solyc01g	Solyc01g	Laccase-	GO:0055	GO:0055	contig312	Solyc01g	Laccase-	GO:0055	SL2.40ch	AT3G133	sks11	sks11 (S	chr3:435	28.6377	2.19028	2.16505	2.0023	37.4314	32.0226
GT	Sense	Sense	0.403	Detected	-0.403	Detected	0.000	1.070	Detected	1.112	Detected	1.091	0.114	GT	Sens	contig312	contig312	Spermidi	TCGACG	contig312	Solyc05g	Solyc05g	Spermidi	GO:0003	GO:0003	contig312	Solyc05g	Spermidi	GO:0004	SL2.40ch	AT1G703	SPDS2	SPDS2 (s	chr1:264	7781.5	4054.93	4950.01	13636.8	11259.5	12218

GT	Sense	Sense	-0.864	Comprom	0.864	Comprom	0.000	1.250	Detected	1.587	Detected	1.419	0.248	GT	Sens
GT	Sense	Sense	0.241	Comprom	-0.241	Comprom	0.000	0.816	Detected	1.344	Detected	1.080	0.094	GT	Sens
GT	Sense	Sense	0.088	Comprom	-0.088	Comprom	0.000	1.235	Detected	1.490	Detected	1.363	0.013	GT	Sens
GT	Sense	Sense	0.763	Detected	-0.763	Detected	0.000	1.252	Detected	1.586	Detected	1.419	0.211	GT	Sens
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	1.337	Detected	1.116	Detected	1.227	0.008	GT	Sens
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	0.884	Detected	1.245	Detected	1.064	0.035	GT	Sens
GT	Sense	Sense	0.659	Detected	-0.659	Detected	0.000	1.107	Detected	1.005	Detected	1.056	0.251	GT	Sens
GT	Sense	Sense	-0.058	Comprom	0.058	Comprom	0.000	0.897	Detected	1.846	Detected	1.371	0.103	GT	Sens
GT	Sense	Sense	0.038	Detected	-0.038	Detected	0.000	1.338	Detected	1.792	Detected	1.565	0.021	GT	Sens
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	1.192	Detected	1.548	Detected	1.370	0.017	GT	Sens
GT	Sense	Sense	0.442	Detected	-0.442	Detected	0.000	1.242	Detected	1.230	Detected	1.236	0.108	GT	Sens
GT	Sense	Sense	-0.118	Comprom	0.118	Comprom	0.000	1.549	Detected	1.499	Detected	1.524	0.006	GT	Sens
GT	Sense	Sense	-0.049	Detected	0.049	Detected	0.000	0.949	Detected	1.252	Detected	1.101	0.020	GT	Sens
GT	Sense	Sense	0.233	Detected	-0.233	Detected	0.000	1.321	Detected	1.518	Detected	1.420	0.030	GT	Sens
GT	Sense	Sense	0.279	Detected	-0.279	Detected	0.000	1.126	Detected	1.026	Detected	1.076	0.063	GT	Sens
GT	Sense	Sense	0.389	Detected	-0.389	Detected	0.000	1.644	Detected	1.529	Detected	1.587	0.056	GT	Sens
GT	Sense	Sense	0.439	Detected	-0.439	Comprom	0.000	1.543	Detected	1.161	Detected	1.352	0.106	GT	Sens
GT	Sense	Sense	0.438	Detected	-0.438	Detected	0.000	1.181	Detected	1.179	Detected	1.180	0.114	GT	Sens
GT	Sense	Sense	0.307	Detected	-0.307	Detected	0.000	1.120	Detected	0.935	Detected	1.027	0.085	GT	Sens
GT	Sense	Sense	0.523	Detected	-0.523	Comprom	0.000	0.879	Detected	1.262	Detected	1.070	0.195	GT	Sens
GT	Sense	Sense	0.772	Detected	-0.772	Comprom	0.000	1.243	Detected	1.092	Detected	1.168	0.271	GT	Sens
GT	Sense	Sense	0.592	Comprom	-0.592	Comprom	0.000	1.790	Detected	1.559	Detected	1.674	0.109	GT	Sens
GT	Sense	Sense	2.134	Detected	-2.134	Detected	0.000	2.761	Detected	1.637	Detected	2.199	0.424	GT	Sens
GT	Sense	Sense	1.047	Detected	-1.047	Comprom	0.000	1.252	Detected	0.818	Detected	1.035	0.435	GT	Sens
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	1.089	Detected	1.048	Detected	1.069	0.002	GT	Sens
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	1.407	Detected	1.150	Detected	1.279	0.012	GT	Sens
GT	Sense	Sense	0.447	Comprom	-0.447	Comprom	0.000	1.925	Detected	2.791	Detected	2.358	0.063	GT	Sens
GT	Sense	Sense	-0.269	Comprom	0.269	Comprom	0.000	1.405	Detected	1.584	Detected	1.495	0.034	GT	Sens
GT	Sense	Sense	0.336	Detected	-0.336	Comprom	0.000	0.823	Detected	1.725	Detected	1.274	0.152	GT	Sens
GT	Sense	Sense	0.378	Detected	-0.378	Detected	0.000	1.354	Detected	0.900	Detected	1.127	0.125	GT	Sens
GT	Sense	Sense	0.007	Detected	-0.007	Detected	0.000	1.917	Detected	2.202	Detected	2.060	0.005	GT	Sens
GT	Sense	Sense	0.002	Detected	-0.002	Detected	0.000	1.554	Detected	1.752	Detected	1.653	0.004	GT	Sens
GT	Sense	Sense	0.485	Detected	-0.485	Detected	0.000	1.201	Detected	1.135	Detected	1.168	0.138	GT	Sens
GT	Sense	Sense	1.562	Detected	-1.562	Detected	0.000	1.258	Detected	1.191	Detected	1.224	0.515	GT	Sens
GT	Sense	Sense	-0.063	Detected	0.063	Detected	0.000	0.983	Detected	1.076	Detected	1.029	0.006	GT	Sens
GT	Sense	Sense	0.224	Detected	-0.224	Detected	0.000	1.094	Detected	1.557	Detected	1.325	0.054	GT	Sens
GT	Sense	Sense	-0.483	Comprom	0.483	Comprom	0.000	1.039	Detected	1.120	Detected	1.079	0.156	GT	Sens
GT	Sense	Sense	0.604	Detected	-0.604	Detected	0.000	1.022	Detected	0.987	Detected	1.005	0.238	GT	Sens
GT	Sense	Sense	0.716	Detected	-0.716	Detected	0.000	0.847	Detected	1.712	Detected	1.279	0.266	GT	Sens
GT	Sense	Sense	0.218	Detected	-0.218	Detected	0.000	0.868	Detected	1.341	Detected	1.104	0.075	GT	Sens
GT	Sense	Sense	0.214	Detected	-0.214	Detected	0.000	1.239	Detected	1.275	Detected	1.257	0.028	GT	Sens
GT	Sense	Sense	-0.356	Comprom	0.356	Detected	0.000	1.225	Detected	1.034	Detected	1.130	0.092	GT	Sens
GT	Sense	Sense	0.340	Comprom	-0.340	Comprom	0.000	1.506	Detected	1.522	Detected	1.514	0.047	GT	Sens
GT	Sense	Sense	0.244	Comprom	-0.244	Comprom	0.000	1.566	Detected	1.880	Detected	1.723	0.027	GT	Sens
GT	Sense	Sense	-1.219	Comprom	1.219	Detected	0.000	3.115	Detected	3.961	Detected	3.538	0.111	GT	Sens
GT	Sense	Sense	-0.513	Comprom	0.513	Comprom	0.000	1.465	Detected	1.355	Detected	1.410	0.112	GT	Sens
GT	Sense	Sense	1.511	Detected	-1.511	Detected	0.000	2.121	Detected	1.976	Detected	2.048	0.308	GT	Sens
GT	Sense	Sense	-0.288	Comprom	0.288	Comprom	0.000	1.187	Detected	1.117	Detected	1.152	0.058	GT	Sens
GT	Sense	Sense	0.317	Comprom	-0.317	Comprom	0.000	1.132	Detected	1.819	Detected	1.475	0.087	GT	Sens
GT	Sense	Sense	1.517	Detected	-1.517	Detected	0.000	2.369	Detected	2.569	Detected	2.469	0.246	GT	Sens
GT	Sense	Sense	2.399	Detected	-2.399	Comprom	0.000	2.381	Detected	2.820	Detected	2.601	0.393	GT	Sens
GT	Sense	Sense	0.408	Detected	-0.408	Detected	0.000	1.618	Detected	0.973	Detected	1.296	0.130	GT	Sens
GT	Sense	Sense	0.229	Comprom	-0.229	Comprom	0.000	1.311	Detected	1.045	Detected	1.178	0.047	GT	Sens
GT	Sense	Sense	0.657	Detected	-0.657	Detected	0.000	1.880	Detected	1.777	Detected	1.829	0.109	GT	Sens
GT	Sense	Sense	0.470	Detected	-0.470	Detected	0.000	1.153	Detected	1.386	Detected	1.270	0.120	GT	Sens
GT	Sense	Sense	0.564	Detected	-0.564	Detected	0.000	1.147	Detected	1.722	Detected	1.435	0.152	GT	Sens
GT	Sense	Sense	-0.054	Detected	0.054	Detected	0.000	0.828	Detected	1.299	Detected	1.064	0.048	GT	Sens
GT	Sense	Sense	0.005	Detected	-0.005	Detected	0.000	1.351	Detected	1.770	Detected	1.561	0.018	GT	Sens
GT	Sense	Sense	0.624	Detected	-0.624	Detected	0.000	1.359	Detected	1.348	Detected	1.353	0.162	GT	Sens
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	1.861	Detected	1.680	Detected	1.771	0.003	GT	Sens
GT	Sense	Sense	0.237	Comprom	-0.237	Comprom	0.000	1.075	Detected	1.268	Detected	1.172	0.045	GT	Sens
GT	Sense	Sense	0.498	Detected	-0.498	Detected	0.000	0.991	Detected	1.370	Detected	1.180	0.157	GT	Sens
GT	Sense	Sense	0.799	Detected	-0.799	Detected	0.000	1.258	Detected	1.610	Detected	1.434	0.222	GT	Sens
GT	Sense	Sense	0.364	Detected	-0.364	Detected	0.000	1.244	Detected	0.904	Detected	1.074	0.116	GT	Sens
GT	Sense	Sense	0.259	Detected	-0.259	Detected	0.000	0.935	Detected	1.351	Detected	1.143	0.075	GT	Sens
GT	Sense	Sense	0.778	Detected	-0.778	Detected	0.000	1.681	Detected	2.103	Detected	1.892	0.143	GT	Sens
GT	Sense	Sense	0.224	Detected	-0.224	Detected	0.000	1.269	Detected	1.547	Detected	1.408	0.033	GT	Sens
GT	Sense	Sense	0.712	Detected	-0.712	Detected	0.000	1.037	Detected	1.541	Detected	1.289	0.230	GT	Sens
GT	Sense	Sense	-0.013	Comprom	0.013	Comprom	0.000	1.316	Detected	1.355	Detected	1.336	0.000	GT	Sens
GT	Sense	Sense	0.331	Detected	-0.331	Detected	0.000	1.333	Detected	1.576	Detected	1.455	0.054	GT	Sens
GT	Sense	Sense	0.402	Detected	-0.402	Detected	0.000	1.083	Detected	1.259	Detected	1.171	0.105	GT	Sens
GT	Sense	Sense	0.581	Detected	-0.581	Detected	0.000	1.060	Detected	1.419	Detected	1.240	0.178	GT	Sens
GT	Sense	Sense	0.935	Detected	-0.935	Detected	0.000	1.322	Detected	1.122	Detected	1.222	0.323	GT	Sens
GT	Sense	Sense	0.287	Comprom	-0.287	Comprom	0.000	1.118	Detected	1.772	Detected	1.445	0.080	GT	Sens
GT	Sense	Sense	0.424	Detected	-0.424	Detected	0.000	1.080	Detected	1.038	Detected	1.059	0.130	GT	Sens
GT	Sense	Sense	-0.216	Detected	0.216	Detected	0.000	1.146	Detected	1.055	Detected	1.101	0.038	GT	Sens
GT	Sense	Sense	0.484	Detected	-0.484	Detected	0.000	1.072	Detected	2.359	Detected	1.715	0.167	GT	Sens
GT	Sense	Sense	0.448	Detected	-0.448	Detected	0.000	1.066	Detected	1.072	Detected	1.069	0.140	GT	Sens
GT	Sense	Sense	0.766	Detected	-0.766	Detected	0.000	1.189	Detected	1.592	Detected	1.391	0.221	GT	Sens
GT	Sense	Sense	0.129	Detected	-0.129	Detected	0.000	1.228	Detected	0.986	Detected	1.107	0.025	GT	Sens
GT	Sense	Sense	0.532	Comprom	-0.532	Comprom	0.000	1.380	Detected	1.186	Detected	1.283	0.141	GT	Sens
GT	Sense	Sense	0.034	Detected	-0.034	Detected	0.000	1.069	Detected	1.369	Detected	1.219	0.015	GT	Sens
GT	Sense	Sense	0.978	Detected	-0.978	Detected	0.000	1.034	Detected	1.564	Detected	1.299	0.329	GT	Sens
GT	Sense	Sense	0.211	Detected	-0.211	Detected	0.000	1.202	Detected	0.890	Detected	1.046	0.057	GT	Sens
GT	Sense	Sense	0.198	Detected	-0.198	Comprom	0.000	0.918	Detected	1.214	Detected	1.066	0.050	GT	Sens
GT	Sense	Sense	0.144	Detected	-0.144	Detected	0.000	1.041	Detected	1.278	Detected	1.160	0.025	GT	Sens
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	0.928	Detected	1.459	Detected	1.194	0.054	GT	Sens
GT	Sense	Sense	0.449	Detected	-0.449	Detected	0.000	0.985	Detected	1.238	Detected	1.112	0.140	GT	Sens
GT	Sense	Sense	0.254	Detected	-0.254	Detected	0.000	0.904	Detected	1.098	Detected	1.001	0.066	GT	Sens
GT	Sense	Sense	0.546	Detected	-0.546	Detected	0.000	1.188	Detected	1.338	Detected	1.263	0.149	GT	Sens
GT	Sense	Sense	0.426	Detected	-0.426	Detected	0.000	1.183	Detected	0.968	Detected	1.075	0.134	GT	Sens
GT	Sense	Sense	0.909	Detected	-0.909	Detected	0.000	1.258	Detected	1.326	Detected	1.292	0.291	GT	Sens
GT	Sense	Sense	0.224	Detected	-0.224	Detected	0.000	1.317	Detected	1.086	Detected	1.201	0.041	GT	Sens
GT	Sense	Sense	-0.279	Detected	0.279	Detected	0.000	0.868	Detected	1.691	Detected	1.279	0.124	GT	Sens
GT	Sense	Sense	0.605	Detected	-0.605	Detected	0.000	0.829	Detected	1.644	Detected	1.237	0.232	GT	Sens
GT	Sense	Sense	1.298	Detected	-1.298	Comprom	0.000	1.513	Detected	0.898	Detected	1.206	0.461	GT	Sens
GT	Sense	Sense	0.464	Detected	-0.464	Detected	0.000	1.306	Detected	0.982	Detected	1.144	0.145	GT	Sens
GT	Sense	Sense	0.810	Detected	-0.810	Detected	0.000	0.950	Detected	1.288	Detected	1.119	0.309	GT	Sens
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	0.805	Detected	1.219	Detected	1.012	0.041	GT	Sens
GT	Sense	Sense	0.821	Detected	-0.821	Detected	0.000	0.878	Detected	2.454	Detected	1.666	0.281	GT	Sens
GT	Sense	Sense	0.463	Detected	-0.463	Detected	0.000	1.187	Detected	1.260	Detected	1.224	0.119	GT	Sens
GT	Sense	Sense	1.509	Detected	-1.509	Detected	0.000	2.790	Detected	1.355	Detected	2.073	0.341	GT	Sens
GT	Sense	Sense	0.387	Detected	-0.387	Comprom	0.000	1.194	Detected	0.844	Detected	1.019	0.139	GT	Sens
GT	Sense	Sense	-0.200	Comprom	0.200	Comprom	0.000	1.545	Detected	1.182	Detected	1.363	0.037	GT	Sens
GT	Sense	Sense	0.311	Detected	-0.311	Detected	0.000	1.529	Detected	1.335	Detected	1.432	0.048	GT	Sens
GT	Sense	Sense	0.937	Detected	-0.937	Comprom	0.000	1.946	Detected	1.191	Detected	1.568	0.261	GT	Sens
GT	Sense	Sense	0.698	Detected	-0.698	Detected	0.000	1.079	Detected	1.417	Detected	1.248	0.224	GT	Sens
GT	Sense	Sense	-0.898	Detected	0.898	Detected	0.000	1.873	Detected	3.435	Detected	2.654	0.155	GT	Sens
GT	Sense	Sense	0.469	Detected	-0.469	Detected	0.000	1.309	Detected	1.278	Detected	1.294	0.110	GT	Sens
GT	Sense	Sense	0.991	Detected	-0.991	Comprom	0.000	1.589	Detected	1.583	Detected	1.586	0.251	GT	Sens
GT	Sense	Sense	0.467	Detected	-0.467	Detected	0.000	1.078	Detected	1.054	Detected	1.066	0.150	GT	Sens
GT	Sense	Sense	0.533	Detected	-0.533	Detected	0.000	1.316	Detected	2.222	Detected	1.769	0.127	GT	Sens
GT	Sense	Sense	0.928	Detected	-0.928	Detected	0.000	2.429	Detected	2.317	Detected	2.373	0.125	GT	Sens
GT	Sense	Sense	0.081	Detected	-0.081	Detected	0.000	0.882	Detected	1.301	Detected	1.092	0.040	GT	Sens
GT	Sense	Sense	-0.663	Comprom	0.663	Comprom	0.000	1.792	Detected	1.664	Detected	1.728	0.122	GT	Sens
GT	Sense	Sense	0.067	Comprom	-0.067	Comprom	0.000	1.405	Detected	3.698	Detected	2.552	0.156	GT	Sens
GT	Sense	Sense	1.267	Detected	-1.267	Detected	0.000	1.159	Detected	1.397	Detected	1.278	0.421	GT	Sens
GT	Sense	Sense	-0.231	Comprom	0.231	Comprom	0.000	1.050	Detected	1.026	Detected	1.038	0.046	GT	Sens
GT	Sense	Sense	0.432	Detected	-0.432	Detected	0.000	1.038	Detected	0.969	Detected	1.004	0.146	GT	Sens
GT	Sense	Sense	1.095	Detected	-1.095	Comprom	0.000	1.483	Detected	3.125	Detected	2.304	0.234	GT	Sens
GT	Sense	Sense	0.547	Detected	-0.547	Detected	0.000	0.917	Detected	1.570	Detected	1.243	0.190	GT	Sens
GT	Sense	Sense	0.801	Detected	-0.801	Detected	0.000	0.855	Detected	1.182	Detected	1.018	0.339	GT	Sens
GT	Sense	Sense	0.164	Detected	-0.164	Detected	0.000	1.041	Detected	1.463	Detected	1.252	0.043	GT	Sens
GT	Sense	Sense	0.282	Detected	-0.282	Detected	0.000	1.013	Detected	0.998	Detected	1.006	0.070	GT	Sens
GT	Sense	Sense	0.997	Detected	-0.997	Detected	0.000	1.859	Detected	2.094	Detected	1.976	0.188	GT	Sens
GT	Sense	Sense	0.982	Detected	-0.982	Detected	0.000	0.826	Detected	1.221	Detected	1.023	0.415	GT	Sens
GT	Sense	Sense	1.115	Detected	-1.115	Detected	0.000	1.807	Detected	1.657	Detected	1.732	0.261	GT	Sens
GT	Sense	Sense	0.625	Detected	-0.625	Comprom	0.000	1.176	Detected	3.556	Detected	2.366	0.220	GT	Sens
GT	Sense	Sense	0.407	Detected	-0.407	Detected	0.000	1.160	Detected	1.424	Detected	1.292	0.094	GT	Sens
GT	Sense	Sense	0.226	Detected	-0.226	Detected	0.000	0.965	Detected	1.112	Detected	1.039	0.048	GT	Sens
GT	Sense	Sense	-0.118	Comprom	0.118	Comprom	0.000	1.308	Detected	1.202	Detected	1.255	0.011	GT	Sens
GT	Sense	Sense	-0.115	Detected	0.115	Detected	0.000	1.697	Detected	1.254	Detected	1.475	0.027	GT	Sens
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	0.962	Detected	1.118	Detected	1.040	0.006	GT	Sens
GT	Sense	Sense	1.444	Detected	-1.444	Comprom	0.000	0.960	Detected	1.048	Detected	1.004	0.559	GT	Sens
GT	Sense	Sense	0.011	Detected	-0.011	Detected	0.000	0.912	Detected	1.540	Detected	1.226	0.060	GT	Sens
GT	Sense	Sense	1.186	Detected	-1.186	Detected	0.000	1.651	Detected	2.571	Detected	2.111	0.239	GT	Sens
GT	Sense	Sense	0.559	Detected	-0.559	Detected	0.000	0.872	Detected	1.583	Detected	1.228	0.205	GT	Sens
GT	Sense	Sense	0.668	Detected	-0.668	Detected	0.000	1.091	Detected	1.169	Detected	1.130	0.233	GT	Sens
GT	Sense	Sense	0.341	Detected	-0.341	Detected	0.000	0.962	Detected	1.524	Detected	1.243	0.107	GT	Sens
GT	Sense	Sense	-0.436	Comprom	0.436	Detected	0.000	1.261	Detected	0.805	Detected	1.033	0.171	GT	Sens
GT	Sense	Sense	1.273	Detected	-1.273	Detected	0.000	2.652	Detected	2.503	Detected	2.578	0.181	GT	Sens
GT	Sense	Sense	0.914	Detected	-0.914	Detected	0.000	1.516	Detected	1.274	Detected	1.395	0.269	GT	Sens
GT	Sense	Sense	-0.155	Comprom	0.155	Comprom	0.000	1.332	Detected	1.308	Detected	1.320	0.014	GT	Sens
GT	Sense	Sense	0.270	Detected	-0.270	Detected	0.000	0.972	Detected	1.101	Detected	1.036	0.065	GT	Sens
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	1.016	Detected	1.094	Detected	1.055	0.070	GT	Sens
GT	Sense	Sense	0.940	Detected	-0.940	Comprom	0.000	2.835	Detected	2.617	Detected	2.726	0.102	GT	Sens
GT	Sense	Sense	0.291	Detected	-0.291	Detected	0.000	0.813	Detected	2.588	Detected	1.700	0.210	GT	Sens
GT	Sense	Sense	0.159	Detected	-0.159	Detected	0.000	1.895	Detected	2.042	Detected	1.969	0.008	GT	Sens
GT	Sense	Sense	0.594	Detected	-0.594	Detected	0.000	1.427	Detected	1.286	Detected	1.356	0.152	GT	Sens
GT	Sense	Sense	-0.619	Detected	0.619	Detected	0.000	2.095	Detected	1.688	Detected	1.892	0.101	GT	Sens
GT	Sense	Sense	0.274	Detected	-0.274	Detected	0.000	1.115	Detected	1.550	Detected	1.332	0.063	GT	Sens
GT	Sense	Sense	0.517	Detected	-0.517	Detected	0.000	1.255	Detected	1.695	Detected	1.475	0.120	GT	Sens
GT	Sense	Sense	1.259	Detected	-1.259	Comprom	0.000	1.443	Detected	1.319	Detected	1.381	0.387	GT	Sens
GT	Sense	Sense	1.373	Detected	-1.373	Detected	0.000	1.977	Detected	1.293	Detected	1.635	0.367	GT	Sens
GT	Sense	Sense	0.322	Detected	-0.322	Detected	0.000	1.801	Detected	2.265	Detected	2.033	0.036	GT	Sens
GT	Sense	Sense	0.536	Detected	-0.536	Detected	0.000	0.874	Detected	1.709	Detected	1.291	0.198	GT	Sens
GT	Sense	Sense	1.626	Detected	-1.626	Comprom	0.000	1.908	Detected	2.727	Detected	2.318	0.301	GT	Sens
GT	Sense	Sense	0.603	Detected	-0.603	Detected	0.000	1.004	Detected	1.295	Detected	1.150	0.205	GT	Sens
GT	Sense	Sense	0.237	Detected	-0.237	Detected	0.000	0.801	Detected	1.201	Detected	1.001	0.084	GT	Sens
GT	Sense	Sense	0.417	Detected	-0.417	Detected	0.000	3.554	Detected	3.958	Detected	3.756	0.015	GT	Sens
GT	Sense	Sense	0.316	Detected	-0.316	Detected	0.000	0.830	Detected	1.182	Detected	1.006	0.109	GT	Sens
GT	Sense	Sense	0.741	Detected	-0.741	Detected	0.000	0.912	Detected	1.109	Detected	1.011	0.309	GT	Sens
GT	Sense	Sense	0.444	Detected	-0.444	Detected	0.000	1.373	Detected	1.722	Detected	1.548	0.083	GT	Sens
GT	Sense	Sense	0.538	Detected	-0.538	Detected	0.000	1.362	Detected	1.300	Detected	1.331	0.132	GT	Sens
GT	Sense	Sense	0.593	Detected	-0.593	Comprom	0.000	1.138	Detected	1.209	Detected	1.173	0.187	GT	Sens
GT	Sense	Sense	-0.386	Comprom	0.386	Comprom	0.000	1.805	Detected	2.647	Detected	2.226	0.060	GT	Sens
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	1.000	Detected	1.107	Detected	1.053	0.003	GT	Sens
GT	Sense	Sense	-0.485	Comprom	0.485	Comprom	0.000	2.688	Detected	2.971	Detected	2.830	0.030	GT	Sens
GT	Sense	Sense	1.318	Detected	-1.318	Comprom	0.000	1.939	Detected	2.080	Detected	2.010	0.267	GT	Sens
GT	Sense	Sense	-0.021	Detected	0.021	Detected	0.000	1.218	Detected	0.957	Detected	1.088	0.014	GT	Sens
GT	Sense	Sense	0.618	Comprom	-0.618	Comprom	0.000	0.938	Detected	1.217	Detected	1.077	0.231	GT	Sens
GT	Sense	Sense	-0.127	Detected	0.127	Detected	0.000	0.952	Detected	2.516	Detected	1.734	0.160	GT	Sens
GT	Sense	Sense	0.941	Detected	-0.941	Detected	0.000	1.678	Detected	1.407	Detected	1.543	0.246	GT	Sens
GT	Sense	Sense	0.220	Detected	-0.220	Detected	0.000	1.208	Detected	1.306	Detected	1.257	0.031	GT	Sens
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	0.872	Detected	1.580	Detected	1.226	0.084	GT	Sens
GT	Sense	Sense	0.254	Detected	-0.254	Detected	0.000	1.129	Detected	1.303	Detected	1.216	0.045	GT	Sens
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	1.184	Detected	1.281	Detected	1.233	0.015	GT	Sens
GT	Sense	Sense	0.563	Detected	-0.563	Detected	0.000	1.041	Detected	1.058	Detected	1.050	0.203	GT	Sens
GT	Sense	Sense	-0.026	Detected	0.026	Detected	0.000	1.175	Detected	1.324	Detected	1.250	0.004	GT	Sens
GT	Sense	Sense	0.145	Detected	-0.145	Detected	0.000	1.457	Detected	1.626	Detected	1.542	0.012	GT	Sens
GT	Sense	Sense	0.387	Detected	-0.387	Comprom	0.000	1.085	Detected	1.101	Detected	1.093	0.106	GT	Sens
GT	Sense	Sense	0.380	Detected	-0.380	Detected	0.000	0.937	Detected	1.127	Detected	1.032	0.119	GT	Sens
GT	Sense	Sense	0.685	Detected	-0.685	Detected	0.000	2.486	Detected	2.347	Detected	2.417	0.072	GT	Sens
GT	Sense	Sense	0.022	Detected	-0.022	Detected	0.000	1.421	Detected	1.086	Detected	1.253	0.018	GT	Sens
GT	Sense	Sense	0.012	Detected	-0.012	Detected	0.000	1.153	Detected	2.221	Detected	1.687	0.087	GT	Sens
GT	Sense	Sense	1.552	Detected	-1.552	Comprom	0.000	1.853	Detected	1.764	Detected	1.809	0.364	GT	Sens
GT	Sense	Sense	-0.286	Comprom	0.286	Comprom	0.000	0.980	Detected	1.337	Detected	1.159	0.075	GT	Sens
GT	Sense	Sense	0.460	Detected	-0.460	Detected	0.000	1.043	Detected	1.207	Detected	1.125	0.138	GT	Sens
GT	Sense	Sense	0.824	Detected	-0.824	Comprom	0.000	0.852	Detected	1.172	Detected	1.012	0.351	GT	Sens
GT	Sense	Sense	0.099	Detected	-0.099	Detected	0.000	1.386	Detected	1.224	Detected	1.305	0.009	GT	Sens
GT	Sense	Sense	-0.070	Detected	0.070	Detected	0.000	1.089	Detected	1.462	Detected	1.276	0.024	GT	Sens
GT	Sense	Sense	0.326	Comprom	-0.326	Comprom	0.000	2.308	Detected	2.063	Detected	2.186	0.025	GT	Sens
GT	Sense	Sense	-0.173	Detected	0.173	Detected	0.000	1.463	Detected	1.406	Detected	1.435	0.015	GT	Sens
GT	Sense	Sense	1.427	Detected	-1.427	Detected	0.000	1.689	Detected	2.524	Detected	2.106	0.292	GT	Sens
GT	Sense	Sense	0.165	Detected	-0.165	Detected	0.000	1.197	Detected	1.831	Detected	1.514	0.051	GT	Sens
GT	Sense	Sense	0.629	Detected	-0.629	Detected	0.000	1.301	Detected	1.721	Detected	1.511	0.150	GT	Sens
GT	Sense	Sense	-0.493	Comprom	0.493	Comprom	0.000	1.157	Detected	1.516	Detected	1.337	0.126	GT	Sens
GT	Sense	Sense	-0.805	Comprom	0.805	Detected	0.000	1.227	Detected	0.847	Detected	1.037	0.336	GT	Sens
GT	Sense	Sense	1.024	Detected	-1.024	Detected	0.000	2.077	Detected	0.896	Detected	1.486	0.336	GT	Sens
GT	Sense	Sense	0.278	Detected	-0.278	Detected	0.000	1.263	Detected	1.037	Detected	1.150	0.062	GT	Sens
GT	Sense	Sense	0.842	Detected	-0.842	Detected	0.000	1.548	Detected	2.384	Detected	1.966	0.172	GT	Sens
GT	Sense	Sense	-0.009	Detected	0.009	Detected	0.000	0.949	Detected	1.212	Detected	1.080	0.015	GT	Sens
GT	Sense	Sense	0.526	Detected	-0.526	Comprom	0.000	1.415	Detected	1.223	Detected	1.319	0.132	GT	Sens
GT	Sense	Sense	0.407	Comprom	-0.407	Comprom	0.000	1.695	Detected	1.858	Detected	1.776	0.051	GT	Sens
GT	Sense	Sense	-0.020	Detected	0.020	Detected	0.000	1.296	Detected	2.144	Detected	1.720	0.056	GT	Sens
GT	Sense	Sense	0.480	Detected	-0.480	Detected	0.000	1.092	Detected	1.351	Detected	1.222	0.133	GT	Sens
GT	Sense	Sense	0.686	Detected	-0.686	Detected	0.000	1.162	Detected	1.792	Detected	1.477	0.189	GT	Sens
GT	Sense	Sense	0.729	Detected	-0.729	Detected	0.000	1.884	Detected	2.652	Detected	2.268	0.111	GT	Sens
GT	Sense	Sense	-0.053	Comprom	0.053	Comprom	0.000	2.092	Detected	2.687	Detected	2.389	0.016	GT	Sens
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	0.947	Detected	1.134	Detected	1.040	0.021	GT	Sens
GT	Sense	Sense	0.520	Detected	-0.520	Detected	0.000	1.205	Detected	1.346	Detected	1.276	0.136	GT	Sens
GT	Sense	Sense	0.009	Detected	-0.009	Detected	0.000	0.992	Detected	1.195	Detected	1.093	0.009	GT	Sens
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	0.903	Detected	1.148	Detected	1.025	0.015	GT	Sens
GT	Sense	Sense	-0.493	Comprom	0.493	Detected	0.000	1.113	Detected	0.954	Detected	1.033	0.174	GT	Sens
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	0.968	Detected	1.275	Detected	1.122	0.029	GT	Sens
GT	Sense	Sense	-0.054	Comprom	0.054	Comprom	0.000	1.291	Detected	0.902	Detected	1.096	0.032	GT	Sens
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	0.876	Detected	1.580	Detected	1.228	0.081	GT	Sens
GT	Sense	Sense	-0.325	Comprom	0.325	Comprom	0.000	1.368	Detected	1.270	Detected	1.319	0.057	GT	Sens
GT	Sense	Sense	1.139	Detected	-1.139	Detected	0.000	1.654	Detected	1.855	Detected	1.754	0.265	GT	Sens
GT	Sense	Sense	0.739	Detected	-0.739	Detected	0.000	1.565	Detected	1.109	Detected	1.337	0.226	GT	Sens
GT	Sense	Sense	-0.398	Comprom	0.398	Comprom	0.000	1.734	Detected	1.451	Detected	1.593	0.064	GT	Sens
GT	Sense	Sense	1.860	Detected	-1.860	Detected	0.000	1.696	Detected	2.133	Detected	1.915	0.414	GT	Sens
GT	Sense	Sense	0.139	Detected	-0.139	Detected	0.000	0.923	Detected	1.144	Detected	1.034	0.028	GT	Sens
GT	Sense	Sense	0.369	Detected	-0.369	Detected	0.000	1.347	Detected	1.486	Detected	1.416	0.064	GT	Sens
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	1.391	Detected	1.133	Detected	1.262	0.015	GT	Sens
GT	Sense	Sense	-0.588	Comprom	0.588	Detected	0.000	0.964	Detected	2.772	Detected	1.868	0.225	GT	Sens
GT	Sense	Sense	0.665	Detected	-0.665	Detected	0.000	1.401	Detected	1.610	Detected	1.506	0.155	GT	Sens
GT	Sense	Sense	0.380	Detected	-0.380	Detected	0.000	1.261	Detected	1.148	Detected	1.205	0.089	GT	Sens
GT	Sense	Sense	-0.311	Detected	0.311	Detected	0.000	1.498	Detected	1.344	Detected	1.421	0.047	GT	Sens
GT	Sense	Sense	0.715	Detected	-0.715	Detected	0.000	0.946	Detected	1.294	Detected	1.120	0.268	GT	Sens
GT	Sense	Sense	0.328	Detected	-0.328	Detected	0.000	0.986	Detected	1.223	Detected	1.105	0.087	GT	Sens
GT	Sense	Sense	0.390	Detected	-0.390	Detected	0.000	1.269	Detected	1.538	Detected	1.403	0.077	GT	Sens
GT	Sense	Sense	0.503	Detected	-0.503	Comprom	0.000	1.538	Detected	0.992	Detected	1.265	0.158	GT	Sens
GT	Sense	Sense	0.148	Detected	-0.148	Detected	0.000	0.927	Detected	1.200	Detected	1.064	0.034	GT	Sens
GT	Sense	Sense	0.440	Detected	-0.440	Detected	0.000	1.355	Detected	0.861	Detected	1.108	0.159	GT	Sens
GT	Sense	Sense	0.720	Detected	-0.720	Detected	0.000	0.951	Detected	1.995	Detected	1.473	0.239	GT	Sens
GT	Sense	Sense	0.653	Detected	-0.653	Detected	0.000	1.051	Detected	2.213	Detected	1.632	0.203	GT	Sens
GT	Sense	Sense	0.358	Detected	-0.358	Detected	0.000	1.084	Detected	1.147	Detected	1.116	0.090	GT	Sens
GT	Sense	Sense	0.123	Detected	-0.123	Detected	0.000	0.877	Detected	1.497	Detected	1.187	0.071	GT	Sens
GT	Sense	Sense	0.600	Detected	-0.600	Detected	0.000	1.459	Detected	1.124	Detected	1.292	0.174	GT	Sens
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	1.128	Detected	1.213	Detected	1.170	0.003	GT	Sens
GT	Sense	Sense	0.104	Detected	-0.104	Detected	0.000	1.087	Detected	1.085	Detected	1.086	0.009	GT	Sens
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	0.977	Detected	1.267	Detected	1.122	0.028	GT	Sens
GT	Sense	Sense	0.815	Detected	-0.815	Detected	0.000	0.989	Detected	1.379	Detected	1.184	0.293	GT	Sens

GT	Sense	Sense	0.490	Detected	-0.490	Detected	0.000	0.810	Detected	1.804	Detected	1.307	0.202	GT	Sens	X72730	X72730	ERT10	CCGGTGTCCCGATTTCTCATCCCTCTAGTATAGAGAAAACAAATTAGAAAAATAAGGAT																7402.59	3419.48	7095.39	7792.06	8419.6	17679.2
GT	Sense	Sense	0.348	Detected	-0.348	Detected	0.000	1.373	Detected	0.805	Detected	1.089	0.136	GT	Sens	contig101	contig101	Proline ri	AATTAAA	contig101	Solyc12g	Solyc12g	Proline ri	GO:00051	GO:00051	contig101	Solyc12g	Proline ri	GO:00051	SL2.40ch	AT5G26740.3		unknown	chr5:929	52.7739	29.683	166.637	175.062	97.8522	69.5761
GT	Sense	Sense	0.391	Detected	-0.391	Detected	0.000	1.014	Detected	1.210	Detected	1.112	0.110	GT	Sens	contig102	contig102	Unknown	GCCGTG	contig102	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig102	Solyc05g	Unknown Protein (A		SL2.40ch	AT1G52360.1		coatome	chr1:194	602.12	319.406	269.213	752.532	845.449	1020.93
GT	Sense	Sense	0.530	Detected	-0.530	Detected	0.000	1.206	Detected	2.195	Detected	1.700	0.144	GT	Sens	contig103	contig103	Unknown	TATATCA	contig103	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig103	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G015	ANAC068	NTM1 (N/	chr4:670	40.1644	17.5688	18.8581	27.5636	58.5052	122.33
GT	Sense	Sense	0.287	Detected	-0.287	Detected	0.000	0.933	Detected	2.028	Detected	1.480	0.139	GT	Sens	contig103	contig103	Unknown	GCAAAAT	contig103	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig103	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G015	ANAC068	NTM1 (N/	chr4:670	130.681	80.0236	79.5541	105.499	186.414	419.453
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	0.918	Detected	1.642	Detected	1.280	0.072	GT	Sens	contig102	contig102	Receptor	ACCGACA	contig102	Solyc07g	Solyc07g	Receptor	GO:00055	GO:00055	contig102	Solyc07g	Receptor	GO:00055	SL2.40ch	AT4G323	SD2-5	SD2-5 (S	chr4:155	123.084	118.462	101.84	192.732	217.784	379.147
GT	Sense	Sense	0.488	Detected	-0.488	Detected	0.000	0.848	Detected	2.084	Detected	1.466	0.204	GT	Sens	contig104	contig104	Protein s	TGAAGAT	contig104	Solyc02g	Solyc02g	Protein s	GO:00064	GO:00064	contig104	Solyc02g	Protein s	GO:00428	SL2.40ch	AT5G670	MAPKKK	MAPKKK	chr5:267	1695.62	785.641	1085.32	1581.18	1983.15	4923.48
GT	Sense	Sense	0.563	Detected	-0.563	Detected	0.000	1.022	Detected	2.423	Detected	1.723	0.195	GT	Sens	contig105	contig105	Protein s	TTCAGGA	contig105	Solyc07g	Solyc07g	Protein s	GO:00064	GO:00064	contig105	Solyc07g	Protein s	GO:00428	SL2.40ch	AT3G46370.1		leucine-r	chr3:170	304.657	127.319	260.379	382.875	381.796	1062.78
GT	Sense	Sense	1.175	Detected	-1.175	Detected	0.000	1.348	Detected	1.018	Detected	1.183	0.424	GT	Sens	contig106	contig106	Wound in	TAGAAGG	contig106	Solyc07g	Solyc07g	Wound induced protein (AHRD			contig106	Solyc07g	Wound induced pro		SL2.40ch	AT4G10270.1		wound-re	chr4:637	2306.93	412.329	773.146	1974.58	2370.43	1987.48
GT	Sense	Sense	1.149	Detected	-1.149	Detected	0.000	0.909	Detected	2.162	Detected	1.536	0.362	GT	Sens	contig107	contig107	UDP-gluc	TTGAATT	contig107	Solyc11g	Solyc11g	UDP-gluc	GO:00081	GO:00081	contig107	Solyc11g	UDP-gluc	GO:00081	SL2.40ch	AT4G30500.1		unknown	chr4:149	334.815	62.0279	228.049	255.227	258.409	648.799
GT	Sense	Sense	1.109	Detected	-1.109	Detected	0.000	2.006	Detected	1.364	Detected	1.685	0.282	GT	Sens	contig107	contig107	Aminotra	TGGTGG	contig107	Solyc12g	Solyc12g	Aminotra	GO:00301	GO:00301	contig107	Solyc12g	Aminotra	GO:00301	SL2.40ch	AT3G222	POP2. GA	POP2 (PO	chr3:783	854.063	167.456	612.906	3781.72	1450.78	979.125
GT	Sense	Sense	-0.122	Detected	0.122	Detected	0.000	1.584	Detected	1.045	Detected	1.315	0.047	GT	Sens	contig107	contig107	Unknown	AACATCC	contig107	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig107	Solyc04g	Unknown Protein (A		SL2.40ch	AT4G20160.1		LOCATE	chr4:108	107.102	115.645	242.943	416.6	318.66	231.058
GT	Sense	Sense	0.496	Detected	-0.496	Detected	0.000	1.096	Detected	1.146	Detected	1.121	0.152	GT	Sens	contig108	contig108	Breast ca	GGTTGAT	contig108	Solyc05g	Solyc05g	Breast ca	GO:00037	GO:00037	contig108	Solyc05g	Breast ca	GO:00037	SL2.40ch	AT5G08500.1		transmem	chr5:274	1181.18	541.788	649.248	1578.61	1632.83	1781.23
GT	Sense	Sense	0.322	Detected	-0.322	Detected	0.000	1.173	Detected	1.208	Detected	1.190	0.066	GT	Sens	contig109	contig109	Proteinas	GACCCTA	contig109	Solyc00g	Solyc00g	Proteinas	GO:00048	GO:00048	contig109	Solyc00g	Proteinas	GO:00048	SL2.40ch	AT4G123	MYB42. A	MYB42 (N	chr4:732	1792.29	1045.01	3325.22	4013.7	2945.36	3181.04
GT	Sense	Sense	0.442	Detected	-0.442	Detected	0.000	0.803	Detected	1.804	Detected	1.304	0.190	GT	Sens	contig110	contig110	Ycf2 (AHF	TTTCCTC	contig110	Solyc02g	Solyc02g	Ycf2 (AHF	GO:00095	GO:00095	contig110	Solyc09g	RING fing	GO:00065	SL2.40ch	AT3G218	ATXR2. S	ATXR2 (H	chr3:768	694.889	343.397	247.536	443.93	813.632	1716.4
GT	Sense	Sense	0.671	Detected	-0.671	Detected	0.000	1.298	Detected	1.358	Detected	1.328	0.187	GT	Sens	contig112	contig112	Xanthine	ACTGATC	contig112	Solyc11g	Solyc11g	Xanthine	GO:00551	GO:00551	contig112	Solyc11g	Xanthine	GO:00090	SL2.40ch	AT4G348	ATXDH1.	XDH1 (XA	chr4:166	6997.4	2515.85	4131.22	12748.4	9850.2	10822.6
GT	Sense	Sense	-0.455	Comprom	0.455	Comprom	0.000	2.279	Detected	2.963	Detected	2.621	0.044	GT	Sens	contig115	contig115	Mutator-li	TTTCTAC	contig115	Solyc04g	Solyc04g	Mutator-like transposase (AHF			contig115	Solyc01g	Mutator-like transpo		SL2.40ch	AT5G18550.1		nucleic a	chr5:616	2.22956	3.81756	3.81621	6.47123	13.5161	22.8922
GT	Sense	Sense	0.473	Detected	-0.473	Detected	0.000	1.126	Detected	1.013	Detected	1.070	0.154	GT	Sens	contig116	contig116	CST com	AGGAACT	contig116	Solyc12g	Solyc12g	CST complex subunit CTC1 (A			contig116	Solyc12g	CST complex subun		SL2.40ch	AT3G22150.1		pentatric	chr3:781	45.4295	21.4914	18.6483	60.0685	65.129	63.4352
GT	Sense	Sense	-0.198	Detected	0.198	Detected	0.000	1.482	Detected	1.691	Detected	1.586	0.019	GT	Sens	contig119	contig119	1-aminoc	TTTGAAC	contig119	Solyc09g	Solyc09g	1-aminocyclopropane-1-carbo			contig119	Solyc09g089700.2.1				AT3G61400.1		2-oxoglu	chr3:227	28.4169	34.0959	85.2071	292.076	83.0118	101.104
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	1.142	Detected	0.968	Detected	1.055	0.008	GT	Sens	contig123	contig123	Aquapori	AATTCTC	contig123	Solyc10g	Solyc10g	Aquapori	GO:00160	GO:00160	contig123	Solyc10g	Aquapori	GO:00152	SL2.40ch	AT2G168	PIP3B. PI	PIP2:8 (P	chr2:730	209.374	181.645	245.919	661.012	410.839	383.779
GT	Sense	Sense	-0.058	Detected	0.058	Detected	0.000	1.297	Detected	1.041	Detected	1.169	0.014	GT	Sens	contig124	contig124	Aquapori	GCCATGC	contig124	Solyc10g	Solyc10g	Aquapori	GO:00160	GO:00160	contig124	Solyc10g	Aquapori	GO:00152	SL2.40ch	AT2G168	PIP3B. PI	PIP2:8 (P	chr2:730	483.111	477.519	659.96	1545.59	1126.86	994.259
GT	Sense	Sense	0.377	Detected	-0.377	Detected	0.000	1.167	Detected	1.478	Detected	1.323	0.083	GT	Sens	contig127	contig127	Glucose-	TTGCCAC	contig127	Solyc12g	Solyc12g	Glucose-	GO:00090	GO:00090	contig127	Solyc07g	Glucose-	GO:00088	SL2.40ch	AT5G483	ADG1. AF	ADG1 (AI	chr5:195	740.617	400.18	447.931	1494.35	1167.35	1525.4
GT	Sense	Sense	0.521	Detected	-0.521	Detected	0.000	1.075	Detected	1.547	Detected	1.311	0.149	GT	Sens	contig128	contig128	Sulfate ad	ACTGCCC	contig128	Solyc09g	Solyc09g	Sulfate ad	GO:00001	GO:00001	contig128	Solyc09g	Sulfate ad	GO:00047	SL2.40ch	AT4G146	APS3	APS3: su	chr4:841	361.46	160.066	261.47	527.599	483.972	706.917
GT	Sense	Sense	0.278	Detected	-0.278	Detected	0.000	1.189	Detected	0.861	Detected	1.025	0.087	GT	Sens	contig128	contig128	Unknown	AACAATT	contig128	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig128	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G43550.1				137.05	84.9519	65.2158	255.214	234.832	197.147
GT	Sense	Sense	-1.201	Comprom	1.201	Detected	0.000	1.770	Detected	1.414	Detected	1.592	0.320	GT	Sens	contig131	contig131	Kinase-lik	AATTTCC	contig131	Solyc04g	Solyc04g	Kinase-lik	GO:00064	GO:00064	contig131	Solyc04g	Receptor	GO:00046	SL2.40ch	AT5G478	CCR4	CCR4 (AF	chr5:193	3.04195	14.6541	8.05394	27.0003	21.747	17.9025
GT	Sense	Sense	0.269	Comprom	-0.269	Comprom	0.000	1.121	Detected	1.221	Detected	1.171	0.050	GT	Sens	contig131	contig131	Homeobo	AGTCTCA	contig131	Solyc02g	Solyc02g	Homeobo	GO:00435	GO:00435	contig131	Solyc02g	Homeobo	GO:00435	SL2.40ch	AT1G052	HDG2	HDG2 (HC	chr1:151	10.912	6.85594	9.66785	26.5565	17.962	20.2776
GT	Sense	Sense	0.232	Detected	-0.232	Detected	0.000	1.097	Detected	1.176	Detected	1.137	0.040	GT	Sens	contig132	contig132	class I he	GAGCAAT	contig132	Solyc09g	Solyc09g	class I he	GO:00510	GO:00510	contig132	Solyc09g	class I he	GO:00510	SL2.40ch	AT5G597	HSP18.2	HSP18.2	chr5:240	91.6868	60.6183	66.9241	138.183	152.299	169.48
GT	Sense	Sense	-0.789	Comprom	0.789	Comprom	0.000	1.356	Detected	1.005	Detected	1.180	0.282	GT	Sens	contig139	contig139	Unknown	CAATTAC	contig139	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig139	Solyc11g	Genomic DNA chror		SL2.40ch	AT5G059	DHS	DHS (DE	chr5:177	3.15631	8.58871	5.55702	8.06585	12.7218	10.5087
GT	Sense	Sense	0.694	Detected	-0.694	Detected	0.000	1.343	Detected	1.574	Detected	1.458	0.174	GT	Sens	contig141	contig141	Protein ki	GCTTCAC	contig141	Solyc01g	Solyc01g	Protein ki	GO:00167	GO:00167	contig141	Solyc01g	Serine/thr	GO:00046	SL2.40ch	AT1G500	TOR	TOR (TAI	chr1:185	367.682	128.167	139.734	484.177	525.636	650.342
GT	Sense	Sense	1.427	Detected	-1.427	Comprom	0.000	1.436	Detected	1.840	Detected	1.638	0.374	GT	Sens	contig143	contig143	Ferric red	CTGGTG	contig143	Solyc01g	Solyc01g	Ferric red	GO:00160	GO:00160	contig143	Solyc01g	Ferric red	GO:00002	SL2.40ch	AT5G497	ATFRO7.	ATFRO7	chr5:202	17.2832	2.17955	4.18962	18.7781	15.8551	22.1034
GT	Sense	Sense	2.499	Detected	-2.499	Detected	0.000	2.049	Detected	4.326	Detected	3.188	0.366	GT	Sens	contig144	contig144	N-hydrox	TATACTT	contig144	Solyc05g	Solyc05g	N-hydrox	GO:00167	GO:00167	contig144	Solyc05g	N-hydrox	GO:00167	SL2.40ch	AT2G39980.1		transfera	chr2:166	2682.41	76.5144	1527.03	1518.07	1789.97	9142.57
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	1.481	Detected	1.646	Detected	1.563	0.008	GT	Sens	contig144	contig144	Naringeni	GGTATTT	contig144	Solyc04g	Solyc04g	Naringeni	GO:00164	GO:00164	contig144	Solyc09g	1-aminoc	GO:00098	SL2.40ch	AT3G52140.1		tetratrico	chr3:193	117.078	91.0105	196.564	369.077	275.077	324.955
GT	Sense	Sense	1.541	Detected	-1.541	Detected	0.000	2.183	Detected	1.601	Detected	1.892	0.351	GT	Sens	contig146	contig146	Chalcone	CTGGTG	contig146	Solyc05g	Solyc05g	Chalcone	GO:00081	GO:00081	contig146	Solyc05g	Chalcone	GO:00084	SL2.40ch	AT5G139	CHS. TT4	TT4 (TRA	chr5:448	21048.5	2265.19	7900.7	34016.4	29939	21066.3
GT	Sense	Sense	1.388	Detected	-1.388	Detected	0.000	1.718	Detected	2.610	Detected	2.164	0.276	GT	Sens	contig146	contig146	Zinc finge	TGCTATT	contig146	Solyc12g	Solyc12g	Zinc finge	GO:00056	GO:00056	contig146	Solyc12g	Zinc finge	GO:00056	SL2.40ch	AT3G205	POLGAM	POLGAM	chr3:716	83.4419	11.1134	79.1388	67.0816	95.6523	187.085
GT	Sense	Sense	0.260	Detected	-0.260	Detected	0.000	1.260	Detected	1.275	Detected	1.268	0.040	GT	Sens	contig151	contig151	Photosys	GGCCTAC	contig151	Solyc12g	Solyc12g	Photosys	GO:00095	GO:00095	contig151	Solyc12g	Photosys	GO:00095	SL2.40ch	AT1G522	PSAH2. P	PSAH2 (F	chr1:194	206.902	131.579	306.474	570.356	377.281	401.707
GT	Sense	Sense	0.958	Detected	-0.958	Detected	0.000	1.362	Detected	1.775	Detected	1.569	0.250	GT	Sens	contig157	contig157	Heat shoc	AGTGGT	contig157	Solyc04g	Solyc04g	Heat shock cognate protein 2 (			contig157	Solyc04g	Heat shock cognate		SL2.40ch	AT3G32030.1				14005.7	3385.01	7578.6	11173.9	16903.8	23707
GT	Sense	Sense	0.342	Detected	-0.342	Detected	0.000	0.885	Detected	1.553	Detected	1.219	0.125	GT	Sens	contig157	contig157	Catalase	ATGCTCT	contig157	Solyc01g	Solyc01g	Catalase	GO:00551	GO:00551	contig157	Solyc01g	Catalase	GO:00551	SL2.40ch	AT4G350	CAT2	CAT2 (CA	chr4:167	720.29	408.947	573.502	1743.63	957.081	1602.17
GT	Sense	Sense	-1.387	Comprom	1.387	Detected	0.000	1.929	Detected	1.664	Detected	1.797	0.326	GT	Sens	contig158	contig158	Ripening-	TGTAGAT	contig158	Solyc03g	Solyc03g	Ripening-related protein 3 (AH			contig158	Solyc03g013300.1.1				AT3G16800.1		protein p	chr3:572	2.82623	17.627	29.3835	32.473	25.6651	22.5
GT	Sense	Sense	0.218	Comprom	-0.218	Comprom	0.000	2.147	Detected	2.120	Detected	2.134	0.010	GT	Sens	contig158	contig158	Zeatin O-	TCTCCAT	contig158	Solyc07g	Solyc07g	Zeatin O-glucosyltransferase (			contig158	Solyc07g	UDP-gluc	GO:00080	SL2.40ch	AT3G496	UBP26. S	UBP26 (U	chr3:183	7.20324	4.8554	7.00388	75.6412	25.0167	25.866
GT	Sense	Sense	0.292	Detected	-0.292	Detected	0.000	1.245	Detected	0.998	Detected	1.121	0.071	GT	Sens	contig160	contig160	Susceptib	GAAAAAT	contig160	Solyc01g	Solyc01g	Susceptib	GO:00055	GO:00055	contig160	Solyc01g	Susceptib	GO:00055	SL2.40ch	AT5G49600.1		unknown	chr5:201	575.193	349.781	558.826	1674.39	1014.78	901.243
GT	Sense	Sense	0.630	Detected	-0.630	Detected	0.000	0.916	Detected	1.411	Detected	1.164	0.228	GT	Sens	contig160	contig160	Cysteine	TACACGT	contig160	Solyc09g	Solyc09g	Cysteine	GO:00082	GO:00082	contig160	Solyc11g	Cysteine	GO:00065	SL2.40ch	AT3G54940.2		cysteine-	chr3:203	32.5338	12.3874	9.29332	26.8454	36.167	53.7199
GT	Sense	Sense	1.366	Detected	-1.366	Comprom	0.000	1.300	Detected	1.718	Detected	1.509	0.389	GT	Sens	contig163	contig163	Primary a	ATAATGC	contig163	Solyc09g	Solyc09g	Primary a	GO:00551	GO:00551	contig163	Solyc09g	Primary a	GO:00551	SL2.40ch	AT1G62810.1		copper a	chr1:232	43.74	6.00262	24.3956	56.385	38.0857	53.6318
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	0.851	Detected	1.194	Detected	1.023	0.028	GT	Sens	contig164	contig164	PAR-1c p	GACTCTT	contig164	Solyc03g	Solyc03g	PAR-1c protein (AHRD V1 ***- C			contig164	Solyc03g	PAR-1c protein (AHF		SL2.40ch	AT5G52390.1		photoass	chr5:212	5266.92	5066.82	2468.8	4365.3	8899.4	11891.1
GT	Sense	Sense	0.489	Detected	-0.489	Detected	0.000	1.087	Detected	1.740	Detected	1.413	0.138	GT	Sens	contig164	contig164	Receptor-	ATACTAT	contig164	Solyc11g	Solyc11g	Receptor-like protein kinase (A			contig164	Solyc11g	Receptor-like protei		SL2.40ch	AT3G29785.1		unknown	chr3:116	122.235	56.5674	107.368	158.514	168.7	279.341
GT	Sense	Sense	0.375	Detected	-0.375	Detected	0.000	1.333	Detected	1.789	Detected	1.561	0.071	GT	Sens	contig166	contig166	Subtilisin	ATAGTGC	contig166	Solyc01g	Solyc01g	Subtilisin	GO:00042	GO:00042	contig166	Solyc01g	Subtilisin	GO:00042	SL2.40ch	AT2G041	AIR3	AIR3: ser	chr2:140	45.3959	24.6061	73.1732	108.289	80.4067	116.209
GT	Sense	Sense	0.745	Detected	-0.745	Detected	0.000	1.225	Detected	1.318	Detected	1.271	0.230	GT	Sens	contig167	contig167	Glutathio	AAAGCTC	contig167	Solyc12g	Solyc12g	Glutathione S-transferase (AHI			contig167	Solyc09g	Glutathio	GO:00451	SL2.40ch	AT4G09467.1				1794.48	582.763	1093.47	3294.65	2282.84	2564.07
GT	Sense	Sense	0.579	Detected	-0.579	Detected	0.000	0.866	Detected	2.034	Detected	1.450	0.220	GT	Sens	contig168	contig168	Glutathio	CAAGAGA	contig168	Solyc09g	Solyc09g	Glutathio	GO:00043	GO:00043	contig168	Solyc09g	Glutathio	GO:00043	SL2.40ch	AT1G699	ATGSTU1	ATGSTU	chr1:263	24395.4	9965.06	26384.1	29296.1	27128.6	64240.2
GT	Sense	Sense	0.297	Detected	-0.297	Detected	0.000	0.973	Detected	1.077	Detected	1.025	0.077	GT	Sens	contig168	contig168	Proteinas	GGTGTT	contig168	Solyc09g	Solyc09g	Proteinas	GO:00096	GO:00096	contig168	Solyc09g	Proteinas	GO:00096	SL2.40ch	AT5G553	EDM2	EDM2: tr	chr5:224	14614	8824.41	11755.9	22110.1	21281.6	24104.7
GT	Sense	Sense	-0.397	Comprom	0.397	Comprom	0.000	8.353	Detected	7.400	Detected	7.876	0.006	GT	Sens	contig170	contig170	Gag poly	CTGCATC	contig170	Solyc00g	Solyc00g	Gag poly	GO:00082	GO:00082	contig170	Solyc11g	Kinase fa	GO:00064	SL2.40ch	AT5G286	WRKY74.	WRKY74	chr5:106	2.41241	3.81124	3473.48	8.06126	946.609	515.17
GT	Sense	Sense	0.250	Detected	-0.250	Detected	0.000	1.040	Detected	1.156	Detected	1.098	0.051	GT	Sens	contig171	contig171	Helicase (	CAATGTT	contig171	Solyc06g	Solyc06g	Helicase (AHRD V1 *--- B3LLX3			contig171	Solyc06g	Helicase (	GO:00055	SL2.40ch	AT1G054	SDE3	SDE3 (SI	chr1:160	680.4	438.725	349.4	791.58	1072.32	1224.91
GT	Sense	Sense	0.168	Detected	-0.168	Detected	0.000	2.981	Detected	2.474	Detected	2.728	0.012	GT	Sens	contig171	contig171	Acetylorn	TCAGGG	contig171	Solyc08g	Solyc08g	Acetylorn	GO:00081	GO:00081	contig171	Solyc08g	Acetylorn	GO:00167	SL2.40ch	AT4G17830.1		peptidas	chr4:991	14.8988	10.7658	12.9231	75.7103	95.4844	70.7939
GT	Sense	Sense	0.337	Detected	-0.337	Detected	0.000	1.266	Detected	0.925	Detected	1.096	0.101	GT	Sens	contig171	contig171	Pumilio-li	AATGGG	contig171	Solyc06g	Solyc06g	Pumilio-li	GO:00037	GO:00037	contig171	Solyc06g	Pumilio-li	GO:00054	SL2.40ch	AT1G26500.1				79.1839	45.255	35.0394	154.015	137.446	114.375
GT	Sense	Sense	0.602	Detected	-0.602	Detected	0.000	0.818	Detected	1.289	Detected	1.053	0.245	GT	Sens	contig175	contig175	Multidrug	ACGAATT	contig175	Solyc12g	Solyc12g	Multidrug resistance protein A			contig175	Solyc12g	Multidrug	GO:00171	SL2.40ch	AT3G212	ATMRP6.	ATMRP6	chr3:745	49.0599	19.4245	95.6581	204.16	51.9609	75.8744
GT	Sense	Sense	0.595	Detected	-0.595	Detected	0.000	1.243	Detected	1.561	Detected	1.402	0.151	GT	Sens	contig175	contig175	Multidrug	CTCTCTT	contig175	Solyc03g	Solyc03g	Multidrug	GO:00152	GO:00152	contig175	Solyc07g	Hypersen	GO:00338	SL2.40ch	AT1G66980.1		protein k	chr1:249	21054.4	8414.02	17035.5	42453.7	30072	39519.1
GT	Sense	Sense	0.080	Detected	-0.080	Detected	0.000	1.863	Detected	2.025	Detected	1.944	0.003	GT	Sens	contig175	contig175	FAM65A r	AGGTGG	contig175	Solyc05g	Solyc05g	FAM65A protein related (AHRD			contig175	Solyc05g	FAM65A protein rela		SL2.40ch	AT2G18380.1		transcrip	chr2:798	26.5747	21.6936	38.0649	130.78	83.4113	98.2965
GT	Sense	Sense	0.428	Detected	-0.428	Detected	0.000	1.319	Detected	1.440	Detected	1.380	0.086	GT	Sens	contig176	contig176	Acid phos	CTAAAGC	contig176	Solyc06g	Solyc06g	Acid phos	GO:00039	GO:00039	contig176	Solyc06g	Acid phos	GO:00039	SL2.40ch	AT4G29270.1		acid pho	chr4:144	30467.9	15347	29637	49389.4	51513	59041
GT	Sense	Sense	0.564	Detected	-0.564	Detected	0.000	1.056	Detected	1.659	Detected	1.357	0.168	GT	Sens	contig177	contig177	Xanthine	CCAGGA	contig177	Solyc11g	Solyc11g	Xanthine	GO:00506	GO:00506	contig177	Solyc11g071610.1.1				AT1G045	AAO4. AT	AAO4 (AF	chr1:125	814.508	339.659	302.084	965.245	1044.09	1670.59
GT	Sense	Sense	0.576	Detected	-0.576	Detected	0.000	1.188	Detected	1.902	Detected	1.545	0.150	GT	Sens	contig178	contig178	ATP-bind	CCTGCT	contig178	Solyc05g	Solyc05g	ATP-bind	GO:00168	GO:00168	contig178	Solyc05g	ATP-bind	GO:00426	SL2.40ch	AT1G155	PDR12. A	PDR12 (F	chr1:533	9155.64	3754.3	7261.62	9699.3	12755.2	22048.7
GT	Sense	Sense	0.588	Detected	-0.588	Detected	0.000	1.480	Detected	1.552	Detected	1.516	0.124	GT	Sens	contig185	contig185	Callose s	GCAGATT	contig185	Solyc01g	Solyc01g	Callose synthase 1 (AHRD V1 *			contig185	Solyc01g	Callose synthase 1		SL2.40ch	AT5G130	ATGSL12	ATGSL12	chr5:411	4193.09	1692.16	2578.65	7795.82	7096.62	7858.31
GT	Sense	Sense	0.266	Detected	-0.266	Detected	0.000	1.538	Detected	0.955	Detected	1.246	0.087	GT	Sens	contig185	contig185	Unknown	GGAGTT	contig185	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig185	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G19200.1		unknown	chr3:664	172.483	108.814	104.399	232.224	379.794	267.209
GT	Sense	Sense	0.306	Detected	-0.306	Detected	0.000	1.427	Detected	1.659	Detected	1.543	0.042	GT	Sens	contig186	contig186	Oxidored	ATTAAGC	contig186	Solyc01g	Solyc01g	Oxidored	GO:00081	GO:00081	contig186	Solyc01g	Oxidored	GO:00081	SL2.40ch	AT5G16990.1		NADP-de	chr5:558	83.746	49.9517	215.326	250.234	166.009	205.535
GT	Sense	Sense	0.607	Detected	-0.607	Detected	0.000	1.728	Detected	1.490	Detected	1.609	0.122	GT	Sens	contig187	contig187	Argonaut	AATGGAT	contig187	Solyc06g	Solyc06g	Argonaut	GO:00036	GO:00036	contig187	Solyc06g	Argonaut	GO:00198	SL2.40ch	AT2G270	AGO4. OC	AGO4 (AI	chr2:115	713.57	280.257	413.624	1314.19	1414.84	1263.26
GT	Sense	Sense	0.267	Detected	-0.267	Detected	0.000	1.566	Detected	1.382	Detected	1.474	0.035	GT	Sens	contig190	contig190	Rhamnog	CAAAGTC	contig190	Solyc04g	Solyc04g	Rhamnog	GO:00302	GO:00302	contig190	Solyc04g	Rhamnog	GO:00302	SL2.40ch	AT1G09890.1		lyase	chr1:321	904.506	569.238	804.892	1364.87	2028.09	1881.39
GT	Sense	Sense	-0.460	Detected	0.460	Detected	0.000	2.089	Detected	1.720	Detected	1.905	0.061	GT	Sens	contig195	contig195	FAD-bind	GAGCTTT	contig195	Solyc10g	Solyc10g	FAD-bind	GO:00506	GO:00506	contig195	Solyc02g	FAD-bind	GO:00090	SL2.40ch	AT5G44410.1		FAD-bind	chr5:178	123.28	212.581	101.079	362.769	657.542	536.598
GT	Sense	Sense	-0.559	Comprom	0.559	Detected	0.000	1.039	Detected	1.259	Detected	1.149	0.181	GT	Sens	contig195	contig195	Genomic	TTATTCT	contig195	Solyc02g	Solyc02g	Genomic DNA chromosome 5			contig195	Solyc02g	Genomic DNA chror		SL2.40ch	AT5G66090.1		unknown	chr5:264	6.77186	13.3963	10.6491	12.5808	18.6845	22.9338
GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	0.972	Detected	1.759	Detected	1.365	0.085	GT	Sens	contig204	contig204	Transcrip	TGTTTCA	contig204	Solyc02g	Solyc02g	Transcrip	GO:00056	GO:00056	contig204	Solyc02g	Transcrip	GO:00037	SL2.40ch	AT3G28857.1		transcrip	chr3:108	34.1365	38.9927	42.1916	60.6776	68.3098	124.185
GT	Sense	Sense	0.801	Detected	-0.801	Detected	0.000	1.392	Detected	1.229	Detected	1.310	0.245	GT	Sens	contig205	contig205	Ovate pro	CATTATC	contig205	Solyc02g	Solyc02g	Ovate protein (AHRD V1 **-- O8			contig205	Solyc02g	Ovate protein (AHRD		SL2.40ch	AT5G16290.2		acetolact	chr5:533	1338.92	401.935	397.98	1780.28	1837.61	1729.88
GT	Sense	Sense	0.890	Comprom	-0.890	Comprom	0.000	1.536	Detected	1.783	Detected	1.659	0.206	GT	Sens	contig205	contig205	Guanine	AGCTGC	contig205	Solyc08g	Solyc08g	Guanine	GO:00455	GO:00455	contig205	Solyc10g	WD-40 repeat family		SL2.40ch	AT5G53500.1		WD-40 re	chr5:217	9.98736	2.65107	4.14038	9.53366	14.2427	17.8128
GT	Sense	Sense	0.429	Detected	-0.429	Detected	0.000	1.048	Detected	1.000	Detected	1.024	0.140	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. ZIF	AGO7 (AI	chr1:261	258.999	130.258	112.13	303.222	362.495	369.582
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	3.461	Detected	3.014	Detected	3.238	0.006	GT	Sens	contig209	contig209	1-aminoc	GACTACT	contig209	Solyc09g	Solyc09g	1-aminocyclopropane-1-carbo			contig209	Solyc09g	1-aminocyclopropa		SL2.40ch	AT3G49030.1		F-box far	chr3:181	51.144	38.848	147.195	336.195	468.78	362.308
GT	Sense	Sense	0.292	Detected	-0.292	Detected	0.000	1.460	Detected	0.846	Detected	1.153	0.113	GT	Sens	contig212	contig212	Unknown	GGAGTT	contig212	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig212	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G19200.1		unknown	chr3:664	174.307	106.065	121.41	232.058	357.194	245.793
GT	Sense	Sense	0.627	Detected	-0.627	Detected	0.000	1.068	Detected	1.996	Detected	1.532	0.189	GT	Sens	contig212	contig212	ATP-bind	GTTATTT	contig212	Solyc05g	Solyc05g	ATP-bind	GO:00168	GO:00168	contig212	Solyc05g	ATP-bind	GO:00085	SL2.40ch	AT1G155	PDR12. A	PDR12 (F	chr1:533	8100.63	3095.94	5440.21	7130.99	10025.4	20101.4
GT	Sense	Sense	0.463	Detected	-0.463	Detected	0.000	1.625	Detected	1.721	Detected	1.673	0.069	GT	Sens	contig213	contig213	Ulp1 prot	CATCAAT	contig213	Solyc11g	Solyc11g	Ulp1 prot	GO:00065	GO:00065	contig213	Solyc12g	DUF599 family prote		SL2.40ch	AT5G60430.2		antiporte	chr5:243	64.5001	30.9393	30.1517	114.078	131.585	148.196
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	1.089	Detected	1.537	Detected	1.313	0.031	GT	Sens	contig214	contig214	Proteinas	ATCCATA	contig214	Solyc09g	Solyc09g	Proteinas	GO:00096	GO:00096	contig214	Solyc09g	Proteinas	GO:00096	SL2.40ch	AT5G28350.2		FUNCTIC	chr5:103	13306.3	10833.9	12943.5	24454.6	24386.6	35041.1
GT	Sense	Sense	0.179	Detected	-0.179	Detected	0.000	1.060	Detected	1.223	Detected	1.141	0.028	GT	Sens	contig215	contig215	Unknown	CAATGCC	contig215	Solyc03g	Solyc03g	Unknown	GO:00082	GO:00082	contig215	Solyc12g	Mutator-li	GO:00082	SL2.40ch	AT2G35880.1		FUNCTIC	chr2:150	120.511	85.7524	116.828	164.688	202.341	238.646
GT	Sense	Sense	0.161	Detected	-0.161	Detected	0.000	1.458	Detected	1.638	Detected	1.548	0.014	GT	Sens	contig219	contig219	UDP-gluc	GGATTCA	contig219	Solyc04g	Solyc04g	UDP-gluc	GO:00081	GO:00081	contig219	Solyc04g	UDP-gluc	GO:00081	SL2.40ch	AT5G228	EMB1030	EMB1030	chr5:761	1121.84	818.725	1111.75	2706.03	2513.07	3000.5
GT	Sense	Sense	0.656	Detected	-0.656	Comprom	0.000	1.666	Detected	1.348	Detected	1.507	0.155	GT	Sens	contig220	contig220	Unknown	AAACTAA	contig220	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig220	Solyc02g	Unknown Protein (A		SL2.40ch	AT4G341	UGT73B1	UGT73B1	chr4:163	17.3105	6.36004	10.8173	19.6578	31.7996	26.861
GT	Sense	Sense	0.098	Comprom	-0.098	Comprom	0.000	2.487	Detected	2.059	Detected	2.273	0.011	GT	Sens	contig225	contig225	Arginine	TACTCTT	contig225	Solyc07g	Solyc07g	Arginine	GO:00038	GO:00038	contig225	Solyc07g	Lysine de	GO:00089	SL2.40ch	AT5G37130.1		binding	chr5:146	2.74377	2.18261	5.59747	16.5853	13.1026	10.2598
GT	Sense	Sense	-0.058	Detected	0.058	Detected	0.000	0.869	Detected	1.646	Detected	1.257	0.085	GT	Sens	contig227	contig227	Transcrip	GTTGCTC	contig227	Solyc06g	Solyc06g	Transcrip	GO:00056	GO:00056	contig227	Solyc06g	Transcrip	GO:00056	SL2.40ch	AT4G118	AGL14	AGL14 (a	chr4:714	84.6438	83.6219	129.01	171.095	146.714	264.795
GT	Sense	Sense	-0.295	Detected	0.295	Detected	0.000	1.013	Detected	1.062	Detected	1.037	0.073	GT	Sens	contig229	contig229	Chloroph	AAATCTC	contig229	Solyc02g	Solyc02g	Chloroph	GO:00161	GO:00161	contig229	Solyc02g	Chloroph	GO:00161	SL2.40ch	AT1G299	CAB1. AB	CAB1 (CI	chr1:104	949.792	1303.23	1459.96	2950.82	2144.08	2336.13
GT	Sense	Sense	0.332	Detected	-0.332	Comprom	0.000	1.094	Detected	1.346	Detected	1.220	0.075	GT	Sens	contig229	contig229	Serine/thr	AAATAAC	contig229	Solyc01g	Solyc01g	Serine/thr	GO:00191	GO:00191	contig229	Solyc01g	RLK. Rec	GO:00191	SL2.40ch	AT1G70520.1		protein k	chr1:265	16.917	9.73361	21.9594	18.5799	26.1619	32.8267
GT	Sense	Sense	-0.359	Detected	0.359	Detected	0.000	1.912	Detected	1.853	Detected	1.882	0.035	GT	Sens	contig230	contig230	1-aminoc	TCAGTTC	contig230	Solyc09g	Solyc09g	1-aminoc	GO:00164	GO:00164	contig230	Solyc09g	1-aminoc	GO:00164	SL2.40ch	AT3G61400.1		2-oxoglu	chr3:227	488.275	732.363	2381.04	5413.75	2148.3	2172.6
GT	Sense	Sense	-0.607	Comprom	0.607	Comprom	0.000	2.115	Detected	1.731	Detected	1.923	0.094	GT	Sens	contig234	contig234	Ulp1 prot	ACTGAGC	contig234	Solyc04g	Solyc04g	Ulp1 protease family C-termina			contig234	Solyc04g015890.1.1				AT3G53100.1		GDSL-m	chr3:196	2.19774	4.6472	8.99378	1.94048	13.2151	10.6711
GT	Sense	Sense	2.382	Detected	-2.382	Detected	0.000	3.032	Detected	4.642	Detected	3.837	0.267	GT	Sens	contig234	contig234	Hydroxyc	AATTCAC	contig234	Solyc05g	Solyc05g	Hydroxyc	GO:00167	GO:00167	contig234	Solyc05g	Hydroxyc	GO:00167	SL2.40ch	AT2G39980.1		transfera	chr2:166	1702.94	57.1329	1239.16	1539.64	2435.4	7836.8
GT	Sense	Sense	0.900	Detected	-0.900	Detected	0.000	0.897	Detected	1.748	Detected	1.322	0.316	GT	Sens	contig235	contig235	Phenylala	TGGTGG	contig235	Solyc03g	Solyc03g	Phenylala	GO:00090	GO:00090	contig235	Solyc09g	Phenylala	GO:00043	SL2.40ch	AT2G370	pal1. ATP	pal1 (Phe	chr2:155	186.134	48.7022	88.1982	265.698	169.267	321.735
GT	Sense	Sense	0.238	Detected	-0.238	Detected	0.000	0.971	Detected	1.376	Detected	1.173	0.064	GT	Sens	contig235	contig235	Inositol-3	GATTTCC	contig235	Solyc05g	Solyc05g	Inositol-3	GO:00086	GO:00086	contig235	Solyc05g	Inositol-3	GO:00428	SL2.40ch	AT2G222	ATMIPS2	MIPS2 (M	chr2:945	4975.45	3260.4	4130.02	11020.4	7535.86	10518.2
GT	Sense	Sense	-0.031	Detected	0.031	Detected	0.000	1.222	Detected	1.179	Detected	1.200	0.001	GT	Sens	contig237	contig237	MuDR far	AGGATAC	contig237	Solyc03g	Solyc03g	MuDR family transposase con			contig237	Solyc02g055340.1.1				AT5G44730.1		haloacid	chr5:180	71.2493	67.7909	70.7351	97.0275	154.768	158.248
GT	Sense	Sense	-0.086	Detected	0.086	Detected	0.000	1.165	Detected	1.221	Detected	1.193	0.006	GT	Sens	contig237	contig237	Leucine-r	TTCCATT	contig237	Solyc12g	Solyc12g	Leucine-rich repeat receptor-li			contig237	Solyc01g	Receptor	GO:00428	SL2.40ch	AT3G04190.1				26.94	27.6759	32.9014	70.082	58.4731	64.0206
GT	Sense	Sense	0.132	Detected	-0.132	Detected	0.000	1.023	Detected	1.464	Detected	1.243	0.040	GT	Sens	contig238	contig238	Chymotry	CCATAGC	contig238	Solyc09g	Solyc09g	Chymotry	GO:00096	GO:00096	contig238	Solyc09g	Chymotry	GO:00096	SL2.40ch	AT5G28350.2		FUNCTIC	chr5:103	6487.6	4925.68	4192.15	14903.7	10966.8	15686.3
GT	Sense	Sense	0.268	Detected	-0.268	Detected	0.000	0.965	Detected	1.202	Detected	1.083	0.066	GT	Sens	contig239	contig239	Unknown	TTCAAGA	contig239	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig239	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G31070.1		pentatric	chr4:151	985.443	619.271	676.631	1292.66	1456.16	1807.49
GT	Sense	Sense	1.025	Detected	-1.025	Detected	0.000	1.447	Detected	2.506	Detected	1.976	0.229	GT	Sens	contig240	contig240	EIN3-bind	CACAAGC	contig240	Solyc05g	Solyc05g	EIN3-binding F-box protein 1 (/			contig240	Solyc07g	SCF E3 u	GO:00055	SL2.40ch	AT4G02750.1		pentatric	chr4:122	3867.58	851.563	3017.33	3461.87	4723.94	10369.6
GT	Sense	Sense	0.797	Detected	-0.797	Detected	0.000	1.087	Detected	0.944	Detected	1.015	0.332	GT	Sens	contig242	contig242	Agmatina	TCCGTGC	contig242	Solyc01g	Solyc01g	Agmatina	GO:00468	GO:00468	contig242	Solyc01g	Agmatina	GO:00468	SL2.40ch	AT4G08870.1		arginase	chr4:564	65769.8	19864.7	32115.4	79219.3	73315.4	69932.5
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	1.963	Detected	1.098	Detected	1.531	0.073	GT	Sens	contig246	contig246	Unknown	GACTTGT	contig246	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig246	Solyc05g024230.1.1				AT4G344	CHB3. AT	CHB3: DI	chr4:164	154.934	127.931	86.148	143.648	524.235	303.091
GT	Sense	Sense	0.588	Detected	-0.588	Detected	0.000	0.810	Detected	1.265	Detected	1.038	0.242	GT	Sens	contig246	contig246	CBL-inter	TACGTTA	contig246	Solyc11g	Solyc11g	CBL-inter	GO:00064	GO:00064	contig246	Solyc12g	CBL-inter	GO:00064	SL2.40ch	AT1G48260.1				1050.92	423.94	709.879	1500.78	1117.66	1613.44
GT	Sense	Sense	0.358	Detected	-0.358	Detected	0.000	1.067	Detected	1.656	Detected	1.361	0.099	GT	Sens	contig247	contig247	Stress-ind	TATGAAT	contig247	Solyc11g	Solyc11g	Stress-induced receptor-like k			contig247	Solyc11g	Stress-induced rece		SL2.40ch	AT3G14980.1		PHD fing	chr3:503	57.2028	31.7391	52.7247	84.7569	85.2188	135.054
GT	Sense	Sense	0.080	Detected	-0.080	Detected	0.000	1.106	Detected	1.194	Detected	1.150	0.006	GT	Sens	contig248	contig248	Unknown	TCCTGCT	contig248	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig248	Solyc12g	Kinesin-like calmod		SL2.40ch	AT1G03590.1		catalytic/	chr1:894	77.1735	62.9971	67.6776	126.17	143.26	160.461
GT	Sense	Sense	-0.643	Detected	0.643	Detected	0.000	1.644	Detected	1.327	Detected	1.486	0.154	GT	Sens	contig250	contig250	Unknown	GCTCTTC	contig250	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig250	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G03970.2		binding	chr3:102	11.6728	25.9444	21.6226	7.07801	51.9407	43.9224
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	1.929	Detected	2.893	Detected	2.411	0.038	GT	Sens	contig250	contig250	Cytochro	TTGGGAT	contig250	Solyc04g	Solyc04g	Cytochro	GO:00198	GO:00198	contig250	Solyc04g	Cytochro	GO:00198	SL2.40ch	AT4G319	CYP82C4	CYP82C4	chr4:154	58.4598	51.428	51.2711	180.349	199.358	409.64
GT	Sense	Sense	0.923	Comprom	-0.923	Comprom	0.000	2.290	Detected	1.943	Detected	2.116	0.153	GT	Sens	contig253	contig253	Amino ac	TGGTATT	contig253	Solyc05g	Solyc05g	Amino acid transporter (AHRD			contig253	Solyc05g	Amino ac	GO:00151	SL2.40ch	AT5G14470.1				8.41428	2.13332	5.72436	5.11702	19.7792	16.3906
GT	Sense	Sense	-0.355	Comprom	0.355	Comprom	0.000	2.213	Detected	2.744	Detected	2.478	0.031	GT	Sens	contig253	contig253	Carboxyl-	CCTATGA	contig253	Solyc07g	Solyc07g	Carboxyl-	GO:00055	GO:00055	contig253	Solyc07g	Carboxyl-	GO:00055	SL2.40ch	AT2G472	LACS1	long-cha	chr2:193	6.51705	9.72169	103.742	76.282	35.2268	53.6571
GT	Sense	Sense	0.667	Detected	-0.667	Detected	0.000	1.242	Detected	1.087	Detected	1.165	0.225	GT	Sens	contig253	contig253	Unknown	GAAGAGC	contig253	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)%:			contig253	Solyc09g	Unknown Protein (A		SL2.40ch	AT5G14610.1		ATP bind	chr5:471	622.987	225.229	457.504	1127.12	846.076	800.541
GT	Sense	Sense	-0.558	Detected	0.558	Detected	0.000	1.195	Detected	1.235	Detected	1.215	0.161	GT	Sens	contig253	contig253	Cytochro	AAATGAT	contig253	Solyc12g	Solyc12g	Cytochro	GO:00198	GO:00198	contig253	Solyc04g	Cytochro	GO:00198	SL2.40ch	AT1G25360.1		pentatric	chr1:889	14.8161	29.2712	6.59797	22.9419	45.5263	49.3134
GT	Sense	Sense	0.501	Detected	-0.501	Detected	0.000	1.131	Detected	1.916	Detected	1.524	0.139	GT	Sens	contig255	contig255	ATP-bind	TATTTTC	contig255	Solyc05g	Solyc05g	ATP-bind	GO:00171	GO:00171	contig255	Solyc05g	ATP-bind	GO:00426	SL2.40ch	AT1G155	PDR12. A	PDR12 (F	chr1:533	8049.67	3664.07	5617.66	7984.83	11359.6	20620.2
GT	Sense	Sense	0.586	Detected	-0.586	Detected	0.000	1.416	Detected	1.502	Detected	1.459	0.131	GT	Sens	contig256	contig256	D-alanine	ACAATTA	contig256	Solyc09g	Solyc09g	D-alanine	GO:00092	GO:00092	contig256	Solyc09g015130.2.1				AT3G08840.2		D-alanine	chr3:267	158.726	64.1981	68.4407	184.799	257.268	287.713
GT	Sense	Sense	0.370	Detected	-0.370	Detected	0.000	0.822	Detected	1.412	Detected	1.117	0.142	GT	Sens	contig261	contig261	Receptor	TCAAAGC	contig261	Solyc04g	Solyc04g	Receptor	GO:00064	GO:00064	contig261	Solyc04g	Receptor	GO:00055	SL2.40ch	AT1G51830.1		ATP bind	chr1:192	2090.02	1141.34	1577.09	2702	2606.12	4134.99
GT	Sense	Sense	0.268	Comprom	-0.268	Comprom	0.000	1.328	Detected	1.635	Detected	1.482	0.041	GT	Sens	contig261	contig261	Hcr9-4E (	CCATAAC	contig261	Solyc12g	Solyc12g	Hcr9-4E (AHRD V1 *-*- O50024			contig261	Solyc12g	LRR recei	GO:00163	SL2.40ch	AT3G09035.1		legume l	chr3:275	8.90247	5.59975	9.39865	8.82012	16.924	22.0635
GT	Sense	Sense	0.503	Detected	-0.503	Detected	0.000	1.122	Detected	0.999	Detected	1.061	0.171	GT	Sens	contig262	contig262	Acid phos	CACTTAT	contig262	Solyc06g	Solyc06g	Acid phos	GO:00039	GO:00039	contig262	Solyc06g	Acid phos	GO:00039	SL2.40ch	AT5G247	VSP2. AT	VSP2 (VE	chr5:850	61.7274	28.0091	56.392	120.729	86.4353	83.6278
GT	Sense	Sense	0.708	Detected	-0.708	Comprom	0.000	1.230	Detected	2.418	Detected	1.824	0.187	GT	Sens	contig267	contig267	N-hydrox	GAAAAAT	contig267	Solyc05g	Solyc05g	N-hydrox	GO:00167	GO:00167	contig267	Solyc05g	N-hydrox	GO:00167	SL2.40ch	AT2G39980.1		transfera	chr2:166	17.6669	6.03862	10.7586	13.672	23.14	55.5239
GT	Sense	Sense	0.555	Detected	-0.555	Detected	0.000	1.027	Detected	1.348	Detected	1.188	0.176	GT	Sens	contig267	contig267	Glycerald	TTTTGGC	contig267	Solyc03g	Solyc03g	Glycerald	GO:00043	GO:00043	contig267	Solyc03g	Glycerald	GO:00043	SL2.40ch	AT3G041	GAPC. GA	GAPC1 ((	chr3:108	1418.12	599.032	616.321	1552.79	1793.64	2360.49
GT	Sense	Sense	0.002	Detected	-0.002	Detected	0.000	1.611	Detected	1.676	Detected	1.644	0.000	GT	Sens	contig267	contig267	Mutator-li	ATGGGG	contig267	Solyc09g	Solyc09g	Mutator-li	GO:00082	GO:00082	contig267	Solyc10g	Mutator-like transpo		SL2.40ch	AT5G20980.2				35.9868	32.7023	33.7663	51.4891	100.065	110.296
GT	Sense	Sense	0.754	Detected	-0.754	Detected	0.000	0.947	Detected	2.169	Detected	1.558	0.250	GT	Sens	contig270	contig270	Zinc finge	GTAGAGC	contig270	Solyc12g	Solyc12g	Zinc finge	GO:00056	GO:00056	contig270	Solyc12g	Zinc finge	GO:00056	SL2.40ch	AT5G584	TAF15b	TAF15b (	chr5:236	42.059	13.4849	44.7772	23.2304	43.8315	107.745
GT	Sense	Sense	0.301	Comprom	-0.301	Comprom	0.000	1.814	Detected	1.212	Detected	1.513	0.071	GT	Sens	contig270	contig270	Cytochro	TTAGCAT	contig270	Solyc00g	Solyc00g	Cytochro	GO:00198	GO:00198	contig270	Solyc04g	Cytochro	GO:00198	SL2.40ch	AT1G25360.1		pentatric	chr1:889	8.12981	4.88231	4.80468	5.79526	21.1494	14.6802
GT	Sense	Sense	0.613	Detected	-0.613	Detected	0.000	1.471	Detected	1.060	Detected	1.266	0.189	GT	Sens	contig270	contig270	Purple ac	TATAAGC	contig270	Solyc07g	Solyc07g	Purple ac	GO:00055	GO:00055	contig270	Solyc07g	Purple ac	GO:00047	SL2.40ch	AT5G504	ATPAP27	PAP27 (P	chr5:205	13142.5	5123.02	8375.65	29029.8	21725.7	17204.9
GT	Sense	Sense	0.599	Detected	-0.599	Detected	0.000	1.102	Detected	1.344	Detected	1.223	0.183	GT	Sens	contig273	contig273	Dehydrog	ACCAATC	contig273	Solyc03g	Solyc03g	Dehydrog	GO:00469	GO:00469	contig273	Solyc03g	Dehydrog	GO:00469	SL2.40ch	AT4G23430.2		short-cha	chr4:122	2879.26	1144.54	1499.97	4457.87	3720.39	4635.62
GT	Sense	Sense	0.992	Detected	-0.992	Comprom	0.000	1.020	Detected	1.017	Detected	1.019	0.412	GT	Sens	contig273	contig273	Salicylic a	TTTGAAC	contig273	Solyc09g	Solyc09g	Salicylic a	GO:00081	GO:00081	contig273	Solyc09g	Salicylic a	GO:00087	SL2.40ch	AT3G448	FAMT	FAMT (fa	chr3:163	29.0134	6.68583	16.4956	75.8699	26.9646	28.362
GT	Sense	Sense	0.228	Detected	-0.228	Detected	0.000	1.361	Detected	1.678	Detected	1.519	0.032	GT	Sens	contig273	contig273	Maltose e	AATCCCC	contig273	Solyc03g	Solyc03g	Maltose excess protein 1-like%			contig273	Solyc04g	Maltose e	GO:00053	SL2.40ch	AT4G372	MYB73. A	MYB73 (I	chr4:175	199.463	132.489	173.992	437.622	398.562	523.184
GT	Sense	Sense	0.384	Detected	-0.384	Detected	0.000	2.431	Detected	2.859	Detected	2.645	0.027	GT	Sens	contig274	contig274	Hydroxypr	TCTGAGT	contig274	Solyc02g	Solyc02g	Hydroxyproline-rich glycoprot			contig274	Solyc02g	Hydroxyproline-rich		SL2.40ch	AT5G65660.1		hydroxyp	chr5:262	53.4825	28.6358	20.0596	87.0191	201.531	285.616
GT	Sense	Sense	0.363	Detected	-0.363	Detected	0.000	1.042	Detected	1.375	Detected	1.208	0.094	GT	Sens	contig275	contig275	TBC1 dor	TTCGTGC	contig275	Solyc03g	Solyc03g	TBC1 dor	GO:00056	GO:00056	contig275	Solyc03g	TBC1 dor	GO:00056	SL2.40ch	AT3G49350.1		RAB GTF	chr3:182	868.279	478.695	437.462	1043.87	1267.1	1682.33
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	0.844	Detected	1.357	Detected	1.101	0.051	GT	Sens	contig275	contig275	Unknown	CACCTAA	contig275	Solyc12g	Solyc12g	Unknown	GO:00082	GO:00082	contig275	Solyc03g078750.1.1				AT2G35880.1		FUNCTIC	chr2:150	106.346	92.1701	88.6382	139.738	169.735	255.184
GT	Sense	Sense	0.171	Detected	-0.171	Detected	0.000	1.271	Detected	1.349	Detected	1.310	0.018	GT	Sens	contig276	contig276	class I he	TCGAGG	contig276	Solyc09g	Solyc09g	class I heat shock protein (AHI			contig276	Solyc09g	class I heat shock p		SL2.40ch	AT5G597	HSP18.2	HSP18.2	chr5:240	159.905	114.969	145.643	220.265	312.474	347.389
GT	Sense	Sense	-0.279	Detected	0.279	Detected	0.000	1.150	Detected	1.226	Detected	1.188	0.052	GT	Sens	contig279	contig279	Oxygen-e	TTCCTTC	contig279	Solyc07g	Solyc07g	Oxygen-e	GO:00198	GO:00198	contig279	Solyc02g	Oxygen-e	GO:00082	SL2.40ch	AT3G508	PSBO2. F	PSBO2 (I	chr3:188	1742.07	2336.72	3014.58	6568.26	4275.62	4748.65
GT	Sense	Sense	-0.015	Detected	0.015	Detected	0.000	1.362	Detected	1.208	Detected	1.285	0.004	GT	Sens	contig280	contig280	Chloroph	TTAGAGA	contig280	Solyc12g	Solyc12g	Chloroph	GO:00160	GO:00160	contig280	Solyc12g	Chloroph	GO:00160	SL2.40ch	AT5G542	LHCB3. L	LHCB3 (L	chr5:220	640.822	596.501	755.519	1756.15	1517.01	1436.84
GT	Sense	Sense	0.236	Detected	-0.236	Detected	0.000	1.181	Detected	1.128	Detected	1.155	0.040	GT	Sens	contig280	contig280	Mutator-li	GTGCAG	contig280	Solyc12g	Solyc12g	Mutator-li	GO:00082	GO:00082	contig280	Solyc12g	Mutator-li	GO:00082	SL2.40ch	AT2G37080.1		myosin h	chr2:155	68.5119	45.03	53.7967	99.2099	120.276	122.108
GT	Sense	Sense	0.544	Detected	-0.544	Comprom	0.000	1.264	Detected	0.904	Detected	1.084	0.199	GT	Sens	contig280	contig280	Ulp1 prot	GAAGAA	contig280	Solyc12g	Solyc12g	Ulp1 protease family C-termina			contig280	Solyc12g036270.1.1				AT1G12750.2				13.2675	5.69324	8.58968	8.18132	19.9223	16.3568
GT	Sense	Sense	0.235	Comprom	-0.235	Comprom	0.000	1.124	Detected	2.408	Detected	1.766	0.123	GT	Sens	contig280	contig280	Ethylene	GGGAAC	contig280	Solyc03g	Solyc03g	Ethylene	GO:00055	GO:00055	contig280	Solyc03g	Ethylene	GO:00055	SL2.40ch	AT5G472	ERF5. AT	ERF5 (ET	chr5:191	11.6899	7.69379	10.6557	10.8648	19.7329	50.6262
GT	Sense	Sense	-0.339	Comprom	0.339	Comprom	0.000	0.865	Detected	1.172	Detected	1.019	0.112	GT	Sens	contig283	contig283	Cysteine-	GATAATA	contig283	Solyc02g	Solyc02g	Cysteine-	GO:00064	GO:00064	contig283	Solyc02g	Serine/thr	GO:00191	SL2.40ch	AT1G56120.1		kinase	chr1:209	9.98056	14.5596	15.5374	19.1313	20.9586	27.3303
GT	Sense	Sense	0.072	Detected	-0.072	Detected	0.000	1.933	Detected	1.125	Detected	1.529	0.065	GT	Sens	contig284	contig284	Unknown	GCTGAGT	contig284	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig284	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G571	ATPAP28	PAP28 (P	chr5:231	129.971	107.21	96.7323	269.024	430.423	259
GT	Sense	Sense	0.200	Detected	-0.200	Detected	0.000	1.357	Detected	1.172	Detected	1.265	0.029	GT	Sens	contig285	contig285	Cyclopro	TTGAGCA	contig285	Solyc09g	Solyc09g	Cyclopro	GO:00086	GO:00086	contig285	Solyc09g	Cyclopro	GO:00086	SL2.40ch	AT3G23530.1		cyclopro	chr3:843	844.35	583.167	625.992	1881.19	1716.23	1591.05
GT	Sense	Sense	0.193	Detected	-0.193	Detected	0.000	0.860	Detected	1.250	Detected	1.055	0.061	GT	Sens	contig286	contig286	Genomic	ACAGTTC	contig286	Solyc07g	Solyc07g	Genomic DNA chromosome 3			contig286	Solyc07g	Enhancer	GO:00001	SL2.40ch	AT1G206	CAT1	CAT1 (CA	chr1:714	379.628	265.013	258.459	555.169	549.646	758.94
GT	Sense	Sense	0.135	Detected	-0.135	Detected	0.000	1.266	Detected	1.226	Detected	1.246	0.012	GT	Sens	contig286	contig286	Mutator-li	GTTGTGC	contig286	Solyc09g	Solyc09g	Mutator-li	GO:00082	GO:00082	contig286	Solyc09g	Mutator-li	GO:00082	SL2.40ch	AT1G27020.1		unknown	chr1:937	309.936	234.316	275.62	399.39	618.718	634.194
GT	Sense	Sense	0.270	Detected	-0.270	Detected	0.000	0.958	Detected	1.308	Detected	1.133	0.072	GT	Sens	contig287	contig287	Malate de	AGATCTT	contig287	Solyc11g	Solyc11g	Malate de	GO:00300	GO:00300	contig287	Solyc11g	Malate de	GO:00300	SL2.40ch	AT5G58330.1		malate de	chr5:235	5503.22	3448.9	4645.19	10185.8	8082.48	10850.5
GT	Sense	Sense	-0.977	Comprom	0.977	Detected	0.000	1.187	Detected	1.226	Detected	1.207	0.342	GT	Sens	contig287	contig287	Reverse t	GACCAGT	contig287	Solyc01g	Solyc01g	Reverse t	GO:00062	GO:00062	contig287	Solyc03g	Pol polyp	GO:00062	SL2.40ch	AT3G19410.1				6.67952	23.5864	15.1692	7.76052	27.2838	29.5406
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	1.063	Detected	1.504	Detected	1.284	0.036	GT	Sens	contig288	contig288	Chymotry	CCATATC	contig288	Solyc09g	Solyc09g	Chymotry	GO:00096	GO:00096	contig288	Solyc09g	Chymotry	GO:00096	SL2.40ch	AT4G123	CYP706A	CYP706A	chr4:731	3644.59	2831.17	2638.06	9800.16	6409.15	9163.94
GT	Sense	Sense	0.295	Detected	-0.295	Detected	0.000	1.515	Detected	1.408	Detected	1.462	0.040	GT	Sens	contig288	contig288	Unknown	AAAGACC	contig288	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig288	Solyc01g	Unknown Protein (A		SL2.40ch	AT3G09950.1		unknown	chr3:306	12004.2	7274.02	15456.6	40179.8	25502.1	24944.6
GT	Sense	Sense	0.451	Detected	-0.451	Detected	0.000	1.142	Detected	1.323	Detected	1.233	0.116	GT	Sens	contig288	contig288	Epoxide I	AAGGCTC	contig288	Solyc05g	Solyc05g	Epoxide I	GO:00038	GO:00038	contig288	Solyc05g	Epoxide I	GO:00043	SL2.40ch	AT2G267	ATSEH	ATSEH (/	chr2:113	4365.63	2129.49	2706.96	7229.79	6424.98	7673.77
GT	Sense	Sense	0.186	Detected	-0.186	Detected	0.000	0.960	Detected	1.198	Detected	1.079	0.039	GT	Sens	contig293	contig293	Cytochro	TGATTAC	contig293	Solyc08g	Solyc08g	Cytochro	GO:00198	GO:00198	contig293	Solyc08g	Cytochro	GO:00198	SL2.40ch	AT4G001	GAE3	GAE3 (UI	chr4:387	999.33	704.06	781.02	1218.99	1557.6	1936.51
GT	Sense	Sense	1.559	Detected	-1.559	Comprom	0.000	2.121	Detected	2.376	Detected	2.248	0.287	GT	Sens	contig295	contig295	class II he	ATTTGAC	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	34.4491	3.61605	11.6723	39.6173	46.3473	58.2688
GT	Sense	Sense	0.413	Detected	-0.413	Detected	0.000	1.619	Detected	1.964	Detected	1.792	0.057	GT	Sens	contig295	contig295	Serine ca	AGCTCCA	contig295	Solyc06g	Solyc06g	Serine ca	GO:00065	GO:00065	contig295	Solyc06g	Serine ca	GO:00428	SL2.40ch	AT4G129	scpl20	scpl20 (s	chr4:755	1810.37	931.171	2201.64	5024.1	3808.52	5096.43
GT	Sense	Sense	0.649	Detected	-0.649	Detected	0.000	1.401	Detected	0.919	Detected	1.160	0.236	GT	Sens	contig296	contig296	Unknown	CATCCA	contig296	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig296	Solyc08g	Unknown Protein (A		SL2.40ch	AT2G33435.1		RNA reco	chr2:141	49.9278	18.5028	19.3996	75.9822	76.6171	57.8158
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	1.288	Detected	1.212	Detected	1.250	0.004	GT	Sens	contig298	contig298	Mutator-li	ATAGCAC	contig298	Solyc05g	Solyc05g	Mutator-li	GO:00082	GO:00082	contig298	Solyc10g	Mutator-like transpo		SL2.40ch	AT3G22910.1		calcium-t	chr3:811	69.8873	70.6428	69.831	102.333	163.836	163.785
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	1.310	Detected	1.517	Detected	1.413	0.009	GT	Sens	contig299	contig299	Mutator-li	GCAAGAT	contig299	Solyc12g	Solyc12g	Mutator-li	GO:00082	GO:00082	contig299	Solyc10g	Mutator-like transpo		SL2.40ch	AT2G26210.1				21.6901	17.4797	20.9896	14.3516	46.0884	56.0618
GT	Sense	Sense	-0.411	Comprom	0.411	Detected	0.000	1.187	Detected	1.067	Detected	1.127	0.113	GT	Sens	contig299	contig299	Unknown	TCGGTGC	contig299	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig299	Solyc09g	Ethylene-	GO:00036	SL2.40ch	AT2G30280.1		unknown	chr2:129	6.78848	10.935	11.7206	3.7679	18.7286	18.1549
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	1.033	Detected	1.290	Detected	1.161	0.015	GT	Sens	contig302	contig302	Photosys	TTCTGGT	contig302	Solyc06g	Solyc06g	Photosys	GO:00095	GO:00095	contig302	Solyc06g	Photosys	GO:00095	SL2.40ch	AT4G128	PSAL	PSAL (ph	chr4:752	693.131	579.286	742.781	1553.65	1237.97	1558.48
GT	Sense	Sense	0.909	Detected	-0.909	Detected	0.000	1.636	Detected	1.491	Detected	1.563	0.229	GT	Sens	contig303	contig303	Ovate pro	TTTTCCT	contig303	Solyc02g	Solyc02g	Ovate protein (AHRD V1 ***- O8			contig303	Solyc02g	Ovate protein (AHRD		SL2.40ch	AT5G07820.1		FUNCTIC	chr5:249	468.147	121.065	114.659	569.21	706.383	672.994
GT	Sense	Sense	-0.838	Comprom	0.838	Detected	0.000	1.571	Detected	1.286	Detected	1.429	0.235	GT	Sens	contig304	contig304	Unknown	TCCAATC	contig304	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig304	Solyc11g	Ulp1 protease family		SL2.40ch	AT4G098	RPS18C	RPS18C	chr4:617	4.13593	12.0526	8.10546	2.22855	20.0286	17.3228
GT	Sense	Sense	0.222	Comprom	-0.222	Comprom	0.000	3.657	Detected	5.464	Detected	4.560	0.039	GT	Sens	contig305	contig305	Cytochro	TTAAACT	contig305	Solyc04g	Solyc04g	Cytochro	GO:00198	GO:00198	contig305	Solyc04g	Cytochro	GO:00198	SL2.40ch	AT4G319	CYP82C4	CYP82C4	chr4:154	5.53556	3.7092	11.4501	33.1789	54.5575	201.177
GT	Sense	Sense	1.275	Detected	-1.275	Comprom	0.000	0.888	Detected	2.301	Detected	1.595	0.388	GT	Sens	contig306	contig306	Major late	GATTAAC	contig306	Solyc04g	Solyc04g	Major late	GO:00096	GO:00096	contig306	Solyc04g	Major late	GO:00096	SL2.40ch	AT5G643	AGP1. AT	AGP1 (AI	chr5:257	50.6286	7.88112	23.3038	65.4011	35.2975	99.0303
GT	Sense	Sense	0.350	Detected	-0.350	Detected	0.000	1.143	Detected	1.470	Detected	1.306	0.077	GT	Sens	contig307	contig307	Auxin res	ATCTTCC	contig307	Solyc00g	Solyc00g	Auxin res	GO:00063	GO:00063	contig307	Solyc00g	Auxin res	GO:00056	SL2.40ch	AT1G303	ARF6	ARF6 (AU	chr1:106	328.963	184.573	149.011	441.731	519.527	686.662
GT	Sense	Sense	0.358	Detected	-0.358	Detected	0.000	0.885	Detected	1.502	Detected	1.193	0.128	GT	Sens	contig311	contig311	Cytochro	TCAAAGA	contig311	Solyc08g	Solyc08g	Cytochro	GO:00198	GO:00198	contig311	Solyc08g	cytochron	GO:00198	SL2.40ch	AT4G123	CYP706A	CYP706A	chr4:730	437.862	242.954	274.183	672.162	575.132	929.169
GT	Sense	Sense	0.850	Detected	-0.850	Detected	0.000	2.173	Detected	2.933	Detected	2.553	0.111	GT	Sens	contig340	contig340	Receptor	TATTAGC	contig340	Solyc10g	Solyc10g	Receptor	GO:00055	GO:00055	contig340	Solyc10g	LRR recei	GO:00055	SL2.40ch	AT4G08450.1		disease r	chr4:536	304.497	85.4902	190.944	312.236	694.527	1239.97
GT	Sense	Sense	0.616	Detected	-0.616	Detected	0.000	2.045	Detected	2.765	Detected	2.405	0.078	GT	Sens	contig342	contig342	Disease r	TTCAAGC	contig342	Solyc10g	Solyc10g	Disease resistance protein (AH			contig342	Solyc10g	Lrr. resistance prot		SL2.40ch	AT3G231	AtRLP38	AtRLP38	chr3:822	1268.23	492.343	1049.1	1502.75	3113.31	5405.11
GT	Sense	Sense	-0.016	Comprom	0.016	Comprom	0.000	1.015	Detected	1.104	Detected	1.060	0.002	GT	Sens	contig347	contig347	Unknown	TCACAAC	contig347	Solyc04g	Solyc04g	Unknown	GO:00036	GO:00036	contig347	Solyc04g	Unknown	GO:00036	SL2.40ch	AT1G582	SAB	SAB (SAI	chr1:215	10.3326	9.62815	13.702	18.3115	19.2522	21.5637
GT	Sense	Sense	1.260	Detected	-1.260	Comprom	0.000	2.246	Detected	1.934	Detected	2.090	0.242	GT	Sens	contig377	contig377	Polyphen	TGAAGGT	contig377	Solyc08g	Solyc08g	Polyphen	GO:00081	GO:00081	contig377	Solyc08g	Polyphen	GO:00081	SL2.40ch	AT3G52700.1		unknown	chr3:195	47.7262	7.58166	15.4562	362.654	86.1424	73.0995
GT	Sense	Sense	-1.163	Comprom	1.163	Detected	0.000	1.015	Detected	1.341	Detected	1.178	0.422	GT	Sens	contig397	contig397	Unknown	CAAGGCC	contig397	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig397	Solyc07g	Unknown Protein (A		SL2.40ch	AT2G44065.2		ribosoma	chr2:182	2.31374	10.5834	6.88604	7.63066	9.55057	12.6076
GT	Sense	Sense	-0.040	Comprom	0.040	Comprom	0.000	3.602	Detected	2.893	Detected	3.248	0.012	GT	Sens	contig405	contig405	Unannota	CCATAAGCGGCAGCATGGTGTTATGCTGTAATTTTACTATCTCAAGAAA							contig405	Solyc06g	Beta-fruct	GO:00059	SL2.40ch	AT3G45800.1				2.22102	2.1394	59.1632	77.4843	25.2707	16.2913
GT	Sense	Sense	-0.056	Comprom	0.056	Comprom	0.000	4.045	Detected	4.091	Detected	4.068	0.000	GT	Sens	contig419	contig419	Unannota	CTCACCATTCAAATTTGTACATCATCGAATGGGAAATCTCTATCTTCTA							contig419	Solyc03g	Polyprote	GO:00065	SL2.40ch	AT5G64667.1				2.12306	2.09068	4.49941	10.3268	33.2	36.1206
GT	Sense	Sense	0.163	Detected	-0.163	Detected	0.000	0.936	Detected	1.381	Detected	1.159	0.052	GT	Sens	contig430	contig430	Nicotia ta	CTCACTCAGCAACTTTCTTCTCTTCCAAACGGAGAAGCAAATAACTAAA							contig430	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	35.776	26.0298	31.5628	63.8663	55.7472	79.9542
GT	Sense	Sense	0.094	Detected	-0.094	Detected	0.000	1.284	Detected	1.291	Detected	1.287	0.005	GT	Sens	contig447	contig447	Mutator-li	GAGCAG	contig447	Solyc10g	Solyc10g	Mutator-li	GO:00082	GO:00082	contig447	Solyc10g	Mutator-li	GO:00082	SL2.40ch	AT4G18580.2		unknown	chr4:102	54.6854	43.7895	49.299	76.7304	113.763	120.446
GT	Sense	Sense	0.836	Detected	-0.836	Detected	0.000	1.677	Detected	2.094	Detected	1.886	0.160	GT	Sens	contig456	contig456	ClpB cha	GAGTTAT	contig456	Solyc06g	Solyc06g	ClpB cha	GO:00055	GO:00055	contig456	Solyc03g	ClpB chai	GO:00195	SL2.40ch	AT1G743	ATHSP10	ATHSP10	chr1:279	1284.12	367.187	512.985	1362.44	2095.99	2949.86
GT	Sense	Sense	0.201	Detected	-0.201	Detected	0.000	0.834	Detected	1.539	Detected	1.187	0.100	GT	Sens	contig471	contig471	Receptor-	TCGGGT	contig471	Solyc02g	Solyc02g	Receptor	GO:00046	GO:00046	contig471	Solyc02g	Receptor-	GO:00046	SL2.40ch	AT1G56120.1		kinase	chr1:209	3948.05	2725.07	3196.78	6226.14	5582.81	9590.04
GT	Sense	Sense	0.549	Detected	-0.549	Detected	0.000	0.942	Detected	1.874	Detected	1.408	0.190	GT	Sens	contig480	contig480	Unknown	AATAATC	contig480	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)%:			contig480	Solyc12g	H-ATPase	GO:00160	SL2.40ch	AT2G13720.1				1581.95	674.001	537.374	1108.18	1894.42	3808.8
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	1.121	Detected	1.351	Detected	1.236	0.034	GT	Sens	contig483	contig483	Metacasp	CAGAAGA	contig483	Solyc01g	Solyc01g	Metacasp	GO:00057	GO:00057	contig483	Solyc01g	Metacasp	GO:00065	SL2.40ch	AT5G502	OS. OLD5	OS (OUIN	chr5:204	83.8033	57.4642	114.832	218.374	144.074	178.09
GT	Sense	Sense	0.290	Detected	-0.290	Detected	0.000	1.022	Detected	1.120	Detected	1.071	0.068	GT	Sens	contig488	contig488	1-aminoc	AAGATAT	contig488	Solyc02g	Solyc02g	1-aminoc	GO:00166	GO:00166	contig488	Solyc02g071480.2.1				AT4G25310.1		oxidored	chr4:129	127.429	77.7005	113.357	80.2312	192.938	217.5
GT	Sense	Sense	1.034	Detected	-1.034	Detected	0.000	1.371	Detected	2.499	Detected	1.935	0.242	GT	Sens	contig497	contig497	EIN3-bind	GCTGCTC	contig497	Solyc05g	Solyc05g	EIN3-binding F-box protein 1 (/			contig497	Solyc07g	SCF E3 u	GO:00055	SL2.40ch	AT4G30020.1		subtilase	chr4:146	4421.41	961.517	3440.57	4061	5092.13	11729
GT	Sense	Sense	0.270	Detected	-0.270	Detected	0.000	0.853	Detected	1.544	Detected	1.199	0.112	GT	Sens	contig513	contig513	Dienelact	GGAGGA	contig513	Solyc09g	Solyc09g	Dienelact	GO:00055	GO:00055	contig513	Solyc09g	Dienelact	GO:00055	SL2.40ch	AT3G23600.2		dienelact	chr3:847	116.947	73.3555	70.9891	187.893	159.743	271.718
GT	Sense	Sense	0.922	Detected	-0.922	Comprom	0.000	0.864	Detected	1.299	Detected	1.082	0.372	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	39.1195	9.93511	7.96023	32.5822	34.2644	48.8006
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	1.237	Detected	0.890	Detected	1.063	0.058	GT	Sens	contig564	contig564	BURP do	AGCTGA	contig564	Solyc05g	Solyc05g	BURP do	GO:00046	GO:00046	contig564	Solyc05g	BURP do	GO:00046	SL2.40ch	AT1G70370.1		BURP do	chr1:265	59.1986	40.7256	23.5062	85.6048	110.49	91.5437
GT	Sense	Sense	0.670	Detected	-0.670	Detected	0.000	1.078	Detected	1.505	Detected	1.291	0.208	GT	Sens	contig589	contig589	Subtilisin	TACCTCA	contig589	Solyc10g	Solyc10g	Subtilisin	GO:00065	GO:00065	contig589	Solyc10g	Subtilisin	GO:00065	SL2.40ch	AT1G308	ARPC2A.	DIS2 (DIS	chr1:109	2353.63	847.286	1097.07	3722.58	2845.84	4031.52
GT	Sense	Sense	0.722	Detected	-0.722	Detected	0.000	1.173	Detected	1.147	Detected	1.160	0.249	GT	Sens	contig623	contig623	Chromod	CTTGATA	contig623	Solyc10g	Solyc10g	Chromod	GO:00055	GO:00055	contig623	Solyc05g	Chromod	GO:00055	SL2.40ch	AT1G05120.1		SNF2 dor	chr1:147	161.628	54.1818	46.0858	249.73	201.523	208.544
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	1.251	Detected	1.253	Detected	1.252	0.001	GT	Sens	contig628	contig628	B3 domai	GGAGGC	contig628	Solyc02g	Solyc02g	B3 domai	GO:00063	GO:00063	contig628	Solyc04g	B3 domai	GO:00063	SL2.40ch	AT1G20970.1		FUNCTIC	chr1:731	21.1567	18.1756	18.3514	37.4163	44.5705	47.0325
GT	Sense	Sense	0.237	Detected	-0.237	Detected	0.000	1.042	Detected	1.400	Detected	1.221	0.054	GT	Sens	contig628	contig628	Cytochro	AGCTGCA	contig628	Solyc04g	Solyc04g	Cytochro	GO:00198	GO:00198	contig628	Solyc04g	Cytochro	GO:00198	SL2.40ch	AT5G479	CYP705A	CYP705A	chr5:194	3544.98	2325.54	2839.57	4752.72	5646.03	7624.51
GT	Sense	Sense	1.033	Comprom	-1.033	Comprom	0.000	1.609	Detected	1.825	Detected	1.717	0.240	GT	Sens	contig629	contig629	Malonyl C	ACCATGT	contig629	Solyc10g	Solyc10g	Malonyl CoA anthocyanin 5-O-			contig629	Solyc10g	Malonyl CoA anthoc		SL2.40ch	AT3G50840.1		phototro	chr3:188	10.1373	2.20793	9.79131	31.5009	13.7754	16.8684
GT	Sense	Sense	0.336	Detected	-0.336	Detected	0.000	1.241	Detected	0.876	Detected	1.058	0.110	GT	Sens	contig639	contig639	Susceptib	CCCAAAA	contig639	Solyc01g	Solyc01g	Susceptib	GO:00055	GO:00055	contig639	Solyc01g	Susceptib	GO:00055	SL2.40ch	AT5G49600.1		unknown	chr5:201	1113.04	636.849	1509.38	3557.12	1899.45	1553.9
GT	Sense	Sense	-0.092	Detected	0.092	Detected	0.000	1.235	Detected	1.407	Detected	1.321	0.009	GT	Sens	contig643	contig643	Mutator-li	ATGAGGT	contig643	Solyc03g	Solyc03g	Mutator-li	GO:00082	GO:00082	contig643	Solyc03g111480.1.1				AT2G35880.1		FUNCTIC	chr2:150	82.472	85.3784	85.3101	140.11	188.589	223.908
GT	Sense	Sense	0.340	Detected	-0.340	Detected	0.000	1.063	Detected	1.467	Detected	1.265	0.085	GT	Sens	contig666	contig666	Kinesin-li	AGATATT	contig666	Solyc12g	Solyc12g	Kinesin-like calmodulin bindin			contig666	Solyc12g	Kinesin-like calmod		SL2.40ch	AT1G11420.1		agenet d	chr1:384	111.988	63.7216	50.7684	144.895	168.557	234.865
GT	Sense	Sense	0.564	Detected	-0.564	Detected	0.000	0.823	Detected	1.184	Detected	1.003	0.232	GT	Sens	contig686	contig686	Leucine-r	CATGAAA	contig686	Solyc01g	Solyc01g	Leucine-r	GO:00055	GO:00055	contig686	Solyc01g	LRR recei	GO:00163	SL2.40ch	AT5G48360.1		formin ho	chr5:195	104.737	43.6964	59.057	209.711	114.24	154.634
GT	Sense	Sense	0.439	Detected	-0.439	Detected	0.000	1.736	Detected	1.881	Detected	1.809	0.056	GT	Sens	contig691	contig691	Serine ca	AGACAGA	contig691	Solyc06g	Solyc06g	Serine ca	GO:00055	GO:00055	contig691	Solyc06g	Serine ca	GO:00055	SL2.40ch	AT4G129	scpl20	scpl20 (s	chr4:755	612.068	303.444	736.302	1748.13	1371.11	1596.61
GT	Sense	Sense	0.501	Comprom	-0.501	Comprom	0.000	1.679	Detected	3.281	Detected	2.480	0.120	GT	Sens	contig705	contig705	Cytochro	ATATGGA	contig705	Solyc04g	Solyc04g	Cytochro	GO:00200	GO:00200	contig705	Solyc04g	Cytochro	GO:00198	SL2.40ch	AT4G139	AtRLP50	AtRLP50	chr4:804	4.9893	2.27215	2.17663	5.58358	10.2915	32.9259
GT	Sense	Sense	0.301	Detected	-0.301	Detected	0.000	1.177	Detected	1.214	Detected	1.195	0.058	GT	Sens	contig713	contig713	Nitrogen	ATATTCT	contig713	Solyc01g	Solyc01g	Nitrogen	GO:00081	GO:00081	contig713	Solyc06g	Nitrogen	GO:00055	SL2.40ch	AT5G462	KAS I	KAS I (3-k	chr5:187	1250.92	751.549	973.483	2217.73	2093.68	2262.26
GT	Sense	Sense	1.670	Detected	-1.670	Comprom	0.000	3.113	Detected	2.139	Detected	2.626	0.270	GT	Sens	contig732	contig732	Globulin-	AATCAAA	contig732	Solyc09g	Solyc09g	Globulin-	GO:00457	GO:00457	contig732	Solyc09g	Vicilin-like	GO:00457	SL2.40ch	AT2G43560.1		immunor	chr2:180	23.5183	2.11736	46.3239	74.3155	58.2794	31.2744
GT	Sense	Sense	0.387	Detected	-0.387	Detected	0.000	1.063	Detected	1.194	Detected	1.128	0.103	GT	Sens	contig733	contig733	Spermidi	TTATCCA	contig733	Solyc08g	Solyc08g	Spermidi	GO:00038	GO:00038	contig733	Solyc05g	Spermidi	GO:00047	SL2.40ch	AT5G531	SPDS3. S	SPDS3 (S	chr5:215	7444.75	3968	4271.1	11538.9	10839.3	12507.6
GT	Sense	Sense	0.484	Detected	-0.484	Detected	0.000	1.009	Detected	1.448	Detected	1.229	0.147	GT	Sens	contig737	contig737	NEDD8 ac	TATGACA	contig737	Solyc12g	Solyc12g	NEDD8 ac	GO:00038	GO:00038	contig737	Solyc12g	NEDD8 ac	GO:00081	SL2.40ch	AT1G051	AXR1	AXR1 (AU	chr1:149	157.525	73.3844	103.974	225.564	206.631	295.105
GT	Sense	Sense	0.669	Detected	-0.669	Detected	0.000	1.021	Detected	0.994	Detected	1.008	0.271	GT	Sens	contig782	contig782	Serine ca	GATGATC	contig782	Solyc10g	Solyc10g	Serine ca	GO:00065	GO:00065	contig782	Solyc10g	Serine ca	GO:00167	SL2.40ch	AT5G559	emb2731	emb2731	chr5:226	361.15	130.165	211.535	555.633	420.079	434.453
GT	Sense	Sense	1.437	Detected	-1.437	Detected	0.000	2.962	Detected	1.928	Detected	2.445	0.250	GT	Sens	contig799	contig799	Hydroxyc	TTTCCAA	contig799	Solyc07g	Solyc07g	Hydroxyc	GO:00167	GO:00167	contig799	Solyc07g	Hydroxyc	GO:00167	SL2.40ch	AT5G484	ATGLR1.	ATGLR1.	chr5:196	259.406	32.2753	235.829	1968.03	680.6	350.385
GT	Sense	Sense	0.172	Detected	-0.172	Detected	0.000	0.992	Detected	1.441	Detected	1.216	0.050	GT	Sens	contig803	contig803	Glutared	GTGAAGC	contig803	Solyc01g	Solyc01g	Glutared	GO:00454	GO:00454	contig803	Solyc01g	Glutared	GO:00454	SL2.40ch	AT1G610	CPSF73-I	CPSF73-	chr1:224	34.6501	24.8817	14.3835	46.9036	55.7613	80.1901
GT	Sense	Sense	1.018	Detected	-1.018	Comprom	0.000	1.822	Detected	1.475	Detected	1.648	0.252	GT	Sens	contig817	contig817	Ulp1 prot	AGCGCAC	contig817	Solyc04g	Solyc04g	Ulp1 protease family C-termina			contig817	Solyc10g	Ulp1 protease family		SL2.40ch	AT4G14746.1				13.0784	2.90644	2.19577	16.0256	20.8082	17.2372
GT	Sense	Sense	0.330	Detected	-0.330	Detected	0.000	0.872	Detected	1.521	Detected	1.196	0.123	GT	Sens	contig833	contig833	Major late	CTCATCA	contig833	Solyc04g	Solyc04g	Major late	GO:00096	GO:00096	contig833	Solyc04g	Major late	GO:00096	SL2.40ch	AT1G744	MYB95. A	MYB95 (I	chr1:279	536.056	309.305	256.514	672.121	711.351	1175.42
GT	Sense	Sense	0.715	Detected	-0.715	Detected	0.000	2.225	Detected	2.830	Detected	2.527	0.083	GT	Sens	contig860	contig860	Gibberelli	TACTGTC	contig860	Solyc04g	Solyc04g	Gibberellin-regulated family pr			contig860	Solyc04g	Gibberellin-regulate		SL2.40ch	AT1G10588.2		Encodes	chr1:350	155.282	52.5341	183.533	936.649	403.106	646.139
GT	Sense	Sense	0.434	Detected	-0.434	Detected	0.000	1.168	Detected	1.103	Detected	1.135	0.121	GT	Sens	contig884	contig884	Cytochro	AAATCTT	contig884	Solyc04g	Solyc04g	Cytochrome P450 (AHRD V1 *-:			contig884	Solyc07g	Cytochro	GO:00198	SL2.40ch	AT5G657	HSL2	HSL2 (HA	chr5:262	3979.26	1987.8	2571.22	9617.45	6033.19	6076.24
GT	Sense	Sense	0.513	Detected	-0.513	Comprom	0.000	1.399	Detected	1.007	Detected	1.203	0.160	GT	Sens	contig887	contig887	GTP-bind	TTTATAC	contig887	Solyc10g	Solyc10g	GTP-bind	GO:00056	GO:00056	contig887	Solyc10g	GTP-bind	GO:00056	SL2.40ch	AT4G350	ARAC3. R	ARAC3 (A	chr4:166	19.1559	8.58199	11.4688	38.815	32.2873	25.9174
GT	Sense	Sense	0.339	Detected	-0.339	Detected	0.000	0.924	Detected	1.108	Detected	1.016	0.101	GT	Sens	contig900	contig900	Ulp1 prot	ATGCAGA	contig900	Solyc02g	Solyc02g	Ulp1 protease family C-termina			contig900	Solyc02g	Ulp1 protease family		SL2.40ch	AT3G439	DCL3. AT	ribonucle	chr3:157	78.1041	44.5364	47.0041	55.939	106.881	127.87
GT	Sense	Sense	-0.085	Comprom	0.085	Comprom	0.000	4.212	Detected	4.525	Detected	4.368	0.002	GT	Sens	contig906	contig906	1-aminoc	GTCCAGA	contig906	Solyc09g	Solyc09g	1-aminoc	GO:00164	GO:00164	contig906	Solyc09g	1-aminoc	GO:00098	SL2.40ch	AT1G06640.1		2-oxoglu	chr1:203	2.36694	2.42657	18.6931	45.3562	42.3995	55.5051
GT	Sense	Sense	0.726	Detected	-0.726	Detected	0.000	1.001	Detected	1.042	Detected	1.022	0.295	GT	Sens	contig913	contig913	Agmatina	ATGACTC	contig913	Solyc01g	Solyc01g	Agmatina	GO:00468	GO:00468	contig913	Solyc01g	Agmatina	GO:00468	SL2.40ch	AT4G08900.1		arginase	chr4:570	67128.1	22366.6	36890.6	79115.9	74057.5	80289
GT	Sense	Sense	-0.352	Detected	0.352	Detected	0.000	1.109	Detected	1.201	Detected	1.155	0.083	GT	Sens	contig959	contig959	Chloroph	AGTGAAA	contig959	Solyc02g	Solyc02g	Chloroph	GO:00161	GO:00161	contig959	Solyc02g	Chloroph	GO:00161	SL2.40ch	AT2G344	LHB1B2.	LHB1B2:	chr2:145	367.469	545.726	652.464	1224.52	922.204	1035.66
GT	Sense	Sense	0.369	Detected	-0.369	Detected	0.000	1.073	Detected	1.075	Detected	1.074	0.101	GT	Sens	contig973	contig973	Chromod	AATCTTA	contig973	Solyc07g	Solyc07g	Chromod	GO:00055	GO:00055	contig973	Solyc05g	Chromod	GO:00055	SL2.40ch	AT5G43530.1		SNF2 dor	chr5:174	889.553	486.206	406.467	1373.35	1320.85	1393.98
GT	Sense	Sense	0.603	Detected	-0.603	Detected	0.000	1.225	Detected	1.560	Detected	1.393	0.156	GT	Sens	EF667342	EF667342	SlARF8: (	CACAACTAAATACGTGCTCCAACTCATCATCACTTCCAACTTACGGGAAAGATACATTCA																321.887	127.151	123.805	437.433	451.614	600.257
GT	Sense	Sense	0.891	Detected	-0.891	Detected	0.000	1.015	Detected	1.006	Detected	1.011	0.374	GT	Sens	LeKNOT1	LeKNOT1	Lycopers	AAATGGATCATCTGATGAAGAGGTTGACGTGAATAACAGTTTCATCGACCCCCAGGCTGA																994.964	263.809	264.684	1068.38	988.692	1035.13

		12h_AZ_Control					12h_AZ_TAPG + TPRP vs. 12h_AZ_Control					
ProbeNar	Orientatio	Fold 12h	Flag 12h	Fold 12h	Flag 12h	Geomean	Fold 12h	Flag 12h	Fold 12h	Flag 12h	Geomean	P-value
A 96 P01	Sense	-0.556	Detected	0.556	Detected	0.000	-2.687	Detected	-1.778	Detected	-2.232	0.090
A 96 P01	Sense	-0.297	Detected	0.297	Detected	0.000	-0.909	Detected	-1.714	Detected	-1.312	0.120
A 96 P01	Sense	-0.081	Detected	0.081	Detected	0.000	-1.049	Detected	-1.106	Detected	-1.077	0.006
A 96 P01	Sense	-0.118	Detected	0.118	Detected	0.000	-2.770	Detected	-3.610	Detected	-3.190	0.018
A 96 P01	Sense	-0.549	Detected	0.549	Detected	0.000	-1.936	Detected	-1.649	Detected	-1.792	0.087
A 96 P02	Sense	-0.114	Detected	0.114	Detected	0.000	-1.435	Detected	-1.645	Detected	-1.540	0.010
A 96 P03	Sense	-0.027	Detected	0.027	Detected	0.000	-1.578	Comprom	-1.702	Comprom	-1.640	0.002
A 96 P03	Sense	-0.341	Detected	0.341	Detected	0.000	-1.009	Detected	-2.908	Detected	-1.958	0.192
A 96 P04	Sense	-0.196	Detected	0.196	Detected	0.000	-1.921	Detected	-2.168	Detected	-2.045	0.013
A 96 P05	Sense	-0.107	Detected	0.107	Detected	0.000	-1.040	Detected	-0.985	Detected	-1.012	0.012
A 96 P06	Sense	-0.246	Detected	0.246	Detected	0.000	-0.957	Detected	-1.467	Comprom	-1.212	0.076
A 96 P07	Sense	-1.031	Detected	1.031	Detected	0.000	-3.149	Detected	-4.200	Detected	-3.674	0.086
A 96 P08	Sense	-0.360	Detected	0.360	Detected	0.000	-1.357	Detected	-1.667	Detected	-1.512	0.061
A 96 P08	Sense	0.091	Detected	-0.091	Detected	0.000	-1.508	Detected	-1.502	Detected	-1.505	0.004
A 96 P08	Sense	-0.027	Detected	0.027	Detected	0.000	-4.300	Comprom	-2.222	Detected	-3.261	0.088
A 96 P08	Sense	0.308	Detected	-0.308	Detected	0.000	-1.641	Detected	-3.788	Detected	-2.714	0.136
A 96 P08	Sense	-0.094	Detected	0.094	Detected	0.000	-1.227	Detected	-1.177	Detected	-1.202	0.006
A 96 P10	Sense	-0.396	Detected	0.396	Detected	0.000	-1.334	Detected	-1.065	Detected	-1.199	0.103
A 96 P10	Sense	-0.456	Detected	0.456	Detected	0.000	-1.503	Detected	-1.430	Detected	-1.467	0.085
A 96 P11	Sense	-0.524	Detected	0.524	Detected	0.000	-1.281	Detected	-1.056	Detected	-1.169	0.161
A 96 P13	Sense	-0.269	Detected	0.269	Detected	0.000	-1.842	Detected	-1.121	Detected	-1.481	0.081
A 96 P13	Sense	-0.298	Detected	0.298	Detected	0.000	-1.895	Detected	-2.408	Detected	-2.151	0.032
A 96 P13	Sense	-0.554	Detected	0.554	Detected	0.000	-1.933	Detected	-1.664	Detected	-1.799	0.087
A 96 P13	Sense	-0.050	Detected	0.050	Detected	0.000	-1.348	Detected	-1.178	Detected	-1.263	0.006
A 96 P13	Sense	-0.093	Detected	0.093	Detected	0.000	-1.503	Detected	-1.387	Detected	-1.445	0.006
A 96 P13	Sense	-0.137	Detected	0.137	Detected	0.000	-1.280	Detected	-1.396	Detected	-1.338	0.012
A 96 P13	Sense	-0.005	Detected	0.005	Detected	0.000	-2.411	Detected	-2.075	Detected	-2.243	0.006
A 96 P13	Sense	-0.082	Detected	0.082	Detected	0.000	-1.138	Detected	-1.173	Detected	-1.156	0.005
A 96 P14	Sense	-0.067	Detected	0.067	Detected	0.000	-1.280	Detected	-0.834	Detected	-1.057	0.045
A 96 P14	Sense	-0.059	Detected	0.059	Detected	0.000	-1.598	Detected	-1.406	Detected	-1.502	0.006
A 96 P15	Sense	-0.294	Detected	0.294	Detected	0.000	-0.874	Detected	-1.338	Detected	-1.106	0.098
A 96 P16	Sense	-0.155	Detected	0.155	Detected	0.000	-1.249	Detected	-1.550	Detected	-1.399	0.023
A 96 P16	Sense	0.103	Detected	-0.103	Detected	0.000	-1.285	Detected	-0.872	Detected	-1.079	0.043
A 96 P18	Sense	0.373	Detected	-0.373	Detected	0.000	-1.024	Detected	-1.442	Detected	-1.233	0.102
A 96 P19	Sense	-0.249	Detected	0.249	Detected	0.000	-2.004	Detected	-1.677	Detected	-1.840	0.025
A 96 P19	Sense	0.100	Detected	-0.100	Detected	0.000	-2.100	Detected	-1.762	Detected	-1.931	0.010
A 96 P21	Sense	0.168	Detected	-0.168	Detected	0.000	-1.470	Detected	-1.707	Detected	-1.589	0.016
A 96 P21	Sense	0.003	Detected	-0.003	Detected	0.000	-1.663	Comprom	-3.858	Comprom	-2.761	0.128
A 96 P22	Sense	-0.053	Detected	0.053	Detected	0.000	-2.892	Detected	-2.842	Detected	-2.867	0.000
A 96 P22	Sense	0.308	Detected	-0.308	Detected	0.000	-1.645	Detected	-3.630	Detected	-2.637	0.127
A 96 P23	Sense	-0.012	Detected	0.012	Detected	0.000	-0.963	Detected	-1.572	Detected	-1.267	0.053
A 96 P24	Sense	0.021	Detected	-0.021	Detected	0.000	-3.059	Comprom	-2.368	Comprom	-2.713	0.016
A 96 P25	Sense	-0.280	Detected	0.280	Detected	0.000	-0.977	Detected	-1.886	Detected	-1.431	0.115
GT Sense	Sense	-1.430	Detected	1.430	Detected	0.000	-1.144	Detected	-1.649	Detected	-1.397	0.438
GT Sense	Sense	-0.339	Detected	0.339	Detected	0.000	-1.089	Detected	-2.400	Detected	-1.744	0.142
GT Sense	Sense	-0.800	Detected	0.800	Detected	0.000	-1.115	Detected	-1.017	Detected	-1.066	0.315
GT Sense	Sense	0.307	Detected	-0.307	Detected	0.000	-1.848	Comprom	-1.710	Comprom	-1.779	0.030
GT Sense	Sense	-0.423	Detected	0.423	Detected	0.000	-1.240	Detected	-1.560	Detected	-1.400	0.090
GT Sense	Sense	0.076	Detected	-0.076	Detected	0.000	-1.229	Detected	-1.867	Detected	-1.548	0.042
GT Sense	Sense	-0.080	Detected	0.080	Detected	0.000	-1.207	Detected	-1.067	Detected	-1.137	0.009
GT Sense	Sense	-0.017	Detected	0.017	Detected	0.000	-2.217	Detected	-1.038	Detected	-1.628	0.110
GT Sense	Sense	0.219	Detected	-0.219	Detected	0.000	-1.150	Detected	-1.757	Detected	-1.454	0.060
GT Sense	Sense	-0.251	Detected	0.251	Detected	0.000	-1.852	Detected	-2.127	Detected	-1.990	0.020
GT Sense	Sense	-0.502	Detected	0.502	Detected	0.000	-0.939	Detected	-2.821	Comprom	-1.880	0.220
GT Sense	Sense	-0.121	Detected	0.121	Detected	0.000	-1.503	Detected	-1.983	Detected	-1.743	0.023
GT Sense	Sense	-0.589	Detected	0.589	Detected	0.000	-1.994	Detected	-1.553	Detected	-1.773	0.106
GT Sense	Sense	-0.139	Detected	0.139	Detected	0.000	-1.511	Detected	-1.029	Detected	-1.270	0.045
GT Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-2.277	Comprom	-1.077	Comprom	-1.677	0.108
GT Sense	Sense	-0.197	Detected	0.197	Detected	0.000	-2.093	Detected	-2.356	Detected	-2.224	0.011
GT Sense	Sense	0.111	Detected	-0.111	Detected	0.000	-2.260	Detected	-0.800	Detected	-1.530	0.174
GT Sense	Sense	0.357	Detected	-0.357	Detected	0.000	-1.989	Comprom	-1.122	Comprom	-1.555	0.110
GT Sense	Sense	-0.428	Detected	0.428	Detected	0.000	-2.817	Detected	-2.344	Detected	-2.580	0.034
GT Sense	Sense	0.483	Detected	-0.483	Detected	0.000	-1.721	Comprom	-2.385	Comprom	-2.053	0.073
GT Sense	Sense	-0.274	Detected	0.274	Detected	0.000	-1.308	Comprom	-1.108	Comprom	-1.208	0.054
GT Sense	Sense	-0.206	Detected	0.206	Detected	0.000	-1.400	Comprom	-1.145	Comprom	-1.272	0.034
GT Sense	Sense	-0.519	Detected	0.519	Detected	0.000	-1.782	Detected	-1.451	Detected	-1.617	0.097
GT Sense	Sense	-0.335	Detected	0.335	Detected	0.000	-0.830	Detected	-1.268	Detected	-1.049	0.120
GT Sense	Sense	-0.051	Detected	0.051	Detected	0.000	-0.870	Comprom	-2.475	Comprom	-1.672	0.173
GT Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-2.509	Detected	-2.461	Detected	-2.485	0.001
GT Sense	Sense	-0.673	Detected	0.673	Detected	0.000	-1.086	Detected	-0.949	Detected	-1.018	0.272
GT Sense	Sense	-0.252	Detected	0.252	Detected	0.000	-2.448	Detected	-3.887	Comprom	-3.168	0.053
GT Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-1.304	Detected	-1.069	Detected	-1.186	0.028
GT Sense	Sense	-0.757	Detected	0.757	Detected	0.000	-1.286	Detected	-1.599	Detected	-1.443	0.203
GT Sense	Sense	0.160	Detected	-0.160	Detected	0.000	-1.759	Detected	-1.743	Detected	-1.751	0.008
GT Sense	Sense	0.360	Detected	-0.360	Detected	0.000	-1.450	Detected	-1.302	Detected	-1.376	0.064
GT Sense	Sense	0.027	Detected	-0.027	Detected	0.000	-2.500	Detected	-1.010	Detected	-1.755	0.143
GT Sense	Sense	0.234	Detected	-0.234	Detected	0.000	-1.486	Detected	-1.504	Detected	-1.495	0.024
GT Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-1.276	Detected	-2.638	Detected	-1.957	0.107
GT Sense	Sense	-0.307	Detected	0.307	Detected	0.000	-0.929	Detected	-1.201	Detected	-1.065	0.087
GT Sense	Sense	-0.432	Detected	0.432	Detected	0.000	-1.614	Detected	-1.468	Detected	-1.541	0.072
GT Sense	Sense	0.150	Detected	-0.150	Detected	0.000	-1.734	Detected	-1.207	Detected	-1.470	0.040
GT Sense	Sense	-0.412	Detected	0.412	Detected	0.000	-2.123	Detected	-1.637	Detected	-1.880	0.059
GT Sense	Sense	0.624	Detected	-0.624	Detected	0.000	-2.267	Detected	-1.068	Detected	-1.667	0.194
GT Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-1.559	Detected	-1.300	Detected	-1.429	0.019
GT Sense	Sense	-0.529	Detected	0.529	Detected	0.000	-3.037	Detected	-2.070	Detected	-2.553	0.071
GT Sense	Sense	-0.416	Detected	0.416	Detected	0.000	-1.371	Detected	-1.841	Detected	-1.606	0.078
GT Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-1.223	Detected	-1.116	Detected	-1.170	0.002
GT Sense	Sense	-0.598	Detected	0.598	Detected	0.000	-1.362	Detected	-2.208	Detected	-1.785	0.135
GT Sense	Sense	-0.205	Detected	0.205	Detected	0.000	-1.294	Detected	-1.556	Detected	-1.425	0.028
GT Sense	Sense	-0.260	Detected	0.260	Detected	0.000	-1.159	Detected	-2.651	Comprom	-1.905	0.137
GT Sense	Sense	0.404	Detected	-0.404	Detected	0.000	-1.331	Detected	-0.871	Detected	-1.101	0.141
GT Sense	Sense	-0.148	Detected	0.148	Detected	0.000	-1.059	Detected	-1.130	Detected	-1.095	0.019
GT Sense	Sense	-0.041	Detected	0.041	Detected	0.000	-0.862	Comprom	-1.240	Comprom	-1.051	0.032
GT Sense	Sense	-0.400	Detected	0.400	Detected	0.000	-1.234	Detected	-1.352	Detected	-1.293	0.085
GT Sense	Sense	-0.258	Detected	0.258	Detected	0.000	-1.342	Comprom	-0.901	Comprom	-1.121	0.081
GT Sense	Sense	-0.167	Detected	0.167	Detected	0.000	-2.123	Comprom	-1.628	Comprom	-1.875	0.024
GT Sense	Sense	-0.391	Detected	0.391	Detected	0.000	-2.926	Detected	-1.582	Detected	-2.254	0.101
GT Sense	Sense	0.172	Detected	-0.172	Detected	0.000	-1.713	Detected	-2.826	Detected	-2.270	0.060
GT Sense	Sense	0.248	Detected	-0.248	Detected	0.000	-1.090	Detected	-1.931	Comprom	-1.511	0.091
GT Sense	Sense	-0.600	Detected	0.600	Detected	0.000	-1.468	Detected	-1.970	Detected	-1.719	0.118
GT Sense	Sense	-0.287	Detected	0.287	Detected	0.000	-1.373	Detected	-1.788	Detected	-1.581	0.047
GT Sense	Sense	0.139	Detected	-0.139	Detected	0.000	-1.141	Detected	-1.314	Detected	-1.227	0.017
GT Sense	Sense	-0.311	Detected	0.311	Detected	0.000	-0.950	Detected	-1.127	Detected	-1.039	0.085
GT Sense	Sense	-0.021	Detected	0.021	Detected	0.000	-1.915	Detected	-1.064	Detected	-1.489	0.073
GT Sense	Sense	-0.280	Detected	0.280	Detected	0.000	-1.659	Comprom	-0.869	Detected	-1.264	0.121
GT Sense	Sense	-0.340	Detected	0.340	Detected	0.000	-2.432	Detected	-2.223	Detected	-2.327	0.023
GT Sense	Sense	-0.486	Detected	0.486	Detected	0.000	-1.091	Detected	-1.850	Comprom	-1.470	0.140
GT Sense	Sense	-0.529	Detected	0.529	Detected	0.000	-2.972	Comprom	-3.248	Comprom	-3.110	0.030
GT Sense	Sense	-0.087	Detected	0.087	Detected	0.000	-1.715	Comprom	-1.472	Comprom	-1.593	0.009
GT Sense	Sense	-0.459	Detected	0.459	Detected	0.000	-1.206	Detected	-1.787	Detected	-1.497	0.110
GT Sense	Sense	-0.503	Detected	0.503	Detected	0.000	-1.977	Detected	-2.451	Detected	-2.214	0.058
GT Sense	Sense	-0.386	Detected	0.386	Detected	0.000	-2.072	Comprom	-1.561	Comprom	-1.817	0.059
GT Sense	Sense	-0.211	Detected	0.211	Detected	0.000	-1.721	Comprom	-1.668	Comprom	-1.694	0.015
GT Sense	Sense	-0.209	Detected	0.209	Detected	0.000	-1.023	Detected	-1.578	Detected	-1.300	0.065
GT Sense	Sense	-0.080	Detected	0.080	Detected	0.000	-1.010	Detected	-1.280	Detected	-1.145	0.018
GT Sense	Sense	-0.014	Detected	0.014	Detected	0.000	-1.382	Comprom	-2.009	Comprom	-1.696	0.033
GT Sense	Sense	-0.793	Detected	0.793	Detected	0.000	-1.048	Detected	-1.706	Detected	-1.377	0.250
GT Sense	Sense	0.117	Detected	-0.117	Detected	0.000	-1.093	Detected	-1.725	Detected	-1.409	0.053
GT Sense	Sense	-0.309	Detected	0.309	Detected	0.000	-0.895	Detected	-1.295	Detected	-1.095	0.097
GT Sense	Sense	-0.284	Detected	0.284	Detected	0.000	-0.918	Detected	-1.260	Detected	-1.089	0.082
GT Sense	Sense	-0.434	Detected	0.434	Detected	0.000	-1.076	Detected	-2.821	Detected	-1.948	0.184
GT Sense	Sense	0.033	Detected	-0.033	Detected	0.000	-1.899	Detected	-1.636	Detected	-1.768	0.006
GT Sense	Sense	-0.569	Detected	0.569	Detected	0.000	-1.209	Detected	-1.557	Detected	-1.383	0.146
GT Sense	Sense	-0.515	Detected	0.515	Detected	0.000	-1.741	Detected	-2.098	Detected	-1.919	0.072
GT Sense	Sense	-0.401	Detected	0.401	Detected	0.000	-1.419	Detected	-1.018	Detected	-1.219	0.113
GT Sense	Sense	0.092	Detected	-0.092	Detected	0.000	-1.082	Detected	-1.839	Comprom	-1.460	0.064
GT Sense	Sense	-0.165	Detected	0.165	Detected	0.000	-1.369	Comprom	-1.356	Comprom	-1.362	0.014
GT Sense	Sense	-0.108	Detected	0.108	Detected	0.000	-0.983	Detected	-1.371	Detected	-1.177	0.034
GT Sense	Sense	0.387	Detected	-0.387	Detected	0.000	-1.305	Detected	-2.895	Comprom	-2.100	0.141
GT Sense	Sense	-0.269	Detected	0.269	Detected	0.000	-1.526	Detected	-0.844	Detected	-1.185	0.112
GT Sense	Sense	-0.327	Detected	0.327	Detected	0.000	-2.674	Comprom	-2.560	Comprom	-2.617	0.016
GT Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.130	Detected	-0.999	Detected	-1.065	0.004
GT Sense	Sense	0.240	Detected	-0.240	Detected	0.000	-3.486	Detected	-2.725	Detected	-3.106	0.020
GT Sense	Sense	0.049	Detected	-0.049	Detected	0.000	-2.021	Detected	-1.555	Detected	-1.788	0.017
GT Sense	Sense	-0.160	Detected	0.160	Detected	0.000	-0.963	Detected	-1.638	Detected	-1.301	0.073
GT Sense	Sense	1.317	Detected	-1.317	Detected	0.000	-2.509	Detected	-3.125	Comprom	-2.817	0.173
GT Sense	Sense	-0.596	Detected	0.596	Detected	0.000	-1.164	Detected	-3.053	Comprom	-2.109	0.200
GT Sense	Sense	-0.535	Detected	0.535	Detected	0.000	-1.346	Detected	-2.410	Comprom	-1.878	0.131
GT Sense	Sense	-0.833	Detected	0.833	Detected	0.000	-3.185	Comprom	-3.238	Comprom	-3.212	0.061
GT Sense	Sense	0.177	Detected	-0.177	Detected	0.000	-2.179	Detected	-1.641	Detected	-1.910	0.027
GT Sense	Sense	1.309	Detected	-1.309	Detected	0.000	-2.170	Detected	-0.842	Detected	-1.506	0.413
GT Sense	Sense	-0.182	Detected	0.182	Detected	0.000	-1.689	Detected	-1.113	Detected	-1.401	0.054
GT Sense	Sense	-0.024	Detected	0.024	Detected	0.000	-1.718	Detected	-1.093	Detected	-1.405	0.046
GT Sense	Sense	-0.744	Detected	0.744	Detected	0.000	-0.937	Detected	-2.170	Detected	-1.553	0.249
GT Sense	Sense	-0.286	Detected	0.286	Detected	0.000	-0.991	Detected	-1.129	Detected	-1.060	0.069
GT Sense	Sense	-0.843	Detected	0.843	Detected	0.000	-0.936	Detected	-1.482	Detected	-1.209	0.306
GT Sense	Sense	-0.171	Detected	0.171	Detected	0.000	-2.167	Detected	-2.273	Detected	-2.220	0.006
GT Sense	Sense	-0.092	Detected	0.092	Detected	0.000	-0.898	Detected	-1.779	Detected	-1.338	0.097
GT Sense	Sense	-0.656	Detected	0.656	Detected	0.000	-2.327	Detected	-1.784	Detected	-2.055	0.101
GT Sense	Sense	-1.008	Detected	1.008	Detected	0.000	-1.775	Detected	-2.298	Detected	-2.037	0.190
GT Sense	Sense	-0.984	Detected	0.984	Detected	0.000	-1.701	Detected	-1.744	Detected	-1.722	0.222
GT Sense	Sense	0.057	Detected	-0.057	Detected	0.000	-1.560	Detected	-1.423	Detected	-1.491	0.004
GT Sense	Sense	-0.208	Detected	0.208	Detected	0.000	-1.327	Detected	-2.100	Comprom	-1.714	0.060
GT Sense	Sense	-0.518	Detected	0.518	Detected	0.000	-1.264	Detected	-2.364	Detected	-1.814	0.138
GT Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-0.886	Detected	-1.796	Detected	-1.341	0.099
GT Sense	Sense	-0.572	Detected	0.572	Detected	0.000	-1.143	Detected	-2.412	Detected	-1.777	0.173
GT Sense	Sense	-0.181	Detected	0.181	Detected	0.000	-1.236	Detected	-1.487	Detected	-1.362	0.025
GT Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.545	Comprom	-0.801	Detected	-1.173	0.089
GT Sense	Sense	-0.327	Detected	0.327	Detected	0.000	-1.576	Detected	-1.582	Detected	-1.579	0.040
GT Sense	Sense	-1.357	Detected	1.357	Detected	0.000	-1.074	Detected	-1.311	Detected	-1.192	0.474
GT Sense	Sense	0.073	Detected	-0.073	Detected	0.000	-2.304	Detected	-1.816	Detected	-2.060	0.015
GT Sense	Sense	-0.053	Detected	0.053	Detected	0.000	-1.129	Detected	-2.510	Detected	-1.820	0.119
GT Sense	Sense	-0.443	Detected	0.443	Detected	0.000	-0.931	Detected	-1.753	Detected	-1.342	0.157
GT Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-1.330	Detected	-1.724	Detected	-1.527	0.018
GT Sense	Sense	-0.253	Detected	0.253	Detected	0.000	-1.276	Detected	-1.075	Detected	-1.176	0.050
GT Sense	Sense	-0.273	Detected	0.273	Detected	0.000	-1.104	Detected	-1.558	Detected	-1.331	0.064
GT Sense	Sense	-0.967	Detected	0.967	Detected	0.000	-1.040	Detected	-1.215	Detected	-1.128	0.365
GT Sense	Sense	-0.502	Detected	0.502	Detected	0.000	-0.873	Detected	-1.556	Detected	-1.215	0.184
GT Sense	Sense	0.108	Detected	-0.108	Detected	0.000	-1.517	Detected	-2.507	Detected	-2.012	0.058
GT Sense	Sense	-0.199	Detected	0.199	Detected	0.000	-1.327	Detected	-1.699	Detected	-1.513	0.031
GT Sense	Sense	-0.103	Detected	0.103	Detected	0.000	-0.807	Detected	-1.660	Comprom	-1.233	0.107
GT Sense	Sense	-0.079	Detected	0.079	Detected	0.000	-0.934	Comprom	-1.497	Comprom	-1.215	0.053
GT Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-2.791	Detected	-2.551	Detected	-2.671	0.003
GT Sense	Sense	-0.541	Detected	0.541	Detected	0.000	-1.852	Detected	-3.235	Detected	-2.544	0.101
GT Sense	Sense	-0.265	Detected	0.265	Detected	0.000	-1.024	Detected	-1.779	Comprom	-1.401	0.094
GT Sense	Sense	-0.516	Detected	0.516	Detected	0.000	-0.954	Detected	-1.307	Detected	-1.130	0.174
GT Sense	Sense	-0.140	Detected	0.140	Detected	0.000	-1.327	Detected	-1.069	Detected	-1.198	0.024
GT Sense	Sense	-0.511	Detected	0.511	Detected	0.000	-1.827	Detected	-1.686	Detected	-1.756	0.076
GT Sense	Sense	-0.511	Detected	0.511	Detected	0.000	-2.809	Comprom	-2.204	Comprom	-2.506	0.052
GT Sense	Sense	-0.271	Detected	0.271	Detected	0.000	-1.581	Detected	-1.964	Detected	-1.772	0.033
GT Sense	Sense	0.244	Detected	-0.244	Detected	0.000	-2.860	Detected	-4.000	Detected	-3.430	0.031
GT Sense	Sense	-0.155	Detected	0.155	Detected	0.000	-0.921	Detected	-1.627	Detected	-1.274	0.081
GT Sense	Sense	-0.289	Detected	0.289	Detected	0.000	-2.463	Detected	-2.203	Detected	-2.333	0.018
GT Sense	Sense	0.248	Detected	-0.248	Detected	0.000	-0.903	Detected	-1.125	Detected	-1.014	0.065
GT Sense	Sense	-0.029	Detected	0.029	Detected	0.000	-1.093	Detected	-0.930	Detected	-1.011	0.007
GT Sense	Sense	-0.371	Detected	0.371	Detected	0.000	-1.329	Detected	-1.943	Detected	-1.636	0.077
GT Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-0.822	Comprom	-2.173	Comprom	-1.498	0.163
GT Sense	Sense	-0.010	Detected	0.010	Detected	0.000	-0.848	Detected	-2.001	Detected	-1.425	0.132
GT Sense	Sense	0.065	Detected	-0.065	Detected	0.000	-1.180	Detected	-3.011	Comprom	-2.095	0.150
GT Sense	Sense	0.147	Detected	-0.147	Detected	0.000	-0.876	Detected	-1.265	Detected	-1.070	0.048
GT Sense	Sense	-0.188	Detected	0.188	Detected	0.000	-2.051	Comprom	-2.210	Comprom	-2.131	0.009
GT Sense	Sense	-0.216	Detected	0.216	Detected	0.000	-1.802	Detected	-1.136	Detected	-1.469	0.066
GT Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-3.121	Detected	-2.775	Detected	-2.948	0.004
GT Sense	Sense	0.272	Detected	-0.272	Detected	0.000	-1.145	Detected	-1.563	Detected	-1.354	0.059
GT Sense	Sense	-0.184	Detected	0.184	Detected	0.000	-0.850	Detected	-1.707	Comprom	-1.278	0.111
GT Sense	Sense	0.214	Detected	-0.214	Detected	0.000	-1.516	Comprom	-1.119	Comprom	-1.318	0.046
GT Sense	Sense	-0.403	Detected	0.403	Detected	0.000	-1.624	Detected	-1.790	Detected	-1.707	0.053
GT Sense	Sense	-0.766	Detected	0.766	Detected	0.000	-1.790	Detected	-2.830	Comprom	-2.310	0.130
GT Sense	Sense	-1.007	Detected	1.007	Detected	0.000	-1.995	Detected	-3.118	Detected	-2.557	0.157
GT Sense	Sense	0.585	Detected	-0.585	Detected	0.000	-1.308	Detected	-1.012	Detected	-1.160	0.195
GT Sense	Sense	0.281	Detected	-0.281	Detected	0.000	-1.479	Detected	-0.986	Detected	-1.233	0.081
GT Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.647	Detected	-1.174	Detected	-1.411	0.027
GT Sense	Sense	-0.351	Detected	0.351	Detected	0.000	-0.971	Detected	-1.261	Detected	-1.116	0.099
GT Sense	Sense	0.063	Detected	-0.063	Detected	0.000	-1.912	Detected	-0.969	Detected	-1.440	0.094
GT Sense	Sense	-0.292	Detected	0.292	Detected	0.000	-1.216	Detected	-0.959	Detected	-1.088	0.076
GT Sense	Sense	-0.154	Detected	0.154	Detected	0.000	-1.362	Detected	-0.972	Detected	-1.167	0.043
GT Sense	Sense	0.774	Detected	-0.774	Detected	0.000	-1.069	Detected	-1.358	Detected	-1.213	0.263
GT Sense	Sense	-0.159	Detected	0.159	Detected	0.000	-1.662	Detected	-1.639	Detected	-1.651	0.009
GT Sense	Sense	-0.357	Detected	0.357	Detected	0.000	-1.610	Comprom	-1.299	Comprom	-1.455	0.065
GT Sense	Sense	-0.240	Detected	0.240	Detected	0.000	-1.436	Detected	-1.241	Detected	-1.338	0.035
GT Sense	Sense	-0.754	Detected	0.754	Detected	0.000	-2.334	Detected	-3.035	Detected	-2.684	0.084
GT Sense	Sense	-0.196	Detected	0.196	Detected	0.000	-1.302	Detected	-1.350	Detected	-1.326	0.022
GT Sense	Sense	0.079	Detected	-0.079	Detected	0.000	-2.709	Comprom	-2.797	Comprom	-2.753	0.001
GT Sense	Sense	-0.098	Detected	0.098	Detected	0.000	-0.989	Detected	-1.267	Detected	-1.128	0.022
GT Sense	Sense	-0.016	Detected	0.016	Detected	0.000	-1.915	Comprom	-1.004	Detected	-1.460	0.085
GT Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-3.382	Comprom	-2.194	Detected	-2.788	0.043
GT Sense	Sense	-0.479	Detected	0.479	Detected	0.000	-0.942	Detected	-1.321	Detected	-1.132	0.159
GT Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-1.263	Detected	-1.426	Detected	-1.345	0.005
GT Sense	Sense	1.074	Detected	-1.074	Detected	0.000	-1.292	Detected	-0.925	Detected	-1.109	0.416
GT Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-0.819	Detected	-2.047	Detected	-1.433	0.147
GT Sense	Sense	-0.020	Detected	0.020	Detected	0.000	-2.188	Comprom	-2.378	Comprom	-2.283	0.002
GT Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-1.788	Detected	-1.022	Detected	-1.405	0.067
GT Sense	Sense	-0.613	Detected	0.613	Detected	0.000	-0.931	Detected	-1.777	Detected	-1.354	0.211
GT Sense	Sense	-0.365	Detected	0.365	Detected	0.000	-0.909	Detected	-1.475	Detected	-1.192	0.123
GT Sense	Sense	-0.110	Detected	0.110	Detected	0.000	-1.916	Comprom	-3.035	Comprom	-2.476	0.049
GT Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-2.132	Detected	-1.503	Detected	-1.818	0.034
GT Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-0.909	Detected	-1.112	Detected	-1.011	0.010
GT Sense	Sense	-0.089	Detected	0.089	Detected	0.000	-1.002	Detected	-1.538	Detected	-1.270	0.046
GT Sense	Sense	-0.667	Detected	0.667	Detected	0.000	-1.327	Detected	-1.916	Detected	-1.621	0.156
GT Sense	Sense	-0.872	Detected	0.872	Detected	0.000	-1.380	Detected	-1.942	Comprom	-1.661	0.212
GT Sense	Sense	0.421	Detected	-0.421	Detected	0.000	-1.332	Detected	-1.048	Detected	-1.190	0.116
GT Sense	Sense	-0.620	Detected	0.620	Detected	0.000	-0.882	Detected	-1.286	Comprom	-1.084	0.238
GT Sense	Sense	-0.620	Detected	0.620	Detected	0.000	-1.040	Detected	-1.408	Detected	-1.224	0.199
GT Sense	Sense	-0.918	Detected	0.918	Detected	0.000	-1.142	Detected	-3.070	Detected	-2.106	0.254
GT Sense	Sense	-0.369	Detected	0.369	Detected	0.000	-1.390	Detected	-1.514	Detected	-1.452	0.061
GT Sense	Sense	0.423	Detected	-0.423	Detected	0.000	-2.798	Detected	-1.793	Detected	-2.295	0.073
GT Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-1.485	Detected	-2.536	Detected	-2.011	0.062
GT Sense	Sense	-0.318	Detected	0.318	Detected	0.000	-1.186	Detected	-1.050	Detected	-1.118	0.075
GT Sense	Sense	-0.503	Detected	0.503	Detected	0.000	-0.877	Detected	-1.348	Detected	-1.112	0.183
GT Sense	Sense	0.019	Detected	-0.019	Detected	0.000	-1.924	Detected	-1.589	Detected	-1.756	0.009
GT Sense	Sense	-0.706	Detected	0.706	Detected	0.000	-0.892	Detected	-1.324	Detected	-1.108	0.272
GT Sense	Sense	-0.207	Detected	0.207	Detected	0.000	-1.455	Detected	-0.811	Detected	-1.133	0.098

GT	Sens	Sense	-0.050	Detected	0.050	Detected	0.000	-2.941	Comprom	-3.004	Comprom	-2.972	0.000	GT	Sens	contig168	contig168	Lipase-lik	GAGGCT
GT	Sens	Sense	-0.150	Detected	0.150	Detected	0.000	-1.449	Detected	-3.808	Comprom	-2.629	0.158	GT	Sens	contig168	contig168	Hydrolas	TTATCAT
GT	Sens	Sense	-0.276	Detected	0.276	Detected	0.000	-0.806	Detected	-1.290	Detected	-1.048	0.104	GT	Sens	contig168	contig168	Receptor	TCAAAT
GT	Sens	Sense	-0.221	Detected	0.221	Detected	0.000	-2.724	Detected	-2.257	Detected	-2.491	0.016	GT	Sens	contig169	contig169	40S ribos	TGATGT
GT	Sens	Sense	-0.204	Detected	0.204	Detected	0.000	-1.092	Detected	-1.452	Detected	-1.272	0.043	GT	Sens	contig169	contig169	Unknown	TCTTTT
GT	Sens	Sense	-0.057	Detected	0.057	Detected	0.000	-0.950	Detected	-2.512	Detected	-1.731	0.158	GT	Sens	contig170	contig170	Unknown	TTTTGC
GT	Sens	Sense	-0.668	Detected	0.668	Detected	0.000	-1.548	Detected	-1.340	Detected	-1.444	0.166	GT	Sens	contig170	contig170	Receptor	CTTGGA
GT	Sens	Sense	-0.660	Detected	0.660	Detected	0.000	-1.316	Detected	-2.667	Detected	-1.991	0.170	GT	Sens	contig171	contig171	Cytochro	AAAGGA
GT	Sens	Sense	0.097	Detected	-0.097	Detected	0.000	-1.868	Detected	-2.059	Detected	-1.964	0.005	GT	Sens	contig171	contig171	Myb-relat	TTGGAC
GT	Sens	Sense	-0.304	Detected	0.304	Detected	0.000	-1.437	Detected	-4.419	Comprom	-2.928	0.194	GT	Sens	contig172	contig172	Nudix hy	GAACTC
GT	Sens	Sense	-0.043	Detected	0.043	Detected	0.000	-0.946	Detected	-1.286	Detected	-1.116	0.024	GT	Sens	contig172	contig172	UDP-gluc	ATGCAA
GT	Sens	Sense	-1.075	Detected	1.075	Detected	0.000	-2.108	Detected	-4.720	Detected	-3.414	0.181	GT	Sens	contig172	contig172	Unknown	CACTTG
GT	Sens	Sense	-0.023	Detected	0.023	Detected	0.000	-1.254	Detected	-2.279	Detected	-1.766	0.075	GT	Sens	contig173	contig173	Long cell	CGATGA
GT	Sens	Sense	-0.446	Detected	0.446	Detected	0.000	-1.274	Detected	-1.747	Detected	-1.511	0.096	GT	Sens	contig173	contig173	Peroxida	ATGCCT
GT	Sens	Sense	0.167	Detected	-0.167	Detected	0.000	-1.707	Detected	-0.961	Detected	-1.334	0.082	GT	Sens	contig174	contig174	Major alle	TAATATT
GT	Sens	Sense	-0.267	Detected	0.267	Detected	0.000	-3.544	Detected	-2.479	Detected	-3.012	0.037	GT	Sens	contig174	contig174	UDP-gluc	GGACTA
GT	Sens	Sense	-0.459	Detected	0.459	Detected	0.000	-1.322	Detected	-2.667	Detected	-1.994	0.134	GT	Sens	contig174	contig174	Receptor	TCAGAA
GT	Sens	Sense	-0.098	Detected	0.098	Detected	0.000	-2.196	Detected	-0.875	Detected	-1.536	0.148	GT	Sens	contig175	contig175	Unknown	GTTAAG
GT	Sens	Sense	-0.271	Detected	0.271	Detected	0.000	-1.189	Detected	-1.553	Detected	-1.371	0.052	GT	Sens	contig175	contig175	ACT dom	TAAAGG
GT	Sens	Sense	-0.270	Detected	0.270	Detected	0.000	-1.132	Detected	-3.631	Detected	-2.382	0.203	GT	Sens	contig176	contig176	Xylanase	GACAAT
GT	Sens	Sense	0.133	Detected	-0.133	Detected	0.000	-3.655	Comprom	-2.072	Comprom	-2.863	0.070	GT	Sens	contig177	contig177	Transcrip	CAGTGG
GT	Sens	Sense	-0.986	Detected	0.986	Detected	0.000	-2.007	Detected	-2.458	Detected	-2.233	0.158	GT	Sens	contig178	contig178	Transcrip	TTGTCT
GT	Sens	Sense	-0.355	Detected	0.355	Detected	0.000	-0.961	Detected	-1.681	Detected	-1.321	0.121	GT	Sens	contig178	contig178	Receptor	TTTGGA
GT	Sens	Sense	-0.415	Detected	0.415	Detected	0.000	-1.146	Detected	-1.022	Detected	-1.084	0.123	GT	Sens	contig178	contig178	Fasciclin	ACCTAT
GT	Sens	Sense	-0.294	Detected	0.294	Detected	0.000	-1.389	Detected	-1.037	Detected	-1.213	0.071	GT	Sens	contig178	contig178	MYB tran	GAAAGT
GT	Sens	Sense	0.842	Detected	-0.842	Detected	0.000	-1.453	Detected	-1.423	Detected	-1.438	0.230	GT	Sens	contig178	contig178	Glycosylt	AATACA
GT	Sens	Sense	-0.215	Detected	0.215	Detected	0.000	-0.819	Detected	-1.354	Detected	-1.086	0.087	GT	Sens	contig178	contig178	Unknown	GATTGA
GT	Sens	Sense	-0.319	Detected	0.319	Detected	0.000	-1.654	Detected	-1.228	Detected	-1.441	0.064	GT	Sens	contig179	contig179	Ethylene	GAAGTT
GT	Sens	Sense	-0.378	Detected	0.378	Detected	0.000	-0.972	Detected	-1.105	Detected	-1.038	0.114	GT	Sens	contig179	contig179	Uncharac	TAGAGC
GT	Sens	Sense	-0.220	Detected	0.220	Detected	0.000	-1.416	Detected	-1.668	Detected	-1.542	0.026	GT	Sens	contig180	contig180	GRAM-co	TAAACC
GT	Sens	Sense	-0.309	Detected	0.309	Detected	0.000	-1.450	Detected	-1.374	Detected	-1.412	0.045	GT	Sens	contig180	contig180	Kinase fa	CGCCAT
GT	Sens	Sense	-0.093	Detected	0.093	Detected	0.000	-1.248	Comprom	-2.399	Comprom	-1.824	0.089	GT	Sens	contig180	contig180	Vacuolar	CTAAAG
GT	Sens	Sense	-0.255	Detected	0.255	Detected	0.000	-0.801	Detected	-1.643	Comprom	-1.222	0.131	GT	Sens	contig180	contig180	Unknown	GAACAA
GT	Sens	Sense	-0.232	Detected	0.232	Detected	0.000	-0.946	Comprom	-1.312	Comprom	-1.129	0.062	GT	Sens	contig181	contig181	Unknown	CTATAT
GT	Sens	Sense	0.046	Detected	-0.046	Detected	0.000	-1.182	Detected	-0.873	Detected	-1.028	0.024	GT	Sens	contig181	contig181	RNase H	CAGAGC
GT	Sens	Sense	0.155	Detected	-0.155	Detected	0.000	-1.213	Detected	-1.039	Detected	-1.126	0.024	GT	Sens	contig181	contig181	Myb fami	CTAACG
GT	Sens	Sense	-0.222	Detected	0.222	Detected	0.000	-2.266	Detected	-1.928	Detected	-2.097	0.017	GT	Sens	contig181	contig181	Non-spec	AGCCTT
GT	Sens	Sense	-0.344	Detected	0.344	Detected	0.000	-1.928	Detected	-1.674	Detected	-1.801	0.039	GT	Sens	contig181	contig181	Calcium-I	CCAACT
GT	Sens	Sense	0.345	Detected	-0.345	Detected	0.000	-1.304	Detected	-0.856	Detected	-1.080	0.120	GT	Sens	contig182	contig182	Kunitz-ty	CGACTA
GT	Sens	Sense	-0.300	Detected	0.300	Detected	0.000	-1.121	Detected	-1.309	Detected	-1.215	0.061	GT	Sens	contig182	contig182	S-recepto	TCTGGT
GT	Sens	Sense	0.183	Detected	-0.183	Detected	0.000	-3.077	Comprom	-1.717	Comprom	-2.397	0.076	GT	Sens	contig182	contig182	Unknown	AGCTGG
GT	Sens	Sense	-0.470	Detected	0.470	Detected	0.000	-2.270	Detected	-2.142	Detected	-2.206	0.043	GT	Sens	contig182	contig182	Calmodul	GTTTTG
GT	Sens	Sense	-0.178	Detected	0.178	Detected	0.000	-1.554	Detected	-2.071	Detected	-1.812	0.029	GT	Sens	contig182	contig182	Unknown	GTGTAT
GT	Sens	Sense	-0.094	Detected	0.094	Detected	0.000	-2.145	Comprom	-2.455	Comprom	-2.300	0.006	GT	Sens	contig182	contig182	Cathepsi	TTGTCT
GT	Sens	Sense	-0.067	Detected	0.067	Detected	0.000	-1.237	Detected	-1.283	Detected	-1.260	0.003	GT	Sens	contig182	contig182	Unknown	TTTGAT
GT	Sens	Sense	0.116	Detected	-0.116	Detected	0.000	-1.534	Detected	-1.153	Detected	-1.343	0.026	GT	Sens	contig182	contig182	Endochiti	TAATGC
GT	Sens	Sense	1.538	Detected	-1.538	Detected	0.000	-1.527	Detected	-2.160	Detected	-1.844	0.361	GT	Sens	contig183	contig183	Unknown	GGTAGG
GT	Sens	Sense	-0.249	Detected	0.249	Detected	0.000	-1.121	Detected	-1.094	Detected	-1.107	0.047	GT	Sens	contig183	contig183	Homeodo	GGAGAT
GT	Sens	Sense	-0.101	Detected	0.101	Detected	0.000	-1.674	Comprom	-0.882	Comprom	-1.278	0.089	GT	Sens	contig183	contig183	ABC tran	CAACTC
GT	Sens	Sense	-0.179	Detected	0.179	Detected	0.000	-1.272	Comprom	-1.679	Comprom	-1.476	0.032	GT	Sens	contig185	contig185	Gag-Pol	CAAAAA
GT	Sens	Sense	-0.525	Detected	0.525	Detected	0.000	-2.565	Detected	-3.578	Detected	-3.071	0.052	GT	Sens	contig185	contig185	Xylogluca	GCTAAG
GT	Sens	Sense	0.488	Detected	-0.488	Detected	0.000	-2.204	Detected	-3.397	Comprom	-2.800	0.068	GT	Sens	contig185	contig185	Peroxida	TCATGG
GT	Sens	Sense	0.482	Detected	-0.482	Detected	0.000	-1.915	Detected	-1.940	Detected	-1.927	0.057	GT	Sens	contig186	contig186	Ethylene	CAGAAG
GT	Sens	Sense	-0.769	Detected	0.769	Detected	0.000	-1.299	Detected	-3.228	Comprom	-2.264	0.208	GT	Sens	contig187	contig187	Sensitivit	AGGCTA
GT	Sens	Sense	0.047	Detected	-0.047	Detected	0.000	-1.094	Detected	-1.122	Detected	-1.108	0.002	GT	Sens	contig187	contig187	Unknown	TGGCGT
GT	Sens	Sense	-0.653	Detected	0.653	Detected	0.000	-3.466	Comprom	-1.675	Detected	-2.571	0.146	GT	Sens	contig187	contig187	Pathogen	GGACAT
GT	Sens	Sense	0.081	Detected	-0.081	Detected	0.000	-1.613	Detected	-1.142	Detected	-1.378	0.031	GT	Sens	contig188	contig188	Thaumati	TTTGTT
GT	Sens	Sense	0.324	Detected	-0.324	Detected	0.000	-0.931	Detected	-2.065	Detected	-1.498	0.149	GT	Sens	contig188	contig188	Unknown	AGAGAA
GT	Sens	Sense	0.149	Detected	-0.149	Detected	0.000	-1.100	Detected	-1.133	Detected	-1.116	0.017	GT	Sens	contig190	contig190	Aspartic	TCGGAG
GT	Sens	Sense	-0.211	Detected	0.211	Detected	0.000	-1.180	Detected	-1.060	Detected	-1.120	0.036	GT	Sens	contig190	contig190	cDNA clo	GAGCTT
GT	Sens	Sense	-0.582	Detected	0.582	Detected	0.000	-1.345	Detected	-1.305	Detected	-1.325	0.151	GT	Sens	contig191	contig191	LOB dom	CTTGTC
GT	Sens	Sense	-0.178	Detected	0.178	Detected	0.000	-1.388	Detected	-1.602	Detected	-1.495	0.019	GT	Sens	contig191	contig191	Mutator-li	CTTTGG
GT	Sens	Sense	-0.785	Detected	0.785	Detected	0.000	-0.888	Detected	-2.632	Detected	-1.760	0.272	GT	Sens	contig191	contig191	Laccase-	TCTAGG
GT	Sens	Sense	-0.346	Detected	0.346	Detected	0.000	-1.279	Detected	-1.401	Detected	-1.340	0.062	GT	Sens	contig192	contig192	Coatome	CTCAAC
GT	Sens	Sense	-0.962	Detected	0.962	Detected	0.000	-0.839	Detected	-2.165	Detected	-1.502	0.328	GT	Sens	contig192	contig192	Integrase	TCCTAA
GT	Sens	Sense	-0.232	Detected	0.232	Detected	0.000	-2.537	Detected	-2.301	Detected	-2.419	0.011	GT	Sens	contig192	contig192	CHP-rich	GTTGAA
GT	Sens	Sense	-0.620	Detected	0.620	Detected	0.000	-0.868	Detected	-2.475	Detected	-1.672	0.241	GT	Sens	contig192	contig192	Heat stres	GAAAAA
GT	Sens	Sense	0.330	Detected	-0.330	Detected	0.000	-3.455	Comprom	-2.952	Comprom	-3.203	0.016	GT	Sens	contig193	contig193	Unknown	GAAAAA
GT	Sens	Sense	-0.299	Detected	0.299	Detected	0.000	-1.024	Detected	-1.217	Detected	-1.120	0.070	GT	Sens	contig193	contig193	Unknown	AACTTC
GT	Sens	Sense	-0.135	Detected	0.135	Detected	0.000	-1.534	Detected	-1.773	Detected	-1.654	0.012	GT	Sens	contig193	contig193	CHP-rich	GCGGGA
GT	Sens	Sense	-0.176	Detected	0.176	Detected	0.000	-1.086	Comprom	-2.966	Comprom	-2.026	0.168	GT	Sens	contig193	contig193	Serine/thr	AAGTGC
GT	Sens	Sense	-0.027	Detected	0.027	Detected	0.000	-1.685	Detected	-1.105	Detected	-1.395	0.041	GT	Sens	contig194	contig194	Bifunctio	GGAGAG
GT	Sens	Sense	-0.111	Detected	0.111	Detected	0.000	-0.891	Detected	-1.613	Detected	-1.252	0.080	GT	Sens	contig194	contig194	RING fing	TCATCT
GT	Sens	Sense	0.010	Detected	-0.010	Detected	0.000	-1.868	Detected	-1.447	Detected	-1.658	0.016	GT	Sens	contig194	contig194	(E)-beta-c	TAGAACT
GT	Sens	Sense	-0.409	Detected	0.409	Detected	0.000	-1.096	Detected	-4.007	Detected	-2.551	0.234	GT	Sens	contig194	contig194	Pectinest	CATGGC
GT	Sens	Sense	-0.719	Detected	0.719	Detected	0.000	-2.684	Comprom	-2.315	Comprom	-2.499	0.078	GT	Sens	contig195	contig195	Phytosulf	GTGATG
GT	Sens	Sense	-0.312	Detected	0.312	Detected	0.000	-0.976	Detected	-1.775	Detected	-1.375	0.113	GT	Sens	contig195	contig195	Os01g07	GGAGAG
GT	Sens	Sense	0.313	Detected	-0.313	Detected	0.000	-0.985	Detected	-1.982	Detected	-1.484	0.128	GT	Sens	contig195	contig195	Inositol o	CTGCTT
GT	Sens	Sense	-0.441	Detected	0.441	Detected	0.000	-1.012	Detected	-1.489	Detected	-1.251	0.130	GT	Sens	contig196	contig196	Nudix hy	CTCACA
GT	Sens	Sense	-0.379	Detected	0.379	Detected	0.000	-1.065	Detected	-0.995	Detected	-1.030	0.114	GT	Sens	contig196	contig196	Indole-3-a	GCTCCA
GT	Sens	Sense	-0.763	Detected	0.763	Detected	0.000	-1.111	Detected	-1.911	Detected	-1.511	0.221	GT	Sens	contig196	contig196	Gag-pol	AGCAGA
GT	Sens	Sense	-0.295	Detected	0.295	Detected	0.000	-1.290	Detected	-1.241	Detected	-1.265	0.050	GT	Sens	contig197	contig197	Unknown	TGAGAA
GT	Sens	Sense	-0.498	Detected	0.498	Detected	0.000	-1.344	Detected	-1.509	Detected	-1.426	0.106	GT	Sens	contig197	contig197	Cysteine-	GATTGG
GT	Sens	Sense	-0.607	Detected	0.607	Detected	0.000	-1.514	Comprom	-1.753	Comprom	-1.634	0.118	GT	Sens	contig197	contig197	Os03g08	CAATTG
GT	Sens	Sense	-0.150	Detected	0.150	Detected	0.000	-2.343	Detected	-2.028	Detected	-2.185	0.010	GT	Sens	contig198	contig198	PAR-1c	GCAAAA
GT	Sens	Sense	-0.008	Detected	0.008	Detected	0.000	-1.684	Detected	-1.572	Detected	-1.628	0.001	GT	Sens	contig198	contig198	D5-type c	AAATTG
GT	Sens	Sense	-0.615	Detected	0.615	Detected	0.000	-1.586	Detected	-2.359	Detected	-1.973	0.113	GT	Sens	contig200	contig200	Pectinest	ATAGTT
GT	Sens	Sense	0.000	Detected	0.000	Detected	0.000	-1.206	Comprom	-1.043	Comprom	-1.125	0.005	GT	Sens	contig201	contig201	Actin dep	AGACAA
GT	Sens	Sense	-0.080	Detected	0.080	Detected	0.000	-1.026	Detected	-0.976	Detected	-1.001	0.007	GT	Sens	contig201	contig201	Fasciclin-	CTCCAG
GT	Sens	Sense	-0.274	Detected	0.274	Detected	0.000	-1.078	Detected	-1.086	Detected	-1.082	0.059	GT	Sens	contig201	contig201	Unknown	AATGGT
GT	Sens	Sense	-0.107	Detected	0.107	Detected	0.000	-1.516	Detected	-1.485	Detected	-1.500	0.005	GT	Sens	contig202	contig202	Gibberell	CTCCTC
GT	Sens	Sense	0.044	Detected	-0.044	Detected	0.000	-1.288	Detected	-1.296	Detected	-1.292	0.001	GT	Sens	contig202	contig202	Polyprote	TTGTAA
GT	Sens	Sense	-0.244	Detected	0.244	Detected	0.000	-1.917	Detected	-0.809	Detected	-1.363	0.153	GT	Sens	contig202	contig202	Unknown	TATGGT
GT	Sens	Sense	-0.223	Detected	0.223	Detected	0.000	-1.044	Detected	-1.311	Detected	-1.178	0.045	GT	Sens	contig202	contig202	RING fing	ATTTAC
GT	Sens	Sense	-0.146	Detected	0.146	Detected	0.000	-1.592	Detected	-1.564	Detected	-1.578	0.009	GT	Sens	contig202	contig202	COBRA-li	AAGAAT
GT	Sens	Sense	-0.015	Detected	0.015	Detected	0.000	-1.222	Detected	-0.808	Detected	-1.015	0.039	GT	Sens	contig203	contig203	WRKY tra	TAAAAT
GT	Sens	Sense	-0.174	Detected	0.174	Detected	0.000	-3.358	Comprom	-1.705	Detected	-2.531	0.096	GT	Sens	contig203	contig203	ATP bind	CCTGAC
GT	Sens	Sense	-0.934	Detected	0.934	Detected	0.000	-1.453	Detected	-1.964	Detected	-1.709	0.220	GT	Sens	contig203	contig203	AP2-like	TGGTAA
GT	Sens	Sense	-0.375	Detected	0.375	Detected	0.000	-1.400	Detected	-0.917	Detected	-1.159	0.122	GT	Sens	contig203	contig203	NAD-depe	GATGCT
GT	Sens	Sense	-0.449	Detected	0.449	Detected	0.000	-1.574	Comprom	-2.725	Comprom	-2.150	0.099	GT	Sens	contig204	contig204	Receptor	ATGTTG
GT	Sens	Sense	-0.219	Detected	0.219	Detected	0.000	-1.540	Detected	-1.744	Detected	-1.642	0.021	GT	Sens	contig204	contig204	LuxR fam	TTGTTT
GT	Sens	Sense	-0.418	Detected	0.418	Detected	0.000	-3.200	Comprom	-3.477	Comprom	-3.338	0.017	GT	Sens	contig204	contig204	Subtilisin	GAGGGA
GT	Sens	Sense	0.000	Detected	0.000	Detected	0.000	-1.432	Detected	-1.328	Detected	-1.380	0.001	GT	Sens	contig204	contig204	Os07g01	GATCTT
GT	Sens	Sense	-0.508	Detected	0.508	Detected	0.000	-1.569	Detected	-1.456	Detected	-1.513	0.098	GT	Sens	contig204	contig204	Calmodul	GATAAT
GT	Sens	Sense	0.200	Detected	-0.200	Detected	0.000	-1.262	Detected	-1.208	Detected	-1.235	0.026	GT	Sens	contig205	contig205	ATP-bind	GAAAGG
GT	Sens	Sense	-0.147	Detected	0.147	Detected	0.000	-0.961	Detected	-1.064	Detected	-1.013	0.023	GT	Sens	contig205	contig205	Serine/thr	CATGGG
GT	Sens	Sense	-0.289	Detected	0.289	Detected	0.000	-1.270	Detected	-1.909	Detected	-1.590	0.066	GT	Sens	contig205	contig205	Non-spec	CAAACA
GT	Sens	Sense	-0.522	Detected	0.522	Detected	0.000	-3.353	Comprom	-4.032	Comprom	-3.693	0.027	GT	Sens	contig205	contig205	Unknown	CTCTAT
GT	Sens	Sense	0.577	Detected	-0.577	Detected	0.000	-1.535	Detected	-1.670	Detected	-1.602	0.110	GT	Sens	contig205	contig205	Abscisic	GCACAG
GT	Sens	Sense	-0.182	Detected	0.182	Detected	0.000	-1.254	Detected	-1.257	Detected	-1.256	0.020	GT	Sens	contig205	contig205	Unknown	TCAATC
GT	Sens	Sense	-0.369	Detected	0.369	Detected	0.000	-2.273	Detected	-1.521	Detected	-1.897	0.069	GT	Sens	contig206	contig206	F-box fam	ATATGA
GT	Sens	Sense	-0.829	Detected	0.829	Detected	0.000	-1.233	Detected	-1.408	Detected	-1.321	0.254	GT	Sens	contig207	contig207	Unknown	AGTCAA
GT	Sens	Sense	-0.003	Detected	0.003	Detected	0.000	-1.559	Detected	-1.416	Detected	-1.488	0.002	GT	Sens	contig207	contig207	(R)-limon	TCTCTT
GT	Sens	Sense	0.104	Detected	-0.104	Detected	0.000	-2.410	Detected	-1.894	Detected	-2.152	0.016	GT	Sens	contig209	contig209	Unknown	GAAGTT
GT	Sens	Sense	-0.620	Detected	0.620	Detected	0.000	-2.059	Detected	-4.288	Comprom	-3.174	0.131	GT	Sens	contig210	contig210	Calmodul	CAACTG
GT	Sens	Sense	-0.797	Detected	0.797	Detected	0.000	-3.523	Comprom	-3.529	Comprom	-3.526	0.048	GT	Sens	contig211	contig211	Non-spec	CCACAT
GT	Sens	Sense	-0.488	Detected	0.488	Detected	0.000	-1.198	Detected	-3.146	Comprom	-2.172	0.184	GT	Sens	contig211	contig211	Cell numl	CCAGAG
GT	Sens	Sense	-1.094	Detected	1.094	Detected	0.000	-2.258	Comprom	-0.880	Detected	-1.569	0.349	GT	Sens	contig211	contig211	Pentatric	GTTGAT
GT	Sens	Sense	-0.489	Detected	0.489	Detected	0.000	-1.031	Detected	-1.917	Detected	-1.474	0.155	GT	Sens	contig212	contig212	Dehydrat	CAGAAG
GT	Sens	Sense	-0.450	Detected	0.450	Detected	0.000	-1.702	Detected	-2.123	Detected	-1.913	0.061	GT	Sens	contig212	contig212	U-box do	AACTCA
GT	Sens	Sense	0.088	Detected	-0.088	Detected	0.000	-1.114	Detected	-1.119	Detected	-1.117	0.006	GT	Sens	contig213	contig213	Unknown	TAGTTG
GT	Sens	Sense	-0.247	Detected	0.247	Detected	0.000	-1.156	Detected	-1.385	Detected	-1.271	0.043	GT	Sens	contig213	contig213	Dynamin-	TCTGAT
GT	Sens	Sense	-0.194	Detected	0.194	Detected	0.000	-0.875	Comprom	-1.140	Comprom	-1.008	0.050	GT	Sens	contig214	contig214	Auxin-ind	AGTTTG
GT	Sens	Sense	0.024	Detected	-0.024	Detected	0.000	-1.199	Detected	-1.271	Detected	-1.235	0.001	GT	Sens	contig214	contig214	Proteinas	TGAAGG
GT	Sens	Sense	-0.367	Detected	0.367	Detected	0.000	-1.600	Detected	-2.044	Detected	-1.822	0.051	GT	Sens	contig214	contig214	Protein tc	CAGAAC
GT	Sens	Sense	-0.107	Detected	0.107	Detected	0.000	-1.015	Comprom	-1.803	Comprom	-1.409	0.075	GT	Sens	contig215	contig215	MuDR far	CAATTG
GT	Sens	Sense	-0.009	Detected	0.009	Detected	0.000	-1.738	Detected	-1.209	Detected	-1.474	0.031	GT	Sens	contig216	contig216	Harpin-in	GGGATG
GT	Sens	Sense	-0.043	Detected	0.043	Detected	0.000	-1.046	Detected	-1.109	Detected	-1.077	0.002	GT	Sens	contig216	contig216	Kunitz-ty	CTGCTA
GT	Sens	Sense	-0.158	Detected	0.158	Detected	0.000	-0.842	Detected	-1.564	Detected	-1.203	0.093	GT	Sens	contig216	contig216	Late emb	ACTGGA
GT	Sens	Sense	0.370	Detected	-0.370	Detected	0.000	-1.052	Detected	-1.502	Detected	-1.277	0.098	GT	Sens	contig216	contig216	Amino ac	GTGCTA
GT	Sens	Sense	-0.728	Detected	0.728	Detected	0.000	-1.180	Detected	-1.603	Detected	-1.392	0.208	GT	Sens	contig216	contig216	Leucine-r	CCAAAT
GT	Sens	Sense	-0.577	Detected	0.577	Detected	0.000	-1.018	Detected	-1.395	Detected	-1.206	0.185	GT	Sens	contig216	contig216	Ribosoma	TATGGA
GT	Sens	Sense	-0.325	Detected	0.325	Detected	0.000	-1.791	Detected	-2.090	Detected	-1.940	0.032	GT	Sens	contig217	contig217	Ubiquitin-	GTATAA
GT	Sens	Sense	-0.278	Detected	0.278	Detected	0.000	-1.089	Detected	-1.187	Detected	-1.138	0.056	GT	Sens	contig217	contig217	Aspartic	TTCTCC
GT	Sens	Sense	-0.787	Detected	0.787	Detected	0.000	-3.703	Detected	-4.716	Detected	-4.209	0.046	GT	Sens	contig217	contig217	Cytochro	GATTTG
GT	Sens	Sense	-0.111	Detected	0.111	Detected	0.000	-1.991	Detected	-1.305	Detected	-1.648	0.045	GT	Sens	contig217	contig217	Glutathio	AGCAAA
GT	Sens	Sense	-0.083	Detected	0.083	Detected	0.000	-1.126	Detected	-0.891	Detected	-1.008	0.020	GT	Sens	contig217	contig217	Arabinog	TGTTGT
GT	Sens	Sense	-0.721	Detected	0.721	Detected	0.000	-0.807	Detected	-1.244	Detected	-1.025	0.307	GT	Sens	contig219	contig219	Tir-nbs re	TTTTCA
GT	Sens	Sense	-0.040	Detected	0.040	Detected	0.000	-1.016	Detected	-1.566	Detected	-1.291	0.043	GT	Sens	contig219	contig219	Unknown	TGGTGA
GT	Sens	Sense	-0.351	Detected	0.351	Detected	0.000	-1.540	Detected	-2.428	Detected	-1.984	0.073	GT	Sens	contig219	contig219	AT5G281	AGAAGA
GT	Sens	Sense	-0.283	Detected	0.283	Detected	0.000	-1.498	Detected	-1.683	Detected	-1.591	0.033	GT	Sens	contig219	contig219	Unknown	GCTATG
GT	Sens	Sense	-0.690	Detected	0.690	Detected	0.000	-2.153	Detected	-2.760	Detected	-2.456	0.083	GT	Sens	contig220	contig220	Unknown	ATTAGC
GT	Sens	Sense	-0.483	Detected	0.483	Detected	0.000	-1.297	Comprom	-3.311	Comprom	-2.304	0.175	GT	Sens	contig220	contig220	NBS-LRR	TGAGCA
GT	Sens	Sense	-0.733	Detected	0.733	Detected	0.000	-0.900	Detected	-1.937	Detected	-1.418	0.255	GT	Sens	contig220	contig220	Genomic	CTCTGC
GT	Sens	Sense	-0.250	Detected	0.250	Detected	0.000	-1.176	Detected	-1.080	Detected	-1.128	0.047	GT	Sens	contig221	contig221	Unknown	ATTAGA
GT	Sens	Sense	-0.013	Detected	0.013	Detected	0.000	-0.939	Detected	-2.473	Comprom	-1.706	0.156	GT	Sens	contig221	contig221	Chalcone	GTGTAT
GT	Sens	Sense	-0.305	Detected	0.305	Detected	0.000	-1.632	Detected	-1.115	Detected	-1.374	0.075	GT	Sens	contig221	contig221	Os03g02	ATCAAT
GT	Sens	Sense	-0.552	Detected	0.552	Detected	0.000	-0.899	Detected	-2.178	Detected	-1.539	0.210	GT	Sens	contig221	contig221	Ethylene	ATCAGG
GT	Sens	Sense	-0.290	Detected	0.290	Detected	0.000	-2.756	Comprom	-2.015	Comprom	-2.386	0.037	GT	Sens	contig222	contig222	Calmodul	ATCTTA
GT	Sens	Sense	0.052	Detected	-0.052	Detected	0.000	-1.656	Detected	-2.374	Detected	-2.015	0.031	GT	Sens	contig223	contig223	Lipase fa	CGTTTA
GT	Sens	Sense	-0.329	Detected	0.329	Detected	0.000	-1.276	Comprom	-0.827	Detected	-1.051	0.119	GT	Sens	contig223	contig223	Unknown	GAGTTG
GT	Sens	Sense	-0.174	Detected	0.174	Detected	0.000	-1.118	Detected	-1.587	Detected	-1.353	0.044	GT	Sens	contig224	contig224	Predicted	TACTTG
GT	Sens	Sense	-0.023	Detected	0.023	Detected	0.000	-1.300	Comprom	-1.361	Comprom	-1.330	0.001	GT	Sens	contig224	contig224	Tropinon	TGACCC
GT	Sens	Sense	-0.015	Detected	0.015	Detected	0.000	-1.385	Detected	-1.266	Detected	-1.326	0.002	GT	Sens	contig224	contig224	Cytochro	CCAAGT
GT	Sens	Sense	-0.698	Detected	0.698	Detected	0.000	-1.224	Detected	-1.882	Detected	-1.553	0.182	GT	Sens	contig224	contig224	Ycf2 (AHF	CAAAAA
GT	Sens	Sense	-0.520	Detected	0.520	Detected	0.000	-1.564	Detected	-2.045	Detected	-1.805	0.088	GT	Sens	contig224	contig224	Auxin-res	GGCTAT
GT	Sens	Sense	-0.431	Detected	0.431	Detected	0.000	-1.454	Detected	-1.539	Detected	-1.496	0.074	GT	Sens	contig225	contig225	Methylen	TCGAAA
GT	Sens	Sense	-0.240	Detected	0.240	Detected	0.000	-1.277	Detected	-0.828	Detected	-1.053	0.085	GT	Sens	contig225	contig225	Cell divis	TTCAAG
GT	Sens	Sense	-0.404	Detected	0.404	Detected	0.000	-1.123	Detected	-1.529	Detected	-1.326	0.099	GT	Sens	contig225	contig225	Unknown	TGACAT
GT	Sens	Sense	-0.020	Detected	0.020	Detected	0.000	-1.160	Comprom	-0.997	Comprom	-1.079	0.006	GT	Sens	contig225	contig225	DNA poly	TAAGGA
GT	Sens	Sense	-0.288	Detected	0.288	Detected	0.000	-1.119	Detected	-1.044	Detected	-1.082	0.065	GT	Sens	contig225	contig225	BZIP tran	GCTGCT
GT	Sens	Sense	-0.487	Detected	0.487	Detected	0.000	-1.544	Detected	-2.152	Detected	-1.848	0.084	GT	Sens	contig226	contig226	Strictosid	AAATTT
GT	Sens	Sense	-0.533	Detected	0.533	Detected	0.000	-2.862	Comprom	-2.395	Comprom	-2.629	0.046	GT	Sens	contig226	contig226	Unknown	TCTTGA
GT	Sens	Sense	0.121	Detected	-0.121	Detected	0.000	-1.635	Detected	-3.300	Detected	-2.467	0.099	GT	Sens	contig226	contig226	Nitric oxi	TTAGGA
GT	Sens	Sense	-0.167	Detected	0.167	Detected	0.000	-1.187	Detected	-1.111	Detected	-1.149	0.021	GT	Sens	contig226	contig226	Glycine-ri	GATATT
GT	Sens	Sense	0.602	Detected	-0.602	Detected	0.000	-1.843	Detected	-1.645	Detected	-1.744	0.104	GT	Sens	contig227	contig227	Transcrip	AGTAGG
GT	Sens	Sense	0.008	Detected	-0.008	Detected	0.000	-1.078	Detected	-1.839	Detected	-1.458	0.062	GT	Sens	contig227	contig227	Unknown	TCACGT
GT	Sens	Sense	0.392	Detected	-0.392	Detected	0.000	-3.225	Comprom	-2.340	Comprom	-2.783	0.042	GT	Sens	contig227	contig227	Polyubiq	AGATTG
GT	Sens	Sense	-0.482	Detected	0.482	Detected	0.000	-1.256	Detected	-2.758	Detected	-2.007	0.154	GT	Sens	contig228	contig228	GATA tra	AAATGA
GT	Sens	Sense	-0.046	Detected	0.046	Detected	0.000	-1.812	Detected	-1.407	Detected	-1.610	0.016	GT	Sens	contig228	contig228	Peroxida	GAAGTA
GT	Sens	Sense	0.167	Detected	-0.167	Detected	0.000	-1.416	Detected	-2.001	Detected	-1.709	0.037	GT	Sens	contig228	contig228	MYB tran	TTTGAT
GT	Sens	Sense	-0.369	Detected	0.369	Detected	0.000	-2.024	Comprom	-1.804	Comprom	-1.914	0.038	GT	Sens	contig228	contig228	Actin (AH	GAAGAA
GT	Sens	Sense	-0.700	Detected	0.700	Detected	0.000	-2.114	Detected	-2.344	Detected	-2.229	0.088	GT	Sens	contig228	contig228	Transcrip	AGTTGA
GT	Sens	Sense	0.867	Detected	-0.867	Detected	0.000	-1.000	Detected	-2.445	Comprom	-1.722	0.267	GT	Sens	contig228	contig228	GTP bind	GACAAA
GT	Sens	Sense	-0.556	Detected	0.556	Detected	0.000	-1.540	Detected	-2.102	Detected	-1.821	0.100	GT	Sens	contig229	contig229	Genomic	CTGAAC
GT	Sens	Sense	-0.054	Detected	0.054	Detected	0.000	-1.479	Detected	-1.130	Detected	-1.304	0.019	GT	Sens	contig229	contig229	Pectinest	CTCAGA
GT	Sens	Sense	0.116	Detected	-0.116	Detected	0.000	-1.898	Detected	-2.575	Detected	-2.236	0.025	GT	Sens	contig230	contig230	Fatty acid	GTAGAT
GT	Sens	Sense	-0.242	Detected	0.242	Detected	0.000	-2.610	Detected	-3.346	Detected	-2.978	0.021	GT	Sens	contig230	contig230	ABC tran	CCTAAT
GT	Sens	Sense	0.093	Detected	-0.093	Detected	0.000	-1.898	Detected	-2.573	Detected	-2.236	0.024	GT	Sens	contig230	contig230	N-acetylt	GAATGG
GT	Sens	Sense	-0.897	Detected	0.897	Detected	0.000	-1.177	Detected	-1.673	Detected	-1.425	0.265	GT	Sens	contig230	contig230	Expansin	TACAAT
GT	Sens	Sense	-0.188	Detected	0.188	Detected	0.000	-1.188	Detected	-1.252	Detected	-1.220	0.024	GT	Sens	contig230	contig230	Receptor	GTGACA
GT	Sens	Sense	0.607	Detected	-0.607	Detected	0.000	-1.716	Detected	-2.926	Detected	-2.321	0.114	GT	Sens	contig231	contig231	Tryptoph	GTCATG
GT	Sens	Sense	-0.196	Detected	0.196	Detected	0.000	-1.465	Detected	-2.404	Detected	-1.935	0.063	GT	Sens	contig232	contig232	Mutant re	AAGAGT
GT	Sens	Sense	-0.298	Detected	0.298	Detected	0.000	-1.363	Detected	-1.424	Detected	-1.393	0.043	GT	Sens	contig233	contig233	Diacylgly	AGGATA
GT	Sens	Sense	0.003	Detected	-0.003	Detected	0.000	-1.069	Detected	-0.975	Detected	-1.022	0.002	GT	Sens	contig234	contig234	Receptor	AATGTG
GT	Sens	Sense	-0.270	Detected	0.270	Detected	0.000	-0.887	Comprom	-1.346	Comprom	-1.116	0.088	GT	Sens	contig234	contig234	Unknown	ATTCAG
GT	Sens	Sense	-0.361	Detected	0.361	Detected	0.000	-1.227	Detected	-1.211	Detected	-1.219	0.078	GT	Sens	contig234	contig234	Cytochro	TCCTTT
GT	Sens	Sense	-0.147	Detected	0.147	Detected	0.000	-1.094	Detected	-0.937	Detected	-1.016	0.026	GT	Sens	contig236	contig236	Potassiu	GTTTGC
GT	Sens	Sense	-0.278	Detected	0.278	Detected	0.000	-1.550	Detected	-1.669	Detected	-1.610	0.030	GT	Sens	contig236	contig236	Myb-relat	ATGGAA
GT	Sens	Sense	0.007	Detected	-0.007	Detected	0.000	-1.037	Detected	-1.420	Detected	-1.228	0.024	GT	Sens	contig236	contig236	Unknown	ATATGG
GT	Sens	Sense	-0.242	Detected	0.242	Detected	0.000	-1.109	Detected	-1.232	Detected	-1.170	0.043	GT	Sens	contig236	contig236	NBS-codi	GGCTAA
GT	Sens	Sense	-0.402	Detected	0.402	Detected	0.000	-1.119	Detected	-1.020	Detected	-1.069	0.119	GT	Sens	contig238	contig238	Low affin	TTACTT
GT	Sens	Sense	-1.089	Detected	1.089	Detected	0.000	-3.239	Comprom	-3.875	Comprom	-3.557	0.088	GT	Sens	contig238	contig238	Expansin	ATGCAA
GT	Sens	Sense	-0.119	Detected	0.119	Detected	0.000	-1.191	Detected	-1.588	Detected	-1.389	0.027	GT	Sens	contig239	contig239	Auxin res	CGTTCG
GT	Sens	Sense	0.467	Detected	-0.467	Detected	0.000	-2.038	Detected	-2.146	Detected	-2.092	0.047	GT	Sens	contig239	contig239	Ethylene-	ATGGCA
GT	Sens	Sense	-0.689	Detected	0.689	Detected	0.000	-1.355	Detected	-1.768	Detected	-1.562	0.162	GT	Sens	contig240	contig240	SKIP inte	CTCGAA
GT	Sens	Sense	-0.308	Detected	0.308	Detected	0.000	-1.124	Detected	-1.763	Detected	-1.444	0.083	GT	Sens	contig240	contig240	Pathogen	GTAGAT
GT	Sens	Sense	-0.227	Detected	0.227	Detected	0.000	-0.947	Detected	-1.075	Detected	-1.011	0.050	GT	Sens	contig241	contig241	Fatty acid	TTCAAA
GT	Sens	Sense	-0.537	Detected	0.537	Detected	0.000	-1.873	Detected	-2.343	Detected	-2.108	0.069	GT	Sens	contig241	contig241	CXE carb	AACAAT
GT	Sens	Sense	0.046	Detected	-0.046	Detected	0.000	-1.455	Detected	-1.018	Detected	-1.237	0.031	GT	Sens	contig241	contig241	Stearoyl-	GTGCAC
GT	Sens	Sense	0.181	Detected	-0.181	Detected	0.000	-0.819	Detected	-1.341	Comprom	-1.080	0.077	GT	Sens	contig241	contig241	Unknown	TGCAGA
GT	Sens	Sense	-0.288	Detected	0.288	Detected	0.000	-1.491	Detected	-1.137	Detected	-1.314	0.060	GT	Sens	contig241	contig241	Laccase	GGCAAT
GT	Sens	Sense	0.261	Detected	-0.261	Detected	0.000	-1.291	Detected	-1.341	Detected	-1.316	0.037	GT	Sens	contig241	contig241	cDNA clo	TCTGAT
GT	Sens	Sense	-0.339	Detected	0.339	Detected	0.000	-1.117	Detected	-1.233	Detected	-1.175	0.076	GT	Sens	contig242	contig242	Unknown	GGCAGC
GT	Sens	Sense	-0.544	Detected	0.544	Detected	0.000	-2.174	Detected	-2.051	Detected	-2.112	0.061	GT	Sens	contig242	contig242	Unknown	AGTAGT
GT	Sens	Sense	-0.135	Detected	0.135	Detected	0.000	-0.989	Detected	-1.487	Detected	-1.238	0.049	GT	Sens	contig242	contig242	5-AMP-ac	TATTGA
GT	Sens	Sense	0.103	Detected	-0.103	Detected	0.000	-3.243	Comprom	-2.124	Detected	-2.683	0.042	GT	Sens	contig242	contig242	Fatty acid	GGTGTC
GT	Sens	Sense	0.155	Detected	-0.155	Detected	0.000	-1.673	Comprom	-1.339	Comprom	-1.506	0.022	GT	Sens	contig243	contig243	IFA-bindi	CTGAAG
GT	Sens	Sense	-0.502	Detected	0.502	Detected	0.000	-1.430	Detected	-2.581	Detected	-2.006	0.120	GT	Sens	contig243	contig243	Copper tr	TGTTTT
GT	Sens	Sense	-0.127	Detected	0.127	Detected	0.000	-1.436	Detected	-0.804	Detected	-1.120	0.081	GT	Sens	contig243	contig243	Beta-ocin	GGAACT
GT	Sens	Sense	-0.823	Detected	0.823	Detected	0.000	-0.812	Detected	-1.777	Detected	-1.295	0.308	GT	Sens	contig244	contig244	Gag/pol	AGGATT
GT	Sens	Sense	-0.080	Detected	0.080	Detected	0.000	-1.608	Comprom	-2.319	Comprom	-1.964	0.033	GT	Sens	contig244	contig244	Reverse	AATAAT
GT	Sens	Sense	-0.406	Detected	0.406	Detected	0.000	-1.914	Detected	-2.873	Detected	-2.393	0.063	GT	Sens	contig244	contig244	CM0216.2	GTATCA
GT	Sens	Sense	-0.586	Detected	0.586	Detected	0.000	-1.472	Comprom	-0.949	Detected	-1.210	0.200	GT	Sens	contig245	contig245	Unknown	TGTGGA
GT	Sens	Sense	0.005	Detected	-0.005	Detected	0.000	-0.958	Detected	-1.395	Detected	-1.177	0.033	GT	Sens	contig245	contig245	Transmem	CCATAT
GT	Sens	Sense	-0.075	Detected	0.075	Detected	0.000	-1.458	Detected	-1.238	Detected	-1.348	0.010	GT	Sens	contig245	contig245	Zinc finge	CAGAAA
GT	Sens	Sense	-0.018	Detected	0.018	Detected	0.000	-1.867	Comprom	-1.892	Comprom	-1.880	0.000	GT	Sens	contig245	contig245	Unknown	AGGATT
GT	Sens	Sense	-0.203	Detected	0.203	Detected	0.000	-1.065	Detected	-1.189	Detected	-1.127	0.034	GT	Sens	contig246	contig246	C4-dicarb	AGCAAC
GT	Sens	Sense	0.282	Detected	-0.282	Detected	0.000	-0.872	Detected	-2.628	Comprom	-1.750	0.198	GT	Sens	contig246	contig246	Unknown	AGCAGC
GT	Sens	Sense	-0.109	Detected	0.109	Detected	0.000	-1.240	Detected	-1.157	Detected	-1.199	0.009	GT	Sens	contig247	contig247	Hypotheti	GGATAT
GT	Sens	Sense	-0.822	Detected	0.822	Detected	0.000	-1.410	Detected	-2.813	Detected	-2.111	0.190	GT	Sens	contig247	contig247	Phosphat	GAGCAG
GT	Sens	Sense	-0.654	Detected	0.654	Detected	0.000	-1.039	Detected	-1.088	Detected	-1.063	0.246	GT	Sens	contig247	contig247	Xylogluca	GGGATC
GT	Sens	Sense	0.031	Detected	-0.031	Detected	0.000	-1.265	Detected	-0.923	Detected	-1.094	0.024	GT	Sens	contig247	contig247	Glutathio	TTCTTG
GT	Sens	Sense	-0.271	Detected	0.271	Detected	0.000	-1.326	Detected	-1.650	Detected	-1.488	0.042	GT	Sens	contig248	contig248	Unknown	CTAAAA
GT	Sens	Sense	-0.353	Detected	0.353	Detected	0.000	-0.894	Detected	-1.563	Detected	-1.228	0.128	GT	Sens	contig248	contig248	Delta-6 de	GTGTGT
GT	Sens	Sense	-0.027	Detected	0.027	Detected	0.000	-1.587	Detected	-2.148	Detected	-1.867	0.022	GT	Sens	contig249	contig249	Inosine-u	AAGACT
GT	Sens	Sense	0.036	Detected	-0.036	Detected	0.000	-2.534	Detected	-1.680	Detected	-2.107	0.039	GT	Sens	contig249	contig249	Gibberell	GTTATT
GT	Sens	Sense	0.411	Detected	-0.411	Detected	0.000	-1.583	Detected	-1.064	Detected	-1.323	0.113	GT	Sens	contig249	contig249	RNase H	AACATT
GT	Sens	Sense	-0.179	Detected	0.179	Detected	0.000	-1.231	Detected	-1.256	Detected	-1.243	0.020	GT	Sens	contig249	contig249	C4-dicarb	CTCAGT
GT	Sens	Sense	0.125	Detected	-0.125	Detected	0.000	-2.015	Comprom	-1.551	Comprom	-1.783	0.021	GT	Sens	contig249	contig249	Ripening-	TCACCT
GT	Sens	Sense	0.202	Detected	-0.202	Detected	0.000	-1.029	Detected	-1.098	Detected	-1.064	0.035	GT	Sens	contig251	contig251	Unknown	GCTGCT
GT	Sens	Sense	-0.036	Detected	0.036	Detected	0.000	-1.126	Comprom	-1.167	Comprom	-1.147	0.001	GT	Sens	contig252	contig252	Disease r	TGCAGG
GT	Sens	Sense	0.064	Detected	-0.064	Detected	0.000	-2.376	Detected	-1.301	Detected	-1.839	0.077	GT	Sens	contig252	contig252	Alpha-hu	GTGTGG
GT	Sens	Sense	0.633	Detected	-0.633	Detected	0.000	-1.796	Comprom	-2.548	Comprom	-2.172	0.098	GT	Sens	contig252	contig252	Coiled-co	CTTTTC
GT	Sens	Sense	-0.828	Detected	0.828	Detected	0.000	-1.408	Detected	-1.706	Detected	-1.557	0.206	GT	Sens	contig253	contig253	Ring H2 fi	CAGAAG
GT	Sens	Sense	1.166	Detected	-1.166	Detected	0.000	-2.993	Comprom	-2.756	Comprom	-2.874	0.134	GT	Sens	contig253	contig253	Unknown	GTATGG
GT	Sens	Sense	-0.366	Detected	0.366	Detected	0.000	-2.695	Comprom	-2.345	Comprom	-2.520	0.025	GT	Sens	contig253	contig253	IFA bindi	TTTGGT
GT	Sens	Sense	0.567	Detected	-0.567	Detected	0.000	-1.092	Detected	-1.385	Detected	-1.238	0.169	GT	Sens	contig254	contig254	Transpos	TATCAA
GT	Sens	Sense	-0.269	Detected	0.269	Detected	0.000	-1.228	Detected	-1.086	Detected	-1.157	0.053	GT	Sens	contig254	contig254	GDP-man	AAACCA
GT	Sens	Sense	-0.320	Detected	0.320	Detected	0.000	-1.416	Comprom	-2.919	Comprom	-2.168	0.118	GT	Sens	contig254	contig254	Glycosylt	TTTAGT
GT	Sens	Sense	-0.327	Detected	0.327	Detected	0.000	-2.340	Comprom	-2.430	Comprom	-2.385	0.019	GT	Sens	contig254	contig254	Beta-gala	GTGAGC
GT	Sens	Sense	-1.284	Detected	1.284	Detected	0.000	-3.485	Comprom	-3.639	Comprom	-3.562	0.109	GT	Sens	contig254	contig254	Amino ac	ATGAGT
GT	Sens	Sense	-0.084	Detected	0.084	Detected	0.000	-2.788	Comprom	-1.841	Detected	-2.314	0.041	GT	Sens	contig254	contig254	Glucosylt	ATTTATT
GT	Sens	Sense	-0.777	Detected	0.777	Detected	0.000	-1.595	Detected	-1.347	Detected	-1.471	0.202	GT	Sens	contig255	contig255	Zinc finge	GGTTGG

GT	Sense	Sense	-0.160	Detected	0.160	Detected	0.000	-0.943	Detected	-1.183	Detected	-1.063	0.034	GT	Sens	contig255	contig255	Proteinas	ATTTTGT	contig255	Solyc07g	Solyc07g	Proteinas	GO:00048	GO:00048	contig255	Solyc07g	Proteinas	GO:00048	SL2.40ch	AT1G15760.1		FUNCTIO	chr1:542	90473.4	102912	84451.4	71638.6	47925	42748.5
GT	Sense	Sense	-0.014	Detected	0.014	Detected	0.000	-3.126	Detected	-2.829	Detected	-2.978	0.003	GT	Sens	contig255	contig255	Pathogen	AGATGT	contig255	Solyc01g	Solyc01g	Pathogen	GO:00055	GO:00055	contig255	Solyc01g	Pathogen	GO:00055	SL2.40ch	AT3G61410.1		FUNCTIO	chr3:227	1520.86	1412.8	1125.81	1037.71	160.274	207.506
GT	Sense	Sense	0.753	Detected	-0.753	Detected	0.000	-1.060	Detected	-1.175	Detected	-1.118	0.277	GT	Sens	contig255	contig255	Unknown	AGCCAG	contig255	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig255	Solyc03g	Retinobla	GO:00056	SL2.40ch	AT5G15170.1		tyrosyl-D	chr5:492	84.0748	26.9888	28.7617	29.6537	21.8105	21.2204
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	-1.147	Detected	-0.967	Detected	-1.057	0.023	GT	Sens	contig256	contig256	Calcium-t	TTATCAT	contig256	Solyc09g	Solyc09g	Calcium-t	GO:00053	GO:00053	contig256	Solyc09g	Calcium-t	GO:00053	SL2.40ch	AT1G69430.1		unknown	chr1:260	256.391	281.495	187.328	340.332	115.807	138.239
GT	Sense	Sense	-0.155	Detected	0.155	Detected	0.000	-3.540	Comprom	-1.747	Detected	-2.643	0.101	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	42.8429	48.3942	6.68586	59.8836	3.73814	13.6478
GT	Sense	Sense	-0.292	Detected	0.292	Detected	0.000	-1.357	Detected	-0.966	Detected	-1.161	0.081	GT	Sens	contig256	contig256	60S ribos	TCTGTA	contig256	Solyc04g	Solyc04g	60S ribos	GO:00055	GO:00055	contig256	Solyc06g	Ribosoma	GO:00055	SL2.40ch	AT2G37190.1		60S ribos	chr2:156	55.8394	76.2874	44.6897	67.5774	24.332	33.6088
GT	Sense	Sense	-0.082	Detected	0.082	Detected	0.000	-1.208	Detected	-1.597	Detected	-1.402	0.022	GT	Sens	contig257	contig257	Ring H2 fi	CAATAT	contig257	Solyc01g	Solyc01g	Ring H2 fi	GO:00082	GO:00082	contig257	Solyc01g	Ring H2 fi	GO:00082	SL2.40ch	AT2G25409.1		unknown	chr2:108	67.8299	69.3231	49.0062	41.6718	28.3391	22.8058
GT	Sense	Sense	-0.086	Detected	0.086	Detected	0.000	-1.171	Comprom	-1.560	Comprom	-1.365	0.023	GT	Sens	contig257	contig257	Unknown	GTGTTC	contig257	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig257	Solyc11g	Ulp1 protease family		SL2.40ch	AT5G13860.1				14.4074	14.8005	13.9974	7.21749	6.19281	4.98361
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-1.098	Detected	-1.057	Detected	-1.077	0.002	GT	Sens	contig259	contig259	HAT famil	ATGTTGT	contig259	Solyc07g	Solyc07g	HAT family dimerisation domai			contig259	Solyc04g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	390.021	380.226	283.075	372.851	171.816	186.172
GT	Sense	Sense	-0.516	Detected	0.516	Detected	0.000	-1.374	Detected	-1.174	Detected	-1.274	0.136	GT	Sens	contig259	contig259	Omega-3	CAGGGG	contig259	Solyc06g	Solyc06g	Omega-3	GO:00423	GO:00423	contig259	Solyc06g	Omega-3	GO:00423	SL2.40ch	AT3G111	FAD7. FA	FAD7 (FA	chr3:349	85.8732	160.098	96.7696	166.843	43.1969	52.2659
GT	Sense	Sense	0.948	Detected	-0.948	Detected	0.000	-2.438	Comprom	-2.846	Comprom	-2.642	0.112	GT	Sens	contig259	contig259	ATP-bind	GAACTAT	contig259	Solyc06g	Solyc06g	ATP-bind	GO:00171	GO:00171	contig259	Solyc06g	ATP-bind	GO:00426	SL2.40ch	AT5G617	ATATH11	ATATH11	chr5:248	59.6634	14.6237	3.77935	15.2322	5.20556	4.1334
GT	Sense	Sense	-0.088	Detected	0.088	Detected	0.000	-1.116	Detected	-1.393	Detected	-1.255	0.017	GT	Sens	contig259	contig259	Pentatric	CAAGAA	contig259	Solyc03g	Solyc03g	Pentatric	GO:00037	GO:00037	contig259	Solyc03g	Pentatric	GO:00037	SL2.40ch	AT3G15200.1		pentatric	chr3:511	150.409	155.003	103.988	121.023	67.2699	58.4704
GT	Sense	Sense	-0.005	Detected	0.005	Detected	0.000	-2.170	Detected	-2.836	Detected	-2.503	0.017	GT	Sens	contig260	contig260	Kelch-like	TTCTGAT	contig260	Solyc03g	Solyc03g	Kelch-like protein (AHRD V1 *-*			contig260	Solyc03g	Kelch-like protein (A		SL2.40ch	AT2G44130.1		kelch rep	chr2:182	303.224	278.177	212.883	355.509	61.6094	40.9308
GT	Sense	Sense	-0.395	Detected	0.395	Detected	0.000	-2.299	Detected	-2.697	Detected	-2.498	0.030	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	2079.88	3278.3	1093.23	1941.19	506.784	405.016
GT	Sense	Sense	0.128	Detected	-0.128	Detected	0.000	-2.078	Comprom	-1.139	Detected	-1.609	0.081	GT	Sens	contig260	contig260	Mutator-li	GTGCAC	contig260	Solyc10g	Solyc10g	Mutator-like transposase (AHF			contig260	Solyc08g	Mutator-li	GO:00082	SL2.40ch	AT3G51120.1		DNA bind	chr3:189	37.2808	28.4666	24.4131	19.4177	7.36613	14.8794
GT	Sense	Sense	0.045	Detected	-0.045	Detected	0.000	-1.274	Detected	-1.467	Detected	-1.371	0.006	GT	Sens	contig260	contig260	UDP-gluc	TTTGCA	contig260	Solyc10g	Solyc10g	UDP-gluc	GO:00081	GO:00081	contig260	Solyc10g	UDP-gluc	GO:00081	SL2.40ch	AT3G531	UGT73C7	UGT73C7	chr3:197	99.2208	85.0257	63.1498	71.3318	36.26	33.4127
GT	Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-1.548	Detected	-1.126	Detected	-1.337	0.024	GT	Sens	contig260	contig260	F-box pro	AACAGT	contig260	Solyc01g	Solyc01g	F-box pro	GO:00302	GO:00302	contig260	Solyc01g	F-box pro	GO:00302	SL2.40ch	AT5G59000.1		zinc fing	chr5:238	1848.22	1716.09	954.094	935.489	581.559	821.059
GT	Sense	Sense	-0.473	Detected	0.473	Detected	0.000	-1.668	Comprom	-2.539	Comprom	-2.104	0.082	GT	Sens	contig261	contig261	WUSCHEL	GTTTAT	contig261	Solyc02g	Solyc02g	WUSCHEL	GO:00063	GO:00063	contig261	Solyc02g	WUSCHEL	GO:00063	SL2.40ch	AT2G353	PLL1	PLL1 (PO	chr2:148	12.7287	22.3502	3.66956	5.38297	5.06737	2.9193
GT	Sense	Sense	-0.466	Detected	0.466	Detected	0.000	-3.214	Comprom	-3.231	Comprom	-3.222	0.020	GT	Sens	contig261	contig261	Unknown	GTTATT	contig261	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig261	Solyc07g	Unknown Protein (A		SL2.40ch	AT3G287	ATHMG.	ATHMG (	chr3:107	25.4975	44.3384	3.21446	15.4401	3.46072	3.60365
GT	Sense	Sense	-0.289	Detected	0.289	Detected	0.000	-1.101	Detected	-0.911	Detected	-1.006	0.080	GT	Sens	contig261	contig261	Acyl-CoA	CCTCAG	contig261	Solyc12g	Solyc12g	Acyl-CoA thioesterase 9 (AHRD			contig261	Solyc12g	Acyl-CoA thioestera		SL2.40ch	AT3G57470.2		peptidas	chr3:212	56.1801	76.4062	31.3054	94.721	29.1601	35.0473
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-0.921	Detected	-1.368	Detected	-1.145	0.048	GT	Sens	contig262	contig262	Serine/thr	CAGATG	contig262	Solyc07g	Solyc07g	Serine/threonine-protein phos			contig262	Solyc07g	Serine/threonine-pr		SL2.40ch	AT5G14410.1				186.241	141.283	76.7092	166.625	81.7761	63.2025
GT	Sense	Sense	-0.439	Detected	0.439	Detected	0.000	-1.744	Detected	-2.523	Detected	-2.133	0.068	GT	Sens	contig262	contig262	Unknown	TGCACA	contig262	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig262	Solyc03g	Unknown Protein (A		SL2.40ch	AT2G35610.1		FUNCTIO	chr2:149	423.034	708.894	292.781	463.019	156.108	95.8616
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-3.237	Detected	-3.044	Detected	-3.140	0.003	GT	Sens	contig263	contig263	Cinnamyl	AGACATT	contig263	Solyc05g	Solyc05g	Cinnamyl alcohol dehydrogen			contig263	Solyc11g	Alcohol d	GO:00081	SL2.40ch	AT1G02330.1		FUNCTIO	chr1:462	144.376	109.444	49.8432	62.9249	12.7332	15.3314
GT	Sense	Sense	-1.164	Detected	1.164	Detected	0.000	-1.053	Detected	-1.311	Detected	-1.182	0.419	GT	Sens	contig263	contig263	Pectate ly	AATTGC	contig263	Solyc09g	Solyc09g	Pectate ly	GO:00168	GO:00168	contig263	Solyc09g	Pectate ly	GO:00168	SL2.40ch	AT4G13710.1		pectate ly	chr4:796	62.9702	288.115	63.7007	101.538	61.9982	54.6127
GT	Sense	Sense	-0.827	Detected	0.827	Detected	0.000	-1.672	Detected	-3.366	Detected	-2.519	0.167	GT	Sens	contig263	contig263	Unknown	GCTACA	contig263	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)%:			contig263	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G207	NPH4. MS	NPH4 (NO	chr5:701	202.82	581.637	74.7703	224.887	102.888	33.5221
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	-2.711	Detected	-2.823	Detected	-2.767	0.000	GT	Sens	contig264	contig264	Hypotheti	AAGTTGT	contig264	Solyc10g	Solyc10g	Hypothetical chloroplast RF1 (			contig264	Solyc10g	Hypothetical chloro		SL2.40ch	AT4G04790.1		FUNCTIO	chr4:243	91.1216	80.3165	41.2985	75.2051	12.478	12.1589
GT	Sense	Sense	-0.765	Detected	0.765	Detected	0.000	-1.368	Detected	-1.649	Detected	-1.509	0.192	GT	Sens	contig264	contig264	Phototro	TTCTCTT	contig264	Solyc07g	Solyc07g	Phototro	GO:00055	GO:00055	contig264	Solyc07g	Phototro	GO:00055	SL2.40ch	AT3G14900.1		unknown	chr3:501	55.7672	146.922	40.3437	77.334	33.4734	29.0379
GT	Sense	Sense	-0.582	Detected	0.582	Detected	0.000	-1.436	Detected	-2.795	Detected	-2.116	0.142	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	165.342	337.784	151.8	314.041	83.3841	34.2482
GT	Sense	Sense	-0.242	Detected	0.242	Detected	0.000	-3.254	Comprom	-2.729	Comprom	-2.991	0.014	GT	Sens	contig264	contig264	Patatin-lik	TGCATC	contig264	Solyc04g	Solyc04g	Patatin-lik	GO:00162	GO:00162	contig264	Solyc04g	Patatin-lik	GO:00457	SL2.40ch	AT2G265	PLP2. PL	PLA2A (F	chr2:112	21.9523	27.9785	23.0925	16.3593	2.48066	3.75992
GT	Sense	Sense	-1.220	Detected	1.220	Detected	0.000	-0.841	Detected	-1.891	Detected	-1.366	0.412	GT	Sens	contig265	contig265	Chloropla	TTGACG	contig265	Solyc05g	Solyc05g	Chloropla	GO:00065	GO:00065	contig265	Solyc05g	Chloropla	GO:00036	SL2.40ch	AT3G25700.2		chloropla	chr3:935	209.777	1037.78	370.139	513.097	248.716	126.545
GT	Sense	Sense	-0.027	Detected	0.027	Detected	0.000	-1.830	Comprom	-1.044	Detected	-1.437	0.068	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	27.2908	25.8316	17.7067	24.2073	7.12826	12.958
GT	Sense	Sense	-0.470	Detected	0.470	Detected	0.000	-1.643	Detected	-1.014	Detected	-1.328	0.143	GT	Sens	contig265	contig265	Auxin res	AGTGAG	contig265	Solyc09g	Solyc09g	Auxin res	GO:00056	GO:00056	contig265	Solyc09g	Auxin res	GO:00170	SL2.40ch	AT5G437	ATAUX2-	ATAUX2-	chr5:175	28.1343	49.2047	16.3036	83.5554	11.3769	18.5367
GT	Sense	Sense	-0.049	Detected	0.049	Detected	0.000	-1.669	Detected	-1.108	Detected	-1.388	0.040	GT	Sens	contig266	contig266	Undecap	GCAATT	contig266	Solyc06g	Solyc06g	Undecap	GO:00455	GO:00455	contig266	Solyc06g	Undecap	GO:00455	SL2.40ch	AT5G58770.1		dehydro	chr5:237	135.62	132.263	47.4473	255.21	40.2197	62.5059
GT	Sense	Sense	-0.815	Detected	0.815	Detected	0.000	-3.270	Comprom	-3.799	Comprom	-3.535	0.054	GT	Sens	contig266	contig266	Unknown	CAAACG	contig266	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig266	Solyc07g	Unknown Protein (A		SL2.40ch	AT3G57720.1				16.4433	46.4112	2.10268	1.94333	2.73381	1.99627
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-1.702	Detected	-1.806	Detected	-1.754	0.005	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	1082.96	1163.66	521.6	742.731	329.464	322.894
GT	Sense	Sense	-0.056	Detected	0.056	Detected	0.000	-1.936	Detected	-1.711	Detected	-1.824	0.005	GT	Sens	contig267	contig267	Receptor-	AGTATG	contig267	Solyc10g	Solyc10g	Receptor-	GO:00311	GO:00311	contig267	Solyc10g	Receptor-	GO:00064	SL2.40ch	AT1G56240.1				1088.2	1072.87	700.702	916.626	269.677	331.935
GT	Sense	Sense	-0.306	Detected	0.306	Detected	0.000	-1.044	Detected	-1.209	Detected	-1.126	0.071	GT	Sens	contig267	contig267	Solute ca	ACAAAA	contig267	Solyc11g	Solyc11g	Solute carrier family 35 memb			contig267	Solyc11g	Solute carrier family		SL2.40ch	AT2G28315.1		LOCATE	chr2:120	63.1723	88.0756	26.6959	76.9927	34.5356	32.4663
GT	Sense	Sense	-0.485	Detected	0.485	Detected	0.000	-1.040	Detected	-1.155	Detected	-1.098	0.154	GT	Sens	contig268	contig268	Ethylene-	GAGTTA	contig268	Solyc12g	Solyc12g	Ethylene-	GO:00063	GO:00063	contig268	Solyc12g	Ethylene-	GO:00036	SL2.40ch	AT5G258	tny	tny (TINY	chr5:898	252.518	451.068	224.471	476.956	156.735	152.425
GT	Sense	Sense	0.226	Detected	-0.226	Detected	0.000	-2.555	Comprom	-1.033	Comprom	-1.794	0.152	GT	Sens	contig268	contig268	Anthranil	ATCCCG	contig268	Solyc03g	Solyc03g	Anthranilate phosphoribosyltr			contig268	Solyc06g	Fumarate	GO:00038	SL2.40ch	AT5G50950.3		fumarate	chr5:207	16.2292	10.8178	3.32934	9.08411	2.15236	6.51212
GT	Sense	Sense	-0.346	Detected	0.346	Detected	0.000	-0.976	Detected	-2.091	Detected	-1.533	0.144	GT	Sens	contig268	contig268	Major alle	TACCTA	contig268	Solyc09g	Solyc09g	Major alle	GO:00096	GO:00096	contig268	Solyc09g	Major alle	GO:00096	SL2.40ch	AT1G069	ATOFP4.	OFP4 (AF	chr1:212	107.712	158.596	113.709	562.589	63.4521	30.8685
GT	Sense	Sense	-0.693	Detected	0.693	Detected	0.000	-1.126	Detected	-1.056	Detected	-1.091	0.256	GT	Sens	contig268	contig268	TIR-NBS-	ATCCAA	contig268	Solyc07g	Solyc07g	TIR-NBS-	GO:00069	GO:00069	contig268	Solyc07g	Nbs-lrr, re	GO:00302	SL2.40ch	AT4G208	TPP2	TPP2 (TF	chr4:111	224.173	533.839	285.35	670.204	151.357	167.335
GT	Sense	Sense	-0.415	Detected	0.415	Detected	0.000	-2.769	Comprom	-3.421	Comprom	-3.095	0.028	GT	Sens	contig268	contig268	Unknown	TGACAA	contig268	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig268	Solyc00g	Unknown Protein (A		SL2.40ch	AT5G07650.1		formin ho	chr5:241	17.2784	27.9934	2.13628	2.38167	3.08112	2.06612
GT	Sense	Sense	0.101	Detected	-0.101	Detected	0.000	-1.291	Detected	-1.445	Detected	-1.368	0.009	GT	Sens	contig268	contig268	UDP-gluc	GGGACT	contig268	Solyc01g	Solyc01g	UDP-gluc	GO:00081	GO:00081	contig268	Solyc01g	UDP-gluc	GO:00081	SL2.40ch	AT1G241	UGT74B1	UGT74B1	chr1:852	218.251	172.894	113.42	204.514	75.7803	71.7571
GT	Sense	Sense	-0.643	Detected	0.643	Detected	0.000	-0.814	Detected	-1.799	Detected	-1.306	0.248	GT	Sens	contig269	contig269	Stachyos	GCATAC	contig269	Solyc01g	Solyc01g	Stachyos	GO:00472	GO:00472	contig269	Solyc01g	Stachyos	GO:00472	SL2.40ch	AT4G019	AtSTS	AtSTS (A	chr4:854	107.732	239.372	123.988	161.455	87.2329	46.4297
GT	Sense	Sense	-0.985	Detected	0.985	Detected	0.000	-1.126	Detected	-0.875	Detected	-1.000	0.420	GT	Sens	contig270	contig270	Unknown	ATGCTT	contig270	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig270	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G66800.1		unknown	chr5:266	34.0497	121.626	84.1065	84.629	28.156	35.2962
GT	Sense	Sense	0.003	Detected	-0.003	Detected	0.000	-0.904	Comprom	-2.371	Comprom	-1.638	0.155	GT	Sens	contig270	contig270	Unknown	GGGTTT	contig270	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig270	Solyc12g	Unknown Protein (A		SL2.40ch	ATCG010	NDHD	Represen	chrC:115	13.0163	11.8172	16.6816	12.1968	6.32739	2.41162
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	-1.123	Detected	-1.048	Detected	-1.085	0.016	GT	Sens	contig270	contig270	Short inte	GAGGAG	contig270	Solyc00g	Solyc00g	Short inte	GO:00037	GO:00037	contig270	Solyc00g	Short inte	GO:00037	SL2.40ch	AT1G755	SRS5	SRS5 (SH	chr1:283	990.261	1083.53	518.403	761.287	454.249	504.135
GT	Sense	Sense	0.399	Detected	-0.399	Detected	0.000	-1.500	Detected	-1.194	Detected	-1.347	0.088	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	238.12	124.891	204.78	205.967	58.1951	75.8513
GT	Sense	Sense	-0.106	Detected	0.106	Detected	0.000	-1.599	Detected	-1.509	Detected	-1.554	0.005	GT	Sens	contig271	contig271	BCS1 pro	TATGAT	contig271	Solyc03g	Solyc03g	BCS1 protein-like protein (AHF			contig271	Solyc03g	BCS1 protein-like pr		SL2.40ch	AT5G14680.1		universa	chr5:473	116.86	123.395	100.9	266.109	37.859	42.4383
GT	Sense	Sense	-0.137	Detected	0.137	Detected	0.000	-1.015	Detected	-1.238	Detected	-1.126	0.024	GT	Sens	contig272	contig272	HAD-supe	TTGAGG	contig272	Solyc07g	Solyc07g	HAD-supe	GO:00085	GO:00085	contig272	Solyc07g	HAD-supe	GO:00039	SL2.40ch	AT3G12900.1		oxidored	chr3:410	1598.29	1762.94	1368.02	1606.71	793.212	716.092
GT	Sense	Sense	-0.103	Detected	0.103	Detected	0.000	-1.703	Detected	-1.583	Detected	-1.643	0.005	GT	Sens	contig272	contig272	Lipoxyge	CACGAC	contig272	Solyc09g	Solyc09g	Lipoxyge	GO:00161	GO:00161	contig272	Solyc09g	Lipoxyge	GO:00161	SL2.40ch	AT1G550	LOX1	LOX1: lip	chr1:205	60.0612	63.1923	60.0652	47.251	18.064	20.6825
GT	Sense	Sense	0.082	Detected	-0.082	Detected	0.000	-2.731	Comprom	-1.507	Comprom	-2.119	0.075	GT	Sens	contig272	contig272	Unknown	CATCTT	contig272	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig272	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G38040.1		UDP-gluc	chr5:151	14.4933	11.7864	3.20757	8.13679	1.87923	4.62463
GT	Sense	Sense	-0.283	Detected	0.283	Detected	0.000	-1.179	Comprom	-0.842	Comprom	-1.011	0.092	GT	Sens	contig272	contig272	Unknown	GAAAGC	contig272	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig272	Solyc06g	Unknown Protein (A		SL2.40ch	AT4G22030.1		F-box far	chr4:116	15.6555	21.1175	7.20309	16.1541	7.66863	10.2015
GT	Sense	Sense	-0.482	Detected	0.482	Detected	0.000	-1.059	Comprom	-1.475	Comprom	-1.267	0.137	GT	Sens	contig272	contig272	Glycogen	GATGAA	contig272	Solyc02g	Solyc02g	Glycogen synthase (AHRD V1			contig272	Solyc02g	Glycogen synthase		SL2.40ch	AT5G65685.1		soluble c	chr5:262	15.8604	28.1871	13.7883	16.7585	9.68787	7.65332
GT	Sense	Sense	0.376	Detected	-0.376	Detected	0.000	-1.149	Detected	-2.396	Comprom	-1.773	0.135	GT	Sens	contig273	contig273	Predicted	GTCAAG	contig273	Solyc05g	Solyc05g	Predicted by genscan and ger			contig273	Solyc05g	Predicted by gensca		SL2.40ch	AT2G01300.1		unknown	chr2:151	57.6491	31.1951	44.8472	31.6393	18.2582	8.10306
GT	Sense	Sense	-0.292	Detected	0.292	Detected	0.000	-0.919	Detected	-1.272	Detected	-1.096	0.085	GT	Sens	contig273	contig273	Tyrosine-	TTTAAAT	contig273	Solyc12g	Solyc12g	Tyrosine-	GO:00096	GO:00096	contig273	Solyc12g038700.1.1				AT1G624	LRX2	LRX2 (LE	chr1:231	57.4156	78.455	53.475	61.9917	33.8815	27.964
GT	Sense	Sense	-0.200	Detected	0.200	Detected	0.000	-1.384	Detected	-1.007	Detected	-1.195	0.049	GT	Sens	contig274	contig274	Serine/thr	TCTACT	contig274	Solyc07g	Solyc07g	Serine/thr	GO:00191	GO:00191	contig274	Solyc07g	Serine/thr	GO:00191	SL2.40ch	AT3G25490.1		wall-asso	chr3:924	885.713	1064.83	628.074	588.903	355.194	486.274
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-0.811	Detected	-1.203	Detected	-1.007	0.036	GT	Sens	contig274	contig274	Plant syn	GGCTAT	contig274	Solyc09g	Solyc09g	Plant synaptotagmin (AHRD V1			contig274	Solyc09g	Plant synaptotagmi		SL2.40ch	AT5G042	SYTC. AT	SYTC	chr5:115	130.839	115.056	65.707	85.6566	66.7604	53.6164
GT	Sense	Sense	-0.538	Detected	0.538	Detected	0.000	-3.435	Detected	-2.992	Detected	-3.214	0.031	GT	Sens	contig274	contig274	FAD-bind	ATTCTT	contig274	Solyc06g	Solyc06g	FAD-bind	GO:00506	GO:00506	contig274	Solyc06g	FAD-bind	GO:00506	SL2.40ch	AT5G44410.1		FAD-bind	chr5:178	1489.8	2861.78	1200.67	552.694	182.325	261.029
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	-0.953	Detected	-2.486	Detected	-1.720	0.182	GT	Sens	contig275	contig275	Unknown	TCTGTG	contig275	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig275	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G532	PAL2. AT	PAL2: ph	chr3:197	87.8034	135.016	34.4933	58.2386	53.7161	19.5451
GT	Sense	Sense	-0.373	Detected	0.373	Detected	0.000	-1.981	Detected	-2.929	Detected	-2.455	0.055	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	330.522	505.086	186.039	373.156	98.8521	53.9597
GT	Sense	Sense	-0.060	Detected	0.060	Detected	0.000	-2.159	Detected	-1.035	Detected	-1.597	0.106	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	412.654	409.012	100.677	766.373	87.8471	201.687
GT	Sense	Sense	-0.495	Detected	0.495	Detected	0.000	-1.892	Detected	-1.830	Detected	-1.861	0.064	GT	Sens	contig276	contig276	Unknown	AGAATA	contig276	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig276	Solyc05g	Unknown Protein (A		SL2.40ch	AT4G38340.1		RWP-RK	chr4:179	133.752	242.079	141.949	256.792	46.2936	50.9164
GT	Sense	Sense	-0.397	Detected	0.397	Detected	0.000	-1.063	Detected	-1.203	Detected	-1.133	0.107	GT	Sens	contig277	contig277	Receptor-	ACACCA	contig277	Solyc02g	Solyc02g	Receptor-	GO:00055	GO:00055	contig277	Solyc02g	Receptor-	GO:00046	SL2.40ch	AT4G213	ARK3	ARK3 (A.	chr4:113	314.403	496.938	188.004	345.265	180.656	172.752
GT	Sense	Sense	-0.532	Detected	0.532	Detected	0.000	-1.224	Detected	-1.706	Detected	-1.465	0.129	GT	Sens	contig277	contig277	Os06g02	CCCCAG	contig277	Solyc12g	Solyc12g	Os06g0207500 protein (Fragm			contig277	Solyc12g	Os06g0207500 prot		SL2.40ch	AT1G48880.1		unknown	chr1:180	33.2076	63.2945	36.0721	44.6044	18.7361	14.1389
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-1.629	Detected	-1.176	Detected	-1.402	0.025	GT	Sens	contig277	contig277	Fatty acyl	GATGGT	contig277	Solyc09g	Solyc09g	Fatty acyl	GO:00166	GO:00166	contig277	Solyc09g	Fatty acyl	GO:00166	SL2.40ch	AT3G567	FAR6	FAR6 (FA	chr3:209	233.313	213.562	70.6192	598.879	68.9212	99.3757
GT	Sense	Sense	-0.450	Detected	0.450	Detected	0.000	-2.122	Detected	-3.193	Comprom	-2.658	0.063	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	43.2293	73.5773	17.8165	30.1946	12.3688	6.20332
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-1.658	Detected	-1.198	Detected	-1.428	0.025	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	888.053	804.769	494.937	845.95	255.846	370.643
GT	Sense	Sense	-0.463	Detected	0.463	Detected	0.000	-1.589	Detected	-1.853	Detected	-1.721	0.070	GT	Sens	contig278	contig278	Squamos	AAATTCA	contig278	Solyc10g	Solyc10g	Squamos	GO:00056	GO:00056	contig278	Solyc10g	Squamos	GO:00056	SL2.40ch	AT1G020	SPL8	SPL8 (SO	chr1:365	98.8359	171.206	84.1216	283.675	41.294	36.2209
GT	Sense	Sense	-0.380	Detected	0.380	Detected	0.000	-1.772	Detected	-1.562	Detected	-1.667	0.052	GT	Sens	contig278	contig278	Tyrosine-	TTTCAA	contig278	Solyc10g	Solyc10g	Tyrosine-	GO:00053	GO:00053	contig278	Solyc10g	Tyrosine-	GO:00053	SL2.40ch	AT2G33260.1		tryptoph	chr2:141	862.197	1331.89	448.094	567.784	299.56	365.152
GT	Sense	Sense	0.084	Detected	-0.084	Detected	0.000	-2.187	Detected	-1.041	Detected	-1.614	0.108	GT	Sens	contig278	contig278	Avr9/Cf-9	CGCGGA	contig278	Solyc08g	Solyc08g	Avr9/Cf-9 rapidly elicited prote			contig278	Solyc08g	Avr9/Cf-9 rapidly eli		SL2.40ch	AT4G178	UBP20	UBP20 (U	chr4:993	2406.24	1952.67	1269.63	1818.05	454.654	1059.76
GT	Sense	Sense	-0.402	Detected	0.402	Detected	0.000	-1.080	Detected	-1.196	Detected	-1.138	0.107	GT	Sens	contig279	contig279	Cyclin-de	CAATCA	contig279	Solyc01g	Solyc01g	Cyclin-de	GO:00055	GO:00055	contig279	Solyc01g	Cyclin-de	GO:00055	SL2.40ch	AT2G447	CYCP4:1	CYCP4:1	chr2:184	72.9907	116.122	52.4647	76.7152	41.5703	40.4151
GT	Sense	Sense	-0.808	Detected	0.808	Detected	0.000	-1.068	Detected	-2.362	Detected	-1.715	0.239	GT	Sens	contig279	contig279	Unknown	GGAGGA	contig279	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig279	Solyc04g	Unknown Protein (A		SL2.40ch	AT4G39840.1		unknown	chr4:184	207.92	581.017	219.509	311.486	158.259	68.0016
GT	Sense	Sense	-0.049	Detected	0.049	Detected	0.000	-1.859	Detected	-1.587	Detected	-1.723	0.007	GT	Sens	contig280	contig280	Unknown	TTGTTT	contig280	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig280	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G11000.1		unknown	chr5:347	618.488	603.236	548.667	624.74	160.773	204.553
GT	Sense	Sense	0.663	Detected	-0.663	Detected	0.000	-2.652	Detected	-1.386	Detected	-2.019	0.159	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	220.806	80.2401	21.0395	204.685	20.2254	51.2462
GT	Sense	Sense	-0.646	Detected	0.646	Detected	0.000	-2.153	Detected	-1.798	Detected	-1.975	0.098	GT	Sens	contig281	contig281	Regulator	GGTAAT	contig281	Solyc08g	Solyc08g	Regulatory protein (AHRD V1 *			contig281	Solyc08g	Regulatory protein (		SL2.40ch	AT1G14590.1		FUNCTIO	chr1:499	179.199	399.877	106.662	236.367	57.4777	77.4651
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-1.098	Detected	-1.999	Detected	-1.548	0.078	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	67.0139	53.7253	20.8405	87.2679	26.7672	15.1047
GT	Sense	Sense	-0.205	Detected	0.205	Detected	0.000	-1.410	Detected	-1.282	Detected	-1.346	0.025	GT	Sens	contig282	contig282	Heat shoc	CTATGA	contig282	Solyc01g	Solyc01g	Heat shoc	GO:00055	GO:00055	contig282	Solyc01g	Heat shoc	GO:00055	SL2.40ch	AT5G285	BIP1	BIP1: AT	chr5:105	78.2818	94.8513	49.1893	34.2082	30.9545	35.6438
GT	Sense	Sense	-0.695	Detected	0.695	Detected	0.000	-0.940	Detected	-1.177	Detected	-1.058	0.272	GT	Sens	contig283	contig283	Glucosylt	CATAGG	contig283	Solyc01g	Solyc01g	Glucosylt	GO:00081	GO:00081	contig283	Solyc09g	Peptide tr	GO:00429	SL2.40ch	AT2G36810.1		binding	chr2:154	508.094	1213.17	596.369	809.571	390.793	349.432
GT	Sense	Sense	-0.329	Detected	0.329	Detected	0.000	-1.194	Detected	-1.046	Detected	-1.120	0.080	GT	Sens	contig283	contig283	B3 domai	GATGAT	contig283	Solyc01g	Solyc01g	B3 domai	GO:00063	GO:00063	contig283	Solyc01g	B3 domai	GO:00063	SL2.40ch	AT5G45460.1		unknown	chr5:184	916.574	1318.42	471.194	683.876	458.858	535.709
GT	Sense	Sense	-0.070	Detected	0.070	Detected	0.000	-2.609	Detected	-1.302	Detected	-1.956	0.097	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:779	75.0125	75.3515	62.0917	86.3608	11.7622	30.6772
GT	Sense	Sense	0.103	Detected	-0.103	Detected	0.000	-2.275	Comprom	-2.681	Comprom	-2.478	0.008	GT	Sens	contig284	contig284	Unknown	ATACAG	contig284	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig284	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G10810.1		zinc fing	chr3:338	14.2604	11.2764	29.1566	41.2351	2.50102	1.9893
GT	Sense	Sense	-0.685	Detected	0.685	Detected	0.000	-2.280	Comprom	-2.602	Comprom	-2.441	0.074	GT	Sens	contig284	contig284	Pathogen	CATTATA	contig284	Solyc08g	Solyc08g	Pathogen	GO:00055	GO:00055	contig284	Solyc08g	Pathogen	GO:00055	SL2.40ch	AT3G19690.1		pathogen	chr3:684	14.026	33.041	36.2393	37.6711	4.2335	3.56621
GT	Sense	Sense	-0.306	Detected	0.306	Detected	0.000	-0.930	Detected	-1.247	Detected	-1.088	0.087	GT	Sens	contig284	contig284	Ethylene-	AGAAGA	contig284	Solyc10g	Solyc10g	Ethylene-	GO:00063	GO:00063	contig284	Solyc10g	Ethylene-	GO:00036	SL2.40ch	AT5G18450.1		AP2 dom	chr5:611	26.0182	36.2352	7.21041	15.6076	15.3901	13.0175
GT	Sense	Sense	-0.264	Detected	0.264	Detected	0.000	-1.191	Comprom	-1.187	Comprom	-1.189	0.046	GT	Sens	contig285	contig285	Calmodul	TACGAA	contig285	Solyc10g	Solyc10g	Calmodulin binding protein (A			contig285	Solyc10g	Calmodulin binding		SL2.40ch	AT3G52870.1		calmodu	chr3:195	12.4089	16.3053	2.44269	14.2865	5.94757	6.28422
GT	Sense	Sense	-0.303	Detected	0.303	Detected	0.000	-3.802	Comprom	-2.337	Detected	-3.069	0.061	GT	Sens	contig285	contig285	Unknown	TGAAAT	contig285	Solyc02g	Solyc02g	Unknown	GO:00160	GO:00160	contig285	Solyc03g	SPFH domain/band		SL2.40ch	AT5G22550.2		unknown	chr5:748	51.7884	71.828	35.874	58.5304	4.17536	12.1443
GT	Sense	Sense	-1.384	Detected	1.384	Detected	0.000	-0.935	Detected	-5.581	Comprom	-3.258	0.351	GT	Sens	contig286	contig286	Acetyl xy	AGATGC	contig286	Solyc12g	Solyc12g	Acetyl xylan esterase A (AHRD			contig286	Solyc12g	Acetyl xylan esteras		SL2.40ch	AT3G477	ATATH1.	ATATH1:	chr3:175	48.0417	298.272	56.8936	54.6092	59.7825	2.51615
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.969	Comprom	-2.705	Comprom	-2.337	0.024	GT	Sens	contig286	contig286	Cys2/His2	CAAAAG	contig286	Solyc05g	Solyc05g	Cys2/His2	GO:00037	GO:00037	contig286	Solyc05g	Cys2/His2	GO:00037	SL2.40ch	AT3G10470.1		zinc fing	chr3:326	16.8525	14.5405	2.21837	6.69074	3.81658	2.41509
GT	Sense	Sense	-0.807	Detected	0.807	Detected	0.000	-0.908	Detected	-1.691	Detected	-1.299	0.284	GT	Sens	contig287	contig287	Pectate ly	GTAGCC	contig287	Solyc03g	Solyc03g	Pectate ly	GO:00168	GO:00168	contig287	Solyc03g	Pectate ly	GO:00168	SL2.40ch	AT4G24780.1		pectate ly	chr4:127	8853.6	24700.1	7536.91	9921.58	7526.29	4609.02
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	-1.775	Detected	-1.428	Detected	-1.602	0.061	GT	Sens	contig287	contig287	Lipoxyge	CTCCAG	contig287	Solyc01g	Solyc01g	Lipoxyge	GO:00161	GO:00161	contig287	Solyc01g	Lipoxyge	GO:00055	SL2.40ch	AT3G451	LOX2. AT	LOX2 (LI	chr3:165	400.245	615.686	526.982	345.127	138.512	185.547
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-1.702	Detected	-1.719	Detected	-1.710	0.000	GT	Sens	contig290	contig290	Unknown	CATTTA	contig290	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig290	Solyc01g	Transport protein p		SL2.40ch	AT5G439	MYA2. AT	MYA2 (AI	chr5:176	291.134	257.776	186.399	291.49	80.4063	83.7098
GT	Sense	Sense	-0.392	Detected	0.392	Detected	0.000	-1.455	Comprom	-1.628	Comprom	-1.542	0.062	GT	Sens	contig290	contig290	Peptidogl	GTTCTT	contig290	Solyc10g	Solyc10g	Peptidogl	GO:00169	GO:00169	contig290	Solyc10g	Peptidogl	GO:00169	SL2.40ch	AT3G52790.1		peptidog	chr3:195	11.6969	18.3556	3.53484	16.7355	5.1031	4.76882
GT	Sense	Sense	-0.563	Detected	0.563	Detected	0.000	-1.336	Detected	-2.733	Detected	-2.034	0.151	GT	Sens	contig290	contig290	Unknown	GAGGTT	contig290	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig290	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G14370.1		LOCATE	chr5:463	296.659	590.169	165.689	351.76	158.28	63.3206
GT	Sense	Sense	-0.895	Detected	0.895	Detected	0.000	-1.148	Detected	-1.374	Detected	-1.261	0.297	GT	Sens	contig291	contig291	Unknown	GACAAA	contig291	Solyc06g	Solyc06g	Unknown Protein (AHRD V1):O			contig291	Solyc05g	Eukaryoti	GO:00037	SL2.40ch	AT5G35680.2		eukaryot	chr5:138	1632.35	5144.39	1384.57	2098.82	1248.44	1124.77
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-1.328	Detected	-0.979	Detected	-1.153	0.022	GT	Sens	contig291	contig291	UDP-gluc	GCTTTC	contig291	Solyc07g	Solyc07g	UDP-gluc	GO:00054	GO:00054	contig291	Solyc07g	UDP-gluc	GO:00054	SL2.40ch	AT4G32272.1		FUNCTIO	chr4:155	49.3469	45.1545	18.3749	25.8703	17.9551	24.0887
GT	Sense	Sense	-0.674	Detected	0.674	Detected	0.000	-1.950	Comprom	-1.654	Comprom	-1.802	0.121	GT	Sens	contig291	contig291	Unknown	ATCTGA	contig291	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig291	Solyc02g	Unknown Protein (A		SL2.40ch	ATCG001	RPOB	Chloropl	chrC:231	13.2001	30.6173	4.64005	4.70846	4.96803	6.42543
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	-1.604	Detected	-1.032	Detected	-1.318	0.048	GT	Sens	contig291	contig291	Copper c	CTTTCA	contig291	Solyc01g	Solyc01g	Copper c	GO:00300	GO:00300	contig291	Solyc01g	Copper c	GO:00300	SL2.40ch	AT5G02600.1		heavy-m	chr5:585	137.585	141.566	40.5619	298.056	43.8207	68.6756
GT	Sense	Sense	-0.153	Detected	0.153	Detected	0.000	-1.226	Detected	-1.023	Detected	-1.124	0.026	GT	Sens	contig292	contig292	Calmodul	AACAAGT	contig292	Solyc12g	Solyc12g	Calmodulin-binding protein (A			contig292	Solyc12g	Calmodulin-binding		SL2.40ch	AT2G26190.1		calmodu	chr2:111	2015.82	2270.61	1162.57	2067.05	873.467	1059.33
GT	Sense	Sense	-0.094	Detected	0.094	Detected	0.000	-1.061	Detected	-2.683	Comprom	-1.872	0.149	GT	Sens	contig293	contig293	Ulp1 prot	GAAAGA	contig293	Solyc10g	Solyc10g	Ulp1 protease family C-termina			contig293	Solyc10g	Ulp1 protease family		SL2.40ch	AT3G44440.1				22.4334	23.3036	16.3067	13.2362	10.4627	3.58079
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-1.564	Detected	-1.439	Detected	-1.502	0.002	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	453.418	425.986	354.041	435.161	141.956	163.013
GT	Sense	Sense	0.020	Detected	-0.020	Detected	0.000	-1.250	Detected	-1.410	Detected	-1.330	0.004	GT	Sens	contig293	contig293	Peroxiso	TTCAACT	contig293	Solyc06g	Solyc06g	Peroxiso	GO:00055	GO:00055	contig293	Solyc06g	Peroxiso	GO:00055	SL2.40ch	AT4G14305.1		FUNCTIO	chr4:823	1023.87	908.081	1281.05	1232.75	386.998	365.052
GT	Sense	Sense	-0.168	Detected	0.168	Detected	0.000	-1.090	Comprom	-1.105	Comprom	-1.098	0.023	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	15.7371	18.0998	15.861	19.7266	7.56818	7.89401
GT	Sense	Sense	-0.018	Detected	0.018	Detected	0.000	-1.189	Detected	-1.127	Detected	-1.158	0.001	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	172.327	161.087	89.528	190.437	69.7609	76.7652
GT	Sense	Sense	-0.444	Detected	0.444	Detected	0.000	-2.609	Detected	-1.481	Detected	-2.045	0.104	GT	Sens	contig294	contig294	ATP-bind	AATGACT	contig294	Solyc09g	Solyc09g	ATP-bind	GO:00171	GO:00171	contig294	Solyc09g	ATP-bind	GO:00426	SL2.40ch	AT2G299	PDR3. AT	PDR3 (PL	chr2:127	6091.74	10277	3275.18	3007.75	1238.44	2850.81
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	-1.801	Comprom	-1.323	Comprom	-1.562	0.027	GT	Sens	contig294	contig294	Inositol o	ACAACA	contig294	Solyc11g	Solyc11g	Inositol o	GO:00057	GO:00057	contig294	Solyc11g	Inositol o	GO:00057	SL2.40ch	AT4G262	MIOX4	MIOX4: i	chr4:132	11.7058	12.4616	5.20618	11.6017	3.30967	4.85795
GT	Sense	Sense	-0.439	Detected	0.439	Detected	0.000	-0.849	Detected	-1.654	Detected	-1.252	0.170	GT	Sens	contig294	contig294	Myb fami	GATGTC	contig294	Solyc10g	Solyc10g	Myb fami	GO:0045449		contig294	Solyc10g	Myb fami	GO:00454	SL2.40ch	AT3G04030.3		myb fam	chr3:104	808.023	1353.36	720.338	922.475	554.189	334.311
GT	Sense	Sense	-0.352	Detected	0.352	Detected	0.000	-1.554	Detected	-1.588	Detected	-1.571	0.047	GT	Sens	contig294	contig294	MYB tran	CTACGC	contig294	Solyc02g	Solyc02g	MYB tran	GO:00037	GO:00037	contig294	Solyc02g	MYB tran	GO:00037	SL2.40ch	AT4G051	AtMYB74	AtMYB74	chr4:261	107.99	160.42	76.5722	162.325	42.8023	44.0303
GT	Sense	Sense	-0.064	Detected	0.064	Detected	0.000	-1.801	Comprom	-0.963	Comprom	-1.382	0.083	GT	Sens	contig295	contig295	Unknown	AGAAAG	contig295	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig295	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G07050.1		GTP-bind	chr3:222	14.49	14.4456	12.8127	13.515	3.96383	7.46476
GT	Sense	Sense	-0.555	Detected	0.555	Detected	0.000	-1.188	Detected	-2.150	Detected	-1.669	0.151	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	50.0971	98.6379	57.6618	34.6413	29.466	15.938
GT	Sense	Sense	-0.473	Detected	0.473	Detected	0.000	-1.516	Detected	-2.536	Detected	-2.026	0.100	GT	Sens	contig296	contig296	Glutared	GAAAAT	contig296	Solyc10g	Solyc10g	Glutared	GO:00454	GO:00454	contig296	Solyc10g	Glutared	GO:00055	SL2.40ch	AT1G03850.2		glutared	chr1:977	660.958	1160.41	387.909	703.487	292.338	151.896
GT	Sense	Sense	-0.281	Detected	0.281	Detected	0.000	-1.514	Detected	-2.303	Detected	-1.909	0.059	GT	Sens	contig296	contig296	Glutamat	CGGCTA	contig296	Solyc04g	Solyc04g	Glutamat	GO:00043	GO:00043	contig296	Solyc04g	Glutamat	GO:00043	SL2.40ch	AT5G173	GAD. GAI	GAD: cal	chr5:571	1117.35	1504.22	1069.97	1658.66	433.316	264.339
GT	Sense	Sense	0.470	Detected	-0.470	Detected	0.000	-1.953	Detected	-1.446	Detected	-1.700	0.086	GT	Sens	contig296	contig296	Monooxy	GGGGAA	contig296	Solyc09g	Solyc09g	Monooxy	GO:00551	GO:00551	contig296	Solyc09g	Monooxy	GO:00551	SL2.40ch	AT3G14170.1		unknown	chr3:469	1984.71	943.449	618.011	772.741	337.402	505.092
GT	Sense	Sense	0.068	Detected	-0.068	Detected	0.000	-1.580	Detected	-0.860	Detected	-1.220	0.080	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	1027.8	852.733	336.892	1984.14	299.007	518.978
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-1.968	Detected	-1.103	Detected	-1.535	0.074	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	995.952	802.07	711.958	457.77	218.159	418.629
GT	Sense	Sense	-0.814	Detected	0.814	Detected	0.000	-1.930	Comprom	-3.954	Comprom	-2.942	0.152	GT	Sens	contig300	contig300	Gibberelli	TGTTTA	contig300	Solyc04g	Solyc04g	Gibberellin regulated protein (			contig300	Solyc04g	Gibberellin regulate		SL2.40ch	AT1G74670.1		gibberell	chr1:280	23.1369	65.1612	30.3038	61.5525	9.73121	2.51952
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-1.008	Detected	-1.138	Detected	-1.073	0.007	GT	Sens	contig300	contig300	Unknown	GGAGTA	contig300	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig300	Solyc12g	Unknown Protein (A		SL2.40ch	AT4G08450.1		disease r	chr4:536	406.27	401.73	373.678	589.972	191.843	184.645
GT	Sense	Sense	0.397	Detected	-0.397	Detected	0.000	-2.836	Detected	-2.677	Detected	-2.757	0.021	GT	Sens	contig300	contig300	UDP-gluc	TGGAAT	contig300	Solyc10g	Solyc10g	UDP-gluc	GO:00081	GO:00081	contig300	Solyc10g	UDP-gluc	GO:00081	SL2.40ch	AT1G584	XF1. SOE	XF1: squ	chr1:217	100.038	52.6341	14.3979	32.4673	9.70161	11.4151
GT	Sense	Sense	-0.278	Detected	0.278	Detected	0.000	-1.584	Detected	-1.061	Detected	-1.322	0.074	GT	Sens	contig300	contig300	Unknown	GTATTT	contig300	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig300	Solyc10g036650.1.1				AT4G31100.1		wall-asso	chr4:151	849.626	1139.57	789.662	1172.5	313.457	474.388
GT	Sense	Sense	-0.299	Detected	0.299	Detected	0.000	-1.902	Detected	-1.291	Detected	-1.596	0.065	GT	Sens	contig301	contig301	Serine/thr	CGTTAG	contig301	Solyc07g	Solyc07g	Serine/thr	GO:00055	GO:00055	contig301	Solyc07g	Serine/thr	GO:00055	SL2.40ch	AT1G52540.1		protein k	chr1:195	71.7641	99.0178	52.4527	50.0932	21.5421	34.6513
GT	Sense	Sense	-0.177	Detected	0.177	Detected	0.000	-1.644	Comprom	-1.267	Detected	-1.456	0.030	GT	Sens	contig301	contig301	Phospho	ATTCAA	contig301	Solyc04g	Solyc04g	Phosphol	GO:00046	GO:00046	contig301	Solyc04g	Phosphol	GO:00046	SL2.40ch	AT4G357	ATPLDDE	ATPLDDI	chr4:169	22.2543	25.9422	15.4844	13.8488	7.33849	10.046
GT	Sense	Sense	-0.813	Detected	0.813	Detected	0.000	-1.034	Detected	-2.002	Detected	-1.518	0.250	GT	Sens	contig302	contig302	Plant-spe	TGCAATT	contig302	Solyc12g	Solyc12g	Plant-specific domain TIGR015			contig302	Solyc12g	Plant-specific doma		SL2.40ch	AT5G42680.1		unknown	chr5:171	829.272	2332.06	909.598	1368.23	648.537	349.16
GT	Sense	Sense	-0.332	Detected	0.332	Detected	0.000	-0.990	Detected	-1.689	Detected	-1.340	0.109	GT	Sens	contig303	contig303	F-box fam	ATATCA	contig303	Solyc09g	Solyc09g	F-box family protein (AHRD V1			contig303	Solyc09g	F-box family protein		SL2.40ch	AT3G25250.1				62.3359	90.0731	40.1029	55.9719	36.0159	23.3756
GT	Sense	Sense	-0.148	Detected	0.148	Detected	0.000	-1.877	Detected	-0.895	Detected	-1.386	0.114	GT	Sens	contig304	contig304	Cytochro	TTAGAAT	contig304	Solyc04g	Solyc04g	Cytochro	GO:00198	GO:00198	contig304	Solyc04g	Cytochro	GO:00198	SL2.40ch	AT1G649	CYP89A2	CYP89A2	chr1:241	264.958	296.733	54.9438	256.706	72.8877	151.644
GT	Sense	Sense	-0.270	Detected	0.270	Detected	0.000	-1.111	Detected	-1.898	Detected	-1.504	0.088	GT	Sens	contig304	contig304	Unknown	ATACAC	contig304	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig304	Solyc04g	Unknown Protein (A		SL2.40ch	AT5G53700.1		INVOLVE	chr5:218	141.708	187.752	78.8265	119.468	72.121	44.0333
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	-1.065	Detected	-1.932	Detected	-1.499	0.076	GT	Sens	contig305	contig305	Homeobo	CTTGGA	contig305	Solyc05g	Solyc05g	Homeobo	GO:00056	GO:00056	contig305	Solyc05g	Homeobo	GO:00165	SL2.40ch	AT5G653	ATHB5. A	ATHB5 (A	chr5:261	4427.22	3694.23	2725.61	3265.53	1845.25	1066.19
GT	Sense	Sense	-0.527	Detected	0.527	Detected	0.000	-2.833	Detected	-1.994	Detected	-2.413	0.070	GT	Sens	contig305	contig305	Glutathio	GTGAAA	contig305	Solyc09g	Solyc09g	Glutathio	GO:00043	GO:00043	contig305	Solyc09g	Glutathio	GO:00043	SL2.40ch	AT1G783	ATGSTU2	ATGSTU	chr1:294	84.396	159.805	64.6316	89.2186	15.5598	29.3388
GT	Sense	Sense	-0.548	Detected	0.548	Detected	0.000	-1.467	Detected	-2.257	Detected	-1.862	0.110	GT	Sens	contig305	contig305	Tropinon	TTCAGG	contig305	Solyc06g	Solyc06g	Tropinon	GO:00081	GO:00081	contig305	Solyc06g	Tropinon	GO:00081	SL2.40ch	AT2G29310.1		tropinone	chr2:125	849.006	1654.12	624.533	1000.53	409.27	249.427
GT	Sense	Sense	-0.430	Detected	0.430	Detected	0.000	-1.155	Detected	-2.065	Comprom	-1.610	0.124	GT	Sens	contig305	contig305	Unknown	TAAATCA	contig305	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig305	Solyc09g	Unknown Protein (A		SL2.40ch	AT1G241	ARL1	ARL1 (AF	chr1:852	23.8669	39.4986	19.2144	51.2549	13.1646	7.38237
GT	Sense	Sense	-0.155	Detected	0.155	Detected	0.000	-1.720	Detected	-0.952	Detected	-1.336	0.084	GT	Sens	contig305	contig305	Auxin-reg	TAGAAG	contig305	Solyc11g	Solyc11g	Auxin-regulated protein (AHRD			contig305	Solyc11g	Auxin-regulated pro		SL2.40ch	AT5G10150.1		unknown	chr5:318	34.1846	38.6495	25.4164	47.0532	10.5371	18.9047
GT	Sense	Sense	-0.528	Detected	0.528	Detected	0.000	-1.809	Detected	-2.836	Detected	-2.322	0.088	GT	Sens	contig306	contig306	Unknown	AACTTAT	contig306	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig306	Solyc12g	Unknown Protein (A		SL2.40ch	AT3G010	WRKY58.	WRKY58	chr3:255	1328.85	2520.09	1012.06	1388.88	498.799	257.749
GT	Sense	Sense	0.115	Detected	-0.115	Detected	0.000	-1.420	Detected	-1.414	Detected	-1.417	0.006	GT	Sens	contig306	contig306	Unknown	AAGGGT	contig306	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig306	Solyc06g	TO54-2 (Fragment) (		SL2.40ch	AT3G48185.1		unknown	chr3:177	378.76	294.611	277.026	368.472	119.19	126.114
GT	Sense	Sense	-0.497	Detected	0.497	Detected	0.000	-1.825	Detected	-1.733	Detected	-1.779	0.070	GT	Sens	contig306	contig306	ELF4-like	ATAGCAT	contig306	Solyc06g	Solyc06g	ELF4-like protein (AHRD V1 ***			contig306	Solyc06g	ELF4-like protein (A		SL2.40ch	AT2G400	ELF4	ELF4 (EA	chr2:167	135.09	245.241	91.903	91.059	49.058	55.0673
GT	Sense	Sense	-0.412	Detected	0.412	Detected	0.000	-1.524	Detected	-1.535	Detected	-1.529	0.066	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	54.9153	88.663	21.3579	68.3662	23.1667	24.2313
GT	Sense	Sense	-0.384	Detected	0.384	Detected	0.000	-0.964	Detected	-1.455	Detected	-1.210	0.117	GT	Sens	contig306	contig306	RING fing	ATGTGA	contig306	Solyc04g	Solyc04g	RING fing	GO:00055	GO:00055	contig306	Solyc04g	RING fing	GO:00055	SL2.40ch	AT3G094	PLL3	PLL3: ca	chr3:289	1402.74	2177.48	930.431	1670.98	855.285	641.116
GT	Sense	Sense	0.156	Detected	-0.156	Detected	0.000	-2.381	Detected	-0.891	Detected	-1.636	0.165	GT	Sens	contig307	contig307	Undecap	GCTTAC	contig307	Solyc08g	Solyc08g	Undecap	GO:00455	GO:00455	contig307	Solyc08g	Undecap	GO:00455	SL2.40ch	AT5G58770.1		dehydro	chr5:237	2666.77	1957.39	540.361	5075.43	418.842	1239.03
GT	Sense	Sense	-0.182	Detected	0.182	Detected	0.000	-1.239	Detected	-2.445	Detected	-1.842	0.100	GT	Sens	contig307	contig307	DNA-3-me	TGCACAT	contig307	Solyc10g	Solyc10g	DNA-3-me	GO:00062	GO:00062	contig307	Solyc10g	DNA-3-me	GO:00062	SL2.40ch	AT5G44680.1		methylad	chr5:180	364.494	427.386	124.731	184.694	159.66	72.9378
GT	Sense	Sense	0.406	Detected	-0.406	Detected	0.000	-1.053	Detected	-1.063	Detected	-1.058	0.121	GT	Sens	contig308	contig308	ATP-bind	GAAAAA	contig308	Solyc06g	Solyc06g	ATP-bind	GO:00171	GO:00171	contig308	Solyc03g	ATP-bind	GO:00168	SL2.40ch	AT3G477	ATATH1.	ATATH1:	chr3:175	62.6843	32.5591	16.9357	28.914	20.7865	21.7488
GT	Sense	Sense	-0.257	Detected	0.257	Detected	0.000	-1.325	Detected	-0.864	Detected	-1.095	0.086	GT	Sens	contig308	contig308	Glutathio	AGAGAT	contig308	Solyc09g	Solyc09g	Glutathio	GO:00043	GO:00043	contig308	Solyc09g	Glutathio	GO:00043	SL2.40ch	AT3G562	CCH	CCH (CO	chr3:208	30703.3	39953.6	25766.8	28812.3	13351.2	19352
GT	Sense	Sense	-0.098	Detected	0.098	Detected	0.000	-2.896	Detected	-2.343	Detected	-2.619	0.012	GT	Sens	contig308	contig308	Heat stres	GATGAA	contig308	Solyc04g	Solyc04g	Heat stres	GO:00056	GO:00056	contig308	Solyc04g	Heat stres	GO:00036	SL2.40ch	AT2G416	AT-HSFB	AT-HSFB	chr2:173	428.279	447.327	209.159	208.958	56.1532	86.7735
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-1.177	Detected	-2.350	Detected	-1.763	0.097	GT	Sens	contig309	contig309	IST1 hom	AACAGA	contig309	Solyc05g	Solyc05g	IST1 homolog (AHRD V1 *--- IS			contig309	Solyc05g	IST1 homolog (AHR		SL2.40ch	AT1G13340.1		unknown	chr1:456	282.855	294.178	184.655	364.262	121.789	56.9377
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	-2.094	Detected	-1.078	Detected	-1.586	0.089	GT	Sens	contig309	contig309	Tumor-re	CAAATCA	contig309	Solyc10g	Solyc10g	Tumor-related protein (AHRD \			contig309	Solyc10g	Tumor-related prote		SL2.40ch	AT5G523	CYP96A4	CYP96A4	chr5:212	581.568	538.664	146.491	1342.45	125.16	266.704
GT	Sense	Sense	-0.558	Detected	0.558	Detected	0.000	-1.274	Detected	-2.399	Detected	-1.837	0.146	GT	Sens	contig310	contig310	Receptor-	CTAGATA	contig310	Solyc11g	Solyc11g	Receptor-	GO:00064	GO:00064	contig310	Solyc11g	Receptor-	GO:00055	SL2.40ch	AT1G70250.1		receptor	chr1:264	388.092	767.122	486.206	666.938	215.413	104.048
GT	Sense	Sense	-0.251	Detected	0.251	Detected	0.000	-0.973	Detected	-1.056	Detected	-1.014	0.057	GT	Sens	contig310	contig310	CONSTAN	GAATTA	contig310	Solyc07g	Solyc07g	CONSTAN	GO:00305	GO:00305	contig310	Solyc07g	CONSTAN	GO:00305	SL2.40ch	AT5G571	CIA2	CIA2 (CH	chr5:231	803.449	1036.9	580.008	1333.58	444.122	441.628
GT	Sense	Sense	-0.021	Detected	0.021	Detected	0.000	-1.760	Comprom	-1.723	Comprom	-1.741	0.000	GT	Sens	contig310	contig310	Unknown	GACTTA	contig310	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig310	Solyc09g	Unknown Protein (A		SL2.40ch	ATCG003	PSAA	Encodes	chrC:396	16.2827	15.2882	4.21577	20.1601	4.44794	4.80849
GT	Sense	Sense	-0.037	Detected	0.037	Detected	0.000	-2.181	Detected	-1.435	Detected	-1.808	0.040	GT	Sens	contig312	contig312	Laccase	CCTCTT	contig312	Solyc04g	Solyc04g	Laccase	GO:00480	GO:00480	contig312	Solyc04g	Laccase	GO:00043	SL2.40ch	AT2G302	LAC3	LAC3 (lac	chr2:128	5646.89	5421.22	3212.55	1920.73	1164.78	2058.11
GT	Sense	Sense	-0.018	Detected	0.018	Detected	0.000	-3.228	Comprom	-3.201	Comprom	-3.214	0.000	GT	Sens	contig312	contig312	3%26apo	GTGATG	contig312	Solyc01g	Solyc01g	3%26apo	GO:00036	GO:00036	contig312	Solyc01g	3&apos-5	GO:00036	SL2.40ch	AT4G01800.1		preprote	chr4:770	18.5512	17.3483	13.8222	2.88621	1.82849	1.96266
GT	Sense	Sense	-0.291	Detected	0.291	Detected	0.000	-3.673	Detected	-1.820	Detected	-2.746	0.106	GT	Sens	contig312	contig312	Kunitz-typ	ATTTGTT	contig312	Solyc03g	Solyc03g	Kunitz-typ	GO:00048	GO:00048	contig312	Solyc03g	Kunitz-typ	GO:00048	SL2.40ch	AT5G440	CESA4. IF	CESA4 (C	chr5:177	6950.07	9484.09	3109.47	3073.35	607.851	2313.33
GT	Sense	Sense	-0.320	Detected	0.320	Detected	0.000	-1.693	Detected	-2.654	Detected	-2.173	0.064	GT	Sens	contig312	contig312	Unknown	TCAGTCA	contig312	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig312	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G18930.2		zinc fing	chr3:652	175.852	249.805	45.61	176.735	61.9097	33.4943
GT	Sense	Sense	-0.295	Detected	0.295	Detected	0.000	-0.920	Detected	-1.367	Detected	-1.144	0.091	GT	Sens	contig313	contig313	Unannota	GGGAAGAAACTTGTGTTCCAGATATACTTGATATGGCAATTAGAAAATC							contig313	Solyc08g	CUGBP E	GO:00036	SL2.40ch	AT1G51790.1				42.6536	58.5386	52.0908	46.4456	25.2182	19.4845
GT	Sense	Sense	-0.268	Detected	0.268	Detected	0.000	-1.422	Detected	-1.656	Detected	-1.539	0.034	GT	Sens	contig313	contig313	Unannota	TAATGAAATTTGTTTAGAGGAAAATTCAACAAGTTATGATGATGTTAGA							contig313	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G24190.1		ABC1 far	chr3:874	35.4904	46.896	24.8237	27.3913	14.5351	13.0254
GT	Sense	Sense	0.004	Detected	-0.004	Detected	0.000	-2.196	Comprom	-2.612	Comprom	-2.404	0.007	GT	Sens	contig313	contig313	Unannota	TTTTCTTAAAATGGGATTCTTCATATGAAATAATGTTTGATCACTAATAA							contig313	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G28770.1		unknown	chr3:107	12.8519	11.6468	2.1591	7.55503	2.54863	2.01325
GT	Sense	Sense	-0.746	Detected	0.746	Detected	0.000	-0.901	Detected	-1.341	Detected	-1.121	0.286	GT	Sens	contig313	contig313	Unannota	CCAGTTTATTCACTGCACTTGAACCTCCTTTGTTTTTCAAAACTAAACA							contig313	Solyc06g	Protein T	GO:00054	SL2.40ch	AT5G155	EMB2773	EMB2773	chr5:504	19.5446	50.1455	14.5955	29.8648	16.0092	12.4324
GT	Sense	Sense	-0.885	Detected	0.885	Detected	0.000	-1.072	Detected	-1.554	Detected	-1.313	0.288	GT	Sens	contig313	contig313	Unannota	GAGTTTGTTCACTTTGGAGCATTTTTCATTTCTCTTTTCTGTTCCTGTT							contig313	Solyc11g	Gibberelli	GO:00055	SL2.40ch	AT3G52700.1		unknown	chr3:195	185.298	575.77	149.683	216.741	148.295	111.88
GT	Sense	Sense	-0.271	Detected	0.271	Detected	0.000	-1.118	Detected	-1.071	Detected	-1.095	0.057	GT	Sens	contig314	contig314	Unannota	GTGATAAATTAGTGATCTTTGGTGGTAGTGGTGAAGGTGAGGCAAACT							contig314	Solyc01g	Kelch domain-conta		SL2.40ch	AT1G65040.3		protein b	chr1:241	25.1308	33.3738	16.2368	23.0707	12.7355	13.8669
GT	Sense	Sense	-0.004	Detected	0.004	Detected	0.000	-1.077	Comprom	-2.120	Comprom	-1.598	0.092	GT	Sens	contig314	contig314	Unannota	AAAGAGTACATACTCAGCAAGCCAGAAACTCAGAAACCCAAACTTAACT							contig314	Solyc08g	Unknown Protein (A		SL2.40ch	AT5G43560.2		meprin a	chr5:175	12.8318	11.7566	4.67507	8.43087	5.55855	2.8434
GT	Sense	Sense	-0.082	Detected	0.082	Detected	0.000	-1.458	Detected	-0.812	Detected	-1.135	0.077	GT	Sens	contig315	contig315	Unannota	AGTGATGAATGGATGAAGAAATCCCTAATTTTCCCAGCAGAATCTCAAT							contig315	Solyc05g009440.1.1				AT1G680	ATMAP7	ATMAP7	chr1:255	81.3317	83.0966	39.1046	97.6872	28.5735	47.1122
GT	Sense	Sense	0.174	Detected	-0.174	Detected	0.000	-1.515	Comprom	-1.873	Comprom	-1.694	0.021	GT	Sens	contig315	contig315	Dof zinc f	TGGAAG	contig315	Solyc05g	Solyc05g	Dof zinc f	GO:0045449		contig315	Solyc05g	Dof zinc f	GO:00454	SL2.40ch	AT5G66940.1		Dof-type	chr5:267	16.8625	12.081	12.3879	13.8974	4.76685	3.92062
GT	Sense	Sense	-0.240	Detected	0.240	Detected	0.000	-0.980	Detected	-1.312	Comprom	-1.146	0.059	GT	Sens	contig316	contig316	Unannota	CCGTGTTACATAGTCTATAGTGATGAGATTAATCAAAATTCTGAACTTA							contig316	Solyc10g	Nodulin M	GO:00160	SL2.40ch	AT5G540	AT-HSFA	AT-HSFA	chr5:219	20.3311	25.8545	30.8734	16.5938	11.095	9.29166
GT	Sense	Sense	-0.419	Detected	0.419	Detected	0.000	-1.096	Detected	-1.200	Detected	-1.148	0.113	GT	Sens	contig316	contig316	Unannota	TTTAAGTATGCAATTGGAACAACGTATCGTTTCTTCTTCTCTGTTTCTC							contig316	Solyc01g	Auxin-ind	GO:00055	SL2.40ch	AT4G38840.1		auxin-res	chr4:181	23.1132	37.6584	22.5549	23.5163	13.1752	12.9202
GT	Sense	Sense	-0.223	Detected	0.223	Detected	0.000	-0.916	Detected	-1.509	Detected	-1.213	0.082	GT	Sens	contig316	contig316	Unannota	CTTGATCTATGTCTTGATCTCTGACATCTAAGAGGTGATTTGTCGGGTT							contig316	Solyc10g	MYB tran	GO:00036	SL2.40ch	AT2G076	ATMRP1	ATMRP1	chr2:351	26.5711	32.9832	15.9544	14.5806	14.9781	10.4625
GT	Sense	Sense	-0.079	Detected	0.079	Detected	0.000	-1.669	Comprom	-1.627	Comprom	-1.648	0.002	GT	Sens	contig317	contig317	Unknown	TTTTAAC	contig317	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig317	Solyc07g	Multidrug	GO:00052	SL2.40ch	AT5G24140.1				15.621	15.8818	4.22347	7.81421	4.72901	5.12951
GT	Sense	Sense	-0.417	Detected	0.417	Detected	0.000	-1.986	Comprom	-1.194	Detected	-1.590	0.110	GT	Sens	contig317	contig317	Unannota	GAAGTGAGCAATTTAAAGAATTTTGTTGTGAACCATGACATGGCACATG							contig317	Solyc09g	HAT famil	GO:00469	SL2.40ch	AT3G52700.1		unknown	chr3:195	11.0688	18.0009	3.17016	9.96793	3.40137	6.20787
GT	Sense	Sense	0.189	Detected	-0.189	Detected	0.000	-1.003	Comprom	-1.633	Comprom	-1.318	0.070	GT	Sens	contig317	contig317	Unannota	TCGAATTTGTGTTTGTTGAAGGTTGGTGAAACAAGATTTGCCTCAAACA							contig317	Solyc09g	HAT famil	GO:00469	SL2.40ch	AT3G52700.1		unknown	chr3:195	15.4253	10.8233	3.35055	15.4019	6.15397	4.19179
GT	Sense	Sense	-0.144	Detected	0.144	Detected	0.000	-1.399	Comprom	-1.228	Comprom	-1.314	0.016	GT	Sens	contig317	contig317	Unannota	CAGTTGTTATGAACAGTATCGAATAAAGGGTATTGTCTAGGAAACTGTC							contig317	Solyc04g	F-box/kelch-repeat		SL2.40ch	AT5G43190.1		F-box far	chr5:173	18.8203	20.9601	13.2771	16.7668	7.19067	8.52968
GT	Sense	Sense	-0.676	Detected	0.676	Detected	0.000	-1.143	Detected	-2.268	Comprom	-1.706	0.192	GT	Sens	contig317	contig317	Unannota	GATACTATTGGATTCAAGATGTGTTGGATTCTAGGTTGCTTGAACTTAC							contig317	Solyc06g	Gag-Pol polyprotein		SL2.40ch	AT4G12740.1		adenine-	chr4:749	21.7528	50.6478	20.013	16.8822	13.5342	6.9307
GT	Sense	Sense	-0.392	Detected	0.392	Detected	0.000	-1.753	Comprom	-1.604	Comprom	-1.678	0.052	GT	Sens	contig317	contig317	Unannota	CTTTTGATTGGCAGAAAGTAATGATCCGGATGTCGGTTGCTTTGTCGT							contig317	Solyc02g	Hydrolase	GO:00038	SL2.40ch	AT1G17330.1		metal-de	chr1:592	13.4033	21.0268	3.22161	6.87346	4.75659	5.55674
GT	Sense	Sense	-0.182	Detected	0.182	Detected	0.000	-1.246	Detected	-1.189	Detected	-1.217	0.022	GT	Sens	contig318	contig318	Unannota	GAGTCAGTGAGTTCAAAAATATGTGTGTGGTTTAATTGTATCGATACAT							contig318	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G68390.1		unknown	chr1:256	755.613	886.806	763.969	661.982	329.585	361.174
GT	Sense	Sense	-0.328	Detected	0.328	Detected	0.000	-2.807	Comprom	-1.682	Comprom	-2.244	0.075	GT	Sens	contig318	contig318	Unannota	GCTCTTTAATGTCTACATTTTAATGTTTTGCTTTGTTTTAGGTTCCTGT							contig318	Solyc05g	Unknown Protein (A		SL2.40ch	AT5G06690.2				14.0379	20.1549	13.0021	7.72007	2.29521	5.27332
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	-1.403	Detected	-1.571	Detected	-1.487	0.061	GT	Sens	contig318	contig318	Unannota	GGTATTGAAAAAGAGAAGAGCCAAGTTGAGGACGATCAAGAACAAATTT							contig318	Solyc12g	Katanin p	GO:00055	SL2.40ch	AT2G04850.1				79.9801	123.006	56.0593	62.3195	35.8142	33.5746
GT	Sense	Sense	-0.376	Detected	0.376	Detected	0.000	-1.206	Detected	-1.932	Detected	-1.569	0.095	GT	Sens	contig318	contig318	Unannota	GGAGGGAATTTTATGTTTTGAAGTGGTCAAATTGAAGAAAATGAGGAGT							contig318	Solyc01g	Sterol 4-a	GO:00080	SL2.40ch	AT1G53035.1		unknown	chr1:197	92.2782	141.697	68.1	92.4695	47.3185	30.1536
GT	Sense	Sense	-0.416	Detected	0.416	Detected	0.000	-1.334	Detected	-2.059	Detected	-1.696	0.092	GT	Sens	contig318	contig318	Unannota	TAATTCAACAAATCTCTTGAGTTATTATGTACTTATAATTGGTGTTTCT							contig318	Solyc01g	Sterol 4-a	GO:00080	SL2.40ch	AT1G53035.1		unknown	chr1:197	45.6133	74.0712	31.73	34.4058	22.0133	14.0376
GT	Sense	Sense	-1.045	Detected	1.045	Detected	0.000	-1.533	Detected	-1.078	Detected	-1.306	0.346	GT	Sens	contig318	contig318	Unannota	AAGTCTACGCACTTACCAATGATCTGCAATTCCTGGAAATGCACAAGCC							contig318	Solyc04g	Pentatric	GO:00037	SL2.40ch	AT3G05240.1		pentatric	chr3:149	16.8419	65.3316	14.5984	18.8142	10.9423	15.8051
GT	Sense	Sense	0.323	Detected	-0.323	Detected	0.000	-1.114	Detected	-1.004	Detected	-1.059	0.084	GT	Sens	contig319	contig319	Unannota	GAGGTAAGAATAAGATTTATATACATTTCATGACCTGCTTATGAAATCAT							contig319	Solyc10g	Linalool s	GO:00340	SL2.40ch	AT5G38850.1		disease r	chr5:155	39.46	23.0001	15.1375	32.478	13.292	15.1144
GT	Sense	Sense	0.109	Detected	-0.109	Detected	0.000	-1.717	Detected	-1.683	Detected	-1.700	0.004	GT	Sens	contig320	contig320	Unannota	CCAAGGCTTCACCAAATTTGAAAGAATTAGAAAATGTTTATGTTACTGG							contig320	Solyc06g	Adaptin e	GO:00055	SL2.40ch	AT5G093	LAC14	LAC14 (la	chr5:290	886.517	694.595	442.511	603.872	227.948	245.86
GT	Sense	Sense	0.046	Detected	-0.046	Detected	0.000	-2.262	Comprom	-1.594	Comprom	-1.928	0.029	GT	Sens	contig321	contig321	Unannota	TGACAAGAAAATACAAAGTCAAGAGGAGGGCTATACAGTCGTTGGAAA							contig321	Solyc12g	Potassiu	GO:00160	SL2.40ch	AT2G32000.2		DNA topo	chr2:136	17.277	14.7722	4.35233	6.06468	3.17911	5.32327
GT	Sense	Sense	-0.134	Detected	0.134	Detected	0.000	-1.339	Detected	-1.780	Detected	-1.560	0.026	GT	Sens	contig321	contig321	Unannota	TACAGTGTCCTTTCTGTTGTTGGGGAAAAATCGAAGATTTCACATGGTA							contig321	Solyc01g065760.1.1				AT4G10540.1		subtilase	chr4:651	164.088	180.094	210.678	231.267	64.8609	50.3474
GT	Sense	Sense	0.408	Detected	-0.408	Detected	0.000	-3.130	Comprom	-4.607	Comprom	-3.868	0.044	GT	Sens	contig322	contig322	Unannota	ATGCTCCATTTGCTACTTACCATAGACACAACTATGATCACCTCCGTTC							contig322	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G432	WRKY49.	WRKY49	chr5:173	69.5417	35.9918	3.22443	1.93578	5.45803	2.06486
GT	Sense	Sense	0.124	Detected	-0.124	Detected	0.000	-2.710	Comprom	-2.729	Comprom	-2.719	0.002	GT	Sens	contig322	contig322	Unannota	CATTTACCTAGAAGATTAGAAGCAACTTTCGAAATCTTCAGGAAATCTG							contig322	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G432	WRKY49.	WRKY49	chr5:173	15.8992	12.2043	2.10193	2.01506	2.03277	2.11424
GT	Sense	Sense	-0.230	Detected	0.230	Detected	0.000	-1.018	Detected	-1.198	Detected	-1.108	0.046	GT	Sens	contig323	contig323	Ycf2 (AHF	AAATAAC	contig323	Solyc01g	Solyc01g	Ycf2 (AHRD V1 *-*- A6YA57_9M			contig323	Solyc01g	Ycf2 (AHRD V1 *-*- A		SL2.40ch	ATCG012	ORF77.2	hypothet	chrC:144	35.3201	44.2648	47.0965	45.0333	18.6433	17.3366
GT	Sense	Sense	-0.332	Detected	0.332	Detected	0.000	-1.263	Detected	-1.342	Detected	-1.302	0.060	GT	Sens	contig324	contig324	Unannota	GCGATGGTGCCTTTTATGCAAGATTTTTTCATACTTGTATTGAAAATCG							contig324	Solyc08g	Genomic DNA chron		SL2.40ch	AT5G486	ATSMC3.	ATSMC3	chr5:197	1680.75	2428.92	1141.39	1493.53	803.774	802.022
GT	Sense	Sense	-0.127	Detected	0.127	Detected	0.000	-1.026	Detected	-1.215	Detected	-1.120	0.019	GT	Sens	contig324	contig324	Unannota	GTCCTGAAATCTATAATTAGTCTACTCTGATTACAGATAGATAACCTAC							contig324	Solyc04g	Ribonucle	GO:00036	SL2.40ch	AT5G432	SPL2	SPL2 (SO	chr5:173	45.0184	48.9537	41.8233	26.327	22.0138	20.3478
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-0.869	Detected	-1.209	Detected	-1.039	0.034	GT	Sens	contig324	contig324	Unannota	AGCCCCCAAGTGCCTTTGCATGGTAGCAGCACTTTCTTTTTTAGTCAAT							contig324	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G40490.1		RNA reco	chr5:162	41.0016	32.7163	17.8322	20.0105	19.1456	15.9391
GT	Sense	Sense	-0.045	Detected	0.045	Detected	0.000	-1.233	Comprom	-3.046	Comprom	-2.140	0.142	GT	Sens	contig324	contig324	Unannota	GGAAGTAAGACTTCCATTTTCTTTTCATCTAAACATTTGTAGAGGATAT							contig324	Solyc04g	Auxin F-box protein		SL2.40ch	AT4G165	ATPRMT7	PRMT7 (I	chr4:933	16.9937	16.5005	9.29953	20.0495	6.80163	2.03929
GT	Sense	Sense	-0.198	Detected	0.198	Detected	0.000	-1.401	Detected	-1.477	Detected	-1.439	0.019	GT	Sens	contig326	contig326	Aspartic	GCTTTT	contig326	Solyc08g	Solyc08g	Aspartic	GO:00065	GO:00065	contig326	Solyc08g	Aspartic	GO:00036	SL2.40ch	AT4G35280.1		zinc fing	chr4:167	1647.98	1976.3	1771.33	2293.81	652.643	652.131
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-1.794	Detected	-0.832	Detected	-1.313	0.114	GT	Sens	contig327	contig327	Unannota	GACACACCAAAGTAGAGAAGTAATAGAGAGTAGAGAGAGTAATCCACA							contig327	Solyc05g	Transposon Ty1-A		SL2.40ch	AT4G13650.1		pentatric	chr4:793	771.492	778.567	285.386	490.969	213.351	437.949
GT	Sense	Sense	-0.389	Detected	0.389	Detected	0.000	-1.275	Detected	-1.203	Detected	-1.239	0.087	GT	Sens	contig327	contig327	Unannota	CTACGAATGAAAGCTATTCTTGACCCACAAATGAGGAAACTTTGCCCTC							contig327	Solyc05g	Transposon Ty1-A		SL2.40ch	AT4G13650.1		pentatric	chr4:793	1729.75	2704.08	1158.51	1277.57	853.331	945.212
GT	Sense	Sense	0.295	Detected	-0.295	Detected	0.000	-1.316	Detected	-1.053	Detected	-1.184	0.067	GT	Sens	contig327	contig327	Unannota	TATATATTGTAGCCTCCAGTAAGAATAAGATGATGTTGGATCTTTGAG							contig327	Solyc02g	Cell divisi	GO:00168	SL2.40ch	AT3G28510.1		AAA-type	chr3:106	2680.59	1623.44	1343.34	1610.32	800.263	1011.76
GT	Sense	Sense	-0.317	Detected	0.317	Detected	0.000	-1.494	Comprom	-1.827	Comprom	-1.660	0.043	GT	Sens	contig327	contig327	Unannota	TTTGATCAACGAAAAAACAGAGACTCACGAAAACGAAGAGGGGATAGGT							contig327	Solyc08g	ORM1-like	GO:00428	SL2.40ch	AT5G42000.1		ORMDL f	chr5:167	16.3287	23.0897	5.65888	4.95374	6.58264	5.50594
GT	Sense	Sense	0.204	Detected	-0.204	Detected	0.000	-1.971	Comprom	-1.892	Comprom	-1.932	0.011	GT	Sens	contig327	contig327	Unannota	TGCCTTCCTGTTTCTAATCAGACACCAGAGCAGAGTCACCTCACAAAGC							contig327	Solyc04g	Early resp	GO:00055	SL2.40ch	AT3G52700.1		unknown	chr3:195	26.0904	17.9166	14.6311	11.8884	5.26417	5.86151
GT	Sense	Sense	-0.221	Detected	0.221	Detected	0.000	-1.299	Detected	-2.086	Detected	-1.693	0.064	GT	Sens	contig328	contig328	Unannota	TTTCTGCAACATTGAAGTCGTAATTTATAGTCATCAACAATATATATAT							contig328	Solyc12g	Translatio	GO:00422	SL2.40ch	AT5G101	AST68. S	AST68: s	chr5:319	90.1248	111.655	52.3481	101.749	38.9134	23.7701
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	-0.961	Detected	-1.728	Detected	-1.345	0.075	GT	Sens	contig328	contig328	Unannota	AAGAAGAAATTCCAATAACATTTGAACAGGCCCAAACAATTTTGGGTCA							contig328	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G30640.1		protein k	chr1:108	682.108	692.709	346.104	541.16	337.04	208.76
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.049	Detected	-1.466	Detected	-1.257	0.027	GT	Sens	contig328	contig328	Unannota	GGACAGGTCATTGAATTTGGAATTTGGGCTAAAAGCACAAGTTCAATAT							contig328	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G30640.1		protein k	chr1:108	1394.26	1244.29	699.035	1060.8	607.771	479.671
GT	Sense	Sense	0.184	Detected	-0.184	Detected	0.000	-1.310	Detected	-1.007	Detected	-1.158	0.040	GT	Sens	contig328	contig328	High mob	AATCTAT	contig328	Solyc12g	Solyc12g	High mob	GO:00050	GO:00050	contig328	Solyc12g	High mob	GO:00050	SL2.40ch	AT1G76110.1		high mob	chr1:285	56.5313	39.9545	64.0232	38.722	18.3009	23.7911
GT	Sense	Sense	-0.293	Detected	0.293	Detected	0.000	-1.145	Detected	-1.443	Detected	-1.294	0.059	GT	Sens	contig328	contig328	Unannota	GCGAAAATTAAACAAATGCTAGAACAGACGACTATTGCTTCCTGATTTT							contig328	Solyc07g	LanC-like	GO:00104	SL2.40ch	AT1G15510.1		pentatric	chr1:532	104.95	143.573	84.3573	133.895	53.0078	45.4285
GT	Sense	Sense	-0.212	Detected	0.212	Detected	0.000	-3.436	Comprom	-2.598	Comprom	-3.017	0.023	GT	Sens	contig328	contig328	Unannota	TTGTGTTTCAATTATATATGTATGCCTTTTTTAATTAAGAATAAAAGAA							contig328	Solyc01g	Legumin-	GO:00082	SL2.40ch	AT4G39753.1				33.515	41.0107	20.1879	56.9949	3.27024	6.16167
GT	Sense	Sense	-0.149	Detected	0.149	Detected	0.000	-1.258	Detected	-1.483	Detected	-1.371	0.018	GT	Sens	contig329	contig329	Unannota	CGATAATATGAATTTTCACTGATCATATCGATTCGGATAATCTCATATA							contig329	Solyc09g	Unknown	GO:00055	SL2.40ch	AT1G15040.2		glutamin	chr1:518	51.7944	58.0685	29.2926	50.6832	21.8918	19.7317
GT	Sense	Sense	0.153	Detected	-0.153	Detected	0.000	-0.930	Detected	-2.021	Comprom	-1.476	0.121	GT	Sens	contig329	contig329	Unannota	GGTGGAAAATAAGAGAAAGAACTGTACATCATCTGAAATCTTCTGTAC							contig329	Solyc09g	Unknown	GO:00055	SL2.40ch	AT1G15040.2		glutamin	chr1:518	23.2506	17.157	16.1871	16.6822	10.0111	4.94945
GT	Sense	Sense	-0.022	Detected	0.022	Detected	0.000	-1.133	Detected	-1.583	Detected	-1.358	0.027	GT	Sens	contig329	contig329	Unannota	GGCTTTAGTGATGTAGCTTCTGCTTTTTAGACTTTTAGCAGTAGTATAC							contig329	Solyc01g011270.1.1				AT4G08910.1				641.386	602.923	746.135	1428.66	270.694	208.872
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-1.246	Detected	-1.505	Detected	-1.375	0.010	GT	Sens	contig329	contig329	Unannota	TTTTAGCAAAGACTTTTCCTCCATTTTCTACCTATCCATTATTTTTTTAC							contig329	Solyc01g011270.1.1				AT4G08910.1				391.487	377.005	474.543	857.895	154.642	136.187
GT	Sense	Sense	-0.683	Detected	0.683	Detected	0.000	-1.598	Comprom	-1.868	Comprom	-1.733	0.131	GT	Sens	contig329	contig329	Unannota	GCAAGGGCATGGATAGTTTCTCACTACTCTACATTTTATGCATTTTCA							contig329	Solyc11g	Unknown Protein (A		SL2.40ch	AT1G05370.1		FUNCTIO	chr1:156	15.617	36.716	14.828	11.7272	7.5502	6.60044
GT	Sense	Sense	-0.521	Detected	0.521	Detected	0.000	-1.370	Detected	-1.565	Detected	-1.468	0.109	GT	Sens	contig329	contig329	Unannota	GGGTAATGTATGGCCATTTGGAATTTTGAGAACAAAATCTTGATGGGG							contig329	Solyc11g	Unknown Protein (A		SL2.40ch	AT1G05370.1		FUNCTIO	chr1:156	46.2501	86.7811	39.4638	37.8079	23.3993	21.5404
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-0.845	Detected	-2.194	Comprom	-1.519	0.153	GT	Sens	contig329	contig329	Unannota	ATCTCATCTATTGTACAAGCAAAACTGTTCTCTGTACATTAGGTCTACA							contig329	Solyc12g	Photosys	GO:00160	SL2.40ch	AT1G069	ATTIC110	TIC110 (I	chr1:213	17.1787	16.8293	8.08044	15.0958	9.18132	3.79568
GT	Sense	Sense	-0.283	Detected	0.283	Detected	0.000	-2.089	Detected	-2.409	Detected	-2.249	0.020	GT	Sens	contig330	contig330	Unannota	AATTGATGTATTGAACTTTTTCATTTTTACAAAATCGTCTGAATTTGTT							contig330	Solyc11g	Flowering	GO:00084	SL2.40ch	AT3G19080.1				239.761	323.465	132.929	251.679	62.5166	52.7421

GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-1.211	Comprom	-1.861	Comprom	-1.536	0.042	GT	Sens	contig345	contig345	Unannota	ACAACCTTTTTGCCAAAAATCGTCCCATTCTAGAACAGGATTAGGAGAA	contig345	Solvc04g	Unknown Protein (A		SL2.40ch	AT4G14490.1		forkhead	chr4:833	12.3399	11.8892	3.22665	8.23941	4.9942	3.35445
GT	Sense	Sense	0.612	Detected	-0.612	Detected	0.000	-2.808	Comprom	-2.180	Comprom	-2.494	0.068	GT	Sens	contig345	contig345	Unknown	AATCAG(contig345 Solvc05g Solvc05g Unknown Protein (AHRD V1)	contig345	Solvc05g	Unknown Protein (A		SL2.40ch	AT5G46920.1		intron ma	chr5:190	28.5609	11.141	11.4795	16.0932	2.4319	3.96035
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-0.978	Comprom	-1.329	Comprom	-1.154	0.024	GT	Sens	contig347	contig347	Unannota	GGCATAGAGCACATAACATTGTGTCAGTTAATGTTACTGTTTATTTTGT	contig347	Solvc06g	N-(5&apo	GO:0008	SL2.40ch	AT3G07810.1				14.1608	13.7934	4.61076	10.1951	6.77323	5.5969
GT	Sense	Sense	-0.133	Detected	0.133	Detected	0.000	-1.217	Detected	-2.725	Detected	-1.971	0.124	GT	Sens	contig347	contig347	Unannota	TTTTTTGGGGTGTTGTCTTTGTAATTTTGAGGAAATTTTATTTGTGTGT	contig347	Solvc01g	Gibberelli	GO:0005	SL2.40ch	AT1G161	WAKL2	WAKL2 (	chr1:552	45861.7	50283.2	50675.3	45264	19721.1	7305.09
GT	Sense	Sense	-0.261	Detected	0.261	Detected	0.000	-1.534	Detected	-3.194	Detected	-2.364	0.113	GT	Sens	contig347	contig347	Unannota	TCTGGTGTAATATTTATTCTGGTTTGCATTGTATTGTATAATAAGATGA	contig347	Solvc01g	Gibberelli	GO:0005	SL2.40ch	AT1G161	WAKL2	WAKL2 (	chr1:552	29882.6	39146.1	28662.1	28032.9	11273.8	3758.46
GT	Sense	Sense	-0.652	Detected	0.652	Detected	0.000	-2.333	Comprom	-2.661	Comprom	-2.497	0.065	GT	Sens	contig348	contig348	Unannota	CAGATGGTTACTGAGAGTGCCTTCGGTACAAAATACAAAATTTATCCTC	contig348	Solvc11g	Pto-like. S	GO:0004	SL2.40ch	AT1G773	MEI1	MEI1 (me	chr1:290	12.5718	28.2934	3.36713	8.6287	3.5738	3.00058
GT	Sense	Sense	0.032	Detected	-0.032	Detected	0.000	-1.902	Comprom	-1.543	Comprom	-1.723	0.011	GT	Sens	contig349	contig349	Unannota	ACATCTAGTAAGTTTCCAAAAGATAATGCTTAGGCTAGTTCAATATAAT	contig349	Solvc09g	WRKY-like	GO:0005	SL2.40ch	AT1G05805.1		basic hel	chr1:174	21.8302	19.0358	5.92057	13.9196	5.2069	7.03546
GT	Sense	Sense	-0.133	Detected	0.133	Detected	0.000	-0.980	Detected	-2.059	Comprom	-1.519	0.112	GT	Sens	contig349	contig349	class I he	CCTCAA(contig349 Solvc12g Solvc12g class I heat shock protein (AH	contig349	Solvc12g	class I heat shock p		SL2.40ch	AT5G41020.1		mvb fami	chr5:164	20.6542	22.6314	10.9307	22.8603	10.4658	5.22008
GT	Sense	Sense	-0.078	Detected	0.078	Detected	0.000	-2.403	Comprom	-1.096	Comprom	-1.750	0.117	GT	Sens	contig350	contig350	Unannota	CTTCTTGAGATAATAACTATTTAGCAAAGTGACCATATGAGAAATCAAT	contig350	Solvc02g	Aldehyde	GO:0004	SL2.40ch	AT1G238	ALDH2B7	ALDH2B7	chr1:841	12.9991	13.2028	5.6835	11.8848	2.36526	6.16341
GT	Sense	Sense	-0.474	Detected	0.474	Detected	0.000	-0.928	Detected	-1.465	Detected	-1.196	0.159	GT	Sens	contig351	contig351	Unannota	ACAACAAATAAAGAATTTTGTTGTAATAATTTACCGGGTAGTATAACTG	contig351	Solvc03g	Zinc trans	GO:0016	SL2.40ch	AT4G09770.1		meprin a	chr4:615	746.581	1313.54	590.065	655.787	497.102	360.787
GT	Sense	Sense	0.059	Detected	-0.059	Detected	0.000	-2.847	Comprom	-1.944	Comprom	-2.396	0.034	GT	Sens	contig352	contig352	Unannota	AGCGAGGAATAACCAACCTTTTGCTATTTTTCTCACATTTCCTTCATGT	contig352	Solvc09g	HAT famil	GO:0046	SL2.40ch	AT4G311	DCAF1	DCAF1 (D	chr4:151	16.0543	13.4924	4.53089	19.3656	1.95254	3.84677
GT	Sense	Sense	-0.316	Detected	0.316	Detected	0.000	-1.055	Detected	-1.988	Detected	-1.521	0.114	GT	Sens	contig352	contig352	Unannota	CTCCTCTTTTTGAGAACAATAGTTCGTTTTAAGTATGACTTGATAGTGG	contig352	Solvc02g	Malonyl-CoA decarb		SL2.40ch	AT3G17010.1				42.5147	60.0375	32.6845	43.7587	23.2227	12.8123
GT	Sense	Sense	-0.274	Detected	0.274	Detected	0.000	-0.915	Detected	-1.927	Detected	-1.421	0.132	GT	Sens	contig352	contig352	Unannota	GTACACCATTCGAGCTGAACAGAAGTCTAAACACACCGACAACAAAAAA	contig352	Solvc04g	Cellular retinaldehy		SL2.40ch	AT5G11160.1				71.224	94.9264	67.9748	34.7526	41.6401	21.756
GT	Sense	Sense	0.330	Detected	-0.330	Detected	0.000	-0.974	Detected	-1.947	Comprom	-1.460	0.131	GT	Sens	contig352	contig352	Unannota	GGCAAAGCATCCATCTTCCGTGTGACTTTCGACCTCCCAAATATTAACA	contig352	Solvc04g	Cellular retinaldehy		SL2.40ch	AT5G11160.1				29.7663	17.1782	12.9771	7.03589	10.9938	5.9017
GT	Sense	Sense	-0.174	Detected	0.174	Detected	0.000	-0.976	Detected	-1.047	Detected	-1.011	0.029	GT	Sens	contig352	contig352	Unannota	TGTGTGTTTGATTTTCAGGTTTGATTTAAATTGATTGATTTAAGGAACG	contig352	Solvc12g	Arf GTPa	GO:0005	SL2.40ch	AT5G43950.1		unknowr	chr5:176	32.2532	37.415	34.3381	51.2642	16.8624	16.9167
GT	Sense	Sense	-0.501	Detected	0.501	Detected	0.000	-1.356	Detected	-1.280	Detected	-1.318	0.120	GT	Sens	contig353	contig353	Unannota	ACAGGTTAGATTCCGTTAGCACCATTTCTTGAAATTGCTTATTCTTTAT	contig353	Solvc08g	BHLH trai	GO:0030	SL2.40ch	AT3G52700.1		unknowr	chr3:195	24.7119	45.0946	14.1485	31.9807	12.4482	13.8273
GT	Sense	Sense	-0.332	Detected	0.332	Detected	0.000	-1.081	Comprom	-1.166	Comprom	-1.124	0.078	GT	Sens	contig353	contig353	Unannota	GCCCCCGAAGAGAAGAGATATCTAAAAAAGTTAAAACCTTCATTGCTAC	contig353	Solvc08g	BHLH trai	GO:0030	SL2.40ch	AT3G52700.1		unknowr	chr3:195	12.7684	18.4491	5.66485	15.5879	6.92487	6.88169
GT	Sense	Sense	-0.007	Detected	0.007	Detected	0.000	-1.679	Comprom	-1.024	Detected	-1.352	0.054	GT	Sens	contig354	contig354	Unannota	TCGTAAGTTGCTCTGGTGGTTATTACAATATGATTAAAATTCTGGGAAG	contig354	Solvc05g	Protein re	GO:0003	SL2.40ch	AT1G02440.1				30.6485	28.2074	14.1457	24.1534	8.76485	14.549
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	-1.115	Comprom	-1.558	Comprom	-1.336	0.027	GT	Sens	contig355	contig355	Unannota	TACAGAAGAATACAAGTAAGAAAGAATAACATGGCTGGGGTCCTCAAAC	contig355	Solvc02g	Unknown Protein (A		SL2.40ch	AT3G02930.1		unknowr	chr3:655	11.8759	11.4819	4.97635	5.90091	5.14901	3.99081
GT	Sense	Sense	0.908	Detected	-0.908	Detected	0.000	-1.868	Comprom	-2.447	Comprom	-2.157	0.152	GT	Sens	contig355	contig355	Unannota	AACAATTTTCATAGTTTTCATGGGTTTCACTTCCCTGCGCTTCGTCTAC	contig355	Solvc03g	DNA excis	GO:0017	SL2.40ch	AT4G14180.1				48.4513	12.5419	3.21265	8.01941	6.4475	4.5486
GT	Sense	Sense	0.424	Detected	-0.424	Detected	0.000	-1.487	Detected	-1.214	Detected	-1.350	0.094	GT	Sens	contig355	contig355	Unannota	CTTGCGCCCCCTTGTGTGACTGATCATCGTCTCAGACCAGTTACAGAT	contig355	Solvc00g	Unknown Protein (A		SL2.40ch	AT4G04570.2		protein k	chr4:229	180.091	91.19	125.396	123.434	43.6617	55.5726
GT	Sense	Sense	-0.531	Detected	0.531	Detected	0.000	-2.931	Detected	-4.528	Detected	-3.730	0.060	GT	Sens	contig356	contig356	Unknown	TTTGGG, contig356 Solvc08g Solvc08g Unknown Protein (AHRD V1)%:	contig356	Solvc08g	Unknown Protein (A		SL2.40ch	AT5G16520.1		unknowr	chr5:539	192.231	365.653	164.85	593.912	33.2	11.5574
GT	Sense	Sense	-0.286	Detected	0.286	Detected	0.000	-1.387	Comprom	-0.903	Comprom	-1.145	0.092	GT	Sens	contig356	contig356	Unannota	CACAGAACTCAGTGTACAATCAATGATGATCAATACAAGTATCACTCTC	contig356	Solvc04g	5&apos-3	GO:0004	SL2.40ch	AT3G27906.1				11.2376	15.2211	7.88051	13.7722	4.77595	7.03479
GT	Sense	Sense	-0.055	Detected	0.055	Detected	0.000	-0.998	Detected	-1.216	Detected	-1.107	0.012	GT	Sens	contig357	contig357	Os05g02	TGACCC contig357 Solvc04g Solvc04g Os05g0235100 protein (Fragm	contig357	Solvc04g	Os05g0235100 prot		SL2.40ch	AT4G35040.1				59.2467	58.266	29.2318	40.0455	28.0932	25.4454
GT	Sense	Sense	-0.640	Detected	0.640	Detected	0.000	-0.843	Detected	-1.216	Detected	-1.029	0.263	GT	Sens	contig357	contig357	Unannota	GTAGAGAGAGTTCAATGATGTCATATGCTAGATTGGAAGGCATTCTAC	contig357	Solvc02g	Proteaso	GO:0019	SL2.40ch	AT5G541	ILL3	ILL3: IAA	chr5:219	42.4974	94.1446	48.996	42.3091	33.6777	27.3977
GT	Sense	Sense	-0.243	Detected	0.243	Detected	0.000	-1.095	Comprom	-1.134	Comprom	-1.115	0.045	GT	Sens	contig357	contig357	Unknown	TTTGCC contig357 Solvc11g Solvc11g Unknown Protein (AHRD V1)	contig357	Solvc11g	Unknown Protein (A		SL2.40ch	AT5G57670.2		protein k	chr5:233	11.1791	14.2835	10.0304	14.302	5.6478	5.79206
GT	Sense	Sense	-0.002	Detected	0.002	Detected	0.000	-0.802	Comprom	-1.617	Comprom	-1.209	0.097	GT	Sens	contig357	contig357	Unannota	AAGAGCACATACAGGCCATCCACAAGAAGGTCTTCTGTTCTGCATTTAT	contig357	Solvc07g	RING-H2 f	GO:0008	SL2.40ch	AT2G18938.1				12.6243	11.5391	3.28048	6.9953	6.60908	3.95916

GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-2.208	Detected	-1.370	Detected	-1.789	0.051	GT	Sens	contig419	contig419	Unannota	TAAAAAGAGTACCAAGTGTTTGACATTTAATTTAATGTTATTGTCTACT							contig419	Solyc02g	Protectio	GO:0000	SL2.40ch	AT5G43570.1		serine-ty	chr5:175	56.9005	55.4694	25.0846	43.339	11.6081	21.8681
GT	Sense	Sense	-0.111	Detected	0.111	Detected	0.000	-1.313	Comprom	-0.946	Comprom	-1.129	0.034	GT	Sens	contig419	contig419	Unannota	AGGCAGTTAACTTGTGTTATATGGCACTAGGAAGAAGGGAAGACGAAC							contig419	Solyc09g	Cysteine-	GO:0030	SL2.40ch	AT5G56200.1		zinc fing	chr5:227	13.6905	14.565	4.24722	5.30331	5.42577	7.37529
GT	Sense	Sense	-0.019	Detected	0.019	Detected	0.000	-1.460	Detected	-1.620	Detected	-1.540	0.003	GT	Sens	contig420	contig420	Unannota	GAGCTAGCTTTTGGGGTTGAGTTACGTTAGACTGGATGTCATATCTTG							contig420	Solyc07g	Carboxyl-	GO:0005	SL2.40ch	AT5G42320.1		metalloca	chr5:169	199.455	186.718	94.4295	193.914	66.9585	63.1809
GT	Sense	Sense	-0.118	Detected	0.118	Detected	0.000	-1.428	Comprom	-1.182	Comprom	-1.305	0.017	GT	Sens	contig421	contig421	Unannota	TGTCATTCCACTATACACCATTACATGAAACACTTATTTGCTCCTACTC							contig421	Solyc12g	F-box family protein		SL2.40ch	AT4G123	CYP706A	CYP706A	chr4:731	12.8859	13.8288	8.69758	12.3288	4.73563	5.91965
GT	Sense	Sense	-0.729	Detected	0.729	Detected	0.000	-2.151	Detected	-5.740	Comprom	-3.945	0.179	GT	Sens	contig421	contig421	Unannota	GCATATTAATTGAATCCGAGTCCTTTTCCTCTTATTAATTAAACCTGGC							contig421	Solyc07g	Protein ki	GO:0005	SL2.40ch	AT3G27680.1				64.6123	161.875	37.6984	76.8781	21.9933	1.9252
GT	Sense	Sense	-0.261	Detected	0.261	Detected	0.000	-1.657	Comprom	-1.923	Comprom	-1.790	0.026	GT	Sens	contig421	contig421	Unannota	TAAGCATAAGGTATACTAATTGACTACGAGTGTAATAAGAGCATCAGTC							contig421	Solyc09g	Ycf2 (AHF	GO:0009	SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:145	30.9695	40.5619	33.6149	38.3452	10.7291	9.40342
GT	Sense	Sense	-0.190	Detected	0.190	Detected	0.000	-0.856	Detected	-1.262	Detected	-1.059	0.063	GT	Sens	contig421	contig421	Unannota	TCATTTTCGAAGTCAATTTGAGGTTAGATCTATGTGATACAAGCGGGG							contig421	Solyc04g	Mutator-li	GO:0008	SL2.40ch	AT5G081	MIR162A	MIR162A	chr5:263	218.736	259.569	129.339	187.598	125.721	99.9175
GT	Sense	Sense	0.788	Detected	-0.788	Detected	0.000	-1.764	Detected	-1.270	Detected	-1.517	0.208	GT	Sens	contig422	contig422	Unannota	TATAACGAGATCAAGTCCCCCATCCTACCACCATATAGGACAACAATAT							contig422	Solyc06g	NAC dom	GO:0045	SL2.40ch	AT5G465	PGP7	PGP7 (P-	chr5:188	180.224	55.1248	45.7029	52.941	28.0154	41.5815
GT	Sense	Sense	0.114	Detected	-0.114	Detected	0.000	-0.940	Detected	-2.100	Detected	-1.520	0.124	GT	Sens	contig422	contig422	Unannota	CACGATCTGAATATTTCAGGGCATATAATCCTTGTGCTTTCCAAATTAC							contig422	Solyc05g	Dof zinc f	GO:0005	SL2.40ch	AT5G10650.2				94.4723	73.5224	38.2183	98.0688	41.4682	19.5609
GT	Sense	Sense	0.088	Detected	-0.088	Detected	0.000	-1.126	Comprom	-1.082	Comprom	-1.104	0.007	GT	Sens	contig422	contig422	Unannota	GCTAGCGAATGAATGTTGCAGGTCCAAAACAGTTCTGAATTTGGTCAG							contig422	Solyc02g	Unknown Protein (A		SL2.40ch	AT3G465	RPP13	RPP13 (F	chr3:171	16.719	13.491	11.1754	13.5283	6.57155	7.13903
GT	Sense	Sense	-0.067	Detected	0.067	Detected	0.000	-1.183	Detected	-1.612	Detected	-1.398	0.025	GT	Sens	contig422	contig422	Unannota	GTTAGACAATAGCATGGAACAATAGATTTAGTTGTTGGATGGGTTTAG							contig422	Solyc08g	Neurochondrin fami		SL2.40ch	AT5G04050.2		FUNCTIO	chr5:109	33.3343	33.3264	15.8504	26.8932	14.0151	10.9699
GT	Sense	Sense	-0.202	Detected	0.202	Detected	0.000	-0.988	Detected	-1.415	Detected	-1.201	0.055	GT	Sens	contig422	contig422	Unannota	CTCGATTAGCGACAGATCATCTATGGACAAACACATATGTTATGTGGC							contig422	Solyc08g	Neurochondrin fami		SL2.40ch	AT5G04050.2		FUNCTIO	chr5:109	80.8741	97.5982	45.5739	80.681	42.773	33.5241
GT	Sense	Sense	-0.819	Detected	0.819	Detected	0.000	-1.008	Detected	-1.992	Detected	-1.500	0.257	GT	Sens	contig423	contig423	Unannota	CAAATCTTGATAAAAACCTAATCTCTTTTTAATGATGATGCCTTGGTAA							contig423	Solyc11g045300.1.1				AT1G75530.1		forkhead	chr1:283	211.178	599.582	188.59	116.525	168.943	89.9952
GT	Sense	Sense	-0.168	Detected	0.168	Detected	0.000	-0.850	Comprom	-1.219	Comprom	-1.035	0.054	GT	Sens	contig423	contig423	Unannota	ATGAAGAAACAGGTGTCCTAAGGGAAGCCCCTGGAAGAGAATGAGAAT							contig423	Solyc04g	MYB tran	GO:0003	SL2.40ch	AT4G081	KNAT1, B	KNAT1 (h	chr4:514	14.3115	16.4655	5.94241	13.4525	8.13061	6.63257
GT	Sense	Sense	-0.364	Detected	0.364	Detected	0.000	-1.586	Comprom	-1.058	Comprom	-1.322	0.099	GT	Sens	contig424	contig424	Cyclin-de	GCGGAA	contig424	Solyc01g	Solyc01g	Cyclin-de	GO:0005	GO:0005	contig424	Solyc01g	Cyclin-de	GO:0005	SL2.40ch	AT1G496	KRP7, ICI	ICK5: cy	chr1:183	11.6033	17.515	4.07231	13.4899	4.53393	6.88717
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	-1.063	Detected	-1.150	Detected	-1.106	0.017	GT	Sens	contig425	contig425	Unannota	GATGATTTAGTTGATCACTCCATTTGGGTACACTGAAGCTCTTAAACTC							contig425	Solyc11g	Cc-nbs-lr	GO:0005	SL2.40ch	AT5G452	RPS4	RPS4 (RE	chr5:183	1972.23	2178.95	2189.94	3046.87	947.484	939.633
GT	Sense	Sense	-0.100	Detected	0.100	Detected	0.000	-1.097	Detected	-1.480	Detected	-1.289	0.027	GT	Sens	contig425	contig425	Unannota	GAAGTCATTAGATTCCCCATTAACAAGTACAAAGTACCAATTATTTGAT							contig425	Solyc11g	Cc-nbs-lr	GO:0005	SL2.40ch	AT5G452	RPS4	RPS4 (RE	chr5:183	206.606	216.272	205.667	304.816	94.327	76.2285
GT	Sense	Sense	0.834	Detected	-0.834	Detected	0.000	-1.445	Detected	-1.351	Detected	-1.398	0.236	GT	Sens	contig425	contig425	Unannota	TCGCCTTAGGGGCCGACTAACCCTGCGCAGATTAGCTTTACGCAGGAA							contig425	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G10990.1				84.6012	24.2657	19.7318	24.5977	15.8917	17.8628
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	-1.437	Detected	-1.072	Detected	-1.254	0.031	GT	Sens	contig427	contig427	Histone H	GGTGTTGAAGCAGGTTCATCCAGAATTCTTAGATTTAGATTTGTTTGTT							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1016.39	1111.78	732.854	987.373	374.899	508.762
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.198	Detected	-2.320	Detected	-1.759	0.089	GT	Sens	contig427	contig427	F22L4.5 p	AAAGAAAGGCCTTGAAGACAGTTTCCGCTCTAACAGGGATTGATGAGA							contig427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	130.3	112.234	58.117	85.605	50.3105	24.3626
GT	Sense	Sense	-0.073	Detected	0.073	Detected	0.000	-1.038	Detected	-1.176	Detected	-1.107	0.008	GT	Sens	contig428	contig428	Putative (	CACCCAGTCAGCTATCCCTTAATTTTTACTGAATTTTCATATCTATTGA							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	32.1516	32.4191	15.4521	34.9338	15.0078	14.3737
GT	Sense	Sense	-0.100	Detected	0.100	Detected	0.000	-0.878	Detected	-1.767	Detected	-1.322	0.101	GT	Sens	contig428	contig428	Calcium-t	TGTGTTCACTGCAAAAGCCATAGCAACAGAATGTGGAATTCTTCATCCT							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	43.4897	45.565	14.4545	57.7405	23.1347	13.1545
GT	Sense	Sense	0.064	Detected	-0.064	Detected	0.000	-1.164	Detected	-1.355	Detected	-1.260	0.008	GT	Sens	contig428	contig428	At5g5949	GAAGACAGCTACAAGGGAGTTTCGGAGCCAAAATATGAGTGCCTTCTG							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	249.073	207.845	177.598	195.044	96.9451	89.4518
GT	Sense	Sense	0.174	Detected	-0.174	Detected	0.000	-1.552	Detected	-4.064	Detected	-2.808	0.157	GT	Sens	contig428	contig428	Peroxida	TGAGTGGAGGATCTACCGATGATATTGTTTTAGAATATAGCAATAGCCC							contig428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	10931.3	7830.54	6378.05	10145.6	3011.61	556.651
GT	Sense	Sense	-0.488	Detected	0.488	Detected	0.000	-0.897	Detected	-1.781	Detected	-1.339	0.179	GT	Sens	contig429	contig429	Calcium-t	TTCATGGGAATCATCGGAATAACATTGGTTCTCCAAGTGGTGATGGTG							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1336.14	2396.77	795.807	2134.51	917.727	523.721
GT	Sense	Sense	-0.105	Detected	0.105	Detected	0.000	-1.296	Comprom	-1.253	Comprom	-1.275	0.007	GT	Sens	contig429	contig429	AT3G208	GGCTTAGCTCTGTAGCTAAATGACAGATACAAGAGCTACAACAAGATAT							contig429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	14.5627	15.3583	3.90647	13.5126	5.81539	6.31108
GT	Sense	Sense	-0.082	Detected	0.082	Detected	0.000	-1.748	Detected	-2.185	Detected	-1.966	0.014	GT	Sens	contig430	contig430	Unknown	CCTTTGGAGGCCAATGGCAGATCTGTTAATTTTGAGGAAACTAGGTGC							contig430	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	16992.3	17353.9	10115.6	13828	4882.29	3799.14
GT	Sense	Sense	-0.415	Detected	0.415	Detected	0.000	-1.079	Detected	-1.204	Detected	-1.141	0.113	GT	Sens	contig431	contig431	N.tabacum	GCAGTTCAACTCTGGAGTTACCAGAGATATCAGTATCTACTATAATAAA							contig431	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1203.55	1949.32	1069.18	1966.95	692.078	669.077
GT	Sense	Sense	-0.343	Detected	0.343	Detected	0.000	-1.833	Detected	-2.908	Detected	-2.370	0.065	GT	Sens	contig432	contig432	Nicotia ta	ACCTTAAATGCTAAACCTAAGTGGTTACAGCTACTAGTGTGTGTTTTCT							contig432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	59643.2	87496.3	47796	52019.2	19363.8	9682.94
GT	Sense	Sense	-0.887	Detected	0.887	Detected	0.000	-0.809	Detected	-1.817	Detected	-1.313	0.327	GT	Sens	contig432	contig432	Nicotia ta	TAATCTAGAGCAAATTGAGTTTCCCCTCAAGTAACTTCATGGTGCAGAA							contig432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	22.3499	69.6678	34.2852	22.0485	21.5016	11.2686
GT	Sense	Sense	-0.987	Detected	0.987	Detected	0.000	-1.360	Detected	-2.072	Detected	-1.716	0.244	GT	Sens	contig432	contig432	Nicotia ta	CAGTGTTGGTCTTGTTAGATGTTTTAAGGCTTTTATTCTTGTCCTTAGG							contig432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	3489.73	12498.4	2515.08	3667.73	2457.08	1579.8
GT	Sense	Sense	0.259	Detected	-0.259	Detected	0.000	-3.112	Comprom	-2.068	Detected	-2.590	0.047	GT	Sens	contig433	contig433	Nicotia ta	AACTCAAAACTGTTTGTAAACAAATCATAGAACAAAAGAACAATAAGGAT							contig433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	73.2475	46.6061	38.9618	24.3552	6.45457	14.0136
GT	Sense	Sense	0.026	Detected	-0.026	Detected	0.000	-0.826	Comprom	-1.789	Comprom	-1.308	0.113	GT	Sens	contig433	contig433	Nicotia ta	TGGCTTCAAAAGCTAGCAATTCATATGTGTGGTCGGAAGGACAGCTTCC							contig433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	14.704	12.9364	6.11283	13.4368	7.4275	4.01458
GT	Sense	Sense	-0.509	Detected	0.509	Detected	0.000	-1.245	Detected	-1.108	Detected	-1.177	0.149	GT	Sens	contig433	contig433	Nicotia ta	GTTATATAAAATACATCTTCTAATCATTGTAAAAAGGCTATGCCTTGTTT							contig433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	16113.5	29736.3	13574.2	21228.6	8816.22	10214.5
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-1.362	Detected	-1.290	Detected	-1.326	0.001	GT	Sens	contig433	contig433	Nicotia ta	TCACATCGCCAAGTGTAAAAGGGGGCTTCGAAGATGGAACTCTTTGGA							contig433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	36.2686	32.4232	27.2437	55.0158	12.7361	14.1068
GT	Sense	Sense	-0.296	Detected	0.296	Detected	0.000	-1.033	Detected	-1.275	Detected	-1.154	0.069	GT	Sens	contig434	contig434	Nicotiana	CTACAG	contig434	Solyc01g	Solyc01g	Nicotiana	GO:0030	GO:0030	contig434	Solyc01g	Nicotiana	GO:0030	SL2.40ch	AT5G560	ATNAS2,	NAS2 (NI	chr5:227	387.033	531.945	305.796	270.602	211.749	188.684
GT	Sense	Sense	-0.348	Detected	0.348	Detected	0.000	-1.317	Detected	-1.290	Detected	-1.303	0.065	GT	Sens	contig434	contig434	NTU7432	CTAGTATTTACTAGATTTCACACAAATAAAACTAACTTCGCATATTGCG							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	382.507	564.952	276.436	472.011	178.199	191.287
GT	Sense	Sense	-0.028	Detected	0.028	Detected	0.000	-1.313	Detected	-0.826	Detected	-1.069	0.049	GT	Sens	contig434	contig434	N.tabacum	AAATGATGTGATTATTTAATAACTTGGATTAATTAGAAGAATGATCATG							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	5019.72	4756.49	3035.87	4384.03	1878.22	2772.26
GT	Sense	Sense	-0.365	Detected	0.365	Detected	0.000	-1.142	Detected	-1.071	Detected	-1.106	0.094	GT	Sens	contig434	contig434	N.tabacum	TTGAAATTGTTTGTTCTTTTGGTCATAGTGTAAGTTCTGCTTTTACTTT							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	746.241	1128	535.709	964.993	397.037	439.295
GT	Sense	Sense	0.102	Detected	-0.102	Detected	0.000	-1.119	Detected	-1.122	Detected	-1.120	0.008	GT	Sens	contig442	contig442	Adenylate	TATAGG	contig442	Solyc02g	Solyc02g	Adenylate	GO:0006	GO:0006	contig442	Solyc02g	Adenylate	GO:0006	SL2.40ch	AT5G623	VND6, AN	ANAC101	chr5:250	183.893	145.526	120.144	167.94	71.9162	75.6356
GT	Sense	Sense	-0.119	Detected	0.119	Detected	0.000	-1.095	Comprom	-1.049	Comprom	-1.072	0.013	GT	Sens	contig448	contig448	Unknown	GAAAAT	contig448	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig448	Solyc10g	Cell divisi	GO:0006	SL2.40ch	AT5G19855.1				16.912	18.1768	14.0484	13.9486	7.83554	8.52693
GT	Sense	Sense	-0.304	Detected	0.304	Detected	0.000	-1.232	Detected	-1.649	Detected	-1.441	0.060	GT	Sens	contig450	contig450	Glucan 1	GGATTA	contig450	Solyc12g	Solyc12g	Glucan 1	GO:0005	GO:0005	contig450	Solyc12g	Glucan 1	GO:0005	SL2.40ch	AT1G178	ATEGY3,	EGY3 (ET	chr1:615	6096.64	8475.72	5990.15	5891.18	2921.42	2305.88
GT	Sense	Sense	-0.375	Detected	0.375	Detected	0.000	-2.202	Detected	-1.879	Detected	-2.041	0.038	GT	Sens	contig450	contig450	WRKY tra	CAAAAT	contig450	Solyc08g	Solyc08g	WRKY tra	GO:0045449		contig450	Solyc08g	WRKY tra	GO:0045	SL2.40ch	AT5G528	WRKY27,	WRKY27	chr5:214	41.1001	62.9814	11.3712	31.6682	10.5561	13.9142
GT	Sense	Sense	-0.301	Detected	0.301	Detected	0.000	-1.562	Detected	-1.992	Detected	-1.777	0.041	GT	Sens	contig456	contig456	Dienelact	TAAATG	contig456	Solyc01g	Solyc01g	Dienelact	GO:0005	GO:0005	contig456	Solyc01g	Dienelact	GO:0005	SL2.40ch	AT5G45160.1		root hair	chr5:182	865.343	1198.16	679.192	714.706	329.382	257.441
GT	Sense	Sense	-0.398	Detected	0.398	Detected	0.000	-0.841	Detected	-1.279	Detected	-1.060	0.145	GT	Sens	contig462	contig462	Unknown	GGCTGG	contig462	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)%:			contig462	Solyc08g	Unknown Protein (A		SL2.40ch	AT1G62500.1		protease	chr1:231	96.2546	152.35	74.4061	136.502	64.5478	50.1881
GT	Sense	Sense	-0.501	Detected	0.501	Detected	0.000	-3.333	Detected	-2.684	Detected	-3.009	0.037	GT	Sens	contig464	contig464	Peroxida	ATAGTA	contig464	Solyc06g	Solyc06g	Peroxida	GO:0005	GO:0005	contig464	Solyc06g	Peroxida	GO:0005	SL2.40ch	AT5G64120.1		peroxida	chr5:256	177.751	324.648	36.8967	70.0926	22.756	37.6077
GT	Sense	Sense	-0.483	Detected	0.483	Detected	0.000	-1.371	Detected	-1.569	Detected	-1.470	0.097	GT	Sens	contig468	contig468	Unknown	ATGAAG	contig468	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig468	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G29450.1		leucine-r	chr4:144	191.38	340.988	137.986	165.405	94.2991	86.591
GT	Sense	Sense	-0.470	Detected	0.470	Detected	0.000	-0.912	Detected	-2.771	Detected	-1.842	0.219	GT	Sens	contig481	contig481	CHP-rich	GATACC	contig481	Solyc01g	Solyc01g	CHP-rich zinc finger protein-lik			contig481	Solyc01g	CHP-rich zinc finger		SL2.40ch	AT5G25590.1		INVOLVE	chr5:890	120.129	210	85.9094	157.4	80.5777	23.4087
GT	Sense	Sense	-0.470	Detected	0.470	Detected	0.000	-1.316	Detected	-0.972	Detected	-1.144	0.150	GT	Sens	contig483	contig483	Serine/thr	AATTGT	contig483	Solyc02g	Solyc02g	Serine/thr	GO:0019	GO:0019	contig483	Solyc02g	Serine/thr	GO:0019	SL2.40ch	AT4G231	CRK6	CRK6 (C	chr4:121	26.7641	46.8138	20.425	24.3607	13.5777	18.1554
GT	Sense	Sense	-0.239	Detected	0.239	Detected	0.000	-0.919	Detected	-1.517	Detected	-1.218	0.086	GT	Sens	contig486	contig486	Acyltrans	CAAGAC	contig486	Solyc12g	Solyc12g	Acyltrans	GO:0016	GO:0016	contig486	Solyc12g	Acyltrans	GO:0016	SL2.40ch	AT1G35460.1		basic hel	chr1:130	5357.73	6798.96	7980.01	7685.92	3047.83	2121.58
GT	Sense	Sense	-0.461	Detected	0.461	Detected	0.000	-2.426	Detected	-3.341	Detected	-2.884	0.047	GT	Sens	contig505	contig505	WRKY tra	TCGTAT	contig505	Solyc10g	Solyc10g	WRKY tra	GO:0045449		contig505	Solyc10g	WRKY tra	GO:0045	SL2.40ch	AT5G415	WRKY24,	WRKY24	chr5:166	3110.16	5368.79	1319.05	2193.69	725.817	405.585
GT	Sense	Sense	-0.172	Detected	0.172	Detected	0.000	-1.152	Comprom	-1.122	Comprom	-1.137	0.022	GT	Sens	contig515	contig515	Leucine-r	GAGGAC	contig515	Solyc01g	Solyc01g	Leucine-r	GO:0005	GO:0005	contig515	Solyc01g	LRR recei	GO:0004	SL2.40ch	AT2G251	HSP98.7,	CLPB4 (C	chr2:106	15.741	18.2137	13.0648	17.9207	7.27507	7.82523
GT	Sense	Sense	-0.139	Detected	0.139	Detected	0.000	-2.917	Comprom	-1.743	Comprom	-2.330	0.061	GT	Sens	contig517	contig517	C4-dicarb	GCTTAA	contig517	Solyc03g	Solyc03g	C4-dicarb	GO:0016	GO:0016	contig517	Solyc08g	50S ribos	GO:0032	SL2.40ch	AT4G245	REN1	REN1 (RC	chr4:126	27.0038	29.8528	19.8966	40.9485	3.58997	8.53484
GT	Sense	Sense	-0.110	Detected	0.110	Detected	0.000	-2.188	Detected	-1.678	Detected	-1.933	0.020	GT	Sens	contig518	contig518	Calmodul	ACTTTT	contig518	Solyc12g	Solyc12g	Calmodulin-binding protein-lik			contig518	Solyc12g	Calmodulin-binding		SL2.40ch	AT1G73805.1		calmodu	chr1:277	1800.4	1911.6	865.712	1902.66	388.614	583.124
GT	Sense	Sense	0.119	Detected	-0.119	Detected	0.000	-1.023	Comprom	-1.379	Comprom	-1.201	0.030	GT	Sens	contig520	contig520	Ethylene-	TGATTA	contig520	Solyc03g	Solyc03g	Ethylene-	GO:0003	GO:0003	contig520	Solyc03g	Ethylene-	GO:0003	SL2.40ch	AT5G197	RAP2.11	RAP2.11	chr5:668	18.4355	14.261	2.09031	8.38144	7.61738	6.27163
GT	Sense	Sense	-0.182	Detected	0.182	Detected	0.000	-1.521	Detected	-1.466	Detected	-1.494	0.015	GT	Sens	contig521	contig521	Mitochon	AAAGTG	contig521	Solyc06g	Solyc06g	Mitochon	GO:0001	GO:0001	contig521	Solyc06g	Mitochon	GO:0001	SL2.40ch	AT5G03030.1		DNAJ he	chr5:708	1447.56	1699.27	945.12	853.523	521.764	571.149
GT	Sense	Sense	-0.002	Detected	0.002	Detected	0.000	-1.039	Detected	-1.176	Detected	-1.108	0.004	GT	Sens	contig528	contig528	ATP bind	CACCAA	contig528	Solyc07g	Solyc07g	ATP bind	GO:0005	GO:0005	contig528	Solyc07g	ATP bind	GO:0005	SL2.40ch	AT2G05940.1		protein k	chr2:228	70.848	64.8088	19.7275	51.0803	31.4762	30.1732
GT	Sense	Sense	-0.321	Detected	0.321	Detected	0.000	-0.968	Comprom	-1.150	Comprom	-1.059	0.086	GT	Sens	contig532	contig532	AT5G281	ACATTC	contig532	Solyc11g	Solyc11g	AT5G28150-like protein (Fragn			contig532	Solyc11g	AT5G28150-like pro		SL2.40ch	AT2G27770.1		unknown	chr2:118	11.9101	16.9413	12.8949	18.5954	6.93201	6.44138
GT	Sense	Sense	-0.276	Detected	0.276	Detected	0.000	-0.909	Detected	-1.596	Detected	-1.253	0.105	GT	Sens	contig539	contig539	Serine/thr	TTCTAT	contig539	Solyc12g	Solyc12g	Serine/threonine protein kinas			contig539	Solyc12g	Serine/threonine pr		SL2.40ch	AT5G161	GLT1, PG	PGLCT (I	chr5:527	209.054	279.491	230.941	320.854	122.901	80.4411
GT	Sense	Sense	-0.286	Detected	0.286	Detected	0.000	-1.084	Detected	-1.553	Detected	-1.319	0.070	GT	Sens	contig542	contig542	Unknown	TACGAG	contig542	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig542	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G25160.1		protein k	chr4:129	3806.29	5155.2	2776.31	3544.18	1994.71	1518.79
GT	Sense	Sense	-0.353	Detected	0.353	Detected	0.000	-1.381	Detected	-2.202	Detected	-1.791	0.080	GT	Sens	contig548	contig548	Genomic	TCATTC	contig548	Solyc11g	Solyc11g	Genomic DNA chromosome 5			contig548	Solyc11g	Genomic DNA chror		SL2.40ch	AT5G59350.1		unknown	chr5:239	332.635	494.518	204.534	252.988	148.732	88.6951
GT	Sense	Sense	0.024	Detected	-0.024	Detected	0.000	-1.595	Detected	-1.309	Detected	-1.452	0.010	GT	Sens	contig550	contig550	Unknown	GAAAAT	contig550	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig550	Solyc08g	AT-hook	GO:0003	SL2.40ch	AT3G20270.2		lipid-bind	chr3:706	153.549	135.448	100.369	131.27	45.5861	58.559
GT	Sense	Sense	-0.726	Detected	0.726	Detected	0.000	-2.188	Detected	-3.462	Comprom	-2.825	0.100	GT	Sens	contig561	contig561	Legumin	ATTAGA	contig561	Solyc09g	Solyc09g	Legumin	GO:0045	GO:0045	contig561	Solyc09g	Legumin	GO:0045	SL2.40ch	AT5G25590.1		INVOLVE	chr5:890	54.5563	136.054	71.737	32.1568	18.0563	7.86671
GT	Sense	Sense	-0.581	Detected	0.581	Detected	0.000	-1.686	Detected	-2.542	Detected	-2.114	0.099	GT	Sens	contig562	contig562	Thiamin r	GATAAT	contig562	Solyc09g	Solyc09g	Thiamin r	GO:0009	GO:0009	contig562	Solyc09g	Thiamin r	GO:0004	SL2.40ch	AT1G028	TPK1	TPK1 (TH	chr1:643	1657.75	3380.07	1019.16	1419.3	702.503	408.988
GT	Sense	Sense	-0.487	Detected	0.487	Detected	0.000	-1.837	Comprom	-2.603	Comprom	-2.220	0.070	GT	Sens	contig564	contig564	Reverse t	GGGGGG	contig564	Solyc09g	Solyc09g	Reverse t	GO:0006	GO:0006	contig564	Solyc04g	BZIP tran	GO:0003	SL2.40ch	#N/A	#N/A	#N/A	#N/A	12.1388	21.7452	10.3301	3.75849	4.3422	2.69065
GT	Sense	Sense	-0.726	Detected	0.726	Detected	0.000	-0.961	Detected	-1.834	Detected	-1.398	0.241	GT	Sens	contig573	contig573	Plant-spe	TTTATT	contig573	Solyc11g	Solyc11g	Plant-specific domain TIGR015			contig573	Solyc11g	Plant-specific doma		SL2.40ch	AT5G649	CIP8	CIP8 (CO	chr5:259	305.675	762.145	184.054	402.331	236.767	136.173
GT	Sense	Sense	-0.001	Detected	0.001	Detected	0.000	-1.464	Detected	-1.201	Detected	-1.333	0.010	GT	Sens	contig577	contig577	WD-40 re	ATGACA	contig577	Solyc01g	Solyc01g	WD-40 re	GO:0000	GO:0000	contig577	Solyc01g	WD-40 re	GO:0000	SL2.40ch	AT3G50390.1		transduc	chr3:187	1318.28	1202.81	980.152	1547.76	435.739	551.089
GT	Sense	Sense	0.266	Detected	-0.266	Detected	0.000	-2.948	Detected	-1.715	Detected	-2.332	0.074	GT	Sens	contig583	contig583	Syntaxin	CTGGAG	contig583	Solyc01g	Solyc01g	Syntaxin	GO:0043	GO:0043	contig583	Solyc01g	Syntaxin	GO:0043	SL2.40ch	AT3G118	SYP121,	SYP121 (	chr3:372	647.379	408.15	268.881	403.557	63.593	157.527
GT	Sense	Sense	-0.077	Detected	0.077	Detected	0.000	-1.285	Detected	-0.883	Detected	-1.084	0.037	GT	Sens	contig587	contig587	Cullin 1-li	ATTACC	contig587	Solyc01g	Solyc01g	Cullin 1-li	GO:0031	GO:0031	contig587	Solyc01g	Cullin 1-li	GO:0031	SL2.40ch	AT1G59790.1		cullin-rel	chr1:220	133.31	135.149	106.553	207.419	52.6059	73.2135
GT	Sense	Sense	0.018	Detected	-0.018	Detected	0.000	-1.308	Comprom	-2.979	Comprom	-2.144	0.124	GT	Sens	contig589	contig589	Cytochro	GTTCCC	contig589	Solyc06g	Solyc06g	Cytochro	GO:0019	GO:0019	contig589	Solyc06g	Cytochro	GO:0019	SL2.40ch	AT1G016	CYP86A4	CYP86A4	chr1:219	16.4085	14.5871	2.10076	2.93335	5.96445	1.97404
GT	Sense	Sense	-0.641	Detected	0.641	Detected	0.000	-1.396	Detected	-2.346	Comprom	-1.871	0.144	GT	Sens	contig591	contig591	Ulp1 prot	TATATG	contig591	Solyc12g	Solyc12g	Ulp1 prot	GO:0006	GO:0006	contig591	Solyc12g	Ulp1 prot	GO:0006	SL2.40ch	AT1G69980.1		unknown	chr1:263	17.7177	39.2598	19.9121	18.3299	9.56944	5.21806
GT	Sense	Sense	-0.302	Detected	0.302	Detected	0.000	-1.907	Detected	-2.165	Detected	-2.036	0.025	GT	Sens	contig596	contig596	Acyl-CoA	CATACA	contig596	Solyc02g	Solyc02g	Acyl-CoA	GO:0018	GO:0018	contig596	Solyc02g	Acyl-CoA	GO:0018	SL2.40ch	AT1G658	BZO1	BZO1 (BE	chr1:245	112.972	156.576	177.393	328.847	33.8502	29.8336
GT	Sense	Sense	-0.410	Detected	0.410	Detected	0.000	-0.966	Detected	-1.163	Detected	-1.065	0.128	GT	Sens	contig596	contig596	Unknown	AGCTAG	contig596	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig596	Solyc05g	Unknown Protein (A		SL2.40ch	AT1G48330.1		unknown	chr1:178	198.472	319.62	224.847	255.938	123.081	113.151
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.449	Detected	-1.252	Detected	-1.351	0.006	GT	Sens	contig597	contig597	Acyl-CoA	TTAATT	contig597	Solyc03g	Solyc03g	Acyl-CoA	GO:0005	GO:0005	contig597	Solyc03g	Acyl-CoA	GO:0005	SL2.40ch	AT3G23480.1		cyclopro	chr3:842	106.164	90.6462	30.1248	197.489	34.2978	41.431
GT	Sense	Sense	-0.286	Detected	0.286	Detected	0.000	-2.605	Detected	-1.243	Detected	-1.924	0.121	GT	Sens	contig599	contig599	Nudix hyd	GGATGG	contig599	Solyc05g	Solyc05g	Nudix hyd	GO:0051	GO:0051	contig599	Solyc05g	Nudix hyd	GO:0051	SL2.40ch	AT2G044	ATNUDT6	ATNUDT	chr2:154	61.7106	83.6396	26.202	28.8747	11.2787	30.5426
GT	Sense	Sense	-0.504	Detected	0.504	Detected	0.000	-1.440	Detected	-1.286	Detected	-1.363	0.116	GT	Sens	contig602	contig602	Glyoxalas	AAGCTG	contig602	Solyc02g	Solyc02g	Glyoxalas	GO:0004	GO:0004	contig602	Solyc02g	Glyoxalas	GO:0004	SL2.40ch	AT1G80160.2		lactoylgl	chr1:301	4368.76	8007.21	3340.38	5444.67	2081.1	2439.79
GT	Sense	Sense	-0.987	Detected	0.987	Detected	0.000	-1.282	Detected	-1.407	Detected	-1.345	0.307	GT	Sens	contig609	contig609	GATA tra	GATGTT	contig609	Solyc01g	Solyc01g	GATA tra	GO:0006	GO:0006	contig609	Solyc01g	GATA tra	GO:0006	SL2.40ch	AT3G20750.1		zinc fing	chr3:725	70.8711	253.709	41.3526	91.4954	52.6325	50.8591
GT	Sense	Sense	-0.855	Detected	0.855	Detected	0.000	-1.019	Detected	-1.083	Detected	-1.051	0.344	GT	Sens	contig609	contig609	Arabinoga	TGAGAC	contig609	Solyc07g	Solyc07g	Arabinogalactan-protein (AHRI			contig609	Solyc07g	Arabinogalactan-pr		SL2.40ch	AT5G19340.1		unknown	chr5:651	2280.19	6797.36	1629.49	2695.71	1854.29	1870.05
GT	Sense	Sense	-0.872	Detected	0.872	Detected	0.000	-1.964	Detected	-3.887	Detected	-2.925	0.153	GT	Sens	contig609	contig609	Calmodul	AAGTCA	contig609	Solyc06g	Solyc06g	Calmodul	GO:0005	GO:0005	contig609	Solyc06g	Calmodul	GO:0005	SL2.40ch	AT3G47480.1		calcium-l	chr3:174	371.473	1134.6	331.172	854.112	158.893	44.1587
GT	Sense	Sense	-0.080	Detected	0.080	Detected	0.000	-1.805	Detected	-0.847	Detected	-1.326	0.112	GT	Sens	contig610	contig610	Aromatic	GTGGGT	contig610	Solyc07g	Solyc07g	Aromatic	GO:0006	GO:0004	contig610	Solyc07g	Aromatic	GO:0004	SL2.40ch	AT2G20340.1		tyrosine	chr2:877	865.587	881.644	264.163	1721.22	238.753	488.728
GT	Sense	Sense	-0.223	Detected	0.223	Detected	0.000	-1.132	Detected	-1.079	Detected	-1.106	0.039	GT	Sens	contig610	contig610	Bifunctio	TATGTT	contig610	Solyc05g	Solyc05g	Bifunctio	GO:0008	GO:0008	contig610	Solyc05g	Bifunctio	GO:0048	SL2.40ch	AT3G464	UXS5	UXS5: UD	chr3:170	41.9456	52.1027	11.4827	48.1782	20.3669	22.2569
GT	Sense	Sense	-0.211	Detected	0.211	Detected	0.000	-1.196	Detected	-1.045	Detected	-1.120	0.038	GT	Sens	contig611	contig611	Metalloca	GCAAGA	contig611	Solyc07g	Solyc07g	Metalloca	GO:0004	GO:0004	contig611	Solyc07g	Metalloca	GO:0008	SL2.40ch	AT4G36980.2		unknown	chr4:174	3695.79	4515.77	2830.29	1906.01	1702.56	1992.3
GT	Sense	Sense	-0.017	Detected	0.017	Detected	0.000	-1.261	Detected	-0.969	Detected	-1.115	0.017	GT	Sens	contig613	contig613	Ankyrin r	GGAGCT	contig613	Solyc08g	Solyc08g	Ankyrin r	GO:0005	GO:0005	contig613	Solyc08g	Ankyrin r	GO:0005	SL2.40ch	AT4G002	XSP1	XSP1 (xy	chr4:939	440.2	410.866	276.486	541.514	169.46	218.514
GT	Sense	Sense	-0.247	Detected	0.247	Detected	0.000	-2.042	Detected	-3.320	Detected	-2.681	0.059	GT	Sens	contig616	contig616	Unknown	TATTTT	contig616	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig616	Solyc06g	Unknown Protein (A		SL2.40ch	AT5G07800.1		flavin-co	chr5:248	117.155	150.422	127.439	410.774	30.7707	13.3718
GT	Sense	Sense	-0.395	Detected	0.395	Detected	0.000	-0.969	Detected	-1.181	Comprom	-1.075	0.119	GT	Sens	contig618	contig618	Neuralize	GACGTT	contig618	Solyc10g	Solyc10g	Neuralize	GO:0008	GO:0008	contig618	Solyc10g	Neuralize	GO:0008	SL2.40ch	AT5G01590.1		unknown	chr5:224	17.2301	27.1634	12.4206	19.8284	10.5504	9.59694
GT	Sense	Sense	-0.125	Detected	0.125	Detected	0.000	-1.656	Detected	-0.824	Detected	-1.240	0.104	GT	Sens	contig620	contig620	FIP1 (AHF	CCAGTG	contig620	Solyc03g	Solyc03g	FIP1 (AHRD V1 **-- B6TFD3_MA			contig620	Solyc03g	FIP1 (AHRD V1 **-- B		SL2.40ch	AT5G23350.1		GRAM do	chr5:785	756.434	820.665	425.528	632.787	238.79	447.731
GT	Sense	Sense	0.043	Detected	-0.043	Detected	0.000	-2.574	Comprom	-1.437	Comprom	-2.006	0.072	GT	Sens	contig623	contig623	Heat shoc	TTTCAT	contig623	Solyc04g	Solyc04g	Heat shoc	GO:0006	GO:0006	contig623	Solyc04g	Heat shoc	GO:0006	SL2.40ch	AT4G01920.1		DC1 dom	chr4:829	14.0846	12.0965	68.8682	15.0955	2.09247	4.84913
GT	Sense	Sense	-0.124	Detected	0.124	Detected	0.000	-1.670	Detected	-1.976	Detected	-1.823	0.011	GT	Sens	contig623	contig623	WRKY tra	AATTCA	contig623	Solyc05g	Solyc05g	WRKY tra	GO:0045449		contig623	Solyc05g	WRKY tra	GO:0045	SL2.40ch	AT2G472	WRKY23,	WRKY23	chr2:194	139.703	151.174	57.3027	119.54	43.595	37.1601
GT	Sense	Sense	-0.129	Detected	0.129	Detected	0.000	-1.065	Detected	-1.015	Detected	-1.040	0.016	GT	Sens	contig625	contig625	Non-spec	GCGACG	contig625	Solyc03g	Solyc03g	Non-spec	GO:0008	GO:0008	contig625	Solyc03g	Non-spec	GO:0008	SL2.40ch	AT5G60300.3		lectin pro	chr5:242	2105.71	2296.07	1056.63	2251.65	1003.45	1094.29
GT	Sense	Sense	-0.676	Detected	0.676	Detected	0.000	-1.268	Detected	-2.109	Detected	-1.689	0.168	GT	Sens	contig625	contig625	Unknown	GTTGAC	contig625	Solyc08g	Solyc08g	Unknown Protein (AHRD V1)			contig625	Solyc08g	Unknown Protein (A		SL2.40ch	AT3G46160.1		protein k	chr3:169	768.739	1789.68	511.433	809.237	465.011	273.45
GT	Sense	Sense	-0.100	Detected	0.100	Detected	0.000	-1.037	Detected	-1.599	Detected	-1.318	0.048	GT	Sens	contig632	contig632	Pyrimidin	AGGCAT	contig632	Solyc06g	Solyc06g	Pyrimidin	GO:0008	GO:0008	contig632	Solyc06g	Pyrimidin	GO:0008	SL2.40ch	AT5G59480.2		haloacid	chr5:239	799.294	837.349	697.265	667.446	380.559	271.608
GT	Sense	Sense	-0.339	Detected	0.339	Detected	0.000	-0.987	Detected	-1.195	Detected	-1.091	0.091	GT	Sens	contig638	contig638	Unknown	AAGAAG	contig638	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig638	Solyc01g	Unknown Protein (A		SL2.40ch	AT2G21640.1		Encodes	chr2:925	315.827	460.548	328.596	437.182	183.769	167.595
GT	Sense	Sense	-0.231	Detected	0.231	Detected	0.000	-1.060	Detected	-1.445	Detected	-1.252	0.053	GT	Sens	contig643	contig643	Multidrug	TGGGAA	contig643	Solyc01g	Solyc01g	Multidrug	GO:0015	GO:0015	contig643	Solyc01g	Multidrug	GO:0015	SL2.40ch	AT5G49130.1		MATE eff	chr5:199	3119.89	3918.49	1190.73	2070.71	1601.43	1292.24
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-1.125	Comprom	-1.474	Comprom	-1.299	0.022	GT	Sens	contig645	contig645	Plant-spe	TGCAGA	contig645	Solyc06g	Solyc06g	Plant-specific domain TIGR016			contig645	Solyc06g	Plant-specific doma		SL2.40ch	AT3G25240.1		unknown	chr3:919	17.0668	13.7439	8.92715	17.7621	6.70639	5.54776
GT	Sense	Sense	-0.923	Detected	0.923	Detected	0.000	-1.158	Detected	-2.144	Detected	-1.651	0.255	GT	Sens	contig647	contig647	Integrase	CAGCAT	contig647	Solyc06g	Solyc06g	Integrase core domain contair			contig647	Solyc06g	Integrase core dom		SL2.40ch	AT5G46380.1		unknown	chr5:188	126.37	414.279	116.063	66.0058	97.8719	52.0913
GT	Sense	Sense	-0.515	Detected	0.515	Detected	0.000	-0.993	Detected	-2.746	Comprom	-1.870	0.207	GT	Sens	contig651	contig651	Lipid tran	TTGTCT	contig651	Solyc03g	Solyc03g	Lipid tran	GO:0006	GO:0006	contig651	Solyc03g	Lipid tran	GO:0006	SL2.40ch	AT4G35987.1		unknown	chr4:170	16.1961	30.1374	10.8297	14.7566	10.6005	3.3119
GT	Sense	Sense	-0.268	Detected	0.268	Detected	0.000	-1.862	Comprom	-1.506	Comprom	-1.684	0.035	GT	Sens	contig652	contig652	Zinc finge	TCGTTG	contig652	Solyc05g	Solyc05g	Zinc finge	GO:0003	GO:0003	contig652	Solyc05g	Zinc finge	GO:0003	SL2.40ch	AT1G64880.1		ribosoma	chr1:241	14.1043	18.6444	6.14139	13.7292	4.25911	5.74443
GT	Sense	Sense	-0.620	Detected	0.620	Detected	0.000	-1.552	Detected	-1.451	Detected	-1.502	0.137	GT	Sens	contig652	contig652	Acetyl co	GTATGT	contig652	Solyc07g	Solyc07g	Acetyl co	GO:0010	GO:0010	contig652	Solyc07g	Acetyl co	GO:0010	SL2.40ch	AT3G034	CHAT	CHAT (ac	chr3:828	2376.8	5116.17	4103.5	13579.3	1135.38	1283.18
GT	Sense	Sense	-0.357	Detected	0.357	Detected	0.000	-1.832	Comprom	-1.460	Comprom	-1.646	0.055	GT	Sens	contig653	contig653	Unknown	CCACTA	contig653	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig653	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G67610.2		unknown	chr5:269	14.0853	21.0651	7.07424	11.9184	4.62022	6.30017
GT	Sense	Sense	0.023	Detected	-0.023	Detected	0.000	-1.301	Detected	-1.568	Detected	-1.434	0.009	GT	Sens	contig654	contig654	Centrin (A	GGATTT	contig654	Solyc03g	Solyc03g	Centrin (A	GO:0005	GO:0005	contig654	Solyc03g	Centrin (A	GO:0005	SL2.40ch	AT5G65207.1		unknown	chr5:260	77.397	68.3908	54.3628	101.986	28.191	24.6884
GT	Sense	Sense	-1.299	Detected	1.299	Detected	0.000	-3.516	Comprom	-4.677	Comprom	-4.096	0.102	GT	Sens	contig655	contig655	Xylanase	GGAGAA	contig655	Solyc02g	Solyc02g	Xylanase	GO:0006	GO:0006	contig655	Solyc02g	Xylanase	GO:0006	SL2.40ch	AT5G60250.1		zinc fing	chr5:242	30.1825	166.704	33.7258	54.2705	5.92138	2.78958
GT	Sense	Sense	-0.766	Detected	0.766	Detected	0.000	-1.371	Detected	-3.327	Comprom	-2.349	0.199	GT	Sens	contig664	contig664	Unknown	GAAAAA	contig664	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig664	Solyc11g	Unknown Protein (A		SL2.40ch	AT1G48300.1		unknown	chr1:178	22.2247	58.5766	4.43096	4.66819	13.3198	3.61757
GT	Sense	Sense	-0.318	Detected	0.318	Detected	0.000	-1.527	Detected	-1.065	Detected	-1.296	0.081	GT	Sens	contig667	contig667	Metacasp	ACCCTA	contig667	Solyc10g	Solyc10g	Metacasp	GO:0006	GO:0006	contig667	Solyc10g	Metacasp	GO:0006	SL2.40ch	AT5G042	AtMC9	AtMC9 (m	chr5:115	401.284	568.486	222.25	460.758	158.266	229.711
GT	Sense	Sense	0.007	Detected	-0.007	Detected	0.000	-1.313	Comprom	-1.076	Comprom	-1.194	0.010	GT	Sens	contig676	contig676	Pre-mRNA	CAAGAG	contig676	Solyc02g	Solyc02g	Pre-mRNA	GO:0005	GO:0005	contig676	Solyc02g	Pre-mRNA	GO:0005	SL2.40ch	AT5G23480.1		DNA bind	chr5:791	16.4608	14.8645	2.24832	2.82359	6.01323	7.46632
GT	Sense	Sense	-0.901	Detected	0.901	Detected	0.000	-1.228	Detected	-1.105	Detected	-1.167	0.326	GT	Sens	contig682	contig682	3-methyl-	GGAGAA	contig682	Solyc06g	Solyc06g	3-methyl-	GO:0008	GO:0008	contig682	Solyc06g	3-methyl-	GO:0003	SL2.40ch	AT5G09300.2		2-oxoiso	chr5:288	61.7073	196.137	89.5889	154.667	44.8554	51.4355
GT	Sense	Sense	-0.321	Detected	0.321	Detected	0.000	-1.643	Detected	-1.782	Detected	-1.713	0.035	GT	Sens	contig684	contig684	Tobacco	CAGAAT	contig684	Solyc07g	Solyc07g	Tobacco rattle virus-induced r			contig684	Solyc07g	Tobacco rattle virus		SL2.40ch	AT1G735	PIN1, ATF	PIN1 (PIN	chr1:276	43.4847	61.8371	47.6459	56.5289	15.8482	15.1667
GT	Sense	Sense	-0.469	Detected	0.469	Detected	0.000	-1.118	Detected	-1.018	Detected	-1.068	0.152	GT	Sens	contig686	contig686	Chaperon	GAGTCT	contig686	Solyc05g	Solyc05g	Chaperon	GO:0031	GO:0031	contig686	Solyc05g	Chaperon	GO:0031	SL2.40ch	AT1G71000.1		heat sho	chr1:267	229.455	400.777	205.226	214.607	133.429	150.686
GT	Sense	Sense	-0.023	Detected	0.023	Detected	0.000	-0.944	Detected	-1.081	Detected	-1.013	0.005	GT	Sens	contig687	contig687	LL-diamin	TTCCTG	contig687	Solyc11g	Solyc11g	LL-diamin	GO:0030	GO:0030	contig687	Solyc11g	LL-diamin	GO:0010	SL2.40ch	AT2G138	ALD1	ALD1 (AG	chr2:576	248.301	233.797	218.318	278.656	119.571	114.548
GT	Sense	Sense	0.108	Detected	-0.108	Detected	0.000	-2.477	Comprom	-0.912	Comprom	-1.695	0.165	GT	Sens	contig687	contig687	Os05g02	TTTATG	contig687	Solyc02g	Solyc02g	Os05g0272200 protein (Fragm			contig687	Solyc02g	Os05g0272200 prot		SL2.40ch	AT1G17030.1		unknown	chr1:582	18.217	14.2929	2.37879	11.4687	2.76707	8.62508
GT	Sense	Sense	-0.385	Detected	0.385	Detected	0.000	-1.642	Detected	-1.433	Detected	-1.537	0.061	GT	Sens	contig700	contig700	1-aminoc	CAGCTC	contig700	Solyc12g	Solyc12g	1-aminoc	GO:0016	GO:0016	contig700	Solyc12g	1-aminoc	GO:0016	SL2.40ch	AT1G623	ACO2, AT	ACO2 (AC	chr1:230	7413.15	11525.6	11564.3	4575.12	2828.67	3444.65
GT	Sense	Sense	-0.356	Detected	0.356	Detected	0.000	-1.261	Detected	-1.129	Detected	-1.195	0.081	GT	Sens	contig703	contig703	Unknown	CCCTGT	contig703	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)%:			contig703	Solyc11g	Unknown Protein (A		SL2.40ch	AT3G44940.1		unknown	chr3:164	4746.53	7089.25	4022.69	4146.58	2311.16	2668.18
GT	Sense	Sense	-0.398	Detected	0.398	Detected	0.000	-0.890	Detected	-1.631	Detected	-1.261	0.146	GT	Sens	contig704	contig704	Cytochro	GAAGTA	contig704	Solyc07g	Solyc07g	Cytochro	GO:0055	GO:0055	contig704	Solyc07g	Cytochro	GO:0020	SL2.40ch	AT5G144	CYP724A	CYP724A	chr5:464	554.925	878.073	535.782	263.22	359.621	226.693
GT	Sense	Sense	-0.885	Detected	0.885	Detected	0.000	-1.119	Detected	-1.150	Detected	-1.134	0.328	GT	Sens	contig706	contig706	Zinc finge	ATAATG	contig706	Solyc10g	Solyc10g	Zinc finge	GO:0005	GO:0005	contig706	Solyc10g	Zinc finge	GO:0005	SL2.40ch	AT5G066	GIS2	GIS2 (GL	chr5:204	47.0362	146.183	74.461	138.342	36.462	37.6028
GT	Sense	Sense	0.773	Detected	-0.773	Detected	0.000	-1.600	Detected	-2.640	Comprom	-2.120	0.151	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	65.9968	20.6179	330.438	109.843	11.6222	5.9522
GT	Sense	Sense	-0.162	Detected	0.162	Detected	0.000	-1.522	Detected	-2.662	Detected	-2.092	0.072	GT	Sens	contig710	contig710	Homeobo	TTGAAA	contig710	Solyc01g	Solyc01g	Homeobo	GO:0005	GO:0005	contig710	Solyc01g	Homeobo	GO:0016	SL2.40ch	AT3G618	ATHB-12,	ATHB-12	chr3:229	358.845	409.422	126.846	677.684	127.412	60.9148
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	-2.149	Comprom	-1.215	Comprom	-1.682	0.070	GT	Sens	contig714	contig714	LOB dom	TCTCTC	contig714	Solyc03g	Solyc03g	LOB dom	GO:0005	GO:0005	contig714	Solyc03g	LOB dom	GO:0005	SL2.40ch	AT1G656	AS2	AS2 (ASY	chr1:244	17.4771	15.1794	4.85921	7.32665	3.50583	7.05794
GT	Sense	Sense	0.856	Detected	-0.856	Detected	0.000	-1.595	Detected	-1.476	Detected	-1.536	0.215	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	113.393	31.5553	20.2365	272.735	18.9046	21.6307
GT	Sense	Sense	-0.132	Detected	0.132	Detected	0.000	-0.905	Detected	-1.181	Detected	-1.043	0.032	GT	Sens	contig724	contig724	WRKY tra	CTACAA	contig724	Solyc08g	Solyc08g	WRKY tra	GO:0003	GO:0003	contig724	Solyc08g	WRKY tra	GO:0003	SL2.40ch	AT4G238	WRKY53,	WRKY53	chr4:123	1639.37	1794.87	1126.02	1185.65	874.544	760.932
GT	Sense	Sense	-0.412	Detected	0.412	Detected	0.000	-1.551	Detected	-1.980	Detected	-1.765	0.063	GT	Sens	contig726	contig726	Acyltrans	TGATCA	contig726	Solyc02g	Solyc02g	Acyltrans	GO:0016	GO:0016	contig726	Solyc02g	Acyltrans	GO:0016	SL2.40ch	AT1G03390.1		transfera	chr1:841	110.26	178.015	55.6012	91.9497	45.6549	35.7375
GT	Sense	Sense	0.036	Detected	-0.036	Detected	0.000	-1.624	Detected	-1.161	Detected	-1.393	0.027	GT	Sens	contig729	contig729	Calmodul	TCCAAA	contig729	Solyc03g	Solyc03g	Calmodul	GO:0005	GO:0005	contig729	Solyc03g	Calmodul	GO:0005	SL2.40ch	AT1G73805.1		calmodu	chr1:277	883.448	766.724	287.743	579.651	254.956	370.203
GT	Sense	Sense	-0.040	Detected	0.040	Detected	0.000	-1.831	Detected	-1.628	Detected	-1.729	0.004	GT	Sens	contig740	contig740	HMG type	GCAGAT	contig740	Solyc06g	Solyc06g	HMG type	GO:0003	GO:0003	contig740	Solyc06g	HMG type	GO:0003	SL2.40ch	AT5G54550.1		unknown	chr5:221	510.175	491.622	69.8449	243.181	134.366	163.051
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-1.065	Comprom	-1.400	Comprom	-1.233	0.021	GT	Sens	contig744	contig744	Unknown	ACAAAC	contig744	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig744	Solyc00g	Unknown Protein (A		SL2.40ch	AT5G46870.1		RNA reco	chr5:190	13.1522	13.2557	3.95574	11.9435	6.02549	5.03243
GT	Sense	Sense	-0.255	Detected	0.255	Detected	0.000	-2.697	Detected	-2.535	Detected	-2.616	0.010	GT	Sens	contig747	contig747	Patatin-lik	GGGGGA	contig747	Solyc04g	Solyc04g	Patatin-lik	GO:0016	GO:0016	contig747	Solyc04g	Patatin-lik	GO:0045	SL2.40ch	AT4G370	PLP5, PL	PLP5 (PA	chr4:174	71.6902	93.0295	58.6683	97.3688	12.0211	14.1734
GT	Sense	Sense	-0.039	Detected	0.039	Detected	0.000	-0.919	Detected	-1.985	Detected	-1.452	0.113	GT	Sens	contig751	contig751	Inositol 2-	CATGAT	contig751	Solyc08g	Solyc08g	Inositol 2-	GO:0008	GO:0008	contig751	Solyc08g	Inositol 2-	GO:0008	SL2.40ch	AT4G17370.1		oxidored	chr4:970	186.554	179.605	148.83	190.822	92.4082	46.5313
GT	Sense	Sense	-0.256	Detected	0.256	Detected	0.000	-1.466	Detected	-1.692	Detected	-1.579	0.030	GT	Sens	contig751	contig751	Zinc finge	GGAATT	contig751	Solyc12g	Solyc12g	Zinc finge	GO:0005	GO:0005	contig751	Solyc12g	Zinc finge	GO:0005	SL2.40ch	AT5G498	MMT	MMT: S-	chr5:202	175.711	228.33	96.007	214.625	69.2396	62.3536
GT	Sense	Sense	-0.674	Detected	0.674	Detected	0.000	-1.035	Detected	-0.969	Detected	-1.002	0.276	GT	Sens	contig753	contig753	Polyprote	TTGGTG	contig753	Solyc05g	Solyc05g	Polyprote	GO:0008	GO:0008	contig753	Solyc05g	Polyprote	GO:0008	SL2.40ch	AT5G40700.3		unknown	chr5:162	18.814	43.6903	11.9795	14.5108	13.3608	14.7317
GT	Sense	Sense	-0.582	Detected	0.582	Detected	0.000	-1.109	Detected	-1.657	Comprom	-1.383	0.164	GT	Sens	contig755	contig755	Unknown	TCATTT	contig755	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig755	Solyc01g	Unknown Protein (A		SL2.40ch	AT5G063	FLA17	FLA17 (F	chr5:195	17.1256	34.9787	12.0483	20.2404	10.834	7.80805
GT	Sense	Sense	0.071	Detected	-0.071	Detected	0.000	-1.037	Detected	-1.086	Detected	-1.061	0.005	GT	Sens	contig767	contig767	Unknown	TTGCTT	contig767	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig767	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G185	PUCHI	PUCHI: D	chr5:616	64.408	53.2331	58.0511	59.0484	27.2554	27.7536
GT	Sense	Sense	-0.375	Detected	0.375	Detected	0.000	-2.153	Detected	-1.666	Detected	-1.909	0.051	GT	Sens	contig769	contig769	Centrin 2	GCTCAT	contig769	Solyc10g	Solyc10g	Centrin 2	GO:0031	GO:0031	contig769	Solyc10g	Centrin 2	GO:0031	SL2.40ch	AT5G544	PBP1	PBP1 (PI	chr5:221	134.661	206.468	81.7456	216.76	35.8081	52.875
GT	Sense	Sense	-1.082	Detected	1.082	Detected	0.000	-0.916	Detected	-2.636	Detected	-1.776	0.327	GT	Sens	contig772	contig772	AAA-ATP	CTCGAA	contig772	Solyc12g	Solyc12g	AAA-ATP	GO:0017	GO:0017	contig772	Solyc12g	AAA-ATP	GO:0005	SL2.40ch	AT5G57480.1		AAA-type	chr5:232	33.5476	137.019	60.2705	67.0473	34.2995	10.9724
GT	Sense	Sense	-1.049	Detected	1.049	Detected	0.000	-1.360	Detected	-2.912	Detected	-2.136	0.243	GT	Sens	contig781	contig781	Pectinest	CTCTGA	contig781	Solyc11g	Solyc11g	Pectinest	GO:0030	GO:0030	contig781	Solyc11g	Pectinest	GO:0030	SL2.40ch	AT5G62360.1		invertase	chr5:250	1592.14	6214.22	1728.39	3233.07	1170.03	420.533
GT	Sense	Sense	-1.156	Detected	1.156	Detected	0.000	-2.786	Comprom	-3.159	Comprom	-2.973	0.126	GT	Sens	contig782	contig782	Glutathio	TTGTGG	contig782	Solyc07g	Solyc07g	Glutathio	GO:0004	GO:0004	contig782	Solyc07g	Glutathio	GO:0004	SL2.40ch	AT1G17180.1				11.2166	50.7591	11.5519	131.313	3.30221	2.68687
GT	Sense	Sense	0.060	Detected	-0.060	Detected	0.000	-1.599	Detected	-1.075	Detected	-1.337	0.038	GT	Sens	contig786	contig786	Ferric red	GAATGT	contig786	Solyc00g	Solyc00g	Ferric red	GO:0000	GO:0000	contig786	Solyc00g	Ferric red	GO:0000	SL2.40ch	AT5G028	UPL4	UPL4: ub	chr5:662	336.039	281.927	81.7936	217.678	97.0128	146.984
GT	Sense	Sense	-0.123	Detected	0.123	Detected	0.000	-1.203	Comprom	-2.191	Comprom	-1.697	0.079	GT	Sens	contig792	contig792	Cellulose	TGTTAA	contig792	Solyc01g	Solyc01g	Cellulose	GO:0016	GO:0016	contig792	Solyc01g	Cellulose	GO:0016	SL2.40ch	AT5G647	CESA6, IX	CESA6 (C	chr5:258	11.3575	12.2853	5.91456	4.64056	4.89815	2.60241
GT	Sense	Sense	0.402	Detected	-0.402	Detected	0.000	-2.071	Detected	-3.820	Detected	-2.946	0.092	GT	Sens	contig796	contig796	Peroxida	TAGTGG	contig796	Solyc11g	Solyc11g	Peroxida	GO:0055	GO:0055	contig796	Solyc11g	Peroxida	GO:0055	SL2.40ch	AT2G41480.1		electron	chr2:172	1528.17	797.536	1035.3	1148.85	250.846	78.628
GT	Sense	Sense	0.412	Detected	-0.412	Detected	0.000	-1.947	Detected	-1.112	Detected	-1.529	0.121	GT	Sens	contig796	contig796	Unknown	TGAAGC	contig796	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig796	Solyc07g026990.1.1				AT5G24280.1		EXPRESS	chr5:825	390.173	200.93	245.926	234.79	69.3271	130.36
GT	Sense	Sense	-0.143	Detected	0.143	Detected	0.000	-1.443	Detected	-1.669	Detected	-1.556	0.013	GT	Sens	contig798	contig798	Ring H2 fi	TAACGA	contig798	Solyc04g	Solyc04g	Ring H2 fi	GO:0008	GO:0008	contig798	Solyc04g	Ring H2 fi	GO:0004	SL2.40ch	AT5G42200.1		zinc fing	chr5:168	272.093	302.273	142.45	244.932	100.742	90.7274
GT	Sense	Sense	-0.947	Detected	0.947	Detected	0.000	-1.726	Detected	-1.055	Detected	-1.391	0.300	GT	Sens	contig799	contig799	RING fing	GTATGT	contig799	Solyc01g	Solyc01g	RING fing	GO:0008	GO:0008	contig799	Solyc01g	RING fing	GO:0008	SL2.40ch	AT5G57540.1		xylogluca	chr5:233	45.6325	154.629	51.3704	97.4928	24.2447	40.6587
GT	Sense	Sense	-0.953	Detected	0.953	Detected	0.000	-1.941	Detected	-3.723	Detected	-2.832	0.162	GT	Sens	contig804	contig804	Expansin	CAATCA	contig804	Solyc04g	Solyc04g	Expansin	GO:0009	GO:0009	contig804	Solyc04g	Expansin	GO:0005	SL2.40ch	AT1G201	ATEXPA1	ATEXPA1	chr1:699	3018.89	10314.8	2362.51	4037.58	1387.46	425.093
GT	Sense	Sense	0.027	Detected	-0.027	Detected	0.000	-3.092	Detected	-2.178	Detected	-2.635	0.029	GT	Sens	contig805	contig805	Calmodul	CGATGG	contig805	Solyc03g	Solyc03g	Calmodul	GO:0005	GO:0005	contig805	Solyc03g	Calmodul	GO:0005	SL2.40ch	AT5G58000.1		LOCATE	chr5:234	108.766	95.5059	43.6619	77.4452	11.4126	22.6567
GT	Sense	Sense	-0.062	Detected	0.062	Detected	0.000	-1.626	Detected	-1.294	Detected	-1.460	0.014	GT	Sens	contig815	contig815	Ring fing	GTGAGA	contig815	Solyc04g	Solyc04g	Ring fing	GO:0008	GO:0008	contig815	Solyc04g	Protein pl	GO:0005	SL2.40ch	AT2G18938.1				33.711	33.506	29.4519	48.9569	10.394	13.7899
GT	Sense	Sense	-0.146	Detected	0.146	Detected	0.000	-1.194	Comprom	-2.586	Comprom	-1.890	0.117	GT	Sens	contig820	contig820	Xylanase	CGGGCA	contig820	Solyc01g	Solyc01g	Xylanase	GO:0006	GO:0006	contig820	Solyc01g	Xylanase	GO:0006	SL2.40ch	AT1G636	ATMURE,	MURE: A	chr1:236	16.5556	18.4845	5.2168	12.0356	7.29877	2.93049
GT	Sense	Sense	-0.252	Detected	0.252	Detected	0.000	-1.787	Detected	-1.716	Detected	-1.752	0.020	GT	Sens	contig821	contig821	Unknown	AATTGA	contig821	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig821	Solyc12g	Unknown Protein (A		SL2.40ch	AT4G24275.1		Identified	chr4:125	350.531	453.247	217.421	202.808	110.249	122.079
GT	Sense	Sense	0.009	Detected	-0.009	Detected	0.000	-0.977	Detected	-1.053	Detected	-1.015	0.001	GT	Sens	contig823	contig823	BZIP tran	GTTGAG	contig823	Solyc12g	Solyc12g	BZIP tran	GO:0006	GO:0006	contig823	Solyc12g	BZIP tran	GO:0005	SL2.40ch	AT2G423	ATBZIP34	bZIP tran	chr2:176	31.4268	28.2925	36.0036	43.3391	14.4599	14.462
GT	Sense	Sense	-0.737	Detected	0.737	Detected	0.000	-1.437	Comprom	-1.388	Comprom	-1.412	0.195	GT	Sens	contig825	contig825	Gag-pol p	CGATAC	contig825	Solyc01g	Solyc01g	Gag-pol polyprotein (AHRD V1			contig825	Solyc01g	Gag-pol polyprotein		SL2.40ch	AT4G357	RecQl3	RecQl3:	chr4:169	12.5108	31.6663	12.02	12.9595	7.01788	7.65296
GT	Sense	Sense	-0.112	Detected	0.112	Detected	0.000	-1.125	Detected	-0.982	Detected	-1.053	0.015	GT	Sens	contig827	contig827	Patatin-lik	TTGGTA	contig827	Solyc02g	Solyc02g	Patatin-lik	GO:0004	GO:0004	contig827	Solyc02g	Patatin-lik	GO:0004	SL2.40ch	AT1G61390.2		S-locus	chr1:226	449.576	478.535	286.356	565.143	203.095	236.205
GT	Sense	Sense	-0.289	Detected	0.289	Detected	0.000	-0.859	Detected	-1.217	Detected	-1.038	0.093	GT	Sens	contig827	contig827	Seed mat	TCAAGA	contig827	Solyc03g	Solyc03g	Seed maturation protein PM41			contig827	Solyc03g	Seed maturation pr		SL2.40ch	AT3G11920.1		glutared	chr3:377	677.729	922.014	442.841	821.894	416.175	342.182
GT	Sense	Sense	-0.732	Detected	0.732	Detected	0.000	-0.809	Detected	-1.500	Detected	-1.155	0.290	GT	Sens	contig827	contig827	Pto-like s	GACACC	contig827	Solyc07g	Solyc07g	Pto-like s	GO:0005	GO:0005	contig827	Solyc07g	Pto-like. S	GO:0005	SL2.40ch	AT1G30570.1		protein k	chr1:108	662.498	1665.27	647.584	1185.9	572.364	373.523
GT	Sense	Sense	-0.831	Detected	0.831	Detected	0.000	-0.974	Detected	-1.882	Detected	-1.428	0.270	GT	Sens	contig831	contig831	Transpos	TGCAAA	contig831	Solyc12g	Solyc12g	Transposon Ty1-BL Gag-Pol p			contig831	Solyc12g	Transposon Ty1-BL		SL2.40ch	AT5G563	ATCRT1	zinc fing	chr5:228	47.2682	136.356	37.6112	27.909	39.011	21.9085
GT	Sense	Sense	-0.412	Detected	0.412	Detected	0.000	-1.612	Detected	-2.279	Detected	-1.945	0.067	GT	Sens	contig834	contig834	Os01g06	CTTAGA	contig834	Solyc06g	Solyc06g	Os01g0611000 protein (Fragm			contig834	Solyc06g	Os01g0611000 prot		SL2.40ch	AT5G25460.1		unknown	chr5:886	4126.97	6662.58	8169.93	5698.58	1638.33	1086.64
GT	Sense	Sense	-0.096	Detected	0.096	Detected	0.000	-1.335	Detected	-1.308	Detected	-1.322	0.005	GT	Sens	contig837	contig837	Proteaso	GAAATT	contig837	Solyc07g	Solyc07g	Proteaso	GO:0019	GO:0019	contig837	Solyc07g	Proteaso	GO:0019	SL2.40ch	AT1G164	PAB1	PAB1 (PF	chr1:562	449.489	468.438	312.645	417.349	173.674	186.415
GT	Sense	Sense	-0.439	Detected	0.439	Detected	0.000	-0.897	Detected	-3.294	Comprom	-2.096	0.242	GT	Sens	contig837	contig837	Os04g05	TCATCT	contig837	Solyc06g	Solyc06g	Os04g0585900 protein (Fragm			contig837	Solyc06g	Os04g0585900 prot		SL2.40ch	AT5G47060.1		senescen	chr5:191	17.2709	28.9368	11.874	20.6633	11.4625	2.29238
GT	Sense	Sense	-0.191	Detected	0.191	Detected	0.000	-0.885	Detected	-1.490	Detected	-1.187	0.080	GT	Sens	contig845	contig845	Unknown	TAACTT	contig845	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig845	Solyc10g	Unknown Protein (A		SL2.40ch	AT3G23450.1		unknown	chr3:841	38.2793	45.4617	14.6287	21.6562	21.5648	14.943
GT	Sense	Sense	-0.492	Detected	0.492	Detected	0.000	-1.798	Detected	-1.000	Detected	-1.399	0.158	GT	Sens	contig848	contig848	Auxin effl	GATCCT	contig848	Solyc03g	Solyc03g	Auxin effl	GO:0009	GO:0009	contig848	Solyc03g	Auxin effl	GO:0009	SL2.40ch	AT1G20925.1		auxin effl	chr1:729	42.5284	76.657	24.6928	52.4402	15.6719	28.7261
GT	Sense	Sense	-0.570	Detected	0.570	Detected	0.000	-1.107	Detected	-1.075	Detected	-1.091	0.196	GT	Sens	contig849	contig849	F-box/LRI	CCTAAC	contig849	Solyc03g	Solyc03g	F-box/LRR-repeat protein At3g			contig849	Solyc09g	Unknown Protein (A		SL2.40ch	AT3G22580.1		protease	chr3:800	103.886	208.808	84.7594	91.375	65.299	70.35
GT	Sense	Sense	0.067	Detected	-0.067	Detected	0.000	-1.050	Detected	-1.177	Detected	-1.113	0.007	GT	Sens	contig849	contig849	Unknown	ATATAC	contig849	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig849	Solyc09g	Unknown Protein (A		SL2.40ch	AT4G10790.1		UBX dom	chr4:664	2523.18	2096.73	1693.47	2440.04	1060.67	1023.62
GT	Sense	Sense	-0.463	Detected	0.463	Detected	0.000	-0.843	Detected	-2.491	Comprom	-1.667	0.220	GT	Sens	contig850	contig850	Serine/thr	GCAGGA	contig850	Solyc11g	Solyc11g	Serine/thr	GO:0006	GO:0006	contig850	Solyc11g	Serine/thr	GO:0006	SL2.40ch	AT3G442	ATNEK6,	NEK6 ("N	chr3:159	35.919	62.1961	21.9485	33.0837	25.1651	8.45654
GT	Sense	Sense	0.175	Detected	-0.175	Detected	0.000	-1.301	Detected	-1.221	Detected	-1.261	0.020	GT	Sens	contig851	contig851	Glutathio	GCTGAA	contig851	Solyc06g	Solyc06g	Glutathio	GO:0004	GO:0004	contig851	Solyc06g	Glutathio	GO:0004	SL2.40ch	AT5G594	ZEU1	ZEU1 (ZE	chr5:239	1234.42	882.831	1163.24	1567.65	404.455	450.54
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-1.220	Detected	-1.733	Detected	-1.476	0.034	GT	Sens	contig853	contig853	Pseudo r	TTGACA	contig853	Solyc03g	Solyc03g	Pseudo r	GO:0010	GO:0010	contig853	Solyc03g	Timing of	GO:0030	SL2.40ch	AT5G613	TOC1, AP	TOC1 (TI	chr5:246	1625.87	1267.98	712.558	932.343	588.704	434.374
GT	Sense	Sense	-0.203	Detected	0.203	Detected	0.000	-1.507	Detected	-1.187	Detected	-1.347	0.035	GT	Sens	contig862	contig862	Cysteine-	TTAGTT	contig862	Solyc03g	Solyc03g	Cysteine-rich receptor-like prc			contig862	Solyc08g	Protein s	GO:0016	SL2.40ch	AT4G38950.2				210.163	253.949	168.69	251.264	77.587	102.051
GT	Sense	Sense	-0.321	Detected	0.321	Detected	0.000	-1.305	Detected	-1.284	Detected	-1.295	0.056	GT	Sens	contig866	contig866	UDP-gluc	TGACCA	contig866	Solyc12g	Solyc12g	UDP-gluc	GO:0008	GO:0008	contig866	Solyc12g	UDP-gluc	GO:0008	SL2.40ch	AT1G01390.1		UDP-gluc	chr1:148	95.8431	136.391	65.547	107.032	44.1731	47.2404
GT	Sense	Sense	-0.363	Detected	0.363	Detected	0.000	-1.224	Detected	-1.893	Comprom	-1.559	0.087	GT	Sens	contig878	contig878	O-methyl	TTTAGT	contig878	Solyc02g	Solyc02g	O-methyl	GO:0046	GO:0046	contig878	Solyc02g	O-methyl	GO:0008	SL2.40ch	AT5G541	ATOMT1,	ATOMT1	chr5:219	28.4238	42.8768	15.6255	20.8839	14.2697	9.45302
GT	Sense	Sense	-0.337	Detected	0.337	Detected	0.000	-1.642	Detected	-1.795	Detected	-1.719	0.038	GT	Sens	contig881	contig881	Beta-fruc	GTTTAC	contig881	Solyc03g	Solyc03g	Beta-fruc	GO:0005	GO:0005	contig881	Solyc03g	Beta-fruc	GO:0004	SL2.40ch	AT5G119	AtcwINV6	AtcwINV6	chr5:383	328.188	477.537	203.564	412.555	121.091	114.772
GT	Sense	Sense	-0.537	Detected	0.537	Detected	0.000	-0.858	Detected	-1.598	Detected	-1.228	0.200	GT	Sens	contig888	contig888	Kinase-S	CTTGCA	contig888	Solyc06g	Solyc06g	Kinase-S	GO:0035	GO:0035	contig888	Solyc06g	Kinase-S	GO:0035	SL2.40ch	AT2G28320.1		pleckstri	chr2:120	203.839	391.043	102.56	229.19	148.712	93.7937
GT	Sense	Sense	-0.011	Detected	0.011	Detected	0.000	-1.139	Detected	-1.295	Detected	-1.217	0.004	GT	Sens	contig889	contig889	Transcrip	TTGCAG	contig889	Solyc06g	Solyc06g	Transcrip	GO:0003	GO:0003	contig889	Solyc06g	Transcrip	GO:0003	SL2.40ch	AT5G59570.1		myb fami	chr5:240	181.946	168.437	93.9911	111.423	75.8736	71.7937
GT	Sense	Sense	0.440	Detected	-0.440	Detected	0.000	-0.861	Detected	-1.361	Detected	-1.111	0.159	GT	Sens	contig892	contig892	Proline d	TGCAAC	contig892	Solyc02g	Solyc02g	Proline d	GO:0004	GO:0004	contig892	Solyc02g	Proline d	GO:0005	SL2.40ch	AT3G307	ERD5, PR	ERD5 (EA	chr3:124	808.245	400.484	281.319	458.82	298.983	222.863
GT	Sense	Sense	0.516	Detected	-0.516	Detected	0.000	-0.871	Detected	-1.570	Detected	-1.220	0.189	GT	Sens	contig895	contig895	Potassiu	GCAAGG	contig895	Solyc07g	Solyc07g	Potassiu	GO:0055	GO:0055	contig895	Solyc07g	Potassiu	GO:0015	SL2.40ch	AT2G17970.2		oxidored	chr2:781	65.6652	29.2574	16.6108	96.4423	22.8812	14.8527
GT	Sense	Sense	-0.182	Detected	0.182	Detected	0.000	-0.896	Detected	-1.381	Detected	-1.138	0.064	GT	Sens	contig899	contig899	ATP-bind	AATTTG	contig899	Solyc05g	Solyc05g	ATP-bind	GO:0017	GO:0017	contig899	Solyc05g	ATP-bind	GO:0042	SL2.40ch	AT2G299	PDR3, AT	PDR3 (PL	chr2:127	864.379	1014.2	461.024	928.272	480.537	361.744
GT	Sense	Sense	-0.417	Detected	0.417	Detected	0.000	-0.925	Detected	-1.260	Detected	-1.093	0.136	GT	Sens	contig902	contig902	cDNA clo	GAAAAG	contig902	Solyc11g	Solyc11g	cDNA clone J033118E13 full in			contig902	Solyc11g	cDNA clone J03311		SL2.40ch	AT3G52900.1		unknown	chr3:196	50.1654	81.5558	21.3656	54.0311	32.1583	26.8626
GT	Sense	Sense	0.025	Detected	-0.025	Detected	0.000	-1.211	Detected	-1.161	Detected	-1.186	0.001	GT	Sens	contig910	contig910	Unknown	ACTTTC	contig910	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig910	Solyc08g	Pectinace	GO:0004	SL2.40ch	AT1G26976.1				1103.13	971.482	1172.18	1403.64	426.962	465.778
GT	Sense	Sense	-0.229	Detected	0.229	Detected	0.000	-1.492	Detected	-1.463	Detected	-1.477	0.023	GT	Sens	contig914	contig914	Disease r	GTGTTT	contig914	Solyc10g	Solyc10g	Disease resistance response (			contig914	Solyc10g	Disease resistance		SL2.40ch	AT5G542	MRE11, A	MRE11 (r	chr5:220	1420.86	1780.57	1116.41	2941.7	539.969	580.569
GT	Sense	Sense	-0.030	Detected	0.030	Detected	0.000	-1.739	Detected	-0.870	Detected	-1.305	0.096	GT	Sens	contig917	contig917	Lysine de	AGGTAT	contig917	Solyc07g	Solyc07g	Lysine de	GO:0003	GO:0003	contig917	Solyc07g	Lysine de	GO:0008	SL2.40ch	AT4G31810.1		enoyl-Co	chr4:153	118.204	112.34	13.2742	67.2327	32.96	63.4062
GT	Sense	Sense	-0.031	Detected	0.031	Detected	0.000	-2.530	Detected	-2.113	Detected	-2.321	0.008	GT	Sens	contig925	contig925	Beta-1 3-	TCCAAT	contig925	Solyc04g	Solyc04g	Beta-1 3-	GO:0005	GO:0005	contig925	Solyc04g	Beta-1 3-	GO:0008	SL2.40ch	AT3G49800.1		BSD dom	chr3:184	326.762	311.176	233.853	74.1279	52.7205	74.1583
GT	Sense	Sense	-0.359	Detected	0.359	Detected	0.000	-0.948	Detected	-1.935	Detected	-1.441	0.142	GT	Sens	contig930	contig930	RNA-bind	CATGCT	contig930	Solyc04g	Solyc04g	RNA-bind	GO:0003	GO:0003	contig930	Solyc04g	RNA-bind	GO:0003	SL2.40ch	AT1G78260.2		RNA reco	chr1:294	361.452	542.313	624.874	520.994	219.061	116.519
GT	Sense	Sense	0.124	Detected	-0.124	Detected	0.000	-1.018	Detected	-1.323	Detected	-1.171	0.027	GT	Sens	contig930	contig930	F-box pro	AGATTT	contig930	Solyc12g	Solyc12g	F-box protein PP2-B1 (AHRD V			contig930	Solyc12g	F-box protein PP2-B		SL2.40ch	AT5G63120.2		ethylene	chr5:253	60.8996	46.7468	51.4852	232.385	25.1524	21.4518
GT	Sense	Sense	-0.214	Detected	0.214	Detected	0.000	-1.271	Detected	-1.113	Detected	-1.192	0.035	GT	Sens	contig937	contig937	Calmodul	TGTGAT	contig937	Solyc01g	Solyc01g	Calmodul	GO:0005	GO:0005	contig937	Solyc01g	Calmodul	GO:0005	SL2.40ch	AT3G568	CAM3, ac	CAM3 (C	chr3:210	621.481	762.396	485.645	707.189	272.308	320.225
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	-2.630	Comprom	-2.531	Comprom	-2.581	0.001	GT	Sens	contig938	contig938	Unknown	GTAATG	contig938	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig938	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G38600.1		proline-r	chr5:154	57.1322	49.5932	22.4559	56.4137	8.20784	9.26261
GT	Sense	Sense	0.142	Detected	-0.142	Detected	0.000	-1.914	Detected	-2.063	Detected	-1.988	0.006	GT	Sens	contig954	contig954	Zinc finge	GCCAAG	contig954	Solyc07g	Solyc07g	Zinc finger family protein (AHR			contig954	Solyc03g	E3 ubiqui	GO:0005	SL2.40ch	AT2G02960.3		zinc fing	chr2:862	2817.26	2109.61	1665.77	2636.73	617.691	587.048
GT	Sense	Sense	-0.494	Detected	0.494	Detected	0.000	-1.729	Detected	-2.824	Detected	-2.276	0.091	GT	Sens	contig955	contig955	BZIP tran	GAGTTA	contig955	Solyc07g	Solyc07g	BZIP tran	GO:0006	GO:0006	contig955	Solyc07g	BZIP tran	GO:0016	SL2.40ch	AT3G581	ATBZIP61	BZIP61:	chr3:215	117.84	213.036	42.6	86.3263	45.631	22.5167
GT	Sense	Sense	0.113	Detected	-0.113	Detected	0.000	-1.153	Detected	-1.503	Detected	-1.328	0.024	GT	Sens	contig956	contig956	Unknown	TTATCC	contig956	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig956	Solyc01g	Unknown Protein (A		SL2.40ch	AT4G29180.1		leucine-r	chr4:143	77.502	60.4516	41.5908	44.6124	29.399	24.286
GT	Sense	Sense	0.144	Detected	-0.144	Detected	0.000	-1.000	Detected	-1.175	Detected	-1.088	0.023	GT	Sens	contig959	contig959	Ring H2 fi	GGATTT	contig959	Solyc12g	Solyc12g	Ring H2 fi	GO:0008	GO:0008	contig959	Solyc12g	Ring H2 fi	GO:0008	SL2.40ch	AT4G28890.1		protein b	chr4:142	44.9335	33.5522	19.1906	44.1759	18.5345	17.294
GT	Sense	Sense	-0.260	Detected	0.260	Detected	0.000	-1.895	Detected	-2.181	Detected	-2.038	0.021	GT	Sens	contig960	contig960	Unknown	AAGAAA	contig960	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig960	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G50000.1		protein k	chr5:203	333.996	436.504	175.021	240.191	98.0075	84.6883
GT	Sense	Sense	-0.408	Detected	0.408	Detected	0.000	-1.525	Detected	-2.201	Detected	-1.863	0.072	GT	Sens	contig961	contig961	Zinc finge	TTGCAC	contig961	Solyc11g	Solyc11g	Zinc finge	GO:0005	GO:0005	contig961	Solyc11g	Zinc finge	GO:0005	SL2.40ch	AT5G26770.3		unknown	chr5:940	164.529	263.918	89.5995	138.191	69.1378	45.5885
GT	Sense	Sense	-0.723	Detected	0.723	Detected	0.000	-1.237	Detected	-1.905	Detected	-1.571	0.187	GT	Sens	contig961	contig961	Expresse	AATGTC	contig961	Solyc10g	Solyc10g	Expressed protein (Fragment)			contig961	Solyc10g	Expressed protein (		SL2.40ch	AT2G172	EXL5	EXL5 (EX	chr2:749	170.146	422.673	152.003	205.405	108.598	72.0591
GT	Sense	Sense	-0.279	Detected	0.279	Detected	0.000	-1.166	Detected	-1.178	Detected	-1.172	0.052	GT	Sens	contig974	contig974	Ovarian c	CACCAT	contig974	Solyc11g	Solyc11g	Ovarian c	GO:0017	GO:0017	contig974	Solyc11g	Ovarian c	GO:0017	SL2.40ch	AT5G65400.1		unknown	chr5:261	1362.41	1828.44	773.353	1318.25	671.594	701.718
GT	Sense	Sense	0.186	Detected	-0.186	Detected	0.000	-1.242	Detected	-1.039	Detected	-1.141	0.033	GT	Sens	contig975	contig975	B3 domai	GGAGGA	contig975	Solyc02g	Solyc02g	B3 domai	GO:0006	GO:0006	contig975	Solyc02g026080.1.1				AT3G44440.1				1463.23	1030.54	843.47	1266.14	495.672	600.99
GT	Sense	Sense	-0.473	Detected	0.473	Detected	0.000	-1.147	Detected	-2.148	Detected	-1.648	0.139	GT	Sens	contig976	contig976	Protein s	GGCAAA	contig976	Solyc12g	Solyc12g	Protein s	GO:0006	GO:0006	contig976	Solyc12g	Protein s	GO:0006	SL2.40ch	AT5G668	MAPKKK	MAPKKK	chr5:266	234.153	411.23	127.527	231.705	133.783	70.4256
GT	Sense	Sense	0.133	Detected	-0.133	Detected	0.000	-1.599	Detected	-1.936	Detected	-1.768	0.014	GT	Sens	contig983	contig983	Calcium-l	AATGGA	contig983	Solyc02g	Solyc02g	Calcium-l	GO:0031	GO:0031	contig983	Solyc02g	Calcium-l	GO:0031	SL2.40ch	AT5G08570.1		pyruvate	chr5:277	295.99	224.37	74.88	314.732	81.2029	67.7319
GT	Sense	Sense	0.194	Detected	-0.194	Detected	0.000	-2.435	Comprom	-2.254	Comprom	-2.345	0.008	GT	Sens	contig985	contig985	Unknown	TGTTGG	contig985	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig985	Solyc09g020030.1.1				AT1G69800.2		CBS dom	chr1:262	19.991	13.9187	5.17164	6.92377	2.94446	3.51709
GT	Sense	Sense	-0.438	Detected	0.438	Detected	0.000	-1.922	Detected	-1.347	Detected	-1.635	0.089	GT	Sens	contig102	contig102	UDP-gluc	AGCCAA	contig102	Solyc10g	Solyc10g	UDP-gluc	GO:0008	GO:0008	contig102	Solyc10g	UDP-gluc	GO:0008	SL2.40ch	AT5G12890.1		UDP-gluc	chr5:406	56.9645	95.3098	32.1124	127.247	18.5628	29.1355
GT	Sense	Sense	-0.292	Detected	0.292	Detected	0.000	-1.716	Detected	-1.476	Detected	-1.596	0.037	GT	Sens	contig102	contig102	UDP-gluc	TTTTTG	contig102	Solyc10g	Solyc10g	UDP-gluc	GO:0008	GO:0008	contig102	Solyc10g	UDP-gluc	GO:0008	SL2.40ch	AT5G12890.1		UDP-gluc	chr5:406	55.7283	76.125	41.121	132.637	18.9326	23.5505
GT	Sense	Sense	-0.549	Detected	0.549	Detected	0.000	-2.385	Detected	-1.592	Detected	-1.988	0.099	GT	Sens	contig104	contig104	Disease r	GAAAGG	contig104	Solyc01g	Solyc01g	Disease resistance response r			contig104	Solyc01g	Disease resistance		SL2.40ch	AT1G58170.1		disease r	chr1:215	51.6517	100.734	13.9345	87.5782	13.1877	24.0697
GT	Sense	Sense	-0.433	Detected	0.433	Detected	0.000	-0.950	Detected	-1.880	Detected	-1.415	0.156	GT	Sens	contig106	contig106	Transcrip	CTGAGC	contig106	Solyc06g	Solyc06g	Transcrip	GO:0003	GO:0003	contig106	Solyc06g	Transcrip	GO:0003	SL2.40ch	AT3G07340.1		basic hel	chr3:234	156.818	260.51	135.044	121.714	99.8772	55.2265
GT	Sense	Sense	0.021	Detected	-0.021	Detected	0.000	-2.064	Detected	-2.169	Detected	-2.116	0.001	GT	Sens	contig100	contig100	Proteinas	TCCATC	contig100	Solyc03g	Solyc03g	Proteinas	GO:0004	GO:0004	contig100	Solyc03g	Proteinas	GO:0004	SL2.40ch	AT5G44680.1		methylad	chr5:180	11987.4	10620.1	16946.7	8525.58	2576.6	2524.75
GT	Sense	Sense	-0.318	Detected	0.318	Detected	0.000	-1.827	Comprom	-1.340	Detected	-1.584	0.058	GT	Sens	contig101	contig101	Serine/thr	TCAACT	contig101	Solyc07g	Solyc07g	Serine/thr	GO:0019	GO:0019	contig101	Solyc07g	Serine/thr	GO:0019	SL2.40ch	AT1G11300.1		ATP bind	chr1:379	30.1002	42.6159	9.75937	14.8199	9.63543	14.2285
GT	Sense	Sense	-0.594	Detected	0.594	Detected	0.000	-1.445	Detected	-1.336	Detected	-1.390	0.145	GT	Sens	contig101	contig101	Unknown	GTTCCC	contig101	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig101	Solyc06g	Unknown Protein (A		SL2.40ch	AT3G076	IBM1	IBM1 (inc	chr3:242	39.3832	81.8403	47.4096	49.2636	19.9108	22.6283
GT	Sense	Sense	-0.733	Detected	0.733	Detected	0.000	-1.043	Detected	-2.094	Detected	-1.568	0.224	GT	Sens	contig101	contig101	Pol polyp	GGGTGC	contig101	Solyc10g	Solyc10g	Pol polyp	GO:0006	GO:0006	contig101	Solyc10g	Pol polyp	GO:0006	SL2.40ch	AT4G103	HKT1, AT	HKT1 (HI	chr4:639	116.704	294.048	124.213	76.283	85.8581	43.6625
GT	Sense	Sense	-0.318	Detected	0.318	Detected	0.000	-2.045	Detected	-1.371	Detected	-1.708	0.066	GT	Sens	contig106	contig106	Sulfotran	TTACAG	contig106	Solyc04g	Solyc04g	Sulfotran	GO:0008	GO:0008	contig106	Solyc04g	Sulfotran	GO:0008	SL2.40ch	AT1G59680.1				36.7522	52.0593	35.3067	57.2936	10.1232	17.0147
GT	Sense	Sense	0.053	Detected	-0.053	Detected	0.000	-1.887	Detected	-2.512	Detected	-2.200	0.020	GT	Sens	contig109	contig109	HIN1-like	ATCCTA	contig109	Solyc10g	Solyc10g	HIN1-like protein (Fragment) (A			contig109	Solyc10g	HIN1-like protein (Fr		SL2.40ch	AT5G63900.1		PHD fing	chr5:255	783.557	664.091	312.452	605.218	186.19	127.219
GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-0.947	Detected	-1.991	Detected	-1.469	0.115	GT	Sens	contig110	contig110	CM0216.3	CAACAT	contig110	Solyc02g	Solyc02g	CM0216.330.nc protein (AHRD			contig110	Solyc02g	CM0216.330.nc prot		SL2.40ch	AT5G05160.1		leucine-r	chr5:152	92.9766	106.211	78.8759	124.709	49.2253	25.1561
GT	Sense	Sense	-0.842	Detected	0.842	Detected	0.000	-0.854	Detected	-2.226	Detected	-1.540	0.292	GT	Sens	contig111	contig111	Unknown	ACAAGA	contig111	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig111	Solyc06g	Unknown Protein (A		SL2.40ch	AT5G03870.1		glutared	chr5:103	317.25	929.398	283.44	169.821	286.906	116.737
GT	Sense	Sense	-0.464	Detected	0.464	Detected	0.000	-1.857	Detected	-1.673	Detected	-1.765	0.065	GT	Sens	contig111	contig111	Long-cha	GAAAAT	contig111	Solyc02g	Solyc02g	Long-cha	GO:0018	GO:0018	contig111	Solyc02g	Long-cha	GO:0004	SL2.40ch	AT1G68270.1		AMP-dep	chr1:255	162.208	281.433	380.082	718.736	56.3292	67.4189
GT	Sense	Sense	-0.175	Detected	0.175	Detected	0.000	-1.056	Detected	-1.351	Detected	-1.204	0.034	GT	Sens	contig112	contig112	Cc-nbs-lr	GAGAAG	contig112	Solyc11g	Solyc11g	Cc-nbs-lrr resistance protein (			contig112	Solyc05g014620.1.1				AT1G086	ZIGA4	ZIGA4 (A	chr1:276	9804.11	11389	6385.15	9393.22	4851.4	4165.89
GT	Sense	Sense	-0.240	Detected	0.240	Detected	0.000	-1.129	Detected	-1.399	Detected	-1.264	0.044	GT	Sens	contig115	contig115	Ribosoma	ACGCCA	contig115	Solyc11g	Solyc11g	Ribosoma	GO:0005	GO:0005	contig115	Solyc11g	Ribosoma	GO:0005	SL2.40ch	ATMG002	RPL5	encodes	chrM:57	81.3785	103.53	58.0796	69.6481	40.061	35.0021
GT	Sense	Sense	-0.377	Detected	0.377	Detected	0.000	-1.688	Detected	-1.199	Detected	-1.443	0.085	GT	Sens	contig115	contig115	Trachear	CTAATA	contig115	Solyc03g	Solyc03g	Tracheary element differentiat			contig115	Solyc03g	Tracheary element		SL2.40ch	AT2G177	ATBZIP2	ATBZIP2	chr2:772	73.2182	112.568	68.754	118.527	26.8975	39.7945
GT	Sense	Sense	-0.696	Detected	0.696	Detected	0.000	-0.870	Detected	-1.808	Detected	-1.339	0.252	GT	Sens	contig115	contig115	Ycf15 (AH	ATATTC	contig115	Solyc11g	Solyc11g	Ycf15 (AHRD V1 ***- D2KLP6_C			contig115	Solyc11g	Ycf15 (AHRD V1 ***-		SL2.40ch	ATCG012	ORF77.2	hypothet	chrC:144	434.185	1038.48	381.4	313.572	350.763	192.88
GT	Sense	Sense	0.427	Detected	-0.427	Detected	0.000	-1.201	Detected	-0.847	Detected	-1.024	0.157	GT	Sens	contig117	contig117	Myb-relat	GCTCCT	contig117	Solyc07g	Solyc07g	Myb-relat	GO:0045449		contig117	Solyc07g	Myb-relat	GO:0003	SL2.40ch	AT5G102	MYB92, A	ATMYB9	chr5:323	105.606	53.2842	169.205	152.525	31.1648	41.9388
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-1.557	Detected	-1.106	Detected	-1.332	0.035	GT	Sens	contig118	contig118	Leucine-r	GTAATT	contig118	Solyc02g	Solyc02g	Leucine-r	GO:0019	GO:0019	contig118	Solyc02g	Receptor	GO:0004	SL2.40ch	AT3G051	RBK2	RBK2 (Ro	chr3:143	103.296	79.1606	81.6844	120.911	29.3437	42.249
GT	Sense	Sense	0.230	Detected	-0.230	Detected	0.000	-1.388	Detected	-1.172	Detected	-1.280	0.037	GT	Sens	contig119	contig119	Developm	TTCTGC	contig119	Solyc10g	Solyc10g	Developmentally-regulated GT			contig119	Solyc10g	Developmentally-re		SL2.40ch	AT1G72660.3		developm	chr1:273	116.648	77.267	45.9726	97.5128	34.6329	42.3856
GT	Sense	Sense	0.042	Detected	-0.042	Detected	0.000	-1.557	Detected	-0.926	Detected	-1.241	0.060	GT	Sens	contig120	contig120	Alpha-hyd	GAGTGT	contig120	Solyc07g	Solyc07g	Alpha-hyd	GO:0080	GO:0080	contig120	Solyc07g	Alpha-hyd	GO:0080	SL2.40ch	AT3G049	WNK1, ZI	WNK1 (W	chr3:135	261.83	225.358	56.8864	477.74	78.8451	128.602
GT	Sense	Sense	0.143	Detected	-0.143	Detected	0.000	-1.415	Detected	-1.229	Detected	-1.322	0.016	GT	Sens	contig120	contig120	Cytochro	GTGATT	contig120	Solyc04g	Solyc04g	Cytochro	GO:0019	GO:0019	contig120	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT5G19640.1		proton-d	chr5:663	177.234	132.491	150.985	226.667	54.8864	65.7768
GT	Sense	Sense	0.375	Detected	-0.375	Detected	0.000	-2.368	Detected	-1.075	Detected	-1.722	0.148	GT	Sens	contig121	contig121	Decarbox	CGAGAA	contig121	Solyc08g	Solyc08g	Decarbox	GO:0030	GO:0030	contig121	Solyc08g	Decarbox	GO:0030	SL2.40ch	AT1G437	emb1075	emb1075	chr1:164	604.992	327.878	233.364	418.248	82.3761	212.622
GT	Sense	Sense	-0.804	Detected	0.804	Detected	0.000	-1.616	Detected	-2.667	Detected	-2.142	0.155	GT	Sens	contig121	contig121	Retrotran	AGGAAT	contig121	Solyc07g	Solyc07g	Retrotran	GO:0015	GO:0015	contig121	Solyc00g	Pol polyp	GO:0003	SL2.40ch	AT5G66790.1				325.508	904.028	282.242	137.105	168.914	85.9381
GT	Sense	Sense	-0.266	Detected	0.266	Detected	0.000	-0.952	Comprom	-3.230	Comprom	-2.091	0.216	GT	Sens	contig122	contig122	Unknown	GCAGCA	contig122	Solyc06g	Solyc06g	Unknown Protein (AHRD V1)			contig122	Solyc11g	Avr9/Cf-9 rapidly eli		SL2.40ch	AT5G094	EICBP.B	EICBP.B	chr5:292	16.3492	21.5557	14.569	30.1646	9.26794	2.01213
GT	Sense	Sense	-0.264	Detected	0.264	Detected	0.000	-4.021	Detected	-3.163	Detected	-3.592	0.019	GT	Sens	contig126	contig126	Patatin-lik	CCTCAG	contig126	Solyc04g	Solyc04g	Patatin-lik	GO:0016	GO:0016	contig126	Solyc04g	Patatin-lik	GO:0045	SL2.40ch	AT4G370	PLP4, PL	PLP4 (PA	chr4:174	3978.74	5232.9	1186.07	498.622	268.444	512.43
GT	Sense	Sense	-0.722	Detected	0.722	Detected	0.000	-1.050	Detected	-2.161	Comprom	-1.605	0.220	GT	Sens	contig127	contig127	Nitrate tra	GACAAC	contig127	Solyc06g	Solyc06g	Nitrate tra	GO:0080	GO:0080	contig127	Solyc06g	Nitrate tra	GO:0080	SL2.40ch	AT3G45680.1		proton-d	chr3:167	29.4521	73.0107	4.43314	27.4446	21.3896	10.4279
GT	Sense	Sense	-0.402	Detected	0.402	Detected	0.000	-1.350	Detected	-2.080	Detected	-1.715	0.087	GT	Sens	contig128	contig128	Pol polyp	GGTTTT	contig128	Solyc04g	Solyc04g	Pol polyp	GO:0006	GO:0006	contig128	Solyc04g040100.1.1				AT5G40450.2		unknown	chr5:161	369.785	588.314	325.032	226.849	174.741	111.007
GT	Sense	Sense	-0.322	Detected	0.322	Detected	0.000	-1.509	Detected	-2.268	Comprom	-1.889	0.063	GT	Sens	contig128	contig128	Long-cha	GCAAGA	contig128	Solyc09g	Solyc09g	Long-cha	GO:0008	GO:0008	contig128	Solyc09g	Long-cha	GO:0004	SL2.40ch	AT3G059	LACS6, A	LACS6 (lo	chr3:178	38.7514	55.2039	19.3821	67.7039	15.5139	9.66123
GT	Sense	Sense	0.221	Detected	-0.221	Detected	0.000	-1.315	Detected	-1.231	Detected	-1.273	0.030	GT	Sens	contig129	contig129	Unknown	GTGAAA	contig129	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig129	Solyc08g061470.1.1				AT3G45040.1		phospha	chr3:164	3632.29	2439.16	2567.37	4312.74	1142.26	1275.29
GT	Sense	Sense	-0.553	Detected	0.553	Detected	0.000	-1.037	Comprom	-1.505	Comprom	-1.271	0.168	GT	Sens	contig129	contig129	UDP-gluc	GGAAAG	contig129	Solyc12g	Solyc12g	UDP-gluc	GO:0008	GO:0008	contig129	Solyc12g	UDP-gluc	GO:0008	SL2.40ch	AT1G223	AtUGT85	AtUGT85	chr1:789	15.3367	30.0901	19.3064	35.5124	9.99615	7.61154
GT	Sense	Sense	0.097	Detected	-0.097	Detected	0.000	-1.169	Comprom	-1.321	Comprom	-1.245	0.010	GT	Sens	contig130	contig130	60s acidic	CTTTGA	contig130	Solyc07g	Solyc07g	60s acidic	GO:0005	GO:0005	contig130	Solyc06g	Receptor-	GO:0005	SL2.40ch	AT5G40710.1		zinc fing	chr5:162	16.6397	13.2655	8.11142	9.73736	6.31057	5.98359
GT	Sense	Sense	-0.089	Detected	0.089	Detected	0.000	-1.584	Detected	-1.836	Detected	-1.710	0.008	GT	Sens	contig132	contig132	F-box fam	TATAGT	contig132	Solyc08g	Solyc08g	F-box fam	GO:0004	GO:0004	contig132	Solyc12g	Pistil exte	GO:0009	SL2.40ch	AT5G130	ATGSL12	ATGSL12	chr5:411	48.0478	49.5661	57.3005	53.9145	15.5454	13.7469
GT	Sense	Sense	-0.846	Detected	0.846	Detected	0.000	-3.186	Comprom	-4.496	Comprom	-3.841	0.070	GT	Sens	contig132	contig132	Acyltrans	GTGTGT	contig132	Solyc11g	Solyc11g	Acyltrans	GO:0016	GO:0016	contig132	Solyc11g	Acyltrans	GO:0016	SL2.40ch	AT5G59400.2		unknown	chr5:239	27.2923	80.4485	166.472	171.544	4.91668	2.08836
GT	Sense	Sense	-0.154	Detected	0.154	Detected	0.000	-1.399	Detected	-0.816	Detected	-1.108	0.078	GT	Sens	contig135	contig135	Copper io	TGGGGC	contig135	Solyc10g	Solyc10g	Copper ion binding protein (AI			contig135	Solyc10g	Copper ion binding		SL2.40ch	AT5G07650.1		formin ho	chr5:241	148.809	168	48.6339	100.171	57.2467	90.3311
GT	Sense	Sense	-0.706	Detected	0.706	Detected	0.000	-1.833	Comprom	-3.421	Comprom	-2.627	0.132	GT	Sens	contig136	contig136	Transpos	GGGTCC	contig136	Solyc08g	Solyc08g	Transposase (AHRD V1 **-- O6			contig136	Solyc11g	Transposase (AHRD		SL2.40ch	AT4G38650.1				17.2123	41.7583	9.92817	9.30473	7.1827	2.51732
GT	Sense	Sense	-0.113	Detected	0.113	Detected	0.000	-1.477	Detected	-1.155	Detected	-1.316	0.022	GT	Sens	contig140	contig140	Unknown	TTTGGA	contig140	Solyc05g	Solyc05g	Unknown Protein (AHRD V1)			contig140	Solyc05g	Unknown Protein (A		SL2.40ch	AT1G708	MLP34	MLP34 (M	chr1:267	79.7867	85.132	22.8881	178.2	28.2703	37.2413
GT	Sense	Sense	0.047	Detected	-0.047	Detected	0.000	-1.306	Detected	-0.874	Detected	-1.090	0.039	GT	Sens	contig142	contig142	Pectinest	CTGATT	contig142	Solyc02g	Solyc02g	Pectinest	GO:0030	GO:0030	contig142	Solyc02g	Pectinest	GO:0005	SL2.40ch	AT1G02810.1		pectines	chr1:618	1520.03	1297.63	495.79	3150.15	542.345	770.698
GT	Sense	Sense	-0.562	Detected	0.562	Detected	0.000	-0.893	Detected	-1.121	Detected	-1.007	0.221	GT	Sens	contig143	contig143	Receptor	ATCAGT	contig143	Solyc03g	Solyc03g	Receptor	GO:0005	GO:0004	contig143	Solyc03g	Receptor-	GO:0004	SL2.40ch	AT5G24080.1		protein k	chr5:813	558.4	1109.84	388.927	909.613	404.639	364.07
GT	Sense	Sense	-0.389	Detected	0.389	Detected	0.000	-1.004	Comprom	-1.600	Comprom	-1.302	0.117	GT	Sens	contig143	contig143	Cytochro	AACAGA	contig143	Solyc04g	Solyc04g	Cytochro	GO:0019	GO:0019	contig143	Solyc04g	Cytochro	GO:0019	SL2.40ch	AT4G319	CYP82C4	CYP82C4	chr4:154	11.6076	18.1343	2.56044	10.3818	6.90588	4.81496
GT	Sense	Sense	0.411	Detected	-0.411	Detected	0.000	-2.548	Detected	-1.132	Detected	-1.840	0.154	GT	Sens	contig148	contig148	Decarbox	GTGCAA	contig148	Solyc08g	Solyc08g	Decarbox	GO:0019	GO:0019	contig148	Solyc08g	Decarbox	GO:0030	SL2.40ch	AT1G437	emb1075	emb1075	chr1:164	816.42	420.983	346.722	489.762	95.7322	269.027
GT	Sense	Sense	0.594	Detected	-0.594	Detected	0.000	-0.815	Detected	-1.350	Detected	-1.083	0.238	GT	Sens	contig148	contig148	Proteinas	TGGATT	contig148	Solyc03g	Solyc03g	Proteinas	GO:0004	GO:0004	contig148	Solyc03g	Proteinas	GO:0004	SL2.40ch	AT4G15830.1		binding	chr4:899	1438.34	575.875	486.036	971.395	493.862	359.142
GT	Sense	Sense	-0.836	Detected	0.836	Detected	0.000	-0.852	Detected	-1.986	Detected	-1.419	0.295	GT	Sens	contig154	contig154	%26apos	TACAGA	contig154	Solyc11g	Solyc11g	%26apos	GO:0005	GO:0005	contig154	Solyc11g	&aposchi	GO:0005	SL2.40ch	AT3G58090.1		FUNCTIO	chr3:215	4151.68	12054.8	4151.68	2423.9	3743.1	1796.66
GT	Sense	Sense	-0.748	Detected	0.748	Detected	0.000	-2.196	Detected	-1.601	Detected	-1.898	0.142	GT	Sens	contig157	contig157	Peroxida	ATCGGT	contig157	Solyc01g	Solyc01g	Peroxida	GO:0055	GO:0055	contig157	Solyc01g	Peroxida	GO:0004	SL2.40ch	AT5G19890.1		peroxida	chr5:672	12996.3	33400	12196.2	17656	4342.35	6908.14
GT	Sense	Sense	-0.455	Detected	0.455	Detected	0.000	-1.379	Detected	-1.042	Detected	-1.210	0.130	GT	Sens	contig157	contig157	Dirigent-l	ATGGAA	contig157	Solyc01g	Solyc01g	Dirigent-like protein 1 (AHRD V			contig157	Solyc01g	Disease resistance		SL2.40ch	AT1G58170.1		disease r	chr1:215	825.465	1413.72	277.344	1430.57	396.522	527.949
GT	Sense	Sense	0.169	Detected	-0.169	Detected	0.000	-1.238	Detected	-1.175	Detected	-1.206	0.020	GT	Sens	contig159	contig159	Pathogen	TGCAAT	contig159	Solyc00g	Solyc00g	Pathogen	GO:0005	GO:0005	contig159	Solyc00g	Pathogen	GO:0005	SL2.40ch	AT2G198	MIOX2	MIOX2 (M	chr2:853	748.568	539.851	1216.87	639.775	257.362	283.297
GT	Sense	Sense	-0.154	Detected	0.154	Detected	0.000	-2.150	Comprom	-1.708	Comprom	-1.929	0.019	GT	Sens	contig160	contig160	Ycf1 (AHF	ACTCCA	contig160	Solyc11g	Solyc11g	Ycf1 (AHRD V1 ***- D2KLR1_OI			contig160	Solyc11g	Ycf1 (AHRD V1 ***- D		SL2.40ch	AT5G48830.1		unknown	chr5:198	21.7585	24.5435	10.7793	14.3865	4.97228	7.11448
GT	Sense	Sense	0.482	Detected	-0.482	Detected	0.000	-1.215	Detected	-2.006	Detected	-1.610	0.123	GT	Sens	contig160	contig160	Glutathio	TTTACA	contig160	Solyc01g	Solyc01g	Glutathione S-transferase (AHI			contig160	Solyc01g	Glutathione S-transf		SL2.40ch	AT2G294	ATGSTU1	ATGSTU	chr2:126	205.781	96.1942	43.2078	73.1015	57.8752	35.2414
GT	Sense	Sense	0.207	Detected	-0.207	Detected	0.000	-2.271	Detected	-1.844	Detected	-2.057	0.020	GT	Sens	contig161	contig161	Unknown	CCTGTG	contig161	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig161	Solyc02g067600.1.1				AT5G25590.1		INVOLVE	chr5:890	472.243	322.935	258.682	320.128	77.2778	109.444
GT	Sense	Sense	0.372	Detected	-0.372	Detected	0.000	-2.251	Detected	-1.964	Detected	-2.108	0.034	GT	Sens	contig162	contig162	Peroxida	AATGAG	contig162	Solyc10g	Solyc10g	Peroxida	GO:0055	GO:0055	contig162	Solyc10g	Peroxida	GO:0055	SL2.40ch	AT5G06720.1		peroxida	chr5:207	15336.3	8349.95	8836.68	3803.65	2269.18	2918.22
GT	Sense	Sense	0.010	Detected	-0.010	Detected	0.000	-3.755	Comprom	-3.024	Comprom	-3.389	0.011	GT	Sens	contig163	contig163	Stearoyl-	AAGAAG	contig163	Solyc06g	Solyc06g	Stearoyl-	GO:0004	GO:0004	contig163	Solyc06g	Stearoyl-	GO:0004	SL2.40ch	AT1G13940.1				30.6381	27.5418	7.52034	55.1873	2.05493	3.59241
GT	Sense	Sense	-0.036	Detected	0.036	Detected	0.000	-1.246	Detected	-0.928	Detected	-1.087	0.022	GT	Sens	contig164	contig164	Transcrip	TCAGAT	contig164	Solyc06g	Solyc06g	Transcription factor homolog			contig164	Solyc07g	Nascent r	GO:0051	SL2.40ch	AT5G25500.1		unknown	chr5:888	762.855	731.229	535.328	1058.45	300.695	394.98
GT	Sense	Sense	0.035	Detected	-0.035	Detected	0.000	-1.488	Detected	-1.773	Detected	-1.630	0.008	GT	Sens	contig165	contig165	Unknown	ACGACC	contig165	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig165	Solyc10g	Ulp1 protease family		SL2.40ch	AT2G32360.1				102.624	89.1261	64.649	69.1258	32.5596	28.1524
GT	Sense	Sense	0.247	Detected	-0.247	Detected	0.000	-1.661	Detected	-1.158	Detected	-1.409	0.057	GT	Sens	contig165	contig165	NAC dom	AACAAG	contig165	Solyc07g	Solyc07g	NAC dom	GO:0045449		contig165	Solyc02g	Calcium-t	GO:0016	SL2.40ch	AT1G277	ACA1, PE	ACA1 (AU	chr1:967	62.8444	40.6907	34.3928	31.1647	15.2709	22.8015
GT	Sense	Sense	-0.067	Detected	0.067	Detected	0.000	-1.571	Detected	-1.742	Detected	-1.657	0.004	GT	Sens	contig173	contig173	Delta 12 f	TTACAC	contig173	Solyc12g	Solyc12g	Delta 12 fatty acid desaturase			contig173	Solyc12g	Delta 12 fatty acid d		SL2.40ch	ATCG012	YCF2.2	hypothet	chrC:145	291.88	291.962	199.21	342.165	93.8003	87.7893

GT	Sense	Sense	0.592	Detected	-0.592	Detected	0.000	-4.373	Comprom	-3.271	Comprom	-3.822	0.042	GT	Sens	contig174	contig174	Peroxidas	ATAAAAC	contig174	Solyc12g	Solyc12g	Peroxidas	GO:00551	GO:00551	contig174	Solyc10g	Peroxidas	GO:00551	SL2.40ch	AT2G38500.1		FUNCTIO	chr2:161	68.1613	27.3682	33.2366	11.1152	1.98989	4.50101
GT	Sense	Sense	0.095	Detected	-0.095	Detected	0.000	-0.920	Detected	-1.283	Detected	-1.102	0.033	GT	Sens	contig177	contig177	Unknown	TGACTT	contig177	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig177	Solyc12g	Protein kinase like r		SL2.40ch	AT4G181	AML3	AML3 (AI	chr4:100	49.4772	39.5354	17.0079	20.0623	22.3157	18.2843
GT	Sense	Sense	-0.312	Detected	0.312	Detected	0.000	-1.867	Detected	-1.647	Detected	-1.757	0.034	GT	Sens	contig178	contig178	Equilibrat	TATGTC	contig178	Solyc02g	Solyc02g	Equilibrat	GO:0005	GO:0005	contig178	Solyc02g079330.2.1				AT4G05140.1		equilibra	chr4:265	162.357	228.212	33.9608	109.37	50.3672	61.8439
GT	Sense	Sense	-0.253	Detected	0.253	Detected	0.000	-1.146	Detected	-2.341	Comprom	-1.743	0.115	GT	Sens	contig178	contig178	CM0216.3	CCTTTC	contig178	Solyc02g	Solyc02g	CM0216.330.nc protein (AHRD			contig178	Solyc02g	CM0216.330.nc prot		SL2.40ch	AT3G15080.1		exonucle	chr3:507	26.2267	33.9325	13.2491	37.1659	12.8742	5.92431
GT	Sense	Sense	-0.335	Detected	0.335	Detected	0.000	-1.176	Comprom	-2.732	Comprom	-1.954	0.147	GT	Sens	contig179	contig179	UDP-gluc	CAACGC	contig179	Solyc10g	Solyc10g	UDP-gluc	GO:0080	GO:0080	contig179	Solyc10g	UDP-gluc	GO:0080	SL2.40ch	AT2G36970.1		UDP-gluc	chr2:155	13.4693	19.5457	11.362	60.2437	6.85548	2.45714
GT	Sense	Sense	0.153	Detected	-0.153	Detected	0.000	-1.160	Detected	-1.504	Detected	-1.332	0.029	GT	Sens	contig181	contig181	Xylogluca	TCTTCT	contig181	Solyc03g	Solyc03g	Xylogluca	GO:0005	GO:0005	contig181	Solyc03g	Xylogluca	GO:00167	SL2.40ch	AT4G258	XTR6. XT	XTR6 (XY	chr4:131	11505.4	8481.73	5702.75	8700.11	4221.98	3504.54
GT	Sense	Sense	-0.548	Detected	0.548	Detected	0.000	-1.392	Detected	-2.145	Comprom	-1.769	0.117	GT	Sens	contig184	contig184	DC1 dom	ACTGCA	contig184	Solyc01g	Solyc01g	DC1 domain containing protei			contig184	Solyc01g	CHP-rich zinc finger		SL2.40ch	AT2G16250.1		leucine-r	chr2:703	21.6011	42.0916	30.2246	83.8904	10.9665	6.85629
GT	Sense	Sense	0.121	Detected	-0.121	Detected	0.000	-2.048	Detected	-1.041	Detected	-1.544	0.097	GT	Sens	contig185	contig185	Polygalac	AAAGAG	contig185	Solyc12g	Solyc12g	Polygalac	GO:0005	GO:0005	contig185	Solyc12g	Polygalac	GO:0005	SL2.40ch	AT5G14650.1		polygala	chr5:472	41572.3	32028.5	19540.3	31017.1	8424.29	17844
GT	Sense	Sense	-0.130	Detected	0.130	Detected	0.000	-1.191	Detected	-1.184	Detected	-1.187	0.012	GT	Sens	contig186	contig186	Aberrant	ATTTGC	contig186	Solyc10g	Solyc10g	Aberrant	GO:0016	GO:0016	contig186	Solyc10g	Aberrant	GO:0016	SL2.40ch	AT5G196	STT3A	STT3A (S	chr5:665	24.2153	26.4196	5.5397	64.8694	10.5802	11.1994
GT	Sense	Sense	-0.110	Detected	0.110	Detected	0.000	-1.156	Detected	-0.928	Detected	-1.042	0.022	GT	Sens	contig186	contig186	Calcium-t	TACCTG	contig186	Solyc09g	Solyc09g	Calcium-t	GO:0016	GO:0016	contig186	Solyc09g	Calcium-t	GO:0005	SL2.40ch	AT5G196	SULTR3:	SULTR3:	chr5:661	83.4127	88.6205	61.6781	106.381	36.8304	45.4564
GT	Sense	Sense	0.127	Detected	-0.127	Detected	0.000	-1.462	Detected	-0.829	Detected	-1.146	0.078	GT	Sens	contig188	contig188	Sulfotran	GAAGAG	contig188	Solyc05g	Solyc05g	Sulfotran	GO:00081	GO:00081	contig188	Solyc05g	Sulfotrans	GO:00801	SL2.40ch	AT3G137	AtcwINV5	AtcwINV5	chr3:452	682.686	522.036	157.27	1265.77	206.901	337.986
GT	Sense	Sense	-0.322	Detected	0.322	Detected	0.000	-0.981	Detected	-1.209	Detected	-1.095	0.085	GT	Sens	contig189	contig189	Reverse t	ATGGTT	contig189	Solyc04g	Solyc04g	Reverse t	GO:0006	GO:0006	contig189	Solyc01g	Glutamate	GO:0006	SL2.40ch	AT5G11410.1		protein k	chr5:363	50.043	71.287	48.8861	73.4969	28.9	25.9925
GT	Sense	Sense	-0.217	Detected	0.217	Detected	0.000	-1.671	Detected	-2.480	Detected	-2.076	0.046	GT	Sens	contig189	contig189	Mutant re	CTCCAA	contig189	Solyc08g	Solyc08g	Mutant required to maintain re			contig189	Solyc08g077640.1.1				AT4G38200.1		guanine	chr4:179	551.196	678.734	267.187	299.067	183.406	110.285
GT	Sense	Sense	-0.072	Detected	0.072	Detected	0.000	-3.263	Detected	-2.401	Detected	-2.832	0.023	GT	Sens	contig19	contig19	Unknown	ATAGGA	contig19	Solyc07g	Solyc07g	Unknown	GO:0045449		contig19	Solyc10g045250.1.1				AT3G02900.1		unknown	chr3:645	254.854	256.704	160.38	240.026	25.4397	48.7255
GT	Sense	Sense	-0.749	Detected	0.749	Detected	0.000	-1.408	Detected	-1.152	Detected	-1.280	0.234	GT	Sens	contig190	contig190	Unknown	CATGGG	contig190	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig190	Solyc01g	Disease resistance		SL2.40ch	AT3G13650.1				1421.4	3660.4	711.599	3394.51	820.739	1032.51
GT	Sense	Sense	-0.231	Detected	0.231	Detected	0.000	-0.874	Detected	-1.262	Detected	-1.068	0.071	GT	Sens	contig191	contig191	Mutator-li	ACAATA	contig191	Solyc01g	Solyc01g	Mutator-li	GO:0008	GO:0008	contig191	Solyc12g	Unknown	GO:0008	SL2.40ch	AT4G36400.2		FAD linke	chr4:171	12069.9	15147.4	11651.5	9962.03	7043.75	5670.47
GT	Sense	Sense	0.125	Detected	-0.125	Detected	0.000	-1.222	Detected	-1.033	Detected	-1.127	0.019	GT	Sens	contig191	contig191	Unknown	GCATCA	contig191	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig191	Solyc07g	Unknown Protein (A		SL2.40ch	AT5G08630.1		DDT dom	chr5:279	49.282	37.7847	28.0084	46.4116	17.6662	21.2209
GT	Sense	Sense	-0.210	Detected	0.210	Detected	0.000	-1.139	Detected	-1.049	Detected	-1.094	0.037	GT	Sens	contig192	contig192	Cytochro	TTTCAA	contig192	Solyc03g	Solyc03g	Cytochro	GO:0020	GO:0020	contig192	Solyc03g	Cytochro	GO:0004	SL2.40ch	AT3G483	CYP71A2	CYP71A2	chr3:178	168.401	205.492	196.041	730.416	80.6482	90.4164
GT	Sense	Sense	-0.099	Detected	0.099	Detected	0.000	-1.442	Detected	-1.750	Detected	-1.596	0.013	GT	Sens	contig192	contig192	Unknown	GGTGGT	contig192	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig192	Solyc10g	Unknown Protein (A		SL2.40ch	AT4G030	BSL1	kelch rep	chr4:135	3048.14	3188.46	2586.21	2736.74	1095.67	932.463
GT	Sense	Sense	0.041	Detected	-0.041	Detected	0.000	-1.591	Detected	-1.143	Detected	-1.367	0.027	GT	Sens	contig194	contig194	Unknown	CAAATG	contig194	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig194	Solyc01g	Unknown Protein (A		SL2.40ch	AT1G20970.1		FUNCTIO	chr1:731	2204.81	1898.83	666.892	5302.4	648.28	932.131
GT	Sense	Sense	0.090	Detected	-0.090	Detected	0.000	-2.228	Detected	-1.362	Detected	-1.795	0.056	GT	Sens	contig196	contig196	Unknown	AGGTAC	contig196	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig196	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G07630.1		lipid tran	chr5:241	64.3203	51.7413	47.502	45.5462	11.7574	22.5803
GT	Sense	Sense	0.134	Detected	-0.134	Detected	0.000	-1.879	Detected	-1.521	Detected	-1.700	0.017	GT	Sens	contig198	contig198	Unknown	ATCAAG	contig198	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig198	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G05470.1		formin ho	chr3:157	60.16	45.5522	33.6436	67.3463	13.5911	18.3476
GT	Sense	Sense	-0.003	Detected	0.003	Detected	0.000	-0.996	Detected	-1.254	Detected	-1.125	0.013	GT	Sens	contig198	contig198	Receptor-	TTAAAC	contig198	Solyc08g	Solyc08g	Receptor	GO:0005	GO:0005	contig198	Solyc08g	Receptor	GO:0004	SL2.40ch	AT1G24650.1		leucine-r	chr1:873	714.164	653.831	418.278	392.493	327.168	288.193
GT	Sense	Sense	-0.465	Detected	0.465	Detected	0.000	-1.099	Detected	-1.402	Comprom	-1.251	0.125	GT	Sens	contig198	contig198	FIP1 (AHF	TATCTG	contig198	Solyc11g	Solyc11g	FIP1 (AHRD V1 **-- B6U778_MA			contig198	Solyc11g	FIP1 (AHRD V1 **-- B		SL2.40ch	AT5G08350.1		GRAM do	chr5:268	17.0885	29.6968	9.38459	3.71047	10.0406	8.57373
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-2.790	Detected	-1.674	Detected	-2.232	0.058	GT	Sens	contig200	contig200	Gibberelli	TTTCGC	contig200	Solyc09g	Solyc09g	Gibberelli	GO:0004	GO:0004	contig200	Solyc09g	Gibberelli	GO:0004	SL2.40ch	AT3G08530.1		clathrin h	chr3:258	943.585	790.978	556.255	410.198	119.277	272.319
GT	Sense	Sense	-0.613	Detected	0.613	Detected	0.000	-0.915	Detected	-1.363	Detected	-1.139	0.223	GT	Sens	contig200	contig200	Expansin	AATAAT	contig200	Solyc01g	Solyc01g	Expansin	GO:00051	GO:00051	contig200	Solyc05g	Expansin	GO:00051	SL2.40ch	AT2G030	ATEXPA1	ATEXPA1	chr2:917	84.6239	180.37	66.3275	103.381	62.5427	48.331
GT	Sense	Sense	-0.258	Detected	0.258	Detected	0.000	-1.219	Detected	-2.095	Detected	-1.657	0.083	GT	Sens	contig201	contig201	Unknown	TGAAAA	contig201	Solyc00g	Solyc00g	Unknown Protein (AHRD V1)			contig201	Solyc06g	Unknown Protein (A		SL2.40ch	AT2G01021.1		unknown	chr2:657	32515	42395.9	22515.7	29562.1	15224.8	8744.97
GT	Sense	Sense	-0.168	Detected	0.168	Detected	0.000	-1.042	Detected	-1.234	Detected	-1.138	0.028	GT	Sens	contig207	contig207	Unknown	TGTCAT	contig207	Solyc03g	Solyc03g	Unknown	GO:0005	GO:0005	contig207	Solyc03g	Unknown	GO:0005	SL2.40ch	AT1G042	SHY2. IAA	SHY2 (SH	chr1:112	234.48	269.736	133.736	374.108	116.577	107.589
GT	Sense	Sense	0.136	Detected	-0.136	Detected	0.000	-2.144	Comprom	-1.244	Detected	-1.694	0.069	GT	Sens	contig208	contig208	Sulfotran	ACTCAA	contig208	Solyc05g	Solyc05g	Sulfotran	GO:00081	GO:00081	contig208	Solyc05g	Sulfotrans	GO:00081	SL2.40ch	AT2G27570.1		sulfotran	chr2:117	42.0092	31.7121	17.845	50.2236	7.88512	15.4976
GT	Sense	Sense	-0.042	Detected	0.042	Detected	0.000	-1.154	Detected	-1.755	Detected	-1.455	0.041	GT	Sens	contig208	contig208	Unknown	AAGGAG	contig208	Solyc04g	Solyc04g	Unknown Protein (AHRD V1)			contig208	Solyc04g	Unknown Protein (A		SL2.40ch	AT3G32180.1		unknown	chr3:131	77.1341	74.5232	81.8498	69.4451	32.5286	22.5903
GT	Sense	Sense	-0.150	Detected	0.150	Detected	0.000	-1.114	Detected	-1.423	Detected	-1.269	0.028	GT	Sens	contig208	contig208	FIP1 (AHF	CAAAAG	contig208	Solyc04g	Solyc04g	FIP1 (AHRD V1 **-- B6U778_MA			contig208	Solyc04g	FIP1 (AHRD V1 **-- B		SL2.40ch	AT5G08350.1		GRAM do	chr5:268	29.503	33.1214	15.349	21.8816	13.7877	11.7278
GT	Sense	Sense	-0.048	Detected	0.048	Detected	0.000	-2.014	Comprom	-1.590	Comprom	-1.802	0.014	GT	Sens	contig210	contig210	Endochiti	TTCTTT	contig210	Solyc10g	Solyc10g	Endochiti	GO:0005	GO:0005	contig210	Solyc10g	Endochiti	GO:0008	SL2.40ch	AT3G125	ATHCHIB	ATHCHIB	chr3:396	29.0333	28.2805	11.5936	19.5641	6.7722	9.57805
GT	Sense	Sense	-0.616	Detected	0.616	Detected	0.000	-2.197	Detected	-2.043	Detected	-2.120	0.076	GT	Sens	contig212	contig212	Receptor-	CATTGC	contig212	Solyc06g	Solyc06g	Receptor-	GO:0005	GO:0004	contig212	Solyc06g	Receptor-	GO:0004	SL2.40ch	AT5G24080.1		protein k	chr5:813	126.046	269.781	81.1321	181.881	38.391	45.001
GT	Sense	Sense	0.099	Detected	-0.099	Detected	0.000	-1.092	Detected	-0.927	Detected	-1.009	0.016	GT	Sens	contig213	contig213	Cullin 1-li	GATAAC	contig213	Solyc01g	Solyc01g	Cullin 1-li	GO:0030	GO:0030	contig213	Solyc01g	Cullin 1-li	GO:0030	SL2.40ch	AT4G025	ATCUL1.	ATCUL1	chr4:112	219.303	174.36	136.391	226.461	87.6108	103.443
GT	Sense	Sense	0.031	Detected	-0.031	Detected	0.000	-1.379	Detected	-0.983	Detected	-1.181	0.028	GT	Sens	contig213	contig213	Decarbox	GCCAGG	contig213	Solyc08g	Solyc08g	Decarbox	GO:00197	GO:00197	contig213	Solyc08g	Decarbox	GO:00301	SL2.40ch	AT1G437	emb1075	emb1075	chr1:164	2309.69	2017.84	1270.87	2491.97	792.612	1098.97
GT	Sense	Sense	0.158	Detected	-0.158	Detected	0.000	-1.026	Detected	-1.644	Detected	-1.335	0.062	GT	Sens	contig215	contig215	Xylogluca	TCTTCT	contig215	Solyc03g	Solyc03g	Xylogluca	GO:00167	GO:00167	contig215	Solyc03g	Xylogluca	GO:00167	SL2.40ch	AT4G258	XTR6. XT	XTR6 (XY	chr4:131	19626.9	14367.8	10492.4	15747.7	7874.58	5403.62
GT	Sense	Sense	0.143	Detected	-0.143	Detected	0.000	-1.045	Detected	-1.536	Detected	-1.290	0.045	GT	Sens	contig218	contig218	Xylogluca	TCTTCT	contig218	Solyc03g	Solyc03g	Xylogluca	GO:0005	GO:0005	contig218	Solyc03g	Xylogluca	GO:00167	SL2.40ch	AT4G258	XTR6. XT	XTR6 (XY	chr4:131	18108	13546.7	9745.3	14765.9	7249.4	5434.65
GT	Sense	Sense	-0.429	Detected	0.429	Detected	0.000	-1.187	Detected	-0.900	Detected	-1.043	0.147	GT	Sens	contig218	contig218	Short cha	TCATCT	contig218	Solyc06g	Solyc06g	Short cha	GO:0005	GO:0005	contig218	Solyc06g	Short cha	GO:0005	SL2.40ch	AT2G29310.1		tropinone	chr2:125	254.853	420.869	170.589	322.451	137.322	176.589
GT	Sense	Sense	-0.319	Detected	0.319	Detected	0.000	-1.244	Detected	-1.062	Detected	-1.153	0.074	GT	Sens	contig221	contig221	Unknown	TACATA	contig221	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig221	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G018	PEX11C	PEX11C	chr1:296	58.3733	82.8212	84.725	71.8475	28.0222	33.4917
GT	Sense	Sense	-0.290	Detected	0.290	Detected	0.000	-1.430	Comprom	-1.093	Detected	-1.262	0.064	GT	Sens	contig222	contig222	Trachear	GAACCT	contig222	Solyc03g	Solyc03g	Tracheary element differentiat			contig222	Solyc03g	Tracheary element (		SL2.40ch	AT4G033	SRF3	SRF3 (ST	chr4:149	23.9363	32.6335	13.1336	29.5619	9.90291	13.1787
GT	Sense	Sense	0.013	Detected	-0.013	Detected	0.000	-1.034	Detected	-1.011	Detected	-1.023	0.000	GT	Sens	contig223	contig223	Unknown	GATGAG	contig223	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig223	Solyc06g	En/Spm-like transpo		SL2.40ch	AT5G584	ATEXO70	ATEXO7(	chr5:236	48.3369	43.2691	22.8124	49.3158	21.3211	22.8215
GT	Sense	Sense	0.203	Detected	-0.203	Detected	0.000	-1.187	Detected	-1.084	Detected	-1.136	0.032	GT	Sens	contig223	contig223	Transcrip	AGGAGA	contig223	Solyc03g	Solyc03g	Transcrip	GO:0045449		contig223	Solyc11g	Cellular n	GO:0008	SL2.40ch	AT4G37250.1		leucine-r	chr4:175	472.42	325.065	263.73	414.123	164.333	185.935
GT	Sense	Sense	-0.097	Detected	0.097	Detected	0.000	-2.503	Comprom	-2.343	Detected	-2.423	0.003	GT	Sens	contig223	contig223	Periaxin-l	AGGAAG	contig223	Solyc01g	Solyc01g	Periaxin-like protein (AHRD V1			contig223	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G42090.1		LOCATE	chr5:168	71.4672	74.5432	48.4168	90.6033	12.2952	14.4694
GT	Sense	Sense	-0.128	Detected	0.128	Detected	0.000	-1.825	Detected	-1.355	Detected	-1.590	0.027	GT	Sens	contig228	contig228	Unknown	GAGATC	contig228	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig228	Solyc07g	Unknown Protein (A		SL2.40ch	AT3G19520.2				196.438	213.857	125.489	192.473	55.2168	80.5852
GT	Sense	Sense	-0.114	Detected	0.114	Detected	0.000	-1.642	Detected	-2.152	Detected	-1.897	0.021	GT	Sens	contig229	contig229	Receptor-	AATAAA	contig229	Solyc02g	Solyc02g	Receptor-	GO:0006	GO:0006	contig229	Solyc02g	Receptor-	GO:0006	SL2.40ch	AT4G23240.1				398.922	426.144	264.541	370.429	126.131	93.339
GT	Sense	Sense	-0.057	Detected	0.057	Detected	0.000	-1.596	Comprom	-1.254	Detected	-1.425	0.016	GT	Sens	contig230	contig230	Trachear	ATTCGG	contig230	Solyc07g	Solyc07g	Tracheary element differentiat			contig230	Solyc07g	Tracheary element (		SL2.40ch	AT1G56040.1		binding /	chr1:209	28.3735	28.0061	21.1339	35.123	8.90419	11.8871
GT	Sense	Sense	-0.726	Detected	0.726	Detected	0.000	-1.107	Detected	-2.713	Detected	-1.910	0.220	GT	Sens	contig230	contig230	Unknown	GCTACG	contig230	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig230	Solyc12g	Unknown Protein (A		SL2.40ch	AT5G18570.1		GTP1/OB	chr5:617	1226.45	3061.06	1125.62	643.895	858.723	297.373
GT	Sense	Sense	-0.821	Detected	0.821	Detected	0.000	-0.892	Detected	-1.909	Detected	-1.401	0.284	GT	Sens	contig231	contig231	Pro-Pol p	ATTCAG	contig231	Solyc01g	Solyc01g	Pro-Pol p	GO:0015	GO:0015	contig231	Solyc11g	Pol polyp	GO:0003	SL2.40ch	AT4G394	BRI1. CBI	BRI1 (BR	chr4:183	4696.46	13370.4	4731.11	2624.56	4077.58	2122.07
GT	Sense	Sense	-0.345	Detected	0.345	Detected	0.000	-1.296	Comprom	-0.935	Detected	-1.116	0.103	GT	Sens	contig231	contig231	Mutator-li	AGTTAG	contig231	Solyc01g	Solyc01g	Mutator-like transposase (AHF			contig231	Solyc01g	Mutator-like transpo		SL2.40ch	AT5G03406.1		ATP bind	chr5:839	21.4928	31.6241	18.4144	40.0122	10.1384	13.7143
GT	Sense	Sense	-0.273	Detected	0.273	Detected	0.000	-0.920	Comprom	-1.602	Comprom	-1.261	0.102	GT	Sens	contig231	contig231	Solute ca	GGGATT	contig231	Solyc02g	Solyc02g	Solute ca	GO:0015	GO:0015	contig231	Solyc02g	Solute ca	GO:0015	SL2.40ch	AT2G18480.1		mannitol	chr2:800	12.8945	17.158	4.07219	14.9154	7.50585	4.93004
GT	Sense	Sense	-0.121	Detected	0.121	Detected	0.000	-1.227	Detected	-1.271	Detected	-1.249	0.010	GT	Sens	contig232	contig232	Cytochro	CTTTGT	contig232	Solyc07g	Solyc07g	Cytochro	GO:0019	GO:0019	contig232	Solyc07g	Cytochro	GO:0019	SL2.40ch	AT4G395	CYP96A1	CYP96A1	chr4:183	1670.02	1799.87	872.242	1170.91	706.94	722.958
GT	Sense	Sense	0.075	Detected	-0.075	Detected	0.000	-2.047	Detected	-0.866	Detected	-1.457	0.134	GT	Sens	contig234	contig234	Decarbox	ATTTCA	contig234	Solyc08g	Solyc08g	Decarbox	GO:00197	GO:00197	contig234	Solyc08g	Decarbox	GO:00301	SL2.40ch	AT4G332	XI-I. ATXI	XI-I: moto	chr4:160	414.651	340.725	100.472	824.319	86.8297	207.433
GT	Sense	Sense	-0.387	Detected	0.387	Detected	0.000	-1.363	Comprom	-2.069	Comprom	-1.716	0.082	GT	Sens	contig235	contig235	Leucine-r	TGGCTT	contig235	Solyc12g	Solyc12g	Leucine-r	GO:0005	GO:0005	contig235	Solyc12g	LRR recep	GO:0004	SL2.40ch	AT1G055	SYTE. AT	NTMC2T	chr1:162	17.2834	26.9425	9.06022	15.1963	8.00874	5.1736
GT	Sense	Sense	-0.761	Detected	0.761	Detected	0.000	-2.557	Detected	-1.564	Detected	-2.060	0.152	GT	Sens	contig235	contig235	Subtilisin	CTACCA	contig235	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:0004	contig235	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT3G19540.1		unknown	chr3:678	379.524	994.009	1560.43	1290.66	99.6613	208.961
GT	Sense	Sense	0.206	Detected	-0.206	Detected	0.000	-1.785	Detected	-1.633	Detected	-1.709	0.016	GT	Sens	contig236	contig236	Unknown	AGAAGA	contig236	Solyc01g	Solyc01g	Unknown Protein (AHRD V1)			contig236	Solyc03g	Iron-sulfu	GO:00081	SL2.40ch	AT1G01240.3				1264.97	866.504	781.314	1156.53	290.112	339.489
GT	Sense	Sense	0.264	Detected	-0.264	Detected	0.000	-0.965	Detected	-1.082	Detected	-1.023	0.063	GT	Sens	contig239	contig239	Mutator-li	ATAGGT	contig239	Solyc08g	Solyc08g	Mutator-like transposase (AHF			contig239	Solyc08g	Mutator-like transpo		SL2.40ch	AT5G30490.2		FUNCTIO	chr5:116	82.4653	52.1069	41.094	51.2539	32.0736	31.1503
GT	Sense	Sense	0.089	Detected	-0.089	Detected	0.000	-2.575	Detected	-2.844	Detected	-2.710	0.004	GT	Sens	contig239	contig239	Chromod	GAAGTG	contig239	Solyc07g	Solyc07g	Chromod	GO:0008	GO:0008	contig239	Solyc09g	UDP-gluc	GO:0080	SL2.40ch	AT3G52700.1		unknown	chr3:195	2083.14	1678.97	917.071	1034.23	299.664	261.954
GT	Sense	Sense	-0.936	Detected	0.936	Detected	0.000	-0.949	Detected	-1.877	Detected	-1.413	0.309	GT	Sens	contig240	contig240	Transpos	CAAGAT	contig240	Solyc01g	Solyc01g	Transpos	GO:0003	GO:0003	contig240	Solyc01g	Transpos	GO:0003	SL2.40ch	AT1G493	ATPI4K A	ATPI4K A	chr1:182	64.3225	214.625	62.938	37.1698	58.1032	32.1791
GT	Sense	Sense	-0.796	Detected	0.796	Detected	0.000	-0.864	Detected	-2.373	Detected	-1.618	0.278	GT	Sens	contig241	contig241	Peroxidas	AAGAAT	contig241	Solyc05g	Solyc05g	Peroxidas	GO:0005	GO:0005	contig241	Solyc05g046020.2.1				AT3G21770.1		peroxida	chr3:767	71.1334	195.406	68.3396	90.1894	61.866	22.8973
GT	Sense	Sense	-0.909	Detected	0.909	Detected	0.000	-1.051	Detected	-1.156	Detected	-1.103	0.349	GT	Sens	contig244	contig244	Indole-3-a	TCAAGA	contig244	Solyc08g	Solyc08g	Indole-3-a	GO:00801	GO:00801	contig244	Solyc08g	Indole-3-a	GO:00801	SL2.40ch	AT4G034	DFL2. GH	DFL2 (DW	chr4:149	23.0244	73.9657	18.6646	48.7015	19.0204	18.6306
GT	Sense	Sense	-0.754	Detected	0.754	Detected	0.000	-2.818	Detected	-1.970	Detected	-2.394	0.109	GT	Sens	contig247	contig247	Subtilisin	ACATTT	contig247	Solyc08g	Solyc08g	Subtilisin	GO:0004	GO:0004	contig247	Solyc08g	Subtilisin	GO:0004	SL2.40ch	AT3G19540.1		unknown	chr3:678	1008.3	2613.91	4015.71	2916.78	219.876	416.76
GT	Sense	Sense	-0.825	Detected	0.825	Detected	0.000	-1.334	Detected	-3.332	Comprom	-2.333	0.213	GT	Sens	contig248	contig248	Pol polyp	CCATAT	contig248	Solyc08g	Solyc08g	Pol polyp	GO:0008	GO:0008	contig248	Solyc08g	Pol polyp	GO:0008	SL2.40ch	AT5G28210.1		mRNA ca	chr5:101	53.6525	153.439	47.8851	26.4373	34.3531	9.06259
GT	Sense	Sense	-0.107	Detected	0.107	Detected	0.000	-2.608	Comprom	-2.646	Comprom	-2.627	0.002	GT	Sens	contig249	contig249	O-methyl	GAAGGA	contig249	Solyc02g	Solyc02g	O-methyl	GO:0033	GO:0033	contig249	Solyc02g	O-methyl	GO:0030	SL2.40ch	AT4G393	CESA2. A	CESA2 (C	chr4:182	12.6153	13.3405	3.86582	6.90103	2.03117	2.08521
GT	Sense	Sense	0.014	Detected	-0.014	Detected	0.000	-1.412	Detected	-1.632	Detected	-1.522	0.005	GT	Sens	contig251	contig251	Unknown	CGACCC	contig251	Solyc03g	Solyc03g	Unknown Protein (AHRD V1)			contig251	Solyc03g	Unknown Protein (A		SL2.40ch	AT5G47490.1		unknown	chr5:192	146.268	130.805	94.976	101.405	49.643	44.9035
GT	Sense	Sense	-0.834	Detected	0.834	Detected	0.000	-0.842	Detected	-2.445	Detected	-1.644	0.291	GT	Sens	contig251	contig251	Unknown	AGACAA	contig251	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig251	Solyc10g	Unknown Protein (A		SL2.40ch	AT5G115	MYB3R-4	MYB3R-4	chr5:368	1038.9	3009.44	1047.44	598.697	941.633	326.659
GT	Sense	Sense	-0.609	Detected	0.609	Detected	0.000	-1.415	Detected	-2.253	Detected	-1.834	0.131	GT	Sens	contig253	contig253	Unknown	ACCCAA	contig253	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig253	Solyc02g	Unknown Protein (A		SL2.40ch	AT2G358	CPK25	CPK25: A	chr2:150	493.849	1046.74	437.341	465.912	257.454	151.712
GT	Sense	Sense	-0.171	Detected	0.171	Detected	0.000	-1.609	Detected	-2.333	Detected	-1.971	0.039	GT	Sens	contig254	contig254	GTP bind	GGATCA	contig254	Solyc08g	Solyc08g	GTP binding protein (AHRD V1			contig254	Solyc08g	GTP binding protein		SL2.40ch	AT1G771	VPS45. A	VPS45 (V	chr1:289	187.347	216.618	178.387	159.594	63.0398	40.2219
GT	Sense	Sense	-0.778	Detected	0.778	Detected	0.000	-1.048	Detected	-1.980	Comprom	-1.514	0.237	GT	Sens	contig256	contig256	Polyprote	CGGGAA	contig256	Solyc09g	Solyc09g	Polyprote	GO:0008	GO:0008	contig256	Solyc09g	Polyprote	GO:0008	SL2.40ch	AT2G464	ATCNGC	ATCNGC	chr2:190	12.7275	34.1209	9.90089	11.9378	9.62467	5.31337
GT	Sense	Sense	0.093	Detected	-0.093	Detected	0.000	-1.080	Detected	-1.194	Detected	-1.137	0.009	GT	Sens	contig257	contig257	Unknown	GAAAAG	contig257	Solyc10g	Solyc10g	Unknown Protein (AHRD V1)			contig257	Solyc03g	Unknown Protein (A		SL2.40ch	AT3G053	ALY2. AT	DNA bind	chr3:154	129.536	103.862	81.0714	74.6916	52.3869	50.9911
GT	Sense	Sense	0.590	Detected	-0.590	Detected	0.000	-0.935	Detected	-2.126	Comprom	-1.531	0.209	GT	Sens	contig258	contig258	RNA-direc	ACTGGG	contig258	Solyc11g	Solyc11g	RNA-direc	GO:0006	GO:0006	contig258	Solyc05g	Phosphat	GO:0044	SL2.40ch	AT1G596	ZCW32. B	ZCW32: I	chr1:219	60.3709	24.3054	24.4971	76.8341	19.1295	8.82722
GT	Sense	Sense	-0.533	Detected	0.533	Detected	0.000	-1.137	Detected	-1.450	Detected	-1.293	0.145	GT	Sens	contig260	contig260	Peptide tr	ATTGGC	contig260	Solyc09g	Solyc09g	Peptide tr	GO:0042	GO:0042	contig260	Solyc05g	Peptide tr	GO:0042	SL2.40ch	AT5G46040.1		proton-d	chr5:186	167.235	319.364	147.76	228.263	100.35	85.0998
GT	Sense	Sense	-0.063	Detected	0.063	Detected	0.000	-1.142	Comprom	-2.014	Comprom	-1.578	0.070	GT	Sens	contig261	contig261	Unknown	CTATAA	contig261	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig261	Solyc02g	Unknown Protein (A		SL2.40ch	AT5G65230.1				21.2806	21.1672	8.62808	14.2582	9.18333	5.28572
GT	Sense	Sense	-0.111	Detected	0.111	Detected	0.000	-2.792	Detected	-2.860	Detected	-2.826	0.002	GT	Sens	contig261	contig261	FAD-bind	ACATTG	contig261	Solyc06g	Solyc06g	FAD-bind	GO:0050	GO:0050	contig261	Solyc06g	FAD-bind	GO:0050	SL2.40ch	AT4G20840.1		FAD-bind	chr4:111	98.2577	104.421	49.9098	29.6912	13.9642	14.0376
GT	Sense	Sense	-0.152	Detected	0.152	Detected	0.000	-2.565	Comprom	-3.512	Comprom	-3.039	0.026	GT	Sens	contig263	contig263	Blue copp	GAAAAT	contig263	Solyc07g	Solyc07g	Blue copp	GO:0009	GO:0009	contig263	Solyc07g	Blue copp	GO:0009	SL2.40ch	AT1G03055.2		unknown	chr1:710	21.197	23.8652	13.5268	31.0781	3.62973	1.9827
GT	Sense	Sense	0.169	Detected	-0.169	Detected	0.000	-1.302	Comprom	-0.915	Comprom	-1.109	0.050	GT	Sens	contig264	contig264	Laccase (	TTCGAT	contig264	Solyc09g	Solyc09g	Laccase (	GO:00551	GO:00551	contig264	Solyc09g011000.2.1				AT5G600	LAC17. A	LAC17 (la	chr5:241	17.1339	12.3592	4.23795	23.3612	5.63447	7.76397
GT	Sense	Sense	0.324	Detected	-0.324	Detected	0.000	-1.702	Detected	-0.916	Detected	-1.309	0.124	GT	Sens	contig267	contig267	Omega-6	GTTGTA	contig267	Solyc04g	Solyc04g	Omega-6	GO:0042	GO:0042	contig267	Solyc04g	Omega-6	GO:0042	SL2.40ch	AT3G121	FAD2	FAD2 (FA	chr3:386	653.173	379.939	396.822	737.457	146.22	265.662
GT	Sense	Sense	-0.647	Detected	0.647	Detected	0.000	-0.831	Detected	-2.360	Detected	-1.595	0.252	GT	Sens	contig268	contig268	Pol polyp	CAGTAC	contig268	Solyc10g	Solyc10g	Pol polyprotein (AHRD V1 ***- P			contig268	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT4G29750.1		RNA bind	chr4:145	488.891	1092.17	550.591	301.811	392.207	143.229
GT	Sense	Sense	0.267	Detected	-0.267	Detected	0.000	-1.620	Comprom	-2.385	Comprom	-2.002	0.050	GT	Sens	contig268	contig268	Ulp1 pept	CACAAC	contig268	Solyc08g	Solyc08g	Ulp1 pept	GO:0006	GO:0006	contig268	Solyc08g	Ulp1 pept	GO:0006	SL2.40ch	AT3G26140.1		glycosyl	chr3:955	38.0257	23.9445	17.6073	14.1989	9.37546	5.81095
GT	Sense	Sense	0.293	Detected	-0.293	Detected	0.000	-1.936	Comprom	-1.297	Detected	-1.616	0.065	GT	Sens	contig268	contig268	Thioester	ACAAAC	contig268	Solyc03g	Solyc03g	Thioester	GO:0005	GO:0005	contig268	Solyc03g	Thioester	GO:0005	SL2.40ch	AT2G47250.1				38.3027	23.2696	11.8062	59.6862	7.44928	12.223
GT	Sense	Sense	-0.176	Detected	0.176	Detected	0.000	-1.001	Detected	-1.262	Detected	-1.131	0.035	GT	Sens	contig268	contig268	Chitinase	AGCAAA	contig268	Solyc07g	Solyc07g	Chitinase	GO:0008	GO:0008	contig268	Solyc07g	Chitinase	GO:0008	SL2.40ch	AT4G01290.2		unknown	chr4:538	102118	118818	66078.5	63864.2	52539.4	46215.9
GT	Sense	Sense	-0.449	Detected	0.449	Detected	0.000	-2.339	Detected	-1.887	Detected	-2.113	0.052	GT	Sens	contig270	contig270	Tir-nbs-lr	TCACTT	contig270	Solyc12g	Solyc12g	Tir-nbs-lr	GO:0031	GO:0031	contig270	Solyc12g	Tir. resist	GO:0031	SL2.40ch	AT2G271	AAO3	AAO3 (AI	chr2:116	154.156	262.072	91.8955	251.866	37.9218	54.6711
GT	Sense	Sense	0.201	Detected	-0.201	Detected	0.000	-1.848	Detected	-1.576	Detected	-1.712	0.020	GT	Sens	contig272	contig272	Unknown	CTGTGA	contig272	Solyc02g	Solyc02g	Unknown Protein (AHRD V1)			contig272	Solyc02g	Unknown Protein (A		SL2.40ch	AT1G18170.1		immunop	chr1:625	917.221	632.578	603.691	691.766	202.092	256.991
GT	Sense	Sense	-0.866	Detected	0.866	Detected	0.000	-2.406	Detected	-2.306	Detected	-2.356	0.113	GT	Sens	contig272	contig272	Acyl-CoA	ATCTTG	contig272	Solyc07g	Solyc07g	Acyl-CoA	GO:00081	GO:00081	contig272	Solyc07g	Acyl-CoA	GO:0015	SL2.40ch	AT2G17650.1		AMP-dep	chr2:767	73.3075	222.013	67.9133	32.8679	22.9811	25.9542
GT	Sense	Sense	-0.695	Detected	0.695	Detected	0.000	-1.352	Detected	-2.590	Detected	-1.971	0.169	GT	Sens	contig272	contig272	Pol polyp	CTATTC	contig272	Solyc10g	Solyc10g	Pol polyp	GO:0015	GO:0015	contig272	Solyc00g	Pol polyp	GO:0003	SL2.40ch	AT5G59980.2		RNase P	chr5:241	674.965	1613.51	557.697	297.982	390.446	174.374
GT	Sense	Sense	-0.075	Detected	0.075	Detected	0.000	-1.247	Detected	-1.487	Detected	-1.367	0.010	GT	Sens	contig274	contig274	F-box fam	TTTTTTT	contig274	Solyc04g	Solyc04g	F-box family protein (AHRD V1			contig274	Solyc11g	Unknown Protein (A		SL2.40ch	#N/A	#N/A	#N/A	#N/A	7415.62	7499.68	5992.73	7225.36	2999.07	2676.76
GT	Sense	Sense	0.622	Detected	-0.622	Detected	0.000	-2.620	Detected	-4.031	Comprom	-3.325	0.072	GT	Sens	contig274	contig274	Peroxidas	ACATCA	contig274	Solyc10g	Solyc10g	Peroxidas	GO:00551	GO:00551	contig274	Solyc10g	Peroxidas	GO:00551	SL2.40ch	AT5G06720.1		peroxida	chr5:207	115.34	44.4115	53.1985	24.1833	11.1176	4.4039
GT	Sense	Sense	-0.374	Detected	0.374	Detected	0.000	-1.405	Comprom	-2.054	Comprom	-1.730	0.073	GT	Sens	contig279	contig279	Serine/thr	TGATAG	contig279	Solyc05g	Solyc05g	Serine/threonine-protein phos			contig279	Solyc09g	Serine/threonine-pr		SL2.40ch	AT4G046	APR1. AP	APR1 (AF	chr4:232	15.7805	24.1776	7.11231	19.6584	7.04027	4.73097
GT	Sense	Sense	0.077	Detected	-0.077	Detected	0.000	-1.432	Detected	-1.193	Detected	-1.312	0.012	GT	Sens	contig282	contig282	F-box fam	GTTGAT	contig282	Solyc05g	Solyc05g	F-box family protein (AHRD V1			contig282	Solyc05g	F-box family protein		SL2.40ch	AT2G362	ABI5. GIA	ABI5 (AB	chr2:152	11290.8	9255.92	8319.45	12928.1	3617.01	4499.67
GT	Sense	Sense	-0.680	Detected	0.680	Detected	0.000	-0.994	Detected	-2.346	Detected	-1.670	0.224	GT	Sens	contig284	contig284	Polyprote	CTACTG	contig284	Solyc11g	Solyc11g	Polyprotein (AHRD V1 ***- Q6AT			contig284	Solyc11g	Pol polyp	GO:0003	SL2.40ch	AT4G29750.1		RNA bind	chr4:145	1302.34	3047.6	1029.73	655.339	955.263	394.325
GT	Sense	Sense	-0.767	Detected	0.767	Detected	0.000	-0.835	Detected	-2.501	Detected	-1.668	0.279	GT	Sens	contig284	contig284	Polyprote	TTTTGT	contig284	Solyc12g	Solyc12g	Polyprotein (Fragment) (AHRD			contig284	Solyc11g	Pol polyp	GO:0003	SL2.40ch	ATMG00750.1				2483.04	6555.9	2384.79	1454.97	2160.26	716.847
GT	Sense	Sense	0.061	Detected	-0.061	Detected	0.000	-2.669	Detected	-1.203	Detected	-1.936	0.119	GT	Sens	contig286	contig286	Major late	GATGAA	contig286	Solyc05g	Solyc05g	Major late	GO:0009	GO:0009	contig286	Solyc05g	Major late	GO:0009	SL2.40ch	AT5G02620.1				95.7962	80.2993	16.2143	188.448	13.1699	38.3255
GT	Sense	Sense	-0.145	Detected	0.145	Detected	0.000	-1.371	Detected	-1.491	Detected	-1.431	0.012	GT	Sens	contig287	contig287	MuDR far	GAGTTT	contig287	Solyc06g	Solyc06g	MuDR family transposase con			contig287	Solyc12g	Unknown	GO:0016	SL2.40ch	AT5G46470.1		disease r	chr5:188	10259.1	11440.6	6129.01	11398.6	3997.87	3876.81
GT	Sense	Sense	0.192	Detected	-0.192	Detected	0.000	-1.339	Detected	-1.421	Detected	-1.380	0.020	GT	Sens	contig290	contig290	Cytochro	TGACAC	contig290	Solyc09g	Solyc09g	Cytochrome P450 (AHRD V1 **			contig290	Solyc11g	Cytochro	GO:0019	SL2.40ch	AT5G64600.1		unknown	chr5:258	223.006	155.753	240.489	157.114	70.3606	69.9987
GT	Sense	Sense	-0.438	Detected	0.438	Detected	0.000	-2.148	Comprom	-3.918	Comprom	-3.033	0.092	GT	Sens	contig290	contig290	Chitinase	TTTTCT	contig290	Solyc10g	Solyc10g	Chitinase	GO:0016	GO:0016	contig290	Solyc10g	Chitinase	GO:0005	SL2.40ch	AT3G125	ATHCHIB	ATHCHIB	chr3:396	33.8288	56.6236	26.3333	23.3067	9.42643	2.91261
GT	Sense	Sense	-0.046	Detected	0.046	Detected	0.000	-2.508	Detected	-1.782	Detected	-2.145	0.028	GT	Sens	contig291	contig291	Phospho	ACTAGC	contig291	Solyc05g	Solyc05g	Phospho	GO:0004	GO:0004	contig291	Solyc05g	Phospho	GO:0004	SL2.40ch	AT4G15830.1		binding	chr4:899	1508.9	1467.08	606.218	451.391	249.745	435.213
GT	Sense	Sense	-0.385	Detected	0.385	Detected	0.000	-0.925	Detected	-1.876	Detected	-1.400	0.149	GT	Sens	contig291	contig291	Receptor-	ATGTTG	contig291	Solyc09g	Solyc09g	Receptor-	GO:0006	GO:0006	contig291	Solyc09g	Receptor-	GO:0006	SL2.40ch	AT1G161	WAKL2	WAKL2 (I	chr1:552	44.515	69.1744	34.4088	51.2384	27.9093	15.208
GT	Sense	Sense	-0.360	Detected	0.360	Detected	0.000	-1.312	Detected	-1.043	Detected	-1.177	0.092	GT	Sens	contig292	contig292	FAD-bind	AATCTC	contig292	Solyc02g	Solyc02g	FAD-bind	GO:0050	GO:0050	contig292	Solyc02g	FAD-bind	GO:0050	SL2.40ch	AT5G44410.1		FAD-bind	chr5:178	71.7534	107.823	38.9191	62.354	33.8216	42.9533
GT	Sense	Sense	-0.184	Detected	0.184	Detected	0.000	-1.410	Comprom	-1.805	Comprom	-1.607	0.027	GT	Sens	contig293	contig293	Strictosid	GCAGGG	contig293	Solyc03g	Solyc03g	Strictosid	GO:0004	GO:0004	contig293	Solyc03g	Strictosid	GO:0004	SL2.40ch	AT4G36690.3				13.0978	15.4159	2.14714	11.2063	5.10572	4.09078
GT	Sense	Sense	-0.131	Detected	0.131	Detected	0.000	-1.175	Detected	-1.769	Comprom	-1.472	0.045	GT	Sens	contig294	contig294	Serine/thr	GGGATT	contig294	Solyc09g	Solyc09g	Serine/threonine-protein phos			contig294	Solyc09g	Serine/threonine-pr		SL2.40ch	AT3G13228.1				29.2006	31.9343	19.3214	27.7232	12.9168	9.01189
GT	Sense	Sense	0.015	Detected	-0.015	Detected	0.000	-1.286	Detected	-0.887	Detected	-1.086	0.032	GT	Sens	contig295	contig295	60S ribos	GGCTTC	contig295	Solyc09g	Solyc09g	60S ribos	GO:0003	GO:0003	contig295	Solyc09g	60S ribos	GO:0003	SL2.40ch	AT2G34480.1		60S ribos	chr2:145	166.937	149.052	124.301	170.625	61.7646	85.8369
GT	Sense	Sense	-0.013	Detected	0.013	Detected	0.000	-1.358	Detected	-0.990	Detected	-1.174	0.024	GT	Sens	contig299	contig299	Decarbox	CCAGGC	contig299	Solyc08g	Solyc08g	Decarbox	GO:00197	GO:00197	contig299	Solyc08g	Decarbox	GO:00301	SL2.40ch	AT1G437	emb1075	emb1075	chr1:164	1683.56	1563.06	1026.67	1981.54	604.07	821.773
GT	Sense	Sense	-0.331	Detected	0.331	Detected	0.000	-1.303	Detected	-2.096	Comprom	-1.699	0.081	GT	Sens	contig300	contig300	Pol polyp	TTTTAG	contig300	Solyc12g	Solyc12g	Pol polyp	GO:0006	GO:0006	contig300	Solyc08g	Pol polyp	GO:0008	SL2.40ch	AT5G40450.2		unknown	chr5:161	34.1161	49.2381	32.0626	21.0709	15.8629	9.64673
GT	Sense	Sense	-0.471	Detected	0.471	Detected	0.000	-1.058	Detected	-1.908	Detected	-1.483	0.144	GT	Sens	contig300	contig300	Cytochro	CGTTGA	contig300	Solyc12g	Solyc12g	Cytochro	GO:00551	GO:00551	contig300	Solyc12g	Cytochro	GO:0019	SL2.40ch	AT2G251	CYP82F1	CYP82F1	chr2:107	1120.38	1961.98	1217.79	1160.43	679.778	397.303
GT	Sense	Sense	-0.181	Detected	0.181	Detected	0.000	-2.143	Detected	-1.890	Detected	-2.017	0.012	GT	Sens	contig301	contig301	Wound-in	AGCAGA	contig301	Solyc06g	Solyc06g	Wound-induced basic protein			contig301	Solyc06g	Wound-induced bas		SL2.40ch	AT3G07230.1		wound-re	chr3:229	84.7532	99.3079	32.406	44.2218	19.8325	24.894
GT	Sense	Sense	-0.558	Detected	0.558	Detected	0.000	-1.406	Detected	-2.657	Detected	-2.031	0.136	GT	Sens	contig302	contig302	Pol polyp	CAGTAT	contig302	Solyc01g	Solyc01g	Pol polyprotein (AHRD V1 *-*- F			contig302	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT3G27025.1				228.406	451.55	185.745	106.656	115.733	51.2404
GT	Sense	Sense	-0.491	Detected	0.491	Detected	0.000	-2.422	Detected	-1.346	Detected	-1.884	0.123	GT	Sens	contig309	contig309	Serine/thr	ACTTCT	contig309	Solyc02g	Solyc02g	Serine/thr	GO:00191	GO:00191	contig309	Solyc02g	Serine/thr	GO:00191	SL2.40ch	AT1G61610.1		S-locus l	chr1:227	197.457	355.447	102.859	207.635	47.1843	104.863
GT	Sense	Sense	-0.883	Detected	0.883	Detected	0.000	-1.011	Detected	-2.083	Detected	-1.547	0.273	GT	Sens	contig310	contig310	Polyprote	TTGATC	contig310	Solyc10g	Solyc10g	Polyprote	GO:0003	GO:0003	contig310	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT2G03740.1				357.566	1109.02	327.502	216.186	298.4	149.547
GT	Sense	Sense	-0.731	Detected	0.731	Detected	0.000	-0.995	Detected	-1.340	Detected	-1.167	0.260	GT	Sens	contig311	contig311	Cytochro	GGGAAT	contig311	Solyc06g	Solyc06g	Cytochro	GO:0020	GO:0020	contig311	Solyc06g	Cytochro	GO:0020	SL2.40ch	AT4G231	CRK6	CRK6 (CY	chr4:121	66.8677	167.918	74.9884	85.1307	50.7796	42.1202
GT	Sense	Sense	-0.381	Detected	0.381	Detected	0.000	-0.944	Detected	-1.185	Detected	-1.064	0.117	GT	Sens	contig317	contig317	Auxin-ind	GCAGCA	contig317	Solyc02g	Solyc02g	Auxin-ind	GO:0005	GO:0005	contig317	Solyc02g	Auxin-ind	GO:0005	SL2.40ch	AT2G18010.1		auxin-res	chr2:783	33.5228	51.8536	9.23674	24.4927	20.6958	18.4532
GT	Sense	Sense	-0.223	Detected	0.223	Detected	0.000	-1.867	Detected	-2.515	Detected	-2.191	0.031	GT	Sens	contig322	contig322	Peroxidas	GATGGA	contig322	Solyc05g	Solyc05g	Peroxidas	GO:0005	GO:0005	contig322	Solyc05g	Peroxidas	GO:0004	SL2.40ch	AT3G21770.1		peroxida	chr3:767	141.902	176.119	137.629	187.182	41.3741	27.8195
GT	Sense	Sense	-0.416	Detected	0.416	Detected	0.000	-0.904	Detected	-1.211	Detected	-1.057	0.140	GT	Sens	contig323	contig323	Legumin-	TCTCCC	contig323	Solyc01g	Solyc01g	Legumin-	GO:0008	GO:0008	contig323	Solyc01g	Legumin-	GO:0008	SL2.40ch	AT3G54600.1		DJ-1 fam	chr3:202	1696.88	2752.68	1170.81	2607.09	1102.71	939.388
GT	Sense	Sense	-0.478	Detected	0.478	Detected	0.000	-1.052	Detected	-1.045	Detected	-1.049	0.159	GT	Sens	contig340	contig340	Ulp1 prot	TTCAGA	contig340	Solyc11g	Solyc11g	Ulp1 protease family C-termina			contig340	Solyc01g	Endo-1 4-	GO:0008	SL2.40ch	AT2G42870.1				289.807	512.355	306.378	277.5	177.397	187.837
GT	Sense	Sense	-0.059	Detected	0.059	Detected	0.000	-1.691	Detected	-1.187	Detected	-1.439	0.031	GT	Sens	contig344	contig344	Serine/thr	ATCAAC	contig344	Solyc07g	Solyc07g	Serine/thr	GO:00191	GO:00191	contig344	Solyc07g	Serine/thr	GO:00191	SL2.40ch	AT1G11340.1		S-locus l	chr1:381	201.398	199.301	93.0896	78.674	59.2649	88.5431
GT	Sense	Sense	-1.060	Detected	1.060	Detected	0.000	-0.889	Detected	-1.233	Detected	-1.061	0.428	GT	Sens	contig355	contig355	Endogluc	TTACAA	contig355	Solyc08g	Solyc08g	Endogluc	GO:0005	GO:0005	contig355	Solyc08g	Endogluc	GO:0030	SL2.40ch	AT1G643	AtGH9C2	AtGH9C2	chr1:239	55.1296	218.612	54.5963	124.309	56.6182	46.9785
GT	Sense	Sense	-0.734	Detected	0.734	Detected	0.000	-0.827	Detected	-2.294	Detected	-1.560	0.271	GT	Sens	contig366	contig366	Pol polyp	ATGCTT	contig366	Solyc11g	Solyc11g	Pol polyp	GO:0008	GO:0008	contig366	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT5G036	PTL	PTL (PET	chr5:957	1790.37	4513.16	1586.06	964.486	1529.86	583.275
GT	Sense	Sense	-0.793	Detected	0.793	Detected	0.000	-0.912	Detected	-2.151	Detected	-1.531	0.267	GT	Sens	contig371	contig371	Pol polyp	TCGCTA	contig371	Solyc08g	Solyc08g	Pol polyp	GO:0006	GO:0006	contig371	Solyc08g	Pol polyp	GO:0008	SL2.40ch	AT5G40450.2		unknown	chr5:161	2164	5920.35	1986.06	1179.86	1816.55	810.684
GT	Sense	Sense	-0.694	Detected	0.694	Detected	0.000	-0.811	Detected	-2.443	Detected	-1.627	0.268	GT	Sens	contig374	contig374	Unknown	AACCTC	contig374	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig374	Solyc11g	Unknown Protein (A		SL2.40ch	AT2G45990.4		unknown	chr2:189	584.617	1394.56	726.347	431.088	491.393	167.034
GT	Sense	Sense	-0.761	Detected	0.761	Detected	0.000	-1.075	Detected	-1.767	Detected	-1.421	0.231	GT	Sens	contig383	contig383	Gag-pol p	GATCTT	contig383	Solyc12g	Solyc12g	Gag-pol polyprotein (AHRD V1			contig383	Solyc12g	Gag-pol polyprotein		SL2.40ch	AT5G65910.1		BSD dom	chr5:263	70.0374	183.297	49.9196	40.6567	51.3387	33.4857
GT	Sense	Sense	0.065	Detected	-0.065	Detected	0.000	-1.172	Detected	-0.869	Detected	-1.021	0.025	GT	Sens	contig387	contig387	Terminal	AATTGT	contig387	Solyc01g	Solyc01g	Terminal ear1-like 2 protein (A			contig387	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G53200.2				2231.59	1859.35	1408.15	2299.55	863.2	1121.7
GT	Sense	Sense	-0.220	Detected	0.220	Detected	0.000	-0.829	Detected	-1.668	Detected	-1.248	0.119	GT	Sens	contig391	contig391	Unknown	ATGCTT	contig391	Solyc01g	Solyc01g	Unknown	GO:0006	GO:0006	contig391	Solyc01g	Unknown	GO:0006	SL2.40ch	AT5G40750.1		FUNCTIO	chr5:163	34.2088	42.2918	13.9174	21.9726	20.4477	12.0402
GT	Sense	Sense	-0.380	Detected	0.380	Detected	0.000	-1.803	Detected	-2.348	Detected	-2.075	0.047	GT	Sens	contig391	contig391	Unannota	GCGACCAACGCGATTAAGCCATTGCTAGGAGATTATTACCAAGTTGAT							contig391	Solyc12g	Omega-6	GO:0042	SL2.40ch	AT3G121	FAD2	FAD2 (FA	chr3:386	6774.69	10458.9	7098.4	11976.8	2303.89	1663.1
GT	Sense	Sense	-0.449	Detected	0.449	Detected	0.000	-3.159	Detected	-2.465	Detected	-2.812	0.038	GT	Sens	contig402	contig402	Long-cha	ATAGCA	contig402	Solyc09g	Solyc09g	Long-cha	GO:00081	GO:00081	contig402	Solyc09g	Long-cha	GO:0004	SL2.40ch	AT3G059	LACS6. A	LACS6 (lo	chr3:178	72.2341	122.799	38.4285	84.3045	10.0689	17.1616
GT	Sense	Sense	-0.305	Detected	0.305	Detected	0.000	-1.732	Detected	-2.196	Detected	-1.964	0.036	GT	Sens	contig406	contig406	Endo-1 3	TATCCG	contig406	Solyc12g	Solyc12g	Endo-1 31 4-beta-D-glucanase			contig406	Solyc01g	Dienelact	GO:0005	SL2.40ch	AT1G15130.1		hydroxyl	chr1:520	2074.15	2885.96	1613.92	1651.11	703.201	537.302
GT	Sense	Sense	-0.184	Detected	0.184	Detected	0.000	-0.907	Detected	-1.284	Detected	-1.095	0.053	GT	Sens	contig409	contig409	Unannota	AACTTAGAATCATTTCATGCATTTAACTTGGCTTTAAAAAATATTTCAAA							contig409	Solyc11g	Unknown Protein (A		SL2.40ch	AT5G463	FLS2	FLS2 (FL	chr5:187	96.2745	113.199	55.4136	119.391	53.1698	43.1325
GT	Sense	Sense	-0.295	Detected	0.295	Detected	0.000	-1.365	Comprom	-1.163	Comprom	-1.264	0.056	GT	Sens	contig409	contig409	Unannota	GACTACTTTTATTCAAGTCACGCTTCCCTTTCTTTCTCCGAGCTGGAGA							contig409	Solyc12g	TNP2 (AHRD V1 *--- (		SL2.40ch	AT3G204	ATMSH5.	MSH5 (M	chr3:714	11.3811	15.6268	11.7321	9.23981	4.94288	5.98996
GT	Sense	Sense	-0.074	Detected	0.074	Detected	0.000	-1.018	Detected	-1.146	Detected	-1.082	0.008	GT	Sens	contig411	contig411	Unannota	AATAGATGTTGAATATTGATAGTTATTGAATTGGTTTTATTAATGAGTT							contig411	Solyc03g	Polyprote	GO:0006	SL2.40ch	AT3G24530.1		AAA-type	chr3:894	218.223	220.432	169.85	241.901	103.437	99.7162
GT	Sense	Sense	-0.466	Detected	0.466	Detected	0.000	-1.792	Detected	-1.854	Detected	-1.823	0.060	GT	Sens	contig411	contig411	Tir-nbs-lr	CCATCA	contig411	Solyc07g	Solyc07g	Tir-nbs-lr	GO:0031	GO:0031	contig411	Solyc07g	Tir. resist	GO:0031	SL2.40ch	AT5G44900.1		transmen	chr5:181	104.163	181.184	93.8948	235.059	37.8776	38.2275
GT	Sense	Sense	-0.259	Detected	0.259	Detected	0.000	-1.279	Detected	-1.740	Detected	-1.509	0.049	GT	Sens	contig412	contig412	Unannota	GACGTTAGGCAAACTTTAGGCCGATAATTATTGCTTTATTGTGTGTATT							contig412	Solyc01g	ATP depe	GO:0008	SL2.40ch	AT4G235	AtGH9B1	AtGH9B1	chr4:122	815.065	1063.6	547.676	1052.6	366.314	280.501
GT	Sense	Sense	-0.214	Detected	0.214	Detected	0.000	-1.319	Detected	-1.524	Detected	-1.422	0.027	GT	Sens	contig415	contig415	Unannota	CGCTGATAAACAGTAATTATCCGCTAAAGTACGATGCTAATAGTGACTA							contig415	Solyc12g	Ulp1 protease family		SL2.40ch	AT5G24880.1		INVOLVE	chr5:855	353.256	433.441	309.322	472.79	149.725	136.844
GT	Sense	Sense	-0.904	Detected	0.904	Detected	0.000	-1.202	Detected	-2.859	Comprom	-2.031	0.240	GT	Sens	contig421	contig421	Unannota	GCTCCTGTTGTGAAGTTAATCTCTATTTGAATTCTGTTGAGAATTGTTG							contig421	Solyc06g	Peroxiso	GO:0005	SL2.40ch	AT2G22400.1		NOL1/NO	chr2:950	30.5869	97.6947	33.2	18.9644	22.6819	7.58121
GT	Sense	Sense	-0.370	Detected	0.370	Detected	0.000	-2.110	Detected	-2.608	Detected	-2.359	0.034	GT	Sens	contig423	contig423	Fatty acid	CCAAGT	contig423	Solyc12g	Solyc12g	Fatty acid desaturase (AHRD V			contig423	Solyc12g100240.1.1				AT3G121	FAD2	FAD2 (FA	chr3:386	8654.44	13170.9	8452.45	13309.7	2361.42	1761.17
GT	Sense	Sense	0.401	Detected	-0.401	Detected	0.000	-2.980	Detected	-2.897	Detected	-2.939	0.018	GT	Sens	contig430	contig430	Cross hy	ATCAGGATCGGTCGATGGTGCGCCCCGAGGGGTTCCCACCTCCGTTCA							contig430	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	518.913	271.423	176.186	164.298	45.4121	50.6794
GT	Sense	Sense	-0.396	Detected	0.396	Detected	0.000	-1.994	Detected	-3.022	Detected	-2.508	0.061	GT	Sens	contig434	contig434	Nicotia ta	ACTAGTACTCGTACTTGCCTTCACTCTAACTTTTGCATGGCCTTTATAC							contig434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	4770.26	7529.73	3769.14	4535.79	1436.39	742.098
GT	Sense	Sense	-0.161	Detected	0.161	Detected	0.000	-1.505	Comprom	-2.098	Comprom	-1.801	0.033	GT	Sens	contig454	contig454	Gibberelli	AGAATC	contig454	Solyc05g	Solyc05g	Gibberelli	GO:0004	GO:0004	contig454	Solyc05g	Gibberelli	GO:0004	SL2.40ch	AT3G08660.1		phototro	chr3:263	24.9256	28.4157	8.13075	26.0715	8.95508	6.25364
GT	Sense	Sense	-0.754	Detected	0.754	Detected	0.000	-0.991	Detected	-2.062	Detected	-1.526	0.241	GT	Sens	contig460	contig460	Reverse t	TATACT	contig460	Solyc02g	Solyc02g	Reverse t	GO:0006	GO:0006	contig460	Solyc11g	Pol polyp	GO:0006	SL2.40ch	AT4G292	PFK1	PFK1 (PH	chr4:144	170.023	440.956	190.411	106.63	131.511	65.9842
GT	Sense	Sense	1.061	Detected	-1.061	Detected	0.000	-1.029	Detected	-2.189	Detected	-1.609	0.315	GT	Sens	contig476	contig476	Tryptoph	CACGGC	contig476	Solyc10g	Solyc10g	Tryptoph	GO:00081	GO:00081	contig476	Solyc10g	Tryptoph	GO:0004	SL2.40ch	AT3G12100.2		cation ef	chr3:385	1130.1	236.618	832.316	427.062	242.032	114.06
GT	Sense	Sense	0.261	Detected	-0.261	Detected	0.000	-1.791	Comprom	-1.864	Comprom	-1.827	0.020	GT	Sens	contig499	contig499	Unknown	TCAAAT	contig499	Solyc12g	Solyc12g	Unknown Protein (AHRD V1)			contig499	Solyc12g	Unknown Protein (A		SL2.40ch	AT1G35330.1				33.2819	21.1209	23.1811	21.3047	7.31609	7.32865
GT	Sense	Sense	-0.269	Detected	0.269	Detected	0.000	-1.490	Detected	-1.186	Detected	-1.338	0.049	GT	Sens	contig518	contig518	Glutathio	AGGAAT	contig518	Solyc09g	Solyc09g	Glutathio	GO:0004	GO:0004	contig518	Solyc09g	Glutathio	GO:0004	SL2.40ch	AT3G092	ATGSTU	ATGSTU	chr3:284	42.881	56.7273	49.7446	92.0411	16.7612	21.8
GT	Sense	Sense	0.096	Detected	-0.096	Detected	0.000	-1.201	Comprom	-1.072	Detected	-1.137	0.010	GT	Sens	contig521	contig521	Disease r	AGCAGA	contig521	Solyc07g	Solyc07g	Disease r	GO:0006	GO:0006	contig521	Solyc07g	Nbs-lrr. re	GO:0006	SL2.40ch	AT3G51080.1		zinc fing	chr3:189	26.7537	21.3622	12.419	24.3829	9.92723	11.4393
GT	Sense	Sense	-0.543	Detected	0.543	Detected	0.000	-0.880	Detected	-2.214	Detected	-1.547	0.214	GT	Sens	contig526	contig526	Reverse t	AGAATG	contig526	Solyc01g	Solyc01g	Reverse t	GO:0006	GO:0006	contig526	Solyc09g	Polyprote	GO:0008	SL2.40ch	AT5G124	CPK7	CPK7 (ca	chr5:404	806.424	1561.17	762.585	471.259	582.274	243.205
GT	Sense	Sense	-0.733	Detected	0.733	Detected	0.000	-0.800	Detected	-2.129	Detected	-1.465	0.277	GT	Sens	contig545	contig545	Retrotran	ATATTG	contig545	Solyc08g	Solyc08g	Retrotransposon gag protein (			contig545	Solyc08g022190.1.1				AT5G14050.1		transduc	chr5:453	1942.48	4891.17	1943.29	1113.27	1690.15	708.776
GT	Sense	Sense	0.189	Detected	-0.189	Detected	0.000	-1.693	Detected	-1.641	Detected	-1.667	0.013	GT	Sens	contig582	contig582	Helicase-l	CAATGG	contig582	Solyc01g	Solyc01g	Helicase-like protein (AHRD V1			contig582	Solyc01g	Helicase-like protein		SL2.40ch	AT3G20700.1				2985.21	2093.38	1704.56	2850.43	738.191	806.532
GT	Sense	Sense	-0.432	Detected	0.432	Detected	0.000	-1.430	Detected	-1.395	Detected	-1.412	0.082	GT	Sens	contig585	contig585	GRAM-co	TGGGAT	contig585	Solyc11g	Solyc11g	GRAM-containing/ABA-respon			contig585	Solyc11g	GRAM-containing/A		SL2.40ch	AT4G13600.1		EXPRES	chr4:791	338.785	562.451	192.895	184.553	154.681	166.992
GT	Sense	Sense	-0.962	Detected	0.962	Detected	0.000	-3.975	Detected	-5.736	Comprom	-4.856	0.065	GT	Sens	contig600	contig600	Acyltrans	CCAAGT	contig600	Solyc11g	Solyc11g	Acyltrans	GO:00167	GO:00167	contig600	Solyc11g	Acyltrans	GO:00167	SL2.40ch	AT4G37950.1		lyase	chr4:178	127.508	440.856	974.968	687.009	14.3909	4.47379
GT	Sense	Sense	0.297	Detected	-0.297	Detected	0.000	-1.506	Detected	-1.880	Detected	-1.693	0.040	GT	Sens	contig612	contig612	Cysteine	AAGTAC	contig612	Solyc11g	Solyc11g	Cysteine	GO:00081	GO:00081	contig612	Solyc11g	Cysteine	GO:00081	SL2.40ch	AT4G30260.1		integral r	chr4:148	156.83	94.7395	94.9074	91.4033	40.9746	33.326
GT	Sense	Sense	-0.394	Detected	0.394	Detected	0.000	-0.870	Detected	-1.236	Comprom	-1.053	0.136	GT	Sens	contig657	contig657	Unknown	AATGCA	contig657	Solyc09g	Solyc09g	Unknown Protein (AHRD V1)			contig657	Solyc09g055770.1.1				AT2G43180.2		catalytic	chr2:179	17.1884	27.0474	19.0903	20.3071	11.2665	9.21064
GT	Sense	Sense	-0.901	Detected	0.901	Detected	0.000	-2.643	Comprom	-1.975	Detected	-2.309	0.138	GT	Sens	contig671	contig671	Cytochro	GTTCAA	contig671	Solyc10g	Solyc10g	Cytochro	GO:0020	GO:0020	contig671	Solyc10g	Cytochro	GO:0046	SL2.40ch	AT2G408	CYP98A3	CYP98A3	chr2:170	32.636	103.689	48.9006	72.7259	8.89411	14.8818
GT	Sense	Sense	0.040	Detected	-0.040	Detected	0.000	-1.183	Detected	-1.765	Comprom	-1.474	0.038	GT	Sens	contig681	contig681	SWIB com	CTGATG	contig681	Solyc01g	Solyc01g	SWIB complex BAF60b domai			contig681	Solyc01g	SWIB complex BAF6		SL2.40ch	AT5G37950.2		transfera	chr5:151	31.3788	27.0763	17.2462	28.0052	12.259	8.62631
GT	Sense	Sense	0.377	Detected	-0.377	Detected	0.000	-1.866	Detected	-3.104	Detected	-2.485	0.076	GT	Sens	contig683	contig683	Pyridine	GTGAAA	contig683	Solyc11g	Solyc11g	Pyridine	GO:00551	GO:00551	contig683	Solyc11g	Nitric oxide reducta		SL2.40ch	AT3G102	LYC	LYC (LYC	chr3:316	170.661	92.2888	58.2191	99.5149	32.8742	14.6811
GT	Sense	Sense	-0.352	Detected	0.352	Detected	0.000	-2.075	Detected	-2.628	Detected	-2.352	0.034	GT	Sens	contig705	contig705	Unknown	ACAAAA	contig705	Solyc11g	Solyc11g	Unknown Protein (AHRD V1)			contig705	Solyc05g	Unknown Protein (A		SL2.40ch	AT3G52700.1		unknown	chr3:195	3746.89	5562.6	3223.93	2593.32	1034.6	742.738
GT	Sense	Sense	-0.320	Detected	0.320	Detected	0.000	-1.268	Detected	-1.625	Detected	-1.446	0.059	GT	Sens	contig729	contig729	Beta-fruc	GAGAAT	contig729	Solyc09g	Solyc09g	Beta-fruc	GO:0005	GO:0005	contig729	Solyc10g	Beta-fruc	GO:0005	SL2.40ch	AT3G52700.1		unknown	chr3:195	27607.2	39240.6	24451.5	27687.4	13053.3	10735.7
GT	Sense	Sense	-0.163	Detected	0.163	Detected	0.000	-2.546	Detected	-3.681	Detected	-3.114	0.034	GT	Sens	contig749	contig749	Abscisic	ACCGTT	contig749	Solyc04g	Solyc04g	Abscisic	GO:0006	GO:0006	contig749	Solyc04g	Abscisic	GO:0006	SL2.40ch	AT1G76940.1		RNA reco	chr1:289	206.613	235.959	110.47	206.928	36.0859	17.3174
GT	Sense	Sense	1.235	Detected	-1.235	Detected	0.000	-1.167	Detected	-1.970	Detected	-1.568	0.351	GT	Sens	contig752	contig752	Phosphat	AGAGTA	contig752	Solyc09g	Solyc09g	Phosphatidylinositol 3-kinase			contig752	Solyc09g	Phosphatidylinosito		SL2.40ch	AT2G479	SCC3. AT	SCC3 (SI	chr2:196	116.166	19.108	16.0373	19.8493	20.0327	12.0998
GT	Sense	Sense	-0.332	Detected	0.332	Detected	0.000	-1.391	Detected	-1.379	Detected	-1.385	0.053	GT	Sens	contig756	contig756	Peroxidas	TTTTCA	contig756	Solyc02g	Solyc02g	Peroxidas	GO:0005	GO:0005	contig756	Solyc02g	Peroxidas	GO:0004	SL2.40ch	AT1G14540.1		anionic p	chr1:497	6256.07	9035.69	3666.48	7000.69	2738	2908.93
GT	Sense	Sense	0.432	Detected	-0.432	Detected	0.000	-2.489	Detected	-1.842	Detected	-2.165	0.057	GT	Sens	contig796	contig796	Peroxidas	TATTTG	contig796	Solyc10g	Solyc10g	Peroxidas	GO:00551	GO:00551	contig796	Solyc10g	Peroxidas	GO:00551	SL2.40ch	AT5G05340.1		peroxida	chr5:157	790.561	395.785	392.68	182.398	95.162	156.939
GT	Sense	Sense	-0.289	Detected	0.289	Detected	0.000	-2.278	Detected	-4.424	Comprom	-3.351	0.095	GT	Sens	contig810	contig810	Abscisic	CACCGT	contig810	Solyc04g	Solyc04g	Abscisic	GO:0006	GO:0006	contig810	Solyc04g071590.1.1				AT3G44590.1		60S acid	chr3:161	185.739	252.85	108.357	163.777	42.6478	10.1528
GT	Sense	Sense	0.205	Detected	-0.205	Detected	0.000	-3.526	Comprom	-3.195	Detected	-3.361	0.006	GT	Sens	contig816	contig816	Auxin-ind	TCTTCA	contig816	Solyc07g	Solyc07g	Auxin-induced protein-like (AH			contig816	Solyc07g	Auxin-induced prote		SL2.40ch	AT3G07730.1		unknown	chr3:246	115.687	79.3672	30.9333	38.6362	7.94173	10.5224
GT	Sense	Sense	-0.165	Detected	0.165	Detected	0.000	-1.201	Detected	-1.948	Detected	-1.575	0.061	GT	Sens	contig838	contig838	CM0216.3	AGTGGA	contig838	Solyc02g	Solyc02g	CM0216.330.nc protein (AHRD			contig838	Solyc02g083000.1.1				AT4G38200.1		guanine	chr4:179	217.54	249.194	178.541	293.581	96.6694	60.6945
GT	Sense	Sense	0.321	Detected	-0.321	Detected	0.000	-3.354	Detected	-3.596	Detected	-3.475	0.010	GT	Sens	contig843	contig843	Glutathio	GGCGTA	contig843	Solyc01g	Solyc01g	Glutathione-S-transferase (AHI			contig843	Solyc01g	Glutathione-S-transf		SL2.40ch	AT3G492	emb1796	emb1796	chr3:182	8489.13	4961.94	513.761	1047.72	606.05	539.994
GT	Sense	Sense	-0.264	Detected	0.264	Detected	0.000	-1.023	Detected	-1.126	Detected	-1.074	0.057	GT	Sens	contig856	contig856	Cytochro	TCAAAA	contig856	Solyc03g	Solyc03g	Cytochro	GO:0020	GO:0020	contig856	Solyc03g	Cytochro	GO:0004	SL2.40ch	AT3G483	CYP71A2	CYP71A2	chr3:178	344.075	452.213	339.538	1386.01	185.391	181.842
GT	Sense	Sense	-0.732	Detected	0.732	Detected	0.000	-1.463	Detected	-2.049	Detected	-1.756	0.156	GT	Sens	contig870	contig870	AP2/ERF	AAGAAG	contig870	Solyc10g	Solyc10g	AP2/ERF	GO:0006	GO:0006	contig870	Solyc10g	AP2/ERF	GO:0006	SL2.40ch	AT5G500	ERF110	DNA bind	chr5:203	38.1231	95.8849	15.4533	22.7262	20.9378	14.702
GT	Sense	Sense	0.063	Detected	-0.063	Detected	0.000	-1.356	Detected	-0.813	Detected	-1.085	0.060	GT	Sens	contig888	contig888	Pectinest	ATCATA	contig888	Solyc02g	Solyc02g	Pectinest	GO:0030	GO:0030	contig888	Solyc02g	Pectinest	GO:0005	SL2.40ch	AT1G02810.1		pectinest	chr1:618	1456.9	1217.44	418.989	2633.64	496.646	762.548
GT	Sense	Sense	-0.050	Detected	0.050	Detected	0.000	-3.432	Comprom	-2.208	Detected	-2.820	0.044	GT	Sens	contig909	contig909	Inosine-u	GCATAC	contig909	Solyc01g	Solyc01g	Inosine-u	GO:00167	GO:00167	contig909	Solyc01g	Inosine-u	GO:00167	SL2.40ch	AT5G18890.1		inosine-u	chr5:630	67.0494	65.4699	41.8032	52.9607	5.86063	14.4221
GT	Sense	Sense	-0.687	Detected	0.687	Detected	0.000	-1.062	Detected	-1.375	Detected	-1.218	0.226	GT	Sens	contig911	contig911	Pectate ly	ATTTTG	contig911	Solyc06g	Solyc06g	Pectate ly	GO:0016	GO:0016	contig911	Solyc06g071840.1.1				AT4G24780.1		pectate ly	chr4:127	921.116	2175.69	571.786	843.592	647.339	549.178
GT	Sense	Sense	0.006	Detected	-0.006	Detected	0.000	-2.704	Comprom	-3.470	Comprom	-3.087	0.015	GT	Sens	contig929	contig929	Self-incom	CCTGGC	contig929	Solyc05g	Solyc05g	Self-incompatibility protein-like			contig929	Solyc05g	Self-incompatibility		SL2.40ch	AT4G12430.1		trehalose	chr4:736	51.4911	46.5236	24.3738	20.014	7.17353	4.44445
GT	Sense	Sense	-0.456	Detected	0.456	Detected	0.000	-1.572	Detected	-1.649	Detected	-1.611	0.072	GT	Sens	contig931	contig931	Auxin-ind	ATACCT	contig931	Solyc01g	Solyc01g	Auxin-ind	GO:0005	GO:0005	contig931	Solyc01g	Auxin-ind	GO:0005	SL2.40ch	AT4G38840.1		auxin-res	chr4:181	2737.77	4695.58	2935.39	2798.37	1151.09	1150.37
GT	Sense	Sense	-0.435	Detected	0.435	Detected	0.000	-2.243	Detected	-3.190	Detected	-2.717	0.052	GT	Sens	contig934	contig934	Fatty acid	TGTAGA	contig934	Solyc12g	Solyc12g	Fatty acid desaturase (AHRD V			contig934	Solyc12g	Fatty acid desatura		SL2.40ch	AT3G121	FAD2	FAD2 (FA	chr3:386	6885.38	11470.2	7197.64	11521.2	1792.07	979.819
GT	Sense	Sense	-0.326	Detected	0.326	Detected	0.000	-1.394	Detected	-1.422	Detected	-1.408	0.050	GT	Sens	contig938	contig938	Laccase (	GTTATT	contig938	Solyc05g	Solyc05g	Laccase (	GO:0048	GO:0048	contig938	Solyc07g	Laccase (	GO:0005	SL2.40ch	AT5G589	LAC16	LAC16 (la	chr5:237	521.589	747.133	215.383	469.152	226.767	234.413
GT	Sense	Sense	0.120	Detected	-0.120	Detected	0.000	-0.962	Detected	-1.667	Detected	-1.315	0.072	GT	Sens	contig956	contig956	Ulp1 prot	CAGCAA	contig956	Solyc11g	Solyc11g	Ulp1 protease family C-termina			contig956	Solyc07g041690.1.1				AT1G08040.2		unknown	chr1:249	657.832	507.842	433.392	589.402	283.214	183.075
GT	Sense	Sense	-0.095	Detected	0.095	Detected	0.000	-2.178	Detected	-1.585	Detected	-1.881	0.026	GT	Sens	contig993	contig993	Glutathio	CACGCA	contig993	Solyc09g	Solyc09g	Glutathio	GO:0004	GO:0004	contig993	Solyc09g	Glutathio	GO:0004	SL2.40ch	AT3G21940.1		receptor	chr3:772	1172.29	1219.76	971.439	1184.36	252.329	400.96
GT	Sense	Sense	-0.087	Detected	0.087	Detected	0.000	-1.638	Detected	-0.803	Detected	-1.221	0.104	GT	Sens	contig993	contig993	Unknown	TATTAG	contig993	Solyc07g	Solyc07g	Unknown Protein (AHRD V1)			contig993	Solyc04g	30S ribos	GO:0005	SL2.40ch	AT3G460	RPS15AD	RPS15AD	chr3:169	3679.28	3786.77	2740.73	4418.87	1144.92	2152.41
GT	Sense	Sense	-0.678	Detected	0.678	Detected	0.000	-1.161	Comprom	-1.159	Comprom	-1.160	0.229	GT	Sens	GmHAES	GmHAES	Cross hy	AACAGATGACGAGTGTCTTCAAATTAGCTCTCCTTTGCACAAGCTCGTTGCCCTCAACTA																11.8453	27.6566	2.11329	5.00526	7.73071	8.15161
GT	Sense	Sense	-0.047	Detected	0.047	Detected	0.000	-1.381	Detected	-1.134	Detected	-1.257	0.011	GT	Sens	U70481	U70481	LEU7048	CTGGAGGAAGAGCTTCTGGTTTTGAAGAACTTAGTAAATGCTTATAAATTATACAACAAA																133945	130247	98439.8	108698	48415.9	60562.8
GT	Sense	Sense	0.055	Detected	-0.055	Detected	0.000	-1.779	Detected	-1.274	Detected	-1.527	0.027	GT	Sens	U70481	U70481	TAPG4: (	AAGAGCAAGGAGTACAAAATGTGACAGTTAAGATGGTTAGCTTCACAAGTACTGAGAATG																93272.9	78811.9	53485.9	78438	23853.1	35665.1

GO ID	GO ACCESSION	GO Term	p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
8530	GO:0015116	sulfate transmembran	0.00	5	0.74294204	26	0.075085916
5793	GO:0008272|GO:000	sulfate transport	0.00	5	0.74294204	28	0.080861755
8736	GO:0015381	high affinity sulfate tra	0.00	4	0.5943536	18	0.051982556
5792	GO:0008271	secondary active sulfa	0.00	4	0.5943536	18	0.051982556
8584	GO:0015171|GO:001	amino acid transmem	0.00	9	1.3372957	118	0.34077454
2521	GO:0003333	amino acid transmem	0.00	9	1.3372957	118	0.34077454
4951	GO:0006865|GO:000	amino acid transport	0.00	9	1.3372957	123	0.35521415
3761	GO:0005275|GO:000	amine transmembrane	0.00	9	1.3372957	126	0.3638779
9806	GO:0016752	sinapoyltransferase a	0.00	4	0.5943536	23	0.06642216
9807	GO:0016753	O-sinapoyltransferase	0.00	4	0.5943536	23	0.06642216
9808	GO:0016754	sinapoylglucose-malat	0.00	4	0.5943536	23	0.06642216
9114	GO:0015849	organic acid transport	0.00	10	1.4858841	156	0.45051548
22443	GO:0046942	carboxylic acid transp	0.00	10	1.4858841	156	0.45051548
9600	GO:0016491	oxidoreductase activit	0.00	52	7.7265973	1724	4.9787736
9103	GO:0015837	amine transport	0.00	9	1.3372957	135	0.38986918
3801	GO:0005342	organic acid transmen	0.00	9	1.3372957	136	0.3927571
22444	GO:0046943	carboxylic acid transm	0.00	9	1.3372957	136	0.3927571
5729	GO:0008191	metalloendopeptidase	0.00	2	0.2971768	4	0.011551679
23942	GO:0048551	metalloenzyme inhibit	0.00	2	0.2971768	4	0.011551679
7792	GO:0010576	metalloenzyme regula	0.00	2	0.2971768	4	0.011551679
8967	GO:0015698	inorganic anion transp	0.00	10	1.4858841	176	0.5082739
11827	GO:0019898|GO:003	extrinsic to membrane	0.00	4	0.5943536	30	0.086637594
3884	GO:0005524	ATP binding	0.00	20	2.9717681	524	1.51327
21949	GO:0046424	ferulate 5-hydroxylase	0.00	2	0.2971768	5	0.0144396
7220	GO:0009973	adenylyl-sulfate reduc	0.01	2	0.2971768	6	0.01732752
7690	GO:0010466	negative regulation of	0.01	7	1.0401188	110	0.31767118
12946	GO:0030414	peptidase inhibitor act	0.01	7	1.0401188	110	0.31767118
25636	GO:0051346	negative regulation of	0.01	7	1.0401188	110	0.31767118
13041	GO:0030554	adenyl nucleotide bind	0.01	20	2.9717681	550	1.5883559
14965	GO:0032559	adenyl ribonucleotide	0.01	20	2.9717681	550	1.5883559
12547	GO:0022857|GO:000	transmembrane trans	0.01	43	6.389302	1483	4.282785
26711	GO:0052547	regulation of peptidas	0.01	7	1.0401188	112	0.32344702
28100	GO:0061134	peptidase regulator a	0.01	7	1.0401188	112	0.32344702
26931	GO:0055085	transmembrane trans	0.01	44	6.53789	1548	4.4705
5981	GO:0008509	anion transmembrane	0.01	11	1.6344725	245	0.70754033
5704	GO:0008150|GO:000	biological_process	0.01	461	68.49926	22215	64.155136
4917	GO:0006820|GO:000	anion transport	0.01	11	1.6344725	247	0.7133162
26959	GO:0055114	oxidation-reduction pr	0.01	65	9.658247	2490	7.1909204
11776	GO:0019825	oxygen binding	0.01	15	2.228826	389	1.1234008
3472	GO:0004866	endopeptidase inhibit	0.01	6	0.89153045	95	0.27435237
8159	GO:0010951	negative regulation of	0.01	6	0.89153045	95	0.27435237
26712	GO:0052548	regulation of endopep	0.01	6	0.89153045	95	0.27435237
28101	GO:0061135	endopeptidase regula	0.01	6	0.89153045	95	0.27435237
8517	GO:0015103	inorganic anion trans	0.01	8	1.1887072	154	0.44473964
3723	GO:0005215|GO:000	transporter activity	0.01	50	7.4294205	1844	5.325324
19393	GO:0043086	negative regulation of	0.01	9	1.3372957	188	0.54292893
20342	GO:0044092	negative regulation of	0.01	9	1.3372957	188	0.54292893
3464	GO:0004857	enzyme inhibitor activ	0.01	8	1.1887072	157	0.4534034
12516	GO:0022804	active transmembrane	0.01	25	3.7147102	787	2.2727928
25379	GO:0051082	unfolded protein bindi	0.01	6	0.89153045	98	0.28301615
12574	GO:0022892	substrate-specific tra	0.01	41	6.092125	1463	4.2250266
4878	GO:0006772	thiamine metabolic pr	0.02	2	0.2971768	10	0.0288792
6592	GO:0009228	thiamine biosynthetic	0.02	2	0.2971768	10	0.0288792
8651	GO:0015248	sterol transporter acti	0.02	2	0.2971768	10	0.0288792
9178	GO:0015918	sterol transport	0.02	2	0.2971768	10	0.0288792
10072	GO:0017127	cholesterol transporte	0.02	2	0.2971768	10	0.0288792
12859	GO:0030301	cholesterol transport	0.02	2	0.2971768	10	0.0288792
30069	GO:0071705	nitrogen compound tr	0.02	9	1.3372957	202	0.5833598
3380	GO:0004766	spermidine synthase	0.02	2	0.2971768	11	0.03176712
12573	GO:0022891	substrate-specific tra	0.02	35	5.2005944	1241	3.5839086
4261	GO:0006023	aminoglycan biosynth	0.02	1	0.1485884	1	0.00288792
4262	GO:0006024	glycosaminoglycan bi	0.02	1	0.1485884	1	0.00288792
6615	GO:0009252|GO:000	peptidoglycan biosynt	0.02	1	0.1485884	1	0.00288792
7606	GO:0010382	cellular cell wall macr	0.02	1	0.1485884	1	0.00288792
12766	GO:0030203	glycosaminoglycan m	0.02	1	0.1485884	1	0.00288792
20289	GO:0044038	cell wall macromolecu	0.02	1	0.1485884	1	0.00288792
28953	GO:0070589	cellular component m	0.02	1	0.1485884	1	0.00288792
205	GO:0000270|GO:000	peptidoglycan metabo	0.02	1	0.1485884	1	0.00288792
3827	GO:0005372	water transmembrane	0.02	5	0.74294204	81	0.23392151
4927	GO:0006833	water transport	0.02	5	0.74294204	81	0.23392151
8652	GO:0015250	water channel activity	0.02	5	0.74294204	81	0.23392151
18429	GO:0042044	fluid transport	0.02	5	0.74294204	81	0.23392151
6826	GO:0009538	photosystem I reactio	0.02	2	0.2971768	12	0.03465504
19047	GO:0042723	thiamine-containing c	0.02	2	0.2971768	12	0.03465504
19048	GO:0042724	thiamine-containing c	0.02	2	0.2971768	12	0.03465504
4894	GO:0006790	sulfur compound met	0.02	4	0.5943536	55	0.15883559
6515	GO:0009150	purine ribonucleotide	0.02	24	3.5661218	791	2.2843447
9933	GO:0016903	oxidoreductase activit	0.02	6	0.89153045	113	0.32633495
4493	GO:0006298|GO:000	mismatch repair	0.03	3	0.44576523	33	0.09530135
24966	GO:0050660	flavin adenine dinucle	0.03	6	0.89153045	118	0.34077454
4373	GO:0006163	purine nucleotide met	0.03	24	3.5661218	810	2.339215
18000	GO:0035639	purine ribonucleoside	0.03	23	3.4175334	769	2.2208104
6622	GO:0009259|GO:000	ribonucleotide metabo	0.03	24	3.5661218	812	2.344991
12533	GO:0022838	substrate-specific cha	0.03	9	1.3372957	221	0.63823026
9719	GO:0016638	oxidoreductase activit	0.03	5	0.74294204	89	0.25702485
4405	GO:0006195	purine nucleotide cata	0.03	23	3.4175334	773	2.232362
6508	GO:0009143	nucleoside triphospha	0.03	23	3.4175334	773	2.232362
6509	GO:0009144	purine nucleoside trip	0.03	23	3.4175334	773	2.232362
6511	GO:0009146	purine nucleoside trip	0.03	23	3.4175334	773	2.232362
6519	GO:0009154	purine ribonucleotide	0.03	23	3.4175334	773	2.232362

6530	GO:0009166	nucleotide catabolic pr	**0.03**	23	3.4175334	773	2.232362
6567	GO:0009203	ribonucleoside triphos	**0.03**	23	3.4175334	773	2.232362
6569	GO:0009205	purine ribonucleoside	**0.03**	23	3.4175334	773	2.232362
6571	GO:0009207	purine ribonucleoside	**0.03**	23	3.4175334	773	2.232362
6624	GO:0009261	ribonucleotide catabol	**0.03**	23	3.4175334	773	2.232362
17034	GO:0034655	nucleobase, nucleosid	**0.03**	23	3.4175334	773	2.232362
17035	GO:0034656	nucleobase, nucleosid	**0.03**	23	3.4175334	773	2.232362
22209	GO:0046700	heterocycle catabolic	**0.03**	23	3.4175334	773	2.232362
30879	GO:0072523	purine-containing com	**0.03**	23	3.4175334	773	2.232362
20520	GO:0044270	cellular nitrogen comp	**0.03**	23	3.4175334	777	2.2439137
8660	GO:0015267|GO:0015	channel activity	**0.03**	9	1.3372957	226	0.6526699
12515	GO:0022803	passive transmembra	**0.03**	9	1.3372957	226	0.6526699
6810	GO:0009522	photosystem I	**0.03**	2	0.2971768	15	0.043318797
12650	GO:0030060	L-malate dehydrogena	**0.03**	2	0.2971768	15	0.043318797
24968	GO:0050662	coenzyme binding	**0.03**	8	1.1887072	191	0.5515927
30877	GO:0072521	purine-containing com	**0.03**	24	3.5661218	827	2.3883097
6563	GO:0009199	ribonucleoside triphos	**0.04**	23	3.4175334	790	2.2814567
3334	GO:0004713|GO:0004	protein tyrosine kinase	**0.04**	2	0.2971768	16	0.046206716
206	GO:0000271	polysaccharide biosyn	**0.04**	2	0.2971768	16	0.046206716
2878	GO:0004072	aspartate kinase activ	**0.04**	1	0.1485884	2	0.00577584
3013	GO:0004328|GO:0034	formamidase activity	**0.04**	1	0.1485884	2	0.00577584
3069	GO:0004392	heme oxygenase (dec	**0.04**	1	0.1485884	2	0.00577584
3335	GO:0004714	transmembrane recep	**0.04**	1	0.1485884	2	0.00577584
3337	GO:0004716	receptor signaling prot	**0.04**	1	0.1485884	2	0.00577584
3434	GO:0004825	methionine-tRNA ligas	**0.04**	1	0.1485884	2	0.00577584
3595	GO:0005017	platelet-derived growt	**0.04**	1	0.1485884	2	0.00577584
3664	GO:0005128	erythropoietin recepto	**0.04**	1	0.1485884	2	0.00577584
3709	GO:0005176	ErbB-2 class receptor	**0.04**	1	0.1485884	2	0.00577584
3751	GO:0005251	delayed rectifier potas	**0.04**	1	0.1485884	2	0.00577584
3899	GO:0005547	phosphatidylinositol-3,	**0.04**	1	0.1485884	2	0.00577584
4907	GO:0006808	regulation of nitrogen	**0.04**	1	0.1485884	2	0.00577584
5907	GO:0008413	8-oxo-7,8-dihydrogua	**0.04**	1	0.1485884	2	0.00577584
5923	GO:0008430	selenium binding	**0.04**	1	0.1485884	2	0.00577584
6023	GO:0008569	minus-end-directed m	**0.04**	1	0.1485884	2	0.00577584
7532	GO:0010307	acetylglutamate kinas	**0.04**	1	0.1485884	2	0.00577584
8513	GO:0015098	molybdate ion transme	**0.04**	1	0.1485884	2	0.00577584
8958	GO:0015689	molybdate ion transpo	**0.04**	1	0.1485884	2	0.00577584
9380	GO:0016151	nickel ion binding	**0.04**	1	0.1485884	2	0.00577584
11186	GO:0019177	dihydroneopterin triph	**0.04**	1	0.1485884	2	0.00577584
23486	GO:0048008	platelet-derived growt	**0.04**	1	0.1485884	2	0.00577584
24640	GO:0050321	tau-protein kinase acti	**0.04**	1	0.1485884	2	0.00577584
24919	GO:0050613|GO:000	delta14-sterol reducta	**0.04**	1	0.1485884	2	0.00577584
24987	GO:0050681	androgen receptor bin	**0.04**	1	0.1485884	2	0.00577584
190	GO:0000247	C-8 sterol isomerase	**0.04**	1	0.1485884	2	0.00577584
10058	GO:0017111	nucleoside-triphospha	**0.04**	25	3.7147102	878	2.5355935
14959	GO:0032553	ribonucleotide binding	**0.04**	23	3.4175334	795	2.2958963
14961	GO:0032555	purine ribonucleotide	**0.04**	23	3.4175334	795	2.2958963
3473	GO:0004867	serine-type endopepti	**0.04**	4	0.5943536	66	0.1906027
6888	GO:0009611|GO:0002	response to wounding	**0.04**	4	0.5943536	66	0.1906027
6506	GO:0009141	nucleoside triphospha	**0.04**	23	3.4175334	796	2.2987843
10033	GO:0017076	purine nucleotide bind	**0.04**	23	3.4175334	797	2.3016722
9923	GO:0016892	endoribonuclease acti	**0.04**	2	0.2971768	17	0.049094636
9925	GO:0016894	endonuclease activity,	**0.04**	2	0.2971768	17	0.049094636
9930	GO:0016899	oxidoreductase activit	**0.04**	2	0.2971768	17	0.049094636
16281	GO:0033897	ribonuclease T2 activi	**0.04**	2	0.2971768	17	0.049094636
11828	GO:0019899	enzyme binding	**0.04**	9	1.3372957	237	0.684437
22409	GO:0046906	tetrapyrrole binding	**0.05**	18	2.6745913	596	1.7212002
4408	GO:0006200	ATP catabolic process	**0.05**	19	2.8231797	641	1.8511566
9918	GO:0016887|GO:0004	ATPase activity	**0.05**	19	2.8231797	641	1.8511566
21600	GO:0046034	ATP metabolic proces	**0.05**	19	2.8231797	641	1.8511566
20532	GO:0044282	small molecule catabo	**0.05**	24	3.5661218	854	2.4662836
5874	GO:0008374	O-acyltransferase acti	**0.05**	5	0.74294204	102	0.29456782
3744	GO:0005244	voltage-gated ion cha	**0.05**	4	0.5943536	72	0.20793022
12528	GO:0022832	voltage-gated channel	**0.05**	4	0.5943536	72	0.20793022
15280	GO:0032879	regulation of localizati	**0.05**	4	0.5943536	72	0.20793022
17141	GO:0034762	regulation of transme	**0.05**	4	0.5943536	72	0.20793022
17144	GO:0034765	regulation of ion trans	**0.05**	4	0.5943536	72	0.20793022
19568	GO:0043269	regulation of ion trans	**0.05**	4	0.5943536	72	0.20793022
25348	GO:0051049	regulation of transport	**0.05**	4	0.5943536	72	0.20793022
2895	GO:0004089	carbonate dehydratas	**0.05**	2	0.2971768	19	0.054870475
20522	GO:0044272	sulfur compound bios	**0.05**	3	0.44576523	44	0.12706847
19253	GO:0042936	dipeptide transporter	**0.05**	5	0.74294204	105	0.3032316
19255	GO:0042938	dipeptide transport	**0.05**	5	0.74294204	105	0.3032316
9579	GO:0016462	pyrophosphatase acti	**0.05**	26	3.8632987	954	2.7550755
9859	GO:0016818	hydrolase activity, acti	0.06	26	3.8632987	956	2.7608514
9768	GO:0016706	oxidoreductase activit	0.06	7	1.0401188	175	0.505386
30066	GO:0071702	organic substance tra	0.06	16	2.3774145	529	1.5277096
4867	GO:0006753	nucleoside phosphate	0.06	25	3.7147102	914	2.6395588
6484	GO:0009117	nucleotide metabolic	0.06	25	3.7147102	914	2.6395588
31431	GO:0080054	low affinity nitrate tran	0.06	3	0.44576523	45	0.1299564
3747	GO:0005247	voltage-gated chloride	0.06	2	0.2971768	20	0.0577584
3754	GO:0005254	chloride channel activ	0.06	2	0.2971768	20	0.0577584
6201	GO:0008794	arsenate reductase (g	0.06	2	0.2971768	20	0.0577584
9707	GO:0016624	oxidoreductase activit	0.06	2	0.2971768	20	0.0577584
13086	GO:0030611	arsenate reductase a	0.06	2	0.2971768	20	0.0577584
13088	GO:0030613	oxidoreductase activit	0.06	2	0.2971768	20	0.0577584
13089	GO:0030614	oxidoreductase activit	0.06	2	0.2971768	20	0.0577584
6636	GO:0009273	peptidoglycan-based	0.06	1	0.1485884	3	0.00866376
18884	GO:0042546	cell wall biogenesis	0.06	1	0.1485884	3	0.00866376
9858	GO:0016817	hydrolase activity, acti	0.06	26	3.8632987	959	2.769515
28364	GO:0065007	biological regulation	0.06	99	14.710253	4376	12.637537

9396	GO:0016168	chlorophyll binding	0.06	3	0.44576523	46	0.13284431
3129	GO:0004467	long-chain fatty acid-C	0.06	2	0.2971768	21	0.060646318
9698	GO:0016615	malate dehydrogenase	0.06	2	0.2971768	21	0.060646318
2986	GO:0004252	serine-type endopeptic	0.06	6	0.89153045	144	0.41586044
7074	GO:0009815	1-aminocyclopropane-	0.07	3	0.44576523	49	0.14150807
25094	GO:0050789|GO:0050	regulation of biological	0.07	97	14.413075	4315	12.461374
4755	GO:0006629	lipid metabolic process	0.07	17	2.526003	590	1.7038727
4478	GO:0006281	DNA repair	0.07	6	0.89153045	149	0.43030006
5037	GO:0006974|GO:0034	response to DNA dam	0.07	6	0.89153045	149	0.43030006
4918	GO:0006821	chloride transport	0.07	2	0.2971768	23	0.06642216
4216	GO:0005976	polysaccharide metab	0.07	3	0.44576523	50	0.14439599
7166	GO:0009914	hormone transport	0.07	3	0.44576523	50	0.14439599
27891	GO:0060918	auxin transport	0.07	3	0.44576523	50	0.14439599
31536	GO:0080161	auxin transmembrane	0.07	3	0.44576523	50	0.14439599
26932	GO:0055086	nucleobase, nucleosid	0.08	25	3.7147102	944	2.7261963
2789	GO:0003968	RNA-directed RNA po	0.08	1	0.1485884	4	0.011551679
3057	GO:0004373	glycogen (starch) synt	0.08	1	0.1485884	4	0.011551679
3084	GO:0004412	homoserine dehydroge	0.08	1	0.1485884	4	0.011551679
3336	GO:0004715	non-membrane spann	0.08	1	0.1485884	4	0.011551679
3557	GO:0004970	ionotropic glutamate re	0.08	1	0.1485884	4	0.011551679
4039	GO:0005751|GO:0005	mitochondrial respirato	0.08	1	0.1485884	4	0.011551679
5641	GO:0008066	glutamate receptor act	0.08	1	0.1485884	4	0.011551679
5942	GO:0008456	alpha-N-acetylgalactos	0.08	1	0.1485884	4	0.011551679
7170	GO:0009918	sterol delta7 reductase	0.08	1	0.1485884	4	0.011551679
7538	GO:0010313	phytochrome binding	0.08	1	0.1485884	4	0.011551679
8594	GO:0015184	L-cystine transmembra	0.08	1	0.1485884	4	0.011551679
8598	GO:0015188	L-isoleucine transmem	0.08	1	0.1485884	4	0.011551679
9072	GO:0015803	branched-chain alipha	0.08	1	0.1485884	4	0.011551679
9080	GO:0015811	L-cystine transport	0.08	1	0.1485884	4	0.011551679
9086	GO:0015818	isoleucine transport	0.08	1	0.1485884	4	0.011551679
9745	GO:0016672	oxidoreductase activity	0.08	1	0.1485884	4	0.011551679
10089	GO:0017151	DEAD/H-box RNA hel	0.08	1	0.1485884	4	0.011551679
15186	GO:0032784	regulation of transcript	0.08	1	0.1485884	4	0.011551679
15188	GO:0032786	positive regulation of t	0.08	1	0.1485884	4	0.011551679
15369	GO:0032968|GO:0090	positive regulation of t	0.08	1	0.1485884	4	0.011551679
16626	GO:0034243|GO:0090	regulation of transcript	0.08	1	0.1485884	4	0.011551679
17623	GO:0035257	nuclear hormone rece	0.08	1	0.1485884	4	0.011551679
17624	GO:0035258	steroid hormone recep	0.08	1	0.1485884	4	0.011551679
20810	GO:0045174	glutathione dehydroge	0.08	1	0.1485884	4	0.011551679
20901	GO:0045277|GO:0045	respiratory chain comp	0.08	1	0.1485884	4	0.011551679
23084	GO:0047598	7-dehydrocholesterol r	0.08	1	0.1485884	4	0.011551679
25055	GO:0050750	low-density lipoprotein	0.08	1	0.1485884	4	0.011551679
25711	GO:0051427	hormone receptor bind	0.08	1	0.1485884	4	0.011551679
28689	GO:0070325	lipoprotein particle rec	0.08	1	0.1485884	4	0.011551679
31507	GO:0080132	fatty acid alpha-hydrox	0.08	1	0.1485884	4	0.011551679
75	GO:0000099	sulfur amino acid trans	0.08	1	0.1485884	4	0.011551679
77	GO:0000101	sulfur amino acid trans	0.08	1	0.1485884	4	0.011551679
4311	GO:0006073	cellular glucan metabo	0.08	2	0.2971768	24	0.06931008
4692	GO:0006563	L-serine metabolic pro	0.08	2	0.2971768	24	0.06931008
20293	GO:0044042	glucan metabolic proc	0.08	2	0.2971768	24	0.06931008
2809	GO:0003993	acid phosphatase acti	0.08	3	0.44576523	52	0.15017183
6424	GO:0009055|GO:0009	electron carrier activity	0.08	6	0.89153045	154	0.44473964
5705	GO:0008152	metabolic process	0.08	357	53.046062	17432	50.34222
21145	GO:0045543	gibberellin 2-beta-diox	0.08	2	0.2971768	25	0.072197996
22007	GO:0046483	heterocycle metabolic	0.09	28	4.1604753	1094	3.1593843
25626	GO:0051336	regulation of hydrolase	0.09	7	1.0401188	196	0.5660323
11224	GO:0019222	regulation of metabolic	0.09	71	10.549777	3115	8.995871
28365	GO:0065008	regulation of biological	0.09	10	1.4858841	316	0.9125827
2962	GO:0004160	dihydroxy-acid dehydr	0.09	1	0.1485884	5	0.0144396
3392	GO:0004779	sulfate adenylyltransfe	0.09	1	0.1485884	5	0.0144396
3394	GO:0004781	sulfate adenylyltransfe	0.09	1	0.1485884	5	0.0144396
5243	GO:0007218	neuropeptide signaling	0.09	1	0.1485884	5	0.0144396
14047	GO:0031625	ubiquitin protein ligase	0.09	1	0.1485884	5	0.0144396
24603	GO:0050284	sinapate 1-glucosyltra	0.09	1	0.1485884	5	0.0144396
4909	GO:0006810|GO:0015	transport	0.09	54	8.023774	2315	6.6855345
25529	GO:0051234	establishment of locali	0.09	54	8.023774	2315	6.6855345
21331	GO:0045735	nutrient reservoir activ	0.10	4	0.5943536	89	0.25702485
8919	GO:0015645	fatty acid ligase activit	0.10	2	0.2971768	27	0.077973835
12794	GO:0030234	enzyme regulator activ	0.10	12	1.7830609	403	1.1638317
25476	GO:0051179	localization	0.10	54	8.023774	2319	6.697086
8673	GO:0015291|GO:0015	secondary active trans	0.10	12	1.7830609	407	1.1753833
6438	GO:0009069	serine family amino ac	0.10	2	0.2971768	28	0.080861755
6809	GO:0009521|GO:0030	photosystem	0.10	2	0.2971768	28	0.080861755
6940	GO:0009672	auxin:hydrogen sympo	0.10	2	0.2971768	28	0.080861755
8028	GO:0010817	regulation of hormone	0.10	3	0.44576523	58	0.16749935
9422	GO:0016209	antioxidant activity	0.10	6	0.89153045	165	0.47650677
20498	GO:0044248	cellular catabolic proce	0.11	23	3.4175334	894	2.5818002
2694	GO:0003844	1,4-alpha-glucan bran	0.11	1	0.1485884	6	0.01732752
2713	GO:0003863	3-methyl-2-oxobutano	0.11	1	0.1485884	6	0.01732752
3029	GO:0004345	glucose-6-phosphate	0.11	1	0.1485884	6	0.01732752
3058	GO:0004375	glycine dehydrogenas	0.11	1	0.1485884	6	0.01732752
3065	GO:0004382	guanosine-diphosphat	0.11	1	0.1485884	6	0.01732752
3777	GO:0005302|GO:0015	L-tyrosine transmemb	0.11	1	0.1485884	6	0.01732752
3845	GO:0005452	inorganic anion excha	0.11	1	0.1485884	6	0.01732752
4532	GO:0006357|GO:0006	regulation of transcript	0.11	1	0.1485884	6	0.01732752
4953	GO:0006868|GO:0015	glutamine transport	0.11	1	0.1485884	6	0.01732752
8586	GO:0015173	aromatic amino acid tr	0.11	1	0.1485884	6	0.01732752
8596	GO:0015186	L-glutamine transmem	0.11	1	0.1485884	6	0.01732752
9070	GO:0015801	aromatic amino acid tr	0.11	1	0.1485884	6	0.01732752
9096	GO:0015828	tyrosine transport	0.11	1	0.1485884	6	0.01732752
9723	GO:0016642	oxidoreductase activity	0.11	1	0.1485884	6	0.01732752
9825	GO:0016774	phosphotransferase a	0.11	1	0.1485884	6	0.01732752
11169	GO:0019156	isoamylase activity	0.11	1	0.1485884	6	0.01732752
13832	GO:0031409	pigment binding	0.11	1	0.1485884	6	0.01732752
22095	GO:0046577	long-chain-alcohol oxi	0.11	1	0.1485884	6	0.01732752

23230	GO:0047746	chlorophyllase activity	0.11	1	0.1485884	6	0.01732752
30707	GO:0072348	sulfur compound trans	0.11	1	0.1485884	6	0.01732752
191	GO:0000248	C-5 sterol desaturase	0.11	1	0.1485884	6	0.01732752
9266	GO:0016020	membrane	0.11	83	12.332838	3741	10.803708
4215	GO:0005975	carbohydrate metaboli	0.11	25	3.7147102	990	2.8590407
3886	GO:0005527	macrolide binding	0.11	2	0.2971768	30	0.086637594
3887	GO:0005528	FK506 binding	0.11	2	0.2971768	30	0.086637594
8526	GO:0015112	nitrate transmembrane	0.12	3	0.44576523	61	0.1761631
8975	GO:0015706|GO:0006	nitrate transport	0.12	3	0.44576523	61	0.1761631
21058	GO:0045454|GO:0030	cell redox homeostasis	0.12	7	1.0401188	211	0.6093511
11931	GO:0020037	heme binding	0.12	15	2.228826	550	1.5883559
20514	GO:0044264	cellular polysaccharide	0.12	2	0.2971768	31	0.08952551
15949	GO:0033554	cellular response to st	0.12	6	0.89153045	173	0.49961013
3242	GO:0004601|GO:0016	peroxidase activity	0.12	5	0.74294204	135	0.38986918
9754	GO:0016684	oxidoreductase activity	0.12	5	0.74294204	135	0.38986918
5766	GO:0008236	serine-type peptidase	0.13	7	1.0401188	214	0.6180149
3717	GO:0005199	structural constituent c	0.13	2	0.2971768	32	0.09241343
21041	GO:0045431	flavonol synthase activ	0.13	2	0.2971768	32	0.09241343
25836	GO:0051552	flavone metabolic proc	0.13	2	0.2971768	32	0.09241343
25837	GO:0051553	flavone biosynthetic pr	0.13	2	0.2971768	32	0.09241343
25838	GO:0051554	flavonol metabolic pro	0.13	2	0.2971768	32	0.09241343
25839	GO:0051555	flavonol biosynthetic p	0.13	2	0.2971768	32	0.09241343
9293	GO:0016051|GO:0006	carbohydrate biosynth	0.13	3	0.44576523	64	0.18482687
3357	GO:0004738	pyruvate dehydrogena	0.13	1	0.1485884	7	0.020215439
3358	GO:0004739	pyruvate dehydrogena	0.13	1	0.1485884	7	0.020215439
3367	GO:0004748|GO:0016	ribonucleoside-diphos	0.13	1	0.1485884	7	0.020215439
4260	GO:0006022	aminoglycan metabolic	0.13	1	0.1485884	7	0.020215439
9786	GO:0016725	oxidoreductase activity	0.13	1	0.1485884	7	0.020215439
9789	GO:0016728	oxidoreductase activity	0.13	1	0.1485884	7	0.020215439
21107	GO:0045505	dynein intermediate ch	0.13	1	0.1485884	7	0.020215439
2632	GO:0003682	chromatin binding	0.13	2	0.2971768	33	0.09530135
4942	GO:0006855	drug transmembrane t	0.14	5	0.74294204	139	0.40142086
8607	GO:0015197|GO:0015	peptide transporter act	0.14	5	0.74294204	139	0.40142086
8608	GO:0015198	oligopeptide transporte	0.14	5	0.74294204	139	0.40142086
8642	GO:0015238|GO:0015	drug transmembrane t	0.14	5	0.74294204	139	0.40142086
9154	GO:0015893	drug transport	0.14	5	0.74294204	139	0.40142086
18832	GO:0042493|GO:0017	response to drug	0.14	5	0.74294204	139	0.40142086
25098	GO:0050794|GO:0051	regulation of cellular p	0.14	87	12.927192	3987	11.514136
3872	GO:0005506	iron ion binding	0.14	15	2.228826	563	1.6258988
10103	GO:0017171	serine hydrolase activi	0.14	7	1.0401188	220	0.63534236
4944	GO:0006857	oligopeptide transport	0.14	5	0.74294204	141	0.4071967
9099	GO:0015833	peptide transport	0.14	5	0.74294204	141	0.4071967
3749	GO:0005249	voltage-gated potassiu	0.14	2	0.2971768	34	0.09818927
5700	GO:0008144	drug binding	0.14	2	0.2971768	34	0.09818927
5827	GO:0008308|GO:0022	voltage-gated anion ch	0.14	2	0.2971768	34	0.09818927
20321	GO:0044070	regulation of anion tra	0.14	2	0.2971768	34	0.09818927
2932	GO:0004130	cytochrome-c peroxida	0.15	1	0.1485884	8	0.023103358
2935	GO:0004133	glycogen debranching	0.15	1	0.1485884	8	0.023103358
3280	GO:0004645	phosphorylase activity	0.15	1	0.1485884	8	0.023103358
3356	GO:0004737	pyruvate decarboxylas	0.15	1	0.1485884	8	0.023103358
3803	GO:0005344|GO:0015	oxygen transporter act	0.15	1	0.1485884	8	0.023103358
4035	GO:0005746	mitochondrial respirato	0.15	1	0.1485884	8	0.023103358
4486	GO:0006289|GO:0045	nucleotide-excision re	0.15	1	0.1485884	8	0.023103358
4664	GO:0006535	cysteine biosynthetic p	0.15	1	0.1485884	8	0.023103358
5724	GO:0008184	glycogen phosphoryla	0.15	1	0.1485884	8	0.023103358
6613	GO:0009250	glucan biosynthetic pr	0.15	1	0.1485884	8	0.023103358
8940	GO:0015669	gas transport	0.15	1	0.1485884	8	0.023103358
8942	GO:0015671	oxygen transport	0.15	1	0.1485884	8	0.023103358
10057	GO:0017110	nucleoside-diphosphat	0.15	1	0.1485884	8	0.023103358
12818	GO:0030259	lipid glycosylation	0.15	1	0.1485884	8	0.023103358
22702	GO:0047209	coniferyl-alcohol gluco	0.15	1	0.1485884	8	0.023103358
28833	GO:0070469	respiratory chain	0.15	1	0.1485884	8	0.023103358
29068	GO:0070704	sterol desaturase activ	0.15	1	0.1485884	8	0.023103358
30696	GO:0072337	modified amino acid tr	0.15	1	0.1485884	8	0.023103358
30708	GO:0072349	modified amino acid tr	0.15	1	0.1485884	8	0.023103358
4530	GO:0006355|GO:0032	regulation of transcript	0.15	58	8.618128	2591	7.4826
25095	GO:0050790	regulation of catalytic a	0.15	13	1.9316493	480	1.3862015
25544	GO:0051252	regulation of RNA met	0.15	58	8.618128	2593	7.488376
9722	GO:0016641	oxidoreductase activity	0.15	3	0.44576523	69	0.19926646
28366	GO:0065009	regulation of molecula	0.15	13	1.9316493	484	1.3977532
9185	GO:0015925	galactosidase activity	0.15	2	0.2971768	36	0.10396511
12626	GO:0030029	actin filament-based p	0.15	2	0.2971768	36	0.10396511
12633	GO:0030036	actin cytoskeleton orga	0.15	2	0.2971768	36	0.10396511
7141	GO:0009889	regulation of biosynthe	0.16	58	8.618128	2605	7.523031
7772	GO:0010556	regulation of macromo	0.16	58	8.618128	2605	7.523031
13756	GO:0031326	regulation of cellular b	0.16	58	8.618128	2605	7.523031
32213	GO:2000112	regulation of cellular m	0.16	58	8.618128	2605	7.523031
3758	GO:0005267	potassium channel act	0.16	2	0.2971768	37	0.10685303
2655	GO:0003725	double-stranded RNA	0.16	1	0.1485884	9	0.025991278
2837	GO:0004028	3-chloroallyl aldehyde	0.16	1	0.1485884	9	0.025991278
19342	GO:0043027	caspase inhibitor activ	0.16	1	0.1485884	9	0.025991278
19343	GO:0043028	caspase regulator acti	0.16	1	0.1485884	9	0.025991278
19458	GO:0043154|GO:0001	negative regulation of	0.16	1	0.1485884	9	0.025991278
19579	GO:0043281|GO:0043	regulation of caspase	0.16	1	0.1485884	9	0.025991278
21104	GO:0045502	dynein binding	0.16	1	0.1485884	9	0.025991278
79	GO:0000103|GO:0019	sulfate assimilation	0.16	1	0.1485884	9	0.025991278
9740	GO:0016667	oxidoreductase activity	0.16	3	0.44576523	72	0.20793022
18953	GO:0042623	ATPase activity, coupl	0.17	14	2.0802376	537	1.550813
5066	GO:0007010	cytoskeleton organizat	0.17	2	0.2971768	38	0.10974095
8588	GO:0015175	neutral amino acid tran	0.17	2	0.2971768	38	0.10974095
9073	GO:0015804	neutral amino acid tran	0.17	2	0.2971768	38	0.10974095
12538	GO:0022843	voltage-gated cation c	0.17	2	0.2971768	38	0.10974095
9703	GO:0016620	oxidoreductase activity	0.17	3	0.44576523	73	0.21081814
11695	GO:0019725	cellular homeostasis	0.17	7	1.0401188	234	0.67577326
7692	GO:0010468	regulation of gene exp	0.18	58	8.618128	2635	7.6096687

2897	GO:0004091|GO:0004	carboxylesterase activ	0.18	6	0.89153045	194	0.5602564
3056	GO:0004372	glycine hydroxymethyl	0.18	1	0.1485884	10	0.0288792
3203	GO:0004557	alpha-galactosidase a	0.18	1	0.1485884	10	0.0288792
3362	GO:0004743	pyruvate kinase activit	0.18	1	0.1485884	10	0.0288792
4663	GO:0006534	cysteine metabolic pro	0.18	1	0.1485884	10	0.0288792
8470	GO:0015037	peptide disulfide oxido	0.18	1	0.1485884	10	0.0288792
8471	GO:0015038	glutathione disulfide ox	0.18	1	0.1485884	10	0.0288792
9659	GO:0016572	histone phosphorylatio	0.18	1	0.1485884	10	0.0288792
10220	GO:0018105	peptidyl-serine phosph	0.18	1	0.1485884	10	0.0288792
10320	GO:0018209	peptidyl-serine modific	0.18	1	0.1485884	10	0.0288792
11205	GO:0019202	amino acid kinase acti	0.18	1	0.1485884	10	0.0288792
11337	GO:0019344	cysteine biosynthetic p	0.18	1	0.1485884	10	0.0288792
13472	GO:0031013	troponin I binding	0.18	1	0.1485884	10	0.0288792
17539	GO:0035173	histone kinase activity	0.18	1	0.1485884	10	0.0288792
17540	GO:0035174	histone serine kinase	0.18	1	0.1485884	10	0.0288792
17541	GO:0035175|GO:0044	histone kinase activity	0.18	1	0.1485884	10	0.0288792
17770	GO:0035404	histone-serine phosph	0.18	1	0.1485884	10	0.0288792
20239	GO:0043987|GO:0043	histone H3-S10 phosp	0.18	1	0.1485884	10	0.0288792
23419	GO:0047938	glucose-6-phosphate	0.18	1	0.1485884	10	0.0288792
26022	GO:0051740	ethylene binding	0.18	1	0.1485884	10	0.0288792
28451	GO:0070085	glycosylation	0.18	1	0.1485884	10	0.0288792
30687	GO:0072328	alkene binding	0.18	1	0.1485884	10	0.0288792
3627	GO:0005085|GO:0008	guanyl-nucleotide exc	0.18	3	0.44576523	75	0.21659398
9801	GO:0016747	transferase activity, tra	0.18	12	1.7830609	456	1.3168914
7072	GO:0009813	flavonoid biosynthetic	0.18	2	0.2971768	40	0.1155168
18925	GO:0042592	homeostatic process	0.18	7	1.0401188	238	0.68732494
5663	GO:0008094|GO:0004	DNA-dependent ATPa	0.18	3	0.44576523	76	0.2194819
8494	GO:0015075	ion transmembrane tra	0.19	20	2.9717681	827	2.3883097
23515	GO:0048037	cofactor binding	0.19	9	1.3372957	327	0.94434977
9767	GO:0016705	oxidoreductase activity	0.19	9	1.3372957	329	0.95012563
5196	GO:0007166	cell surface receptor li	0.19	3	0.44576523	78	0.22525774
2791	GO:0003973	(S)-2-hydroxy-acid oxi	0.19	1	0.1485884	11	0.03176712
2989	GO:0004301	epoxide hydrolase act	0.19	1	0.1485884	11	0.03176712
3202	GO:0004556	alpha-amylase activity	0.19	1	0.1485884	11	0.03176712
6288	GO:0008891	glycolate oxidase activ	0.19	1	0.1485884	11	0.03176712
9849	GO:0016803	ether hydrolase activit	0.19	1	0.1485884	11	0.03176712
11152	GO:0019139|GO:0046	cytokinin dehydrogena	0.19	1	0.1485884	11	0.03176712
3753	GO:0005253	anion channel activity	0.20	2	0.2971768	42	0.121292636
4874	GO:0006767	water-soluble vitamin	0.20	2	0.2971768	42	0.121292636
8461	GO:0015020|GO:0003	glucuronosyltransferas	0.20	2	0.2971768	42	0.121292636
18713	GO:0042364	water-soluble vitamin	0.20	2	0.2971768	42	0.121292636
27228	GO:0060255	regulation of macromo	0.20	58	8.618128	2660	7.6818666
16603	GO:0034220	ion transmembrane tra	0.20	20	2.9717681	833	2.4056373
131	GO:0000166	nucleotide binding	0.20	28	4.1604753	1213	3.5030468
8589	GO:0015179	L-amino acid transmen	0.20	2	0.2971768	43	0.124180555
9076	GO:0015807	L-amino acid transport	0.20	2	0.2971768	43	0.124180555
9875	GO:0016836	hydro-lyase activity	0.20	3	0.44576523	80	0.2310336
11221	GO:0019219	regulation of nucleoba	0.21	58	8.618128	2675	7.7251854
25468	GO:0051171	regulation of nitrogen	0.21	58	8.618128	2675	7.7251854
2838	GO:0004029	aldehyde dehydrogena	0.21	1	0.1485884	12	0.03465504
3037	GO:0004353	glutamate dehydrogen	0.21	1	0.1485884	12	0.03465504
3049	GO:0004365	glyceraldehyde-3-phos	0.21	1	0.1485884	12	0.03465504
3246	GO:0004605	phosphatidate cytidyly	0.21	1	0.1485884	12	0.03465504
4217	GO:0005977	glycogen metabolic pr	0.21	1	0.1485884	12	0.03465504
4344	GO:0006112	energy reserve metab	0.21	1	0.1485884	12	0.03465504
6336	GO:0008943	glyceraldehyde-3-phos	0.21	1	0.1485884	12	0.03465504
6439	GO:0009070	serine family amino ac	0.21	1	0.1485884	12	0.03465504
21503	GO:0045935	positive regulation of r	0.21	1	0.1485884	12	0.03465504
25470	GO:0051173	positive regulation of r	0.21	1	0.1485884	12	0.03465504
25546	GO:0051254	positive regulation of R	0.21	1	0.1485884	12	0.03465504
37	GO:0000049	tRNA binding	0.21	1	0.1485884	12	0.03465504
4873	GO:0006766	vitamin metabolic proc	0.21	2	0.2971768	44	0.12706847
6477	GO:0009110	vitamin biosynthetic pr	0.21	2	0.2971768	44	0.12706847
7071	GO:0009812	flavonoid metabolic pr	0.21	2	0.2971768	44	0.12706847
12532	GO:0022836	gated channel activity	0.21	4	0.5943536	122	0.3523262
3630	GO:0005088	Ras guanyl-nucleotide	0.22	2	0.2971768	45	0.1299564
3787	GO:0005319	lipid transporter activit	0.22	3	0.44576523	83	0.23969735
4912	GO:0006813|GO:0015	potassium ion transpo	0.22	3	0.44576523	84	0.24258527
30168	GO:0071804	cellular potassium ion	0.22	3	0.44576523	84	0.24258527
30169	GO:0071805	potassium ion transme	0.22	3	0.44576523	84	0.24258527
4357	GO:0006139|GO:0055	nucleobase, nucleosid	0.22	70	10.401189	3285	9.486816
2896	GO:0004090	carbonyl reductase (N	0.23	1	0.1485884	13	0.037542958
7551	GO:0010327	acetyl CoA:(Z)-3-hexe	0.23	1	0.1485884	13	0.037542958
8149	GO:0010941	regulation of cell death	0.23	1	0.1485884	13	0.037542958
13443	GO:0030984	kininogen binding	0.23	1	0.1485884	13	0.037542958
19298	GO:0042981	regulation of apoptosis	0.23	1	0.1485884	13	0.037542958
19381	GO:0043067|GO:0043	regulation of programm	0.23	1	0.1485884	13	0.037542958
6425	GO:0009056	catabolic process	0.24	24	3.5661218	1051	3.0352037
31465	GO:0080090	regulation of primary n	0.24	58	8.618128	2710	7.826263
2976	GO:0004176|GO:0004	ATP-dependent peptid	0.24	2	0.2971768	48	0.13862015
2977	GO:0004177	aminopeptidase activit	0.24	1	0.1485884	14	0.040430877
3204	GO:0004558|GO:0004	alpha-glucosidase acti	0.24	1	0.1485884	14	0.040430877
3629	GO:0005087	Ran guanyl-nucleotide	0.24	1	0.1485884	14	0.040430877
5197	GO:0007167	enzyme linked recepto	0.24	1	0.1485884	14	0.040430877
5199	GO:0007169	transmembrane recep	0.24	1	0.1485884	14	0.040430877
7413	GO:0010181	FMN binding	0.24	1	0.1485884	14	0.040430877
9720	GO:0016639	oxidoreductase activity	0.24	1	0.1485884	14	0.040430877
9847	GO:0016801	hydrolase activity, acti	0.24	1	0.1485884	14	0.040430877
28373	GO:0070006	metalloaminopeptidas	0.24	1	0.1485884	14	0.040430877
3756	GO:0005261|GO:0015	cation channel activity	0.25	2	0.2971768	49	0.14150807
9725	GO:0016645	oxidoreductase activity	0.25	2	0.2971768	49	0.14150807
4605	GO:0006457|GO:0007	protein folding	0.25	5	0.74294204	173	0.49961013
8675	GO:0015293	symporter activity	0.25	5	0.74294204	173	0.49961013
13753	GO:0031323	regulation of cellular m	0.25	59	8.766716	2770	7.999538
8635	GO:0015229	L-ascorbic acid transp	0.26	1	0.1485884	15	0.043318797

9144	GO:0015882	L-ascorbic acid transp	0.26	1	0.1485884	15	0.043318797
16081	GO:0033692	cellular polysaccharide	0.26	1	0.1485884	15	0.043318797
2758	GO:0003924	GTPase activity	0.26	4	0.5943536	132	0.3812054
4394	GO:0006184	GTP catabolic process	0.26	4	0.5943536	132	0.3812054
21605	GO:0046039	GTP metabolic proces	0.26	4	0.5943536	132	0.3812054
4906	GO:0006807	nitrogen compound me	0.26	78	11.589896	3725	10.757502
19126	GO:0042803	protein homodimerizat	0.26	7	1.0401188	265	0.7652988
30207	GO:0071843	cellular component bio	0.26	2	0.2971768	51	0.14728391
9800	GO:0016746	transferase activity, tra	0.26	12	1.7830609	498	1.438184
6965	GO:0009699	phenylpropanoid biosy	0.27	2	0.2971768	52	0.15017183
2667	GO:0003777	microtubule motor acti	0.27	1	0.1485884	16	0.046206716
3742	GO:0005242	inward rectifier potass	0.27	1	0.1485884	16	0.046206716
7178	GO:0009927	histidine phosphotrans	0.27	1	0.1485884	16	0.046206716
9189	GO:0015929	hexosaminidase activi	0.27	1	0.1485884	16	0.046206716
9727	GO:0016647	oxidoreductase activity	0.27	1	0.1485884	16	0.046206716
9797	GO:0016742	hydroxymethyl-, formy	0.27	1	0.1485884	16	0.046206716
9898	GO:0016863	intramolecular oxidore	0.27	1	0.1485884	16	0.046206716
13435	GO:0030976	thiamine pyrophospha	0.27	1	0.1485884	16	0.046206716
18757	GO:0042409	caffeoyl-CoA O-methy	0.27	1	0.1485884	16	0.046206716
22110	GO:0046592	polyamine oxidase act	0.27	1	0.1485884	16	0.046206716
72	GO:0000096	sulfur amino acid meta	0.27	1	0.1485884	16	0.046206716
73	GO:0000097	sulfur amino acid biosy	0.27	1	0.1485884	16	0.046206716
219	GO:0000287	magnesium ion bindin	0.27	1	0.1485884	16	0.046206716
2643	GO:0003700|GO:0000	sequence-specific DN	0.27	31	4.6062407	1417	4.0921826
716	GO:0001071	nucleic acid binding tra	0.27	31	4.6062407	1417	4.0921826
8585	GO:0015172	acidic amino acid trans	0.28	1	0.1485884	17	0.049094636
9069	GO:0015800	acidic amino acid trans	0.28	1	0.1485884	17	0.049094636
2674	GO:0003824	catalytic activity	0.29	216	32.095097	10750	31.045137
3724	GO:0005216	ion channel activity	0.29	4	0.5943536	140	0.40430877
8676	GO:0015294	solute:cation symporte	0.29	4	0.5943536	141	0.4071967
5767	GO:0008237	metallopeptidase activ	0.30	2	0.2971768	56	0.16172351
5765	GO:0008235	metalloexopeptidase a	0.30	1	0.1485884	18	0.051982556
6491	GO:0009126	purine nucleoside mon	0.30	1	0.1485884	18	0.051982556
6492	GO:0009127	purine nucleoside mon	0.30	1	0.1485884	18	0.051982556
6517	GO:0009152	purine ribonucleotide b	0.30	1	0.1485884	18	0.051982556
6531	GO:0009167	purine ribonucleoside	0.30	1	0.1485884	18	0.051982556
6532	GO:0009168	purine ribonucleoside	0.30	1	0.1485884	18	0.051982556
8469	GO:0015036	disulfide oxidoreductas	0.30	1	0.1485884	18	0.051982556
8662	GO:0015271	outward rectifier potas	0.30	1	0.1485884	18	0.051982556
22917	GO:0047429	nucleoside-triphospha	0.30	1	0.1485884	18	0.051982556
28931	GO:0070567	cytidylyltransferase ac	0.30	1	0.1485884	18	0.051982556
17020	GO:0034641	cellular nitrogen comp	0.30	76	11.292719	3678	10.621769
5763	GO:0008233	peptidase activity	0.31	13	1.9316493	565	1.6316746
20531	GO:0044281	small molecule metabo	0.31	38	5.6463594	1788	5.1636004
3290	GO:0004656	procollagen-proline 4-c	0.31	1	0.1485884	19	0.054870475
11752	GO:0019798	procollagen-proline dio	0.31	1	0.1485884	19	0.054870475
13966	GO:0031543	peptidyl-proline dioxyg	0.31	1	0.1485884	19	0.054870475
13968	GO:0031545	peptidyl-proline 4-diox	0.31	1	0.1485884	19	0.054870475
4910	GO:0006811	ion transport	0.32	21	3.1203566	959	2.769515
2626	GO:0003674|GO:0005	molecular_function	0.32	480	71.32243	24394	70.447914
2675	GO:0003825	alpha,alpha-trehalose-	0.32	1	0.1485884	20	0.0577584
3628	GO:0005086	ARF guanyl-nucleotide	0.32	1	0.1485884	20	0.0577584
9706	GO:0016623	oxidoreductase activity	0.32	1	0.1485884	20	0.0577584
9784	GO:0016723	oxidoreductase activity	0.32	1	0.1485884	20	0.0577584
24482	GO:0050162	oxalate oxidase activit	0.32	1	0.1485884	20	0.0577584
25477	GO:0051180	vitamin transport	0.32	1	0.1485884	20	0.0577584
25480	GO:0051183	vitamin transporter act	0.32	1	0.1485884	20	0.0577584
122	GO:0000154|GO:0016	rRNA modification	0.32	1	0.1485884	20	0.0577584
225	GO:0000293	ferric-chelate reductas	0.32	1	0.1485884	20	0.0577584
6964	GO:0009698	phenylpropanoid meta	0.33	2	0.2971768	60	0.17327519
8943	GO:0015672	monovalent inorganic	0.33	9	1.3372957	383	1.1060733
11426	GO:0019438	aromatic compound bi	0.33	4	0.5943536	149	0.43030006
2818	GO:0004003	ATP-dependent DNA	0.33	2	0.2971768	61	0.1761631
3474	GO:0004869|GO:0004	cysteine-type endopep	0.34	1	0.1485884	21	0.060646318
3195	GO:0004540	ribonuclease activity	0.34	3	0.44576523	106	0.3061195
5213	GO:0007186	G-protein coupled rece	0.34	2	0.2971768	62	0.17905103
9697	GO:0016614	oxidoreductase activity	0.34	7	1.0401188	293	0.84616053
17016	GO:0034637	cellular carbohydrate b	0.35	2	0.2971768	63	0.18193895
6521	GO:0009156	ribonucleoside monop	0.35	1	0.1485884	22	0.06353424
6525	GO:0009161	ribonucleoside monop	0.35	1	0.1485884	22	0.06353424
7143	GO:0009891	positive regulation of b	0.35	1	0.1485884	22	0.06353424
8489	GO:0015066	alpha-amylase inhibito	0.35	1	0.1485884	22	0.06353424
8774	GO:0015431	glutathione S-conjugat	0.35	1	0.1485884	22	0.06353424
13031	GO:0030544	Hsp70 protein binding	0.35	1	0.1485884	22	0.06353424
13758	GO:0031328	positive regulation of c	0.35	1	0.1485884	22	0.06353424
24858	GO:0050551	myrcene synthase act	0.35	1	0.1485884	22	0.06353424
30359	GO:0071997	glutathione S-conjugat	0.35	1	0.1485884	22	0.06353424
28378	GO:0070011	peptidase activity, acti	0.35	12	1.7830609	537	1.550813
9710	GO:0016628	oxidoreductase activity	0.36	2	0.2971768	65	0.18771479
2633	GO:0003684	damaged DNA binding	0.36	1	0.1485884	23	0.06642216
3662	GO:0005126	cytokine receptor bind	0.36	1	0.1485884	23	0.06642216
7527	GO:0010302	2-oxoglutarate-depend	0.36	1	0.1485884	23	0.06642216
3626	GO:0005083	small GTPase regulato	0.37	3	0.44576523	111	0.3205591
3180	GO:0004521	endoribonuclease acti	0.37	2	0.2971768	66	0.1906027
9765	GO:0016702	oxidoreductase activity	0.37	2	0.2971768	66	0.1906027
11829	GO:0019900	kinase binding	0.37	2	0.2971768	66	0.1906027
2629	GO:0003678|GO:0003	DNA helicase activity	0.38	2	0.2971768	67	0.19349062
8559	GO:0015146	pentose transmembra	0.38	1	0.1485884	24	0.06931008
8561	GO:0015148	D-xylose transmembra	0.38	1	0.1485884	24	0.06931008
8829	GO:0015519	D-xylose:hydrogen sy	0.38	1	0.1485884	24	0.06931008
9019	GO:0015750	pentose transport	0.38	1	0.1485884	24	0.06931008
9022	GO:0015753	D-xylose transport	0.38	1	0.1485884	24	0.06931008
9779	GO:0016717	oxidoreductase activity	0.38	1	0.1485884	24	0.06931008
20488	GO:0044238	primary metabolic proc	0.38	182	27.04309	9167	26.47356
9836	GO:0016787	hydrolase activity	0.39	75	11.144131	3723	10.751725

3620	GO:0005057	receptor signaling prot	0.39	2	0.2971768	69	0.19926646
21710	GO:0046148	pigment biosynthetic p	0.39	2	0.2971768	69	0.19926646
2649	GO:0003713	transcription coactivat	0.40	2	0.2971768	70	0.20215438
5726	GO:0008187	poly-pyrimidine tract b	0.40	2	0.2971768	70	0.20215438
5788	GO:0008266	poly(U) RNA binding	0.40	2	0.2971768	70	0.20215438
3210	GO:0004565	beta-galactosidase ac	0.40	1	0.1485884	26	0.075085916
3415	GO:0004805	trehalose-phosphatase	0.40	1	0.1485884	26	0.075085916
7000	GO:0009734	auxin mediated signali	0.40	1	0.1485884	26	0.075085916
7540	GO:0010315	auxin efflux	0.40	1	0.1485884	26	0.075085916
7553	GO:0010329	auxin efflux transmem	0.40	1	0.1485884	26	0.075085916
17147	GO:0034768	(E)-beta-ocimene synt	0.40	1	0.1485884	26	0.075085916
29729	GO:0071365	cellular response to au	0.40	1	0.1485884	26	0.075085916
126	GO:0000160	two-component signal	0.40	1	0.1485884	26	0.075085916
9764	GO:0016701	oxidoreductase activity	0.41	2	0.2971768	72	0.20793022
5018	GO:0006950	response to stress	0.41	13	1.9316493	611	1.764519
3631	GO:0005089	Rho guanyl-nucleotide	0.41	1	0.1485884	27	0.077973835
9389	GO:0016160	amylase activity	0.41	1	0.1485884	27	0.077973835
9541	GO:0016413	O-acetyltransferase ac	0.41	1	0.1485884	27	0.077973835
18786	GO:0042440	pigment metabolic pro	0.42	2	0.2971768	73	0.21081814
17617	GO:0035251	UDP-glucosyltransfera	0.42	5	0.74294204	218	0.62956655
3284	GO:0004650	polygalacturonase act	0.42	1	0.1485884	28	0.080861755
4374	GO:0006164	purine nucleotide bios	0.42	1	0.1485884	28	0.080861755
6079	GO:0008654	phospholipid biosynthe	0.42	1	0.1485884	28	0.080861755
7145	GO:0009893	positive regulation of r	0.42	1	0.1485884	28	0.080861755
7819	GO:0010604	positive regulation of r	0.42	1	0.1485884	28	0.080861755
8863	GO:0015562	efflux transmembrane	0.42	1	0.1485884	28	0.080861755
9238	GO:0015980	energy derivation by o	0.42	1	0.1485884	28	0.080861755
13144	GO:0030674	protein binding, bridgin	0.42	1	0.1485884	28	0.080861755
13755	GO:0031325	positive regulation of c	0.42	1	0.1485884	28	0.080861755
27064	GO:0060090	binding, bridging	0.42	1	0.1485884	28	0.080861755
139	GO:0000175	3'-5'-exoribonuclease	0.42	1	0.1485884	28	0.080861755
4526	GO:0006351|GO:0006	transcription, DNA-dep	0.42	32	4.754829	1575	4.548474
15176	GO:0032774	RNA biosynthetic proc	0.42	32	4.754829	1575	4.548474
6884	GO:0009607	response to biotic stim	0.42	3	0.44576523	122	0.3523262
25195	GO:0050896|GO:0051	response to stimulus	0.43	38	5.6463594	1881	5.432177
22049	GO:0046527	glucosyltransferase ac	0.43	6	0.89153045	270	0.77973837
3260	GO:0004620	phospholipase activity	0.43	3	0.44576523	123	0.35521415
2975	GO:0004175|GO:0016	endopeptidase activity	0.43	7	1.0401188	320	0.9241344
25510	GO:0051213	dioxygenase activity	0.43	2	0.2971768	75	0.21659398
3490	GO:0004888|GO:0004	transmembrane recep	0.43	12	1.7830609	571	1.6490022
4968	GO:0006886	intracellular protein tra	0.43	1	0.1485884	29	0.083749674
16992	GO:0034613|GO:0016	cellular protein localiza	0.43	1	0.1485884	29	0.083749674
29091	GO:0070727	cellular macromolecule	0.43	1	0.1485884	29	0.083749674
5732	GO:0008194	UDP-glycosyltransfera	0.44	7	1.0401188	322	0.9299102
6529	GO:0009165	nucleotide biosynthetic	0.44	2	0.2971768	77	0.22236982
2666	GO:0003774	motor activity	0.45	1	0.1485884	30	0.086637594
3518	GO:0004930|GO:0001	G-protein coupled rec	0.45	1	0.1485884	30	0.086637594
6216	GO:0008810	cellulase activity	0.45	1	0.1485884	30	0.086637594
6488	GO:0009123	nucleoside monophos	0.45	1	0.1485884	30	0.086637594
6489	GO:0009124	nucleoside monophos	0.45	1	0.1485884	30	0.086637594
8683	GO:0015301|GO:0015	anion:anion antiporter	0.45	1	0.1485884	30	0.086637594
5681	GO:0008116	prostaglandin-I syntha	0.45	2	0.2971768	78	0.22525774
9909	GO:0016877	ligase activity, forming	0.45	2	0.2971768	78	0.22525774
25998	GO:0051716	cellular response to st	0.45	23	3.4175334	1138	3.2864528
19590	GO:0043295	glutathione binding	0.46	1	0.1485884	31	0.08952551
3190	GO:0004532	exoribonuclease activi	0.47	1	0.1485884	32	0.09241343
3265	GO:0004630	phospholipase D activ	0.47	1	0.1485884	32	0.09241343
6942	GO:0009674	potassium:sodium sym	0.47	1	0.1485884	32	0.09241343
9927	GO:0016896	exoribonuclease activi	0.47	1	0.1485884	32	0.09241343
12522	GO:0022820	potassium ion sympor	0.47	1	0.1485884	32	0.09241343
12833	GO:0030275	LRR domain binding	0.47	1	0.1485884	32	0.09241343
23914	GO:0048522|GO:0051	positive regulation of c	0.47	1	0.1485884	32	0.09241343
30878	GO:0072522	purine-containing com	0.48	1	0.1485884	33	0.09530135
16738	GO:0034357	photosynthetic membr	0.48	2	0.2971768	83	0.23969735
4844	GO:0006725	cellular aromatic comp	0.49	4	0.5943536	185	0.53426516
9486	GO:0016298	lipase activity	0.49	4	0.5943536	185	0.53426516
9818	GO:0016765|GO:0016	transferase activity, tra	0.49	4	0.5943536	185	0.53426516
2985	GO:0004222	metalloendopeptidase	0.49	1	0.1485884	34	0.09818927
6004	GO:0008536	Ran GTPase binding	0.49	1	0.1485884	34	0.09818927
4327	GO:0006091	generation of precurso	0.49	2	0.2971768	84	0.24258527
19125	GO:0042802	identical protein bindin	0.49	14	2.0802376	697	2.01288
4538	GO:0006364|GO:0006	rRNA processing	0.50	1	0.1485884	35	0.10107719
6355	GO:0008970	phospholipase A1 acti	0.50	1	0.1485884	35	0.10107719
9310	GO:0016072	rRNA metabolic proce	0.50	1	0.1485884	35	0.10107719
11206	GO:0019203	carbohydrate phospha	0.50	1	0.1485884	35	0.10107719
12817	GO:0030258	lipid modification	0.50	1	0.1485884	35	0.10107719
21146	GO:0045544	gibberellin 20-oxidase	0.50	1	0.1485884	35	0.10107719
23199	GO:0047714	galactolipase activity	0.50	1	0.1485884	35	0.10107719
2657	GO:0003727|GO:0003	single-stranded RNA b	0.50	4	0.5943536	188	0.54292893
5768	GO:0008238	exopeptidase activity	0.50	2	0.2971768	86	0.24836111
4916	GO:0006818	hydrogen transport	0.50	6	0.89153045	292	0.84327257
9246	GO:0015992	proton transport	0.50	6	0.89153045	292	0.84327257
4232	GO:0005992	trehalose biosynthetic	0.51	1	0.1485884	36	0.10396511
5902	GO:0008408	3'-5' exonuclease activ	0.51	1	0.1485884	36	0.10396511
6794	GO:0009505	plant-type cell wall	0.51	1	0.1485884	36	0.10396511
8739	GO:0015385|GO:0015	sodium:hydrogen antip	0.51	1	0.1485884	36	0.10396511
9393	GO:0016165	lipoxygenase activity	0.51	1	0.1485884	36	0.10396511
20649	GO:0044455	mitochondrial membra	0.51	1	0.1485884	36	0.10396511
4641	GO:0006508	proteolysis	0.51	19	2.8231797	965	2.7868426
3318	GO:0004693|GO:0016	cyclin-dependent prote	0.52	1	0.1485884	37	0.10685303
11202	GO:0019199	transmembrane recep	0.52	10	1.4858841	504	1.4555116
13164	GO:0030695	GTPase regulator acti	0.52	3	0.44576523	142	0.4100846
20630	GO:0044436	thylakoid part	0.52	2	0.2971768	90	0.2599128
4231	GO:0005991	trehalose metabolic pr	0.53	1	0.1485884	38	0.10974095
9308	GO:0016070	RNA metabolic proces	0.53	36	5.3491826	1855	5.3570914

3644	GO:0005102	receptor binding	0.53	2	0.2971768	91	0.2628007
6784	GO:0009451|GO:0016	RNA modification	0.53	2	0.2971768	91	0.2628007
6623	GO:0009260	ribonucleotide biosynt	0.54	1	0.1485884	39	0.11262887
16785	GO:0034404	nucleobase, nucleosid	0.54	2	0.2971768	92	0.26568863
17033	GO:0034654	nucleobase, nucleosid	0.54	2	0.2971768	92	0.26568863
12805	GO:0030246	carbohydrate binding	0.54	5	0.74294204	251	0.7248679
3178	GO:0004519	endonuclease activity	0.54	7	1.0401188	356	1.0280994
9895	GO:0016860	intramolecular oxidore	0.54	3	0.44576523	146	0.42163628
20336	GO:0044085	cellular component bio	0.54	2	0.2971768	93	0.26857653
5891	GO:0008395|GO:0008	steroid hydroxylase ac	0.54	1	0.1485884	40	0.1155168
7021	GO:0009755	hormone-mediated sig	0.54	1	0.1485884	40	0.1155168
9843	GO:0016796	exonuclease activity, a	0.54	1	0.1485884	40	0.1155168
15271	GO:0032870	cellular response to ho	0.54	1	0.1485884	40	0.1155168
16446	GO:0034062	RNA polymerase activ	0.54	1	0.1485884	40	0.1155168
23910	GO:0048518|GO:0043	positive regulation of b	0.54	1	0.1485884	40	0.1155168
3808	GO:0005351|GO:0005	sugar:hydrogen sympo	0.55	2	0.2971768	94	0.27146447
3835	GO:0005402	cation:sugar symporte	0.55	2	0.2971768	94	0.27146447
6863	GO:0009579	thylakoid	0.55	2	0.2971768	94	0.27146447
22479	GO:0046983	protein dimerization ac	0.55	10	1.4858841	517	1.4930545
9829	GO:0016779	nucleotidyltransferase	0.55	3	0.44576523	148	0.42741212
22415	GO:0046914	transition metal ion bin	0.55	50	7.4294205	2599	7.5057034
31895	GO:0090304	nucleic acid metabolic	0.55	45	6.6864786	2340	6.7577324
11712	GO:0019748	secondary metabolic p	0.55	2	0.2971768	95	0.27435237
9874	GO:0016835	carbon-oxygen lyase a	0.55	4	0.5943536	202	0.5833598
6666	GO:0009312	oligosaccharide biosyn	0.56	1	0.1485884	42	0.121292636
9370	GO:0016138	glycoside biosynthetic	0.56	1	0.1485884	42	0.121292636
21880	GO:0046351	disaccharide biosynthe	0.56	1	0.1485884	42	0.121292636
3200	GO:0004553|GO:0016	hydrolase activity, hyd	0.57	6	0.89153045	312	0.90103096
8679	GO:0015297	antiporter activity	0.57	3	0.44576523	152	0.4389638
8682	GO:0015300	solute:solute antiporte	0.57	3	0.44576523	152	0.4389638
27562	GO:0060589	nucleoside-triphospha	0.57	3	0.44576523	152	0.4389638
8677	GO:0015295	solute:hydrogen symp	0.57	2	0.2971768	98	0.28301615
8681	GO:0015299	solute:hydrogen antipo	0.57	2	0.2971768	98	0.28301615
20619	GO:0044425	membrane part	0.57	29	4.309064	1523	4.398302
3307	GO:0004675	transmembrane recep	0.57	7	1.0401188	367	1.0598665
16851	GO:0034470	ncRNA processing	0.58	2	0.2971768	99	0.28590405
17039	GO:0034660	ncRNA metabolic proc	0.58	2	0.2971768	99	0.28590405
4954	GO:0006869	lipid transport	0.58	4	0.5943536	208	0.6006873
8085	GO:0010876	lipid localization	0.58	4	0.5943536	208	0.6006873
5797	GO:0008276	protein methyltransfera	0.58	1	0.1485884	44	0.12706847
9186	GO:0015926	glucosidase activity	0.58	1	0.1485884	44	0.12706847
9753	GO:0016682	oxidoreductase activity	0.58	1	0.1485884	44	0.12706847
29859	GO:0071495	cellular response to en	0.58	1	0.1485884	44	0.12706847
16430	GO:0034046	poly(G) RNA binding	0.58	2	0.2971768	100	0.28879198
7229	GO:0009987|GO:0008	cellular process	0.58	204	30.312037	10601	30.614838
8666	GO:0015276	ligand-gated ion chann	0.59	1	0.1485884	45	0.1299564
9893	GO:0016857	racemase and epimera	0.59	1	0.1485884	45	0.1299564
12530	GO:0022834	ligand-gated channel a	0.59	1	0.1485884	45	0.1299564
18956	GO:0042626	ATPase activity, coupl	0.59	4	0.5943536	211	0.6093511
3177	GO:0004518	nuclease activity	0.59	8	1.1887072	427	1.2331418
9699	GO:0016616	oxidoreductase activity	0.59	5	0.74294204	266	0.7681867
9861	GO:0016820	hydrolase activity, acti	0.59	4	0.5943536	212	0.612239
4329	GO:0006096|GO:0019	glycolysis	0.59	1	0.1485884	46	0.13284431
6999	GO:0009733	response to auxin stim	0.59	1	0.1485884	46	0.13284431
12498	GO:0022613	ribonucleoprotein com	0.59	1	0.1485884	46	0.13284431
18614	GO:0042254|GO:0007	ribosome biogenesis	0.59	1	0.1485884	46	0.13284431
26845	GO:0052689	carboxylic ester hydro	0.60	10	1.4858841	538	1.5537009
3421	GO:0004812|GO:0017	aminoacyl-tRNA ligase	0.60	1	0.1485884	47	0.13573223
8497	GO:0015079|GO:0022	potassium ion transme	0.60	1	0.1485884	47	0.13573223
9907	GO:0016875	ligase activity, forming	0.60	1	0.1485884	47	0.13573223
9908	GO:0016876	ligase activity, forming	0.60	1	0.1485884	47	0.13573223
9709	GO:0016627	oxidoreductase activity	0.60	2	0.2971768	104	0.30034366
4849	GO:0006730|GO:0019	one-carbon metabolic	0.61	6	0.89153045	325	0.93857396
9869	GO:0016829	lyase activity	0.61	9	1.3372957	488	1.4093049
4188	GO:0005938	cell cortex	0.61	1	0.1485884	48	0.13862015
20642	GO:0044448	cell cortex part	0.61	1	0.1485884	48	0.13862015
28930	GO:0070566	adenylyltransferase ac	0.61	1	0.1485884	48	0.13862015
113	GO:0000145	exocyst	0.61	1	0.1485884	48	0.13862015
18582	GO:0042221	response to chemical	0.62	6	0.89153045	328	0.94723773
3844	GO:0005451	monovalent cation:hyd	0.62	1	0.1485884	49	0.14150807
31421	GO:0080044	quercetin 7-O-glucosy	0.62	1	0.1485884	49	0.14150807
5055	GO:0006996	organelle organization	0.62	3	0.44576523	164	0.47361887
5909	GO:0008415	acyltransferase activity	0.62	6	0.89153045	330	0.95301354
4459	GO:0006259|GO:0055	DNA metabolic proces	0.62	9	1.3372957	493	1.4237444
3185	GO:0004527|GO:0008	exonuclease activity	0.63	1	0.1485884	50	0.14439599
4622	GO:0006479	protein methylation	0.63	1	0.1485884	50	0.14439599
5750	GO:0008213	protein alkylation	0.63	1	0.1485884	50	0.14439599
9783	GO:0016722	oxidoreductase activity	0.63	1	0.1485884	50	0.14439599
9993	GO:0017016	Ras GTPase binding	0.63	1	0.1485884	50	0.14439599
29674	GO:0071310	cellular response to or	0.63	1	0.1485884	50	0.14439599
13656	GO:0031224	intrinsic to membrane	0.63	22	3.268945	1193	3.4452884
22375	GO:0046872	metal ion binding	0.63	56	8.3209505	2985	8.6204405
7173	GO:0009922	fatty acid elongase act	0.63	1	0.1485884	51	0.14728391
22410	GO:0046907	intracellular transport	0.63	1	0.1485884	51	0.14728391
25925	GO:0051641	cellular localization	0.63	1	0.1485884	51	0.14728391
25933	GO:0051649	establishment of locali	0.63	1	0.1485884	51	0.14728391
5097	GO:0007049	cell cycle	0.64	1	0.1485884	52	0.15017183
20287	GO:0044036	cell wall macromolecu	0.64	1	0.1485884	52	0.15017183
9812	GO:0016758	transferase activity, tra	0.64	9	1.3372957	501	1.4468478
19470	GO:0043167	ion binding	0.64	56	8.3209505	2997	8.655096
19472	GO:0043169	cation binding	0.64	56	8.3209505	2997	8.655096
5070	GO:0007017	microtubule-based pro	0.64	2	0.2971768	112	0.32344702
5071	GO:0007018	microtubule-based mo	0.64	2	0.2971768	112	0.32344702
8680	GO:0015298	solute:cation antiporte	0.64	2	0.2971768	112	0.32344702
9730	GO:0016651	oxidoreductase activity	0.64	2	0.2971768	112	0.32344702

29081	GO:0070717	poly-purine tract bindi	0.64	2	0.2971768	112	0.32344702
17024	GO:0034645|GO:0034	cellular macromolecul	0.65	37	5.4977713	1999	5.7729516
9750	GO:0016679	oxidoreductase activit	0.65	1	0.1485884	53	0.15305975
29246	GO:0070882	cellular cell wall organ	0.65	1	0.1485884	53	0.15305975
6428	GO:0009059|GO:0043	macromolecule biosyn	0.65	37	5.4977713	2003	5.7845035
30205	GO:0071841	cellular component or	0.65	5	0.74294204	285	0.8230572
3156	GO:0004497	monooxygenase activ	0.65	3	0.44576523	172	0.49672222
29251	GO:0070887	cellular response to ch	0.65	1	0.1485884	54	0.15594767
9267	GO:0016021	integral to membrane	0.66	20	2.9717681	1103	3.1853757
3476	GO:0004872|GO:0019	receptor activity	0.66	12	1.7830609	672	1.9406822
4224	GO:0005984	disaccharide metaboli	0.67	1	0.1485884	56	0.16172351
9369	GO:0016137	glycoside metabolic pr	0.67	1	0.1485884	56	0.16172351
9883	GO:0016846	carbon-sulfur lyase ac	0.67	1	0.1485884	56	0.16172351
13697	GO:0031267	small GTPase binding	0.67	1	0.1485884	56	0.16172351
3955	GO:0005634	nucleus	0.67	26	3.8632987	1433	4.138389
20533	GO:0044283	small molecule biosyn	0.67	6	0.89153045	347	1.0021082
3475	GO:0004871|GO:0005	signal transducer activ	0.67	14	2.0802376	787	2.2727928
27063	GO:0060089	molecular transducer	0.67	14	2.0802376	787	2.2727928
25416	GO:0051119	sugar transmembrane	0.67	2	0.2971768	118	0.34077454
19758	GO:0043492	ATPase activity, coupl	0.67	4	0.5943536	235	0.67866117
5715	GO:0008171	O-methyltransferase a	0.67	1	0.1485884	57	0.16461143
7557	GO:0010333	terpene synthase activ	0.67	1	0.1485884	57	0.16461143
9813	GO:0016759	cellulose synthase act	0.67	1	0.1485884	57	0.16461143
3877	GO:0005516	calmodulin binding	0.68	4	0.5943536	236	0.6815491
2628	GO:0003677	DNA binding	0.68	22	3.268945	1224	3.534814
9824	GO:0016773	phosphotransferase a	0.68	27	4.011887	1493	4.311664
3304	GO:0004672|GO:0050	protein kinase activity	0.68	24	3.5661218	1333	3.8495972
3323	GO:0004702	receptor signaling prot	0.68	1	0.1485884	58	0.16749935
4913	GO:0006814|GO:0006	sodium ion transport	0.68	1	0.1485884	58	0.16749935
6665	GO:0009311	oligosaccharide metab	0.68	1	0.1485884	58	0.16749935
8499	GO:0015081|GO:0022	sodium ion transmem	0.68	1	0.1485884	58	0.16749935
8558	GO:0015145	monosaccharide trans	0.68	1	0.1485884	58	0.16749935
9018	GO:0015749	monosaccharide trans	0.68	1	0.1485884	58	0.16749935
18086	GO:0035725	sodium ion transmem	0.68	1	0.1485884	58	0.16749935
29800	GO:0071436	sodium ion export	0.68	1	0.1485884	58	0.16749935
30700	GO:0072341	modified amino acid b	0.69	1	0.1485884	59	0.17038727
5195	GO:0007165|GO:0023	signal transduction	0.69	17	2.526003	961	2.775291
12602	GO:0023052|GO:0023	signaling	0.69	17	2.526003	961	2.775291
9823	GO:0016772	transferase activity, tr	0.69	35	5.2005944	1932	5.579461
2980	GO:0004185	serine-type carboxype	0.69	1	0.1485884	60	0.17327519
5652	GO:0008081|GO:0004	phosphoric diester hy	0.69	1	0.1485884	60	0.17327519
14811	GO:0032403	protein complex bindi	0.69	1	0.1485884	60	0.17327519
25319	GO:0051020	GTPase binding	0.69	1	0.1485884	60	0.17327519
28375	GO:0070008	serine-type exopeptida	0.69	1	0.1485884	60	0.17327519
5610	GO:0008026	ATP-dependent helica	0.69	3	0.44576523	183	0.52848935
28401	GO:0070035	purine NTP-dependen	0.69	3	0.44576523	183	0.52848935
4768	GO:0006644	phospholipid metaboli	0.70	1	0.1485884	61	0.1761631
2978	GO:0004180	carboxypeptidase acti	0.70	1	0.1485884	62	0.17905103
6018	GO:0008559|GO:0005	xenobiotic-transportin	0.70	1	0.1485884	62	0.17905103
11210	GO:0019207	kinase regulator activi	0.70	1	0.1485884	62	0.17905103
17457	GO:0035091	phosphatidylinositol bi	0.70	1	0.1485884	62	0.17905103
19225	GO:0042908	xenobiotic transport	0.70	1	0.1485884	62	0.17905103
19227	GO:0042910	xenobiotic transporter	0.70	1	0.1485884	62	0.17905103
2648	GO:0003712	transcription cofactor	0.71	2	0.2971768	126	0.3638779
634	GO:0000988	protein binding transc	0.71	2	0.2971768	126	0.3638779
635	GO:0000989	transcription factor bin	0.71	2	0.2971768	126	0.3638779
20512	GO:0044262|GO:0006	cellular carbohydrate	0.71	4	0.5943536	248	0.7162041
3068	GO:0004386	helicase activity	0.71	3	0.44576523	189	0.54581684
25820	GO:0051536	iron-sulfur cluster bind	0.72	1	0.1485884	64	0.18482687
25824	GO:0051540	metal cluster binding	0.72	1	0.1485884	64	0.18482687
20521	GO:0044271	cellular nitrogen comp	0.72	6	0.89153045	367	1.0598665
5840	GO:0008324	cation transmembrane	0.72	9	1.3372957	538	1.5537009
11616	GO:0019637	organophosphate met	0.72	1	0.1485884	65	0.18771479
4561	GO:0006399	tRNA metabolic proce	0.73	1	0.1485884	66	0.1906027
5615	GO:0008033	tRNA processing	0.73	1	0.1485884	66	0.1906027
9890	GO:0016854	racemase and epimer	0.73	1	0.1485884	66	0.1906027
30206	GO:0071842	cellular component or	0.73	3	0.44576523	193	0.5573685
9837	GO:0016788	hydrolase activity, acti	0.73	27	4.011887	1534	4.430069
6662	GO:0009308	amine metabolic proce	0.73	5	0.74294204	314	0.9068068
2999	GO:0004312	fatty acid synthase act	0.74	1	0.1485884	68	0.19637854
7691	GO:0010467	gene expression	0.74	35	5.2005944	1974	5.7007537
5809	GO:0008289	lipid binding	0.74	4	0.5943536	258	0.74508333
31420	GO:0080043	quercetin 3-O-glucosy	0.74	1	0.1485884	69	0.19926646
10244	GO:0018130	heterocycle biosynthe	0.75	3	0.44576523	199	0.57469606
8749	GO:0015399	primary active transm	0.75	4	0.5943536	260	0.75085914
8753	GO:0015405	P-P-bond-hydrolysis-d	0.75	4	0.5943536	260	0.75085914
9853	GO:0016811	hydrolase activity, acti	0.75	1	0.1485884	70	0.20215438
9796	GO:0016741	transferase activity, tr	0.75	4	0.5943536	261	0.7537471
20499	GO:0044249	cellular biosynthetic p	0.75	47	6.9836555	2635	7.6096687
6427	GO:0009058	biosynthetic process	0.75	50	7.4294205	2796	8.074624
4612	GO:0006468	protein phosphorylatio	0.75	39	5.794948	2205	6.367863
3306	GO:0004674|GO:0004	protein serine/threoni	0.76	18	2.6745913	1062	3.0669708
9839	GO:0016791|GO:0016	phosphatase activity	0.76	6	0.89153045	383	1.1060733
3895	GO:0005543	phospholipid binding	0.76	2	0.2971768	140	0.40430877
9811	GO:0016757|GO:0016	transferase activity, tr	0.76	12	1.7830609	729	2.1052935
4247	GO:0006007	glucose catabolic pro	0.76	1	0.1485884	73	0.21081814
11313	GO:0019320	hexose catabolic proc	0.76	1	0.1485884	73	0.21081814
20525	GO:0044275	cellular carbohydrate	0.76	1	0.1485884	73	0.21081814
21726	GO:0046164	alcohol catabolic proc	0.76	1	0.1485884	73	0.21081814
21894	GO:0046365	monosaccharide catab	0.76	1	0.1485884	73	0.21081814
18912	GO:0042578	phosphoric ester hydr	0.76	7	1.0401188	444	1.2822365
6046	GO:0008610	lipid biosynthetic proc	0.76	2	0.2971768	141	0.4071967
8557	GO:0015144	carbohydrate transme	0.77	2	0.2971768	143	0.41297254
16602	GO:0034219	carbohydrate transme	0.77	2	0.2971768	143	0.41297254
8810	GO:0015491	cation:cation antiporte	0.77	1	0.1485884	75	0.21659398

9488	GO:0016301	kinase activity	0.78	30	4.457652	1740	5.0249805
3873	GO:0005507	copper ion binding	0.78	2	0.2971768	146	0.42163628
9493	GO:0016310	phosphorylation	0.78	44	6.53789	2504	7.2313514
9877	GO:0016838	carbon-oxygen lyase a	0.78	1	0.1485884	77	0.22236982
6071	GO:0008643|GO:0006	carbohydrate transpor	0.78	2	0.2971768	147	0.42452422
2819	GO:0004004	ATP-dependent RNA	0.78	1	0.1485884	78	0.22525774
5725	GO:0008186|GO:0004	RNA-dependent ATPa	0.78	1	0.1485884	78	0.22525774
8495	GO:0015077	monovalent inorganic	0.79	3	0.44576523	214	0.6180149
4649	GO:0006520|GO:0006	cellular amino acid me	0.79	4	0.5943536	277	0.7999538
2654	GO:0003724	RNA helicase activity	0.79	1	0.1485884	80	0.2310336
9655	GO:0016568	chromatin modification	0.79	1	0.1485884	80	0.2310336
9656	GO:0016569	covalent chromatin mo	0.79	1	0.1485884	80	0.2310336
9657	GO:0016570	histone modification	0.79	1	0.1485884	80	0.2310336
9682	GO:0016597	amino acid binding	0.79	1	0.1485884	80	0.2310336
19479	GO:0043176	amine binding	0.79	1	0.1485884	80	0.2310336
9845	GO:0016798	hydrolase activity, acti	0.79	6	0.89153045	401	1.1580559
9795	GO:0016740	transferase activity	0.80	67	9.955423	3764	10.870131
18674	GO:0042325	regulation of phosphor	0.80	1	0.1485884	81	0.23392151
6991	GO:0009725	response to hormone	0.80	1	0.1485884	82	0.23680943
4558	GO:0006396|GO:0006	RNA processing	0.80	3	0.44576523	219	0.63245445
3048	GO:0004364	glutathione transferase	0.81	1	0.1485884	84	0.24258527
5624	GO:0008047	enzyme activator activ	0.81	1	0.1485884	85	0.24547319
11222	GO:0019220	regulation of phosphat	0.81	1	0.1485884	85	0.24547319
25471	GO:0051174	regulation of phosphor	0.81	1	0.1485884	85	0.24547319
4460	GO:0006260|GO:0055	DNA replication	0.81	3	0.44576523	224	0.64689404
3888	GO:0005529	sugar binding	0.81	2	0.2971768	158	0.45629135
6985	GO:0009719	response to endogeno	0.82	1	0.1485884	86	0.24836111
4246	GO:0006006	glucose metabolic pro	0.82	1	0.1485884	87	0.25124902
4990	GO:0006915|GO:0008	apoptosis	0.82	3	0.44576523	227	0.6555578
8496	GO:0015078	hydrogen ion transmer	0.82	2	0.2971768	160	0.4620672
4032	GO:0005743	mitochondrial inner me	0.82	1	0.1485884	88	0.25413695
119	GO:0000151	ubiquitin ligase comple	0.82	1	0.1485884	88	0.25413695
6796	GO:0009507	chloroplast	0.82	3	0.44576523	229	0.6613336
10304	GO:0018193	peptidyl-amino acid m	0.83	1	0.1485884	89	0.25702485
4911	GO:0006812|GO:0006	cation transport	0.83	10	1.4858841	662	1.9118029
9294	GO:0016052|GO:0006	carbohydrate catabolic	0.83	1	0.1485884	91	0.2628007
30204	GO:0071840	cellular component org	0.83	5	0.74294204	362	1.045427
4476	GO:0006278	RNA-dependent DNA	0.84	2	0.2971768	166	0.4793947
9494	GO:0016311	dephosphorylation	0.84	6	0.89153045	425	1.227366
11803	GO:0019866	organelle inner membr	0.84	1	0.1485884	94	0.27146447
20356	GO:0044106	cellular amine metabo	0.84	4	0.5943536	303	0.8750397
6077	GO:0008652	cellular amino acid bio	0.84	2	0.2971768	169	0.48805845
18633	GO:0042277	peptide binding	0.85	1	0.1485884	95	0.27435237
5756	GO:0008219	cell death	0.85	3	0.44576523	239	0.69021285
8209	GO:0012501|GO:0016	programmed cell deat	0.85	3	0.44576523	239	0.69021285
9462	GO:0016265	death	0.85	3	0.44576523	239	0.69021285
3341	GO:0004722|GO:0000	protein serine/threonin	0.85	2	0.2971768	171	0.4938343
9889	GO:0016853	isomerase activity	0.85	4	0.5943536	306	0.8837035
4897	GO:0006793	phosphorus metabolic	0.85	50	7.4294205	2925	8.4471655
4900	GO:0006796	phosphate metabolic p	0.85	50	7.4294205	2925	8.4471655
5791	GO:0008270	zinc ion binding	0.85	31	4.6062407	1880	5.4292893
2653	GO:0003723	RNA binding	0.85	12	1.7830609	797	2.3016722
12608	GO:0030001	metal ion transport	0.85	5	0.74294204	374	1.080082
13829	GO:0031406	carboxylic acid binding	0.85	1	0.1485884	98	0.28301615
4067	GO:0005783	endoplasmic reticulum	0.85	2	0.2971768	174	0.50249803
5712	GO:0008168|GO:0004	methyltransferase acti	0.86	3	0.44576523	244	0.7046524
3885	GO:0005525	GTP binding	0.86	3	0.44576523	245	0.70754033
11032	GO:0019001	guanyl nucleotide bind	0.86	3	0.44576523	245	0.70754033
14967	GO:0032561	guanyl ribonucleotide	0.86	3	0.44576523	245	0.70754033
7271	GO:0010033	response to organic su	0.86	1	0.1485884	100	0.28879198
11787	GO:0019842	vitamin binding	0.86	2	0.2971768	177	0.5111618
6824	GO:0009536	plastid	0.86	3	0.44576523	247	0.7133162
11311	GO:0019318	hexose metabolic proc	0.86	1	0.1485884	101	0.2916799
2627	GO:0003676	nucleic acid binding	0.86	41	6.092125	2453	7.0840673
13082	GO:0030599	pectinesterase activity	0.86	2	0.2971768	178	0.5140497
6166	GO:0008757	S-adenosylmethionine	0.87	2	0.2971768	180	0.5198256
6663	GO:0009309	amine biosynthetic pro	0.87	2	0.2971768	181	0.5227135
19392	GO:0043085	positive regulation of c	0.87	1	0.1485884	104	0.30034366
20343	GO:0044093	positive regulation of m	0.87	1	0.1485884	104	0.30034366
2668	GO:0003779	actin binding	0.87	1	0.1485884	105	0.3032316
20505	GO:0044255	cellular lipid metabolic	0.88	2	0.2971768	184	0.53137726
20487	GO:0044237	cellular metabolic proc	0.88	147	21.842497	8185	23.637625
3942	GO:0005618	cell wall	0.88	1	0.1485884	107	0.30900744
19473	GO:0043170|GO:0043	macromolecule metab	0.88	116	17.236256	6553	18.92454
11833	GO:0019904	protein domain specifi	0.88	1	0.1485884	109	0.31478328
9285	GO:0016043	cellular component org	0.88	3	0.44576523	261	0.7537471
15436	GO:0033036	macromolecule localiz	0.89	5	0.74294204	397	1.1465042
12868	GO:0030312	external encapsulating	0.89	1	0.1485884	111	0.3205591
4512	GO:0006325	chromatin organization	0.89	1	0.1485884	112	0.32344702
25568	GO:0051276|GO:0007	chromosome organiza	0.89	1	0.1485884	112	0.32344702
29918	GO:0071554	cell wall organization o	0.89	1	0.1485884	112	0.32344702
19686	GO:0043414	macromolecule methy	0.89	1	0.1485884	113	0.32633495
14379	GO:0031966	mitochondrial membra	0.89	1	0.1485884	114	0.32922286
22478	GO:0046982	protein heterodimeriza	0.89	1	0.1485884	114	0.32922286
9535	GO:0016407	acetyltransferase activ	0.90	1	0.1485884	115	0.3321108
9871	GO:0016831	carboxy-lyase activity	0.90	1	0.1485884	115	0.3321108
20510	GO:0044260|GO:0034	cellular macromolecule	0.90	97	14.413075	5577	16.105928
3340	GO:0004721	phosphoprotein phosp	0.90	2	0.2971768	199	0.57469606
4236	GO:0005996	monosaccharide meta	0.91	1	0.1485884	125	0.36099
12741	GO:0030170	pyridoxal phosphate b	0.92	1	0.1485884	126	0.3638779
28643	GO:0070279	vitamin B6 binding	0.92	1	0.1485884	126	0.3638779
14667	GO:0032259	methylation	0.92	3	0.44576523	285	0.8230572
9295	GO:0016053	organic acid biosynthe	0.92	2	0.2971768	211	0.6093511
21922	GO:0046394	carboxylic acid biosyn	0.92	2	0.2971768	211	0.6093511
22376	GO:0046873	metal ion transmembra	0.92	2	0.2971768	213	0.6151269

9852	GO:0016810	hydrolase activity, acti	0.93	1	0.1485884	134	0.38698125
4320	GO:0006082	organic acid metabolic	0.93	4	0.5943536	369	1.0656425
11716	GO:0019752	carboxylic acid metabo	0.93	4	0.5943536	369	1.0656425
19707	GO:0043436	oxoacid metabolic pro	0.93	4	0.5943536	369	1.0656425
5019	GO:0006952|GO:0002	defense response	0.93	2	0.2971768	221	0.63823026
18541	GO:0042180	cellular ketone metabo	0.93	4	0.5943536	375	1.0829699
13531	GO:0031072	heat shock protein bin	0.94	2	0.2971768	230	0.6642216
4304	GO:0006066	alcohol metabolic proc	0.94	1	0.1485884	143	0.41297254
11522	GO:0019538|GO:0006	protein metabolic proc	0.94	68	10.104012	4134	11.938661
4029	GO:0005740	mitochondrial envelop	0.95	1	0.1485884	151	0.4360759
19526	GO:0043227	membrane-bounded o	0.95	32	4.754829	2142	6.185924
19530	GO:0043231	intracellular membrane	0.95	32	4.754829	2142	6.185924
3449	GO:0004842|GO:0004	ubiquitin-protein ligase	0.95	3	0.44576523	326	0.94146186
4609	GO:0006464	protein modification pr	0.95	43	6.389302	2781	8.031305
5661	GO:0008092	cytoskeletal protein bin	0.96	2	0.2971768	249	0.719092
19684	GO:0043412	macromolecule modifi	0.96	45	6.6864786	2900	8.374968
19831	GO:0043565	sequence-specific DN	0.96	1	0.1485884	159	0.45917925
9654	GO:0016567	protein ubiquitination	0.96	3	0.44576523	332	0.9587894
12572	GO:0022890|GO:0015	inorganic cation transm	0.96	3	0.44576523	332	0.9587894
14854	GO:0032446	protein modification by	0.96	3	0.44576523	332	0.9587894
29011	GO:0070647	protein modification by	0.96	3	0.44576523	332	0.9587894
9870	GO:0016830	carbon-carbon lyase a	0.96	1	0.1485884	161	0.4649551
5764	GO:0008234|GO:0004	cysteine-type peptidas	0.96	1	0.1485884	163	0.47073093
20623	GO:0044429	mitochondrial part	0.96	1	0.1485884	165	0.47650677
11747	GO:0019787|GO:0008	small conjugating prote	0.96	3	0.44576523	339	0.9790048
30306	GO:0071944	cell periphery	0.96	2	0.2971768	259	0.74797124
3946	GO:0005623	cell	0.97	140	20.802378	8227	23.758917
20657	GO:0044464	cell part	0.97	140	20.802378	8227	23.758917
3874	GO:0005509	calcium ion binding	0.97	2	0.2971768	279	0.8057296
8466	GO:0015031|GO:0015	protein transport	0.97	1	0.1485884	185	0.53426516
20820	GO:0045184	establishment of prote	0.97	1	0.1485884	185	0.53426516
20517	GO:0044267	cellular protein metabo	0.97	49	7.2808323	3225	9.313541
3863	GO:0005488	binding	0.98	246	36.55275	13903	40.15075
5669	GO:0008104	protein localization	0.98	1	0.1485884	189	0.54581684
9906	GO:0016874	ligase activity	0.98	6	0.89153045	597	1.7240882
14380	GO:0031967	organelle envelope	0.98	1	0.1485884	201	0.5804719
14387	GO:0031975	envelope	0.98	1	0.1485884	205	0.59202355
9913	GO:0016881	acid-amino acid ligase	0.98	3	0.44576523	391	1.1291766
4028	GO:0005739	mitochondrion	0.99	1	0.1485884	219	0.63245445
13547	GO:0031090	organelle membrane	0.99	1	0.1485884	224	0.64689404
3903	GO:0005575|GO:0008	cellular_component	0.99	140	20.802378	8515	24.590637
9911	GO:0016879	ligase activity, forming	0.99	3	0.44576523	456	1.3168914
3716	GO:0005198	structural molecule act	1.00	2	0.2971768	393	1.1349525
3876	GO:0005515|GO:0045	protein binding	1.00	108	16.047548	6933	20.021948
19533	GO:0043234	protein complex	1.00	5	0.74294204	848	2.448956
19525	GO:0043226	organelle	1.00	34	5.052006	3013	8.701303
19528	GO:0043229	intracellular organelle	1.00	34	5.052006	3013	8.701303
20618	GO:0044424	intracellular part	1.00	47	6.9836555	3853	11.127155
4027	GO:0005737	cytoplasm	1.00	18	2.6745913	2001	5.7787275
3945	GO:0005622	intracellular	1.00	59	8.766716	4751	13.720507
4109	GO:0005840|GO:0033	ribosome	1.00	2	0.2971768	682	1.9695613
13018	GO:0030529	ribonucleoprotein com	1.00	2	0.2971768	741	2.1399486
20640	GO:0044446	intracellular organelle	1.00	1	0.1485884	710	2.0504231
20616	GO:0044422	organelle part	1.00	1	0.1485884	712	2.0561988
19527	GO:0043228	non-membrane-bound	1.00	2	0.2971768	923	2.66555
19531	GO:0043232	intracellular non-memb	1.00	2	0.2971768	923	2.66555
20638	GO:0044444	cytoplasmic part	1.00	9	1.3372957	1644	4.7477403
15392	GO:0032991	macromolecular comp	1.00	7	1.0401188	1616	4.666878

GO ID	GO ACCESSION	GO Term	p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
5704	GO:0008150|GO:0000004|G	biological_process	0.00	449	72.41936	22215	64.155136
28101	GO:0061135	endopeptidase regulator acti	0.00	10	1.6129032	95	0.27435237
8159	GO:0010951	negative regulation of endop	0.00	10	1.6129032	95	0.27435237
3472	GO:0004866	endopeptidase inhibitor activ	0.00	10	1.6129032	95	0.27435237
26712	GO:0052548	regulation of endopeptidase	0.00	10	1.6129032	95	0.27435237
3473	GO:0004867	serine-type endopeptidase in	0.00	8	1.2903225	66	0.1906027
25636	GO:0051346	negative regulation of hydrola	0.00	10	1.6129032	110	0.31767118
12946	GO:0030414	peptidase inhibitor activity	0.00	10	1.6129032	110	0.31767118
7690	GO:0010466	negative regulation of peptida	0.00	10	1.6129032	110	0.31767118
26711	GO:0052547	regulation of peptidase activi	0.00	10	1.6129032	112	0.32344702
28100	GO:0061134	peptidase regulator activity	0.00	10	1.6129032	112	0.32344702
3874	GO:0005509	calcium ion binding	0.00	16	2.580645	279	0.8057296
25626	GO:0051336	regulation of hydrolase activi	0.00	12	1.9354838	196	0.5660323
3167	GO:0004508	steroid 17-alpha-monooxyge	0.00	2	0.32258064	2	0.00577584
3464	GO:0004857	enzyme inhibitor activity	0.00	10	1.6129032	157	0.4534034
3048	GO:0004364	glutathione transferase activi	0.00	7	1.1290323	84	0.24258527
4476	GO:0006278	RNA-dependent DNA replica	0.00	10	1.6129032	166	0.4793947
3877	GO:0005516	calmodulin binding	0.00	12	1.9354838	236	0.6815491
8919	GO:0015645	fatty acid ligase activity	0.00	4	0.6451613	27	0.077973835
9816	GO:0016762	xyloglucan:xyloglucosyl trans	0.00	4	0.6451613	27	0.077973835
9869	GO:0016829	lyase activity	0.00	19	3.064516	488	1.4093049
6932	GO:0009664	plant-type cell wall organizati	0.00	5	0.8064516	50	0.14439599
5096	GO:0007047	cellular cell wall organization	0.00	5	0.8064516	50	0.14439599
20857	GO:0045229	external encapsulating struct	0.00	5	0.8064516	50	0.14439599
30033	GO:0071669	plant-type cell wall organizati	0.00	5	0.8064516	50	0.14439599
12805	GO:0030246	carbohydrate binding	0.00	12	1.9354838	251	0.7248679
19393	GO:0043086	negative regulation of catalyt	0.00	10	1.6129032	188	0.54292893
20342	GO:0044092	negative regulation of molecu	0.00	10	1.6129032	188	0.54292893
14101	GO:0031683	G-protein beta/gamma-subu	0.00	3	0.48387095	15	0.043318797
4460	GO:0006260|GO:0055133	DNA replication	0.00	11	1.7741935	224	0.64689404
29246	GO:0070882	cellular cell wall organization	0.00	5	0.8064516	53	0.15305975
9422	GO:0016209	antioxidant activity	0.00	9	1.451613	165	0.47650677
3242	GO:0004601|GO:0016685|G	peroxidase activity	0.00	8	1.2903225	135	0.38986918
9754	GO:0016684	oxidoreductase activity, actin	0.00	8	1.2903225	135	0.38986918
11224	GO:0019222	regulation of metabolic proce	0.00	76	12.258064	3115	8.995871
4459	GO:0006259|GO:0055132	DNA metabolic process	0.00	18	2.903226	493	1.4237444
29919	GO:0071555	cell wall organization	0.00	5	0.8064516	58	0.16749935
9393	GO:0016165	lipoxygenase activity	0.00	4	0.6451613	36	0.10396511
29918	GO:0071554	cell wall organization or biog	0.00	7	1.1290323	112	0.32344702
9096	GO:0015828	tyrosine transport	0.00	2	0.32258064	6	0.01732752
8586	GO:0015173	aromatic amino acid transme	0.00	2	0.32258064	6	0.01732752
9070	GO:0015801	aromatic amino acid transpo	0.00	2	0.32258064	6	0.01732752
3777	GO:0005302|GO:0015508	L-tyrosine transmembrane tr	0.00	2	0.32258064	6	0.01732752
3904	GO:0005576	extracellular region	0.00	9	1.451613	178	0.5140497
21331	GO:0045735	nutrient reservoir activity	0.01	6	0.9677419	89	0.25702485
5705	GO:0008152	metabolic process	0.01	344	55.48387	17432	50.34222
3129	GO:0004467	long-chain fatty acid-CoA lig	0.01	3	0.48387095	21	0.060646318
9818	GO:0016765|GO:0016766	transferase activity, transfer	0.01	9	1.451613	185	0.53426516
6884	GO:0009607	response to biotic stimulus	0.01	7	1.1290323	122	0.3523262
8489	GO:0015066	alpha-amylase inhibitor activi	0.01	3	0.48387095	22	0.06353424
5636	GO:0008061	chitin binding	0.01	3	0.48387095	23	0.06642216
3888	GO:0005529	sugar binding	0.01	8	1.2903225	158	0.45629135
4530	GO:0006355|GO:0032583|G	regulation of transcription, D	0.01	63	10.16129	2591	7.4826
25544	GO:0051252	regulation of RNA metabolic	0.01	63	10.16129	2593	7.488376
6248	GO:0008843	endochitinase activity	0.01	3	0.48387095	24	0.06931008
3213	GO:0004568	chitinase activity	0.01	3	0.48387095	24	0.06931008
7141	GO:0009889	regulation of biosynthetic pro	0.01	63	10.16129	2605	7.523031
13756	GO:0031326	regulation of cellular biosynth	0.01	63	10.16129	2605	7.523031
32213	GO:2000112	regulation of cellular macrom	0.01	63	10.16129	2605	7.523031
7772	GO:0010556	regulation of macromolecule	0.01	63	10.16129	2605	7.523031
9764	GO:0016701	oxidoreductase activity, actin	0.01	5	0.8064516	72	0.20793022
8493	GO:0015074	DNA integration	0.01	4	0.6451613	47	0.13573223
2864	GO:0004058|GO:0016400	aromatic-L-amino-acid deca	0.01	2	0.32258064	9	0.025991278
25094	GO:0050789|GO:0050791	regulation of biological proce	0.01	97	15.645162	4315	12.461374
13753	GO:0031323	regulation of cellular metabo	0.01	66	10.645162	2770	7.999538
11221	GO:0019219	regulation of nucleobase, nu	0.01	64	10.32258	2675	7.7251854
25468	GO:0051171	regulation of nitrogen compo	0.01	64	10.32258	2675	7.7251854
28364	GO:0065007	biological regulation	0.01	98	15.806452	4376	12.637537
7692	GO:0010468	regulation of gene expressio	0.01	63	10.16129	2635	7.6096687
21148	GO:0045547	dehydrodolichyl diphosphate	0.01	2	0.32258064	10	0.0288792
23116	GO:0047631	ADP-ribose diphosphatase a	0.01	2	0.32258064	10	0.0288792
9909	GO:0016877	ligase activity, forming carbo	0.01	5	0.8064516	78	0.22525774
9845	GO:0016798	hydrolase activity, acting on	0.01	14	2.2580645	401	1.1580559
27228	GO:0060255	regulation of macromolecule	0.01	63	10.16129	2660	7.6818666
31465	GO:0080090	regulation of primary metabo	0.01	64	10.32258	2710	7.826263
13082	GO:0030599	pectinesterase activity	0.02	8	1.2903225	178	0.5140497
5702	GO:0008146	sulfotransferase activity	0.02	4	0.6451613	54	0.15594767
9871	GO:0016831	carboxy-lyase activity	0.02	6	0.9677419	115	0.3321108
26845	GO:0052689	carboxylic ester hydrolase ac	0.02	17	2.7419355	538	1.5537009
6424	GO:0009055|GO:0009053|G	electron carrier activity	0.02	7	1.1290323	154	0.44473964
25098	GO:0050794|GO:0051244	regulation of cellular process	0.02	88	14.193548	3987	11.514136
12806	GO:0030247	polysaccharide binding	0.02	3	0.48387095	35	0.10107719
1169	GO:0001871	pattern binding	0.02	3	0.48387095	35	0.10107719
11157	GO:0019144	ADP-sugar diphosphatase a	0.03	2	0.32258064	14	0.040430877
9870	GO:0016830	carbon-carbon lyase activity	0.03	7	1.1290323	161	0.4649551
9765	GO:0016702	oxidoreductase activity, actin	0.03	4	0.6451613	66	0.1906027
3382	GO:0004768|GO:0016214|G	stearoyl-CoA 9-desaturase a	0.03	2	0.32258064	16	0.046206716
9427	GO:0016215	CoA desaturase activity	0.03	2	0.32258064	16	0.046206716
26959	GO:0055114	oxidation-reduction process	0.03	57	9.193548	2490	7.1909204
5952	GO:0008470	isovaleryl-CoA dehydrogena	0.04	1	0.16129032	2	0.00577584
6593	GO:0009229	thiamine diphosphate biosyn	0.04	1	0.16129032	2	0.00577584
9558	GO:0016433	rRNA (adenine) methyltransf	0.04	1	0.16129032	2	0.00577584
9595	GO:0016485	protein processing	0.04	1	0.16129032	2	0.00577584
9638	GO:0016539	intein-mediated protein splici	0.04	1	0.16129032	2	0.00577584
9686	GO:0016602	CCAAT-binding factor comp	0.04	1	0.16129032	2	0.00577584
12948	GO:0030417	nicotianamine metabolic pro	0.04	1	0.16129032	2	0.00577584
12949	GO:0030418	nicotianamine biosynthetic p	0.04	1	0.16129032	2	0.00577584
13372	GO:0030908	protein splicing	0.04	1	0.16129032	2	0.00577584
18706	GO:0042357	thiamine diphosphate metab	0.04	1	0.16129032	2	0.00577584
22759	GO:0047268	galactinol-raffinose galactosy	0.04	1	0.16129032	2	0.00577584
25888	GO:0051604	protein maturation	0.04	1	0.16129032	2	0.00577584
30709	GO:0072350	tricarboxylic acid metabolic p	0.04	1	0.16129032	2	0.00577584
30710	GO:0072351	tricarboxylic acid biosynthetic	0.04	1	0.16129032	2	0.00577584
143	GO:0000179|GO:0043790	rRNA (adenine-N6,N6-)-dim	0.04	1	0.16129032	2	0.00577584
3148	GO:0004489|GO:0008702	methylenetetrahydrofolate re	0.04	1	0.16129032	2	0.00577584
18738	GO:0042389	omega-3 fatty acid desatura	0.04	2	0.32258064	17	0.049094636
23522	GO:0048046	apoplast	0.04	4	0.6451613	70	0.20215438
10899	GO:0018858	benzoate-CoA ligase activity	0.04	2	0.32258064	18	0.051982556
2674	GO:0003824	catalytic activity	0.04	213	34.35484	10750	31.045137
9832	GO:0016782	transferase activity, transfer	0.04	4	0.6451613	74	0.21370606
18750	GO:0042401	cellular biogenic amine biosy	0.04	2	0.32258064	19	0.054870475
25510	GO:0051213	dioxygenase activity	0.05	4	0.6451613	75	0.21659398
3124	GO:0004462	lactoylglutathione lyase activi	0.05	2	0.32258064	20	0.0577584
9877	GO:0016838	carbon-oxygen lyase activity,	0.05	4	0.6451613	77	0.22236982

9486	GO:0016298	lipase activity	**0.05**	7	1.1290323	185	0.53426516
3853	GO:0005463	UDP-N-acetylgalactosamine	**0.05**	1	0.16129032	3	0.00866376
9058	GO:0015789	UDP-N-acetylgalactosamine	**0.05**	1	0.16129032	3	0.00866376
13651	GO:0031219	levanase activity	**0.05**	1	0.16129032	3	0.00866376
21936	GO:0046409	p-coumarate 3-hydroxylase a	**0.05**	1	0.16129032	3	0.00866376
9600	GO:0016491	oxidoreductase activity	0.06	40	6.451613	1724	4.9787736
24858	GO:0050551	myrcene synthase activity	0.06	2	0.32258064	22	0.06353424
9783	GO:0016722	oxidoreductase activity, oxidi	0.06	3	0.48387095	50	0.14439599
12794	GO:0030234	enzyme regulator activity	0.06	12	1.9354838	403	1.1638317
9779	GO:0016717	oxidoreductase activity, actin	0.07	2	0.32258064	24	0.06931008
13657	GO:0031225	anchored to membrane	0.07	2	0.32258064	24	0.06931008
25578	GO:0051287|GO:0051288	NAD binding	0.07	2	0.32258064	24	0.06931008
3399	GO:0004788	thiamine diphosphokinase ac	0.07	1	0.16129032	4	0.011551679
3834	GO:0005395	eye pigment precursor trans	0.07	1	0.16129032	4	0.011551679
5826	GO:0008307	structural constituent of mus	0.07	1	0.16129032	4	0.011551679
5896	GO:0008401	retinoic acid 4-hydroxylase a	0.07	1	0.16129032	4	0.011551679
5934	GO:0008446	GDP-mannose 4,6-dehydrat	0.07	1	0.16129032	4	0.011551679
6293	GO:0008898	homocysteine S-methyltrans	0.07	1	0.16129032	4	0.011551679
7511	GO:0010285|GO:0043742	L,L-diaminopimelate aminotr	0.07	1	0.16129032	4	0.011551679
8130	GO:0010921	regulation of phosphatase ac	0.07	1	0.16129032	4	0.011551679
8598	GO:0015188	L-isoleucine transmembrane	0.07	1	0.16129032	4	0.011551679
8877	GO:0015578|GO:0015589	mannose transmembrane tra	0.07	1	0.16129032	4	0.011551679
9030	GO:0015761	mannose transport	0.07	1	0.16129032	4	0.011551679
9072	GO:0015803	branched-chain aliphatic ami	0.07	1	0.16129032	4	0.011551679
9086	GO:0015818	isoleucine transport	0.07	1	0.16129032	4	0.011551679
16391	GO:0034007	S-linalool synthase activity	0.07	1	0.16129032	4	0.011551679
17669	GO:0035303	regulation of dephosphorylat	0.07	1	0.16129032	4	0.011551679
19932	GO:0043666	regulation of phosphoprotein	0.07	1	0.16129032	4	0.011551679
24433	GO:0050113	inositol oxygenase activity	0.07	1	0.16129032	4	0.011551679
2689	GO:0003839	gamma-glutamylcyclotransfe	0.07	1	0.16129032	4	0.011551679
2753	GO:0003919	FMN adenylyltransferase act	0.07	1	0.16129032	4	0.011551679
3291	GO:0004657	proline dehydrogenase activi	0.07	1	0.16129032	4	0.011551679
9482	GO:0016291|GO:0008778|	acyl-CoA thioesterase activity	0.07	2	0.32258064	25	0.072197996
17147	GO:0034768	(E)-beta-ocimene synthase a	0.08	2	0.32258064	26	0.075085916
7557	GO:0010333	terpene synthase activity	0.08	3	0.48387095	57	0.16461143
18956	GO:0042626	ATPase activity, coupled to t	0.09	7	1.1290323	211	0.6093511
22765	GO:0047274	galactinol-sucrose galactosyl	0.09	1	0.16129032	5	0.0144396
3035	GO:0004351	glutamate decarboxylase act	0.09	1	0.16129032	5	0.0144396
9861	GO:0016820	hydrolase activity, acting on	0.09	7	1.1290323	212	0.612239
30700	GO:0072341	modified amino acid binding	0.09	3	0.48387095	59	0.17038727
14811	GO:0032403	protein complex binding	0.09	3	0.48387095	60	0.17327519
25095	GO:0050790	regulation of catalytic activity	0.09	13	2.096774	480	1.3862015
28366	GO:0065009	regulation of molecular functi	0.10	13	2.096774	484	1.3977532
6216	GO:0008810	cellulase activity	0.10	2	0.32258064	30	0.086637594
9785	GO:0016724	oxidoreductase activity, oxidi	0.10	2	0.32258064	30	0.086637594
2870	GO:0004064	arylesterase activity	0.10	2	0.32258064	30	0.086637594
3009	GO:0004322	ferroxidase activity	0.10	2	0.32258064	30	0.086637594
4953	GO:0006868|GO:0015815	glutamine transport	0.10	1	0.16129032	6	0.01732752
6000	GO:0008531	riboflavin kinase activity	0.10	1	0.16129032	6	0.01732752
6317	GO:0008923	lysine decarboxylase activity	0.10	1	0.16129032	6	0.01732752
8505	GO:0015089	high affinity copper ion trans	0.10	1	0.16129032	6	0.01732752
8596	GO:0015186	L-glutamine transmembrane	0.10	1	0.16129032	6	0.01732752
11899	GO:0019992	diacylglycerol binding	0.10	1	0.16129032	6	0.01732752
19761	GO:0043495	protein anchor	0.10	1	0.16129032	6	0.01732752
31395	GO:0080018	anthocyanin 5-O-glucosyltra	0.10	1	0.16129032	6	0.01732752
5	GO:0000007	low-affinity zinc ion transmen	0.10	1	0.16129032	6	0.01732752
2713	GO:0003863	3-methyl-2-oxobutanoate de	0.10	1	0.16129032	6	0.01732752
2811	GO:0003995|GO:0019109	acyl-CoA dehydrogenase ac	0.10	1	0.16129032	6	0.01732752
19590	GO:0043295	glutathione binding	0.11	2	0.32258064	31	0.08952551
3717	GO:0005199	structural constituent of cell	0.11	2	0.32258064	32	0.09241343
6942	GO:0009674	potassium:sodium symporter	0.11	2	0.32258064	32	0.09241343
12522	GO:0022820	potassium ion symporter acti	0.11	2	0.32258064	32	0.09241343
4705	GO:0006576	cellular biogenic amine meta	0.12	2	0.32258064	33	0.09530135
9812	GO:0016758	transferase activity, transferr	0.12	13	2.096774	501	1.4468478
3443	GO:0004834	tryptophan synthase activity	0.12	1	0.16129032	7	0.020215439
21776	GO:0046219	indolalkylamine biosynthetic	0.12	1	0.16129032	7	0.020215439
128	GO:0000162|GO:0009096	tryptophan biosynthetic proc	0.12	1	0.16129032	7	0.020215439
2945	GO:0004143	diacylglycerol kinase activity	0.12	1	0.16129032	7	0.020215439
3255	GO:0004615|GO:0008971	phosphomannomutase activi	0.12	1	0.16129032	7	0.020215439
11931	GO:0020037	heme binding	0.12	14	2.2580645	550	1.5883559
3873	GO:0005507	copper ion binding	0.12	5	0.8064516	146	0.42163628
22375	GO:0046872	metal ion binding	0.12	62	10	2985	8.6204405
4320	GO:0006082	organic acid metabolic proce	0.13	10	1.6129032	369	1.0656425
11716	GO:0019752	carboxylic acid metabolic pro	0.13	10	1.6129032	369	1.0656425
19707	GO:0043436	oxoacid metabolic process	0.13	10	1.6129032	369	1.0656425
9480	GO:0016289	CoA hydrolase activity	0.13	2	0.32258064	35	0.10107719
24968	GO:0050662	coenzyme binding	0.13	6	0.9677419	191	0.5515927
19470	GO:0043167	ion binding	0.13	62	10	2997	8.655096
19472	GO:0043169	cation binding	0.13	62	10	2997	8.655096
19758	GO:0043492	ATPase activity, coupled to	0.13	7	1.1290323	235	0.67866117
3402	GO:0004791	thioredoxin-disulfide reducta	0.13	1	0.16129032	8	0.023103358
6378	GO:0008999	ribosomal-protein-alanine N-	0.13	1	0.16129032	8	0.023103358
4	GO:0000006	high affinity zinc uptake trans	0.13	1	0.16129032	8	0.023103358
3872	GO:0005506	iron ion binding	0.14	14	2.2580645	563	1.6258988
18541	GO:0042180	cellular ketone metabolic pro	0.14	10	1.6129032	375	1.0829699
9767	GO:0016705	oxidoreductase activity, actin	0.14	9	1.451613	329	0.95012563
3306	GO:0004674|GO:0004695|	protein serine/threonine kina	0.15	24	3.8709676	1062	3.0669708
3694	GO:0005160	transforming growth factor b	0.15	1	0.16129032	9	0.025991278
4697	GO:0006568	tryptophan metabolic proces	0.15	1	0.16129032	9	0.025991278
4715	GO:0006586	indolalkylamine metabolic pr	0.15	1	0.16129032	9	0.025991278
7506	GO:0010279	indole-3-acetic acid amido sy	0.15	1	0.16129032	9	0.025991278
13224	GO:0030755	quercetin 3-O-methyltransfer	0.15	1	0.16129032	9	0.025991278
19254	GO:0042937	tripeptide transporter activity	0.15	1	0.16129032	9	0.025991278
19342	GO:0043027	caspase inhibitor activity	0.15	1	0.16129032	9	0.025991278
19343	GO:0043028	caspase regulator activity	0.15	1	0.16129032	9	0.025991278
19458	GO:0043154|GO:0001719	negative regulation of caspa	0.15	1	0.16129032	9	0.025991278
19579	GO:0043281|GO:0043026	regulation of caspase activity	0.15	1	0.16129032	9	0.025991278
9874	GO:0016835	carbon-oxygen lyase activity	0.16	6	0.9677419	202	0.5833598
5891	GO:0008395|GO:0008394	steroid hydroxylase activity	0.16	2	0.32258064	40	0.1155168
24966	GO:0050660	flavin adenine dinucleotide bi	0.16	4	0.6451613	118	0.34077454
5716	GO:0008172	S-methyltransferase activity	0.17	1	0.16129032	10	0.0288792
7175	GO:0009924	octadecanal decarbonylase	0.17	1	0.16129032	10	0.0288792
9741	GO:0016668|GO:0016654	oxidoreductase activity, actin	0.17	1	0.16129032	10	0.0288792
9828	GO:0016778	diphosphotransferase activity	0.17	1	0.16129032	10	0.0288792
15183	GO:0032781	positive regulation of ATPas	0.17	1	0.16129032	10	0.0288792
19728	GO:0043462	regulation of ATPase activity	0.17	1	0.16129032	10	0.0288792
27563	GO:0060590	ATPase regulator activity	0.17	1	0.16129032	10	0.0288792
30135	GO:0071771	aldehyde decarbonylase acti	0.17	1	0.16129032	10	0.0288792
989	GO:0001671	ATPase activator activity	0.17	1	0.16129032	10	0.0288792
2797	GO:0003979	UDP-glucose 6-dehydrogena	0.17	1	0.16129032	10	0.0288792
4954	GO:0006869	lipid transport	0.17	6	0.9677419	208	0.6006873
8085	GO:0010876	lipid localization	0.17	6	0.9677419	208	0.6006873
9682	GO:0016597	amino acid binding	0.17	3	0.48387095	80	0.2310336
19479	GO:0043176	amine binding	0.17	3	0.48387095	80	0.2310336
13884	GO:0031461	cullin-RING ubiquitin ligase c	0.17	2	0.32258064	42	0.121292636
9795	GO:0016740	transferase activity	0.18	75	12.096774	3764	10.870131
3260	GO:0004620	phospholipase activity	0.18	4	0.6451613	123	0.35521415
8589	GO:0015179	L-amino acid transmembran	0.18	2	0.32258064	43	0.124180555
9076	GO:0015807	L-amino acid transport	0.18	2	0.32258064	43	0.124180555
16183	GO:0033799	myricetin 3'-O-methyltransfe	0.18	1	0.16129032	11	0.03176712
18781	GO:0042435	indole-containing compound	0.18	1	0.16129032	11	0.03176712

19256	GO:0042939	tripeptide transport	0.18	1	0.16129032	11	0.03176712
22376	GO:0046873	metal ion transmembrane tra	0.18	6	0.9677419	213	0.6151269
22409	GO:0046906	tetrapyrrole binding	0.19	14	2.2580645	596	1.7212002
8749	GO:0015399	primary active transmembran	0.19	7	1.1290323	260	0.75085914
8753	GO:0015405	P-P-bond-hydrolysis-driven tr	0.19	7	1.1290323	260	0.75085914
4912	GO:0006813|GO:0015458	potassium ion transport	0.19	3	0.48387095	84	0.24258527
30168	GO:0071804	cellular potassium ion transp	0.19	3	0.48387095	84	0.24258527
30169	GO:0071805	potassium ion transmembran	0.19	3	0.48387095	84	0.24258527
3386	GO:0004773	steryl-sulfatase activity	0.19	1	0.16129032	12	0.03465504
4506	GO:0006313|GO:0006317|G	transposition, DNA-mediated	0.19	1	0.16129032	12	0.03465504
5965	GO:0008484	sulfuric ester hydrolase activi	0.19	1	0.16129032	12	0.03465504
9775	GO:0016713	oxidoreductase activity, actin	0.19	1	0.16129032	12	0.03465504
10743	GO:0018685|GO:0008393	alkane 1-monooxygenase ac	0.19	1	0.16129032	12	0.03465504
14604	GO:0032196	transposition	0.19	1	0.16129032	12	0.03465504
19047	GO:0042723	thiamine-containing compour	0.19	1	0.16129032	12	0.03465504
19048	GO:0042724	thiamine-containing compour	0.19	1	0.16129032	12	0.03465504
31380	GO:0080002	UDP-glucose:4-aminobenzoa	0.19	1	0.16129032	12	0.03465504
3156	GO:0004497	monooxygenase activity	0.20	5	0.8064516	172	0.49672222
3200	GO:0004553|GO:0016800	hydrolase activity, hydrolyzin	0.20	8	1.2903225	312	0.90103096
30204	GO:0071840	cellular component organizat	0.20	9	1.451613	362	1.045427
8497	GO:0015079|GO:0022817	potassium ion transmembran	0.21	2	0.32258064	47	0.13573223
119	GO:0000151	ubiquitin ligase complex	0.21	3	0.48387095	88	0.25413695
7551	GO:0010327	acetyl CoA:(Z)-3-hexen-1-ol	0.21	1	0.16129032	13	0.037542958
8149	GO:0010941	regulation of cell death	0.21	1	0.16129032	13	0.037542958
8578	GO:0015165	pyrimidine nucleotide sugar t	0.21	1	0.16129032	13	0.037542958
9050	GO:0015781	pyrimidine nucleotide-sugar t	0.21	1	0.16129032	13	0.037542958
18777	GO:0042430|GO:0042434	indole-containing compound	0.21	1	0.16129032	13	0.037542958
19298	GO:0042981	regulation of apoptosis	0.21	1	0.16129032	13	0.037542958
19381	GO:0043067|GO:0043070	regulation of programmed ce	0.21	1	0.16129032	13	0.037542958
28930	GO:0070566	adenylyltransferase activity	0.21	2	0.32258064	48	0.13862015
9725	GO:0016645	oxidoreductase activity, actin	0.22	2	0.32258064	49	0.14150807
6075	GO:0008649	rRNA methyltransferase activ	0.22	1	0.16129032	14	0.040430877
31408	GO:0080031	methyl salicylate esterase ac	0.22	1	0.16129032	14	0.040430877
12608	GO:0030001	metal ion transport	0.23	9	1.451613	374	1.080082
9975	GO:0016998	cell wall macromolecule cata	0.23	2	0.32258064	51	0.14728391
3293	GO:0004659	prenyltransferase activity	0.23	2	0.32258064	51	0.14728391
23515	GO:0048037	cofactor binding	0.23	8	1.2903225	327	0.94434977
7520	GO:0010294	abscisic acid glucosyltransfe	0.24	1	0.16129032	15	0.043318797
11733	GO:0019773	proteasome core complex, a	0.24	1	0.16129032	15	0.043318797
2868	GO:0004062	aryl sulfotransferase activity	0.24	1	0.16129032	15	0.043318797
3209	GO:0004564	beta-fructofuranosidase activ	0.24	1	0.16129032	15	0.043318797
20287	GO:0044036	cell wall macromolecule met	0.24	2	0.32258064	52	0.15017183
30066	GO:0071702	organic substance transport	0.24	12	1.9354838	529	1.5277096
3742	GO:0005242	inward rectifier potassium ch	0.25	1	0.16129032	16	0.046206716
13624	GO:0031167	rRNA methylation	0.25	1	0.16129032	16	0.046206716
31396	GO:0080019	fatty-acyl-CoA reductase (ald	0.25	1	0.16129032	16	0.046206716
30205	GO:0071841	cellular component organizat	0.25	7	1.1290323	285	0.8230572
13829	GO:0031406	carboxylic acid binding	0.26	3	0.48387095	98	0.28301615
2986	GO:0004252	serine-type endopeptidase a	0.26	4	0.6451613	144	0.41586044
9533	GO:0016405	CoA-ligase activity	0.26	2	0.32258064	55	0.15883559
11776	GO:0019825	oxygen binding	0.26	9	1.451613	389	1.1234008
30887	GO:0072531	pyrimidine-containing compo	0.26	1	0.16129032	17	0.049094636
31498	GO:0080123	jasmonate-amino synthetase	0.26	1	0.16129032	17	0.049094636
9883	GO:0016846	carbon-sulfur lyase activity	0.27	2	0.32258064	56	0.16172351
9910	GO:0016878	acid-thiol ligase activity	0.27	2	0.32258064	57	0.16461143
9906	GO:0016874	ligase activity	0.28	13	2.096774	597	1.7240882
3832	GO:0005388	calcium-transporting ATPase	0.28	1	0.16129032	18	0.051982556
5776	GO:0008252	nucleotidase activity	0.28	1	0.16129032	18	0.051982556
9726	GO:0016646	oxidoreductase activity, actin	0.28	1	0.16129032	18	0.051982556
12887	GO:0030332	cyclin binding	0.28	1	0.16129032	18	0.051982556
16595	GO:0034212	peptide N-acetyltransferase	0.28	1	0.16129032	18	0.051982556
28368	GO:0070001	aspartic-type peptidase activ	0.28	1	0.16129032	18	0.051982556
2981	GO:0004190	aspartic-type endopeptidase	0.28	1	0.16129032	18	0.051982556
3239	GO:0004596	peptide alpha-N-acetyltransfe	0.28	1	0.16129032	18	0.051982556
8558	GO:0015145	monosaccharide transmemb	0.28	2	0.32258064	58	0.16749935
9018	GO:0015749	monosaccharide transport	0.28	2	0.32258064	58	0.16749935
9800	GO:0016746	transferase activity, transferr	0.28	11	1.7741935	498	1.438184
3304	GO:0004672|GO:0050222	protein kinase activity	0.28	27	4.354839	1333	3.8495972
19253	GO:0042936	dipeptide transporter activity	0.29	3	0.48387095	105	0.3032316
19255	GO:0042938	dipeptide transport	0.29	3	0.48387095	105	0.3032316
3799	GO:0005338|GO:0005339	nucleotide-sugar transmemb	0.29	1	0.16129032	19	0.054870475
9049	GO:0015780	nucleotide-sugar transport	0.29	1	0.16129032	19	0.054870475
9809	GO:0016755	transferase activity, transferr	0.29	1	0.16129032	19	0.054870475
11202	GO:0019199	transmembrane receptor pro	0.29	11	1.7741935	504	1.4555116
8526	GO:0015112	nitrate transmembrane trans	0.30	2	0.32258064	61	0.1761631
8975	GO:0015706|GO:0006872	nitrate transport	0.30	2	0.32258064	61	0.1761631
9801	GO:0016747	transferase activity, transferr	0.30	10	1.6129032	456	1.3168914
3798	GO:0005337	nucleoside transmembrane t	0.30	1	0.16129032	20	0.0577584
6201	GO:0008794	arsenate reductase (glutared	0.30	1	0.16129032	20	0.0577584
9122	GO:0015858	nucleoside transport	0.30	1	0.16129032	20	0.0577584
9707	GO:0016624	oxidoreductase activity, actin	0.30	1	0.16129032	20	0.0577584
9784	GO:0016723	oxidoreductase activity, oxidi	0.30	1	0.16129032	20	0.0577584
13086	GO:0030611	arsenate reductase activity	0.30	1	0.16129032	20	0.0577584
13088	GO:0030613	oxidoreductase activity, actin	0.30	1	0.16129032	20	0.0577584
13089	GO:0030614	oxidoreductase activity, actin	0.30	1	0.16129032	20	0.0577584
122	GO:0000154|GO:0016548	rRNA modification	0.30	1	0.16129032	20	0.0577584
225	GO:0000293	ferric-chelate reductase activ	0.30	1	0.16129032	20	0.0577584
6018	GO:0008559|GO:0005226|G	xenobiotic-transporting ATPa	0.31	2	0.32258064	62	0.17905103
19225	GO:0042908	xenobiotic transport	0.31	2	0.32258064	62	0.17905103
19227	GO:0042910	xenobiotic transporter activity	0.31	2	0.32258064	62	0.17905103
3474	GO:0004869|GO:0004870	cysteine-type endopeptidase	0.32	1	0.16129032	21	0.060646318
5878	GO:0008378	galactosyltransferase activity	0.32	1	0.16129032	21	0.060646318
9902	GO:0016868|GO:0016777	intramolecular transferase ac	0.32	1	0.16129032	21	0.060646318
23518	GO:0048040	UDP-glucuronate decarboxyl	0.32	1	0.16129032	21	0.060646318
22416	GO:0046915	transition metal ion transmen	0.32	2	0.32258064	64	0.18482687
9838	GO:0016790	thiolester hydrolase activity	0.32	2	0.32258064	65	0.18771479
9285	GO:0016043	cellular component organizat	0.33	6	0.9677419	261	0.7537471
3490	GO:0004888|GO:0004926	transmembrane receptor act	0.33	12	1.9354838	571	1.6490022
3828	GO:0005375|GO:0005378|G	copper ion transmembrane t	0.33	1	0.16129032	22	0.06353424
3831	GO:0005385	zinc ion transmembrane tran	0.33	1	0.16129032	22	0.06353424
4920	GO:0006825	copper ion transport	0.33	1	0.16129032	22	0.06353424
4924	GO:0006829	zinc ion transport	0.33	1	0.16129032	22	0.06353424
10032	GO:0017075	syntaxin-1 binding	0.33	1	0.16129032	22	0.06353424
13038	GO:0030551	cyclic nucleotide binding	0.33	1	0.16129032	22	0.06353424
17800	GO:0035434	copper ion transmembrane t	0.33	1	0.16129032	22	0.06353424
29941	GO:0071577	zinc ion transmembrane tran	0.33	1	0.16129032	22	0.06353424
9811	GO:0016757|GO:0016932	transferase activity, transferr	0.33	15	2.419355	729	2.1052935
11829	GO:0019900	kinase binding	0.33	2	0.32258064	66	0.1906027
9837	GO:0016788	hydrolase activity, acting on e	0.34	30	4.83871	1534	4.430069
3662	GO:0005126	cytokine receptor binding	0.34	1	0.16129032	23	0.06642216
22753	GO:0047262|GO:0050375	polygalacturonate 4-alpha-ga	0.34	1	0.16129032	23	0.06642216
2633	GO:0003684	damaged DNA binding	0.34	1	0.16129032	23	0.06642216
32	GO:0000041	transition metal ion transport	0.34	2	0.32258064	68	0.19637854
9836	GO:0016787	hydrolase activity	0.35	70	11.290322	3723	10.751725
8559	GO:0015146	pentose transmembrane tran	0.35	1	0.16129032	24	0.06931008
8561	GO:0015148	D-xylose transmembrane tra	0.35	1	0.16129032	24	0.06931008
8829	GO:0015519	D-xylose:hydrogen symporte	0.35	1	0.16129032	24	0.06931008
9019	GO:0015750	pentose transport	0.35	1	0.16129032	24	0.06931008
9022	GO:0015753	D-xylose transport	0.35	1	0.16129032	24	0.06931008
31407	GO:0080030	methyl indole-3-acetate ester	0.35	1	0.16129032	24	0.06931008
3262	GO:0004622|GO:0045126	lysophospholipase activity	0.35	1	0.16129032	24	0.06931008
17617	GO:0035251	UDP-glucosyltransferase act	0.35	5	0.8064516	218	0.62956655

9824	GO:0016773	phosphotransferase activity,	0.35	29	4.677419	1493	4.311664
8584	GO:0015171|GO:0015359	amino acid transmembrane t	0.35	3	0.48387095	118	0.34077454
2521	GO:0003333	amino acid transmembrane t	0.35	3	0.48387095	118	0.34077454
22049	GO:0046527	glucosyltransferase activity	0.35	6	0.9677419	270	0.77973837
10103	GO:0017171	serine hydrolase activity	0.36	5	0.8064516	220	0.63534236
4503	GO:0006310	DNA recombination	0.36	1	0.16129032	25	0.072197996
21145	GO:0045543	gibberellin 2-beta-dioxygenas	0.36	1	0.16129032	25	0.072197996
31393	GO:0080016	(-)-E-beta-caryophyllene synt	0.36	1	0.16129032	25	0.072197996
31394	GO:0080017	alpha-humulene synthase ac	0.36	1	0.16129032	25	0.072197996
31493	GO:0080118	brassinosteroid sulfotransfera	0.36	1	0.16129032	25	0.072197996
8675	GO:0015293	symporter activity	0.37	4	0.6451613	173	0.49961013
9421	GO:0016208	AMP binding	0.37	1	0.16129032	26	0.075085916
9897	GO:0016862	intramolecular oxidoreductas	0.37	1	0.16129032	26	0.075085916
9899	GO:0016864	intramolecular oxidoreductas	0.37	1	0.16129032	26	0.075085916
25135	GO:0050832|GO:0042831	defense response to fungus	0.37	1	0.16129032	26	0.075085916
2665	GO:0003756	protein disulfide isomerase a	0.37	1	0.16129032	26	0.075085916
3210	GO:0004565	beta-galactosidase activity	0.37	1	0.16129032	26	0.075085916
4951	GO:0006865|GO:0006866	amino acid transport	0.38	3	0.48387095	123	0.35521415
12572	GO:0022890|GO:0015082	inorganic cation transmembr	0.38	7	1.1290323	332	0.9587894
9541	GO:0016413	O-acetyltransferase activity	0.39	1	0.16129032	27	0.077973835
3761	GO:0005275|GO:0005279	amine transmembrane trans	0.39	3	0.48387095	126	0.3638779
3332	GO:0004711	ribosomal protein S6 kinase	0.40	1	0.16129032	28	0.080861755
6940	GO:0009672	auxin:hydrogen symporter ac	0.40	1	0.16129032	28	0.080861755
13634	GO:0031177	phosphopantetheine binding	0.40	1	0.16129032	28	0.080861755
3284	GO:0004650	polygalacturonase activity	0.40	1	0.16129032	28	0.080861755
9913	GO:0016881	acid-amino acid ligase activit	0.40	8	1.2903225	391	1.1291766
6166	GO:0008757	S-adenosylmethionine-depen	0.40	4	0.6451613	180	0.5198256
7558	GO:0010334	sesquiterpene synthase activ	0.41	1	0.16129032	29	0.083749674
11834	GO:0019905	syntaxin binding	0.41	1	0.16129032	29	0.083749674
20887	GO:0045263	proton-transporting ATP synt	0.41	1	0.16129032	29	0.083749674
30865	GO:0072509	divalent inorganic cation tran	0.41	2	0.32258064	78	0.22525774
3975	GO:0005667	transcription factor complex	0.42	1	0.16129032	30	0.086637594
2774	GO:0003950	NAD+ ADP-ribosyltransferas	0.42	1	0.16129032	30	0.086637594
9875	GO:0016836	hydro-lyase activity	0.42	2	0.32258064	80	0.2310336
4612	GO:0006468	protein phosphorylation	0.42	41	6.612903	2205	6.367863
3476	GO:0004872|GO:0019041	receptor activity	0.43	13	2.096774	672	1.9406822
7222	GO:0009975	cyclase activity	0.43	1	0.16129032	31	0.08952551
29202	GO:0070838	divalent metal ion transport	0.43	2	0.32258064	82	0.23680943
9103	GO:0015837	amine transport	0.44	3	0.48387095	135	0.38986918
3787	GO:0005319	lipid transporter activity	0.44	2	0.32258064	83	0.23969735
4108	GO:0005839|GO:0000503	proteasome core complex	0.44	1	0.16129032	32	0.09241343
4481	GO:0006284	base-excision repair	0.44	1	0.16129032	32	0.09241343
4510	GO:0006323	DNA packaging	0.44	1	0.16129032	32	0.09241343
4514	GO:0006334	nucleosome assembly	0.44	1	0.16129032	32	0.09241343
12833	GO:0030275	LRR domain binding	0.44	1	0.16129032	32	0.09241343
13920	GO:0031497	chromatin assembly	0.44	1	0.16129032	32	0.09241343
17107	GO:0034728	nucleosome organization	0.44	1	0.16129032	32	0.09241343
28361	GO:0065004	protein-DNA complex assem	0.44	1	0.16129032	32	0.09241343
29467	GO:0071103	DNA conformation change	0.44	1	0.16129032	32	0.09241343
30188	GO:0071824	protein-DNA complex subuni	0.44	1	0.16129032	32	0.09241343
3265	GO:0004630	phospholipase D activity	0.44	1	0.16129032	32	0.09241343
3475	GO:0004871|GO:0005062|G	signal transducer activity	0.44	15	2.419355	787	2.2727928
12516	GO:0022804	active transmembrane transp	0.44	15	2.419355	787	2.2727928
27063	GO:0060089	molecular transducer activity	0.44	15	2.419355	787	2.2727928
3801	GO:0005342	organic acid transmembrane	0.44	3	0.48387095	136	0.3927571
22444	GO:0046943	carboxylic acid transmembra	0.44	3	0.48387095	136	0.3927571
30867	GO:0072511	divalent inorganic cation tran	0.45	2	0.32258064	84	0.24258527
4493	GO:0006298|GO:0006300	mismatch repair	0.45	1	0.16129032	33	0.09530135
11222	GO:0019220	regulation of phosphate meta	0.45	2	0.32258064	85	0.24547319
25471	GO:0051174	regulation of phosphorus me	0.45	2	0.32258064	85	0.24547319
31895	GO:0090304	nucleic acid metabolic proces	0.45	43	6.935484	2340	6.7577324
4942	GO:0006855	drug transmembrane transpo	0.45	3	0.48387095	139	0.40142086
8607	GO:0015197|GO:0015637	peptide transporter activity	0.45	3	0.48387095	139	0.40142086
8608	GO:0015198	oligopeptide transporter activ	0.45	3	0.48387095	139	0.40142086
8642	GO:0015238|GO:0015239|G	drug transmembrane transpo	0.45	3	0.48387095	139	0.40142086
9154	GO:0015893	drug transport	0.45	3	0.48387095	139	0.40142086
18832	GO:0042493|GO:0017035	response to drug	0.45	3	0.48387095	139	0.40142086
2897	GO:0004091|GO:0004302|G	carboxylesterase activity	0.46	4	0.6451613	194	0.5602564
3749	GO:0005249	voltage-gated potassium cha	0.46	1	0.16129032	34	0.09818927
5717	GO:0008173	RNA methyltransferase activ	0.46	1	0.16129032	34	0.09818927
6072	GO:0008645	hexose transport	0.46	1	0.16129032	34	0.09818927
8562	GO:0015149	hexose transmembrane trans	0.46	1	0.16129032	34	0.09818927
11831	GO:0019902	phosphatase binding	0.46	1	0.16129032	34	0.09818927
11832	GO:0019903	protein phosphatase binding	0.46	1	0.16129032	34	0.09818927
17794	GO:0035428	hexose transmembrane trans	0.46	1	0.16129032	34	0.09818927
4944	GO:0006857	oligopeptide transport	0.46	3	0.48387095	141	0.4071967
9099	GO:0015833	peptide transport	0.46	3	0.48387095	141	0.4071967
4538	GO:0006364|GO:0006365	rRNA processing	0.47	1	0.16129032	35	0.10107719
6355	GO:0008970	phospholipase A1 activity	0.47	1	0.16129032	35	0.10107719
9310	GO:0016072	rRNA metabolic process	0.47	1	0.16129032	35	0.10107719
23199	GO:0047714	galactolipase activity	0.47	1	0.16129032	35	0.10107719
8557	GO:0015144	carbohydrate transmembran	0.47	3	0.48387095	143	0.41297254
16602	GO:0034219	carbohydrate transmembran	0.47	3	0.48387095	143	0.41297254
4513	GO:0006333	chromatin assembly or disas	0.48	1	0.16129032	36	0.10396511
9185	GO:0015925	galactosidase activity	0.48	1	0.16129032	36	0.10396511
3758	GO:0005267	potassium channel activity	0.49	1	0.16129032	37	0.10685303
8934	GO:0015662	ATPase activity, coupled to t	0.49	1	0.16129032	37	0.10685303
30069	GO:0071705	nitrogen compound transport	0.49	4	0.6451613	202	0.5833598
6071	GO:0008643|GO:0006861|G	carbohydrate transport	0.49	3	0.48387095	147	0.42452422
5840	GO:0008324	cation transmembrane transp	0.50	10	1.6129032	538	1.5537009
6893	GO:0009620|GO:0009621	response to fungus	0.50	1	0.16129032	38	0.10974095
8501	GO:0015085	calcium ion transmembrane	0.50	1	0.16129032	38	0.10974095
8588	GO:0015175	neutral amino acid transmem	0.50	1	0.16129032	38	0.10974095
9073	GO:0015804	neutral amino acid transport	0.50	1	0.16129032	38	0.10974095
9637	GO:0016538|GO:0003751|G	cyclin-dependent protein kina	0.50	1	0.16129032	38	0.10974095
12538	GO:0022843	voltage-gated cation channel	0.50	1	0.16129032	38	0.10974095
117	GO:0000149	SNARE binding	0.50	1	0.16129032	38	0.10974095
20336	GO:0044085	cellular component biogenes	0.50	2	0.32258064	93	0.26857653
868	GO:0001510	RNA methylation	0.51	1	0.16129032	39	0.11262887
18633	GO:0042277	peptide binding	0.51	2	0.32258064	95	0.27435237
5732	GO:0008194	UDP-glycosyltransferase act	0.52	6	0.9677419	322	0.9299102
2628	GO:0003677	DNA binding	0.52	22	3.548387	1224	3.534814
4911	GO:0006812|GO:0006819|G	cation transport	0.52	12	1.9354838	662	1.9118029
3449	GO:0004842|GO:0004840|G	ubiquitin-protein ligase activit	0.53	6	0.9677419	326	0.94146186
8943	GO:0015672	monovalent inorganic cation	0.53	7	1.1290323	383	1.1060733
9114	GO:0015849	organic acid transport	0.53	3	0.48387095	156	0.45051548
22443	GO:0046942	carboxylic acid transport	0.53	3	0.48387095	156	0.45051548
4874	GO:0006767	water-soluble vitamin metabo	0.53	1	0.16129032	42	0.121292636
18713	GO:0042364	water-soluble vitamin biosynt	0.53	1	0.16129032	42	0.121292636
5766	GO:0008236	serine-type peptidase activity	0.54	4	0.6451613	214	0.6180149
8495	GO:0015077	monovalent inorganic cation	0.54	4	0.6451613	214	0.6180149
9654	GO:0016567	protein ubiquitination	0.55	6	0.9677419	332	0.9587894
14854	GO:0032446	protein modification by small	0.55	6	0.9677419	332	0.9587894
29011	GO:0070647	protein modification by small	0.55	6	0.9677419	332	0.9587894
4873	GO:0006766	vitamin metabolic process	0.55	1	0.16129032	44	0.12706847
4914	GO:0006816	calcium ion transport	0.55	1	0.16129032	44	0.12706847
6477	GO:0009110	vitamin biosynthetic process	0.55	1	0.16129032	44	0.12706847
20522	GO:0044272	sulfur compound biosynthetic	0.55	1	0.16129032	44	0.12706847
28952	GO:0070588	calcium ion transmembrane	0.55	1	0.16129032	44	0.12706847
409	GO:0000502	proteasome complex	0.55	1	0.16129032	44	0.12706847
5195	GO:0007165|GO:0023033	signal transduction	0.55	17	2.7419355	961	2.775291
12602	GO:0023052|GO:0023046	signaling	0.55	17	2.7419355	961	2.775291

8666	GO:0015276	ligand-gated ion channel acti	0.56	1	0.16129032	45	0.1299564
11780	GO:0019829	cation-transporting ATPase a	0.56	1	0.16129032	45	0.1299564
12530	GO:0022834	ligand-gated channel activity	0.56	1	0.16129032	45	0.1299564
17001	GO:0034622	cellular macromolecular com	0.56	1	0.16129032	45	0.1299564
28360	GO:0065003	macromolecular complex ass	0.56	1	0.16129032	45	0.1299564
31431	GO:0080054	low affinity nitrate transmem	0.56	1	0.16129032	45	0.1299564
9709	GO:0016627	oxidoreductase activity, actin	0.56	2	0.32258064	104	0.30034366
4641	GO:0006508	proteolysis	0.56	17	2.7419355	965	2.7868426
2668	GO:0003779	actin binding	0.56	2	0.32258064	105	0.3032316
12498	GO:0022613	ribonucleoprotein complex bi	0.56	1	0.16129032	46	0.13284431
18614	GO:0042254|GO:0007046	ribosome biogenesis	0.56	1	0.16129032	46	0.13284431
11747	GO:0019787|GO:0008639|G	small conjugating protein liga	0.57	6	0.9677419	339	0.9790048
9911	GO:0016879	ligase activity, forming carbo	0.57	8	1.2903225	456	1.3168914
5714	GO:0008170	N-methyltransferase activity	0.57	1	0.16129032	47	0.13573223
6442	GO:0009073|GO:0016089	aromatic amino acid family b	0.57	1	0.16129032	47	0.13573223
21943	GO:0046417	chorismate metabolic proces	0.57	1	0.16129032	47	0.13573223
17024	GO:0034645|GO:0034961	cellular macromolecule biosy	0.58	35	5.645161	1999	5.7729516
14591	GO:0032183	SUMO binding	0.58	1	0.16129032	48	0.13862015
6428	GO:0009059|GO:0043284	macromolecule biosynthetic	0.58	35	5.645161	2003	5.7845035
3756	GO:0005261|GO:0015281|G	cation channel activity	0.59	1	0.16129032	49	0.14150807
7074	GO:0009815	1-aminocyclopropane-1-carb	0.59	1	0.16129032	49	0.14150807
11830	GO:0019901	protein kinase binding	0.59	1	0.16129032	49	0.14150807
31421	GO:0080044	quercetin 7-O-glucosyltransfe	0.59	1	0.16129032	49	0.14150807
7166	GO:0009914	hormone transport	0.60	1	0.16129032	50	0.14439599
19914	GO:0043648	dicarboxylic acid metabolic p	0.60	1	0.16129032	50	0.14439599
27891	GO:0060918	auxin transport	0.60	1	0.16129032	50	0.14439599
31536	GO:0080161	auxin transmembrane transp	0.60	1	0.16129032	50	0.14439599
7173	GO:0009922	fatty acid elongase activity	0.60	1	0.16129032	51	0.14728391
12492	GO:0022607	cellular component assembly	0.60	1	0.16129032	51	0.14728391
30207	GO:0071843	cellular component biogenes	0.60	1	0.16129032	51	0.14728391
30208	GO:0071844	cellular component assembly	0.60	1	0.16129032	51	0.14728391
9933	GO:0016903	oxidoreductase activity, actin	0.60	2	0.32258064	113	0.32633495
4215	GO:0005975	carbohydrate metabolic proc	0.60	17	2.7419355	990	2.8590407
22478	GO:0046982	protein heterodimerization ac	0.61	2	0.32258064	114	0.32922286
9535	GO:0016407	acetyltransferase activity	0.61	2	0.32258064	115	0.3321108
25635	GO:0051345	positive regulation of hydrola	0.62	1	0.16129032	53	0.15305975
11787	GO:0019842	vitamin binding	0.62	3	0.48387095	177	0.5111618
17918	GO:0035556|GO:0007242|G	intracellular signal transducti	0.62	1	0.16129032	54	0.15594767
25416	GO:0051119	sugar transmembrane transp	0.63	2	0.32258064	118	0.34077454
4894	GO:0006790	sulfur compound metabolic p	0.63	1	0.16129032	55	0.15883559
9493	GO:0016310	phosphorylation	0.64	43	6.935484	2504	7.2313514
15576	GO:0033177	proton-transporting two-sect	0.64	1	0.16129032	56	0.16172351
5712	GO:0008168|GO:0004480	methyltransferase activity	0.64	4	0.6451613	244	0.7046524
5715	GO:0008171	O-methyltransferase activity	0.64	1	0.16129032	57	0.16461143
5964	GO:0008483	transaminase activity	0.64	1	0.16129032	57	0.16461143
6441	GO:0009072	aromatic amino acid family m	0.64	1	0.16129032	57	0.16461143
9813	GO:0016759	cellulose synthase activity	0.64	1	0.16129032	57	0.16461143
9821	GO:0016769	transferase activity, transferr	0.64	1	0.16129032	57	0.16461143
25195	GO:0050896|GO:0051869	response to stimulus	0.64	32	5.16129	1881	5.432177
4913	GO:0006814|GO:0006834|G	sodium ion transport	0.65	1	0.16129032	58	0.16749935
8028	GO:0010817	regulation of hormone levels	0.65	1	0.16129032	58	0.16749935
8499	GO:0015081|GO:0022816	sodium ion transmembrane t	0.65	1	0.16129032	58	0.16749935
11820	GO:0019887	protein kinase regulator activ	0.65	1	0.16129032	58	0.16749935
18086	GO:0035725	sodium ion transmembrane t	0.65	1	0.16129032	58	0.16749935
25989	GO:0051707|GO:0009613|G	response to other organism	0.65	1	0.16129032	58	0.16749935
29800	GO:0071436	sodium ion export	0.65	1	0.16129032	58	0.16749935
3323	GO:0004702	receptor signaling protein se	0.65	1	0.16129032	58	0.16749935
13656	GO:0031224	intrinsic to membrane	0.65	20	3.2258065	1193	3.4452884
25998	GO:0051716	cellular response to stimulus	0.65	19	3.064516	1138	3.2864528
9900	GO:0016866	intramolecular transferase ac	0.66	1	0.16129032	59	0.17038727
2831	GO:0004022	alcohol dehydrogenase (NAD	0.66	1	0.16129032	59	0.17038727
5652	GO:0008081|GO:0004434|G	phosphoric diester hydrolase	0.66	1	0.16129032	60	0.17327519
12741	GO:0030170	pyridoxal phosphate binding	0.66	2	0.32258064	126	0.3638779
28643	GO:0070279	vitamin B6 binding	0.66	2	0.32258064	126	0.3638779
2818	GO:0004003	ATP-dependent DNA helicas	0.67	1	0.16129032	61	0.1761631
22415	GO:0046914	transition metal ion binding	0.67	44	7.096774	2599	7.5057034
11210	GO:0019207	kinase regulator activity	0.67	1	0.16129032	62	0.17905103
17000	GO:0034621	cellular macromolecular com	0.67	1	0.16129032	62	0.17905103
17457	GO:0035091	phosphatidylinositol binding	0.67	1	0.16129032	62	0.17905103
20186	GO:0043933|GO:0034600	macromolecular complex sul	0.67	1	0.16129032	62	0.17905103
20883	GO:0045259|GO:0045255	proton-transporting ATP synt	0.67	1	0.16129032	62	0.17905103
25987	GO:0051704|GO:0051706	multi-organism process	0.67	1	0.16129032	62	0.17905103
2975	GO:0004175|GO:0016809	endopeptidase activity	0.68	5	0.8064516	320	0.9241344
5809	GO:0008289	lipid binding	0.68	4	0.6451613	258	0.74508333
9488	GO:0016301	kinase activity	0.68	29	4.677419	1740	5.0249805
4609	GO:0006464	protein modification process	0.68	47	7.580645	2781	8.031305
25820	GO:0051536	iron-sulfur cluster binding	0.69	1	0.16129032	64	0.18482687
25824	GO:0051540	metal cluster binding	0.69	1	0.16129032	64	0.18482687
9796	GO:0016741	transferase activity, transferr	0.69	4	0.6451613	261	0.7537471
9710	GO:0016628	oxidoreductase activity, actin	0.69	1	0.16129032	65	0.18771479
25314	GO:0051015	actin filament binding	0.69	1	0.16129032	65	0.18771479
10244	GO:0018130	heterocycle biosynthetic proc	0.69	3	0.48387095	199	0.57469606
5651	GO:0008080	N-acetyltransferase activity	0.70	1	0.16129032	67	0.19349062
2629	GO:0003678|GO:0003679	DNA helicase activity	0.70	1	0.16129032	67	0.19349062
18955	GO:0042625	ATPase activity, coupled to t	0.71	1	0.16129032	68	0.19637854
2999	GO:0004312	fatty acid synthase activity	0.71	1	0.16129032	68	0.19637854
3620	GO:0005057	receptor signaling protein act	0.71	1	0.16129032	69	0.19926646
9722	GO:0016641	oxidoreductase activity, actin	0.71	1	0.16129032	69	0.19926646
31420	GO:0080043	quercetin 3-O-glucosyltransfe	0.71	1	0.16129032	69	0.19926646
4408	GO:0006200	ATP catabolic process	0.71	10	1.6129032	641	1.8511566
9918	GO:0016887|GO:0004002	ATPase activity	0.71	10	1.6129032	641	1.8511566
21600	GO:0046034	ATP metabolic process	0.71	10	1.6129032	641	1.8511566
716	GO:0001071	nucleic acid binding transcrip	0.71	23	3.7096775	1417	4.0921826
2643	GO:0003700|GO:0000130	sequence-specific DNA bind	0.71	23	3.7096775	1417	4.0921826
15436	GO:0033036	macromolecule localization	0.72	6	0.9677419	397	1.1465042
3895	GO:0005543	phospholipid binding	0.72	2	0.32258064	140	0.40430877
9191	GO:0015931	nucleobase, nucleoside, nucl	0.72	1	0.16129032	70	0.20215438
9192	GO:0015932	nucleobase, nucleoside, nucl	0.72	1	0.16129032	70	0.20215438
8676	GO:0015294	solute:cation symporter activ	0.72	2	0.32258064	141	0.4071967
12547	GO:0022857|GO:0005386|G	transmembrane transporter a	0.72	24	3.8709676	1483	4.282785
3744	GO:0005244	voltage-gated ion channel ac	0.73	1	0.16129032	72	0.20793022
6475	GO:0009108	coenzyme biosynthetic proce	0.73	1	0.16129032	72	0.20793022
9740	GO:0016667	oxidoreductase activity, actin	0.73	1	0.16129032	72	0.20793022
12528	GO:0022832	voltage-gated channel activit	0.73	1	0.16129032	72	0.20793022
15280	GO:0032879	regulation of localization	0.73	1	0.16129032	72	0.20793022
17141	GO:0034762	regulation of transmembrane	0.73	1	0.16129032	72	0.20793022
17144	GO:0034765	regulation of ion transmembr	0.73	1	0.16129032	72	0.20793022
19568	GO:0043269	regulation of ion transport	0.73	1	0.16129032	72	0.20793022
25348	GO:0051049	regulation of transport	0.73	1	0.16129032	72	0.20793022
21058	GO:0045454|GO:0030503|G	cell redox homeostasis	0.73	3	0.48387095	211	0.6093511
9703	GO:0016620	oxidoreductase activity, actin	0.73	1	0.16129032	73	0.21081814
19684	GO:0043412	macromolecule modification	0.74	48	7.7419353	2900	8.374968
9817	GO:0016763	transferase activity, transferr	0.74	1	0.16129032	74	0.21370606
3965	GO:0005654	nucleoplasm	0.74	1	0.16129032	75	0.21659398
20645	GO:0044451	nucleoplasm part	0.74	1	0.16129032	75	0.21659398
9829	GO:0016779	nucleotidyltransferase activity	0.75	2	0.32258064	148	0.42741212
5663	GO:0008094|GO:0004011	DNA-dependent ATPase act	0.75	1	0.16129032	76	0.2194819
18953	GO:0042623	ATPase activity, coupled	0.75	8	1.2903225	537	1.550813
4478	GO:0006281	DNA repair	0.75	2	0.32258064	149	0.43030006
5037	GO:0006974|GO:0034984	response to DNA damage st	0.75	2	0.32258064	149	0.43030006
11426	GO:0019438	aromatic compound biosynth	0.75	2	0.32258064	149	0.43030006
9538	GO:0016410	N-acyltransferase activity	0.75	1	0.16129032	77	0.22236982

14667	GO:0032259	methylation	0.75	4	0.6451613	285	0.8230572
9823	GO:0016772	transferase activity, transferr	0.76	31	5	1932	5.579461
4358	GO:0006140	regulation of nucleotide meta	0.76	1	0.16129032	80	0.2310336
7146	GO:0009894	regulation of catabolic proce	0.76	1	0.16129032	80	0.2310336
13278	GO:0030811	regulation of nucleotide catab	0.76	1	0.16129032	80	0.2310336
13759	GO:0031329	regulation of cellular catabol	0.76	1	0.16129032	80	0.2310336
15521	GO:0033121	regulation of purine nucleotid	0.76	1	0.16129032	80	0.2310336
8517	GO:0015103	inorganic anion transmembra	0.77	2	0.32258064	154	0.44473964
4357	GO:0006139|GO:0055134	nucleobase, nucleoside, nucl	0.77	54	8.709678	3285	9.486816
18674	GO:0042325	regulation of phosphorylation	0.77	1	0.16129032	81	0.23392151
4990	GO:0006915|GO:0008632	apoptosis	0.77	3	0.48387095	227	0.6555578
19831	GO:0043565	sequence-specific DNA bind	0.78	2	0.32258064	159	0.45917925
5624	GO:0008047	enzyme activator activity	0.79	1	0.16129032	85	0.24547319
3307	GO:0004675	transmembrane receptor pro	0.79	5	0.8064516	367	1.0598665
19473	GO:0043170|GO:0043283	macromolecule metabolic pr	0.79	110	17.741936	6553	18.92454
3723	GO:0005215|GO:0005478	transporter activity	0.79	29	4.677419	1844	5.325324
11695	GO:0019725	cellular homeostasis	0.79	3	0.48387095	234	0.67577326
26931	GO:0055085	transmembrane transport	0.79	24	3.8709676	1548	4.4705
11828	GO:0019899	enzyme binding	0.80	3	0.48387095	237	0.684437
9719	GO:0016638	oxidoreductase activity, actin	0.80	1	0.16129032	89	0.25702485
18925	GO:0042592	homeostatic process	0.80	3	0.48387095	238	0.68732494
4897	GO:0006793	phosphorus metabolic proce	0.80	47	7.580645	2925	8.4471655
4900	GO:0006796	phosphate metabolic process	0.80	47	7.580645	2925	8.4471655
5756	GO:0008219	cell death	0.80	3	0.48387095	239	0.69021285
8209	GO:0012501|GO:0016244	programmed cell death	0.80	3	0.48387095	239	0.69021285
9462	GO:0016265	death	0.80	3	0.48387095	239	0.69021285
14590	GO:0032182	small conjugating protein bin	0.80	1	0.16129032	90	0.2599128
3644	GO:0005102	receptor binding	0.81	1	0.16129032	91	0.2628007
6784	GO:0009451|GO:0016547	RNA modification	0.81	1	0.16129032	91	0.2628007
8494	GO:0015075	ion transmembrane transport	0.81	12	1.9354838	827	2.3883097
9579	GO:0016462	pyrophosphatase activity	0.81	14	2.2580645	954	2.7550755
9859	GO:0016818	hydrolase activity, acting on a	0.81	14	2.2580645	956	2.7608514
16603	GO:0034220	ion transmembrane transport	0.82	12	1.9354838	833	2.4056373
4910	GO:0006811	ion transport	0.82	14	2.2580645	959	2.769515
9858	GO:0016817	hydrolase activity, acting on a	0.82	14	2.2580645	959	2.769515
3808	GO:0005351|GO:0005403	sugar:hydrogen symporter ac	0.82	1	0.16129032	94	0.27146447
3835	GO:0005402	cation:sugar symporter activi	0.82	1	0.16129032	94	0.27146447
15949	GO:0033554	cellular response to stress	0.82	2	0.32258064	173	0.49961013
4526	GO:0006351|GO:0006350|G	transcription, DNA-depender	0.82	24	3.8709676	1575	4.548474
15176	GO:0032774	RNA biosynthetic process	0.82	24	3.8709676	1575	4.548474
28365	GO:0065008	regulation of biological quality	0.82	4	0.6451613	316	0.9125827
4067	GO:0005783	endoplasmic reticulum	0.82	2	0.32258064	174	0.50249803
8967	GO:0015698	inorganic anion transport	0.83	2	0.32258064	176	0.5082739
8677	GO:0015295	solute:hydrogen symporter a	0.83	1	0.16129032	98	0.28301615
8681	GO:0015299	solute:hydrogen antiporter ac	0.83	1	0.16129032	98	0.28301615
25379	GO:0051082	unfolded protein binding	0.83	1	0.16129032	98	0.28301615
4909	GO:0006810|GO:0015457|G	transport	0.83	36	5.806452	2315	6.6855345
25529	GO:0051234	establishment of localization	0.83	36	5.806452	2315	6.6855345
16851	GO:0034470	ncRNA processing	0.83	1	0.16129032	99	0.28590405
17039	GO:0034660	ncRNA metabolic process	0.83	1	0.16129032	99	0.28590405
3716	GO:0005198	structural molecule activity	0.83	5	0.8064516	393	1.1349525
25476	GO:0051179	localization	0.84	36	5.806452	2319	6.697086
4849	GO:0006730|GO:0019753|G	one-carbon metabolic proces	0.84	4	0.6451613	325	0.93857396
16430	GO:0034046	poly(G) RNA binding	0.84	1	0.16129032	100	0.28879198
6663	GO:0009309	amine biosynthetic process	0.84	2	0.32258064	181	0.5227135
5874	GO:0008374	O-acyltransferase activity	0.84	1	0.16129032	102	0.29456782
4844	GO:0006725	cellular aromatic compound	0.85	2	0.32258064	185	0.53426516
19392	GO:0043085	positive regulation of catalytic	0.85	1	0.16129032	104	0.30034366
20343	GO:0044093	positive regulation of molecu	0.85	1	0.16129032	104	0.30034366
12573	GO:0022891	substrate-specific transmem	0.85	18	2.903226	1241	3.5839086
8673	GO:0015291|GO:0015290|G	secondary active transmemb	0.86	5	0.8064516	407	1.1753833
3942	GO:0005618	cell wall	0.86	1	0.16129032	107	0.30900744
11833	GO:0019904	protein domain specific bindi	0.86	1	0.16129032	109	0.31478328
10058	GO:0017111	nucleoside-triphosphatase ac	0.86	12	1.9354838	878	2.5355935
17020	GO:0034641	cellular nitrogen compound m	0.86	58	9.354838	3678	10.621769
12868	GO:0030312	external encapsulating struct	0.87	1	0.16129032	111	0.3205591
4512	GO:0006325	chromatin organization	0.87	1	0.16129032	112	0.32344702
5070	GO:0007017	microtubule-based process	0.87	1	0.16129032	112	0.32344702
5071	GO:0007018	microtubule-based movemen	0.87	1	0.16129032	112	0.32344702
8680	GO:0015298	solute:cation antiporter activi	0.87	1	0.16129032	112	0.32344702
9730	GO:0016651	oxidoreductase activity, actin	0.87	1	0.16129032	112	0.32344702
25568	GO:0051276|GO:0007001|G	chromosome organization	0.87	1	0.16129032	112	0.32344702
29081	GO:0070717	poly-purine tract binding	0.87	1	0.16129032	112	0.32344702
4850	GO:0006732|GO:0006752	coenzyme metabolic process	0.87	1	0.16129032	113	0.32633495
19686	GO:0043414	macromolecule methylation	0.87	1	0.16129032	113	0.32633495
20510	GO:0044260|GO:0034960	cellular macromolecule meta	0.87	90	14.5161295	5577	16.105928
12574	GO:0022892	substrate-specific transporte	0.88	21	3.387097	1463	4.2250266
11522	GO:0019538|GO:0006411	protein metabolic process	0.88	65	10.4838705	4134	11.938661
4906	GO:0006807	nitrogen compound metaboli	0.89	58	9.354838	3725	10.757502
4405	GO:0006195	purine nucleotide catabolic p	0.89	10	1.6129032	773	2.232362
6508	GO:0009143	nucleoside triphosphate cata	0.89	10	1.6129032	773	2.232362
6509	GO:0009144	purine nucleoside triphospha	0.89	10	1.6129032	773	2.232362
6511	GO:0009146	purine nucleoside triphospha	0.89	10	1.6129032	773	2.232362
6519	GO:0009154	purine ribonucleotide catabol	0.89	10	1.6129032	773	2.232362
6530	GO:0009166	nucleotide catabolic process	0.89	10	1.6129032	773	2.232362
6567	GO:0009203	ribonucleoside triphosphate c	0.89	10	1.6129032	773	2.232362
6569	GO:0009205	purine ribonucleoside triphos	0.89	10	1.6129032	773	2.232362
6571	GO:0009207	purine ribonucleoside triphos	0.89	10	1.6129032	773	2.232362
6624	GO:0009261	ribonucleotide catabolic proc	0.89	10	1.6129032	773	2.232362
17034	GO:0034655	nucleobase, nucleoside, nucl	0.89	10	1.6129032	773	2.232362
17035	GO:0034656	nucleobase, nucleoside and	0.89	10	1.6129032	773	2.232362
22209	GO:0046700	heterocycle catabolic proces	0.89	10	1.6129032	773	2.232362
30879	GO:0072523	purine-containing compound	0.89	10	1.6129032	773	2.232362
12532	GO:0022836	gated channel activity	0.89	1	0.16129032	122	0.3523262
9267	GO:0016021	integral to membrane	0.89	15	2.419355	1103	3.1853757
20520	GO:0044270	cellular nitrogen compound c	0.89	10	1.6129032	777	2.2439137
14392	GO:0031981	nuclear lumen	0.89	1	0.16129032	123	0.35521415
25485	GO:0051188	cofactor biosynthetic process	0.89	1	0.16129032	123	0.35521415
9295	GO:0016053	organic acid biosynthetic pro	0.89	2	0.32258064	211	0.6093511
21922	GO:0046394	carboxylic acid biosynthetic p	0.89	2	0.32258064	211	0.6093511
4916	GO:0006818	hydrogen transport	0.90	3	0.48387095	292	0.84327257
9246	GO:0015992	proton transport	0.90	3	0.48387095	292	0.84327257
9583	GO:0016469	proton-transporting two-sect	0.90	1	0.16129032	127	0.36676583
6563	GO:0009199	ribonucleoside triphosphate r	0.90	10	1.6129032	790	2.2814567
6515	GO:0009150	purine ribonucleotide metabo	0.90	10	1.6129032	791	2.2843447
22479	GO:0046983	protein dimerization activity	0.90	6	0.9677419	517	1.4930545
6506	GO:0009141	nucleoside triphosphate meta	0.91	10	1.6129032	796	2.2987843
20356	GO:0044106	cellular amine metabolic proc	0.91	3	0.48387095	303	0.8750397
20619	GO:0044425	membrane part	0.91	21	3.387097	1523	4.398302
19532	GO:0043233	organelle lumen	0.92	1	0.16129032	137	0.39564502
28380	GO:0070013	intracellular organelle lumen	0.92	1	0.16129032	137	0.39564502
4373	GO:0006163	purine nucleotide metabolic p	0.92	10	1.6129032	810	2.339215
6622	GO:0009259|GO:0009121	ribonucleotide metabolic proc	0.92	10	1.6129032	812	2.344991
13531	GO:0031072	heat shock protein binding	0.92	2	0.32258064	230	0.6642216
20531	GO:0044281	small molecule metabolic pro	0.92	25	4.032258	1788	5.1636004
28378	GO:0070011	peptidase activity, acting on	0.92	6	0.9677419	537	1.550813
3724	GO:0005216	ion channel activity	0.92	1	0.16129032	140	0.40430877
6662	GO:0009308	amine metabolic process	0.92	3	0.48387095	314	0.9068068
30877	GO:0072521	purine-containing compound	0.93	10	1.6129032	827	2.3883097
9895	GO:0016860	intramolecular oxidoreductas	0.93	1	0.16129032	146	0.42163628
5791	GO:0008270	zinc ion binding	0.93	26	4.193548	1880	5.4292893
20499	GO:0044249	cellular biosynthetic process	0.93	38	6.129032	2635	7.6096687

18582	GO:0042221	response to chemical stimulu	0.93	3	0.48387095	328	0.94723773
5981	GO:0008509	anion transmembrane transp	0.94	2	0.32258064	245	0.70754033
8679	GO:0015297	antiporter activity	0.94	1	0.16129032	152	0.4389638
8682	GO:0015300	solute:solute antiporter activit	0.94	1	0.16129032	152	0.4389638
27562	GO:0060589	nucleoside-triphosphatase re	0.94	1	0.16129032	152	0.4389638
2660	GO:0003735|GO:0003736|G	structural constituent of ribos	0.94	2	0.32258064	246	0.7104283
5909	GO:0008415	acyltransferase activity	0.94	3	0.48387095	330	0.95301354
4917	GO:0006820|GO:0006822	anion transport	0.94	2	0.32258064	247	0.7133162
14386	GO:0031974	membrane-enclosed lumen	0.94	1	0.16129032	154	0.44473964
5661	GO:0008092	cytoskeletal protein binding	0.94	2	0.32258064	249	0.719092
5763	GO:0008233	peptidase activity	0.94	6	0.9677419	565	1.6316746
20532	GO:0044282	small molecule catabolic pro	0.94	10	1.6129032	854	2.4662836
8496	GO:0015078	hydrogen ion transmembrane	0.94	1	0.16129032	160	0.4620672
20517	GO:0044267	cellular protein metabolic pro	0.94	47	7.580645	3225	9.313541
6427	GO:0009058	biosynthetic process	0.95	40	6.451613	2796	8.074624
9308	GO:0016070	RNA metabolic process	0.95	25	4.032258	1855	5.3570914
9494	GO:0016311	dephosphorylation	0.95	4	0.6451613	425	1.227366
5764	GO:0008234|GO:0004220	cysteine-type peptidase activ	0.95	1	0.16129032	163	0.47073093
5055	GO:0006996	organelle organization	0.95	1	0.16129032	164	0.47361887
25483	GO:0051186	cofactor metabolic process	0.95	1	0.16129032	164	0.47361887
20533	GO:0044283	small molecule biosynthetic p	0.95	3	0.48387095	347	1.0021082
19126	GO:0042803	protein homodimerization act	0.95	2	0.32258064	265	0.7652988
9699	GO:0016616	oxidoreductase activity, actin	0.95	2	0.32258064	266	0.7681867
6077	GO:0008652	cellular amino acid biosynthe	0.95	1	0.16129032	169	0.48805845
4755	GO:0006629	lipid metabolic process	0.95	6	0.9677419	590	1.7038727
22007	GO:0046483	heterocycle metabolic proces	0.96	13	2.096774	1094	3.1593843
3955	GO:0005634	nucleus	0.96	18	2.903226	1433	4.138389
9768	GO:0016706	oxidoreductase activity, actin	0.96	1	0.16129032	175	0.505386
18912	GO:0042578	phosphoric ester hydrolase a	0.96	4	0.6451613	444	1.2822365
4649	GO:0006520|GO:0006519	cellular amino acid metabolic	0.96	2	0.32258064	277	0.7999538
20498	GO:0044248	cellular catabolic process	0.96	10	1.6129032	894	2.5818002
20622	GO:0044428	nuclear part	0.96	1	0.16129032	178	0.5140497
20521	GO:0044271	cellular nitrogen compound b	0.96	3	0.48387095	367	1.0598665
4109	GO:0005840|GO:0033279	ribosome	0.96	7	1.1290323	682	1.9695613
7691	GO:0010467	gene expression	0.96	26	4.193548	1974	5.7007537
5018	GO:0006950	response to stress	0.96	6	0.9677419	611	1.764519
5610	GO:0008026	ATP-dependent helicase acti	0.96	1	0.16129032	183	0.52848935
28401	GO:0070035	purine NTP-dependent helica	0.96	1	0.16129032	183	0.52848935
6425	GO:0009056	catabolic process	0.97	12	1.9354838	1051	3.0352037
4867	GO:0006753	nucleoside phosphate metab	0.97	10	1.6129032	914	2.6395588
6484	GO:0009117	nucleotide metabolic process	0.97	10	1.6129032	914	2.6395588
2657	GO:0003727|GO:0003728	single-stranded RNA binding	0.97	1	0.16129032	188	0.54292893
3068	GO:0004386	helicase activity	0.97	1	0.16129032	189	0.54581684
9697	GO:0016614	oxidoreductase activity, actin	0.97	2	0.32258064	293	0.84616053
9839	GO:0016791|GO:0016302	phosphatase activity	0.97	3	0.48387095	383	1.1060733
2626	GO:0003674|GO:0005554	molecular_function	0.97	416	67.09677	24394	70.447914
30206	GO:0071842	cellular component organizat	0.97	1	0.16129032	193	0.5573685
20488	GO:0044238	primary metabolic process	0.97	144	23.225807	9167	26.47356
3340	GO:0004721	phosphoprotein phosphatase	0.97	1	0.16129032	199	0.57469606
9889	GO:0016853	isomerase activity	0.97	2	0.32258064	306	0.8837035
26932	GO:0055086	nucleobase, nucleoside and	0.98	10	1.6129032	944	2.7261963
13018	GO:0030529	ribonucleoprotein complex	0.98	7	1.1290323	741	2.1399486
4558	GO:0006396|GO:0006394	RNA processing	0.98	1	0.16129032	219	0.63245445
5019	GO:0006952|GO:0002217|G	defense response	0.98	1	0.16129032	221	0.63823026
12533	GO:0022838	substrate-specific channel ac	0.98	1	0.16129032	221	0.63823026
8660	GO:0015267|GO:0015249|G	channel activity	0.98	1	0.16129032	226	0.6526699
12515	GO:0022803	passive transmembrane tran	0.98	1	0.16129032	226	0.6526699
8211	GO:0012505	endomembrane system	0.99	1	0.16129032	242	0.6988766
3178	GO:0004519	endonuclease activity	0.99	2	0.32258064	356	1.0280994
20487	GO:0044237	cellular metabolic process	0.99	123	19.838709	8185	23.637625
30306	GO:0071944	cell periphery	0.99	1	0.16129032	259	0.74797124
2627	GO:0003676	nucleic acid binding	0.99	30	4.83871	2453	7.0840673
3177	GO:0004518	nuclease activity	1.00	2	0.32258064	427	1.2331418
13041	GO:0030554	adenyl nucleotide binding	1.00	3	0.48387095	550	1.5883559
14965	GO:0032559	adenyl ribonucleotide binding	1.00	3	0.48387095	550	1.5883559
19527	GO:0043228	non-membrane-bounded org	1.00	7	1.1290323	923	2.66555
19531	GO:0043232	intracellular non-membrane-b	1.00	7	1.1290323	923	2.66555
19533	GO:0043234	protein complex	1.00	6	0.9677419	848	2.448956
3876	GO:0005515|GO:0045308	protein binding	1.00	97	15.645162	6933	20.021948
7229	GO:0009987|GO:0008151|G	cellular process	1.00	157	25.32258	10601	30.614838
3863	GO:0005488	binding	1.00	212	34.19355	13903	40.15075
3884	GO:0005524	ATP binding	1.00	2	0.32258064	524	1.51327
19125	GO:0042802	identical protein binding	1.00	3	0.48387095	697	2.01288
19526	GO:0043227	membrane-bounded organel	1.00	20	3.2258065	2142	6.185924
19530	GO:0043231	intracellular membrane-boun	1.00	20	3.2258065	2142	6.185924
15392	GO:0032991	macromolecular complex	1.00	13	2.096774	1616	4.666878
9266	GO:0016020	membrane	1.00	42	6.774194	3741	10.803708
131	GO:0000166	nucleotide binding	1.00	8	1.2903225	1213	3.5030468
14959	GO:0032553	ribonucleotide binding	1.00	3	0.48387095	795	2.2958963
14961	GO:0032555	purine ribonucleotide binding	1.00	3	0.48387095	795	2.2958963
10033	GO:0017076	purine nucleotide binding	1.00	3	0.48387095	797	2.3016722
18000	GO:0035639	purine ribonucleoside triphos	1.00	2	0.32258064	769	2.2208104
19525	GO:0043226	organelle	1.00	27	4.354839	3013	8.701303
19528	GO:0043229	intracellular organelle	1.00	27	4.354839	3013	8.701303
2653	GO:0003723	RNA binding	1.00	2	0.32258064	797	2.3016722
20640	GO:0044446	intracellular organelle part	1.00	1	0.16129032	710	2.0504231
20616	GO:0044422	organelle part	1.00	1	0.16129032	712	2.0561988
3945	GO:0005622	intracellular	1.00	49	7.903226	4751	13.720507
4027	GO:0005737	cytoplasm	1.00	13	2.096774	2001	5.7787275
20638	GO:0044444	cytoplasmic part	1.00	9	1.451613	1644	4.7477403
20618	GO:0044424	intracellular part	1.00	36	5.806452	3853	11.127155
3903	GO:0005575|GO:0008372	cellular_component	1.00	101	16.290323	8515	24.590637
3946	GO:0005623	cell	1.00	92	14.83871	8227	23.758917
20657	GO:0044464	cell part	1.00	92	14.83871	8227	23.758917