

Supplemental Table S7. The overlapped DEGs in PagLBD21 RNA-seq & PagLBD3 RNA-se

genes	logFC. x	logCPM. x	PValue. x	FDR. x	OX. WT.	LBDLLJGY. A	LLJGY. B	LLJGY. C
Potri.001	-3.13512	3.626244	3.92E-14	4.01E-11	-1	214	399	228
Potri.001	-0.84518	1.410782	0.001171	0.039407	-1	47	38	40
Potri.001	1.525735	0.918472	0.000125	0.007107	1	12	7	16
Potri.001	0.55523	7.331455	0.000676	0.026114	1	1306	1965	1772
Potri.001	-0.75869	2.329501	0.00016	0.008516	-1	79	78	81
Potri.001	1.647527	2.300543	6.86E-13	5.86E-10	1	37	26	28
Potri.001	0.51275	6.153491	5.85E-06	0.000622	1	784	724	779
Potri.001	0.654147	3.362225	0.000204	0.010422	1	92	121	94
Potri.001	0.5732	5.439324	3.48E-05	0.002637	1	501	483	376
Potri.001	0.47671	7.254934	0.000656	0.025513	1	1883	1392	1728
Potri.001	0.719771	3.519537	2.98E-05	0.002349	1	135	91	110
Potri.001	-0.58717	4.850383	0.000316	0.014595	-1	394	509	434
Potri.001	-0.57131	4.041254	0.000643	0.025104	-1	303	192	269
Potri.001	-0.57569	4.831037	0.000181	0.009396	-1	523	371	434
Potri.001	-0.95512	3.063317	1.17E-06	0.000167	-1	127	130	163
Potri.001	-0.97827	3.169961	5.89E-06	0.000624	-1	141	175	139
Potri.001	0.995222	5.430854	5.81E-09	1.91E-06	1	393	356	374
Potri.001	0.691354	4.032509	6.81E-07	0.000107	1	165	160	160
Potri.001	-0.79479	3.241011	1.26E-05	0.001156	-1	156	152	151
Potri.001	-0.46957	4.776263	0.000134	0.007472	-1	444	403	389
Potri.001	-0.54611	5.968187	0.000527	0.021384	-1	852	1112	913
Potri.001	1.005888	2.519795	5.26E-05	0.003688	1	45	62	38
Potri.001	-0.79283	4.083285	4.34E-08	1.05E-05	-1	286	256	288
Potri.001	-0.63718	5.290515	1.10E-05	0.001027	-1	769	591	502
Potri.001	0.476094	4.644343	0.000258	0.012517	1	310	246	259
Potri.001	0.814917	4.48763	0.000113	0.006532	1	280	156	201
Potri.001	-0.49661	4.130852	0.0004	0.017437	-1	302	233	260
Potri.001	0.755798	6.44516	1.65E-07	3.27E-05	1	1084	629	837
Potri.001	0.566291	5.865582	4.06E-06	0.000461	1	727	520	594
Potri.001	-0.54976	4.871831	2.29E-05	0.00192	-1	466	438	446
Potri.001	0.707213	6.579802	5.96E-06	0.000629	1	764	1096	952
Potri.001	-0.56195	4.096389	4.57E-05	0.003314	-1	294	233	263
Potri.001	-1.46901	1.099163	1.24E-06	0.000173	-1	43	30	40
Potri.001	0.816923	6.304792	3.27E-09	1.19E-06	1	721	841	664
Potri.001	0.985569	3.380787	7.27E-08	1.62E-05	1	96	82	92
Potri.001	0.382987	5.760247	0.001538	0.047254	1	667	618	550
Potri.001	0.522728	7.039502	3.34E-06	0.000395	1	1406	1348	1455
Potri.001	0.432314	7.627102	0.001123	0.038114	1	2284	1828	2464
Potri.001	0.597357	5.799112	5.57E-07	9.02E-05	1	594	589	543
Potri.001	-1.99106	5.031189	9.95E-20	3.29E-16	-1	622	787	607
Potri.001	-2.46939	-0.65892	0.000344	0.015469	-1	7	16	8
Potri.001	-0.57302	5.75023	5.28E-05	0.003691	-1	959	770	785
Potri.001	-1.24878	5.238923	4.14E-07	7.00E-05	-1	559	749	742
Potri.001	0.388254	6.603889	0.001236	0.040569	1	1163	1162	961
Potri.001	1.401929	4.1197	7.88E-15	9.96E-12	1	147	102	123
Potri.001	0.820627	4.471962	3.76E-07	6.55E-05	1	270	165	193
Potri.001	0.582783	3.504078	0.00148	0.046018	1	124	96	131
Potri.001	-0.83854	4.049635	7.56E-09	2.34E-06	-1	307	239	276
Potri.001	0.452777	3.779103	0.001651	0.049927	1	152	151	145
Potri.001	-0.50504	5.018607	7.54E-05	0.004884	-1	593	440	451
Potri.001	-0.51955	5.873937	0.000172	0.009027	-1	805	1019	852

Potri.001	-0.85923	4.969299	2.74E-10	1.32E-07	-1	507	493	565
Potri.001	-0.97416	6.029428	7.76E-07	0.000118	-1	902	1297	1144
Potri.001	-0.46319	4.520176	0.000333	0.015167	-1	376	334	322
Potri.001	-0.53298	3.08634	0.001325	0.042728	-1	128	125	131
Potri.001	0.507613	5.569049	2.06E-05	0.001756	1	542	501	485
Potri.001	-0.44593	4.017667	0.001053	0.036534	-1	252	227	243
Potri.001	-0.84924	6.274699	4.63E-08	1.10E-05	-1	1354	1225	1301
Potri.001	0.614754	3.237927	0.000362	0.016153	1	117	92	79
Potri.001	0.646784	4.457837	0.000211	0.010722	1	188	275	198
Potri.001	-1.4308	0.414602	0.001476	0.045971	-1	12	24	30
Potri.001	-0.87856	3.029737	0.000284	0.013415	-1	125	135	143
Potri.001	-0.61114	3.032776	0.001311	0.04237	-1	120	147	110
Potri.001	-0.48413	5.782281	2.44E-05	0.002014	-1	871	846	781
Potri.001	0.732351	2.73283	0.000315	0.014589	1	64	63	64
Potri.001	0.557111	6.938344	3.27E-06	0.000388	1	1224	1321	1316
Potri.001	-1.53774	2.348601	2.71E-05	0.002179	-1	70	119	94
Potri.001	-2.41269	-0.49038	0.000116	0.006644	-1	15	14	7
Potri.001	0.735158	5.876774	3.99E-07	6.86E-05	1	514	675	521
Potri.001	-1.26445	1.164938	0.001602	0.048792	-1	38	50	26
Potri.001	-0.61748	2.506131	0.00156	0.047688	-1	82	89	89
Potri.001	-1.09081	3.592691	6.86E-10	2.89E-07	-1	193	205	231
Potri.001	-0.9754	2.800004	7.23E-08	1.62E-05	-1	124	116	111
Potri.001	0.731313	4.44416	2.06E-08	5.72E-06	1	222	196	218
Potri.001	-0.49736	6.742809	2.64E-06	0.000326	-1	1740	1538	1615
Potri.001	-0.52087	5.051128	0.000967	0.03447	-1	538	519	461
Potri.001	1.028422	6.339934	6.91E-06	0.000705	1	515	961	579
Potri.001	-1.81756	0.371985	0.000291	0.013712	-1	13	35	20
Potri.001	-0.50759	3.888072	0.000761	0.028803	-1	258	185	230
Potri.001	-0.37551	6.817241	0.001028	0.035839	-1	1936	1515	1536
Potri.001	1.341658	1.801856	0.000131	0.007363	1	31	22	21
Potri.001	0.447768	5.041034	0.000209	0.010648	1	370	364	349
Potri.002	-0.60142	6.238102	3.00E-07	5.42E-05	-1	1294	1146	1110
Potri.002	0.629985	6.569268	1.87E-05	0.001611	1	1035	901	975
Potri.002	-1.28948	1.616772	1.60E-06	0.000212	-1	55	52	53
Potri.002	-0.71892	2.876799	0.000156	0.008383	-1	114	100	134
Potri.002	0.599504	5.379166	3.80E-07	6.59E-05	1	424	424	439
Potri.002	-0.60368	4.136589	9.60E-05	0.005819	-1	245	277	295
Potri.002	-0.62827	3.077539	0.000387	0.017029	-1	153	116	124
Potri.002	-0.58163	6.121173	4.54E-06	0.000503	-1	1307	895	1067
Potri.002	-0.81062	2.74085	0.000251	0.012245	-1	90	127	105
Potri.002	-1.00118	5.622178	5.33E-10	2.26E-07	-1	885	844	825
Potri.002	-0.60124	3.169002	0.001041	0.036244	-1	175	127	115
Potri.002	0.623793	4.087572	0.000268	0.01288	1	219	144	159
Potri.002	0.437132	5.682819	0.000267	0.012871	1	577	564	558
Potri.002	-1.18194	2.393768	3.07E-06	0.000368	-1	86	113	75
Potri.002	-0.54215	4.643873	1.77E-05	0.00154	-1	411	378	361
Potri.002	-0.76727	6.419735	8.39E-06	0.000837	-1	1234	1330	1620
Potri.002	0.864	7.432394	8.69E-06	0.000862	1	1153	1972	1602
Potri.002	-0.95283	2.371896	1.29E-05	0.001178	-1	103	73	82
Potri.002	0.717939	3.963313	5.60E-07	9.03E-05	1	171	137	150
Potri.002	-1.3295	1.169068	2.52E-05	0.002045	-1	46	43	27
Potri.002	0.854925	2.880068	2.23E-05	0.001874	1	68	62	71
Potri.002	0.471667	7.373167	6.66E-06	0.000687	1	1858	1700	1863
Potri.002	-1.51245	1.131792	3.38E-05	0.002585	-1	27	48	41

Potri.002	-1.03671	3.210023	6.62E-09	2.11E-06	-1	166	144	166
Potri.002	0.768995	6.275182	1.91E-10	9.31E-08	1	756	748	728
Potri.002	-0.68999	3.891161	1.50E-06	0.000201	-1	265	215	228
Potri.002	0.766393	6.42309	3.40E-09	1.22E-06	1	824	780	872
Potri.002	-0.36205	6.787399	0.001481	0.046018	-1	1792	1583	1479
Potri.002	-0.94476	4.443899	7.01E-09	2.20E-06	-1	338	409	357
Potri.002	-0.46859	6.088222	0.000107	0.006322	-1	1079	1062	935
Potri.003	-1.24835	1.23633	2.87E-05	0.002274	-1	46	43	31
Potri.003	-0.51647	4.126087	0.00057	0.022728	-1	318	232	248
Potri.003	0.854616	2.960937	0.000352	0.01575	1	65	80	67
Potri.003	0.717787	2.553515	0.000549	0.022035	1	70	43	57
Potri.003	0.676997	4.285084	3.69E-06	0.000426	1	188	212	181
Potri.003	1.682148	2.579024	2.09E-11	1.20E-08	1	38	34	37
Potri.003	0.788922	7.346334	5.46E-05	0.003794	1	1152	1962	1491
Potri.003	1.116424	5.097493	1.04E-12	8.44E-10	1	248	287	303
Potri.003	0.699018	6.800049	5.08E-06	0.000555	1	1015	1254	1030
Potri.003	0.711347	4.369904	4.09E-05	0.003012	1	251	167	194
Potri.003	-0.63878	3.297433	0.001102	0.03764	-1	163	169	127
Potri.003	-0.63823	4.632977	9.31E-05	0.005702	-1	398	400	372
Potri.003	0.552013	6.367706	1.50E-06	0.000201	1	877	910	821
Potri.003	-0.7836	3.562829	6.47E-05	0.004373	-1	191	194	189
Potri.003	0.505143	4.961525	0.000116	0.006644	1	339	343	319
Potri.003	0.813329	6.112858	8.90E-08	1.92E-05	1	783	542	643
Potri.003	0.602275	5.094114	1.19E-05	0.001104	1	374	361	321
Potri.003	-0.72407	4.783236	2.24E-08	6.13E-06	-1	451	459	419
Potri.003	-0.40514	5.436004	0.000397	0.017311	-1	709	583	631
Potri.003	1.065518	1.87097	3.78E-06	0.000433	1	32	25	32
Potri.003	0.424437	5.331467	0.001283	0.041608	1	506	426	410
Potri.003	-1.98732	-0.4646	0.000332	0.015167	-1	14	11	10
Potri.003	0.42403	8.086047	0.001489	0.04619	1	2984	3011	3049
Potri.003	0.760154	9.0103	2.54E-09	9.65E-07	1	4383	5110	5379
Potri.003	-0.61805	4.076674	0.000222	0.011131	-1	346	224	225
Potri.003	0.441681	6.066027	0.000314	0.014582	1	683	764	760
Potri.003	-0.46742	5.655082	0.000195	0.009992	-1	821	657	802
Potri.003	5.488767	-1.43455	0.000135	0.007472	1	0	0	0
Potri.003	0.551493	3.322974	0.000661	0.025659	1	111	96	106
Potri.003	-0.65944	2.968201	8.70E-05	0.005401	-1	129	112	125
Potri.003	-0.50984	5.842655	0.000114	0.006569	-1	811	872	933
Potri.003	0.624865	4.902444	0.000191	0.009847	1	310	338	266
Potri.003	0.482309	5.807377	0.000102	0.006109	1	739	516	576
Potri.003	0.727536	4.582709	0.000147	0.008053	1	324	156	229
Potri.003	-0.43239	5.061458	0.000583	0.023147	-1	502	482	505
Potri.003	-2.85443	-0.01313	0.000139	0.0077	-1	7	30	19
Potri.003	0.585213	5.299015	8.41E-05	0.005283	1	383	487	351
Potri.003	-0.52846	3.591735	0.001144	0.038692	-1	190	178	180
Potri.003	0.566342	5.053538	0.000156	0.008383	1	343	307	391
Potri.003	-0.54563	3.727711	0.001295	0.04196	-1	202	217	186
Potri.003	0.427972	4.376439	0.001603	0.048792	1	233	223	231
Potri.003	-0.74221	2.484828	0.000474	0.019913	-1	95	97	73
Potri.003	-1.45942	0.321644	0.000784	0.029428	-1	25	21	16
Potri.003	0.648803	7.585939	1.39E-07	2.86E-05	1	1824	2157	1836
Potri.004	0.647534	6.195357	2.68E-06	0.000327	1	750	852	620
Potri.004	-1.14755	3.958255	2.80E-06	0.00034	-1	409	236	190
Potri.004	0.804029	5.124847	5.24E-10	2.25E-07	1	364	318	309

Potri.004	0.587352	9.066446	2.38E-07	4.43E-05	1	5890	5176	5678
Potri.004	-0.57524	6.201165	1.26E-06	0.000176	-1	1257	966	1216
Potri.004	-1.04601	4.13805	3.65E-06	0.000422	-1	443	190	294
Potri.004	-0.66726	2.997528	0.000919	0.033221	-1	140	109	126
Potri.004	1.555424	1.517432	1.55E-07	3.14E-05	1	19	19	16
Potri.004	-0.8293	5.811825	6.80E-06	0.000697	-1	750	1092	933
Potri.004	-1.87603	1.029771	5.53E-07	9.00E-05	-1	33	51	30
Potri.004	-0.45979	8.518899	2.33E-05	0.001938	-1	5792	5156	5642
Potri.004	1.358355	2.936321	4.91E-11	2.67E-08	1	68	40	58
Potri.004	0.982763	3.650102	3.75E-07	6.54E-05	1	119	103	105
Potri.004	-1.80445	-0.11552	0.000541	0.021822	-1	17	14	15
Potri.004	0.689231	6.698208	8.14E-07	0.000123	1	897	1057	1131
Potri.004	0.421877	6.73898	0.000302	0.01411	1	1230	1121	1211
Potri.004	-1.54461	3.528254	3.29E-12	2.21E-09	-1	194	239	223
Potri.004	-0.69537	2.62804	0.000309	0.01439	-1	118	85	88
Potri.004	-1.02315	3.408474	1.35E-08	3.96E-06	-1	218	142	188
Potri.004	-0.67172	3.285445	0.000245	0.011977	-1	152	135	172
Potri.004	1.068642	3.34319	3.50E-07	6.21E-05	1	74	80	98
Potri.004	-0.6862	2.399933	0.001537	0.047254	-1	72	95	78
Potri.004	1.885981	4.768346	1.54E-28	1.65E-24	1	142	142	167
Potri.004	-1.08339	1.585227	6.70E-05	0.004491	-1	56	52	42
Potri.004	-1.94835	1.735985	2.73E-05	0.002187	-1	34	107	52
Potri.004	-1.11312	2.045407	2.49E-05	0.002039	-1	98	62	52
Potri.004	0.591571	5.04312	8.71E-06	0.000862	1	394	303	330
Potri.004	1.233569	1.397149	1.83E-05	0.001581	1	19	20	19
Potri.004	-0.42303	4.986564	0.000685	0.026391	-1	543	439	433
Potri.004	0.504944	8.736081	8.86E-07	0.000132	1	4843	4387	4542
Potri.004	0.99788	4.709529	5.35E-05	0.003722	1	296	172	216
Potri.004	-0.77593	2.345836	0.000429	0.018455	-1	103	67	73
Potri.004	-0.36646	7.261809	0.001098	0.037536	-1	2193	2285	2250
Potri.004	-1.24339	4.841806	1.60E-08	4.57E-06	-1	421	628	502
Potri.004	0.372054	7.140819	0.000456	0.019428	1	1650	1566	1583
Potri.004	0.542924	4.659701	2.81E-05	0.002237	1	283	258	259
Potri.004	-0.63226	4.003632	1.93E-05	0.001652	-1	252	252	248
Potri.004	-0.96946	3.339124	9.85E-06	0.000946	-1	127	170	213
Potri.004	-0.39941	6.407688	0.000469	0.019826	-1	1353	1121	1296
Potri.004	-2.07942	3.413293	2.82E-22	1.52E-18	-1	213	241	203
Potri.005	0.739379	5.528423	4.85E-10	2.10E-07	1	454	450	442
Potri.005	0.488963	5.057097	0.000497	0.020517	1	400	339	341
Potri.005	-2.64211	-1.03449	0.000835	0.0309	-1	7	10	5
Potri.005	-0.60486	2.679938	0.001491	0.046207	-1	103	83	108
Potri.005	-2.58858	-0.05375	6.03E-06	0.000635	-1	11	24	18
Potri.005	0.494577	7.126896	6.61E-06	0.000684	1	1632	1479	1422
Potri.005	0.8859	2.579631	6.39E-06	0.000668	1	47	54	59
Potri.005	-0.53521	6.367033	3.70E-06	0.000426	-1	1241	1299	1258
Potri.005	-1.55181	2.523132	4.62E-08	1.10E-05	-1	92	122	108
Potri.005	-0.86009	4.118291	0.000547	0.022008	-1	224	365	269
Potri.005	-1.37263	0.384274	0.000688	0.026483	-1	20	26	18
Potri.005	-0.44271	4.27048	0.001195	0.039872	-1	312	250	300
Potri.005	-0.39338	5.782048	0.001197	0.039872	-1	952	748	742
Potri.005	0.95249	2.781292	2.76E-07	4.99E-05	1	69	47	64
Potri.005	-0.42442	7.614746	0.000176	0.009226	-1	3248	2702	2836
Potri.005	-0.7328	3.362914	0.001002	0.035217	-1	178	123	193
Potri.005	-0.49454	7.551986	4.72E-06	0.00052	-1	2884	2786	2887

Potri.005	-1.0059	1.18914	0.00094	0.033687	-1	37	29	44
Potri.005	-1.45525	3.45393	3.80E-08	9.42E-06	-1	170	234	208
Potri.005	-0.55581	4.206249	0.000386	0.017029	-1	308	260	283
Potri.005	0.794099	5.16942	3.57E-09	1.27E-06	1	394	325	309
Potri.005	0.901551	5.212703	2.27E-08	6.16E-06	1	376	373	259
Potri.005	-1.60457	2.129072	2.78E-08	7.36E-06	-1	108	71	68
Potri.005	0.361505	7.251505	0.001236	0.040569	1	1926	1649	1641
Potri.005	-1.30999	1.384681	4.56E-05	0.003312	-1	37	56	42
Potri.005	-0.46274	6.261908	0.001156	0.039048	-1	1124	1067	1269
Potri.005	0.539118	5.122583	3.11E-05	0.00244	1	446	308	357
Potri.005	0.606765	5.42366	5.81E-07	9.24E-05	1	476	403	448
Potri.005	0.562517	4.934894	4.78E-05	0.003438	1	306	349	303
Potri.005	-0.94076	1.870048	0.000408	0.017723	-1	47	63	68
Potri.005	-0.81174	2.05911	0.000321	0.014773	-1	76	61	62
Potri.005	0.538155	4.233637	0.000838	0.03095	1	178	201	214
Potri.005	-0.48778	4.206288	0.001188	0.039784	-1	311	224	301
Potri.005	-0.72692	3.806899	0.000199	0.010165	-1	214	227	230
Potri.005	0.415951	6.205676	0.000485	0.02021	1	780	819	860
Potri.005	-0.64177	5.302218	5.68E-05	0.003931	-1	771	471	640
Potri.005	0.411214	6.376942	0.00026	0.012614	1	1077	870	845
Potri.005	0.585568	8.338319	5.71E-09	1.89E-06	1	3585	3192	3338
Potri.005	-0.75999	3.214344	4.01E-05	0.002969	-1	158	141	148
Potri.005	-0.58965	7.501352	0.001395	0.044345	-1	4118	1912	2587
Potri.005	0.392352	7.730171	0.000236	0.011654	1	2525	2312	2334
Potri.005	-1.55039	1.260528	4.03E-07	6.90E-05	-1	44	48	37
Potri.006	-0.51823	4.102917	0.001444	0.045275	-1	326	197	264
Potri.006	-1.12007	3.374216	3.89E-07	6.71E-05	-1	233	117	198
Potri.006	0.48723	4.303926	0.001404	0.044478	1	228	187	224
Potri.006	-1.33382	0.308012	0.001074	0.037077	-1	26	20	14
Potri.006	0.939677	3.274996	1.31E-06	0.000181	1	77	103	75
Potri.006	-1.22662	2.908646	5.01E-08	1.17E-05	-1	160	94	148
Potri.006	-0.53989	3.958022	0.001327	0.042746	-1	267	249	196
Potri.006	0.409493	8.166672	0.000486	0.020243	1	3199	2888	3542
Potri.006	-0.78506	5.045792	4.71E-06	0.00052	-1	711	418	508
Potri.006	1.083573	7.480539	6.95E-13	5.86E-10	1	1782	1226	1487
Potri.006	-0.60873	3.688349	0.000459	0.019503	-1	189	215	194
Potri.006	-0.8525	2.942446	1.93E-05	0.001652	-1	111	127	138
Potri.006	0.380875	6.956897	0.001003	0.035217	1	1423	1256	1531
Potri.006	1.007919	1.670261	0.000233	0.011539	1	27	22	30
Potri.006	0.398711	8.035484	0.001092	0.037453	1	3401	2368	3108
Potri.006	-0.40875	6.091339	0.000277	0.013169	-1	1099	977	958
Potri.006	-2.06377	3.719631	2.63E-07	4.79E-05	-1	167	400	239
Potri.006	-0.80242	2.78556	1.26E-05	0.00116	-1	125	93	116
Potri.006	-0.50468	4.733937	0.000134	0.007472	-1	430	370	412
Potri.006	-1.12559	4.1793	2.02E-06	0.000256	-1	235	379	337
Potri.006	1.605001	1.794669	1.02E-06	0.000149	1	15	33	16
Potri.006	1.208376	6.277807	3.97E-17	7.54E-14	1	694	473	669
Potri.006	0.497026	5.916648	0.000128	0.007229	1	604	717	624
Potri.006	-4.00124	-1.07632	3.10E-05	0.002436	-1	12	6	5
Potri.006	0.497241	5.719551	2.85E-05	0.002266	1	587	575	540
Potri.006	0.71698	3.098252	6.83E-05	0.004551	1	82	78	89
Potri.006	0.500677	5.221102	2.58E-05	0.002087	1	432	365	407
Potri.006	0.350799	8.837468	0.000775	0.029208	1	5253	5191	5236
Potri.006	1.904007	-0.38259	0.000178	0.00931	1	5	3	2

Potri.006	0.377252	7.827916	0.000469	0.019828	1	2925	2270	2548
Potri.006	-0.87064	3.504264	2.47E-06	0.000306	-1	204	176	184
Potri.006	-0.39348	7.403529	0.000294	0.013817	-1	2488	2384	2620
Potri.006	-0.69881	2.541187	0.00162	0.049164	-1	99	93	81
Potri.006	-0.70617	5.461544	7.40E-05	0.004815	-1	727	637	761
Potri.006	0.668007	6.379124	1.63E-05	0.001437	1	857	983	663
Potri.006	0.641397	5.397664	2.47E-06	0.000306	1	391	444	443
Potri.006	0.911964	2.512193	0.000142	0.00784	1	51	37	63
Potri.006	-1.11863	1.472404	0.001506	0.04657	-1	26	57	55
Potri.006	-0.38945	8.085736	0.000235	0.011615	-1	4050	4065	3896
Potri.006	0.437533	6.090905	0.000729	0.027736	1	925	638	708
Potri.006	0.680397	2.872806	0.001522	0.046894	1	64	91	60
Potri.006	-0.56201	3.801044	0.000274	0.013072	-1	256	206	181
Potri.006	-0.43383	5.592608	0.000152	0.008207	-1	756	715	687
Potri.006	-0.67645	6.036515	9.22E-09	2.77E-06	-1	1165	1040	945
Potri.006	-3.67759	0.815196	1.14E-13	1.11E-10	-1	44	47	23
Potri.006	-3.87797	3.737086	7.49E-37	3.22E-32	-1	489	244	234
Potri.006	0.680814	7.571514	8.79E-09	2.70E-06	1	1955	1659	2093
Potri.006	-0.92868	2.748867	2.22E-05	0.001871	-1	103	113	118
Potri.006	-2.33619	1.504841	2.51E-05	0.002045	-1	67	68	38
Potri.006	0.759921	4.926295	1.55E-06	0.000206	1	259	342	273
Potri.007	-0.4826	6.227142	0.000159	0.008484	-1	1033	1145	1211
Potri.007	-1.79363	3.332394	1.58E-14	1.79E-11	-1	192	220	184
Potri.007	-0.47456	4.889154	0.000606	0.023849	-1	486	451	402
Potri.007	0.547159	7.837176	2.36E-07	4.41E-05	1	2701	2127	2447
Potri.007	-1.37689	1.109266	9.03E-06	0.000888	-1	45	31	36
Potri.007	-0.66512	4.439421	0.00057	0.022728	-1	351	386	292
Potri.007	-0.4995	8.251177	6.98E-05	0.004642	-1	4527	4769	4601
Potri.007	-0.9743	4.291315	3.99E-05	0.002968	-1	270	405	321
Potri.007	0.667056	2.626518	0.000905	0.032817	1	75	48	60
Potri.007	-0.5271	4.118495	0.000104	0.006177	-1	280	262	251
Potri.007	-0.97186	6.028766	1.34E-05	0.001208	-1	845	1342	1147
Potri.007	-2.20053	0.575166	4.87E-07	8.02E-05	-1	18	32	34
Potri.007	0.825414	2.160488	0.000365	0.01624	1	38	35	49
Potri.007	-0.52221	4.910651	3.29E-05	0.002546	-1	474	418	485
Potri.007	-0.56334	5.786903	0.000153	0.008254	-1	801	1009	742
Potri.007	-1.42187	3.865865	8.54E-11	4.46E-08	-1	239	322	252
Potri.007	-0.50417	4.266085	0.001179	0.039588	-1	327	277	271
Potri.007	-1.02564	2.880539	1.45E-08	4.20E-06	-1	132	120	124
Potri.007	-1.21678	3.316892	1.04E-08	3.12E-06	-1	158	210	163
Potri.007	-0.53861	9.579096	9.64E-07	0.000142	-1	11803	11890	11630
Potri.007	-0.90591	2.168169	0.0009	0.032764	-1	83	80	57
Potri.007	-0.40551	6.00418	0.000825	0.030602	-1	944	1025	874
Potri.007	2.563311	-0.51199	8.78E-05	0.005435	1	2	2	2
Potri.007	0.376592	6.647199	0.000795	0.029742	1	1318	1040	1057
Potri.007	-1.17343	4.510188	1.79E-08	5.05E-06	-1	326	468	419
Potri.007	-0.59394	3.006476	0.000501	0.020621	-1	125	127	117
Potri.007	-0.43665	5.151958	0.000274	0.013082	-1	576	511	504
Potri.007	-0.63465	3.967555	6.46E-06	0.000673	-1	248	250	236
Potri.008	-0.6071	6.705963	3.01E-08	7.84E-06	-1	1827	1606	1491
Potri.008	-0.44044	7.807973	7.32E-05	0.004783	-1	3740	2945	3414
Potri.008	1.321274	1.819899	5.29E-05	0.003691	1	32	14	30
Potri.008	-1.67363	2.282093	1.42E-11	8.22E-09	-1	86	92	99
Potri.008	0.353074	7.892937	0.001375	0.043948	1	2667	2820	2643

Potri.008	-0.57658	3.140712	0.001028	0.035839	-1	140	141	123
Potri.008	-1.16406	3.736152	1.53E-07	3.11E-05	-1	191	288	225
Potri.008	0.330655	8.480291	0.001294	0.041958	1	4608	3792	3985
Potri.008	0.610595	4.406739	6.16E-06	0.000647	1	218	229	204
Potri.008	-0.78517	2.915856	7.13E-05	0.004712	-1	141	106	118
Potri.008	0.468141	6.239946	0.000119	0.006804	1	845	840	786
Potri.008	-0.65809	8.914153	3.48E-05	0.002637	-1	8203	7057	7824
Potri.008	0.585206	7.249599	2.46E-07	4.56E-05	1	1680	1632	1439
Potri.008	-0.4338	7.062808	0.000226	0.011225	-1	1946	2155	1875
Potri.008	-0.5279	6.416613	2.08E-05	0.001765	-1	1319	1430	1175
Potri.008	-0.63917	6.461415	8.04E-08	1.76E-05	-1	1310	1386	1474
Potri.008	-0.53798	6.877833	2.00E-06	0.000255	-1	1796	1744	1884
Potri.008	0.707553	4.755209	6.88E-06	0.000704	1	283	208	308
Potri.008	-1.73518	0.398686	0.000229	0.011386	-1	25	26	18
Potri.008	-0.63263	5.733476	1.80E-07	3.50E-05	-1	868	845	803
Potri.008	0.856411	4.515398	9.19E-09	2.77E-06	1	197	206	228
Potri.008	-0.65897	2.992311	0.000424	0.018302	-1	115	139	117
Potri.008	-3.10096	1.456521	5.25E-12	3.27E-09	-1	87	64	28
Potri.008	0.53808	3.95444	0.000337	0.015298	1	183	130	178
Potri.008	-1.42306	2.767864	0.000112	0.006512	-1	70	180	122
Potri.008	0.830599	3.05757	2.02E-06	0.000256	1	90	73	68
Potri.008	0.776973	10.20572	4.96E-08	1.16E-05	1	13053	11655	9380
Potri.008	0.521554	5.574727	0.000157	0.008405	1	573	405	552
Potri.008	0.466466	5.250619	0.00041	0.017803	1	387	453	400
Potri.008	-0.44543	6.491986	0.000104	0.006159	-1	1521	1256	1280
Potri.008	0.586247	6.374797	0.000472	0.019883	1	867	683	1039
Potri.008	-0.51994	4.86078	0.001204	0.039955	-1	556	435	345
Potri.008	-1.29373	0.757237	0.000915	0.033175	-1	20	36	28
Potri.008	0.563573	6.869962	2.12E-05	0.001794	1	1141	1351	1176
Potri.008	-0.9154	4.667412	7.54E-10	3.11E-07	-1	427	435	423
Potri.008	-0.64399	4.477002	0.000238	0.011732	-1	434	241	384
Potri.008	-0.92918	1.548146	0.001262	0.041153	-1	48	35	58
Potri.008	0.710965	5.00379	3.15E-08	8.00E-06	1	307	330	308
Potri.008	-0.63895	3.954555	4.67E-05	0.003371	-1	247	253	228
Potri.008	0.576597	3.757658	0.000325	0.014903	1	162	138	121
Potri.008	-0.48234	4.425752	0.00032	0.014757	-1	371	295	307
Potri.008	0.796616	6.741656	6.88E-08	1.55E-05	1	1010	1120	914
Potri.008	-0.69611	5.981349	4.88E-06	0.000534	-1	1285	779	1002
Potri.008	0.576804	3.881871	0.000605	0.023827	1	162	162	134
Potri.008	0.590781	2.930927	0.000864	0.031761	1	72	80	81
Potri.009	0.496155	5.508836	8.83E-05	0.00545	1	465	523	479
Potri.009	-0.59484	6.413811	4.77E-07	7.89E-05	-1	1451	1258	1295
Potri.009	-0.74952	2.184992	0.000923	0.033266	-1	72	74	68
Potri.009	-0.49926	4.815857	6.18E-05	0.004211	-1	426	410	443
Potri.009	-0.56398	7.197263	1.15E-06	0.000165	-1	2148	2334	2325
Potri.009	0.709677	4.219195	9.52E-05	0.005802	1	177	149	222
Potri.009	-2.23261	2.770109	2.49E-15	3.35E-12	-1	131	169	124
Potri.009	0.578482	3.893613	6.69E-05	0.004491	1	179	132	152
Potri.009	-0.39685	5.447107	0.000997	0.035168	-1	722	573	639
Potri.009	-1.114	6.062991	6.59E-08	1.51E-05	-1	949	1380	1202
Potri.009	0.632914	5.404899	2.19E-06	0.000277	1	482	390	425
Potri.009	-2.21168	0.353832	2.65E-06	0.000326	-1	23	17	31
Potri.009	-3.61904	1.269807	4.07E-13	3.72E-10	-1	28	72	59
Potri.009	-1.07793	2.978093	1.72E-05	0.001501	-1	108	170	127

Potri.009	-0.37531	6.400678	0.001517	0.046821	-1	1481	1114	1142
Potri.009	-0.99866	4.873567	4.33E-09	1.47E-06	-1	473	499	539
Potri.009	-0.60024	6.418584	9.11E-06	0.000892	-1	1352	1448	1210
Potri.009	0.540768	6.421683	2.46E-06	0.000306	1	998	811	921
Potri.009	1.303156	4.166692	1.88E-16	3.23E-13	1	135	130	137
Potri.009	0.885876	3.92364	6.04E-05	0.004138	1	108	162	140
Potri.009	-0.56834	5.525684	4.11E-05	0.003026	-1	683	761	690
Potri.009	0.512772	5.209402	0.000272	0.013032	1	404	446	335
Potri.009	-0.66464	3.301246	0.000124	0.007071	-1	155	161	147
Potri.009	1.589317	4.583169	1.62E-13	1.54E-10	1	183	170	114
Potri.009	0.335679	6.649222	0.001393	0.044325	1	1223	1094	1147
Potri.009	-0.70447	3.262482	0.000196	0.010059	-1	192	133	133
Potri.009	0.428868	7.699385	9.61E-05	0.005819	1	2388	2304	2221
Potri.009	0.731245	6.099768	2.23E-09	8.55E-07	1	770	580	668
Potri.009	-0.62437	6.029115	1.55E-08	4.47E-06	-1	1078	1024	983
Potri.009	-0.7956	2.217801	0.000284	0.013415	-1	80	70	72
Potri.009	0.426847	7.105002	0.000452	0.019326	1	1729	1340	1529
Potri.009	-2.47474	3.388679	3.68E-17	7.53E-14	-1	195	295	184
Potri.009	-0.7391	2.855223	0.000525	0.021343	-1	96	135	112
Potri.009	0.762583	3.477223	2.36E-06	0.000295	1	112	107	100
Potri.009	0.532368	4.381339	7.94E-05	0.005072	1	236	203	223
Potri.009	-0.74618	3.219596	0.001096	0.037523	-1	193	110	147
Potri.010	-0.49043	5.414903	5.30E-05	0.003693	-1	763	565	619
Potri.010	0.444224	5.628315	0.000135	0.007472	1	613	537	486
Potri.010	0.368176	6.211808	0.001392	0.044325	1	812	856	849
Potri.010	-0.77616	2.012043	0.001211	0.040141	-1	81	59	51
Potri.010	1.020813	1.209087	0.0012	0.039925	1	24	12	20
Potri.010	-0.59619	4.666745	8.67E-06	0.000862	-1	434	380	373
Potri.010	0.771331	3.946148	4.57E-07	7.58E-05	1	162	135	145
Potri.010	-3.05849	1.666163	1.53E-20	6.55E-17	-1	69	81	57
Potri.010	-0.52803	6.416446	3.42E-05	0.002606	-1	1402	1371	1159
Potri.010	0.984428	2.733993	5.31E-06	0.000574	1	76	44	52
Potri.010	0.816288	2.443342	0.001096	0.037523	1	65	28	58
Potri.010	-0.66743	2.821807	0.000327	0.014967	-1	105	102	123
Potri.010	-0.90361	1.610713	0.00141	0.044624	-1	59	46	42
Potri.010	-0.58436	3.404225	0.000434	0.018645	-1	157	161	169
Potri.010	-0.80785	3.451392	4.80E-06	0.000527	-1	188	157	190
Potri.010	0.492235	4.724016	0.001328	0.042746	1	241	304	304
Potri.010	-0.6309	3.704769	0.000127	0.00719	-1	213	212	185
Potri.010	-1.74895	0.262042	2.47E-05	0.002025	-1	22	20	20
Potri.010	-1.39334	0.095728	0.001351	0.043345	-1	15	21	15
Potri.010	-1.21689	4.890178	5.22E-06	0.000567	-1	363	654	573
Potri.010	0.417902	6.592317	0.000222	0.011136	1	1043	1087	1085
Potri.010	-0.59125	5.402578	0.000663	0.025736	-1	587	826	552
Potri.010	2.173831	1.657517	1.75E-12	1.34E-09	1	18	13	12
Potri.010	0.417242	5.986752	0.00034	0.015371	1	713	737	664
Potri.010	-0.40841	5.408198	0.000931	0.033465	-1	639	635	608
Potri.010	-4.64696	-0.63094	1.41E-07	2.88E-05	-1	13	17	6
Potri.010	0.708616	4.89776	3.12E-06	0.000371	1	362	264	259
Potri.010	0.599384	3.015242	0.000268	0.012871	1	86	76	85
Potri.010	-0.84061	4.070334	6.48E-07	0.000102	-1	314	219	302
Potri.010	-0.70568	6.412507	7.30E-05	0.004783	-1	1009	1386	1683
Potri.010	-0.54821	6.453177	5.66E-06	0.000608	-1	1271	1409	1362
Potri.010	0.655169	4.425667	1.62E-06	0.000213	1	243	181	226

Potri.010	-0.57923	5.471732	2.01E-06	0.000256	-1	816	611	650
Potri.010	-0.40018	5.627239	0.001069	0.036992	-1	859	640	699
Potri.010	-0.66664	8.025793	0.000152	0.008207	-1	3827	4425	4174
Potri.010	-1.31428	4.374748	1.47E-09	5.81E-07	-1	497	232	425
Potri.010	-1.18662	4.602913	2.32E-07	4.36E-05	-1	311	493	491
Potri.010	-0.61436	5.306756	5.79E-06	0.000617	-1	650	623	588
Potri.010	-1.25987	1.895245	1.16E-05	0.001082	-1	48	69	77
Potri.010	-0.99277	3.842518	5.85E-08	1.34E-05	-1	212	267	253
Potri.010	-0.48642	5.948115	0.001087	0.03734	-1	795	1027	966
Potri.010	-0.84388	2.806642	4.26E-06	0.000477	-1	124	113	105
Potri.010	-0.38866	6.235802	0.000849	0.031301	-1	1326	985	1035
Potri.010	-1.73882	0.324406	7.02E-05	0.004661	-1	19	16	30
Potri.010	-0.41868	4.543823	0.00123	0.040439	-1	349	324	361
Potri.011	0.612897	4.215865	0.000324	0.014879	1	159	204	204
Potri.011	-0.92493	2.100934	0.000181	0.009403	-1	63	60	87
Potri.011	-0.87764	3.08206	9.92E-06	0.000947	-1	177	120	124
Potri.011	-0.51258	4.120704	0.000566	0.022628	-1	255	270	264
Potri.011	-0.9941	2.614251	3.21E-05	0.002498	-1	141	72	98
Potri.011	-1.04649	1.101579	0.000368	0.016369	-1	38	34	32
Potri.011	0.566079	6.106496	4.26E-06	0.000477	1	844	632	699
Potri.011	-0.74288	3.111409	0.000147	0.008053	-1	176	107	133
Potri.011	0.842869	3.023052	4.88E-05	0.003482	1	66	76	81
Potri.011	0.948361	3.224493	2.35E-06	0.000295	1	74	103	68
Potri.011	0.553241	4.925446	0.000904	0.032814	1	293	259	404
Potri.011	1.057643	1.163375	0.000252	0.012264	1	15	22	16
Potri.011	-1.1034	2.607957	1.43E-05	0.00128	-1	77	118	118
Potri.011	0.765219	2.509178	0.001441	0.045255	1	64	64	33
Potri.011	-0.65298	4.073855	0.00018	0.009396	-1	359	210	233
Potri.011	-0.49131	5.873835	1.16E-05	0.001082	-1	964	873	834
Potri.011	-3.76003	0.873483	7.02E-12	4.31E-09	-1	24	60	35
Potri.011	0.603194	4.416322	3.03E-06	0.000363	1	239	211	209
Potri.011	0.544633	4.000386	0.000254	0.012336	1	157	178	168
Potri.012	-0.3932	10.06187	8.16E-05	0.00521	-1	16456	15243	15695
Potri.012	-0.88689	3.038988	4.51E-06	0.000501	-1	123	144	139
Potri.012	-0.64652	6.521623	0.000458	0.019503	-1	2082	973	1374
Potri.012	-0.49605	4.786454	8.30E-05	0.005247	-1	420	403	429
Potri.012	1.274614	1.020006	0.000108	0.006326	1	15	19	9
Potri.012	-1.84566	2.482419	1.87E-09	7.23E-07	-1	99	133	96
Potri.012	-1.08738	6.406832	4.89E-05	0.003483	-1	988	1909	1539
Potri.012	0.621414	3.416599	8.43E-05	0.005288	1	117	92	116
Potri.012	-0.75041	7.573216	2.96E-09	1.09E-06	-1	3864	2522	3001
Potri.012	0.353265	7.081593	0.001038	0.036167	1	1568	1521	1548
Potri.012	0.574282	5.438353	7.31E-05	0.004783	1	446	494	414
Potri.012	0.604393	5.414095	2.32E-05	0.001936	1	400	490	422
Potri.012	-0.46393	5.302108	0.001627	0.049307	-1	754	496	541
Potri.012	-1.00703	2.186514	0.000483	0.020161	-1	56	67	104
Potri.012	0.50745	6.528601	1.74E-05	0.001518	1	1055	923	999
Potri.012	0.632683	6.334907	5.62E-07	9.03E-05	1	786	884	791
Potri.012	-0.79176	2.982573	5.49E-06	0.000591	-1	144	120	119
Potri.012	1.052703	1.470458	0.001125	0.038141	1	25	18	24
Potri.012	0.510321	6.134953	3.50E-05	0.002643	1	714	759	781
Potri.012	1.829029	0.831006	1.28E-07	2.64E-05	1	8	11	9
Potri.012	-0.60049	7.625639	3.97E-08	9.74E-06	-1	3178	2980	3125
Potri.012	-1.14766	5.867865	5.54E-16	7.93E-13	-1	1132	1044	958

Potri.013	-0.5108	3.804479	0.00117	0.039407	-1	260	196	180
Potri.013	0.474356	6.529862	0.000833	0.03086	1	955	1067	985
Potri.013	-0.8561	4.916857	6.48E-05	0.004379	-1	570	526	417
Potri.013	0.463193	4.669728	0.000592	0.023433	1	334	257	244
Potri.013	1.606807	0.119639	0.000226	0.011225	1	5	7	6
Potri.013	-0.45573	7.946559	8.80E-05	0.00544	-1	4244	3099	3838
Potri.013	-0.42816	5.967918	0.000182	0.009439	-1	1052	882	870
Potri.013	0.396749	6.288164	0.000347	0.015566	1	911	885	834
Potri.013	-0.74385	4.10534	1.32E-05	0.001196	-1	363	257	218
Potri.013	0.595917	3.251936	0.000925	0.03329	1	100	96	96
Potri.013	0.53875	3.737291	0.000538	0.021747	1	139	145	136
Potri.013	0.453424	7.431134	7.69E-05	0.004947	1	2138	1788	1775
Potri.013	-0.84192	5.68138	2.82E-10	1.35E-07	-1	989	824	758
Potri.013	0.531919	4.453812	0.001578	0.048201	1	285	166	249
Potri.013	-1.19111	0.950472	0.000478	0.02004	-1	42	21	33
Potri.013	0.407173	5.808473	0.000956	0.034155	1	602	640	631
Potri.013	0.798832	5.157561	8.37E-06	0.000836	1	299	391	319
Potri.013	-0.97462	4.996132	9.27E-06	0.000903	-1	592	565	486
Potri.013	-0.69383	6.827092	0.000165	0.00871	-1	1780	1738	1944
Potri.013	-0.60348	5.364709	3.47E-05	0.002637	-1	560	730	631
Potri.013	1.17666	2.483799	5.41E-09	1.80E-06	1	47	49	35
Potri.013	-1.11286	1.819942	0.000417	0.018015	-1	60	60	59
Potri.013	1.429892	3.453524	3.40E-08	8.54E-06	1	55	115	57
Potri.013	-0.46587	6.037852	0.001117	0.037942	-1	1039	1012	917
Potri.013	-0.3821	7.79998	0.000816	0.030315	-1	3628	3013	3224
Potri.013	0.534304	5.201606	1.69E-05	0.001485	1	437	348	388
Potri.013	-1.02506	2.14368	1.89E-06	0.000244	-1	79	76	67
Potri.013	-1.5755	0.146643	0.000322	0.014773	-1	21	17	17
Potri.013	-0.69388	3.145737	4.65E-05	0.003371	-1	155	136	128
Potri.014	0.716847	2.594026	0.000968	0.034471	1	70	46	59
Potri.014	0.669176	4.550684	1.38E-05	0.001247	1	266	217	222
Potri.014	0.781881	6.229861	0.000157	0.008405	1	510	893	725
Potri.014	1.224587	3.60906	3.58E-07	6.33E-05	1	58	102	120
Potri.014	0.709614	3.013388	4.07E-05	0.003004	1	74	84	77
Potri.014	-0.76166	3.881969	0.000397	0.017311	-1	325	160	237
Potri.014	0.786005	2.384515	0.00015	0.008156	1	52	37	57
Potri.014	0.537689	5.836482	0.000241	0.011806	1	629	521	668
Potri.014	0.431059	5.093975	0.000923	0.033266	1	443	346	347
Potri.014	-0.61413	4.93841	0.000472	0.019883	-1	552	421	472
Potri.014	-1.11171	3.82359	1.76E-07	3.43E-05	-1	219	275	248
Potri.014	-0.4238	6.60115	0.000113	0.006556	-1	1451	1454	1426
Potri.014	-1.44014	2.08857	3.76E-09	1.32E-06	-1	78	65	89
Potri.014	-2.04707	-0.17839	0.000108	0.006338	-1	12	22	11
Potri.014	-0.48258	4.585692	0.000581	0.02309	-1	360	354	370
Potri.014	-0.47088	4.714936	0.000222	0.011131	-1	422	358	405
Potri.014	-0.97808	4.548095	1.74E-10	8.70E-08	-1	378	417	403
Potri.014	-0.61616	3.453228	0.001166	0.039374	-1	147	187	173
Potri.014	-1.48352	2.996196	8.04E-08	1.76E-05	-1	107	183	154
Potri.014	-1.31084	2.194533	1.10E-05	0.00103	-1	63	108	72
Potri.014	-1.21168	1.508555	5.98E-05	0.004113	-1	37	48	60
Potri.014	0.98539	2.285671	2.94E-05	0.002319	1	40	49	35
Potri.014	1.215104	4.779126	4.30E-09	1.47E-06	1	155	202	281
Potri.014	0.825607	3.090588	1.20E-06	0.000171	1	73	79	84
Potri.014	-0.67851	6.054964	1.33E-06	0.000182	-1	1374	913	925

Potri.014	1.805943	4.036965	2.19E-16	3.62E-13	1	84	108	90
Potri.014	-1.34138	5.469652	2.29E-13	2.14E-10	-1	1109	565	821
Potri.014	-0.84672	2.541504	5.15E-05	0.003629	-1	111	77	96
Potri.014	0.454242	4.609343	0.001311	0.04237	1	242	294	261
Potri.014	0.715266	2.353442	0.00055	0.022035	1	51	50	46
Potri.014	-1.20073	1.532929	1.08E-05	0.001015	-1	54	41	53
Potri.014	0.560526	5.004431	1.48E-05	0.001317	1	343	310	356
Potri.014	0.572474	4.379669	9.93E-05	0.005981	1	268	195	190
Potri.014	-0.48756	4.974276	0.000556	0.022247	-1	538	438	453
Potri.014	-1.09296	3.211246	3.08E-08	7.87E-06	-1	187	117	180
Potri.014	0.499522	6.38417	0.00022	0.011063	1	892	1020	780
Potri.014	0.339452	7.34508	0.001546	0.047352	1	1921	1897	1780
Potri.014	-1.05836	3.301683	1.79E-06	0.000233	-1	148	186	174
Potri.014	-1.11794	1.287278	0.000287	0.013516	-1	35	40	46
Potri.015	0.785063	2.410629	0.00122	0.040267	1	54	44	51
Potri.015	-0.91693	2.963801	1.21E-05	0.001115	-1	110	156	121
Potri.015	-1.93473	2.126491	2.45E-12	1.81E-09	-1	72	106	79
Potri.015	-1.31197	1.961807	8.35E-05	0.005268	-1	42	89	74
Potri.015	-0.4636	4.287848	0.000757	0.028703	-1	319	260	299
Potri.015	-1.42592	1.101525	3.63E-06	0.000422	-1	35	43	34
Potri.015	-2.93066	-0.85263	5.19E-05	0.003652	-1	10	9	8
Potri.015	-0.44237	5.570131	0.000769	0.029031	-1	832	647	659
Potri.015	-1.26801	4.170743	2.60E-09	9.79E-07	-1	280	419	277
Potri.015	0.397551	5.119405	0.001244	0.040732	1	437	367	366
Potri.015	-0.46265	4.480355	0.000784	0.029428	-1	324	311	366
Potri.015	-0.65846	3.695195	0.000111	0.006489	-1	177	217	214
Potri.015	0.464953	4.5529	0.000633	0.024818	1	287	221	260
Potri.016	-0.72581	3.269722	0.001049	0.036462	-1	128	190	140
Potri.016	-0.75911	4.413281	7.63E-08	1.69E-05	-1	379	339	320
Potri.016	0.999797	3.444303	1.12E-07	2.34E-05	1	90	93	97
Potri.016	-0.6171	6.944742	2.49E-06	0.000308	-1	1936	1943	1928
Potri.016	-1.04324	3.040725	2.81E-05	0.002237	-1	123	164	134
Potri.016	-0.84362	2.400486	0.001269	0.041212	-1	71	85	99
Potri.016	0.545251	5.539262	8.19E-05	0.00521	1	564	443	471
Potri.016	0.419679	6.878467	0.000917	0.033207	1	1185	1406	1318
Potri.016	-0.38953	5.025612	0.001432	0.045063	-1	541	430	468
Potri.016	-0.69125	6.017547	3.20E-09	1.18E-06	-1	1009	1037	1063
Potri.016	-0.71134	5.909298	1.22E-06	0.000172	-1	1021	981	903
Potri.016	-0.76664	7.76737	7.59E-05	0.004905	-1	4343	3191	3237
Potri.016	-0.73962	2.807925	0.000709	0.027143	-1	99	137	96
Potri.016	-0.53141	5.084979	5.24E-05	0.003678	-1	510	507	539
Potri.016	-0.41361	7.785919	0.000262	0.01267	-1	3699	2840	3333
Potri.016	-0.45462	5.986484	0.001517	0.046821	-1	884	1060	899
Potri.016	-0.50465	5.0246	8.70E-05	0.005401	-1	511	514	457
Potri.016	0.388414	5.886369	0.000731	0.027803	1	691	627	679
Potri.017	-0.34837	8.335004	0.00161	0.048925	-1	4628	4818	4643
Potri.017	-1.32692	1.336388	0.001427	0.044997	-1	57	28	47
Potri.017	1.025984	1.838813	0.000217	0.010961	1	19	37	32
Potri.017	0.616913	4.967373	7.89E-06	0.000799	1	290	342	325
Potri.017	1.18499	3.018621	1.04E-05	0.000984	1	82	37	73
Potri.017	-1.77243	1.961314	2.27E-06	0.000286	-1	47	103	72
Potri.017	-1.91247	0.306669	3.14E-05	0.002451	-1	29	13	24
Potri.017	-0.88944	4.024208	2.65E-09	9.89E-07	-1	267	291	256
Potri.017	-0.65637	4.548705	8.08E-07	0.000123	-1	437	324	353

Potri.017	0.55476	5.181967	8.04E-06	0.000809	1	364	381	397
Potri.017	1.170851	2.481422	2.48E-08	6.69E-06	1	40	36	55
Potri.017	0.680839	3.950798	0.001181	0.039608	1	198	123	142
Potri.017	-0.94864	3.286415	3.52E-05	0.002659	-1	185	110	199
Potri.017	0.631297	3.020163	0.001215	0.040201	1	94	71	80
Potri.017	-1.45618	1.31499	7.39E-07	0.000115	-1	41	50	41
Potri.017	0.804246	7.618499	8.10E-13	6.69E-10	1	2000	1630	1966
Potri.017	-0.67689	5.511981	9.21E-07	0.000137	-1	861	650	682
Potri.017	-0.91837	1.99254	6.33E-05	0.004298	-1	63	67	64
Potri.018	0.531021	3.866443	0.00014	0.007747	1	162	145	155
Potri.018	-2.22333	2.191267	1.36E-17	3.25E-14	-1	84	93	103
Potri.018	-1.66886	0.130396	0.000123	0.006997	-1	15	19	21
Potri.018	-4.34427	1.948238	6.85E-14	6.84E-11	-1	126	27	120
Potri.018	-0.66843	4.561609	7.81E-05	0.004998	-1	315	441	360
Potri.018	0.358558	6.213251	0.001132	0.038344	1	881	782	873
Potri.018	0.835255	6.688023	0.000434	0.018645	1	615	1320	912
Potri.018	-0.42874	6.156778	0.000206	0.01047	-1	1069	1060	1057
Potri.018	-1.05274	2.751579	1.69E-05	0.001485	-1	106	134	104
Potri.018	0.642177	4.363848	5.08E-05	0.003597	1	203	220	200
Potri.018	-0.62701	3.209869	0.001386	0.044218	-1	116	153	159
Potri.018	1.299021	3.988258	1.81E-08	5.07E-06	1	118	109	128
Potri.018	0.479511	7.142851	2.46E-05	0.002024	1	1569	1445	1591
Potri.018	-0.32683	7.833673	0.001445	0.045275	-1	3410	3185	3310
Potri.018	0.632036	2.687348	0.000712	0.02722	1	64	65	64
Potri.018	0.545604	3.632107	0.000404	0.017592	1	158	118	115
Potri.018	-1.91472	0.450021	9.99E-06	0.000952	-1	36	15	23
Potri.018	-0.50297	4.535215	0.000121	0.006938	-1	410	331	316
Potri.018	-0.77088	2.652302	0.000475	0.019922	-1	96	123	81
Potri.018	-0.57368	4.755013	0.000122	0.006981	-1	534	332	396
Potri.018	0.532966	4.201472	0.001241	0.040668	1	182	231	168
Potri.019	-0.37564	6.969283	0.001018	0.035607	-1	1766	1857	1882
Potri.019	1.506338	4.324928	2.82E-23	1.73E-19	1	159	124	124
Potri.019	0.967293	2.176073	0.001203	0.03995	1	29	44	42
Potri.019	-2.0381	2.316408	2.81E-08	7.39E-06	-1	72	142	84
Potri.019	-2.38374	0.180286	4.19E-07	7.06E-05	-1	21	21	21
Potri.019	-1.27682	1.254077	4.52E-05	0.003296	-1	36	36	50
Potri.019	0.545945	5.258999	0.001201	0.03994	1	475	343	399
Potri.019	-0.63427	8.842316	5.45E-08	1.26E-05	-1	8676	6484	6748
Potri.019	-0.78849	3.422752	1.57E-05	0.001398	-1	216	137	171
Potri.019	-0.42078	7.496723	0.000999	0.0352	-1	3267	2199	2652
Potri.019	-0.68445	8.091765	2.18E-07	4.12E-05	-1	5460	3398	4369
Potri.019	-1.63289	0.441463	4.22E-05	0.003097	-1	18	24	28
Potri.019	-2.04492	3.680571	2.04E-08	5.69E-06	-1	216	377	193
Potri.019	-1.51747	3.171228	4.42E-12	2.92E-09	-1	144	194	169
Potri.019	-0.47819	5.243822	0.000543	0.021896	-1	715	472	539
Potri.019	-0.56209	4.969769	2.88E-05	0.002276	-1	466	510	471
Potri.019	-0.63282	4.850596	9.75E-06	0.000941	-1	506	389	470
Potri.019	-1.36685	1.397053	3.46E-06	0.000405	-1	45	56	37
Potri.019	-1.07574	4.440191	2.44E-12	1.81E-09	-1	469	338	338
Potri.019	-0.91412	6.396962	3.66E-10	1.67E-07	-1	1889	1124	1317
Potri.T01	0.682868	5.49821	1.67E-05	0.00147	1	530	406	421
Potri.T02	1.070686	2.31681	1.31E-06	0.000181	1	39	51	32
Potri.T05	-0.6433	6.326917	0.000102	0.006147	-1	1306	1336	1168
Potri.T05	-0.57638	6.323684	4.46E-05	0.003255	-1	1145	1393	1181

Potri.T07	-0.86985	3.387269	2.74E-08	7.31E-06	-1	198	155	167
Potri.T08	-0.39833	5.344357	0.000673	0.026003	-1	610	604	581
Potri.T09	0.590084	2.987081	0.000923	0.033266	1	86	85	72
Potri.T09	-3.52523	0.112361	4.62E-10	2.05E-07	-1	15	29	21
Potri.T10	1.031965	7.174474	1.38E-14	1.64E-11	1	1367	1346	994
Potri.T11	-0.86897	3.006554	0.000116	0.006644	-1	106	157	131
Potri.T11	-2.76475	2.736297	2.65E-28	2.27E-24	-1	151	159	128
Potri.T12	1.119137	4.327276	1.99E-14	2.19E-11	1	199	133	162
Potri.T13	-0.98467	1.763424	5.13E-05	0.003621	-1	56	51	60
Potri.T17	-5.00992	-1.65814	0.001266	0.041193	-1	2	7	3

q comparison.

LLJGY. M	LLJGY. N	LLJGY. O	F-R	logFC. y	logCPM. y	PValue. y	FDR. y	OX. WT. LBD
39	42	8	0	-1.32387	4.420061	0.001833	0.015165	-1
18	25	22	-2	1.125945	4.536711	6.93E-05	0.000873	1
18	31	47	0	1.631032	0.941618	1.21E-05	0.000183	1
2362	2219	2424	0	2.239473	3.747017	9.50E-19	7.89E-17	1
37	44	51	0	-1.29402	2.694702	4.22E-08	9.99E-07	-1
84	74	110	0	1.714864	0.354332	0.002829	0.022003	1
929	978	1160	0	1.810407	3.907885	1.50E-16	1.00E-14	1
141	151	163	2	-0.64358	2.467035	0.002666	0.02092	-1
674	602	613	2	-0.64966	4.652471	3.51E-06	5.89E-05	-1
1746	2058	2745	0	0.661495	5.961523	3.20E-09	8.97E-08	1
141	170	208	0	1.580581	2.480388	3.35E-12	1.38E-10	1
307	238	292	0	-0.77636	6.131472	5.36E-11	1.92E-09	-1
136	179	165	0	-0.44095	4.623355	0.001527	0.012985	-1
262	326	241	-2	1.189151	3.107414	3.27E-06	5.53E-05	1
69	73	61	0	-1.00234	5.270036	0.000224	0.002448	-1
90	62	64	0	-1.19399	3.541406	7.17E-06	0.000113	-1
522	617	981	0	1.055392	3.884361	7.65E-11	2.67E-09	1
217	245	274	2	-0.507	3.792504	0.00428	0.031244	-1
92	87	68	0	-1.1861	3.67093	3.67E-14	1.87E-12	-1
249	288	300	-2	0.411451	5.120698	0.000219	0.002401	1
688	587	574	0	-0.49734	6.461127	2.91E-08	7.09E-07	-1
68	111	96	2	-0.62463	3.016319	0.000589	0.00568	-1
159	143	146	0	-0.84334	5.174593	9.74E-05	0.001177	-1
343	413	359	0	-0.53912	6.84938	1.64E-07	3.52E-06	-1
361	349	348	0	0.659665	4.25239	3.84E-06	6.40E-05	1
299	262	489	0	3.550998	-0.80613	0.00024	0.002599	1
156	189	182	-2	0.448337	4.685058	0.002229	0.017928	1
1240	1298	1471	0	1.776111	4.892593	5.30E-16	3.38E-14	1
821	786	939	0	1.699455	4.338221	4.48E-13	2.05E-11	1
279	314	270	-2	0.480807	6.092066	5.97E-05	0.000763	1
1432	1320	1589	2	-2.04299	7.438249	1.11E-79	1.77E-76	-1
156	159	186	-2	0.530048	5.804562	0.00527	0.037089	1
10	13	15	0	-1.69533	2.324229	4.85E-13	2.21E-11	-1
1303	1179	1194	2	-0.49416	4.671015	0.001521	0.012959	-1
130	160	214	0	0.614026	4.104071	0.006424	0.043817	1
699	809	731	0	0.448992	4.666434	0.000106	0.001264	1
1662	1888	2142	0	1.157127	6.21347	1.11E-37	3.27E-35	1
2904	2788	2585	2	-0.24995	6.955303	0.007337	0.048903	-1
830	817	797	0	0.560728	4.662394	0.000105	0.001249	1
181	189	103	0	-1.28807	5.391702	4.69E-08	1.10E-06	-1
0	3	2	0	-1.47633	1.256833	3.17E-05	0.000438	-1
391	579	618	0	-0.6767	7.485159	4.54E-09	1.25E-07	-1
357	281	165	0	-1.20599	6.521961	8.79E-05	0.001079	-1
1343	1351	1331	0	0.333106	6.627611	9.39E-05	0.001141	1
223	317	385	0	2.115342	1.153443	9.25E-06	0.000142	1
369	335	325	0	1.386872	3.086039	7.28E-06	0.000114	1
133	153	209	2	-1.0524	2.021223	2.75E-05	0.000384	-1
125	158	147	0	-0.80221	6.324685	7.83E-14	3.86E-12	-1
182	198	195	0	0.956212	3.608688	9.50E-10	2.83E-08	1
306	328	342	0	-0.43357	4.546511	0.001297	0.01128	-1
573	564	622	0	-1.11792	5.931228	8.58E-29	1.47E-26	-1

225	289	298	0	-0.489	9.084197	0.003982	0.029413	-1
603	587	405	0	-0.70245	7.60916	0.003182	0.024349	-1
228	243	229	-2	0.33888	5.975893	0.000755	0.007054	1
74	87	88	-2	0.960827	2.237318	5.50E-05	0.000711	1
704	635	693	0	0.765876	4.479784	4.85E-09	1.32E-07	1
156	159	182	0	-0.45619	4.260514	0.001179	0.010397	-1
684	797	525	-2	2.262505	7.984614	#####	#####	1
140	127	145	2	-0.75926	2.482031	0.000188	0.002103	-1
314	295	369	2	-0.36228	4.363115	0.005361	0.037665	-1
6	7	10	-2	3.486352	3.263784	9.05E-24	1.09E-21	1
93	61	50	0	-1.02151	4.21126	5.36E-08	1.24E-06	-1
74	74	84	0	-0.8742	2.269699	0.001065	0.009545	-1
543	529	603	0	-1.11891	6.181175	4.32E-29	7.64E-27	-1
73	111	115	0	1.393231	2.805717	2.20E-07	4.60E-06	1
1686	1642	2024	2	-0.33279	6.043345	0.001048	0.009402	-1
36	42	13	0	-1.0762	4.088812	1.18E-05	0.000178	-1
5	0	1	0	-1.43977	0.81349	0.000225	0.002453	-1
896	864	920	0	0.319296	5.083432	0.003015	0.023256	1
18	20	6	0	-0.97262	2.765482	0.003653	0.027346	-1
49	56	54	0	-0.83369	2.616788	3.40E-05	0.000464	-1
87	107	83	0	-1.46238	3.830512	1.33E-19	1.16E-17	-1
59	50	58	0	-1.36397	3.370027	6.45E-14	3.22E-12	-1
312	346	331	0	1.332085	4.867344	8.96E-18	6.76E-16	1
1051	1089	1104	0	-0.26448	6.73447	0.002793	0.021765	-1
365	356	264	0	-0.52039	4.132051	0.000353	0.003628	-1
1575	1149	1227	0	1.360651	4.365871	2.40E-08	5.94E-07	1
6	8	4	0	-1.05798	2.901889	0.001113	0.00989	-1
146	143	153	0	-0.70261	6.881315	1.34E-07	2.91E-06	-1
1047	1215	1337	-2	0.377636	7.561883	1.82E-05	0.000266	1
28	63	87	0	0.683373	2.848627	0.000665	0.006302	1
438	440	509	2	-0.43464	5.072462	0.000113	0.00134	-1
745	748	691	0	-0.65275	6.502589	7.99E-12	3.14E-10	-1
1174	1200	1878	0	0.73628	6.449071	1.24E-08	3.20E-07	1
21	26	14	0	-1.6578	4.114317	2.01E-14	1.06E-12	-1
67	64	67	-2	1.12417	3.046789	4.90E-08	1.15E-06	1
561	608	664	2	-1.46595	5.231706	1.42E-32	3.18E-30	-1
173	163	169	0	-0.63554	4.507403	1.83E-07	3.88E-06	-1
84	80	73	-2	1.041456	3.392815	8.88E-07	1.67E-05	1
656	632	750	0	-0.90048	7.33163	7.93E-14	3.90E-12	-1
59	48	66	0	-1.60495	3.881544	2.49E-13	1.16E-11	-1
447	436	304	0	-0.61817	7.34613	0.003737	0.027885	-1
83	91	82	0	-0.82318	3.72981	3.12E-07	6.36E-06	-1
282	239	225	0	0.550679	3.373288	0.001592	0.013439	1
747	695	711	0	0.589064	4.988473	5.01E-06	8.13E-05	1
41	42	30	0	-0.6814	3.512781	0.004809	0.034452	-1
243	250	246	0	-0.46202	5.812512	3.90E-05	0.000524	-1
661	978	672	0	-0.266	7.018217	0.005624	0.039247	-1
2981	2309	2849	2	-1.26978	8.102981	4.13E-18	3.23E-16	-1
44	46	34	0	-0.71325	3.618393	5.18E-06	8.38E-05	-1
224	214	268	0	0.878073	2.576699	2.04E-05	0.000295	1
13	14	16	0	-1.72738	2.351605	9.65E-15	5.25E-13	-1
87	110	146	2	-0.64162	3.555089	0.000104	0.001239	-1
2236	2322	2493	0	0.701603	6.596691	3.62E-07	7.30E-06	1
17	12	9	0	-1.29131	1.873933	0.001265	0.011046	-1

65	87	65	0	-0.97031	3.128493	2.88E-06	4.92E-05	-1
1258	1142	1158	2	-0.38481	4.435552	0.004349	0.031663	-1
135	140	135	0	-1.23251	4.267373	7.51E-18	5.71E-16	-1
1392	1119	1438	2	-0.72777	5.016178	3.32E-05	0.000455	-1
1078	1283	1172	0	-0.26007	6.989957	0.006958	0.046795	-1
181	200	157	0	-0.69287	2.925752	0.001266	0.011049	-1
713	693	673	0	-0.76814	6.46297	6.41E-18	4.93E-16	-1
17	17	13	0	-1.33256	2.86156	2.37E-07	4.92E-06	-1
143	185	194	-2	0.378125	4.221501	0.006947	0.046754	1
95	96	173	2	-1.24777	4.059338	2.56E-11	9.46E-10	-1
78	78	106	0	1.479994	2.042203	2.01E-05	0.00029	1
299	267	306	2	-0.65832	3.82572	1.30E-05	0.000195	-1
139	96	91	0	2.909771	2.866399	5.94E-17	4.12E-15	1
2540	2041	2976	2	-1.70699	8.638716	1.69E-24	2.18E-22	-1
475	526	720	2	-1.23296	5.868262	1.27E-27	2.03E-25	-1
1860	1672	1483	0	0.2855	5.834724	0.003794	0.028252	1
250	280	411	0	0.786784	3.937823	0.000605	0.005806	1
80	114	82	0	-1.51835	2.728557	3.82E-14	1.95E-12	-1
254	262	185	0	-0.51101	4.811348	0.00012	0.001411	-1
1156	1134	1302	2	-0.2969	6.371479	0.002537	0.020044	-1
112	123	76	0	-0.98129	3.818476	3.77E-11	1.36E-09	-1
374	448	516	2	-0.62132	4.726511	2.62E-08	6.44E-07	-1
801	1129	1318	0	0.761509	5.472101	5.60E-08	1.30E-06	1
465	574	461	2	-0.4916	5.143505	0.000134	0.001558	-1
255	243	256	0	-0.59474	5.469743	2.53E-07	5.23E-06	-1
423	459	477	0	-0.5023	6.282206	9.42E-06	0.000144	-1
51	61	63	2	-1.59697	1.643718	3.35E-08	8.07E-07	-1
490	512	690	0	0.677403	3.973411	2.41E-06	4.18E-05	1
3	0	5	0	-1.71179	1.305226	2.73E-07	5.62E-06	-1
4048	4005	3278	0	0.304197	6.050836	0.005527	0.038664	1
7467	7625	8676	2	-0.77084	5.750535	2.04E-06	3.58E-05	-1
160	167	154	0	-0.56279	4.916756	0.000282	0.002983	-1
889	958	973	2	-0.87567	5.697523	5.68E-13	2.56E-11	-1
534	506	499	0	-0.70845	4.62852	1.93E-08	4.84E-07	-1
5	2	9	0	8.351434	1.414641	2.96E-13	1.37E-11	1
147	146	136	2	-0.51564	3.29682	0.004163	0.030526	-1
69	71	77	0	-0.49888	5.090164	4.55E-05	0.000601	-1
609	535	580	0	-0.81336	6.748292	3.65E-14	1.87E-12	-1
441	516	360	2	-0.46533	3.981172	0.000599	0.005757	-1
738	767	884	0	2.283199	1.702605	6.54E-10	2.01E-08	1
398	331	356	0	2.506836	1.3042	1.91E-10	6.34E-09	1
325	375	334	0	-0.55252	5.722264	0.000384	0.00392	-1
5	2	0	0	-1.03088	3.827687	0.00227	0.018211	-1
571	578	573	2	-0.28761	5.181156	0.006712	0.045442	-1
102	141	113	-2	1.223418	5.906738	6.46E-23	7.15E-21	1
500	394	553	0	2.28864	1.600582	4.25E-08	1.01E-06	1
103	123	165	0	-0.84438	6.294651	9.92E-05	0.001194	-1
279	260	329	2	-0.42269	4.759598	9.19E-05	0.001122	-1
54	49	45	0	-0.8119	4.432876	3.66E-06	6.12E-05	-1
4	3	14	0	-2.56639	0.891996	1.31E-10	4.44E-09	-1
2728	2890	2966	2	-0.46431	8.736486	6.89E-08	1.57E-06	-1
1103	1025	1139	2	-0.62031	4.00479	3.45E-05	0.00047	-1
112	144	91	-2	1.106512	1.987807	0.001421	0.012221	1
443	581	601	0	1.169388	2.497525	1.70E-05	0.000249	1

8002	8134	7351	0	0.286678	8.21192	0.000434	0.004354	1
685	728	745	-2	1.474972	6.702549	2.47E-50	1.54E-47	1
113	136	168	-2	1.974384	3.522898	7.23E-20	6.45E-18	1
72	90	58	-2	0.621464	3.615683	5.89E-05	0.000754	1
47	36	67	0	1.530548	2.355615	1.76E-06	3.12E-05	1
572	471	423	0	-0.97084	7.173382	0.000602	0.005785	-1
7	14	8	0	-0.97006	3.041521	0.006661	0.045171	-1
3637	3424	4259	0	-0.55371	9.697988	5.01E-08	1.17E-06	-1
126	152	119	0	1.553675	1.784951	3.95E-07	7.92E-06	1
242	153	208	0	1.898731	0.589307	1.68E-05	0.000246	1
9	1	2	0	-1.40342	2.91785	0.000774	0.007204	-1
1585	1390	1713	2	-1.48522	6.330142	2.65E-26	3.82E-24	-1
1561	1465	1433	0	1.058672	6.564319	1.50E-15	8.92E-14	1
85	76	49	0	-1.47378	5.463925	1.28E-10	4.34E-09	-1
49	54	65	-2	1.499877	2.748154	4.89E-08	1.14E-06	1
88	81	82	-2	1.753874	5.413202	1.97E-43	8.12E-41	1
78	108	84	-2	1.846666	4.65086	2.11E-35	5.62E-33	1
117	193	190	0	1.484325	2.897488	2.22E-11	8.27E-10	1
48	48	47	0	-1.11652	4.348499	3.70E-06	6.18E-05	-1
441	451	685	0	2.230507	0.241293	0.00613	0.042043	1
27	16	23	0	-5.49297	1.915923	1.62E-39	5.24E-37	-1
21	17	9	0	-2.24232	3.57558	8.87E-08	1.99E-06	-1
31	26	34	-2	2.436102	3.574788	1.07E-31	2.24E-29	1
422	448	582	0	0.865923	4.304383	2.27E-06	3.95E-05	1
32	40	57	0	2.925491	-0.66865	0.00387	0.028733	1
296	348	343	0	-0.4287	5.419218	0.000308	0.003222	-1
5979	6193	6116	2	-0.43477	8.360712	4.00E-06	6.64E-05	-1
296	317	676	0	1.121417	2.773171	0.003493	0.026313	1
45	47	40	0	-1.13819	2.087132	4.56E-06	7.46E-05	-1
1588	1672	1638	0	-0.8349	6.633631	2.28E-14	1.19E-12	-1
263	191	159	0	-1.01653	6.78282	4.49E-05	0.000595	-1
1755	1927	2155	0	0.389425	6.477804	0.000158	0.001802	1
369	327	396	2	-0.63865	5.276342	5.20E-05	0.000676	-1
161	150	143	0	-1.4021	3.590554	8.88E-18	6.72E-16	-1
76	83	87	0	-1.13974	5.2305	2.57E-07	5.29E-06	-1
873	924	874	-2	0.900983	7.149946	2.73E-23	3.12E-21	1
64	42	39	0	-1.64465	6.869811	1.75E-05	0.000256	-1
709	659	739	0	2.619794	3.696887	3.85E-22	3.99E-20	1
403	424	599	2	-0.29496	6.049602	0.002629	0.020683	-1
1	2	0	0	-1.88531	0.91779	1.04E-05	0.000159	-1
60	54	67	-2	0.579069	3.360519	0.000369	0.00378	1
4	3	1	0	-1.63407	3.093457	1.36E-15	8.17E-14	-1
2024	1847	2105	2	-0.28806	6.626441	0.002299	0.018407	-1
86	97	95	0	1.347237	0.476018	0.002534	0.020024	1
816	780	865	0	-1.72987	6.778062	1.65E-46	7.88E-44	-1
28	52	23	0	-1.20344	4.413616	1.07E-05	0.000162	-1
170	173	100	0	-1.16189	5.998022	5.43E-05	0.000704	-1
9	4	10	0	-1.26061	3.553481	3.13E-05	0.000432	-1
198	192	203	0	-0.50026	4.28193	0.000319	0.00332	-1
553	616	565	-2	0.85864	5.896276	4.30E-12	1.74E-10	1
103	113	110	0	1.471416	1.474173	0.000281	0.002976	1
1982	2199	1928	0	-1.22129	8.499375	4.43E-32	9.65E-30	-1
116	80	80	-2	0.468505	4.019791	0.000656	0.006223	1
1738	1822	2153	0	-0.61399	8.207769	5.15E-12	2.07E-10	-1

20	18	13	-2	0.694039	1.991337	0.004679	0.033706	1
94	71	43	0	-1.34628	5.569655	7.69E-06	0.00012	-1
165	147	232	0	-0.45093	5.398593	1.03E-05	0.000156	-1
528	480	663	0	1.76255	3.171968	1.94E-09	5.59E-08	1
530	506	736	0	1.60212	3.293423	9.07E-08	2.03E-06	1
26	34	15	-2	0.867274	3.787918	1.36E-05	0.000203	1
2130	2111	2011	0	1.04788	5.160181	1.68E-11	6.36E-10	1
22	11	18	0	-1.38048	2.509672	7.27E-05	0.000911	-1
863	793	688	0	-0.88895	6.395159	3.86E-14	1.97E-12	-1
469	523	514	0	3.013392	4.778719	1.67E-65	1.94E-62	1
651	576	663	0	0.886465	3.970053	9.55E-09	2.51E-07	1
443	463	421	2	-0.36459	6.050021	0.000423	0.004261	-1
29	34	24	0	-0.79999	2.904058	0.004692	0.033777	-1
28	42	36	-2	0.606052	3.658879	0.000336	0.003478	1
227	254	333	2	-0.87616	4.69507	3.52E-14	1.81E-12	-1
176	170	212	0	-0.8781	3.634949	4.94E-08	1.15E-06	-1
161	112	105	-2	0.52609	4.115414	0.000225	0.002459	1
959	983	1147	2	-0.40798	5.658246	0.002199	0.017722	-1
335	325	468	-2	0.489364	6.31642	6.35E-06	0.000101	1
1118	1108	1244	2	-0.29325	5.480802	0.006151	0.04214	-1
4510	4786	4921	0	0.334185	8.319695	3.44E-05	0.00047	1
97	80	69	0	-0.85915	3.971015	1.63E-06	2.91E-05	-1
1741	1617	1935	-2	2.100215	7.446902	3.23E-77	4.62E-74	1
2921	3004	2877	2	-0.35854	7.976971	2.07E-05	0.000298	-1
18	10	13	-2	0.596112	3.616308	0.000386	0.003933	1
163	165	184	-2	2.003795	5.341294	4.52E-60	4.22E-57	1
81	71	82	-2	2.488841	5.488593	8.10E-48	4.35E-45	1
308	275	252	0	0.520192	3.68476	0.003239	0.024726	1
9	6	7	-2	2.550998	0.754906	2.16E-07	4.53E-06	1
162	155	142	2	-0.9186	3.587501	5.82E-10	1.80E-08	-1
45	64	51	0	-1.2384	5.295516	8.95E-15	4.90E-13	-1
164	125	169	-2	0.649863	4.756052	3.59E-08	8.60E-07	1
3936	4107	3935	0	0.296727	7.4916	0.000569	0.005515	1
293	335	251	-2	1.486231	4.788492	7.44E-28	1.21E-25	1
2315	2815	3823	0	2.716613	5.336918	9.67E-47	4.72E-44	1
136	124	107	0	-0.41424	5.011508	8.32E-05	0.001026	-1
52	77	67	0	-0.65275	7.678889	0.000327	0.003396	-1
1707	1664	1764	0	3.866396	1.812111	1.55E-15	9.18E-14	1
58	36	55	0	0.844949	1.785162	0.001477	0.012636	1
3606	3514	3793	0	0.705302	5.983999	2.99E-09	8.42E-08	1
624	726	795	0	-1.58536	6.679576	6.12E-40	2.12E-37	-1
88	67	25	0	-1.11341	5.423299	0.000411	0.004157	-1
55	63	61	0	-0.81467	3.818989	2.32E-07	4.84E-06	-1
283	255	260	0	-0.56635	3.749714	0.002136	0.017293	-1
139	171	100	0	-1.23518	6.497577	2.33E-05	0.000331	-1
63	45	77	2	-2.80866	2.799947	4.11E-26	5.77E-24	-1
1216	1174	1586	0	0.829681	4.537182	0.000246	0.002655	1
859	818	905	2	-0.32829	6.05755	0.001766	0.014714	-1
0	0	1	-2	2.179146	-0.50287	0.002807	0.021865	1
675	817	762	2	-0.55544	6.069485	3.46E-05	0.000471	-1
113	148	123	0	0.846033	2.47351	8.47E-05	0.001041	1
533	503	558	0	0.488991	4.195293	0.000834	0.007689	1
6051	6007	6719	2	-0.37007	8.292816	1.26E-05	0.000189	-1
13	10	13	0	3.339379	1.090663	1.01E-14	5.44E-13	1

2856	3073	3487	0	0.416219	6.568715	5.86E-05	0.000752	1
110	103	74	-2	0.711906	2.910237	9.59E-05	0.001161	1
1642	1762	1958	0	-0.40927	7.45228	1.29E-05	0.000193	-1
49	67	41	0	-2.09372	4.151581	1.05E-31	2.22E-29	-1
485	425	299	-2	1.611688	6.630229	1.23E-31	2.57E-29	1
1348	1135	1241	2	-0.343	6.173106	0.00075	0.007013	-1
649	557	668	2	-0.34553	5.520626	0.001515	0.012913	-1
68	86	114	0	4.718835	3.209736	2.54E-35	6.72E-33	1
22	18	20	0	-0.84785	3.758031	0.000241	0.002609	-1
2746	2746	3122	0	-0.51847	8.930601	3.49E-08	8.38E-07	-1
869	891	1115	0	0.944129	5.247297	9.87E-05	0.001189	1
115	98	111	2	-2.17505	4.004231	1.69E-20	1.58E-18	-1
124	140	143	0	-0.75519	5.769681	2.03E-08	5.07E-07	-1
490	501	505	0	-0.91467	7.122616	2.84E-18	2.28E-16	-1
613	627	601	0	-0.71477	7.205283	5.73E-14	2.88E-12	-1
2	5	1	0	-1.36737	3.027252	1.06E-09	3.13E-08	-1
26	21	13	0	-1.55891	6.699681	2.03E-10	6.71E-09	-1
2534	2826	3239	0	1.539413	5.240028	5.88E-07	1.14E-05	1
60	63	41	0	-0.87682	4.75551	2.92E-11	1.07E-09	-1
20	11	0	0	-1.179	5.1338	0.00229	0.018345	-1
496	451	443	2	-0.60916	4.289325	5.26E-05	0.000683	-1
669	797	821	-2	0.528785	6.620911	4.82E-07	9.50E-06	1
71	53	36	0	-1.3707	5.784631	4.67E-06	7.62E-05	-1
326	296	277	-2	0.447803	5.159513	0.001045	0.009378	1
3103	3319	3522	0	0.702622	6.234356	1.09E-08	2.84E-07	1
16	14	10	0	-1.03822	3.548878	4.55E-05	0.000601	-1
242	209	153	0	-0.56961	4.172996	3.57E-05	0.000483	-1
3311	3030	2855	0	-0.77873	8.779513	1.91E-15	1.12E-13	-1
171	198	106	0	-1.02638	5.34798	2.57E-07	5.30E-06	-1
98	84	89	2	-0.61563	3.216911	0.002087	0.016946	-1
165	160	191	0	-0.30501	5.846626	0.005852	0.040501	-1
636	574	383	0	-0.89485	6.690301	0.000452	0.004524	-1
4	7	6	0	-1.83125	0.963933	2.34E-07	4.88E-06	-1
60	79	64	2	-1.5634	1.246857	2.53E-06	4.37E-05	-1
292	279	328	0	-0.43374	5.11533	0.000189	0.002107	-1
534	567	522	0	-0.89585	5.564457	5.24E-19	4.44E-17	-1
104	112	68	0	-1.37918	6.618521	2.25E-05	0.00032	-1
192	220	163	-2	1.62561	3.250928	3.79E-14	1.93E-12	1
58	48	67	0	-0.93447	5.292362	8.21E-05	0.001013	-1
83	71	60	0	-1.58357	6.095061	1.38E-07	2.99E-06	-1
7718	7589	7471	-2	0.660869	9.931051	2.90E-10	9.36E-09	1
23	52	35	0	-1.0346	3.569103	6.08E-06	9.71E-05	-1
638	649	731	0	-2.30938	7.006421	5.67E-74	7.61E-71	-1
15	5	15	0	5.417922	-0.90468	0.000191	0.002126	1
1355	1394	1387	2	-0.39667	5.441299	0.000198	0.002193	-1
210	154	140	0	-0.93903	4.519984	0.000524	0.005142	-1
78	74	77	0	-1.05881	4.396327	9.88E-16	6.02E-14	-1
361	379	359	0	-0.71618	5.051925	4.80E-11	1.72E-09	-1
134	146	164	-2	0.69615	4.31955	4.48E-06	7.33E-05	1
932	988	1109	0	-1.5404	7.125068	1.16E-32	2.64E-30	-1
2094	2227	2656	0	-0.44055	9.198353	8.32E-05	0.001026	-1
35	69	75	0	3.547631	2.244773	8.88E-24	1.07E-21	1
36	23	22	0	-1.43374	5.308609	3.57E-06	5.99E-05	-1
2963	3352	3453	0	0.3321	7.251417	0.000161	0.001835	1

87	71	96	0	-0.91347	4.237351	6.27E-12	2.50E-10	-1
106	112	77	0	-1.13081	5.027144	0.000535	0.005231	-1
4743	4834	4974	0	0.284244	7.871529	0.000723	0.006788	1
307	313	312	0	0.772524	2.313103	0.001323	0.011475	1
78	62	57	-2	0.603415	4.951279	9.97E-05	0.001199	1
1047	1153	999	2	-0.59656	5.920687	6.93E-09	1.85E-07	-1
5302	4723	3546	-2	0.392368	8.010486	0.005285	0.037172	1
2262	2170	2237	2	-0.35705	6.576223	0.000599	0.005757	-1
1320	1409	1429	0	-0.63386	7.388578	3.22E-14	1.65E-12	-1
826	882	845	0	-0.53713	7.222068	7.01E-07	1.34E-05	-1
773	852	895	0	-0.45707	7.050275	2.18E-05	0.000312	-1
1047	1246	1217	0	-0.40447	6.484785	1.24E-05	0.000186	-1
332	410	485	0	1.305213	2.76467	6.25E-05	0.000795	1
9	10	0	0	-1.0895	3.237796	0.000243	0.002627	-1
513	526	479	-2	0.408012	6.003454	2.67E-05	0.000373	1
372	370	328	2	-0.57512	4.235159	0.000101	0.001218	-1
63	81	77	0	-0.98927	3.350254	5.01E-09	1.36E-07	-1
7	7	5	0	-3.47375	4.130768	1.72E-21	1.72E-19	-1
208	225	234	0	1.270047	1.484	2.14E-05	0.000307	1
45	59	27	0	-1.60491	3.688623	5.92E-08	1.36E-06	-1
109	141	135	0	0.833027	1.466773	0.003918	0.029017	1
20509	16798	17000	0	4.086415	3.963698	3.59E-18	2.82E-16	1
643	753	653	0	0.625073	5.329009	1.44E-05	0.000214	1
495	514	606	0	0.32411	4.988307	0.002181	0.017604	1
820	891	1084	-2	0.616401	7.594507	8.25E-12	3.24E-10	1
1385	1179	1054	2	-0.6516	5.205553	8.02E-05	0.000993	-1
286	318	262	0	-1.08029	5.692906	7.28E-18	5.56E-16	-1
14	10	8	0	-1.80037	1.524696	7.09E-07	1.35E-05	-1
1673	1504	1933	2	-0.53431	5.274052	3.24E-07	6.58E-06	-1
200	251	187	0	-0.72062	6.725772	0.005263	0.037048	-1
211	204	215	0	-1.20147	3.2152	1.12E-06	2.07E-05	-1
24	27	18	0	-0.72743	4.865237	1.10E-05	0.000167	-1
489	455	508	0	0.852853	5.712707	2.93E-12	1.22E-10	1
134	170	134	0	-1.277	5.142723	6.20E-28	1.02E-25	-1
193	214	179	0	0.570215	3.499817	0.001328	0.011506	1
218	220	212	0	-0.61128	5.578583	0.000369	0.00378	-1
1857	1621	1460	2	-0.54957	5.534574	7.13E-07	1.36E-05	-1
495	558	716	0	-0.28588	7.58728	0.003117	0.02393	-1
175	198	271	0	0.600417	3.509828	0.000382	0.0039	1
98	114	118	0	0.485416	3.910049	0.000346	0.003569	1
575	654	721	0	0.407193	4.906693	0.000226	0.002463	1
772	921	785	0	-0.97926	5.628743	3.52E-18	2.76E-16	-1
39	48	32	0	-1.16247	4.012986	4.32E-05	0.000574	-1
267	288	294	0	-0.86234	5.817405	1.30E-08	3.35E-07	-1
1335	1421	1581	0	-0.85449	8.039537	1.07E-23	1.27E-21	-1
289	221	332	0	0.896884	4.257521	0.002138	0.017308	1
35	34	15	0	-2.33765	5.04263	2.50E-14	1.30E-12	-1
215	207	224	0	1.326418	2.911487	3.26E-11	1.19E-09	1
470	440	461	-2	2.038009	5.105666	8.29E-43	3.33E-40	1
566	591	372	0	-1.08218	7.548877	6.13E-05	0.000782	-1
693	555	627	0	0.366228	4.475108	0.002639	0.020742	1
8	5	1	0	-1.71926	1.431348	2.08E-08	5.20E-07	-1
4	3	5	0	-2.19172	6.890786	3.31E-07	6.72E-06	-1
70	63	47	0	-1.00149	5.026286	0.000219	0.002401	-1

791	914	989	0	-0.36284	7.600782	9.51E-05	0.001153	-1
264	258	184	0	-1.2987	6.704461	1.45E-06	2.62E-05	-1
882	840	751	0	-0.52972	6.534888	8.45E-07	1.59E-05	-1
1226	1128	1363	2	-0.40754	4.442771	0.002641	0.020748	-1
241	336	358	0	2.520881	2.482155	1.81E-14	9.60E-13	1
264	169	283	2	-1.61643	4.628102	1.77E-15	1.03E-13	-1
429	510	411	-2	0.444756	5.65112	0.000215	0.002363	1
551	505	528	2	-0.97312	4.449313	4.84E-12	1.95E-10	-1
78	108	88	0	-0.5484	5.520728	0.000227	0.002479	-1
561	341	402	2	-0.65237	3.183658	0.000379	0.003872	-1
1284	1375	1438	2	-2.13469	8.149945	#####	#####	-1
94	91	76	0	-0.97821	4.161214	2.55E-07	5.26E-06	-1
2920	2967	2820	2	-0.61488	8.07256	1.88E-13	8.93E-12	-1
1088	977	1058	0	1.201608	4.487735	0.000135	0.001564	1
593	633	650	0	-0.8408	7.465873	3.15E-11	1.15E-09	-1
27	46	47	0	-0.48489	3.321285	0.004579	0.033087	-1
1690	1787	2325	0	0.860864	7.388256	6.55E-23	7.24E-21	1
53	37	23	0	-0.98797	6.156287	0.001841	0.015217	-1
59	58	77	0	-1.10808	4.105037	2.15E-17	1.57E-15	-1
148	158	203	0	1.053625	2.396295	0.00019	0.002117	1
280	326	290	2	-0.55391	4.386561	6.08E-05	0.000776	-1
88	98	62	0	-0.53244	4.90034	0.001921	0.015804	-1
403	421	471	-2	0.810429	6.541205	8.32E-16	5.16E-14	1
669	674	740	0	0.325518	5.306662	0.002637	0.020727	1
952	1000	1104	0	0.585358	6.42614	9.52E-09	2.50E-07	1
30	39	35	-2	0.859528	3.57419	9.43E-07	1.76E-05	1
26	34	47	0	0.800585	1.614339	0.006197	0.042417	1
264	230	239	0	-0.42482	4.151635	0.001844	0.015233	-1
237	199	271	0	1.890583	2.606553	6.81E-13	3.05E-11	1
6	12	5	0	-1.16881	4.647522	0.000494	0.004886	-1
833	928	788	0	-0.51241	7.247566	1.55E-09	4.53E-08	-1
85	102	132	0	1.053327	2.220349	0.005009	0.035595	1
82	73	93	0	0.865246	3.031834	1.97E-05	0.000284	1
60	65	70	0	-0.72226	4.483059	3.11E-06	5.28E-05	-1
33	17	23	-2	0.738145	3.719466	0.003575	0.026817	1
87	116	102	0	-0.47806	5.038873	0.007337	0.048903	-1
70	111	106	0	-0.95516	5.083104	5.24E-07	1.03E-05	-1
364	339	424	2	-0.56559	4.642269	2.87E-05	0.000399	-1
138	116	114	-2	0.944712	5.976512	1.11E-06	2.05E-05	1
8	5	4	-2	0.873948	2.161642	0.000206	0.002277	1
6	7	5	0	-1.19602	1.695672	0.001636	0.013765	-1
273	228	140	0	-1.1643	5.588783	9.02E-05	0.001104	-1
1297	1298	1442	2	-0.29649	6.928177	0.002027	0.016523	-1
426	422	378	0	-0.59987	6.023394	4.27E-09	1.18E-07	-1
75	45	62	0	1.400616	0.43603	0.001991	0.016279	1
798	882	975	0	0.844049	5.142418	7.14E-08	1.62E-06	1
465	411	452	0	-0.49307	5.619925	1.75E-05	0.000257	-1
0	1	0	0	-1.42647	3.504034	1.46E-06	2.64E-05	-1
364	432	561	0	0.810032	3.609763	7.71E-05	0.000959	1
111	113	127	0	1.776475	2.307122	6.93E-13	3.10E-11	1
163	132	139	-2	1.425818	3.731262	3.64E-06	6.09E-05	1
777	741	848	0	-0.67266	6.256662	5.14E-13	2.34E-11	-1
833	892	873	0	-0.45151	6.819647	3.71E-07	7.46E-06	-1
308	299	351	2	-1.07542	5.043376	1.07E-15	6.51E-14	-1

391	427	482	0	-0.66684	5.824663	1.85E-08	4.65E-07	-1
526	491	536	-2	0.590336	6.291878	6.21E-11	2.19E-09	1
2851	2609	1839	0	-1.00628	7.951045	1.55E-10	5.23E-09	-1
158	133	138	-2	4.103005	3.658929	4.21E-50	2.55E-47	1
191	211	133	0	-1.05352	5.853339	0.000614	0.005878	-1
425	330	381	0	-0.37998	5.51566	0.000573	0.005545	-1
27	29	20	0	-1.08424	2.999888	1.12E-07	2.46E-06	-1
126	119	100	0	-1.12989	5.839006	0.00044	0.00441	-1
630	657	585	0	-1.37334	5.792628	1.39E-12	6.03E-11	-1
63	60	55	0	-0.55499	2.983043	0.002719	0.021299	-1
747	790	849	0	-0.37442	6.392776	0.001946	0.01599	-1
7	6	5	0	-1.3081	1.805888	0.000839	0.007725	-1
217	254	255	0	-0.42776	5.160012	7.31E-05	0.000915	-1
293	236	287	2	-0.51447	4.465668	6.23E-05	0.000793	-1
30	31	43	-2	1.757278	3.2988	1.79E-23	2.09E-21	1
81	59	73	-2	0.905922	4.275618	5.63E-10	1.75E-08	1
181	176	161	-2	0.403263	5.460026	0.003515	0.026435	1
48	42	55	-2	0.552671	3.779651	0.002415	0.01919	1
16	12	19	-2	1.701457	1.719685	3.81E-06	6.36E-05	1
1022	1022	954	0	0.364214	5.113806	0.001447	0.012419	1
62	84	86	-2	0.507106	4.534133	0.000241	0.002601	1
128	96	153	2	-1.51862	3.988197	8.88E-14	4.35E-12	-1
153	132	160	2	-0.99018	3.987961	4.08E-12	1.66E-10	-1
400	406	516	0	1.678095	1.092359	2.37E-06	4.11E-05	1
34	32	38	2	-0.83214	1.510595	0.006323	0.043179	-1
49	49	39	0	-0.81322	3.49838	0.006589	0.044798	-1
76	80	101	2	-1.25146	2.634129	9.55E-08	2.13E-06	-1
145	164	165	-2	0.616771	4.665236	3.89E-06	6.48E-05	1
574	603	601	-2	0.408805	6.197088	1.03E-05	0.000157	1
3	3	2	0	-1.39726	3.947214	0.002321	0.01855	-1
284	330	324	2	-0.71556	3.405057	0.001598	0.013471	-1
208	222	261	2	-0.72312	4.681188	1.47E-06	2.65E-05	-1
10801	11404	11613	0	-0.63606	10.41442	7.09E-15	3.92E-13	-1
65	80	61	0	-0.91166	3.856837	7.17E-08	1.63E-06	-1
816	941	857	-2	1.46914	6.349921	5.30E-14	2.68E-12	1
272	281	279	0	-0.78331	4.77378	2.29E-10	7.49E-09	-1
28	41	29	0	2.549981	-0.0426	3.84E-05	0.000516	1
33	38	14	0	-1.23161	4.136806	0.000107	0.001277	-1
810	720	429	0	-1.00365	6.637265	0.000143	0.001643	-1
156	149	163	0	0.817046	2.877949	0.000567	0.005498	1
1659	1668	1870	-2	0.291503	7.680952	0.004711	0.033898	1
1832	1766	1958	2	-0.25394	6.491808	0.005103	0.036122	-1
699	609	577	2	-0.46714	4.551564	0.000237	0.002567	-1
651	632	589	0	0.645805	4.611771	2.57E-07	5.29E-06	1
433	393	378	-2	0.670954	4.326324	5.62E-07	1.09E-05	1
38	38	30	0	-0.79787	3.683617	0.002015	0.016445	-1
1145	1258	1578	0	0.830123	5.499319	8.31E-16	5.16E-14	1
1185	1250	1145	0	0.395458	5.261567	0.001103	0.009824	1
59	77	71	0	-1.17442	4.910586	2.09E-23	2.44E-21	-1
56	26	48	0	1.663939	1.131948	1.95E-05	0.000282	1
873	1007	1148	2	-1.31859	5.557697	7.32E-29	1.27E-26	-1
37	28	29	0	2.396479	0.864001	1.38E-07	2.99E-06	1
1857	2015	1860	-2	1.73722	8.190759	3.49E-83	6.25E-80	1
459	490	369	0	-1.03495	8.383536	1.68E-12	7.24E-11	-1

123	144	150	0	-0.99849	4.311676	2.28E-13	1.07E-11	-1
1429	1330	1148	2	-0.50286	4.209727	0.002845	0.02209	-1
256	348	172	0	-1.29379	4.837862	4.04E-20	3.66E-18	-1
362	339	373	2	-0.8203	4.620079	8.68E-11	3.00E-09	-1
23	13	16	2	-1.48392	2.47178	2.78E-07	5.69E-06	-1
2531	2473	2599	-2	0.828506	7.465772	1.90E-10	6.32E-09	1
577	689	685	-2	1.043616	6.333535	5.35E-21	5.16E-19	1
971	1100	1182	2	-0.31395	6.211882	0.002395	0.019066	-1
158	153	154	0	-1.03476	5.785532	1.28E-07	2.79E-06	-1
111	130	175	0	0.702614	2.621059	0.000587	0.005666	1
192	167	214	0	0.605521	2.945966	0.002172	0.017536	1
2564	2257	2460	0	0.714257	6.127008	1.92E-06	3.38E-05	1
428	503	406	0	-0.91415	6.826167	6.32E-13	2.84E-11	-1
290	280	376	0	3.132592	3.229149	8.91E-14	4.36E-12	1
12	14	13	0	-0.92517	1.467426	0.005454	0.038227	-1
708	846	780	2	-1.78063	6.253511	4.67E-20	4.19E-18	-1
616	413	624	2	-1.66709	6.02273	8.82E-26	1.21E-23	-1
368	209	196	-2	1.91773	3.59764	0.000421	0.004242	1
1277	1104	755	0	-2.5007	7.367132	2.97E-42	1.16E-39	-1
398	383	410	0	-1.10112	5.943033	1.06E-31	2.24E-29	-1
91	87	100	0	2.466347	2.093316	5.75E-16	3.65E-14	1
25	39	13	0	-0.84687	2.443257	0.000326	0.003389	-1
185	175	221	2	-2.42568	2.795748	1.24E-10	4.21E-09	-1
760	663	579	0	-0.54493	5.735492	2.96E-08	7.19E-07	-1
2041	2257	2814	0	-0.67716	8.392927	1.21E-17	9.03E-16	-1
541	533	511	0	0.728304	3.276518	7.11E-05	0.000892	1
35	32	35	0	-1.1729	1.930014	2.56E-05	0.000361	-1
9	3	5	0	-1.32881	1.586433	9.66E-06	0.000148	-1
87	74	81	0	-0.80564	3.515213	2.30E-06	4.00E-05	-1
95	69	105	0	0.790388	3.453544	1.98E-05	0.000286	1
376	371	296	0	1.931037	1.891905	3.93E-08	9.35E-07	1
1274	910	1282	2	-1.63768	7.250816	2.49E-30	4.82E-28	-1
166	220	237	2	-1.51994	2.494672	9.22E-11	3.18E-09	-1
115	121	125	2	-1.11094	4.735312	1.03E-14	5.56E-13	-1
152	119	122	-2	0.785561	5.134466	1.94E-09	5.58E-08	1
74	79	83	0	1.571519	3.327491	1.03E-15	6.23E-14	1
803	667	1010	0	1.460351	2.944432	6.34E-12	2.52E-10	1
404	477	555	0	1.915153	5.464875	7.43E-45	3.29E-42	1
320	339	216	-2	0.753315	1.969201	0.003048	0.023462	1
120	125	76	0	-0.732	4.118365	2.81E-05	0.000392	-1
925	1010	1100	0	-0.80635	6.694805	3.94E-19	3.37E-17	-1
20	33	27	-2	0.695739	4.170588	1.37E-05	0.000204	1
2	4	4	0	-0.99186	1.004836	0.005206	0.036744	-1
194	251	286	0	-1.1416	4.884204	6.18E-24	7.56E-22	-1
232	278	292	0	-0.87669	5.667742	1.27E-17	9.42E-16	-1
188	215	167	0	-0.84465	6.415275	0.004313	0.031434	-1
103	84	125	0	-1.19322	3.868097	1.32E-12	5.77E-11	-1
61	52	36	0	-1.26088	4.068317	1.49E-07	3.21E-06	-1
32	37	23	0	-1.0441	4.291615	0.000193	0.002152	-1
14	20	25	0	-0.76965	1.682185	0.002798	0.0218	-1
58	78	96	0	0.602055	3.615022	0.001746	0.01457	1
369	467	573	0	1.747593	3.216089	1.94E-09	5.59E-08	1
127	126	140	0	1.072008	3.37305	1.48E-07	3.19E-06	1
595	663	606	-2	2.62923	3.082694	6.14E-24	7.54E-22	1

231	264	444	0	1.244187	2.187522	2.23E-05	0.000318	1
286	346	279	-2	6.600154	1.5785	7.05E-22	7.21E-20	1
55	48	44	-2	1.015599	4.302758	3.27E-12	1.35E-10	1
324	341	363	2	-1.39238	5.617158	5.77E-16	3.66E-14	-1
60	81	86	2	-1.01806	1.899815	0.001149	0.010171	-1
24	15	21	0	-0.91079	2.488737	0.000125	0.001462	-1
468	482	442	2	-0.97312	4.109938	2.73E-13	1.26E-11	-1
266	288	355	0	0.843652	3.041519	1.25E-06	2.28E-05	1
244	329	385	-2	0.959339	6.236312	3.67E-24	4.56E-22	1
61	72	79	-2	1.293612	0.712105	0.001646	0.013832	1
1221	1186	1161	0	0.331451	5.91074	0.000454	0.004541	1
2074	2130	2451	2	-0.24261	7.048706	0.00436	0.031723	-1
97	70	61	0	-1.27255	4.881845	4.09E-06	6.77E-05	-1
24	14	14	0	-0.76563	4.025712	0.000537	0.005243	-1
92	88	59	0	1.505961	1.087776	8.00E-05	0.000991	1
62	65	66	0	-0.96237	3.285647	3.02E-09	8.49E-08	-1
22	23	18	0	-1.13151	3.195596	0.002434	0.019331	-1
24	32	22	0	-1.2233	3.036057	0.000597	0.005744	-1
184	181	232	0	-0.50215	5.275179	3.09E-06	5.24E-05	-1
9	14	16	-2	1.007773	1.912288	0.006992	0.046987	1
2	0	1	0	-3.62531	0.018139	6.63E-08	1.52E-06	-1
482	538	445	0	-0.25737	6.195342	0.004896	0.034928	-1
127	148	106	0	-1.28172	5.514895	8.75E-07	1.65E-05	-1
426	463	557	0	0.574386	4.895992	2.77E-06	4.74E-05	1
208	218	257	0	-0.8131	3.834346	0.000934	0.008492	-1
123	121	118	0	-0.88812	4.435311	1.24E-06	2.27E-05	-1
282	361	350	0	0.663555	3.59606	0.003855	0.028636	1
100	83	77	0	-0.89724	3.669873	4.34E-10	1.37E-08	-1
184	214	175	0	-0.90161	5.533784	6.93E-10	2.12E-08	-1
198	138	189	2	-0.77958	3.119779	0.000295	0.003106	-1
1244	1257	1036	0	-0.45071	7.183405	9.21E-08	2.06E-06	-1
70	79	42	0	-0.75848	4.35111	0.000178	0.001998	-1
58	34	41	0	-0.94617	3.382514	6.78E-08	1.55E-06	-1
549	632	847	0	1.158172	4.642511	1.02E-14	5.51E-13	1
1574	1545	1811	2	-0.38497	6.227181	0.000387	0.003941	-1
341	336	349	-2	0.380001	4.996046	0.000503	0.004962	1
586	579	644	0	-0.65406	6.704444	8.08E-15	4.45E-13	-1
622	570	460	-2	0.861746	6.040472	1.02E-13	4.98E-12	1
2348	2137	1347	0	-0.7742	7.154438	1.84E-12	7.89E-11	-1
59	67	61	0	-0.90081	2.104415	0.000192	0.002138	-1
359	320	329	0	-0.84546	4.878141	2.18E-07	4.55E-06	-1
2045	2257	2645	0	-0.48922	8.455187	3.06E-09	8.62E-08	-1
683	671	591	-2	0.455257	5.106305	0.000423	0.004257	1
322	343	313	-2	1.37913	6.450443	1.06E-37	3.15E-35	1
750	877	823	2	-1.35493	7.186029	1.17E-39	3.86E-37	-1
3478	3331	3576	0	-0.43334	7.543374	2.13E-06	3.74E-05	-1
27	14	7	-2	0.731815	4.13333	0.000421	0.004242	1
58	60	51	0	1.97215	1.042576	7.86E-06	0.000123	1
405	457	523	2	-0.77166	6.179062	9.14E-15	4.99E-13	-1
156	94	156	0	1.277715	3.130288	8.97E-09	2.37E-07	1
24	25	12	0	-1.20417	3.746182	0.000956	0.008672	-1
7	7	2	-2	1.156301	3.888915	4.91E-09	1.34E-07	1
131	127	155	-2	1.295424	7.53268	1.97E-15	1.15E-13	1
206	225	229	0	-0.71877	6.40116	2.85E-08	6.97E-07	-1

506	501	570	0	0.568993	4.71761	3.29E-05	0.000452	1
90	93	94	0	2.814229	0.142513	6.86E-06	0.000108	1
159	221	318	0	0.882816	4.043685	2.27E-10	7.45E-09	1
78	93	67	-2	2.504566	3.624672	1.26E-43	5.27E-41	1
93	110	154	0	0.804514	3.085861	0.006903	0.046513	1
11	19	15	0	-1.00601	2.608895	0.000491	0.004862	-1
3070	2950	3113	0	1.209711	4.960705	5.68E-11	2.02E-09	1
421	478	377	-2	0.664179	5.555447	1.07E-09	3.18E-08	1
35	32	29	0	-0.58081	3.43495	0.000284	0.003	-1
191	215	220	0	1.428511	2.607032	2.36E-09	6.73E-08	1
24	13	19	0	-1.40246	4.923683	1.91E-05	0.000278	-1
5	6	5	0	-1.64293	3.324698	9.61E-14	4.69E-12	-1
5	5	2	-2	4.788822	-0.03649	0.000313	0.00327	1
226	223	212	0	-2.14059	7.233038	1.42E-17	1.05E-15	-1
972	979	1098	0	1.654677	4.449748	8.67E-35	2.20E-32	1
1762	1309	1756	2	-1.45919	7.868844	3.21E-20	2.94E-18	-1
654	725	849	0	-0.9074	7.096061	1.18E-26	1.75E-24	-1
56	63	36	0	-1.17692	3.938111	8.11E-09	2.16E-07	-1
295	248	373	2	-1.45712	4.0787	1.39E-15	8.33E-14	-1
88	82	91	0	-0.62537	3.053872	0.000565	0.00548	-1
170	258	403	0	0.974285	4.111265	4.22E-10	1.33E-08	1
2075	1950	1981	2	-0.49302	5.372862	5.52E-05	0.000713	-1
2260	2507	2647	0	-0.47504	8.633002	5.57E-08	1.29E-06	-1
90	84	107	2	-0.73192	2.404049	0.002123	0.017202	-1
176	172	185	2	-0.55295	3.769134	0.004517	0.032702	-1
5	6	7	0	-1.6448	1.91404	1.21E-07	2.66E-06	-1
222	231	244	-2	0.47653	4.104534	0.000431	0.004332	1
56	54	55	0	-1.84694	6.131724	1.30E-66	1.55E-63	-1
247	252	291	-2	1.095374	6.239375	7.09E-17	4.87E-15	1
229	289	274	2	-0.71936	3.177481	0.000169	0.00191	-1
1313	1282	1391	0	-0.95788	7.337269	8.40E-24	1.02E-21	-1
365	308	409	0	1.453977	1.486294	0.000516	0.005069	1
63	48	103	0	1.089785	0.959711	0.007111	0.047708	1
25	31	12	0	-1.42737	5.652082	5.82E-08	1.34E-06	-1
4	7	0	0	-1.39563	2.738859	2.08E-05	0.000299	-1
20	11	16	0	-1.02046	2.225724	0.002023	0.016497	-1
390	553	731	0	0.42037	6.176011	3.22E-05	0.000444	1
3885	4772	4520	-2	1.215546	9.50909	2.08E-36	5.77E-34	1
96	100	86	-2	1.241369	1.541218	0.000305	0.003201	1
1605	1928	2137	-2	0.300388	8.563322	0.000114	0.001346	1
2398	2583	2679	-2	0.974033	8.158792	2.25E-23	2.62E-21	1
6	7	8	0	-1.26191	1.057107	0.004903	0.034973	-1
84	67	26	0	-1.92877	5.50365	2.23E-12	9.50E-11	-1
63	58	45	0	-1.14738	4.954139	2.05E-06	3.60E-05	-1
375	350	430	-2	1.261346	5.967904	2.15E-32	4.80E-30	1
289	335	296	-2	1.397243	6.763732	6.41E-26	8.95E-24	1
217	278	332	0	-0.37599	5.60847	0.000357	0.003667	-1
18	15	17	0	-1.64504	4.056133	2.83E-09	8.02E-08	-1
170	182	153	-2	1.500071	4.782176	1.20E-18	9.87E-17	1
686	728	718	-2	0.724615	8.37457	1.07E-09	3.18E-08	1
594	547	907	0	0.687321	4.684328	0.003526	0.026503	1
76	82	83	0	1.714674	1.893251	4.94E-08	1.15E-06	1
879	805	585	0	-0.66445	7.339803	5.60E-05	0.000723	-1
775	847	720	0	-1.06272	6.484254	2.43E-22	2.56E-20	-1

84	88	94	-2	1.589608	2.816507	5.64E-10	1.75E-08	1
413	428	436	-2	0.78633	2.476828	0.000161	0.001835	1
117	100	126	0	0.460904	3.35123	0.004559	0.032954	1
2	1	2	0	-1.81905	2.942898	4.61E-06	7.53E-05	-1
2136	2251	2735	2	-0.33802	5.535345	0.003972	0.029354	-1
77	57	69	0	-1.12452	4.256548	7.92E-06	0.000123	-1
19	29	12	0	-0.92703	5.249842	0.000531	0.005198	-1
308	314	382	0	1.977562	3.382459	4.13E-17	2.94E-15	1
21	31	27	0	-0.71724	1.985954	0.003996	0.029505	-1
0	0	0	0	-2.07554	-0.31786	0.002503	0.019826	-1

LLJYT03G	LLJYT03H	LLJYT03I	LLJYT03M	LLJYT03N	LLJYT03O	Best. hit. arabi. symarabi. def
243	216	296	167	156	21	AT3G60130BGLU16 beta gluc
117	155	87	317	439	123	AT3G45140ATLOX2, L0lipoxygen
10	3	7	21	29	19	AT3G45140ATLOX2, L0lipoxygen
47	29	37	125	247	217	AT3G20820.1 Leucine-r
58	91	76	37	44	20	AT2G41560ACA4 autoinhib
8	3	1	14	9	20	AT3G13650.1 Disease r
44	72	47	155	220	244	AT1G15960ATNRAMP6, NRAMP met
59	58	46	30	43	41	AT1G80760NIP6, NIP6NOD26-lik
307	242	215	164	200	169	AT1G04770.1 Tetratric
373	486	346	615	793	671	AT4G13710.1 Pectin ly
18	29	19	67	75	74	AT5G60020ATLAC17, Llacase 1
834	822	565	466	535	414	AT1G27920MAP65-8 microtubu
234	250	221	209	233	131	AT2G33550.1 Homeodoma
49	30	46	77	157	86	AT5G32450.1 RNA bindi
456	403	420	307	321	91	AT4G24140.1 alpha/bet
137	115	147	90	74	30	AT4G24130.1 Protein o
76	82	76	142	234	161	AT1G64390AtGH9C2, Gglycosyl
121	150	131	89	99	119	AT5G41460.1 Protein o
127	170	142	68	78	65	AT5G23750.1 Remorin f
269	243	228	358	427	298	AT1G63020NRPD1, NRPnuclear R
897	899	780	611	771	618	AT1G62990IXR11, KNAKNOTTED-1
71	89	80	60	56	54	AT4G22890PGR5-LIKEPGR5-LIKE
484	369	304	285	306	126	AT4G12350AtMYB42, Mmyb domai
1208	1297	922	783	1017	779	AT1G62710BETA-VPE, beta vacu
145	123	96	200	228	200	AT1G31920.1 Tetratric
1	0	0	5	5	7	
192	152	191	257	339	214	AT1G32540L0L1 lsd one 1
98	138	96	253	501	484	AT3G14310ATPME3, PMpectin me
53	97	83	177	355	300	AT3G14310ATPME3, PMpectin me
449	522	447	756	905	527	AT1G19110.1 inter-alp
2331	2209	2413	559	702	594	AT5G07990CYP75B1, DCytochrom
446	327	362	567	487	708	AT3G15990SULTR3;4 sulfate t
60	62	64	24	27	12	AT3G16360AHP4 HPT phosph
255	294	195	175	184	211	AT3G21360.1 2-oxoglut
152	97	86	150	181	223	AT1G72970EDA17, HTHGlucose-m
185	188	158	267	280	245	AT1G15760.1 Sterile a
380	415	348	914	1034	841	AT5G64570ATBXL4, XYbeta-D-xy
1108	1118	1131	943	1222	943	AT1G15820CP24, LHCBlight har
189	182	136	247	274	290	AT5G21105.1 Plant L-a
385	515	579	217	354	117	AT1G20030.2 Pathogene
33	22	26	14	15	3	AT3G60120BGLU27 beta gluc
1912	1941	1660	1395	1485	921	AT2G44500.1 0-fucosyl
1205	875	1101	622	772	180	AT5G58860CYP86, CYPcytochrom
751	751	679	966	1155	894	AT2G13360AGT, AGT1, alanine:g
9	3	6	13	37	37	AT1G74670.1 Gibberell
50	27	36	68	109	144	AT4G36250ALDH3F1 aldehyde
38	49	44	16	27	26	AT5G58600PMR5, TBL4Plant pro
916	859	770	532	668	412	AT1G07120.1
60	76	66	129	158	142	AT2G14520.1 CBS domai
230	222	214	165	243	138	AT4G34160CYCD3, CYCCYCLIN D3
692	697	694	322	397	334	AT5G03170ATFLA11, FFASCICLIN

6314	4302	5139	4629	3557	3992 AT3G02040SRG3	senescenc
2238	1859	1926	1662	1885	624 AT5G41040.1	HXXXD-typ
475	497	413	557	785	583 AT3G01990ACR6	ACT domai
20	23	32	54	62	45 AT3G27027.1	Protein o
126	148	133	218	289	251 AT1G60550DHNS, ECHI	enoyl-CoA
187	211	153	154	178	109 AT5G40780LHT1	lysine hi
683	805	692	3868	4460	3171 AT3G27400.1	Pectin ly
61	58	51	31	44	35 AT3G01660.1	S-adenosy
185	197	191	175	170	143 AT5G14460.1	Pseudouri
10	17	10	182	213	72 AT5G14650.1	Pectin ly
196	215	205	122	154	62 AT4G18170ATWRKY28, WRKY	DNA-
48	44	58	32	23	34 AT3G13130.1	
877	886	725	421	502	336 AT5G55970.1	RING/U-bo
33	39	21	96	68	98 AT3G58120ATBZIP61,	Basic-leu
634	643	557	527	544	515 AT1G53240mMDH1	Lactate/m
223	178	171	117	142	45 AT3G62730.1	
20	16	21	9	12	2 AT1G68470.1	Exostosin
244	267	237	355	364	302 AT1G78630emb1473	Ribosomal
87	58	73	45	67	14 AT1G53270.1	ABC-2 typ
62	70	59	42	38	37 AT5G53900.2	Serine/th
163	181	175	67	94	47 AT4G27460.1	Cystathio
110	144	115	62	59	36 AT5G53750.1	CBS domai
143	145	122	332	363	422 AT5G54250ATCNGC4,	Ccyclic nu
1022	1029	854	850	1044	761 AT5G54690GAUT12, IR	galacturo
166	185	161	143	158	92 AT1G78380ATGSTU19,	glutathio
113	87	85	285	182	314 AT1G79040PSBR	photosyst
84	80	82	55	65	13 AT4G21390B120	S-locus l
1185	1107	1333	872	993	611 AT2G36840.1	ACT-like
1407	1514	1192	1935	2300	1630 AT4G10550.1	Subtilase
52	43	38	84	74	75 AT2G34780EMB1611,	Mmaternal
340	347	277	277	283	220 AT1G55690.1	Sec14p-li
976	924	866	618	787	535 AT4G35550ATWOX13,	HWUSCHEL r
576	561	496	970	916	1053 AT1G76160sks5	SKU5 simi
203	192	257	94	92	44 AT1G60420.1	DC1 domai
39	50	36	113	118	69 AT3G21570.1	
482	490	408	198	171	174 AT1G19940AtGH9B5,	Gglycosyl
245	224	218	162	189	135 AT2G16400BLH7	BEL1-like
36	68	62	129	157	92 AT2G20500.1	
2047	1765	1441	1027	1273	803 AT3G04810ATNEK2,	NENIMA-rela
195	215	144	71	98	33 AT3G51895AST12,	SULsulfate t
1725	1472	1697	1357	1639	602 AT3G22600.1	Bifunctio
158	131	130	89	108	64 AT2G27310.1	F-box fam
73	61	70	112	135	83 AT1G03600PSB27	photosyst
177	234	216	299	434	307 AT1G43710emb1075	Pyridoxal
108	89	146	74	115	52 AT1G34670AtMYB93,	Mmyb domai
628	534	463	408	513	375 AT1G72220.1	RING/U-bo
1275	1263	1004	965	1261	999 AT2G22540AGL22,	SVPK-box reg
2893	2954	3788	1226	1699	1485 AT4G24220AWI31,	VEPNAD(P)-bi
133	132	112	87	106	60 AT1G46768RAP2.1	related t
27	37	36	60	79	63 AT1G47490ATRBP47C,	RNA-bindi
68	67	56	22	25	16 AT1G02040.1	C2H2-type
136	127	91	85	92	71 AT4G00230XSP1	xylem ser
603	669	566	823	1238	1196 AT4G00570NAD-ME2	NAD-depen
49	20	54	24	21	11 AT2G46130ATWRKY43,	WRKY DNA-

91	106	88	69	44	45 AT2G46770ANAC043, ENAC (No A
193	247	170	172	204	136 AT2G34430LHB1B1, LHlight-har
228	265	182	93	116	104 AT1G03010.1 Phototrop
354	327	323	151	247	263 AT1G12900GAPA-2 glycerald
1157	1207	1094	997	1343	853 AT3G24770CLE41 CLAVATA3/
83	75	71	56	72	29 AT3G25400.1
959	959	858	557	671	557 AT4G28640 IAA11 indole-3-
101	78	76	48	47	17 AT4G37370CYP81D8 cytochrom
148	138	114	160	234	177 AT3G18430.1 Calcium-b
159	190	232	87	90	91 AT3G21250ATMRP6, MRmultidrug
21	18	12	37	44	72 AT1G72970EDA17, HTHGlucose-m
152	142	135	80	117	101 AT1G45688.1
11	18	12	136	71	123 AT1G72610ATGER1, GEgermin-li
4653	4483	5980	1291	2047	1783 AT5G07990CYP75B1, DCytochrom
684	672	687	268	367	319 AT5G07990CYP75B1, DCytochrom
447	433	399	544	615	545 AT1G32470.1 Single hy
108	80	88	144	149	220 AT4G25960PGP2 P-glycopr
71	90	80	33	34	25 AT4G39730.1 Lipase/li
280	301	241	223	265	148 AT4G12350AtMYB42, Mmyb domai
782	760	732	717	726	585 AT4G20360ATRAB8D, ARAB GTPas
174	148	142	83	101	74 AT5G23750.1 Remorin f
255	296	248	185	225	160 AT5G23860TUB8 tubulin b
271	313	236	461	482	557 AT5G12250TUB6 beta-6 tu
358	372	300	256	256	282 AT3G61490.3 Pectin ly
479	496	359	334	371	262 AT1G63910AtMYB103, myb domai
819	803	659	616	719	440 AT5G41800.1 Transmemb
31	38	42	13	14	13 AT4G23990ATCSLG3, Ccellulose
97	117	83	179	179	160 AT4G23990ATCSLG3, Ccellulose
31	33	24	8	7	14 AT3G12720ATMYB67, Amyb domai
440	550	487	580	766	651 AT1G09690.1 Translati
563	702	441	299	356	419 AT5G13870EXGT-A4, Xxylogluca
272	309	313	245	282	145 AT2G33550.1 Homeodoma
611	547	517	316	330	347 AT5G13120ATCYP20-2cyclophil
255	299	212	168	208	138 AT5G14090.1
0	0	0	9	66	54 AT1G24260AGL9, SEP3K-box reg
105	97	82	85	82	51 AT5G43260.1 chaperone
312	361	320	290	263	215 AT2G23520.1 Pyridoxal
1293	1221	921	676	841	624 AT1G27920MAP65-8 microtubu
154	173	127	111	141	108 AT1G04770.1 Tetratric
12	3	10	36	43	55 AT1G64660ATMGL, MGLmethionin
5	2	9	24	42	36 AT1G64660ATMGL, MGLmethionin
647	491	428	399	510	275 AT3G212404CL2, AT4C4-coumara
165	158	147	97	141	24 AT2G03220ATFT1, ATFfucosyltr
344	339	309	310	336	246 AT5G07020.1 proline-r
316	318	260	607	983	710 AT5G12330LRP1 Lateral r
12	7	4	21	57	47 AT3G20820.1 Leucine-r
939	804	770	554	770	256 AT3G57880.1 Calcium-d
255	274	242	208	233	189 AT2G05990ENR1, MOD1NAD(P)-bi
251	241	193	167	178	86 AT3G45240ATSTNAK2, Ggeminivir
21	29	22	3	6	4 AT5G17230PSY PHYTOENE
4390	4119	3840	3332	3585	2888 AT3G13470.1 TCP-1/cpn
166	173	143	123	106	112 AT4G21990APR3, ATAPAPS reduc
10	37	12	46	52	40 AT1G70880.1 Polyketid
30	31	22	67	53	81 AT1G11545XTH8 xylogluca

2232	2451	2001	2822	3280	2796 AT4G05180PSBQ, PSBQphotosyst
455	493	424	1318	1753	1140 AT4G05150.1 Octicosap
38	42	32	136	237	118 AT4G27450.1 Aluminium
89	83	64	123	163	113 AT1G28360ATERF12, EERF domai
35	13	14	58	63	74
1869	1435	1459	1121	1283	345 AT1G28680.1 HXXXD-typ
83	87	96	76	62	14 AT1G06330.1 Heavy met
9312	8762	6707	6092	7224	5192 AT4G18780ATCESA8, Ccellulose
18	8	14	38	43	48 AT1G29670.1 GDSL-like
7	4	2	16	18	20 AT1G17860.1 Kunitz fa
99	97	73	55	53	6 AT3G16520UGT88A1 UDP-gluco
939	902	1105	313	463	386 AT1G65880BZ01 benzoylox
547	555	430	886	1435	1175 AT5G37600ATGLN1;1, glutamine
538	531	548	257	301	97 AT5G37690.1 SGNH hydr
22	39	23	114	77	67 AT1G66400CML23 calmoduli
156	167	158	620	726	447 AT2G01210.1 Leucine-r
81	101	86	353	453	261 AT3G18280.1 Bifunctio
26	38	30	105	86	95 AT5G16030.1
256	234	203	131	176	52 AT5G15900TBL19 TRICHOME
4	1	3	2	15	25 AT1G69530AT-EXP1, Aexpansin
50	69	61	0	2	2 AT3G28917MIF2 mini zinc
230	133	126	43	68	7 AT5G08640ATFLS1, FL flavonol
32	19	38	154	199	178 AT5G42650AOS, CYP74allene ox
113	136	97	187	222	271 AT4G34530CIB1 cryptochr
2	0	0	1	7	11
396	448	380	377	334	281 AT1G75390AtbZIP44, basic leu
3484	3064	2885	2499	2769	2365 AT4G38970FBA2 fructose-
60	28	16	54	81	108 AT4G38770ATPRP4, PRproline-r
53	40	47	21	32	17 AT2G24960.2
985	1180	1016	535	789	633 AT2G16700ADF5, ATADactin dep
1316	1214	1146	763	1007	287 AT4G33790CER4, FAR3Jojoba ac
588	673	658	929	965	854 AT1G08200AXS2 UDP-D-api
330	371	467	235	360	240 AT2G36830GAMMA-TIPgamma ton
138	160	136	70	68	42 AT1G09610.1 Protein o
459	385	438	177	361	124 AT1G59740.1 Major fac
777	956	743	1580	1976	1509 AT4G19420.1 Pectinace
1761	1348	1314	689	795	128 AT4G19380.1 Long-chai
36	30	22	128	212	247 AT1G09240ATNAS3, NAnicotiana
661	592	565	525	626	477 AT5G64740CESA6, E1lcellulose
25	24	18	5	15	0 AT3G52970CYP76G1 cytochrom
64	66	70	108	132	89 AT5G27550.1 P-loop co
102	114	103	47	46	20 AT1G08990PGSIP5 plant gly
951	881	874	782	970	691 AT3G04880DRT102 DNA-damag
7	7	2	15	14	16 AT5G48920TED7 tracheary
1452	1537	1239	541	507	348 AT3G18660GUX1, PGSIplant gly
262	244	232	145	172	44 AT1G34670AtMYB93, Mmyb domai
813	661	723	482	492	134 AT5G23190CYP86B1 cytochrom
172	137	101	72	97	23 AT1G65730YSL7 YELLOW ST
188	184	192	153	178	109 AT1G56170ATHAP5B, Hnuclear f
328	407	319	767	818	517 AT4G35550ATWOX13, HWUSCHEL r
11	9	13	16	41	44 AT2G16850PIP2;8, PIplasma me
4704	4338	3639	2129	2164	1657 AT4G36220CYP84A1, Fferulic a
109	130	96	148	202	158 AT3G50410OBP1 OBF bindi
3271	3114	2568	2097	2408	1896 AT5G67210.1 Protein o

20	30	21	45	46	35	AT1G72200.1	RING/U-bo
576	507	609	315	356	85	AT1G34670AtMYB93,	Mmyb domai
425	406	382	317	385	274	AT5G65170.1	VQ motif-
29	51	20	89	119	155	AT1G22150SULTR1;3	sulfate t
39	48	31	71	143	173	AT1G22150SULTR1;3	sulfate t
64	102	73	118	223	141	AT4G08300.1	nodulin M
204	199	174	320	505	478	AT1G77000ATSKP2;2,	RNI-like
94	72	35	33	39	13	AT1G17950ATMYB52,	Bmyb domai
886	870	963	511	692	428	AT1G71695.1	Peroxiidas
55	50	43	330	543	442	AT5G09970CYP78A7	cytochrom
80	93	96	184	181	178	AT1G03600PSB27	photosyst
630	672	560	551	531	492	AT1G06690.1	NAD(P)-li
85	63	83	65	61	22	AT2G48130.1	Bifunctio
81	78	85	149	162	99	AT4G28530anac074,	NNAC domai
291	283	261	148	204	148	AT1G27680APL2	ADPGLC-PP
133	140	125	78	107	54	AT1G27620.1	HXXXD-typ
125	116	108	174	237	144	AT1G19715.3	Mannose-b
491	493	451	392	357	421	AT4G36360BGAL3	beta-gala
556	560	533	817	1088	660	AT1G19850ARF5,	IAA2Transcrip
388	448	389	320	416	358	AT1G47840HXX3	hexokinas
2352	2459	2245	2979	3747	3030	AT1G76100PETE1	plastocya
170	167	164	98	85	116	AT4G35750.1	SEC14 cyt
527	557	556	2329	3379	2103	AT1G42430.1	
2495	2438	2142	1908	2233	1892	AT1G42970GAPB	glycerald
88	76	74	114	177	107	AT1G21000.2	PLATZ tra
130	153	117	504	732	529	AT4G16480ATINT4,	INinositol
90	138	107	553	985	555	AT4G16480ATINT4,	INinositol
96	81	81	102	168	137	AT4G16410.1	
4	5	1	24	33	10	AT1G22400ATUGT85A1	UDP-Glyco
134	141	114	75	81	69	AT5G04200AtMC9,	MC9metacaspa
535	485	362	244	260	141	AT1G66120.1	AMP-depen
183	181	156	265	372	261	AT3G08550ABI8,	ELD1elongatio
1266	1444	1319	1767	1996	1655	AT3G57490.1	Ribosomal
111	137	110	342	480	287	AT3G53720ATCHX20,	Ccation/H+
76	91	96	561	567	739	AT2G10940.1	Bifunctio
313	310	293	249	283	222	AT2G43290MSS3	Calcium-b
2510	1775	1952	1701	1166	1416	AT2G26660ATSPX2,	SPSPX domai
3	4	3	29	59	75	AT2G37460.1	nodulin M
17	25	15	38	37	37	AT5G02540.1	NAD(P)-bi
381	417	397	589	808	735	AT2G37640ATEXP3,	ATBarwin-li
1459	1343	1054	516	501	386	AT5G60020ATLAC17,	Llaccase 1
498	468	492	310	379	78	AT2G29150.1	NAD(P)-bi
172	150	124	90	118	71	AT5G02090.1	
111	140	145	91	92	108	AT2G38080ATLMCO4,	ILaccase/D
1140	999	1020	581	769	178	AT2G38110ATGPAT6,	Gglycerol-
116	79	106	12	18	17	AT4G00430PIP1;4,	PIplasma me
143	115	153	213	232	344	AT3G51860ATCAX3,	ATcation ex
668	672	514	537	569	502	AT5G05580FAD8	fatty aci
4	0	0	6	5	10	AT1G07080.1	Thioredox
720	777	509	409	564	510	AT5G01930.1	Glycosyl
34	25	35	59	71	56	AT1G14360ATUTR3,	UTUDP-galac
109	138	128	170	207	198	AT3G54210.1	Ribosomal
2967	3168	2708	2353	2697	2411	AT2G36530EN02,	LOS2Enolase
5	1	2	34	29	29	AT5G03795.1	Exostosin

641	729	656	941	1016	986 AT2G36870XTH32	xylogluca
44	46	47	79	100	68 AT2G37170PIP2;2, PI	plasma me
1604	1874	1522	1410	1423	1265 AT5G03170ATFLA11, FF	ASCICLIN
249	258	214	64	90	33 AT2G39200ATML012, M	Seven tra
479	386	349	1410	1716	986 AT2G37130.1	Peroxi
744	681	589	533	653	551 AT5G02790GSTL3	Glutathio
455	409	413	369	389	342 AT3G26060ATPRX Q	Thioredox
7	6	3	201	107	152 AT5G20630ATGER3, GE	germin 3
166	130	133	103	119	44 AT3G212404CL2, AT4C4-	coumara
5237	5191	3983	3705	4150	3147 AT5G17420ATCESA7, C	Cellulose
284	176	184	328	402	600 AT2G26250FDH, KCS103-	ketoacy
165	199	288	52	55	52 AT5G35550ATMYB123, D	uplicate
557	564	584	374	494	257 AT4G38620ATMYB4, M	myb domai
1497	1615	1439	980	977	693 AT5G11890.1	
1512	1517	1541	923	1238	911 AT4G32870.1	Polyketid
109	106	75	53	46	24 AT5G25610ATRD22, R	BURP doma
1529	1211	1137	542	726	219 AT5G25610ATRD22, R	BURP doma
206	131	140	221	642	656 AT5G11420.1	Protein o
275	345	254	165	227	132 AT4G32280 IAA29	indole-3-
464	393	355	251	316	44 AT2G24430ANAC038, AN	AC domai
229	200	158	127	184	113 AT4G31290.1	ChaC-like
590	735	681	1098	1138	932 AT5G23400.1	Leucine-r
736	577	663	354	415	99 AT1G32910.1	HXXXD-ty
261	245	242	331	516	288 AT4G37790HAT22	Homeobox-
527	492	409	689	980	870 AT4G37870PCK1, PE	PCphosphoen
151	118	119	85	95	31 AT5G65500.1	U-box dom
186	192	157	130	169	98 AT2G18060ANAC037, V	vascular
5176	4723	3997	2987	3487	2431 AT4G36220CYP84A1, F	ferulic a
480	413	464	273	345	131 AT2G18360.1	alpha/bet
117	81	78	59	72	66 AT3G50685.1	
574	547	466	479	576	361 AT2G23760BLH4, SA	W2BEL1-like
1211	985	1140	827	914	286 AT2G23540.1	GDSL-like
25	23	21	7	9	5 AT5G66870ASL1, LBD3	ASYMMETRI
26	34	22	10	8	12 AT2G26560PLA IIA, P	phospholi
344	345	303	243	352	216 AT5G67020.1	
498	548	490	308	323	272 AT5G67210.1	Protein o
1271	1000	1252	675	702	162 AT5G23190CYP86B1	cytochrom
40	46	26	112	177	94 AT5G08350.1	GRAM doma
488	418	376	307	333	111 AT5G10280ATMYB64, A	myb domai
976	870	720	424	428	109 AT5G64440AtFAAH, F	A fatty aci
6324	7052	5578	9266	12163	11185 AT5G09220AAP2	amino aci
157	125	112	80	98	36 AT4G33450ATMYB69, M	myb domai
1969	1961	1446	452	408	321 AT3G18660GUX1, PG	S Iplant gly
0	0	0	3	3	10 AT5G48920TED7	tracheary
380	482	371	333	378	312 AT1G58120.1	
230	218	295	155	225	62 AT5G09520.1	hydroxypr
259	229	220	122	152	100 AT4G33580ATBCA5, B	C beta carb
363	347	317	208	260	217 AT4G28500ANAC073, N	NAC domai
137	142	97	233	272	165 AT4G28380.1	Leucine-r
1855	1926	1434	766	641	540 AT5G03760ATCSLA09, N	ucleotid
6352	5771	4811	4635	5658	3487 AT2G37040ATPAL1, P	APHE ammon
4	4	9	93	66	62 AT3G54770.1	RNA-bindi
580	468	397	253	285	65 AT3G55090.1	ABC-2 typ
1188	1186	996	1516	1675	1439 AT5G02500AT-HSC70-	heat shoc

211	219	183	129	137	91 AT3G55420.1
433	338	341	229	292	57 AT5G06090ATGPAT7, Glycerol-
1855	1822	1598	2262	2567	2190 AT2G39730RCA rubisco a
28	41	18	49	68	46 AT2G44920.2 Tetratric
226	200	181	370	426	226 AT5G02070.1 Protein k
628	676	520	402	483	430 AT2G39770CYT1, EMB1Glucose-1
1998	1655	1886	2307	3757	2083 AT5G05960.1 Bifunctio
993	864	815	758	806	715 AT3G55800SBPASE sedoheptu
1704	1897	1503	1162	1359	1076 AT3G55990ESK1, TBL2Plant pro
1564	1506	1346	1212	1291	848 AT2G40320TBL33 TRICHOME
1248	1442	1149	1102	1196	776 AT2G40370LAC5 laccase 5
836	884	824	642	789	674 AT5G05390LAC12 laccase 1
39	30	25	47	87	117 AT5G44680.1 DNA glyco
114	117	85	66	81	19 AT3G12720ATMYB67, Amyb domai
439	511	424	636	813	557 AT3G28960.1 Transmemb
200	205	155	133	132	143 AT1G26820RNS3 ribonucle
100	133	102	64	62	58 AT3G15580APG8H, ATGUbiqutin
317	235	253	34	45	3
12	16	9	30	34	34 AT5G49360ATBXL1, BXbeta-xylo
165	144	171	80	77	20 AT5G49350.1 Glycine-r
15	14	16	26	30	32 AT1G23000.1 Heavy met
10	5	26	122	286	367 AT1G14930.1 Polyketid
220	286	277	514	445	362 AT1G14890.1 Plant inv
230	240	228	304	359	295 AT1G14810.1 semialdeh
1311	1355	1146	2198	2236	1937 AT1G14720ATXTH28, Exylogluca
447	297	374	224	281	275 AT2G37870.1 Bifunctio
520	581	646	286	372	256 AT2G32150.1 Haloacid
34	28	43	18	10	5 AT3G22840ELIP, ELIPChlorophy
374	406	360	277	306	277 AT3G22890APS1 ATP sulfu
1182	1051	1047	855	1097	304 AT2G26640KCS11 3-ketoacy
101	90	126	40	81	34 AT4G14465AHL20 AT-hook m
346	340	223	148	262	192 AT5G07050.1 nodulin M
344	277	304	648	632	549 AT3G23510.1 Cycloprop
434	448	369	206	214	146 AT2G33385arpc2b actin-rel
71	77	74	136	110	113 AT4G17740.1 Peptidase
535	465	438	370	477	205 AT3G21530.1 DNase I-1
454	462	455	308	444	284 AT4G04830ATMSRB5, Mmethionin
1853	1882	1552	1551	1971	1261 AT3G23590MED33A, RFREF4-rela
85	75	61	127	119	119 AT5G19160TBL11 TRICHOME
103	102	102	152	181	139 AT4G02510ATTOC159, transloco
206	246	188	287	371	273 AT2G27920SCPL51 serine ca
523	612	507	308	381	229 AT5G22930.1 Protein o
193	164	194	113	131	34 AT5G57620AtMYB36, Mmyb domai
675	628	516	409	465	234 AT2G28250NCRK Protein k
3005	2957	2516	1716	1974	1455 AT2G28315.1 Nucleotid
161	80	87	126	268	274 AT5G22430.1 Pollen O1
482	455	439	126	152	30 AT2G18370.1 Bifunctio
34	46	23	90	101	91 AT3G46780PTAC16 plastid t
99	139	95	402	650	454 AT5G59080.1
2415	1795	2111	1304	1630	459 AT5G58860CYP86, CYPcytochrom
153	162	164	217	250	210 AT3G63540.1 Mog1/PsbP
34	38	25	11	13	8 AT2G32560.1 F-box fam
1876	1562	1431	558	576	77 AT5G07990CYP75B1, DCytochrom
406	294	376	258	265	83 AT5G19410.1 ABC-2 typ

1989	1791	1671	1574	1707	1364 AT5G12300.1	Calcium-d
1327	1150	1216	710	763	221 AT1G49960.1	Xanthine/
898	1102	750	651	840	595 AT1G10200WLIM1	GATA type
195	209	210	144	189	174 AT4G34215.1	Domain of
11	15	13	58	77	108 AT5G03260LAC11	laccase 1
247	276	401	100	118	114 AT1G19190.1	alpha/bet
328	431	303	519	658	413 AT2G15790CYP40, SQN	peptidyl-
280	228	212	127	144	130 AT3G19000.1	2-oxoglut
520	443	396	364	441	226 AT3G18950.1	Transduci
103	81	88	52	75	63 AT4G39230.1	NmrA-like
3836	4027	3702	1030	1034	820 AT4G39210APL3	Glucose-1
195	178	214	130	134	67 AT2G16385.1	
2896	2737	2503	1837	2236	1757 AT4G38970FBA2	fructose-
153	93	90	152	261	414 AT3G61430ATPIP1, PI	plasma me
1970	1820	1864	1091	1581	852 AT4G38560.2	Arabidops
94	98	94	87	79	58 AT1G20550.1	0-fucosyl
960	1006	995	1917	2225	1764 AT5G22740ATCSLA02,	cellulose
857	702	796	579	627	142 AT5G22810.1	GDSL-like
195	209	181	89	124	85 AT2G29130ATLAC2, LA	laccase 2
23	26	32	48	58	77 AT3G52500.1	Eukaryoti
216	232	171	137	163	159 AT2G36250ATFTSZ2-1	Tubulin/F
300	320	259	232	313	132 AT1G08320bZIP21, TGb	ZIP tran
531	619	535	1148	1216	879 AT3G17510CIPK1, SnR	CBL-inter
281	345	249	372	474	355 AT5G48960.1	HAD-super
530	619	563	1001	1002	808 AT5G26670.1	Pectinace
57	83	66	127	181	105 AT4G21380ARK3, RK3	receptor
15	18	18	24	43	31	
172	169	163	139	172	103 AT3G17210ATHS1, HS1	heat stab
18	20	23	61	91	96 AT3G01680.1	
322	250	287	180	214	41 AT1G24430.1	HXXXD-typ
1438	1656	1375	1081	1281	1063 AT2G33385arpc2b	actin-rel
39	18	15	43	43	74 AT2G33420.1	Protein o
45	51	44	95	83	99 AT5G46050ATPTR3, PT	peptide t
235	241	216	171	195	98 AT5G43420.1	RING/U-bo
73	104	64	162	211	75 AT1G06620.1	2-oxoglut
341	381	235	220	371	172 AT4G24010ATCSLG1, C	cellulose
413	323	374	243	276	121 AT1G04220KCS2	3-ketoacy
265	231	243	164	193	189 AT3G18420.1	Protein p
300	462	312	850	1004	440 AT1G14780.1	MAC/Perfo
26	21	27	53	52	44 AT1G24620.1	EF hand c
34	42	30	10	35	7 AT2G01340At17.1	
580	512	562	369	369	95 AT1G68850.1	Peroxidas
1208	1119	1023	1020	1054	906 AT2G04030AtHsp90.5	Chaperone
718	684	557	437	532	444 AT1G13635.2	DNA glyco
6	4	5	11	16	17 AT4G37580COP3, HLS1	Acyl-CoA
188	246	192	441	532	272 AT1G48100.1	Pectin ly
531	531	377	357	439	323 AT1G79420.1	Protein o
163	117	128	67	84	20 AT3G12720ATMYB67, A	myb domai
78	78	61	107	139	166 AT5G44680.1	DNA glyco
17	12	23	65	76	56 AT1G30820.1	CTP synth
47	88	40	108	297	122 AT2G40390.1	
831	823	695	506	647	466 AT5G05390LAC12	laccase 1
1122	1187	956	876	1003	738 AT2G40320TBL33	TRICHOME
429	330	354	200	212	168 AT5G05690CBB3, CPD,	Cytochrom

595	668	479	340	446	408 AT2G38120AUX1, MAP1	Transmemb
520	539	497	788	1010	776 AT5G05790.1	Duplicate
2921	2334	2944	1558	1989	1029 AT5G05960.1	Bifunctio
11	11	11	141	279	212 AT2G39855.2	
755	545	637	440	501	119 AT3G11430ATGPAT5, G	glycerol-
417	471	402	391	417	281 AT5G54980.1	Uncharact
96	92	79	50	63	26 AT2G37430.1	C2H2 and
731	594	629	427	484	103 AT2G39350.1	ABC-2 typ
802	637	561	352	341	162 AT5G03760ATCSLA09,	Nucleotid
85	80	65	60	71	41 AT3G54240.1	alpha/bet
893	720	748	645	680	662 AT3G11760.1	
47	38	33	25	25	3 AT4G31540ATEX070G1	exocyst s
344	382	297	289	308	235 AT1G16860.1	Ubiquitin
203	216	225	153	204	140 AT3G21690.1	MATE effl
42	36	30	121	163	118 AT5G38280PR5K	PR5-like
100	109	121	201	290	193 AT3G54070.1	Ankyrin r
328	327	286	455	613	315 AT3G54070.1	Ankyrin r
73	86	112	134	179	127 AT3G54070.1	Ankyrin r
5	18	12	27	63	37 AT3G54070.1	Ankyrin r
285	248	218	326	409	325 AT4G05180PSBQ, PSBQ	photosyst
173	155	144	249	308	184 AT1G61660.1	basic hel
199	155	228	81	93	52 AT5G43060.1	Granulin
180	168	175	84	112	93 AT1G09850XBCP3	xylem bar
8	5	9	26	27	25 AT1G29670.1	GDSL-like
35	28	22	14	18	20 AT1G29050TBL38	TRICHOME
135	109	109	77	123	28 AT1G53270.1	ABC-2 typ
60	71	82	24	37	37 AT1G78380ATGSTU19,	glutathio
134	197	164	249	330	254 AT5G06740.1	Concanava
533	560	478	694	925	674 AT2G46770ANAC043,	ENAC (No A
255	173	128	125	98	13 AT5G44440.1	FAD-bindi
126	120	80	79	55	79 AT1G30700.1	FAD-bindi
284	303	211	148	183	193 AT1G23460.1	Pectin ly
14774	14743	12079	9705	11117	8490 AT5G54160ATOMT1,	OM0-methylt
151	170	148	104	114	57 AT3G24770CLE41	CLAVATA3/
294	300	468	829	1407	1049 AT1G74100ATSOT16,	A sulfotran
287	284	289	153	225	172	
2	2	1	5	15	14 AT1G73680ALPHA DOX	alpha dio
223	183	204	118	147	30 AT3G18400anac058,	NNAC domai
1229	923	1144	756	846	259 AT1G74460.1	GDSL-like
49	52	27	83	111	55 AT1G74710ATICS1,	EDADC synth
1526	1604	1474	1871	2710	1669 AT3G01470ATHB-1,	A homeobox
778	848	813	734	850	662 AT5G62790DXR, PDE1	21-deoxy-D
228	253	196	149	212	175 AT5G61640ATMSRA1,	Ppeptideme
167	167	137	267	274	262 AT5G63310ATNDPK2,	Nnucleosid
119	140	122	209	282	178 AT3G48660.1	Protein o
155	129	118	100	122	37 AT1G24140.1	Matrixin
266	289	253	501	643	438 AT5G13980.1	Glycosyl
246	303	273	366	409	403 AT4G25080CHLM	magnesium
363	333	342	171	188	146 AT5G07330.1	
8	7	8	18	26	36 AT2G35640.1	Homeodoma
517	690	481	234	285	220 AT3G54950PLA IIIA,	patatin-l
4	4	4	22	37	13 AT4G25250.1	Plant inv
1032	1215	1115	3795	4729	3776 AT5G62350.1	Plant inv
3830	3889	3499	2245	2563	1280 AT5G23750.2	Remorin f

216	242	201	138	129	94 AT4G25810XTH23, XTRxylogluca
203	165	169	124	133	155 AT1G56580SVB Protein o
364	338	312	154	202	102
253	296	234	134	206	147 AT3G62630.1 Protein o
89	70	41	28	22	27 AT5G06900CYP93D1 cytochrom
954	1031	1174	1686	2589	1940
426	482	404	1032	963	941 AT5G56750NDL1 N-MYC dow
689	687	670	641	691	480 AT3G04790.1 Ribose 5-
721	497	624	405	262	308 AT3G04530ATPPCK2, Pphosphoen
40	41	31	65	66	68 AT3G04760.1 Pentatric
41	51	55	76	105	66 AT3G03900APK3 adenosine
437	520	366	583	911	865 AT5G18170GDH1 glutamate
1241	1295	1168	737	952	496 AT5G56340ATCRT1 RING/U-bo
20	23	4	99	117	218 AT2G03090ATEXP15, Aexpansin
35	26	23	15	27	7 AT3G03700.1 Plasma-me
1008	825	1101	365	407	186 AT5G07990CYP75B1, DCytochrom
761	751	945	216	346	293 AT5G17540.1 HXXXD-typ
22	20	75	52	324	146 AT4G24350.1 Phosphory
2308	2199	2480	330	451	559 AT4G24340.1 Phosphory
702	735	660	358	418	298 AT1G33800.1 Protein o
15	7	8	74	60	49 AT1G75240AtHB33, HBhomeobox
61	58	50	33	52	19 AT1G50420SCL-3, SCLscarecrow
59	95	134	8	25	26 AT4G35160.1 O-methylt
502	561	513	357	465	364 AT4G35020ARAC3, ATRRAC-like
3447	3838	3076	2329	2666	2092 AT3G59690IQD13 IQ-domain
59	62	56	89	113	118 AT1G21500.1
30	51	45	24	21	16 AT4G20970.1 basic hel
35	34	32	21	17	6 AT4G03270CYCD6;1 Cyclin D6
141	115	103	75	94	57 AT2G40470ASL11, LBDLOB domai
80	58	57	101	144	125 AT2G22840AtGRF1, GRgrowth-re
11	11	13	27	71	51 AT3G49940LBD38 LOB domai
1675	1789	2256	586	808	641 AT4G24220AWI31, VEPNAD(P)-bi
70	74	60	29	18	30 AT5G59845.1 Gibberell
342	275	289	157	194	113 AT2G38185.1 RING/U-bo
192	207	237	404	413	383 AT4G37260ATMYB73, Mmyb domai
50	38	34	133	127	135 AT1G60060.1 Serine/th
28	37	33	75	124	98 AT5G67090.1 Subtilisi
174	161	123	641	795	472 AT5G67090.1 Subtilisi
22	27	19	48	48	30 AT5G42380CML37, CMLcalmoduli
143	199	195	138	120	96 AT3G50610.1
1153	1153	989	660	749	649 AT1G19300ATGATL1, GNucleotid
112	112	113	152	262	189 AT5G42610.1 Protein o
16	20	24	15	12	6 AT4G01070GT72B1, UGUDP-Glyco
328	348	337	155	204	146 AT1G75130CYP721A1 cytochrom
582	565	497	327	394	264 AT4G00750.1 S-adenosy
1058	792	874	641	886	205 AT2G37360.1 ABC-2 typ
189	171	145	79	111	54 AT1G01780.1 GATA type
222	172	192	90	142	44 AT2G46130ATWRKY43, WRKY DNA-
238	183	230	138	174	46 AT3G61680.1 alpha/bet
30	35	30	17	26	18 AT1G09530PAP3, PIF3phytochro
90	98	51	147	141	107 AT4G01800AGY1, AtpAlbino or
48	26	29	98	111	164 AT5G19730.1 Pectin ly
70	48	44	140	117	114 AT4G13030.1 P-loop co
20	18	18	88	150	143 AT5G64260EXL2 EXORDIUM

31	14	18	40	70	55 AT4G02290AtGH9B13, glycosyl
1	0	0	24	68	53 AT3G62950.1 Thioredox
105	121	95	251	289	175 AT3G63010ATGID1B, Galpha/bet
537	506	718	200	328	221 AT2G48020.1 Major fac
41	27	50	18	32	15 AT2G48070RPH1 resistanc
54	75	49	38	46	20 AT5G45710AT-HSFA4Cwinged-he
200	187	181	104	127	87 AT2G42610LSH10 Protein o
47	50	45	91	98	90 AT5G14060CARAB-AK-Aspartate
445	465	366	907	990	813 AT3G23690.1 basic hel
5	10	5	13	19	22 AT3G59010PME61 pectin me
463	461	402	596	663	565 AT1G05190emb2394 Ribosomal
1177	1271	1134	1068	1208	1034 AT2G04280.1
358	328	350	201	224	59 AT1G29000.1 Heavy met
167	182	159	143	133	55 AT2G16230.1 O-Glycosy
11	9	4	17	38	21 AT3G28920AtHB34, HBhomeobox
107	117	94	51	76	52 AT1G17950ATMYB52, Bmyb domai
122	76	109	70	75	14 AT3G18170.1 Glycosylt
109	82	90	64	59	12 AT3G18400anac058, NNAC domai
388	371	370	290	348	240 AT5G61340.1
19	18	20	44	69	17 AT1G60190.1 ARM repea
11	18	9	3	0	0 AT5G14740BETA CA2, carbonic
659	712	620	549	714	564 AT1G17100.1 SOUL heme
547	519	546	295	357	98 AT1G08510FATB fatty acy
197	198	196	312	326	322 AT5G45160.1 Root hair
157	142	149	112	132	42 AT5G51460ATTPPA Haloacid
218	262	219	165	174	79 AT5G62350.1 Plant inv
68	91	71	125	103	162 AT3G03620.1 MATE effl
137	149	124	71	93	77 AT5G47635.1 Pollen Ol
587	481	438	352	291	237 AT4G17220ATMAP70-5microtubu
116	88	66	46	69	57 AT5G04200AtMC9, MC9metacaspa
1404	1443	1342	1045	1276	1040 AT5G05110.1 Cystatin/
227	201	207	153	193	74 AT2G05990ENR1, MOD1NAD(P)-bi
125	117	97	74	74	45 AT2G41690AT-HSFB3, heat shoc
142	104	133	287	330	310 AT3G52500.1 Eukaryoti
680	678	750	539	705	537 AT5G062902-Cys Prx2-cystein
244	245	199	299	373	308 AT3G09600.1 Homeodoma
1057	1122	1006	718	856	648 AT2G37090 IRX9 Nucleotid
427	395	340	661	1005	667 AT2G37750.1
1418	1429	1622	941	1132	816 AT3G53980.1 Bifunctio
39	47	48	23	37	19 AT3G09085.1 Protein o
335	319	287	223	240	117 AT2G38060PHT4;2 phosphate
3551	3622	3082	2470	3246	2322 AT2G38120AUX1, MAP1Transmemb
268	269	186	326	390	362 AT5G01360TBL3 Plant pro
358	423	424	1079	1254	1099 AT5G01750.2 Protein o
1872	1797	1568	691	784	754 AT5G01930.1 Glycosyl
1739	1924	1693	1534	1625	1193 AT2G44160MTHFR2 methylene
123	100	99	191	290	119 AT3G59850.1 Pectin ly
4	3	11	29	20	29 AT2G43560.1 FKBP-like
839	752	690	455	565	446 AT5G10610CYP81K1 cytochrom
55	38	30	83	137	108 AT3G45140ATLOX2, LOlipoxygen
193	147	123	102	105	19 AT1G58120.1
60	85	78	180	253	121 AT1G70840MLP31 MLP-like
857	967	848	2582	3276	1470 AT1G17840ABCG11, ATwhite-bro
1005	803	812	601	732	432 AT2G32800AP4.3A protein k

179	187	158	226	328	296 AT3G01480ATCYP38, Ccyclophil
2	1	2	7	18	16 AT3G47800.1 Galactose
98	96	90	168	218	188 AT1G74160.1
32	32	25	156	224	176 AT1G25330.1 basic hel
45	58	48	98	59	123 AT3G47570.1 Leucine-r
80	51	66	38	55	17 AT5G37690.1 SGNH hydr
184	143	137	280	439	451 AT5G37600ATGLN1;1, glutamine
272	310	319	507	582	478 AT1G24625ZFP7 zinc fing
114	110	95	85	78	70 AT1G65730YSL7 YELLOW ST
20	26	32	61	89	81 AT3G57560NAGK N-acetyl-
393	334	367	205	219	45 AT2G24430ANAC038, ANAC domai
128	146	103	53	59	21 AT2G29110ATGLR2.8, glutamate
0	0	1	0	4	34 AT3G63520ATCCD1, ATcaroteno
2013	2040	2066	659	678	222 AT4G32810ATCCD8, CCcaroteno
78	92	88	278	322	289 AT5G25880ATNADP-MENADP-mali
2598	2508	3385	904	1387	1133 AT5G07990CYP75B1, DCytochrom
1520	1600	1346	851	1027	737 AT5G11890.1
184	189	155	70	138	53 AT1G74960ATKAS2, FAfatty aci
216	185	214	97	69	78 AT3G26060ATPRX Q Thioredox
78	97	72	66	62	47 AT3G42725.1 Putative
111	111	65	204	226	185 AT4G29060emb2726 elongatio
361	448	398	255	383	304 AT5G38420.1 Ribulose
3876	4376	3328	2872	3339	2864 AT5G17420ATCESA7, CCellulose
54	44	61	29	38	38 AT5G48930HCT hydroxyci
152	103	143	89	134	79 AT4G30610BRS1, SCPLalpha/bet
62	45	30	15	23	10 AT5G20260.1 Exostosin
118	113	122	182	197	160 AT1G02630.1 Nucleosid
957	904	880	289	286	258 AT1G80130.1 Tetratric
450	367	377	834	1264	742 AT4G10310ATHKT1, HKhigh-affi
79	98	99	54	62	67 AT2G22590.1 UDP-Glyco
1924	1939	1490	980	1180	860 AT2G03200.1 Eukaryoti
7	15	12	19	33	49 AT3G04290ATLTL1, LTLi-tolera
12	7	8	14	21	28 AT5G33370.1 GDSL-like
778	497	550	290	366	111 AT3G05950.1 RmlC-like
85	71	80	48	42	10 AT3G05950.1 RmlC-like
54	47	49	32	43	8 AT5G16770AtMYB9, MYmyb domai
500	613	433	720	846	691 AT5G17020ATCRM1, ATexportin
3312	4317	3362	8986	11230	7828 AT1G71380ATCEL3, ATcellulase
12	11	16	20	43	39 AT4G32480.1 Protein o
2905	2993	2578	3696	4505	3271 AT1G22530PATL2 PATELLIN
1723	1747	1357	3044	4251	3118 AT1G22710ATSUC2, SUSucrose-p
28	14	24	8	20	3 AT2G42360.1 RING/U-bo
601	612	582	197	274	64 AT3G09390ATMT-1, ATmetalloth
383	373	309	182	282	79 AT1G03700.1 Uncharact
327	292	294	754	993	671 AT4G03510ATRMA1, RMRING memb
477	561	453	1670	1608	1036 AT1G05710.5 basic hel
446	494	434	375	487	306 AT3G59690IQD13 IQ-domain
243	169	213	98	96	30 AT2G30210LAC3 laccase 3
126	123	104	362	509	242 AT2G25150.1 HXXXD-typ
2286	2112	1853	3564	5065	2852 AT5G58350WNK4, ZIK2with no 1
187	103	192	235	282	333 AT5G25610ATRD22, RDBURP doma
16	12	12	40	43	60 AT4G27290.1 S-locus 1
1345	1822	1783	844	1646	997 AT2G26560PLA IIA, Pphospholi
943	1214	881	501	562	517 AT5G37478.1 TPX2 (tar

30	27	27	78	83	113 AT5G10180AST68, SULslufate t
30	34	33	62	72	50 AT4G19840ATPP2-A1, phloem pr
75	70	64	111	121	84 AT4G04640ATPC1 ATPase, F
97	91	106	45	44	5 AT2G26560PLA IIA, Pphospholi
484	447	361	388	381	344 AT4G21990APR3, ATAPAPS reduc
239	185	224	129	157	49 AT2G05990ENR1, MOD1NAD(P)-bi
446	419	377	319	319	94 AT1G24430.1 HXXXD-tyr
35	40	27	102	167	169 AT3G01680.1
35	38	44	22	30	26 AT1G79620.1 Leucine-r
13	3	8	4	2	0 AT3G13610.1 2-oxoglut

eline.y
oxidase 16
ase 2
ase 2
rich repeat (LRR) family protein
ited Ca(2+)-ATPase, isoform 4
resistance-responsive (dirigent-like protein) family protein
al ion transporter 6
te intrinsic protein 6;1
opeptide repeat (TPR)-like superfamily protein
ase-like superfamily protein
.7
ile-associated protein 65-8
ain-like superfamily protein
ing (RRM/RBD/RNP motifs) family protein
a-Hydrolases superfamily protein
of unknown function, DUF538
hydrolase 9C2
of unknown function (DUF604)
family protein
RNA polymerase D1A
like homeobox of Arabidopsis thaliana 7
A
n protein 42
olar processing enzyme
opeptide repeat (TPR)-like superfamily protein

like 1
ethylesterase 3
ethylesterase 3
pha-trypsin inhibitor heavy chain-related
ne P450 superfamily protein
ransporter 3;4
hotransmitter 4
arate (2OG) and Fe(II)-dependent oxygenase superfamily protein
ethanol-choline (GMC) oxidoreductase family protein
alpha motif (SAM) domain-containing protein
rlosidase 4
vesting complex photosystem II subunit 6
ascorbate oxidase
esis-related thaumatin superfamily protein
oxidase 27
transferase family protein
ne P450, family 86, subfamily A, polypeptide 1
glyoxylate aminotransferase
in-regulated family protein
dehydrogenase 3F1
tein of unknown function (DUF828)

in-containing protein with a domain of unknown function (DUF21)
;1
-like arabinogalactan-protein 11

pe-related gene 3
pe acyl-transferase family protein
in repeat 6
of unknown function (DUF 3339)
A hydratase/isomerase D
histidine transporter 1
ase-like superfamily protein
L-methionine-dependent methyltransferases superfamily protein
dine synthase family protein
ase-like superfamily protein
-binding protein 28

ox superfamily protein
icine zipper (bZIP) transcription factor family protein
malate dehydrogenase family protein

i family protein
protein L13 family protein
pe transporter family protein
reonine-protein kinase WNK (With No Lysine)-related
mine beta-synthase (CBS) family protein
in-containing protein
cleotide-gated cation channel 4
nosyltransferase 12
one S-transferase TAU 19
em II subunit R
ectin protein kinase family protein
superfamily protein
e family protein
effect embryo arrest 22
like phosphatidylinositol transfer family protein
related homeobox 13
lar 5
in-containing protein

hydrolase 9B5
e homeodomain 7

ated kinase 2
ransporter 3;1
onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
ily protein
em II family protein
phosphate (PLP)-dependent transferases superfamily protein
in protein 93
ox superfamily protein
gion and MADS-box transcription factor family protein
inding Rossmann-fold superfamily protein
o AP2 1
ng protein 47C
e zinc finger family protein
rine peptidase 1
ident malic enzyme 2
-binding protein 43

apical Meristem) domain transcriptional regulator superfamily protein
investing chlorophyll-protein complex II subunit B1
bic-responsive NPH3 family protein
dehyde 3-phosphate dehydrogenase A subunit 2
ESR-RELATED 41

acetic acid inducible 11
e P450, family 81, subfamily D, polypeptide 8
inding EF-hand family protein
g resistance-associated protein 6
ethanol-choline (GMC) oxidoreductase family protein

like protein 1
e P450 superfamily protein
e P450 superfamily protein
brid motif superfamily protein
rotein 2
pooxygenase, PLAT/LH2 family protein
n protein 42
e homolog E1B
family protein
eta 8
bulin
ase-like superfamily protein
n protein 103
rane amino acid transporter family protein
e synthase like G3
e synthase like G3
n protein 67
on protein SH3-like family protein
n endotransglucosylase/hydrolase 5
in-like superfamily protein
in 20-2

gion and MADS-box transcription factor family protein
e protein dnaJ-related
phosphate (PLP)-dependent transferases superfamily protein
ile-associated protein 65-8
opeptide repeat (TPR)-like superfamily protein
e gamma-lyase
e gamma-lyase
ate:CoA ligase 2
ransferase 1
rich family protein
oot primordium (LRP) protein-related
rich repeat (LRR) family protein
ependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family prote
inding Rossmann-fold superfamily protein
rus rep interacting kinase 1
SYNTHASE
60 chaperonin family protein
tase 3
le cyclase/dehydrase and lipid transport superfamily protein
n endotransglucosylase/hydrolase 8

hem II subunit Q-2
heptide/Phox/Bem1p family protein
induced protein with YGL and LRDR motifs
in protein 12

he acyl-transferase family protein
cal transport/detoxification superfamily protein
e synthase family protein
e Lipase/Acylhydrolase superfamily protein
amily trypsin and protease inhibitor protein
osyl transferase 88A1
yglucosinolate 1
e synthase clone R1
colase-type esterase superfamily protein
in like 23
rich repeat protein kinase family protein
onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein

BIREFRINGENCE-LIKE 19

A1
e finger 2
e synthase 1
ide synthase
ome-interacting basic-helix-loop-helix 1

icine-zipper 44
-bisphosphate aldolase 2
rich protein 4

opolymerizing factor 5
yl CoA reductase-related male sterility protein
lose/UDP-D-xylose synthase 2
oplast intrinsic protein
of unknown function (DUF579)
ilitator superfamily protein
etylesterase family protein
in fatty alcohol dehydrogenase family protein
amine synthase 3
e synthase 6
ne P450, family 76, subfamily G, polypeptide 1
ontaining nucleoside triphosphate hydrolases superfamily protein
rocogenin-like starch initiation protein 5
ge-repair/toleration protein (DRT102)
r element differentiation-related 7
rocogenin-like starch initiation protein 1
in protein 93
ne P450, family 86, subfamily B, polypeptide 1
RRIPE like 7
Factor Y, subunit C2
related homeobox 13
embrane intrinsic protein 2;8
acid 5-hydroxylase 1
ing protein 1
of unknown function (DUF579)

ox superfamily protein
in protein 93
-containing protein
transporter 1;3
transporter 1;3
ftN21 /EamA-like transporter family protein
superfamily protein
in protein 52
se superfamily protein
e P450, family 78, subfamily A, polypeptide 7
em II family protein
linked oxidoreductase superfamily protein
onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
in containing protein 74
ase large subunit
e acyl-transferase family protein
inding lectin superfamily protein
ctosidase 3
otional factor B3 family protein / auxin-responsive factor AUX/IAA-related
se 3
min 1
osolic factor family protein / phosphoglyceride transfer family protein

lehyde-3-phosphate dehydrogenase B subunit
nscription factor family protein
transporter 4
transporter 4

osyltransferase superfamily protein
ase 9
ident synthetase and ligase family protein
on defective 1 protein / ELD1 protein
. protein S5 family protein
- exchanger 20
onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
inding EF-hand family protein
in gene 2
ftN21 /EamA-like transporter family protein
inding Rossmann-fold superfamily protein
like endoglucanases superfamily protein
.7
inding Rossmann-fold superfamily protein

Diphenol oxidase family protein
-3-phosphate acyltransferase 6
embrane intrinsic protein 1;4
xchanger 3
ld desaturase 8
tin superfamily protein
hydrolase superfamily protein
tose transporter 3
. protein L17 family protein

n family protein

an endotransglucosylase/hydrolase 32
membrane intrinsic protein 2
V-like arabinogalactan-protein 11
transmembrane MLO family protein
rose superfamily protein
rose S-transferase family protein
rosin superfamily protein

urate:CoA ligase 2
uridine synthase family protein
uridine-CoA synthase 10
uridine homeodomain-like superfamily protein
uridine protein 4

uridine cyclase/dehydrase and lipid transport superfamily protein
uridine-containing protein
uridine-containing protein
uridine of unknown function, DUF642
uridine-acetic acid inducible 29
uridine containing protein 38
uridine family protein
uridine-rich repeat (LRR) family protein
uridine acyl-transferase family protein
uridine-leucine zipper protein family
uridineolpyruvate carboxykinase 1
uridine main-containing protein kinase family protein
uridine related NAC-domain protein 1
uridine acid 5-hydroxylase 1
uridine alpha-Hydrolases superfamily protein

uridine homeodomain 4
uridine Lipase/Acylhydrolase superfamily protein
uridine TIC LEAVES 2-like 1
uridine lipase A 2A

uridine of unknown function (DUF579)
uridine heme P450, family 86, subfamily B, polypeptide 1
uridine main-containing protein / ABA-responsive protein-related
uridine main protein 92
uridine lipid amide hydrolase
uridine lipid permease 2
uridine main protein 69
uridine progesterone-like starch initiation protein 1
uridine r element differentiation-related 7

uridine proline-rich glycoprotein family protein
uridine phosphonic anhydrase 5
uridine main containing protein 73
uridine rich repeat (LRR) family protein
uridine uridine-diphospho-sugar transferases superfamily protein
uridine uridine lyase 1
uridine binding (RRM/RBD/RNP motifs) family protein
uridine uridine transporter family protein
uridine uridine cognate protein 70-1

-3-phosphate acyltransferase 7
 activase
 heptapeptide repeat (TPR)-like superfamily protein
 kinase family protein
 -phosphate adenylyltransferase family protein
 onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
 ilose-bisphosphatase
 rotein of unknown function (DUF828)
 BIREFRINGENCE-LIKE 33
 ;
 .2
 osylase superfamily protein
 in protein 67
 rane amino acid transporter family protein
 ase 3
 r-like superfamily protein

 osidase 1
 rich protein family
 al transport/detoxification superfamily protein
 le cyclase/dehydrase and lipid transport superfamily protein
 ertase/pectin methylesterase inhibitor superfamily protein
 yde dehydrogenase family protein
 in endotransglucosylase/hydrolase 28
 onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
 dehalogenase-like hydrolase (HAD) superfamily protein
 rll A-B binding family protein
 rylase 1
 r1-CoA synthase 11
 otif nuclear-localized protein 20
 ftN21 /EamA-like transporter family protein
 ane-fatty-acyl-phospholipid synthase
 ated protein C2B
 S41 family protein
 like superfamily protein
 ie sulfoxide reductase B5
 ated 1
 BIREFRINGENCE-LIKE 11
 on at the outer envelope membrane of chloroplasts 159
 rboxypeptidase-like 51
 of unknown function (DUF1635)
 in protein 36
 kinase superfamily protein
 le/sugar transporter family protein
 e e 1 allergen and extensin family protein
 onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
 ranscriptionally active 16

 ie P450, family 86, subfamily A, polypeptide 1
 /DUF1795-like photosystem II reaction center PsbP family protein
 ily protein
 ie P450 superfamily protein
 ie transporter family protein

dependent lipid-binding (CaLB domain) family protein
 uracil permease family protein
 zinc finger transcription factor family protein
 unknown function (DUF303)
 1
 -Hydrolases superfamily protein
 -prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase
 -sarcosine (2OG) and Fe(II)-dependent oxygenase superfamily protein
 -WD40 repeat-like superfamily protein
 -negative transcriptional regulator family protein
 -phosphate adenylyltransferase family protein

 -bisphosphate aldolase 2
 membrane intrinsic protein 1A
 -phospholipase-like protein (PEARLI 4) family
 -transferase family protein
 -synthase-like A02
 -Lipase/Acylhydrolase superfamily protein
 2
 -cysteine aspartyl protease family protein
 -ftsZ family protein
 -transcription factor family protein
 -reacting protein kinase 1
 -family hydrolase, subfamily IG, 5\'-nucleotidase
 -phosphatylesterase family protein
 -kinase 3

 -ole protein 1

 -ole acyl-transferase family protein
 -related protein C2B
 -of unknown function (DUF810)
 -transporter 3
 -ox superfamily protein
 -sarcosine (2OG) and Fe(II)-dependent oxygenase superfamily protein
 -synthase like G1
 -thio-CoA synthase 2
 -prenylyltransferase superfamily protein
 -porin domain-containing protein
 -calcium-binding protein family

 -ase superfamily protein
 -protein htpG family protein
 -phosphatase superfamily protein
 -N-acyltransferases (NAT) superfamily protein
 -phosphatase-like superfamily protein
 -of unknown function (DUF620)
 -in protein 67
 -phosphatase superfamily protein
 -phosphatase family protein

 2
 BIREFRINGENCE-LIKE 33
 -type P450 superfamily protein

brane amino acid transporter family protein
ed homeodomain-like superfamily protein
onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein

-3-phosphate acyltransferase 5
erised protein family (UPF0497)
C2HC zinc fingers superfamily protein
e transporter family protein
le-diphospho-sugar transferases superfamily protein
a-Hydrolases superfamily protein

subunit exo70 family protein G1
r-specific protease family C19-related protein
ux family protein
receptor kinase
repeat family protein
repeat family protein
repeat family protein
repeat family protein
em II subunit Q-2
ix-loop-helix (bHLH) DNA-binding superfamily protein
repeat cysteine protease family protein
rk cysteine peptidase 3
e Lipase/Acylhydrolase superfamily protein
BIREFRINGENCE-LIKE 38
e transporter family protein
one S-transferase TAU 19
ilin A-like lectin protein kinase family protein
pical Meristem) domain transcriptional regulator superfamily protein
ng Berberine family protein
ng Berberine family protein
ase-like superfamily protein
ransferase 1
/ESR-RELATED 41
nsferase 16

xygenase
n containing protein 58
e Lipase/Acylhydrolase superfamily protein
ase superfamily protein
1
)-xylulose 5-phosphate reductoisomerase
ethionine sulfoxide reductase 1
le diphosphate kinase 2
of unknown function (DUF 3339)
family protein
hydrolase family 38 protein
r-protoporphyrin IX methyltransferase

ain-like superfamily protein
like protein 6
vertase/pectin methylesterase inhibitor superfamily protein
vertase/pectin methylesterase inhibitor superfamily protein
family protein

in endotransglycosylase 6
of unknown function, DUF538

of unknown function (DUF1645)
in P450, family 93, subfamily D, polypeptide 1

unregulated-like 1
-phosphate isomerase, type A protein
olopyruvate carboxylase kinase 2
peptide repeat (PPR-like) superfamily protein
5'-phosphosulfate (APS) kinase 3
dehydrogenase 1
superfamily protein

A15
membrane choline transporter family protein
in P450 superfamily protein
acyl-transferase family protein
lase superfamily protein
lase superfamily protein
of unknown function (DUF579)
protein 33
-like 3
transferase family protein
3
13

ix-loop-helix (bHLH) DNA-binding superfamily protein
;1
in-containing protein 15
regulating factor 1
in-containing protein 38
inding Rossmann-fold superfamily protein
in-regulated family protein
ox superfamily protein
in protein 73
reonine-protein kinase WNK (With No Lysine)-related
in-like serine endopeptidase family protein
in-like serine endopeptidase family protein
in like 37

le-diphospho-sugar transferases superfamily protein
of unknown function (DUF607)
osyltransferase superfamily protein
in P450, family 721, subfamily A, polypeptide 1
-L-methionine-dependent methyltransferases superfamily protein
e transporter family protein
zinc finger transcription factor family protein
-binding protein 43
a-Hydrolases superfamily protein
ome interacting factor 3
Glassy Yellow 1
ase-like superfamily protein
ontaining nucleoside triphosphate hydrolases superfamily protein
like 2

hydrolase 9B13
tin superfamily protein
ca-Hydrolases superfamily protein
ilitator superfamily protein
e to phytophthora 1
elix DNA-binding transcription factor family protein
of unknown function (DUF640)
e kinase family protein
ix-loop-helix (bHLH) DNA-binding superfamily protein
ethylesterase 61
protein L6 family

al transport/detoxification superfamily protein
l hydrolases family 17 protein
protein 34
n protein 52
ransferase family 61 protein
n containing protein 58

at superfamily protein
anhydrase 2
e-binding family protein
l-ACP thioesterases B
defective 3 GTP-binding protein (RHD3)
dehalogenase-like hydrolase (HAD) superfamily protein
vertase/pectin methylesterase inhibitor superfamily protein
ux family protein
e e 1 allergen and extensin family protein
ile-associated proteins 70-5
ase 9
/monellin family protein
inding Rossmann-fold superfamily protein
ek transcription factor B3
ic aspartyl protease family protein
e peroxiredoxin B
in-like superfamily protein
le-diphospho-sugar transferases superfamily protein

onal inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
of unknown function (DUF962)
e transporter 4;2
rane amino acid transporter family protein
tein of unknown function (DUF828)
of unknown function (DUF567)
hydrolase superfamily protein
etetrahydrofolate reductase 2
rase-like superfamily protein
e peptidyl-prolyl cis-trans isomerase family protein
e P450, family 81, subfamily K, polypeptide 1
ase 2

protein 31
own complex homolog protein 11
kinase family protein

in 38

mutarotase-like superfamily protein

ix-loop-helix (bHLH) DNA-binding superfamily protein

rich repeat protein kinase family protein

colase-type esterase superfamily protein

ynthase clone R1

ger protein 7

RIPE like 7

-l-glutamate kinase

n containing protein 38

receptor 2.8

ld cleavage dioxygenase 1

ld cleavage dioxygenase 8

c enzyme 3

ne P450 superfamily protein

ld biosynthesis 1

kin superfamily protein

membrane lipoprotein

on factor Ts family protein

bisphosphate carboxylase (small chain) family protein

ynthase family protein

nnamoyl-CoA shikimate/quinic acid hydroxycinnamoyl transferase

ca-Hydrolases superfamily protein

n family protein

le transporter family protein

opeptide repeat (TPR)-like superfamily protein

nity K⁺ transporter 1

osyltransferase superfamily protein

c aspartyl protease family protein

nt lipase 1

Lipase/Acylhydrolase superfamily protein

cupins superfamily protein

cupins superfamily protein

n protein 9

1A

3

of unknown function (DUF506)

2

roton symporter 2

ox superfamily protein

nionein 2A

erised protein family (UPF0497)

rane-anchor 1

ix-loop-helix (bHLH) DNA-binding superfamily protein

n 13

}

oe acyl-transferase family protein

ysine (K) kinase 4

uin-containing protein

ectin protein kinase family protein

pase A 2A

argeting protein for Xklp2) protein family

transporter 2;1

protein 2-A1

71 complex, gamma subunit protein

lipase A 2A

stase 3

inding Rossmann-fold superfamily protein

de acyl-transferase family protein

rich repeat protein kinase family protein

arate (2OG) and Fe(II)-dependent oxygenase superfamily protein

