

Monitoring gene expression pattern in somatic hybrid of *Solanum tuberosum* and *S. pinnatisectum* for late blight resistance using microarray analysis

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Supplementary Table S1. Summary of 66 up-regulated and GO-annotated genes in somatic hybrid P-7 after challenge inoculation with *P. infestans*

SN	Gene ID	PGSC description	Fold change	p value	Uniprot ID	GO annotation		
						Biological process	Molecular function	Cellular component
<i>Set 1: Defense response</i>								
1.	PGSC0003DMG400005111	PR1 protein	49.54	0.05	M1A2A4	NA	NA	GO:0005576 (extracellular region)
2.	PGSC0003DMG400011920	SNKR2GH5 protein	26.89	0.05	M1AV76	NA	GO:0043531 (ADP binding)	NA
3.	PGSC0003DMG400002217	NBS-LRR resistance protein	15.42	0.05	M0ZQ85	NA	GO:0043531	NA
4.	PGSC0003DMG400002874	Sn-1 protein	10.39	0.05	M0ZT12	GO:0006952 (defense response)	NA	NA
5.	PGSC0003DMG401002242	Disease resistance protein BS2	10.00	0.05	M0ZQC7	NA	GO:0043531 (ADP binding)	NA
6.	PGSC0003DMG400041706	Zinc knuckle family protein	10.84	0.05	M1DP59	NA	GO:0003676	NA
7.	PGSC0003DMG400016556	Elongation factor 1-alpha	11.32	0.05	M1BDH0	NA	GO:0005525 (GTP binding)	NA
8.	PGSC0003DMG400025481	WRKY domain class transcription factor	10.30	0.05	M1CE46	GO:0006355 (regulation of transcription, DNA-templated)	GO:0003700 (sequence-specific DNA binding transcription factor activity)	NA

9.	PGSC0003DMG400028007	Ripening regulated protein DDTFR10	10.51	0.05	M1CPJ9	GO:0006412 (translation)	GO:0003746 (translation elongation factor activity)	GO:0005853 (eukaryotic translation elongation factor 1 complex)
<i>Set 2: Binding function</i>					0.05			
1.	PGSC0003DMG400023522	Histone H4	17.81	0.05	M1B9C1	GO:0006334 (nucleosome assembly)	GO:0003677 (DNA binding)	GO:0000786 (nucleosome)
2.	PGSC0003DMG400026433	ATP binding protein	15.26	0.05	M1C184	GO:0007165 (signal transduction)	GO:0000166 (nucleotide binding)	NA
3.	PGSC0003DMG400027834	'chromo' domain containing protein	14.60	0.05	M1CNY4	NA	GO:0003676 (nucleic acid binding)	NA
4.	PGSC0003DMG400042845	'chromo' domain containing protein	12.60	0.05	M1DRL5	NA	GO:0003676	NA
5.	PGSC0003DMG400043567	'chromo' domain containing protein	12.16	0.05	M1DT60	NA	GO:0003676	NA
6.	PGSC0003DMG400043731	Polyprotein	11.96	0.05	M1DTJ2	NA	GO:0003676	NA
7.	PGSC0003DMG400045596	Gag-pol polyprotein	11.42	0.05	M1DXJ8	NA	GO:0003676	NA
8.	PGSC0003DMG400044544	'chromo' domain containing protein	10.63	0.05	M1DVA5	NA	GO:0003676	NA
9.	PGSC0003DMG400025418	Retrotransposon protein	10.25	0.05	M1CDV8	GO:0015074 (DNA integration)	GO:0003676	NA
10.	PGSC0003DMG400010462	Bcl-2-associated athanogene	10.08	0.05	M1AP80	NA	GO:0051087 (chaperone binding)	NA
11.	PGSC0003DMG400020534	Protein ycf2	23.47	0.05	M1BU51	NA	GO:0005524 (ATP binding)	GO:0009507
12.	PGSC0003DMG400003335	DNA-directed RNA polymerase subunit alpha	18.73	0.05	M0ZUU3	GO:0006351 (transcription, DNA-templated)	GO:0003677 (DNA binding)	NA
<i>Set 3: Oxidation-reduction and photosynthesis</i>						0.05		
1.	PGSC0003DMG400019709	Lipoxygenase (LOX)	18.36	0.05	M1BQS2	GO:0055114 (oxidation- reduction process)	GO:0016491 (oxidoreductase activity)	NA
2.	PGSC0003DMG400013414	Chlorophyll a-b binding protein 3C, chloroplastic	17.53	0.05	M1B1H1	GO:0015979 (photosynthesis)	GO:0016168 (chlorophyll binding)	GO:0009507 (chloroplast)
3.	PGSC0003DMG400009814	Cytochrome P450	15.50	0.05	M1ALE3	GO:0055114	GO:0016491	NA
4.	PGSC0003DMG400013415	Chlorophyll a-b binding protein 3C, chloroplastic	12.40	0.05	M1B1H2	GO:0015979	GO:0016168	GO:0009507
5.	PGSC0003DMG400020809	Cytochrome P450	12.24	0.05	M1BV90	GO:0055114	GO:0016491	NA

6.	PGSC0003DMG400009811	Cytochrome P450	12.20	0.05	M1ALE1	GO:0055114	GO:0005506 (iron ion binding)	NA
7.	PGSC0003DMG400008476	ATP synthase subunit alpha, chloroplastic	12.00	0.05	M1AFS2	GO:0015991 (ATP hydrolysis coupled proton transport)	GO:0016820 (hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances)	GO:0033178 (proton- transporting two-sector ATPase complex, catalytic domain)
8.	PGSC0003DMG400037286	Ferredoxin II	10.54	0.05	M1DEE2	GO:0022900 (electron transport chain)	GO:0009055 (electron carrier activity)	NA
9.	PGSC0003DMG400009812	Cytochrome P450	10.91	0.05	M1ALE2	GO:0055114	GO:0005506	NA
10.	PGSC0003DMG400000928	NADH dehydrogenase subunit 5	12.84	0.05	M0ZK42	GO:0055114	GO:0016491	NA
11.	PGSC0003DMG400006702	Photosystem I reaction center subunit V, chloroplast	11.83	0.05	M1A8N3	GO:0015979	GO:0016168	GO:0009522 (photosystem I)
12.	PGSC0003DMG400008300	Chlorophyll a/b binding protein	10.80	0.05	M1AF18	GO:0015979	GO:0016168	GO:0009507
13.	PGSC0003DMG400013413	Chlorophyll a/b-binding protein PS II-Type I	12.67	0.05	M1B1G9	GO:0015979	GO:0016168	GO:0009507
14.	PGSC0003DMG400026276	Leucoanthocyanidin dioxygenase	10.66	0.05	M1CHI5	GO:0055114	GO:0016491	NA
<i>Set 4: Metabolic process</i>						0.05		
1.	PGSC0003DMG401010218	Phospholipase A1	22.95	0.05	M1AN73	GO:0006629 (lipid metabolic process)	GO:0016787 (hydrolase activity)	NA
2.	PGSC0003DMG400038064	Beta-glucosidase	19.02	0.05	M1DG35	GO:0005975 (carbohydrate metabolic process)	GO:0004553 (hydrolase activity, hydrolyzing O- glycosyl compounds)	NA
3.	PGSC0003DMG400010490	Acidic class II 1,3-beta-glucanase	17.90	0.05	M1APC4	GO:0005975	GO:0004553	NA
4.	PGSC0003DMG400010771	Pectate lyase	17.25	0.05	M1AQF5	GO:0008150 (biological process)	GO:0016829 (lyase activity)	NA
5.	PGSC0003DMG400024362	Anthranilate N-benzoyltransferase protein	15.83	0.05	M1C9A7	GO:0008152 (metabolic process)	GO:0016747 (transferase activity, transferring acyl groups other than amino-acyl groups)	NA
6.	PGSC0003DMG400002342	Glucan endo-1,3-beta-glucosidase	14.90	0.05	M0ZQQ0	GO:0005975	GO:0004553	NA

7.	PGSC0003DMG401028252	Beta-fructofuranosidase (invertase)	14.79	0.05	M1CQM7	GO:0005975	GO:0004553	NA
8.	PGSC0003DMG400046023	Matrix metalloprotease 1	14.25	0.05	M1DYG9	GO:0006508	GO:0004222 (metalloendopeptidase activity)	GO:0031012 (extracellular matrix)
9.	PGSC0003DMG400029700	Proline-rich protein 1	13.48	0.05	M1CWM5	-	GO:0005199 (structural constituent of cell wall)	NA
10.	PGSC0003DMG401031759	Phospholipase A1	12.46	0.05	M1D4F7	GO:0006629	GO:0016787	NA
11.	PGSC0003DMG400004960	Poly(ADP-ribose) polymerase, catalytic region	12.43	0.05	M1A1N9	GO:0008152	GO:0003950 (NAD+ ADP-ribosyltransferase activity)	NA
12.	PGSC0003DMG400001948	Copalyl diphosphate synthase	12.41	0.05	M0ZP75	GO:0008152	GO:0000287 (Mg ion binding)	NA
13.	PGSC0003DMG400017091	Patatin-01	12.22	0.05	M1BFJ1	GO:0006629	GO:0016787	NA
14.	PGSC0003DMG400002213	Aldehyde dehydrogenase	10.36	0.05	M0ZQ78	GO:0008152	GO:0016491 (oxidoreductase activity)	NA
15.	PGSC0003DMG400005973	AT3G45050 protein	10.21	0.05	M1A5U4	GO:0000023 (maltose metabolic process)	GO:0003674 (molecular function)	NA
16.	PGSC0003DMG400010831	Protein phosphatase 2C	10.20	0.05	M1AQP4	GO:0008152	GO:0003824 (catalytic activity)	NA
<i>Set 5: tRNA processing</i>						0.05		
1.	PGSC0003DMG400026805	Isopentenyltransferase	14.67	0.05	M1CJN5	GO:0008033 (tRNA processing)	NA	NA
2.	PGSC0003DMG400034585	ATP binding protein	13.47	0.05	M1D8K2	GO:0008033	NA	NA
3.	PGSC0003DMG400040970	Isopentenyltransferase	13.23	0.05	M1DMI0	GO:0008033	NA	NA
4.	PGSC0003DMG400038336	Isopentenyltransferase	11.26	0.05	M1DGN8	GO:0008033	NA	NA
5.	PGSC0003DMG400036946	Isopentenyltransferase	10.06	0.05	M1DDQ4	GO:0008033	NA	NA
<i>Set 6: Protein phosphorylation</i>						0.05		
1.	PGSC0003DMG400025595	Kinase	23.56	0.05	M1CEJ1	GO:0006468 (protein phosphorylation)	GO:0004672 (protein kinase activity)	NA
2.	PGSC0003DMG400003982	ATP binding protein	17.60	0.05	M0ZXLO	GO:0006468	GO:0004672	NA
3.	PGSC0003DMG400030581	Receptor kinase	17.06	0.05	M1D0D8	GO:0006468	GO:0004672	NA
4.	PGSC0003DMG402030532	Wall-associated kinase	12.36	0.05	M1D042	GO:0006468	GO:0000166 (nucleotide binding)	NA

5.	PGSC0003DMG403014059	Receptor kinase	12.33	0.05	M1B3R1	GO:0006468	GO:0004672	NA
6.	PGSC0003DMG400017738	Brassinosteroid insensitive 1-associated receptor kinase 1	11.70	0.05	M1BI51	GO:0006468	GO:0004672	NA
7.	PGSC0003DMG400019726	Receptor serine/threonine kinase	12.29	0.05	M1BQV6	GO:0006468	GO:0000166	NA
8.	PGSC0003DMG400010941	Serine/threonine-protein kinase-like domain domain containing protein	11.54	0.05	M1AR19	GO:0006468	GO:0004672	NA
<i>Set 7: Methylation</i>						0.05		
1.	PGSC0003DMG400005231	Ribosomal RNA methyltransferase	14.30	0.05	M1A2T4	GO:0001510 (RNA methylation)	GO:0008168 (methyltransferase activity)	GO:0005634 (nucleus)
2.	PGSC0003DMG401018646	O-methyltransferase	13.32	0.05	M1BLR3	GO:0032259 (methylation)	GO:0008168	NA

Supplementary Table S2. Details of 254 up-regulated genes with GO annotation not found and known/unknown PGSC description

SN	PGSC ID	PGSC Description	Fold change	<i>p</i> value	Uniprot ID	GO term
<i>i) Known PGSC description</i>						
1.	PGSC0003DMG402025507	Hcr2-0A	25.87	0.05	M1CE91	NA
2.	PGSC0003DMG400020533	Protein ycf2	25.36	0.05	M1BU50	NA
3.	PGSC0003DMG400031446	Hcr2-0A	20.65	0.05	M1D3X0	NA
4.	PGSC0003DMG400002886	Serine-threonine protein kinase, plant-type	19.87	0.05	M0ZT24	NA
5.	PGSC0003DMG400046019	Cytokinin synthase	19.39	0.05	M1DYG6	NA

6.	PGSC0003DMG400036709	Gag-pol polyprotein	19.23	0.05	M1DD86	NA
7.	PGSC0003DMG405025785	Dynamin	18.93	0.05	M1CFB1	NA
8.	PGSC0003DMG400039966	Protein kinase	18.07	0.05	M1DKA7	NA
9.	PGSC0003DMG400006652	Hcr9-OR2A	17.91	0.05	M1A8H1	NA
10.	PGSC0003DMG400042019	Mads box protein	17.82	0.05	M1DPU0	NA
11.	PGSC0003DMG400039392	Integrase core domain containing protein	17.25	0.05	M1DJ00	NA
12.	PGSC0003DMG400044207	Singapore isolate B (sub-type 7) whole genome shotgun sequence assembly, scaffold_7	17.22	0.05	M1DUJ2	NA
13.	PGSC0003DMG400036193	Gag-pol polyprotein	16.90	0.05	M1DC58	NA
14.	PGSC0003DMG400041401	Adenylate isopentenyltransferase	16.83	0.05	M1DNH7	NA
15.	PGSC0003DMG400014753	M18S-3Ap	16.81	0.05	M1B6I6	NA
16.	PGSC0003DMG400041287	Integrase core domain containing protein	16.75	0.05	M1DN92	NA
17.	PGSC0003DMG400038411	Low quality protein: amiloride-sensitive sodium channel subunit alpha	16.66	0.05	M1DGU6	NA
18.	PGSC0003DMG400013071	Polyprotein	16.27	0.05	M1B011	NA
19.	PGSC0003DMG400045085	Integrase core domain containing protein	16.19	0.05	M1DWH1	NA
20.	PGSC0003DMG400022876	Late blight resistance protein	16.06	0.05	M1C3F8	NA
21.	PGSC0003DMG400006470	Uncharacterized mitochondrial protein	16.04	0.05	M1A7V5	NA
22.	PGSC0003DMG400024439	NL0D	15.94	0.05	M1C9J5	NA
23.	PGSC0003DMG400001949	Gag-pol polyprotein	15.77	0.05	M0ZP76	NA
24.	PGSC0003DMG400015349	Disease resistance protein	15.75	0.05	M1B8M8	NA
25.	PGSC0003DMG400039336	Integrase core domain containing protein	15.70	0.05	M1DIV8	NA
26.	PGSC0003DMG400007796	DNA-directed RNA polymerase II largest subunit	15.60	0.05	M1AD13	NA
27.	PGSC0003DMG400009680	Zinc knuckle family protein	15.13	0.05	M1AKY4	NA
28.	PGSC0003DMG400037942	Gag-pol polyprotein	15.09	0.05	M1DFU2	NA
29.	PGSC0003DMG400035447	Singapore isolate B (sub-type 7) whole genome shotgun sequence assembly, scaffold_9	14.95	0.05	M1DAG7	NA
30.	PGSC0003DMG400019010	Adhesive plaque matrix protein	14.68	0.05	M1BN19	NA
31.	PGSC0003DMG400042304	Retrotransposon gag protein	14.51	0.05	M1DQF4	NA
32.	PGSC0003DMG400029155	Gag-pol polyprotein	14.22	0.05	M1CUE9	NA
33.	PGSC0003DMG400030168	Late blight resistance protein	14.11	0.05	M1CYK5	NA
34.	PGSC0003DMG400030981	Polygalacturonase non-catalytic subunit AroGP3	13.95	0.05	M1D221	NA
35.	PGSC0003DMG401025507	Hcr2-5D	13.92	0.05	M1CE90	NA
36.	PGSC0003DMG400042948	Gag-pol polyprotein	13.53	0.05	M1DRU6	NA
37.	PGSC0003DMG400044098	Gag-pol polyprotein	13.34	0.05	M1DUB4	NA
38.	PGSC0003DMG400046783	NB-ARC domain containing protein	13.29	0.05	M1E050	NA
39.	PGSC0003DMG400020399	'chromo' domain containing protein	13.29	0.05	M1BTL9	NA
40.	PGSC0003DMG400021063	Gag-pol polyprotein	13.12	0.05	M1BW27	NA
41.	PGSC0003DMG400039442	Gag-pol polyprotein	13.10	0.05	M1DJ38	NA

42.	PGSC0003DMG400043881	Gag-pol protein	13.07	0.05	M1DTV3	NA
43.	PGSC0003DMG400042745	Transcription factor hy5	12.92	0.05	M1DRD9	NA
44.	PGSC0003DMG400040420	'chromo' domain containing protein	12.84	0.05	M1DLB7	NA
45.	PGSC0003DMG400023864	Hcr2-0B	12.77	0.05	M1C7C8	NA
46.	PGSC0003DMG400041103	Leucine-rich repeat resistance protein	12.67	0.05	M1DMU5	NA
47.	PGSC0003DMG400038957	Integrase core domain containing protein	12.60	0.05	M1DI20	NA
48.	PGSC0003DMG400039619	Integrase core domain containing protein	12.58	0.05	M1DJI3	NA
49.	PGSC0003DMG400034767	'chromo' domain containing protein	12.58	0.05	M1D8Y7	NA
50.	PGSC0003DMG400041511	'chromo' domain containing protein	12.54	0.05	M1DNR3	NA
51.	PGSC0003DMG400041728	Integrase core domain containing protein	12.52	0.05	M1DP78	NA
52.	PGSC0003DMG400040435	Gag-pol protein	12.29	0.05	M1DLC9	NA
53.	PGSC0003DMG400027638	Mutator transposase-like polypeptide	12.15	0.05	M1CN58	NA
54.	PGSC0003DMG400004727	Hcr2-0A	12.11	0.05	M1A0M6	NA
55.	PGSC0003DMG400046629	Gag-pol protein	11.95	0.05	M1DZT8	NA
56.	PGSC0003DMG400045212	Gag-pol polyprotein	11.92	0.05	M1DWR4	NA
57.	PGSC0003DMG400022988	EIX receptor 1	11.86	0.05	M1C3X3	NA
58.	PGSC0003DMG400019806	Disease resistance protein RGA3	11.81	0.05	M1BR56	NA
59.	PGSC0003DMG400030939	Integrase core domain containing protein	11.74	0.05	M1D1V9	NA
60.	PGSC0003DMG402023866	Hcr2-0B	11.66	0.05	M1C7D0	NA
61.	PGSC0003DMG400043672	Gag-pol protein	11.62	0.05	M1DTE7	NA
62.	PGSC0003DMG400034692	Integrase core domain containing protein	11.61	0.05	M1D8T1	NA
63.	PGSC0003DMG400042125	'chromo' domain containing protein	11.53	0.05	M1DQ20	NA
64.	PGSC0003DMG402002548	Uncharacterized Cys-rich domain	11.36	0.05	M0ZRJ3	NA
65.	PGSC0003DMG400022095	Retrotransposon protein	11.35	0.05	M1BZX3	NA
66.	PGSC0003DMG400027470	ATP binding protein	11.33	0.05	M1CMI4	NA
67.	PGSC0003DMG400021883	Reverse transcriptase	11.29	0.05	M1BZA7	NA
68.	PGSC0003DMG400038875	Inositol polyphosphate multikinase	11.03	0.05	M1DHW4	NA
69.	PGSC0003DMG400021473	Late blight resistance protein	10.91	0.05	M1BXQ8	NA
70.	PGSC0003DMG400013872	'chromo' domain containing protein	10.85	0.05	M1B347	NA
71.	PGSC0003DMG401006653	Disease resistance protein	10.79	0.05	M1A8H2	NA
72.	PGSC0003DMG400026795	Plant resistance protein	10.63	0.05	M1CJM9	NA
73.	PGSC0003DMG400039609	NB-ARC domain containing protein	10.63	0.05	M1DJH3	NA
74.	PGSC0003DMG400020871	Signal recognition particle receptor subunit beta	10.61	0.05	M1BVH2	NA
75.	PGSC0003DMG400019071	M18S-3Ap	10.51	0.05	M1BN75	NA
76.	PGSC0003DMG400006655	Cf-2.1	10.51	0.05	M1A8H8	NA
77.	PGSC0003DMG400013043	Imp biosynthesis protein	10.50	0.05	M1AZY1	NA
78.	PGSC0003DMG400037911	Gag-pol polyprotein	10.45	0.05	M1DFR7	NA
79.	PGSC0003DMG400044239	Integrase core domain containing protein	10.36	0.05	M1DUL9	NA
80.	PGSC0003DMG400036116	Integrase core domain containing protein	10.35	0.05	M1DBZ8	NA

81.	PGSC0003DMG400046883	Polyprotein	10.33	0.05	M1E0D0	NA
82.	PGSC0003DMG401024806	Myosin heavy chain, striated muscle	10.31	0.05	M1CBA5	NA
83.	PGSC0003DMG400035801	Retrotransposon gag protein	10.29	0.05	M1DBA5	NA
84.	PGSC0003DMG400046879	Gag-pol protein	10.18	0.05	M1E0C7	NA
85.	PGSC0003DMG400039662	Integrase core domain containing protein	10.11	0.05	M1DJL9	NA
86.	PGSC0003DMG400034334	Gag-pol polyprotein	10.04	0.05	M1D7Z9	NA
87.	PGSC0003DMG400042465	Gag-pol polyprotein	10.02	0.05	M1DQT2	NA
<i>ii) Unknown PGSC description</i>						0.05
88.	PGSC0003DMG400021704	Conserved gene of unknown function	10.97	0.05	M1BYQ0	GO:0006508 (proteolysis) (P) GO:0004190 (aspartic-type endopeptidase activity) (F)
89.	PGSC0003DMG400019712	Conserved gene of unknown function	17.45	0.05	M1BQS5	GO:0006468 (protein phosphorylation) (P) GO:0004672 (protein kinase activity) (F)
90.	PGSC0003DMG400014738	Conserved gene of unknown function	25.15	0.05	M1B6H8	NA
91.	PGSC0003DMG400015345	Conserved gene of unknown function	22.95	0.05	M1B8M4	NA
92.	PGSC0003DMG400015347	Conserved gene of unknown function	22.30	0.05	M1B8M5	NA
93.	PGSC0003DMG400041217	Gene of unknown function	19.69	0.05	M1DN34	NA
94.	PGSC0003DMG400045203	Gene of unknown function	19.10	0.05	M1DWQ8	NA
95.	PGSC0003DMG400046406	Gene of unknown function	18.89	0.05	M1DZC2	NA
96.	PGSC0003DMG400034680	Gene of unknown function	17.80	0.05	M1D8S4	NA
97.	PGSC0003DMG400014501	Conserved gene of unknown function	17.80	0.05	M1B5L5	NA
98.	PGSC0003DMG400035232	Gene of unknown function	17.60	0.05	M1D9Z9	NA
99.	PGSC0003DMG400015654	Gene of unknown function	17.59	0.05	M1B9X2	NA
100.	PGSC0003DMG400046976	Unknown protein	17.51	0.05	M1E0K0	NA
101.	PGSC0003DMG400045537	Gene of unknown function	17.15	0.05	M1DXF1	NA
102.	PGSC0003DMG400046856	Gene of unknown function	16.79	0.05	M1E0A8	NA
103.	PGSC0003DMG400047225	Gene of unknown function	16.56	0.05	M1E142	NA
104.	PGSC0003DMG400043979	Gene of unknown function	16.50	0.05	M1DU31	NA
105.	PGSC0003DMG400036612	Gene of unknown function	16.38	0.05	M1DD20	NA
106.	PGSC0003DMG400011927	Gene of unknown function	16.38	0.05	M1AV81	NA
107.	PGSC0003DMG400034679	Gene of unknown function	16.31	0.05	M1D8S3	NA
108.	PGSC0003DMG400035659	Gene of unknown function	16.30	0.05	M1DAY8	NA

109.	PGSC0003DMG400016024	Gene of unknown function	16.14	0.05	M1BBA5	NA
110.	PGSC0003DMG400015348	Conserved gene of unknown function	16.03	0.05	M1B8M7	NA
111.	PGSC0003DMG400014930	Gene of unknown function	15.96	0.05	M1B775	NA
112.	PGSC0003DMG400041219	Gene of unknown function	15.95	0.05	M1DN36	NA
113.	PGSC0003DMG400030655	Gene of unknown function	15.81	0.05	M1D0Q5	NA
114.	PGSC0003DMG400043495	Gene of unknown function	15.58	0.05	M1DT07	NA
115.	PGSC0003DMG400040213	Gene of unknown function	15.19	0.05	M1DKU9	NA
116.	PGSC0003DMG400043474	Gene of unknown function	15.05	0.05	M1DSZ3	NA
117.	PGSC0003DMG400028997	Conserved gene of unknown function	15.02	0.05	M1CTX2	NA
118.	PGSC0003DMG400044330	Gene of unknown function	14.98	0.05	M1DUU0	NA
119.	PGSC0003DMG400044118	Gene of unknown function	14.82	0.05	M1DUC7	NA
120.	PGSC0003DMG400044778	Gene of unknown function	14.78	0.05	M1DVS9	NA
121.	PGSC0003DMG400036676	Gene of unknown function	14.65	0.05	M1DD63	NA
122.	PGSC0003DMG400039715	Conserved gene of unknown function	14.63	0.05	M1DJR5	NA
123.	PGSC0003DMG400037486	Gene of unknown function	14.61	0.05	M1DEU5	NA
124.	PGSC0003DMG400044540	Conserved gene of unknown function	14.44	0.05	M1DVA1	NA
125.	PGSC0003DMG400044682	Gene of unknown function	14.31	0.05	M1DVL9	NA
126.	PGSC0003DMG400046039	Gene of unknown function	14.24	0.05	M1DYI2	NA
127.	PGSC0003DMG400025416	Gene of unknown function	14.21	0.05	M1CDV6	NA
128.	PGSC0003DMG400041586	Gene of unknown function	14.20	0.05	M1DNW8	NA
129.	PGSC0003DMG400043465	Gene of unknown function	14.17	0.05	M1DSY6	NA
130.	PGSC0003DMG400037763	Gene of unknown function	14.10	0.05	M1DFF1	NA
131.	PGSC0003DMG400042177	Gene of unknown function	14.06	0.05	M1DQ58	NA
132.	PGSC0003DMG400046462	Gene of unknown function	14.05	0.05	M1DZG6	NA
133.	PGSC0003DMG400034633	Gene of unknown function	14.00	0.05	M1D8N6	NA
134.	PGSC0003DMG400035498	Gene of unknown function	13.88	0.05	M1DAL0	NA
135.	PGSC0003DMG400043256	Gene of unknown function	13.77	0.05	M1DSH6	NA
136.	PGSC0003DMG400042793	Gene of unknown function	13.74	0.05	M1DRH4	NA
137.	PGSC0003DMG400038033	Gene of unknown function	13.74	0.05	M1DG10	NA
138.	PGSC0003DMG400041443	Gene of unknown function	13.69	0.05	M1DNK6	NA
139.	PGSC0003DMG400039224	Gene of unknown function	13.64	0.05	M1DIM1	NA
140.	PGSC0003DMG400040817	Gene of unknown function	13.60	0.05	M1DM62	NA
141.	PGSC0003DMG400040874	Gene of unknown function	13.56	0.05	M1DMA8	NA
142.	PGSC0003DMG400038037	Gene of unknown function	13.53	0.05	M1DG13	NA
143.	PGSC0003DMG400042010	Gene of unknown function	13.41	0.05	M1DPT5	NA
144.	PGSC0003DMG400011478	Gene of unknown function	13.37	0.05	M1ATH6	NA
145.	PGSC0003DMG400034650	Gene of unknown function	13.36	0.05	M1D8P9	NA
146.	PGSC0003DMG400039630	Gene of unknown function	13.34	0.05	M1DJJ1	NA
147.	PGSC0003DMG400038985	Gene of unknown function	13.32	0.05	M1DI40	NA

148.	PGSC0003DMG400036826	Gene of unknown function	13.30	0.05	M1DDG2	NA
149.	PGSC0003DMG400043622	Gene of unknown function	13.28	0.05	M1DTA5	NA
150.	PGSC0003DMG400023284	Conserved gene of unknown function	13.27	0.05	M1C4U9	NA
151.	PGSC0003DMG400038906	Gene of unknown function	13.27	0.05	M1DHY6	NA
152.	PGSC0003DMG400030299	Conserved gene of unknown function	13.20	0.05	M1CZ10	NA
153.	PGSC0003DMG400041637	Gene of unknown function	13.18	0.05	M1DP06	NA
154.	PGSC0003DMG400013853	Conserved gene of unknown function	13.18	0.05	M1B330	NA
155.	PGSC0003DMG400038854	Gene of unknown function	13.10	0.05	M1DHU8	NA
156.	PGSC0003DMG400043434	Gene of unknown function	13.10	0.05	M1DSV9	NA
157.	PGSC0003DMG400038041	Gene of unknown function	13.08	0.05	M1DG16	NA
158.	PGSC0003DMG400024131	Gene of unknown function	13.04	0.05	M1C8C9	NA
159.	PGSC0003DMG400036734	Gene of unknown function	13.01	0.05	M1DDA2	NA
160.	PGSC0003DMG400043120	Gene of unknown function	12.97	0.05	M1DS69	NA
161.	PGSC0003DMG400038483	Gene of unknown function	12.97	0.05	M1DH08	NA
162.	PGSC0003DMG400035971	Gene of unknown function	12.90	0.05	M1DBN3	NA
163.	PGSC0003DMG400038677	Conserved gene of unknown function	12.88	0.05	M1DHG5	NA
164.	PGSC0003DMG400024358	Conserved gene of unknown function	12.88	0.05	M1C9A6	NA
165.	PGSC0003DMG400038030	Gene of unknown function	12.78	0.05	M1DG08	NA
166.	PGSC0003DMG400024283	Conserved gene of unknown function	12.73	0.05	M1C908	NA
167.	PGSC0003DMG400042785	Conserved gene of unknown function	12.72	0.05	M1DRG7	NA
168.	PGSC0003DMG400039912	Gene of unknown function	12.67	0.05	M1DK66	NA
169.	PGSC0003DMG400034904	Gene of unknown function	12.65	0.05	M1D9A1	NA
170.	PGSC0003DMG400019846	Gene of unknown function	12.59	0.05	M1BRB0	NA
171.	PGSC0003DMG400010864	Gene of unknown function	12.43	0.05	M1AQS4	NA
172.	PGSC0003DMG400045813	Gene of unknown function	12.38	0.05	M1DY09	NA
173.	PGSC0003DMG400035706	Gene of unknown function	12.31	0.05	M1DB21	NA
174.	PGSC0003DMG400040032	Gene of unknown function	12.27	0.05	M1DKF7	NA
175.	PGSC0003DMG400041157	Gene of unknown function	12.17	0.05	M1DMY8	NA
176.	PGSC0003DMG400024760	Gene of unknown function	12.11	0.05	M1CB25	NA
177.	PGSC0003DMG400046034	Gene of unknown function	12.05	0.05	M1DYH9	NA
178.	PGSC0003DMG400043194	Conserved gene of unknown function	12.04	0.05	M1DSC7	NA
179.	PGSC0003DMG400035795	Gene of unknown function	11.98	0.05	M1DB99	NA
180.	PGSC0003DMG400043472	Gene of unknown function	11.91	0.05	M1DSZ2	NA
181.	PGSC0003DMG400039189	Gene of unknown function	11.81	0.05	M1DIJ1	NA
182.	PGSC0003DMG400043885	Gene of unknown function	11.69	0.05	M1DTV7	NA
183.	PGSC0003DMG400044369	Gene of unknown function	11.67	0.05	M1DUX0	NA
184.	PGSC0003DMG400005884	Conserved gene of unknown function	11.64	0.05	M1A5D1	NA
185.	PGSC0003DMG400034435	Gene of unknown function	11.61	0.05	M1D880	NA
186.	PGSC0003DMG400041153	Gene of unknown function	11.61	0.05	M1DMY5	NA

187.	PGSC0003DMG400034512	Gene of unknown function	11.58	0.05	M1D8E8	NA
188.	PGSC0003DMG400044550	Gene of unknown function	11.53	0.05	M1DVB1	NA
189.	PGSC0003DMG400034464	Gene of unknown function	11.53	0.05	M1D8A7	NA
190.	PGSC0003DMG400039902	Gene of unknown function	11.48	0.05	M1DK59	NA
191.	PGSC0003DMG400010921	Conserved gene of unknown function	11.45	0.05	M1AR00	NA
192.	PGSC0003DMG400036663	Gene of unknown function	11.45	0.05	M1DD53	NA
193.	PGSC0003DMG400041456	Gene of unknown function	11.41	0.05	M1DNL8	NA
194.	PGSC0003DMG400016857	Gene of unknown function	11.39	0.05	M1BEL4	NA
195.	PGSC0003DMG400045150	Gene of unknown function	11.34	0.05	M1DWM3	NA
196.	PGSC0003DMG400043930	Gene of unknown function	11.32	0.05	M1DTZ1	NA
197.	PGSC0003DMG400005396	Gene of unknown function	11.29	0.05	M1A3C6	NA
198.	PGSC0003DMG400046217	Gene of unknown function	11.25	0.05	M1DYX7	NA
199.	PGSC0003DMG400042149	Conserved gene of unknown function	11.24	0.05	M1DQ38	NA
200.	PGSC0003DMG400043525	Conserved gene of unknown function	11.23	0.05	M1DT25	NA
201.	PGSC0003DMG400038705	Conserved gene of unknown function	11.21	0.05	M1DHI4	NA
202.	PGSC0003DMG400046215	Gene of unknown function	11.16	0.05	M1DYX5	NA
203.	PGSC0003DMG400013651	Conserved gene of unknown function	11.16	0.05	M1B2E2	NA
204.	PGSC0003DMG400040022	Gene of unknown function	11.12	0.05	M1DKF0	NA
205.	PGSC0003DMG400042464	Gene of unknown function	11.10	0.05	M1DQT1	NA
206.	PGSC0003DMG400035787	Conserved gene of unknown function	11.09	0.05	M1DB94	NA
207.	PGSC0003DMG400034465	Gene of unknown function	11.09	0.05	M1D8A8	NA
208.	PGSC0003DMG400043936	Gene of unknown function	11.08	0.05	M1DTZ6	NA
209.	PGSC0003DMG400044757	Gene of unknown function	10.98	0.05	M1DVR7	NA
210.	PGSC0003DMG400043639	Gene of unknown function	10.96	0.05	M1DTC0	NA
211.	PGSC0003DMG400002344	Conserved gene of unknown function	10.86	0.05	M0ZQQ2	NA
212.	PGSC0003DMG400039420	Gene of unknown function	10.83	0.05	M1DJ22	NA
213.	PGSC0003DMG400040336	Gene of unknown function	10.76	0.05	M1DL48	NA
214.	PGSC0003DMG400040984	Gene of unknown function	10.76	0.05	M1DMJ2	NA
215.	PGSC0003DMG400043430	Gene of unknown function	10.75	0.05	M1DSV5	NA
216.	PGSC0003DMG400038768	Gene of unknown function	10.73	0.05	M1DHN2	NA
217.	PGSC0003DMG400040443	Gene of unknown function	10.68	0.05	M1DLD7	NA
218.	PGSC0003DMG400036728	Gene of unknown function	10.68	0.05	M1DD97	NA
219.	PGSC0003DMG400036599	Gene of unknown function	10.68	0.05	M1DD10	NA
220.	PGSC0003DMG400039591	Gene of unknown function	10.67	0.05	M1DJF7	NA
221.	PGSC0003DMG400020031	Conserved gene of unknown function	10.64	0.05	M1C9I9	NA
222.	PGSC0003DMG400042686	Gene of unknown function	10.63	0.05	M1DRA3	NA
223.	PGSC0003DMG400045782	Gene of unknown function	10.62	0.05	M1DXY7	NA
224.	PGSC0003DMG400036101	Gene of unknown function	10.61	0.05	M1DBY8	NA
225.	PGSC0003DMG400046421	Gene of unknown function	10.53	0.05	M1DZD2	NA

226.	PGSC0003DMG400043335	Gene of unknown function	10.51	0.05	M1DSN0	NA
227.	PGSC0003DMG400044422	Gene of unknown function	10.50	0.05	M1DV08	NA
228.	PGSC0003DMG400045573	Gene of unknown function	10.49	0.05	M1DXH9	NA
229.	PGSC0003DMG400043580	Gene of unknown function	10.43	0.05	M1DT69	NA
230.	PGSC0003DMG400044018	Gene of unknown function	10.42	0.05	M1DU60	NA
231.	PGSC0003DMG400039929	Gene of unknown function	10.41	0.05	M1DK79	NA
232.	PGSC0003DMG400012080	Conserved gene of unknown function	10.40	0.05	M1AVS4	NA
233.	PGSC0003DMG400039564	Gene of unknown function	10.37	0.05	M1DJD2	NA
234.	PGSC0003DMG400035882	Gene of unknown function	10.35	0.05	M1DBG7	NA
235.	PGSC0003DMG400009275	Gene of unknown function	10.33	0.05	M1AJ90	NA
236.	PGSC0003DMG400024418	Gene of unknown function	10.32	0.05	M1C9H4	NA
237.	PGSC0003DMG400044893	Conserved gene of unknown function	10.31	0.05	M1DW16	NA
238.	PGSC0003DMG400044756	Gene of unknown function	10.31	0.05	M1DVR6	NA
239.	PGSC0003DMG400038697	Gene of unknown function	10.31	0.05	M1DHH8	NA
240.	PGSC0003DMG400034731	Gene of unknown function	10.29	0.05	M1D8W0	NA
241.	PGSC0003DMG400042341	Conserved gene of unknown function	10.27	0.05	M1DQH8	NA
242.	PGSC0003DMG400045714	Conserved gene of unknown function	10.26	0.05	M1DXT0	NA
243.	PGSC0003DMG400042891	Gene of unknown function	10.26	0.05	M1DRP8	NA
244.	PGSC0003DMG400040463	Gene of unknown function	10.24	0.05	M1DLF3	NA
245.	PGSC0003DMG400036832	Gene of unknown function	10.22	0.05	M1DDG7	NA
246.	PGSC0003DMG400043805	Conserved gene of unknown function	10.21	0.05	M1DTQ0	NA
247.	PGSC0003DMG400036967	Gene of unknown function	10.21	0.05	M1DDR9	NA
248.	PGSC0003DMG400046731	Gene of unknown function	10.20	0.05	M1E015	NA
249.	PGSC0003DMG400004248	Conserved gene of unknown function	10.17	0.05	M0ZYM9	NA
250.	PGSC0003DMG401025785	Gene of unknown function	10.15	0.05	M1CFA9	NA
251.	PGSC0003DMG400042493	Gene of unknown function	10.11	0.05	M1DQV5	NA
252.	PGSC0003DMG400006230	Gene of unknown function	10.02	0.05	M1A6U5	NA
253.	PGSC0003DMG400045062	Gene of unknown function	10.01	0.05	M1DWF1	NA
254.	PGSC0003DMG400042058	Gene of unknown function	10.01	0.05	M1DPW7	NA

NA: Not available; GO = Gene Ontology; P = GO-biological process; F = GO-molecular function