7. APPENDIX

7.1 Appendix 1: Media and Buffers

7.1.1 Media used

YEG

Yeast extract	2g
Glucose	10g
H_2O	make up to 1 L

YEPD

Yeast extract	5g
Peptone	10g
Glucose	10g
H_2O	make up to 1 L

Oatmeal agar

36.5g oatmeal agar (Hi-Media, India) was added to 800 ml H_2O. The volume was made up to 1 L, and autoclaved

Complete medium for Magnaporthe oryzae

Glucose	10g
Peptone	5g
Yeast extract	1g
CAA	1g
$NaNO_3$	0.6g
KCl	0.5g
$MgSO_4$	0.5g
KH_2PO_4	1.5g
H_2O	make up to 1L

pH	6.5

Minimal medium for Magnaporthe oryzae

Glucose	10g
$NaNO_3$	0.6g
KCl	0.5g
$MgSO_4$	0.5g
KH_2PO_4	1.5g
H_2O	make up to 1L
pH	6.5

AB minimal medium for Agrobacterium

AB liquid	90ml
20x AB buffer	5ml (1x)
20x AB salts	5ml (1x)
AB buffer	(20x)
K_2HPO_4	6g
NaH_2PO_4	2g
H_2O	make up to 100ml

Each salt was dissolved separately in ~50ml H_2O and then mixed to obtain 100ml solution with pH 7.0.

AB salts	***(20x)***
NH_4Cl	2g
$MgSO_4.7H_2O$	0.6g
KCl	0.3g
$CaCl_2$ (anh.)	0.3g
$FeSO_4$	0.005g
H2O	make up to 100ml

AB liquid

0.5g glucose in 90ml H2O

Induction medium for Agrobacterium

20x AB salts	5ml (1x)
Glucose	180mg (10mM)
Glycerol	0.5% w/v
H_2O	make up to 100ml
pH	5.3

Synthetic Dropout (SD) medium for yeast

YNB without amino acids (Hi-media, India)	1x
Ethanol	2%
H_2O	make up to 1L

7.1.2 Reagents and Buffers

1X PBS (Phosphate Buffered Saline)-- Usually a stock of 10X is prepared.
140mM Sodium chloride, 3mM Potassium chloride, 10mM Disodium hydrogen phosphate,
and 2mM Potassium dihydrogen phosphate.

1X Phosphate Buffer(PB)--- Usually a stock of 10X is prepared**.**
10mM Disodium hydrogen phosphate and 2mM Potassium dihydrogen phosphate.

Tris Buffered Saline--- 20mTris-HCl (pH 7.0) and 150mM Sodium chloride.

1XStandard Saline Citrate (SSC)--- Usually a stock of 20X is prepared.
15mM Sodium citrate (pH 7.0) and 150mM Sodium chloride.

Denaturing Solution--- 0.5M Sodium hydroxide and 1.5M Sodium chloride.

$T_{10}E_1$---10mM Tris and 1mM EDTA

1X Tris- glycine electrophoresis buffer---Usually a stock of 5X is prepared.
25mM Tris, 250mM Glycine and 0.1% SDS
1X SDS gel loading buffer---Usually a stock of 5X is prepared.
50mM Tris 1M (pH6.8), 2% SDS, 0.1% Bromophenol blue and 10% Glycerol.

Western Transfer buffer--- 25M Tris and 192mM Glycine.
Dissolved in 700 ml water. Then 200ml of methanol (20%) was added and volume was made up to 1 liter. (It was always made fresh and chilled before each transfer).

Tris Buffered Saline- Tween20 (TBS-T)--- 20mM Tris-HCl (pH7.5), 150mM Sodium chloride and 0.1% Tween20. pH was adjusted to 7.6 by adding 6N HCl, and volume was made up to 1liter.

1X Tris Acetate EDTA (TAE)--- Usually a stock of 50X is prepared. 40mM Tris-H (pH 8.0), 20mM Acetic acid and 2mM EDTA.

1X Tris Borate EDTA (TBE)--- Usually a stock of 10X is prepared. 89mM Tris-HCl (pH 8.0), 89mM Boric acid and 25mM EDTA.

***30% Acrylamide solution --- ***29g Acrylamide and 1g N,N' methylene bis-acrylamide.
Made up volume to 100ml.

Coomassie Blue stain --- 45% Methanol, 12% Acetic acid and 0.1% CBB R250.
Water was added and stirred O/N and filtered through a 0.45u filter paper.

Destainer--- *(for detaining protein gels) and Fixer (for protein gels)*
15% Methanol and 10% Acetic acid.

Bradford solution--- 0.1% (w/v) CBB G250, 4.7% Ethanol and 8.5% Phosphoric acid.
CBB was added to ethanol and phosphoric acid and the solution was stirred for few hours.

Water was then added and it was stirred o/n. Then filtered through a 0.45u filter paper. It was stored at 4^{o}C.

STET buffer

Sucrose	8g
1M Tris-Cl	5ml
TritonX-100	100ul
0.5M EDTA	10ml
H_2O	make up to 100ml

DNA extraction buffer for M. oryzae

1M Tris (pH-8)	15ml
0.5M EDTA (pH-8)	15ml
4M NaCl	18.75ml
H_2O	make up to 100 ml

Add 100μl β-mercaptoethanol before use.

Phosphatase Inhibitor cocktail--- 10mM NaF (0.5M stock, RT), 60mM β-glycerol phosphate (1M, pH-7.5 stock, 4^{0}C), 10mM Na pyrophosphate(100mM stock, -20^{0}C), 2mM Na ortho-vanadate (200mM stock, -20^{0}C), 3μM microcysteine-LR (300mM stock in DMSO, -20^{0}C)

Nonidet-P40 (NP-40) buffer--- 20mM Tris HCL pH-8, 137 mM NaCl, 10% glycerol, 1% nonidet P-40, 2mM EDTA.

7.2 Appendix 2: Summary of Transcriptome data

Up-regulated genes B157 Vs RA6

Test_id	locus	sample_1	sample_2	value_1	value_2	Fold change	log 2 fold change	test_stat	p_value	q_value	significant	Putative function
MGG_08802T0	Chromosome_8.6:73075-74679	B157	RA6	0.082336	46.7622	5.68E+02	9.14960548	9.14013	0	0	yes	GMP synthase
MGG_05828T0	Chromosome_8.3:1629109-1630264	B157	RA6	0.059023	2.96893	5.03E+01	5.652531794	3.95795	7.56E-05	0.006934	yes	chitin deacetylase 1
MGG_18077T0	Chromosome_8.7:3077498-3077846	B157	RA6	1.17771	55.8546	4.74E+01	5.567619863	5.35648	8.49E-08	2.18E-05	yes	*
MGG_05830T0	Chromosome_8.3:1633626-1635636	B157	RA6	0.068309	2.76785	4.05E+01	5.340552614	5.11535	3.13E-07	6.75E-05	yes	allantoin transporter
MGG_00031T0	Chromosome_8.5:4370157-4372812	B157	RA6	0.046656	1.61526	3.46E+01	5.113547603	4.88013	1.06E-06	0.000194	yes	FAD binding domain-containing protein
MGG_17894T0	Chromosome_8.7:708676-709335	B157	RA6	0.172811	4.89795	2.83E+01	4.824911089	3.35138	0.000804	0.043989	yes	*
MGG_05827T0	Chromosome_8.3:1627113-1628442	B157	RA6	0.142004	3.64497	2.57E+01	4.681903467	5.20095	1.98E-07	4.55E-05	yes	glutamyl-tRNA(Gln) amidotransferase subunit A
MGG_09138T0	Chromosome_8.8:61208-62357	B157	RA6	0.558407	10.0264	1.80E+01	4.166342859	6.2107	5.27E-10	2.36E-07	yes	glutathione S-transferase II
MGG_08519T0	Chromosome_8.4:496188-497352	B157	RA6	0.487087	6.72483	1.38E+01	3.787246413	5.31871	1.05E-07	2.60E-05	yes	aflatoxin B1 aldehyde reductase member 3
MGG_11255T0	Chromosome_8.2:2817863-2818893	B157	RA6	109.17	1463.04	1.34E+01	3.744320852	7.92388	2.22E-15	3.50E-12	yes	OP
MGG_10023T0	Chromosome_8.4:4915709-4917386	B157	RA6	0.216054	2.8383	1.31E+01	3.71556324	4.03887	5.37E-05	0.005274	yes	peptidoglycan binding domain
MGG_05413T0	Chromosome_8.1:5137985-5140639	B157	RA6	0.212708	2.57673	1.21E+01	3.598595174	5.02288	5.09E-07	0.000102	yes	MFS transporter
MGG_08977T0	Chromosome_8.2:2350943-2351719	B157	RA6	1.25774	14.8314	1.18E+01	3.559749162	5.38939	7.07E-08	1.85E-05	yes	ctr copper transporter
MGG_11285T0	Chromosome_8.2:2353384-2354179	B157	RA6	1.41327	16.3091	1.15E+01	3.528568152	5.55328	2.80E-08	8.00E-06	yes	*
MGG_08971T0	Chromosome_8.2:2331151-2332099	B157	RA6	0.262328	2.92564	1.12E+01	3.479308547	3.76089	0.000169	0.013019	yes	*

MGG_09354T0	Chromosome_8.6:3580232-3584060	B157	RA6	3.83184	42.3197	1.10E+01	3.465220173	7.62243	2.49E-14	3.10E-11	yes	*
MGG_00156T0	Chromosome_8.5:3919769-3920881	B157	RA6	3.48448	36.16	1.04E+01	3.375379398	6.37789	1.80E-10	9.43E-08	yes	NMRA 1
MGG_07980T0	Chromosome_8.3:6443975-6445860	B157	RA6	0.482832	4.93161	1.02E+01	3.352465514	5.24133	1.59E-07	3.73E-05	yes	metabolite (sugar) transporter
MGG_02379T0	Chromosome_8.1:1616610-1617336	B157	RA6	3.76976	35.8334	9.51E+00	3.248760355	5.87413	4.25E-09	1.46E-06	yes	omo
MGG_04248T0	Chromosome_8.6:1422889-1425832	B157	RA6	13.7029	124.739	9.10E+00	3.186359444	7.50104	6.33E-14	7.43E-11	yes	oligo peptide transporter
MGG_02332T0	Chromosome_8.1:1434443-1435253	B157	RA6	0.844076	7.39428	8.76E+00	3.130964866	4.50909	6.51E-06	0.000942	yes	NPP1 SUPERFAM
MGG_15535T0	Chromosome_8.2:709801-714017	B157	RA6	3.48126	28.1777	8.09E+00	3.016872385	6.86398	6.70E-12	4.89E-09	yes	carbomyl phosphate synthase
MGG_10704T0	Chromosome_8.6:3768979-3770092	B157	RA6	4.5905	35.6618	7.77E+00	2.957656317	5.81841	5.94E-09	1.96E-06	yes	NAT_SF
MGG_05798T0	Chromosome_8.3:3008708-3009990	B157	RA6	1.8072	13.9866	7.74E+00	2.95221722	4.99199	5.98E-07	0.000116	yes	CUTINASE
MGG_05514T0	Chromosome_8.1:5479385-5481064	B157	RA6	0.390941	2.917	7.46E+00	2.899462586	4.05433	5.03E-05	0.005011	yes	*
MGG_01924T0	Chromosome_8.6:636875-639229	B157	RA6	13.1066	97.7744	7.46E+00	2.899163295	6.86016	6.88E-12	4.96E-09	yes	benzoate 4-monooxygenase cytochrome P450
MGG_08675T0	Chromosome_8.1:7770202-7770988	B157	RA6	0.814083	5.60126	6.88E+00	2.7825036	3.78093	0.000156	0.012363	yes	*
MGG_12228T0	Chromosome_8.6:938202-939455	B157	RA6	0.324358	2.18697	6.74E+00	2.753274503	3.4985	0.000468	0.028857	yes	Adh_N
MGG_10694T0	Chromosome_8.6:3793544-3796830	B157	RA6	1.192	7.71716	6.47E+00	2.694685782	5.04678	4.49E-07	9.19E-05	yes	Fungal_transcription_factor
MGG_02119T0	Chromosome_8.1:621766-623611	B157	RA6	3.32482	21.2855	6.40E+00	2.678522837	5.28767	1.24E-07	3.00E-05	yes	high-affinity nicotinic acid transporter
MGG_09874T0	Chromosome_8.6:3827763-3828766	B157	RA6	1.37463	8.68847	6.32E+00	2.660058797	4.00638	6.17E-05	0.005881	yes	METHYL TRANSFERASE
MGG_02637T0	Chromosome_8.7:2103523-2105578	B157	RA6	6.26278	36.8795	5.89E+00	2.557943991	5.31413	1.07E-07	2.64E-05	yes	omo
MGG_01922T0	Chromosome_8.6:641282-642742	B157	RA6	1.71455	9.97963	5.82E+00	2.541156351	4.44667	8.72E-06	0.001187	yes	polysaccharide deacetylase
MGG_09827T0	Chromosome_8.6:3985411-3987706	B157	RA6	3.5807	20.2283	5.65E+00	2.498061524	5.11985	3.06E-07	6.61E-05	yes	sugar transporter
MGG_07957T0	Chromosome_8.3:6382171-6384194	B157	RA6	8.45481	47.4942	5.62E+00	2.489907103	5.73419	9.80E-09	3.03E-06	yes	uridine permease

MGG_17792T0	Chromosome_8.6:3468363-3468890	B157	RA6	69.855	387.063	5.54E+00	2.470133117	5.85894	4.66E-09	1.57E-06	yes	omo
MGG_10439T0	Chromosome_8.2:248389-251403	B157	RA6	1.38302	7.41342	5.36E+00	2.422317229	4.59809	4.26E-06	0.00066	yes	MFS transporter
MGG_13793T0	Chromosome_8.1:7107283-7110884	B157	RA6	12.693	65.4084	5.15E+00	2.365442833	5.7718	7.84E-09	2.54E-06	yes	nitrate transporter
MGG_05829T0	Chromosome_8.3:1630339-1632699	B157	RA6	1.45127	7.44607	5.13E+00	2.35916323	4.30769	1.65E-05	0.001961	yes	Fungal_transcription_factor
MGG_05800T0	Chromosome_8.3:3010744-3013622	B157	RA6	0.759067	3.57224	4.71E+00	2.234529873	3.77936	0.000157	0.012408	yes	*
MGG_06950T0	Chromosome_8.1:3345678-3348326	B157	RA6	10.0083	46.9221	4.69E+00	2.229070642	4.14816	3.35E-05	0.003528	yes	L-serine dehydratase
MGG_07257T0	Chromosome_8.2:6974344-6975837	B157	RA6	20.914	97.9544	4.68E+00	2.227641281	5.37365	7.72E-08	1.99E-05	yes	OP
MGG_00822T0	Chromosome_8.5:1495367-1496434	B157	RA6	9.875	44.0314	4.46E+00	2.156680063	4.5084	6.53E-06	0.000943	yes	*
MGG_09063T0	Chromosome_8.7:2520582-2523687	B157	RA6	10.4754	45.8705	4.38E+00	2.130561299	5.15864	2.49E-07	5.54E-05	yes	urea active transporter
MGG_06980T0	Chromosome_8.1:3451007-3453887	B157	RA6	14.5039	63.4981	4.38E+00	2.130272541	5.14975	2.61E-07	5.72E-05	yes	MFS_1
MGG_03823T0	Chromosome_8.6:2920877-2922508	B157	RA6	1.28178	5.58709	4.36E+00	2.123948396	3.59147	0.000329	0.021932	yes	NADH oxidase
MGG_11535T0	Chromosome_8.5:2212316-2215246	B157	RA6	2.73345	11.8443	4.33E+00	2.115398046	4.38441	1.16E-05	0.001508	yes	neutral ceramidase
MGG_15416T0	Chromosome_8.1:7779653-7780418	B157	RA6	2.76409	11.7605	4.25E+00	2.089072902	3.35118	0.000805	0.043989	yes	*
MGG_00289T0	Chromosome_8.5:3395659-3399392	B157	RA6	172.669	714.955	4.14E+00	2.049843347	3.86343	0.000112	0.009353	yes	amino-acid permease inda1
MGG_00861T0	Chromosome_8.5:1345969-1350801	B157	RA6	2.07753	8.53387	4.11E+00	2.038330824	4.29576	1.74E-05	0.002049	yes	oligopeptide transporter 6

Up regulated genes classified according to their putative functions

Nitrogen metabolism	**transporters/ permeases**	**oxidative stress**	**detox genes**	**CWDE**	**expression regulation/transcriptional factors**	**general metabolism**	**pathogenecity related**	**others**

MGG_08802T0- GMP synthase	MGG_05830T0- allantoin	MGG_03823T0- NADH oxidase	MGG_09138T0- GST-II	MGG_05828T0 chitin deacetylase	MGG_10694T0- transcription factor	MGG_00031T0- FAD binding domain-containing	MGG_02332T0 – necrosis inducing factor	MGG_18077T0
MGG_05827T0 – Gln tRNA amidotransferase	MGG_05413T0- MFS transporter		MGG_08519T0- aflatoxin degradation	MGG_10023T0- peptidoglycan binding protein	MGG_09874T0- methyl transferase-	MGG_12228T0- ADH		MGG_17894T0
MGG_00156T0- NMR1	MGG_08977T0- cu		MGG_10704T0 NAT_SF	MGG_05798T0- cutinase	MGG_05829T0 – transcription factor	MGG_06950T0- L-serine dehydratase		MGG_11255T0
MGG_15535T0- urea cycle	MGG_07980T0- sugar		MGG_01924T0- benzoate mono-xygenase cyt-p450	MGG_01922T0- polysaccharide deacetylase				MGG_11285T0
	MGG_04248T0- OPT							MGG_08971T0
	MGG_02119T0- high aff nicotinic							MGG_09354T0
	MGG_09827T0- sugar							MGG_02379T0
	MGG_07957T0- uridine							MGG_05514T0
	MGG_10439T0 – MFS transporter							MGG_08675T0
	MGG_13793T0- nitrate							MGG_02637T0
	MGG_09063T0- urea							MGG_17792T0
	MGG_06980T0- MFS							MGG_05800T0
	MGG_00289T0- amino acid							MGG_07257T0
	MGG_00861T0- OPT							MGG_00822T0
								MGG_15416T0
								MGG_11535T0
4	14	1	4	4	3	3	1	16

Transcripts expressed only in RA6

Test_id	locus	sample_1	sample_2	value_1	value_2	test_stat	p_value	q_value	significant	Function
MGG_00016T0	Chromosome_8.5:4429064-4430803	B157	RA6	0	9.37735	-1.79769e+308	1.65E-05	0.001961	yes	2-epi-5-epi-valiolone synthase
MGG_00018T0	Chromosome_8.5:4420312-4426205	B157	RA6	0	3.67062	-1.79769e+308	5.10E-05	0.005066	yes	MFS1
MGG_00019T0	Chromosome_8.5:4418625-4419119	B157	RA6	0	16.3901	-1.79769e+308	0.000236	0.016732	yes	*
MGG_08800T0	Chromosome_8.6:77107-78925	B157	RA6	0	5.35672	-1.79769e+308	4.90E-05	0.004919	yes	CAIB/BAIF family enzyme
MGG_08801T0	Chromosome_8.6:75214-76555	B157	RA6	0	32.6743	-1.79769e+308	4.25E-07	8.77E-05	yes	exopolyphosphatase
MGG_08803T0	Chromosome_8.6:70685-72979	B157	RA6	0	4.91594	-1.79769e+308	2.95E-05	0.003145	yes	Git3
MGG_11697T0	Chromosome_8.5:4426466-4428237	B157	RA6	0	7.62598	-1.79769e+308	1.63E-05	0.001951	yes	Carbamoyl Phosphate Synthetase I (CPSI)

Up-regulated gene islands above Log2 fold change cut off- B157 Vs RA6

Test_id	gene_id	sample_1	sample_2	value_1	value_2	Fold change	log 2 fold change	test_stat	p_value	q_value	significant	Putative Function
MGG_01922T0	Chromosome_8.6:641282-642742	B157	RA6	1.71455	9.97963	5.82E+00	2.541156	4.44667	8.72E-06	0.001187	yes	polysaccharide deacetylase
MGG_01924T0	Chromosome_8.6:636875-639229	B157	RA6	13.1066	97.7744	7.46E+00	2.899163	6.86016	6.88E-12	4.96E-09	yes	benzoate 4-monooxygenase cytochrome P450
MGG_05798T0	Chromosome_8.3:3008708-3009990	B157	RA6	1.8072	13.9866	7.74E+00	2.952217	4.99199	5.98E-07	0.000116	yes	CUTINASE
MGG_05800T0	Chromosome_8.3:3010744-3013622	B157	RA6	0.759067	3.57224	4.71E+00	2.23453	3.77936	0.000157	0.012408	yes	*
MGG_05827T0	Chromosome_8.3:1627113-1628442	B157	RA6	0.142004	3.64497	2.57E+01	4.681903	5.20095	1.98E-07	4.55E-05	yes	glutamyl-tRNA(Gln) amidotransferase subunit A

MGG_05828T0	Chromosome_8.3:1629109-1630264	B157	RA6	0.059023	2.96893	5.03E+01	5.652532	3.95795	7.56E-05	0.006934	yes	chitin deacetylase 1
MGG_05829T0	Chromosome_8.3:1630339-1632699	B157	RA6	1.45127	7.44607	5.13E+00	2.359163	4.30769	1.65E-05	0.001961	yes	Fungal_transcription_factor
MGG_05830T0	Chromosome_8.3:1633626-1635636	B157	RA6	0.068309	2.76785	4.05E+01	5.340553	5.11535	3.13E-07	6.75E-05	yes	allantoin transporter
MGG_06950T0	Chromosome_8.1:3345678-3348326	B157	RA6	10.0083	46.9221	4.69E+00	2.229071	4.14816	3.35E-05	0.003528	yes	L-serine dehydratase
MGG_06980T0	Chromosome_8.1:3451007-3453887	B157	RA6	14.5039	63.4981	4.38E+00	2.130273	5.14975	2.61E-07	5.72E-05	yes	MFS_1
MGG_08971T0	Chromosome_8.2:2331151-2332099	B157	RA6	0.262328	2.92564	1.12E+01	3.479309	3.76089	0.000169	0.013019	yes	no domain
MGG_08977T0	Chromosome_8.2:2350943-2351719	B157	RA6	1.25774	14.8314	1.18E+01	3.559749	5.38939	7.07E-08	1.85E-05	yes	ctr copper transporter
MGG_10694T0	Chromosome_8.6:3793544-3796830	B157	RA6	1.192	7.71716	6.47E+00	2.694686	5.04678	4.49E-07	9.19E-05	yes	Fungal_transcription_factor
MGG_10704T0	Chromosome_8.6:3768979-3770092	B157	RA6	4.5905	35.6618	7.77E+00	2.957656	5.81841	5.94E-09	1.96E-06	yes	NAT_SF acetyl transferase

Down regulated genes B157 Vs RA6

Test_id	**locus**	**sample_1**	**sample_2**	**value_1**	**value_2**	**Fold change**	**log 2 fold change**	**test_stat**	**p_value**	**q_value**	**significant**	**Putative function**
MGG_00287T0	Chromosome_8.5:3413312-3414801	B157	RA6	96.8935	13.2217	1.36E-01	-2.873492202	-6.57967	4.71E-11	2.77E-08	yes	OP
MGG_00311T0	Chromosome_8.5:3308795-3312350	B157	RA6	478.144	90.4532	1.89E-01	-2.402201725	-4.67301	2.97E-06	0.000484	yes	peptidase_A4
MGG_00771T0	Chromosome_8.5:1689052-1693961	B157	RA6	508.272	46.1669	9.08E-02	-3.46066999	-6.25193	4.05E-10	1.95E-07	yes	5-oxoprolinase
MGG_00772T0	Chromosome_8.5:1684694-1688648	B157	RA6	38.8643	7.1994	1.85E-01	-2.432496949	-5.85895	4.66E-09	1.57E-06	yes	PX domain-containing protein
MGG_00787T0	Chromosome_8.5:1620248-1621721	B157	RA6	6.05729	1.00436	1.66E-01	-2.592396006	-4.18059	2.91E-05	0.003127	yes	OP

MGG_00942T0	Chromosome_8.5:1045962-1049470	B157	RA6	258.333	50.0748	1.94E-01	-2.367075289	-5.28574	1.25E-07	3.01E-05	yes	aminotransferase class 4
MGG_01041T0	Chromosome_8.5:707747-711666	B157	RA6	53.5804	11.8351	2.21E-01	-2.178633455	-4.23935	2.24E-05	0.002527	yes	cellulose signalling associated protein ENVOY
MGG_01255T0	Chromosome_8.2:2865136-2867181	B157	RA6	3.01006	0.634318	2.11E-01	-2.246514058	-3.39753	0.00068	0.038747	yes	heme binding cytochrome of cellulobiose dehydrogenase
MGG_01365T0	Chromosome_8.2:3266966-3268779	B157	RA6	352.106	58.9192	1.67E-01	-2.579200065	-5.92938	3.04E-09	1.08E-06	yes	FAD binding domain-containing protein
MGG_02082T0	Chromosome_8.1:506856-510148	B157	RA6	8.14186	1.46189	1.80E-01	-2.477523655	-3.45985	0.00054	0.032309	yes	omo
MGG_02112T0	Chromosome_8.1:588845-590368	B157	RA6	3.87304	0.875332	2.26E-01	-2.145564183	-3.32161	0.00089	0.047779	yes	*
MGG_02187T0	Chromosome_8.1:888979-891839	B157	RA6	1.50015	0.301116	2.01E-01	-2.316715489	-3.43619	0.00059	0.034815	yes	*
MGG_02210T0	Chromosome_8.1:948870-950658	B157	RA6	18.3755	2.19003	1.19E-01	-3.068760969	-5.9358	2.92E-09	1.05E-06	yes	vanadium chloroperoxidase
MGG_02234T0	Chromosome_8.1:1088679-1089434	B157	RA6	793.804	6.89043	8.68E-03	-6.848045004	-12.8234	0	0	yes	*
MGG_02541T0	Chromosome_8.7:2431514-2433908	B157	RA6	226.755	54.9159	2.42E-01	-2.045838539	-4.77676	1.78E-06	0.000311	yes	methylcrotonoyl-CoA carboxylase subunit beta
MGG_02814T0	Chromosome_8.7:1410110-1411679	B157	RA6	5.49822	1.03633	1.88E-01	-2.407481159	-3.92903	8.53E-05	0.007522	yes	*
MGG_02818T0	Chromosome_8.7:1402237-1404747	B157	RA6	760.928	189.435	2.49E-01	-2.006057043	-3.8148	0.00014	0.011062	yes	isoamyl alcohol oxidase
MGG_03002T0	Chromosome_8.7:687186-690995	B157	RA6	3.13282	0.735202	2.35E-01	-2.091249284	-3.68774	0.00023	0.016256	yes	blue light harvesting prt
MGG_03034T0	Chromosome_8.7:574551-576407	B157	RA6	28.0796	5.49313	1.96E-01	-2.353822044	-5.04749	4.48E-07	9.18E-05	yes	*
MGG_03335T0	Chromosome_8.4:2218712-2219999	B157	RA6	78.2047	19.3451	2.47E-01	-2.015287128	-4.77544	1.79E-06	0.000312	yes	methylglutaconyl-CoA hydratase
MGG_03363T0	Chromosome_8.4:2130118-2131926	B157	RA6	1.31357	0.133152	1.01E-01	-3.30234708	-3.83899	0.00012	0.010151	yes	no domain
MGG_03364T0	Chromosome_8.4:2129216-2130057	B157	RA6	91.8897	3.04678	3.32E-02	-4.914545922	-9.03417	0	0	yes	DUF4360
MGG_03375T0	Chromosome_8.4:2100075-2102662	B157	RA6	263.342	27.2245	1.03E-01	-3.273960175	-7.48595	7.11E-14	7.88E-11	yes	isotrichodermin C-15 hydroxylase
MGG_03545T0	Chromosome_8.4:1517550-1521784	B157	RA6	8.06149	1.73425	2.15E-01	-2.216734631	-4.59951	4.23E-06	0.000658	yes	*
MGG_03840T0	Chromosome_8.6:2870890-2872354	B157	RA6	144.837	31.2834	2.16E-01	-2.210960976	-5.42201	5.89E-08	1.56E-05	yes	2-oxoisovalerate dehydrogenase subunit alpha

MGG_03847T0	Chromosome_8.6:2837555-2838532	B157	RA6	83.9345	15.8814	1.89E-01	-2.401925834	-5.44434	5.20E-08	1.40E-05	yes	DUF1445
MGG_04034T0	Chromosome_8.6:2168435-2170853	B157	RA6	2658.96	372.441	1.40E-01	-2.835778269	-4.33569	1.45E-05	0.001802	yes	formate dehydrogenase
MGG_04036T0	Chromosome_8.6:2162544-2163835	B157	RA6	4.90475	0.951685	1.94E-01	-2.365623565	-3.4698	0.00052	0.031386	yes	methyl transferase domain .
MGG_04099T0	Chromosome_8.6:1965066-1967270	B157	RA6	70.7807	11.8124	1.67E-01	-2.583053914	-6.11975	9.37E-10	3.79E-07	yes	allantoate permease
MGG_04939T0	Chromosome_8.3:4016019-4017517	B157	RA6	10.2477	1.63642	1.60E-01	-2.646685167	-4.64352	3.43E-06	0.000546	yes	*
MGG_05364T0	Chromosome_8.1:4959441-4960933	B157	RA6	156.416	22.0666	1.41E-01	-2.825451833	-6.66015	2.74E-11	1.69E-08	yes	endoglucanase-4
MGG_05398T0	Chromosome_8.1:5084513-5085420	B157	RA6	8.50225	1.19466	1.41E-01	-2.831244595	-4.22635	2.38E-05	0.002649	yes	OP
MGG_05722T0	Chromosome_8.1:6268280-6271815	B157	RA6	2.0421	0.472815	2.32E-01	-2.110705805	-3.33794	0.00084	0.045691	yes	MFS super family
MGG_06222T0	Chromosome_8.4:4487010-4488886	B157	RA6	1294.73	219.069	1.69E-01	-2.563194022	-4.74098	2.13E-06	0.000363	yes	cobW domain-containing protein
MGG_06511T0	Chromosome_8.4:3474123-3475910	B157	RA6	120.511	29.2722	2.43E-01	-2.041561756	-5.04182	4.61E-07	9.30E-05	yes	2-oxoisovalerate dehydrogenase subunit beta
MGG_06691T0	Chromosome_8.1:2407316-2408576	B157	RA6	700.461	78.7911	1.12E-01	-3.152200145	-6.94978	3.66E-12	3.04E-09	yes	4-hydroxyphenylpyruvate dioxygenase
MGG_07219T0	Chromosome_8.2:6833174-6840086	B157	RA6	65.0785	10.4216	1.60E-01	-2.642604211	-6.23618	4.48E-10	2.08E-07	yes	conidial yellow pigment biosynthesis polyketide synthase
MGG_07227T0	Chromosome_8.2:6869596-6871291	B157	RA6	24.328	4.15967	1.71E-01	-2.548076737	-5.21579	1.83E-07	4.27E-05	yes	Hypothetical
MGG_07411T0	Chromosome_8.3:526917-528046	B157	RA6	13.3629	2.81206	2.10E-01	-2.248533852	-3.92285	8.75E-05	0.007685	yes	*
MGG_07577T0	Chromosome_8.3:1090814-1092787	B157	RA6	10.3267	0.627574	6.08E-02	-4.040449906	-6.72317	1.78E-11	1.15E-08	yes	*
MGG_07598T0	Chromosome_8.3:1157262-1158843	B157	RA6	6.90553	0.462507	6.70E-02	-3.90020504	-5.96044	2.52E-09	9.19E-07	yes	omo
MGG_07631T0	Chromosome_8.3:1271635-1273125	B157	RA6	11.1645	0.864059	7.74E-02	-3.691645005	-6.16486	7.05E-10	2.98E-07	yes	fungal cellulose binding domain-containing protein
MGG_07815T0	Chromosome_8.3:5856828-5857836	B157	RA6	7.4756	0.64356	8.61E-02	-3.538042812	-5.04399	4.56E-07	9.29E-05	yes	ZF-LITAF like domain
MGG_07870T0	Chromosome_8.3:6108544-6110286	B157	RA6	1.92914	0.381281	1.98E-01	-2.3390313	-3.32604	0.00088	0.04711	yes	solid state culture specific gene
MGG_08034T0	Chromosome_8.2:5485081-5485785	B157	RA6	27.7383	2.67785	9.65E-02	-3.372732316	-5.32232	1.02E-07	2.57E-05	yes	*

MGG_08429T0	Chromosome_8.4:169921-172675	B157	RA6	341.785	36.1532	1.06E-01	-3.240893828	-7.24605	4.29E-13	4.14E-10	yes	peptidase_s8
MGG_08589T0	Chromosome_8.4:786380-788212	B157	RA6	18.2174	1.73327	9.51E-02	-3.393748759	-6.22543	4.80E-10	2.18E-07	yes	A,b,hydrolase_6
MGG_08647T0	Chromosome_8.1:7667173-7668680	B157	RA6	6.50458	1.08502	1.67E-01	-2.583734269	-4.24709	2.17E-05	0.002471	yes	*
MGG_08686T0	Chromosome_8.6:462095-464347	B157	RA6	7.09327	0.410967	5.79E-02	-4.109356406	-6.58636	4.51E-11	2.67E-08	yes	omo
MGG_08962T0	Chromosome_8.2:2293505-2294765	B157	RA6	3.76118	0.260182	6.92E-02	-3.85359229	-4.54522	5.49E-06	0.000809	yes	*
MGG_09225T0	Chromosome_8.1:3825648-3826998	B157	RA6	32.7602	5.54716	1.69E-01	-2.562122921	-5.26769	1.38E-07	3.27E-05	yes	may be involved in Zinc metabolism as in humans
MGG_09376T0	Chromosome_8.6:3489148-3490957	B157	RA6	1.71225	0.294222	1.72E-01	-2.540916329	-3.41523	0.00064	0.036889	yes	FAD binding domain-containing protein
MGG_09474T0	Chromosome_8.3:3556481-3556985	B157	RA6	559.553	65.991	1.18E-01	-3.083933603	-7.25375	4.05E-13	3.98E-10	yes	OP
MGG_09645T0	Chromosome_8.7:3086988-3093813	B157	RA6	39.0135	7.00195	1.79E-01	-2.478144767	-6.01875	1.76E-09	6.66E-07	yes	polyketide synthase
MGG_09647T0	Chromosome_8.7:3084083-3085774	B157	RA6	55.8368	12.6745	2.27E-01	-2.139287428	-5.04782	4.47E-07	9.18E-05	yes	acyl-CoA synthetase
MGG_09708T0	Chromosome_8.4:5424884-5425649	B157	RA6	4.79953	0.712726	1.48E-01	-2.751473676	-3.72462	0.0002	0.014537	yes	F-box like prt
MGG_09762T0	Chromosome_8.4:5273514-5275848	B157	RA6	2.2254	0.278269	1.25E-01	-2.999512571	-4.3703	1.24E-05	0.001598	yes	*
MGG_09817T0	Chromosome_8.6:4016281-4020891	B157	RA6	42.004	4.1619	9.91E-02	-3.335212515	-6.28177	3.35E-10	1.66E-07	yes	minor extracellular protease vpr
MGG_09818T0	Chromosome_8.6:4014092-4015685	B157	RA6	18.6101	3.09609	1.66E-01	-2.587566493	-5.08206	3.73E-07	7.85E-05	yes	Aspartate protease
MGG_09941T0	Chromosome_8.1:4421844-4427597	B157	RA6	520.513	65.8516	1.27E-01	-2.982643797	-5.29329	1.20E-07	2.93E-05	yes	nod factor export ATP-binding protein I
MGG_09945T0	Chromosome_8.1:4439239-4441827	B157	RA6	8.55431	1.72803	2.02E-01	-2.307523226	-4.35145	1.35E-05	0.001698	yes	averantin oxidoreductase
MGG_10252T0	Chromosome_8.8:302457-304373	B157	RA6	183.391	22.6952	1.24E-01	-3.014463733	-7.14303	9.13E-13	8.04E-10	yes	hypothetical –Cupin_1 & cupin_2
MGG_10320T0	Chromosome_8.7:117809-120502	B157	RA6	131.096	24.3095	1.85E-01	-2.431031541	-5.86128	4.59E-09	1.56E-06	yes	methylcrotonoyl-CoA carboxylase subunit alpha
MGG_10730T0	Chromosome_8.2:112283-116736	B157	RA6	10.3024	1.90475	1.85E-01	-2.4353069	-5.08365	3.70E-07	7.81E-05	yes	potassium/sodium efflux P-type ATPase
MGG_10781T0	Chromosome_8.5:183047-183757	B157	RA6	24.244	1.36964	5.65E-02	-4.145759102	-6.27923	3.40E-10	1.67E-07	yes	*

MGG_10956T0	Chromosome_8.5:276005-277401	B157	RA6	2.70738	0.389502	1.44E-01	-2.797194753	-3.68117	0.00023	0.016555	yes	amido ligase
MGG_11605T0	Chromosome_8.5:3343738-3347478	B157	RA6	11.3456	2.6113	2.30E-01	-2.11929279	-4.3256	1.52E-05	0.00186	yes	*
MGG_11608T0	Chromosome_8.5:3404246-3406595	B157	RA6	1326.82	27.9636	2.11E-02	-5.56827875	-9.85285	0	0	yes	laccase-2
MGG_11774T0	Chromosome_8.1:3600955-3603724	B157	RA6	4.81364	0.323591	6.72E-02	-3.894884862	-6.12203	9.24E-10	3.77E-07	yes	endoglucanase
MGG_12214T0	Chromosome_8.6:1116077-1127294	B157	RA6	29.8792	7.35622	2.46E-01	-2.02210499	-3.59347	0.00033	0.021789	yes	fatty acid synthase S-acetyltransferase
MGG_12264T0	Chromosome_8.2:5483646-5484733	B157	RA6	10.9635	2.54963	2.33E-01	-2.104348635	-3.54859	0.00039	0.024759	yes	flavodoxin_2 superfamily
MGG_12468T0	Chromosome_8.2:7875877-7878494	B157	RA6	398.982	91.8966	2.30E-01	-2.11824027	-4.54627	5.46E-06	0.000808	yes	CFEM SUPERFAM
MGG_12722T0	Chromosome_8.4:2253263-2255972	B157	RA6	7.93686	1.14056	1.44E-01	-2.798826015	-5.01363	5.34E-07	0.000106	yes	*
MGG_12942T0	Chromosome_8.3:4559112-4559423	B157	RA6	419.81	13.465	3.21E-02	-4.962450398	-8.0499	8.88E-16	1.52E-12	yes	omo
MGG_12978T0	Chromosome_8.3:3704214-3705915	B157	RA6	7.67182	1.81386	2.36E-01	-2.080505764	-3.65449	0.00026	0.018032	yes	kynurenine 3-monooxygenase
MGG_13107T0	Chromosome_8.1:5538176-5540950	B157	RA6	75.7319	16.397	2.17E-01	-2.207469241	-4.20928	2.56E-05	0.002816	yes	HPP_superfam
MGG_13464T0	Chromosome_8.3:1561217-1564067	B157	RA6	465.779	25.8391	5.55E-02	-4.17201787	-8.80197	0	0	yes	laccase
MGG_13622T0	Chromosome_8.4:5033405-5036056	B157	RA6	25.2561	1.70325	6.74E-02	-3.890269766	-7.75219	9.10E-15	1.24E-11	yes	fungal cellulose binding domain-containing protein
MGG_13716T0	Chromosome_8.1:661764-662093	B157	RA6	177.865	43.7109	2.46E-01	-2.024717659	-3.83412	0.00013	0.010326	yes	*
MGG_13908T0	Chromosome_8.3:6222382-6223362	B157	RA6	4.85955	1.0155	2.09E-01	-2.258632485	-3.34163	0.00083	0.04523	yes	OP
MGG_14061T0	Chromosome_8.7:3291739-3293930	B157	RA6	3.28352	0.428703	1.31E-01	-2.937192825	-4.46072	8.17E-06	0.001135	yes	oxalate decarboxylase oxdD
MGG_14269T0	Chromosome_8.1:7670631-7672023	B157	RA6	789.114	126.086	1.60E-01	-2.645825641	-5.6787	1.36E-08	4.09E-06	yes	omo
MGG_14715T0	Chromosome_8.5:3853459-3854236	B157	RA6	224.292	43.2482	1.93E-01	-2.37466617	-5.58458	2.34E-08	6.84E-06	yes	*
MGG_14966T0	Chromosome_8.6:846638-848584	B157	RA6	1252.51	259.879	2.07E-01	-2.268910158	-4.24411	2.19E-05	0.002494	yes	polysacc_deac_1
MGG_15887T0	Chromosome_8.2:6916805-6920969	B157	RA6	13.786	1.02894	7.46E-02	-3.743973158	-3.71775	0.0002	0.014791	yes	OP

MGG_16027T0	Chromosome_8.1:464650-466024	B157	RA6	14.6647	2.7736	1.89E-01	-2.402515911	-4.41234	1.02E-05	0.001358	yes	*
MGG_16361T0	Chromosome_8.1:5235017-5239353	B157	RA6	57.5853	13.0268	2.26E-01	-2.144217844	-5.27487	1.33E-07	3.17E-05	yes	H/K ATPase alpha subunit
MGG_16431T0	Chromosome_8.1:5964193-5964788	B157	RA6	5.75825	0.580993	1.01E-01	-3.309037739	-3.54957	0.00039	0.024759	yes	omo
MGG_16831T0	Chromosome_8.3:4014310-4015443	B157	RA6	3.85904	0.327922	8.50E-02	-3.556817399	-4.4149	1.01E-05	0.001345	yes	PEPTIDASE_S8
MGG_17123T0	Chromosome_8.4:2418693-2423622	B157	RA6	214.194	41.2806	1.93E-01	-2.375382223	-5.20099	1.98E-07	4.55E-05	yes	putative peptidase fam
MGG_17486T0	Chromosome_8.5:3481454-3486511	B157	RA6	7.92192	0.452694	5.71E-02	-4.129242042	-7.52349	5.33E-14	6.51E-11	yes	pectate_lyase_3
MGG_17553T0	Chromosome_8.5:4459060-4460892	B157	RA6	1.02588	0.101386	9.88E-02	-3.33893163	-3.58605	0.00034	0.022344	yes	Retrotrans_gag
MGG_17705T0	Chromosome_8.6:2164908-2165427	B157	RA6	8.3742	0.930478	1.11E-01	-3.169907429	-3.66934	0.00024	0.017197	yes	omo
MGG_17854T0	Chromosome_8.7:144244-145135	B157	RA6	172.39	5.11202	2.97E-02	-5.075638798	-10.1142	0	0	yes	*
MGG_17855T0	Chromosome_8.7:145418-146189	B157	RA6	95.3208	2.1069	2.21E-02	-5.499597314	-9.58659	0	0	yes	*

Down regulated genes classified according to their putative functions

Light regulated	**CWDE and related (plant cell wall degrading)**	**E1 –E2 ATPase**	**Amino acid catabolism**	**miscellaneous**	**transporters / premeases**	**secondary metabolism/ zenobiotic/ metal ion metabolism**	**expression regulation/Transcription factor/Zinc finger like proteins**	**protein degradation**	**others**	
MGG_01041T0- ENVOY	MGG_11608T0 laccase-2	MGG_10730T0- potassium/sodium efflux P-type ATPase	MGG_06691T0- tyrosine metabolism	MGG_04034T0 - formate dehydrogenase	MGG_09941T0- nod factor export ABC transporter	MGG_03375T0- isotrichodermin C-15 hydroxylase	MGG_07815T0- Zn LITAF domain	MGG_16831T0- peptidase S8	MGG_02234T0	MGG_09474T0
MGG_03002T0 Blue light harvesting protein	MGG_13464T0 laccase	MGG_16361T0- H/K ATPase alpha subunit	MGG_10956T0- glutamine metabolism	MGG_09647T0 - acyl-CoA synthetase	MGG_04099T0- allantoate permease	MGG_07219T0 polyketide synthase	MGG_04036T0- methyl transferase SAM dependent methyl transferases	MGG_09817T0- minor extracellular protease vpr	MGG_17855T0	MGG_09762T0
	MGG_17486T		MGG_12978T	MGG_12978T0	MGG_13107T	MGG_09225T		MGG_08429T	MGG_17854T	MGG_00287T

	0- pectate lyase		0- tryptophan metabolism		0- HPP superfam	0- in Zinc metabolism		0- peptidase S8	0	0
	MGG_11774T0 endoglucanase		leucine metabolism-catabolism	MGG_12214T0 - acyl carrier	MGG_05722T0- MFS superfam	MGG_06222T0- cobW domain-containing protein		MGG_09818T0- Aspartate protease	MGG_12942T0	MGG_05398T0
	MGG_13622T0- fungal cellulose binding domain-containing protein		MGG_10320T0	MGG_14061T0 - glyoxylate		MGG_07227T0- cadmium resistance		MGG_00311T0- peptidase A4	MGG_03364T0	MGG_12722T0
	MGG_07631T0- fungal cellulose binding domain-containing protein		MGG_02541T0	MGG_02818T0 - isoamyl alcohol oxidase		MGG_09645T0- polyketide synthase		MGG_17123T0- peptidase superfam	MGG_10781T0	MGG_04939T0
	MGG_05364T0 – endoglucanase 4		MGG_06511T0	MGG_12264T0 - flavidoxin2 supfam.oxidative stress		MGG_09945T0- averantin oxidoreductase		MGG_09708T0- f- box	MGG_08686T0	MGG_14269T0
	MGG_14966T0- polysaccharide deacetylase		MGG_03335T0	MGG_01365T0 - FAD binding					MGG_07577T0	MGG_00787T0
	MGG_01255T0- heme binding cytochrome of cellulobiose dehydrogenase		MGG_03840T0	MGG_09376T0 - FAD binding					MGG_07598T0	MGG_08647T0
				MGG_00942T0 – aminotransferase					MGG_08962T0	MGG_02082T0
				MGG_08589T0 - a,b hydrolase					MGG_15887T0	MGG_02814T0

				2						
				MGG_00771T0 - oxoprolinase, glutathione metabolism					MGG_08034T0	MGG_16027T0
				MGG_02210T0 - choloroperoxide					MGG_16431T0	MGG_03847T0
				MGG_00772T0 - PX domain containing					MGG_03363T0	MGG_14715T0
				MGG_17553T0 - retro_ gag					MGG_17705T0	MGG_03034T0
									MGG_03545T0	MGG_07870T0
									MGG_02112T0	MGG_02187T0
									MGG_11605T0	MGG_13908T0
									MGG_13716T0	MGG_07411T0
									MGG_10252T0	MGG_12468T0
2	9	2	8	15	4	7	2	7	40	

Down regulated gene islands above cut off 4 fold B157 Vs RA6

Test_id	**locus**	**sample_1**	**sample_2**	**value_1**	**value_2**	**log 2 fold change**	**test_stat**	**p_value**	**q_value**	**significant**	**biological function**
MGG_00771T0	Chromosome_8.5:1689052-1693961	B157	RA6	508.272	46.1669	-3.46067	-6.25193	4.05E-10	1.95E-07	yes	5-oxoprolinase
MGG_00772T0	Chromosome_8.5:1684694-1688648	B157	RA6	38.8643	7.1994	-2.4325	-5.85895	4.66E-09	1.57E-06	yes	PX domain-containing protein

MGG_02814T0	Chromosome_8.7:1410110-1411679	B157	RA6	5.49822	1.03633	-2.40748	-3.92903	8.53E-05	0.007522	yes	*
MGG_02818T0	Chromosome_8.7:1402237-1404747	B157	RA6	760.928	189.435	-2.00606	-3.8148	0.000136	0.011062	yes	isoamyl alcohol oxidase
MGG_03363T0	Chromosome_8.4:2130118-2131926	B157	RA6	1.31357	0.133152	-3.30235	-3.83899	0.000124	0.010151	yes	no domain
MGG_03364T0	Chromosome_8.4:2129216-2130057	B157	RA6	91.8897	3.04678	-4.91455	-9.03417	0	0	yes	DUF4360
MGG_03375T0	Chromosome_8.4:2100075-2102662	B157	RA6	263.342	27.2245	-3.27396	-7.48595	7.11E-14	7.88E-11	yes	isotrichodermin C-15 hydroxylase
MGG_04034T0	Chromosome_8.6:2168435-2170853	B157	RA6	2658.96	372.441	-2.83578	-4.33569	1.45E-05	0.001802	yes	formate dehydrogenase
MGG_04036T0	Chromosome_8.6:2162544-2163835	B157	RA6	4.90475	0.951685	-2.36562	-3.4698	0.000521	0.031386	yes	methyl transferase domain
MGG_09645T0	Chromosome_8.7:3086988-3093813	B157	RA6	39.0135	7.00195	-2.47814	-6.01875	1.76E-09	6.66E-07	yes	polyketide synthase
MGG_09647T0	Chromosome_8.7:3084083-3085774	B157	RA6	55.8368	12.6745	-2.13929	-5.04782	4.47E-07	9.18E-05	yes	acyl-CoA synthetase
MGG_09817T0	Chromosome_8.6:4016281-4020891	B157	RA6	42.004	4.1619	-3.33521	-6.28177	3.35E-10	1.66E-07	yes	minor extracellular protease vpr
MGG_09818T0	Chromosome_8.6:4014092-4015685	B157	RA6	18.6101	3.09609	-2.58757	-5.08206	3.73E-07	7.85E-05	yes	Aspartate protease
MGG_09941T0	Chromosome_8.1:4421844-4427597	B157	RA6	520.513	65.8516	-2.98264	-5.29329	1.20E-07	2.93E-05	yes	nod factor export ATP-binding protein I
MGG_09945T0	Chromosome_8.1:4439239-4441827	B157	RA6	8.55431	1.72803	-2.30752	-4.35145	1.35E-05	0.001698	yes	averantin oxidoreductase
MGG_11605T0	Chromosome_8.5:3343738-3347478	B157	RA6	11.3456	2.6113	-2.11929	-4.3256	1.52E-05	0.00186	yes	*
MGG_11608T0	Chromosome_8.5:3404246-3406595	B157	RA6	1326.82	27.9636	-5.56828	-9.85285	0	0	yes	laccase-2

MGG_17854T0	Chromosome_8.7:144244-145135	B157	RA6	172.39	5.11202	-5.07564	-10.1142	0	0	yes	*
MGG_17855T0	Chromosome_8.7:145418-146189	B157	RA6	95.3208	2.1069	-5.4996	-9.58659	0	0	yes	*

Differently expressed genes uniquely expressed in oxidative stress

Up-Regulated Genes

test_id	**sample_1**	**sample_2**	**value_1**	**value_2**	**fold change**	**log2 (fold_change)**	**test_stat**	**p_value**	**q_value**	**significant**	**predicted biological function**
MGG_08801T0	B157H2O2	RA6H2O2	0.041249	31.1698	755.6498339	9.561574038	6.23809	4.43E-10	2.07E-07	yes	exopolyphosphatase
MGG_08800T0	B157H2O2	RA6H2O2	0.02951	6.4637	219.0327412	7.775002731	5.02747	4.97E-07	9.98E-05	yes	CAIB/BAIF family enzyme
MGG_10510T0	B157H2O2	RA6H2O2	0.126097	1.55717	12.3489853	3.626320598	4.03156	5.54E-05	0.005414	yes	ribonuclease T2 (325 aa)
MGG_08258T0	B157H2O2	RA6H2O2	106.43	1087.04	10.21366156	3.352428255	6.07019	1.28E-09	4.94E-07	yes	peptide transporter
MGG_00940T0	B157H2O2	RA6H2O2	38.7819	362.154	9.338222212	3.223147919	7.2692	3.62E-13	3.61E-10	yes	tripeptidyl-peptidase 1
MGG_03368T0	B157H2O2	RA6H2O2	3.44356	27.2369	7.909518057	2.983589791	3.5352	0.000407	0.025844	yes	*
MGG_08817T0	B157H2O2	RA6H2O2	112.346	824.145	7.335775194	2.874949428	6.69697	2.13E-11	1.36E-08	yes	omo
MGG_05386T0	B157H2O2	RA6H2O2	1.74771	9.00172	5.150579902	2.364734874	3.92049	8.84E-05	0.007738	yes	hypothetical integral membrane protein
MGG_03367T0	B157H2O2	RA6H2O2	1.65154	8.34399	5.052248205	2.336925517	3.90989	9.23E-05	0.008028	yes	GPI anchored prt
MGG_01569T0	B157H2O2	RA6H2O2	12.61	63.0268	4.99816019	2.32139714	5.35444	8.58E-08	2.20E-05	yes	minor allergen Alt a 7
MGG_13001T0	B157H2O2	RA6H2O2	23.4993	113.899	4.846910333	2.277065393	5.44972	5.05E-08	1.37E-05	yes	ACT domain containing protein
MGG_02095T0	B157H2O2	RA6H2O2	22.9018	105.655	4.613392834	2.205828144	5.20027	1.99E-07	4.55E-05	yes	NMRA like (isoflavone reductase family like)
MGG_13765T0	B157H2O2	RA6H2O2	3.60615	16.5351	4.585250198	2.197000458	3.65742	0.000255	0.01789	yes	Peptidase_S28
MGG_02378T0	B157H2O2	RA6H2O2	146.531	671.806	4.584736336	2.196838768	4.08571	4.39E-05	0.004476	yes	glutamate decarboxylase
MGG_17222T0	B157H2O2	RA6H2O2	80.348	351.874	4.37937472	2.130724899	4.73457	2.20E-06	0.000371	yes	GST
MGG_09351T0	B157H2O2	RA6H2O2	1.24368	5.39603	4.338760774	2.117283043	3.44284	0.000576	0.034134	yes	aspergillopepsin-F (431 aa)
MGG_05484T0	B157H2O2	RA6H2O2	12.1881	49.9637	4.099383825	2.035407076	3.77485	0.00016	0.012585	yes	AP-2 complex subunit mu-1

MGG_06026T0	B157H2O2	RA6H2O2	5.03582	20.2282	4.016863192	2.006069326	4.52286	6.10E-06	0.000887	yes	PAS_3 domain
MGG_05515T0	B157H2O2	RA6H2O2	2.30712	9.26615	4.016327716	2.005876992	3.54544	0.000392	0.025029	yes	peptidase M35 domain
Down Regulated Genes											
test_id	**sample_1**	**sample_2**	**value_1**	**value_2**	**fold change**	**log2 (fold_change)**	**test_stat**	**p_value**	**q_value**	**significant**	**predicted biological function**
MGG_03365T0	B157H2O2	RA6H2O2	4.33539	0.355573	0.082016381	-3.607944096	-3.54892	0.000387	0.024759	yes	*
MGG_04632T0	B157H2O2	RA6H2O2	7.24576	0.64793	0.089421952	-3.483227157	-5.438	5.39E-08	1.45E-05	yes	DUF 2236
MGG_09377T0	B157H2O2	RA6H2O2	4.64912	0.480485	0.103349666	-3.274394366	-3.76404	0.000167	0.012938	yes	*
MGG_07404T0	B157H2O2	RA6H2O2	1.4595	0.179676	0.123107914	-3.02200459	-3.76318	0.000168	0.012966	yes	tripeptidyl-peptidase 1 (602 aa)
MGG_02884T0	B157H2O2	RA6H2O2	3.3768	0.416198	0.123252191	-3.020314797	-4.49758	6.87E-06	0.000983	yes	beta-Ig-H3/Fasciclin
MGG_10422T0	B157H2O2	RA6H2O2	44.3456	6.18878	0.139557927	-2.841064024	-6.33859	2.32E-10	1.20E-07	yes	Fungal_transcription_factor_2
MGG_03383T0	B157H2O2	RA6H2O2	2.52399	0.365958	0.144991858	-2.785956205	-4.01238	6.01E-05	0.005788	yes	*
MGG_00743T0	B157H2O2	RA6H2O2	2.60347	0.380681	0.146220621	-2.773781311	-4.09324	4.25E-05	0.004356	yes	twin-arginine translocation pathway signal (418 aa)
MGG_09107T0	B157H2O2	RA6H2O2	1.90683	0.300097	0.15738005	-2.667675427	-3.77127	0.000162	0.012684	yes	HET -
MGG_16403T0	B157H2O2	RA6H2O2	101.828	16.4497	0.161543976	-2.630001141	-6.25152	4.06E-10	1.95E-07	yes	*
MGG_10254T0	B157H2O2	RA6H2O2	5.14373	0.864231	0.168016401	-2.57332603	-3.9794	6.91E-05	0.006445	yes	TAU D
MGG_15784T0	B157H2O2	RA6H2O2	7.39566	1.30377	0.176288526	-2.503989517	-3.40169	0.00067	0.038277	yes	omo
MGG_02157T0	B157H2O2	RA6H2O2	148.304	27.4719	0.185240452	-2.432528912	-5.92072	3.21E-09	1.13E-06	yes	OP
MGG_00195T0	B157H2O2	RA6H2O2	95.013	17.888	0.188268974	-2.409132828	-5.83769	5.29E-09	1.76E-06	yes	clock-controlled-9 protein
MGG_16690T0	B157H2O2	RA6H2O2	11.3712	2.168	0.190657099	-2.390947848	-3.74609	0.00018	0.013567	yes	omo
MGG_02543T0	B157H2O2	RA6H2O2	3.4231	0.657906	0.192195963	-2.379350064	-3.32819	0.000874	0.046917	yes	lipase_GDSL_2

MGG_09383T0	B157H2O2	RA6H2O2	13.626	2.62086	0.19234258	-2.378249916	-3.93806	8.21E-05	0.007311	yes	NIMA-interacting protein TinC
MGG_09763T0	B157H2O2	RA6H2O2	3.9779	0.765412	0.192416099	-2.377698584	-3.56133	0.000369	0.023925	yes	*
MGG_04126T0	B157H2O2	RA6H2O2	8.97024	1.79212	0.199785067	-2.323479342	-4.49387	6.99E-06	0.000995	yes	ulphate permease 2
MGG_09015T0	B157H2O2	RA6H2O2	40.3406	8.24734	0.204442671	-2.290231752	-5.04235	4.60E-07	9.30E-05	yes	Bacteriorhodopsin
MGG_08589T0	B157H2O2	RA6H2O2	8.66413	1.78018	0.205465523	-2.283031766	-4.02009	5.82E-05	0.00563	yes	A,b,hydrolase_6
MGG_05116T0	B157H2O2	RA6H2O2	10.6048	2.20453	0.207880394	-2.266174398	-4.56	5.12E-06	0.000768	yes	malic acid transporter (522 aa)
MGG_09383T1	B157H2O2	RA6H2O2	11.6479	2.43737	0.209254029	-2.256672697	-3.32092	0.000897	0.047813	yes	NIMA-interacting protein TinC
MGG_07228T0	B157H2O2	RA6H2O2	4.06598	0.869093	0.213747485	-2.226020648	-3.80935	0.000139	0.011278	yes	OPT
MGG_08486T0	B157H2O2	RA6H2O2	32.5508	7.15988	0.219960185	-2.184685688	-4.93868	7.87E-07	0.00015	yes	beta-lactamase
MGG_10244T0	B157H2O2	RA6H2O2	951.281	209.852	0.220599381	-2.18049935	-5.08561	3.66E-07	7.76E-05	yes	OP
MGG_00433T0	B157H2O2	RA6H2O2	34.3731	7.97167	0.231915946	-2.108326076	-3.9472	7.91E-05	0.007101	yes	omo
MGG_04736T0	B157H2O2	RA6H2O2	208.061	48.3294	0.232284763	-2.106033575	-5.17393	2.29E-07	5.15E-05	yes	NADH(P)_ binding
MGG_07788T0	B157H2O2	RA6H2O2	6.79356	1.644	0.241993888	-2.046957483	-3.39433	0.000688	0.039023	yes	omo
MGG_17458T0	B157H2O2	RA6H2O2	33.9648	8.23435	0.242437759	-2.044313682	-3.65123	0.000261	0.018156	yes	*
MGG_05457T0	B157H2O2	RA6H2O2	12.4325	3.02083	0.242978484	-2.041099529	-4.56341	5.03E-06	0.000757	yes	Tau D
MGG_03464T0	B157H2O2	RA6H2O2	291.142	71.9083	0.246987037	-2.017492769	-4.98056	6.34E-07	0.000122	yes	*
MGG_10846T0	B157H2O2	RA6H2O2	64.2462	15.9453	0.248190554	-2.010479884	-4.50556	6.62E-06	0.000951	yes	omo
MGG_17594T0	B157H2O2	RA6H2O2	11.3466	2.83049	0.249457106	-2.003136328	-3.32733	0.000877	0.047	yes	omo

Up-regulated genes –oxidative stress treated B157 Vs RA6

test_id	**sample_1**	**sample_2**	**value_1**	**value_2**	**fold change**	**log2 (fold_change)**	**test_stat**	**p_value**	**q_value**	**significant**	**Putative function**
MGG_08802T0	B157H2O2	RA6H2O2	0.033609	45.0413	1340.139961	10.38816796	6.79099	1.11E-11	7.58E-09	yes	GMP synthase
MGG_08801T0	B157H2O2	RA6H2O2	0.041249	31.1698	755.6498339	9.561574038	6.23809	4.43E-10	2.07E-07	yes	exopolyphosphatase
MGG_08800T0	B157H2O2	RA6H2O2	0.02951	6.4637	219.0327412	7.775002731	5.02747	4.97E-07	9.98E-05	yes	CAIB/BAIF family enzyme
MGG_18077T0	B157H2O2	RA6H2O2	0.945463	30.5087	32.26852875	5.012055896	4.36558	1.27E-05	0.001619	yes	*
MGG_11255T0	B157H2O2	RA6H2O2	49.4062	1496.39	30.28749428	4.920650322	10.1503	0	0	yes	OP
MGG_08971T0	B157H2O2	RA6H2O2	0.142543	2.98583	20.94687217	4.388662929	3.78667	0.000153	0.012097	yes	*
MGG_09138T0	B157H2O2	RA6H2O2	1.45806	29.5874	20.29230622	4.342860931	7.67955	1.60E-14	2.08E-11	yes	glutathione S-transferase II
MGG_05828T0	B157H2O2	RA6H2O2	0.144466	2.6019	18.01046613	4.170763615	4.27587	1.90E-05	0.002206	yes	chitin deacetylase 1
MGG_00031T0	B157H2O2	RA6H2O2	0.095285	1.52799	16.03592995	4.003236116	4.7809	1.75E-06	0.000306	yes	FAD binding domain-containing protein
MGG_04248T0	B157H2O2	RA6H2O2	3.71161	59.0825	15.91829422	3.992613842	8.62745	0	0	yes	oligo peptide transporter
MGG_02379T0	B157H2O2	RA6H2O2	2.59905	34.3078	13.20013082	3.722480322	6.48049	9.14E-11	4.98E-08	yes	omo
MGG_08977T0	B157H2O2	RA6H2O2	0.512255	6.75338	13.18362925	3.720675671	4.62909	3.67E-06	0.000578	yes	ctr copper transporter
MGG_09354T0	B157H2O2	RA6H2O2	1.89242	24.1742	12.77422559	3.675163929	7.51952	5.51E-14	6.60E-11	yes	*
MGG_10510T0	B157H2O2	RA6H2O2	0.126097	1.55717	12.3489853	3.626320598	4.03156	5.54E-05	0.005414	yes	ribonuclease T2 (325 aa)
MGG_09874T0	B157H2O2	RA6H2O2	0.559993	5.8078	10.37120107	3.374511074	4.32143	1.55E-05	0.001887	yes	METHYL TRANSFERASE
MGG_08258T0	B157H2O2	RA6H2O2	106.43	1087.04	10.21366156	3.352428255	6.07019	1.28E-09	4.94E-07	yes	peptide transporter
MGG_00289T0	B157H2O2	RA6H2O2	63.487	646.107	10.17699687	3.347239994	6.57468	4.88E-11	2.81E-08	yes	amino-acid permease inda1
sMGG_17792T0	B157H2O2	RA6H2O2	49.8772	466.095	9.344850954	3.224171654	7.37539	1.64E-13	1.75E-10	yes	omo

MGG_00940T0	B157H2O2	RA6H2O2	38.7819	362.154	9.338222212	3.223147919	7.2692	3.62E-13	3.61E-10	yes	tripeptidyl-peptidase 1
MGG_10694T0	B157H2O2	RA6H2O2	1.07635	9.04797	8.406159706	3.071446866	5.74873	8.99E-09	2.82E-06	yes	Fungal_transcription_factor
MGG_10704T0	B157H2O2	RA6H2O2	3.99794	33.1871	8.301050041	3.053293842	5.90628	3.50E-09	1.22E-06	yes	NAT_SF
MGG_03368T0	B157H2O2	RA6H2O2	3.44356	27.2369	7.909518057	2.983589791	3.5352	0.000407	0.025844	yes	*
MGG_02119T0	B157H2O2	RA6H2O2	2.51331	18.7695	7.468040154	2.900729685	5.53748	3.07E-08	8.71E-06	yes	high-affinity nicotinic acid transporter
MGG_08817T0	B157H2O2	RA6H2O2	112.346	824.145	7.335775194	2.874949428	6.69697	2.13E-11	1.36E-08	yes	omo
MGG_05827T0	B157H2O2	RA6H2O2	0.270447	1.98006	7.321434514	2.872126348	3.62142	0.000293	0.019886	yes	glutamyl-tRNA(Gln) amidotransferase subunit
MGG_05798T0	B157H2O2	RA6H2O2	0.709727	4.98325	7.021361735	2.811750856	4.05029	5.12E-05	0.005066	yes	cutinase
MGG_11285T0	B157H2O2	RA6H2O2	1.45874	10.2195	7.005703552	2.808529942	4.32826	1.50E-05	0.001845	yes	*
MGG_09827T0	B157H2O2	RA6H2O2	2.36077	15.1786	6.429512405	2.684709332	5.20691	1.92E-07	4.44E-05	yes	sugar transporter
MGG_13793T0	B157H2O2	RA6H2O2	6.29891	36.1525	5.739485086	2.520921312	5.96714	2.41E-09	8.98E-07	yes	nitrate transporter
MGG_09063T0	B157H2O2	RA6H2O2	5.85735	33.4865	5.71700513	2.515259585	5.7904	7.02E-09	2.29E-06	yes	urea active transporter
MGG_01924T0	B157H2O2	RA6H2O2	11.6618	61.2665	5.25360579	2.39330795	5.68456	1.31E-08	3.97E-06	yes	benzoate 4-monooxygenase
MGG_05386T0	B157H2O2	RA6H2O2	1.74771	9.00172	5.150579902	2.364734874	3.92049	8.84E-05	0.007738	yes	hypothetical integral membrane protein
MGG_03367T0	B157H2O2	RA6H2O2	1.65154	8.34399	5.052248205	2.336925517	3.90989	9.23E-05	0.008028	yes	GPI anchored prt
MGG_01569T0	B157H2O2	RA6H2O2	12.61	63.0268	4.99816019	2.32139714	5.35444	8.58E-08	2.20E-05	yes	minor allergen Alt a 7
MGG_13001T0	B157H2O2	RA6H2O2	23.4993	113.899	4.846910333	2.277065393	5.44972	5.05E-08	1.37E-05	yes	ACT domain containing protein
MGG_07957T0	B157H2O2	RA6H2O2	6.27497	29.9278	4.76939332	2.253805763	5.00381	5.62E-07	0.000111	yes	uridine permease
MGG_15535T0	B157H2O2	RA6H2O2	2.71914	12.7742	4.697882419	2.232010605	4.92364	8.50E-07	0.000161	yes	carbomyl phosphate synthase

MGG_02095T0	B157H2O2	RA6H2O2	22.9018	105.655	4.613392834	2.205828144	5.20027	1.99E-07	4.55E-05	yes	NMRA like (isoflavone reductase family like)
MGG_13765T0	B157H2O2	RA6H2O2	3.60615	16.5351	4.585250198	2.197000458	3.65742	0.000255	0.01789	yes	Peptidase_S28
MGG_02378T0	B157H2O2	RA6H2O2	146.531	671.806	4.584736336	2.196838768	4.08571	4.39E-05	0.004476	yes	glutamate decarboxylase
MGG_01922T0	B157H2O2	RA6H2O2	1.17858	5.31976	4.513702931	2.174311471	3.54405	0.000394	0.025108	yes	polysaccharide deacetylase
MGG_17222T0	B157H2O2	RA6H2O2	80.348	351.874	4.37937472	2.130724899	4.73457	2.20E-06	0.000371	yes	GST
MGG_09351T0	B157H2O2	RA6H2O2	1.24368	5.39603	4.338760774	2.117283043	3.44284	0.000576	0.034134	yes	aspergillopepsin-F (431 aa)
MGG_05484T0	B157H2O2	RA6H2O2	12.1881	49.9637	4.099383825	2.035407076	3.77485	0.00016	0.012585	yes	AP-2 complex subunit mu-1
MGG_00822T0	B157H2O2	RA6H2O2	5.96505	24.3869	4.088297667	2.031500242	3.90986	9.23E-05	0.008028	yes	*
MGG_06026T0	B157H2O2	RA6H2O2	5.03582	20.2282	4.016863192	2.006069326	4.52286	6.10E-06	0.000887	yes	PAS_3 domain
MGG_05515T0	B157H2O2	RA6H2O2	2.30712	9.26615	4.016327716	2.005876992	3.54544	0.000392	0.025029	yes	peptidase M35 domain

Up regulated genes under oxidative stress conditions classified according to their putative functions

Nitrogen metabolism	**transporters/ permeases**	**detox genes**	**CWDE**	**expression regulation/ transcriptional factors**	**general metabolism**	**others**	**miscellaneous**	**membrane protein**	**amino acid metabolism**	**protein degradation**	**mycotoxin**
MGG_08802T0- GMP synthase	MGG_04248T0- OPT	MGG_09138T0- GST	MGG_05828T0- Chitin deacetylase	MGG_09874T0- methyl transferase	MGG_00031T0- FAD binding	MGG_18077T0	MGG_10510T0- ribonuclease T2	MGG_05386T0- integral membrane prt	MGG_13001T0-ACT domain containing protein	MGG_00940T0- tripeptidyl peptidase	MGG_09351T0- aspergillo-pepsin
MGG_05827T0- gln tRNA amidotransferase	MGG_08977T0 - Cu trptr	MGG_10704T0- NAT_SF	MGG_05798T0- Cutinase	MGG_10694T0- fungal TF	MGG_08801T0- exopolyphosphatase	MGG_11255T0	MGG_05484T0- AP2 complex-	MGG_03367T0- GPI anchord prt	MGG_02378T0- glutamate decarboxylase	MGG_13765T0- peptidase_S8	MGG_01569T0- Minor allergen Alt a7

MGG_15535T0- carbamyl phosphate synthase	MGG_00289T0- aa permease	MGG_01924T0- benzoate monooxygense	MGG_01922T0- poly sachh_ deacetylase		MGG_08800T0- CAIB/BAIF family enzyme	MGG_08971T0	MGG_06026T0- PAS_3 domain			MGG_05515T0- peptidase _M35	
MGG_02095T0- NMRA like	MGG_02119T0- High affinity	MGG_17222T0- GST 2				MGG_02379T0					
	MGG_09827T0- sugar					MGG_09354T0					
	MGG_13793T0- nitrate					MGG_17792T0					
	MGG_09063T0- urea					MGG_11285T0					
	MGG_07957T0- uridine					MGG_00822T0					
	MGG_08258T0- peptide					MGG_03368T0					
						MGG_08817T0					
Nitrogen metabolism	transporters/ permeases	detox genes	CWDE	expression regulation/transcriptional factors	general metabolism	others	miscellaneous	membrane protein	amino acid metabolism	protein degradation	mycotoxin
4	9	4	3	2	3	10	3	2	2	3	2

Transcripts expressed only in RA6 under oxidative stress

Test_id	sample_1	sample_2	value_1	value_2	test_stat	p_value	q_value	significant	Putative function
MGG_00016T0	B157H2O2	RA6H2O2	0	5.1828	-1.79769e+308	7.94E-05	0.007105	yes	2-epi-5-epi-valiolone synthase
MGG_00018T0	B157H2O2	RA6H2O2	0	2.20458	-1.79769e+308	0.000166	0.012901	yes	integral membrane protein, MFS
MGG_00019T0	B157H2O2	RA6H2O2	0	12.1646	-1.79769e+308	0.000413	0.026028	yes	No domain

Up-regulated gene islands under oxidative stress above Log2 fold change cut off- B157 Vs RA6

test_id	locus	sample_1	sample_2	value_1	value_2	fold change	log2 (fold_change)	test_stat	p_value	q_value	significant	Putative function
MGG_01922T0	Chromosome_8.6:641282-642742	B157H2O2	RA6H2O2	1.17858	5.31976	4.513702931	2.174311471	3.54405	0.000394	0.025108	yes	polysaccharide deacetylase
MGG_01924T0	Chromosome_8.6:636875-639229	B157H2O2	RA6H2O2	11.6618	61.2665	5.25360579	2.39330795	5.68456	1.31E-08	3.97E-06	yes	benzoate 4-monooxygenase cytochrome P450
MGG_02378T0	Chromosome_8.1:1609862-1615708	B157H2O2	RA6H2O2	146.531	671.806	4.584736336	2.196838768	4.08571	4.39E-05	0.004476	yes	glutamate decarboxylase
MGG_02379T0	Chromosome_8.1:1616610-1617336	B157H2O2	RA6H2O2	2.59905	34.3078	13.20013082	3.722480322	6.48049	9.14E-11	4.98E-08	yes	omo
MGG_03367T0	Chromosome_8.4:2116781-2122239	B157H2O2	RA6H2O2	1.65154	8.34399	5.052248205	2.336925517	3.90989	9.23E-05	0.008028	yes	GPI anchored prt
MGG_03368T0	Chromosome_8.4:2116781-2122239	B157H2O2	RA6H2O2	3.44356	27.2369	7.909518057	2.983589791	3.5352	0.000407	0.025844	yes	*
MGG_05827T0	Chromosome_8.3:1627113-1628442	B157H2O2	RA6H2O2	0.270447	1.98006	7.321434514	2.872126348	3.62142	0.000293	0.019886	yes	glutamyl-tRNA(Gln) amidotransferase subunit A
MGG_05828T0	Chromosome_8.3:1629109-1630264	B157H2O2	RA6H2O2	0.144466	2.6019	18.01046613	4.170763615	4.27587	1.90E-05	0.002206	yes	chitin deacetylase 1
MGG_08800T0	Chromosome_8.6:77107-78925	B157H2O2	RA6H2O2	0.02951	6.4637	219.0327412	7.775002731	5.02747	4.97E-07	9.98E-05	yes	CAIB/BAIF family enzyme
MGG_08801T0	Chromosome_8.6:75214-76555	B157H2O2	RA6H2O2	0.041249	31.1698	755.6498339	9.561574038	6.23809	4.43E-10	2.07E-07	yes	exopolyphosphatase
MGG_08802T0	Chromosome_8.6:73075-74679	B157H2O2	RA6H2O2	0.033609	45.0413	1340.139961	10.38816796	6.79099	1.11E-11	7.58E-09	yes	GMP synthase
MGG_08971T0	Chromosome_8.2:2331151-2332099	B157H2O2	RA6H2O2	0.142543	2.98583	20.94687217	4.388662929	3.78667	0.000153	0.012097	yes	*
MGG_08977T0	Chromosome_8.2:2350943-2351719	B157H2O2	RA6H2O2	0.512255	6.75338	13.18362925	3.720675671	4.62909	3.67E-06	0.000578	yes	ctr copper transporter

MGG_09351T0	Chromosome_8.6:3591988-3593387	B157H2O2	RA6H2O2	1.24368	5.39603	4.338760774	2.117283043	3.44284	0.000576	0.034134	yes	aspergillopepsin-F (431 aa)
MGG_09354T0	Chromosome_8.6:3580232-3584060	B157H2O2	RA6H2O2	1.89242	24.1742	12.77422559	3.675163929	7.51952	5.51E-14	6.60E-11	yes	*
MGG_10694T0	Chromosome_8.6:3793544-3796830	B157H2O2	RA6H2O2	1.07635	9.04797	8.406159706	3.071446866	5.74873	8.99E-09	2.82E-06	yes	Fungal_transcription_factor
MGG_10704T0	Chromosome_8.6:3768979-3770092	B157H2O2	RA6H2O2	3.99794	33.1871	8.301050041	3.053293842	5.90628	3.50E-09	1.22E-06	yes	NAT_SF

Down regulated genes B157 Vs RA6 under oxidative stress

test_id	**sample_1**	**sample_2**	**value_1**	**value_2**	**fold change**	**log2 (fold_change)**	**test_stat**	**p_value**	**q_value**	**significant**	**Putative function**
MGG_12942T0	B157H2O2	RA6H2O2	452.383	3.0341	0.006707	-7.22013	-8.44369	0	0	yes	OP
MGG_02234T0	B157H2O2	RA6H2O2	1957.49	28.6626	0.014643	-6.09369	-12.1103	0	0	yes	OP
MGG_03364T0	B157H2O2	RA6H2O2	133.253	2.34987	0.017635	-5.82544	-10.4636	0	0	yes	DUF4360
MGG_11608T0	B157H2O2	RA6H2O2	1331.98	26.124	0.019613	-5.67205	-10.0111	0	0	yes	laccase-2
MGG_09762T0	B157H2O2	RA6H2O2	6.31008	0.194793	0.03087	-5.01764	-7.22669	4.95E-13	4.63E-10	yes	vWFA uperfamily
MGG_11774T0	B157H2O2	RA6H2O2	4.90585	0.160173	0.032649	-4.9368	-6.91499	4.68E-12	3.69E-09	yes	endoglucanase
MGG_07577T0	B157H2O2	RA6H2O2	8.48756	0.305261	0.035966	-4.79723	-7.15503	8.37E-13	7.48E-10	yes	*
MGG_17854T0	B157H2O2	RA6H2O2	63.7224	2.45585	0.03854	-4.69751	-8.64179	0	0	yes	*
MGG_17855T0	B157H2O2	RA6H2O2	32.2256	1.30029	0.04035	-4.6313	-7.28421	3.24E-13	3.34E-10	yes	*
MGG_13464T0	B157H2O2	RA6H2O2	422.114	20.6991	0.049037	-4.34999	-9.24138	0	0	yes	laccase
MGG_07598T0	B157H2O2	RA6H2O2	9.55606	0.564058	0.059026	-4.0825	-6.50852	7.59E-11	4.17E-08	yes	omo
MGG_09645T0	B157H2O2	RA6H2O2	79.2108	5.65632	0.071408	-3.80776	-8.62354	0	0	yes	polyketide synthase
MGG_08034T0	B157H2O2	RA6H2O2	42.4404	3.23249	0.076165	-3.71472	-6.12196	9.24E-10	3.77E-07	yes	*
MGG_08686T0	B157H2O2	RA6H2O2	6.20104	0.48525	0.078253	-3.67571	-5.96831	2.40E-09	8.97E-07	yes	omo

MGG_09376T0	B157H2O2	RA6H2O2	2.76574	0.226616	0.081937	-3.60934	-4.72796	2.27E-06	0.000382	yes	FAD binding domain-containing protein (507 aa)
MGG_03365T0	B157H2O2	RA6H2O2	4.33539	0.355573	0.082016	-3.60794	-3.54892	0.000387	0.024759	yes	*
MGG_04632T0	B157H2O2	RA6H2O2	7.24576	0.64793	0.089422	-3.48323	-5.438	5.39E-08	1.45E-05	yes	DUF 2236
MGG_04099T0	B157H2O2	RA6H2O2	84.2772	7.70796	0.09146	-3.45072	-7.808	5.77E-15	8.23E-12	yes	allantoate permease
MGG_07815T0	B157H2O2	RA6H2O2	8.4046	0.771684	0.091817	-3.4451	-5.07851	3.80E-07	7.97E-05	yes	ZF-LITAF like dimain
MGG_03363T0	B157H2O2	RA6H2O2	2.14536	0.205097	0.0956	-3.38684	-4.40671	1.05E-05	0.001385	yes	*
MGG_09377T0	B157H2O2	RA6H2O2	4.64912	0.480485	0.10335	-3.27439	-3.76404	0.000167	0.012938	yes	*
MGG_17486T0	B157H2O2	RA6H2O2	7.38602	0.768718	0.104077	-3.26427	-6.24697	4.18E-10	1.99E-07	yes	pectate_lyase_3
MGG_05398T0	B157H2O2	RA6H2O2	7.46138	0.779587	0.104483	-3.25866	-4.54402	5.52E-06	0.00081	yes	OP
MGG_07404T0	B157H2O2	RA6H2O2	1.4595	0.179676	0.123108	-3.022	-3.76318	0.000168	0.012966	yes	tripeptidyl-peptidase 1 (602 aa)
MGG_02884T0	B157H2O2	RA6H2O2	3.3768	0.416198	0.123252	-3.02031	-4.49758	6.87E-06	0.000983	yes	beta-Ig-H3/Fasciclin
MGG_08962T0	B157H2O2	RA6H2O2	5.16704	0.65172	0.12613	-2.98701	-4.27104	1.95E-05	0.002245	yes	*
MGG_10252T0	B157H2O2	RA6H2O2	237.194	30.7432	0.129612	-2.94773	-6.92348	4.41E-12	3.57E-09	yes	hypothetical protein
MGG_13107T0	B157H2O2	RA6H2O2	141.359	18.6238	0.131748	-2.92414	-5.80735	6.35E-09	2.08E-06	yes	HPP_superfam
MGG_00771T0	B157H2O2	RA6H2O2	209.132	27.5642	0.131803	-2.92355	-6.21781	5.04E-10	2.27E-07	yes	5-oxoprolinase
MGG_09945T0	B157H2O2	RA6H2O2	9.28816	1.25119	0.134708	-2.89209	-5.31908	1.04E-07	2.60E-05	yes	averantin oxidoreductase
MGG_13622T0	B157H2O2	RA6H2O2	18.9122	2.5501	0.134839	-2.89069	-5.95532	2.60E-09	9.42E-07	yes	fungal cellulose binding domain-containing protein
MGG_10422T0	B157H2O2	RA6H2O2	44.3456	6.18878	0.139558	-2.84106	-6.33859	2.32E-10	1.20E-07	yes	Fungal_transcription_factor_2
MGG_02082T0	B157H2O2	RA6H2O2	9.09885	1.29175	0.141968	-2.81636	-3.57378	0.000352	0.02311	yes	omo
MGG_02818T0	B157H2O2	RA6H2O2	853.974	122.843	0.143849	-2.79738	-5.3307	9.78E-08	2.46E-05	yes	isoamyl alcohol oxidase
MGG_15887T0	B157H2O2	RA6H2O2	14.7712	2.12586	0.143919	-2.79667	-3.35939	0.000781	0.043204	yes	OP
MGG_08429T0	B157H2O2	RA6H2O2	233.406	33.7217	0.144477	-2.79109	-6.51287	7.37E-11	4.09E-08	yes	peptidase_s8
MGG_10781T0	B157H2O2	RA6H2O2	29.2378	4.22827	0.144617	-2.7897	-4.83937	1.30E-06	0.000235	yes	*
MGG_03383T0	B157H2O2	RA6H2O2	2.52399	0.365958	0.144992	-2.78596	-4.01238	6.01E-05	0.005788	yes	*

MGG_00743T0	B157H2O2	RA6H2O2	2.60347	0.380681	0.146221	-2.77378	-4.09324	4.25E-05	0.004356	yes	twin-arginine translocation pathway signal (418 aa)
MGG_02112T0	B157H2O2	RA6H2O2	5.48471	0.816312	0.148834	-2.74822	-4.30989	1.63E-05	0.001953	yes	*
MGG_09647T0	B157H2O2	RA6H2O2	59.7649	9.29319	0.155496	-2.68505	-6.14219	8.14E-10	3.39E-07	yes	acyl-CoA synthetase
MGG_09107T0	B157H2O2	RA6H2O2	1.90683	0.300097	0.15738	-2.66768	-3.77127	0.000162	0.012684	yes	HET -
MGG_17705T0	B157H2O2	RA6H2O2	10.2815	1.61992	0.157557	-2.66606	-3.48456	0.000493	0.030177	yes	omo
MGG_00787T0	B157H2O2	RA6H2O2	5.32169	0.844079	0.158611	-2.65643	-4.17949	2.92E-05	0.003136	yes	OP
MGG_14715T0	B157H2O2	RA6H2O2	406.402	64.9199	0.159743	-2.64617	-6.3504	2.15E-10	1.12E-07	yes	*
MGG_00311T0	B157H2O2	RA6H2O2	354.611	56.9563	0.160616	-2.63831	-5.00926	5.46E-07	0.000108	yes	peptidase_A4
MGG_16403T0	B157H2O2	RA6H2O2	101.828	16.4497	0.161544	-2.63	-6.25152	4.06E-10	1.95E-07	yes	*
MGG_10254T0	B157H2O2	RA6H2O2	5.14373	0.864231	0.168016	-2.57333	-3.9794	6.91E-05	0.006445	yes	TAU D
MGG_12978T0	B157H2O2	RA6H2O2	12.5933	2.14235	0.170118	-2.55539	-4.69953	2.61E-06	0.000435	yes	kynurenine 3-monooxygenase
MGG_00287T0	B157H2O2	RA6H2O2	103.204	17.8458	0.172918	-2.53184	-5.96324	2.47E-09	9.14E-07	yes	OP
MGG_12264T0	B157H2O2	RA6H2O2	16.5132	2.89047	0.17504	-2.51424	-4.39548	1.11E-05	0.001452	yes	flavodoxin_2 superfamily
MGG_04034T0	B157H2O2	RA6H2O2	4011.24	704.972	0.175749	-2.50841	-3.35191	0.000803	0.043989	yes	formate dehydrogenase
MGG_15784T0	B157H2O2	RA6H2O2	7.39566	1.30377	0.176289	-2.50399	-3.40169	0.00067	0.038277	yes	omo
MGG_09474T0	B157H2O2	RA6H2O2	514.763	92.923	0.180516	-2.4698	-5.98812	2.12E-09	8.00E-07	yes	OP
MGG_09941T0	B157H2O2	RA6H2O2	446.637	81.898	0.183366	-2.4472	-4.42152	9.80E-06	0.001313	yes	nod factor export ATP-binding protein I
MGG_02157T0	B157H2O2	RA6H2O2	148.304	27.4719	0.18524	-2.43253	-5.92072	3.21E-09	1.13E-06	yes	OP
MGG_09817T0	B157H2O2	RA6H2O2	31.6522	5.89952	0.186386	-2.42364	-4.67651	2.92E-06	0.000479	yes	minor extracellular protease vpr
MGG_02814T0	B157H2O2	RA6H2O2	6.3046	1.18148	0.1874	-2.41581	-4.02208	5.77E-05	0.0056	yes	*
MGG_00195T0	B157H2O2	RA6H2O2	95.013	17.888	0.188269	-2.40913	-5.83769	5.29E-09	1.76E-06	yes	clock-controlled-9 protein
MGG_14269T0	B157H2O2	RA6H2O2	575.298	109.032	0.189523	-2.39956	-5.37971	7.46E-08	1.93E-05	yes	omo
MGG_16690T0	B157H2O2	RA6H2O2	11.3712	2.168	0.190657	-2.39095	-3.74609	0.00018	0.013567	yes	omo
MGG_02543T0	B157H2O2	RA6H2O2	3.4231	0.657906	0.192196	-2.37935	-3.32819	0.000874	0.046917	yes	lipase_GDSL_2

MGG_09383T0	B157H2O2	RA6H2O2	13.626	2.62086	0.192343	-2.37825	-3.93806	8.21E-05	0.007311	yes	NIMA-interacting protein TinC
MGG_09763T0	B157H2O2	RA6H2O2	3.9779	0.765412	0.192416	-2.3777	-3.56133	0.000369	0.023925	yes	*
MGG_13908T0	B157H2O2	RA6H2O2	5.22366	1.00647	0.192675	-2.37576	-3.52548	0.000423	0.026541	yes	OP
MGG_10730T0	B157H2O2	RA6H2O2	13.0998	2.56043	0.195456	-2.35509	-5.10641	3.28E-07	7.02E-05	yes	potassium/sodium efflux P-type ATPase
MGG_04126T0	B157H2O2	RA6H2O2	8.97024	1.79212	0.199785	-2.32348	-4.49387	6.99E-06	0.000995	yes	sulfate permease 2
MGG_05595T0	B157H2O2	RA6H2O2	0.831907	0.166942	0.200674	-2.31708	-3.39706	0.000681	0.038747	yes	ABC transporter
MGG_09015T0	B157H2O2	RA6H2O2	40.3406	8.24734	0.204443	-2.29023	-5.04235	4.60E-07	9.30E-05	yes	Bacteriorhodopsin
MGG_08589T0	B157H2O2	RA6H2O2	8.66413	1.78018	0.205466	-2.28303	-4.02009	5.82E-05	0.00563	yes	A,b,hydrolase_6
MGG_14966T0	B157H2O2	RA6H2O2	1226.65	252.774	0.206069	-2.2788	-4.28266	1.85E-05	0.00216	yes	polysacc_deac_1
MGG_05116T0	B157H2O2	RA6H2O2	10.6048	2.20453	0.20788	-2.26617	-4.56	5.12E-06	0.000768	yes	malic acid transporter (522 aa)
MGG_09383T1	B157H2O2	RA6H2O2	11.6479	2.43737	0.209254	-2.25667	-3.32092	0.000897	0.047813	yes	NIMA-interacting protein TinC
MGG_04939T0	B157H2O2	RA6H2O2	5.19727	1.09472	0.210634	-2.24719	-3.65235	0.00026	0.018135	yes	*
MGG_07228T0	B157H2O2	RA6H2O2	4.06598	0.869093	0.213747	-2.22602	-3.80935	0.000139	0.011278	yes	OPT
MGG_07219T0	B157H2O2	RA6H2O2	39.7601	8.52514	0.214414	-2.22153	-5.43052	5.62E-08	1.50E-05	yes	conidial yellow pigment biosynthesis polyketide synthase
MGG_14831T0	B157H2O2	RA6H2O2	0.847337	0.184959	0.218283	-2.19573	-3.56124	0.000369	0.023925	yes	fatty acid synthase S-acetyltransferase
MGG_08486T0	B157H2O2	RA6H2O2	32.5508	7.15988	0.21996	-2.18469	-4.93868	7.87E-07	0.00015	yes	beta-lactamase
MGG_10244T0	B157H2O2	RA6H2O2	951.281	209.852	0.220599	-2.1805	-5.08561	3.66E-07	7.76E-05	yes	OP
MGG_13716T0	B157H2O2	RA6H2O2	150.522	33.2253	0.220734	-2.17962	-3.98321	6.80E-05	0.006383	yes	*
MGG_05364T0	B157H2O2	RA6H2O2	149.845	33.2685	0.222019	-2.17124	-5.30219	1.14E-07	2.80E-05	yes	endoglucanase-4
MGG_16361T0	B157H2O2	RA6H2O2	50.2706	11.237	0.22353	-2.16146	-5.3122	1.08E-07	2.66E-05	yes	H/K ATPase alpha subunit
MGG_02210T0	B157H2O2	RA6H2O2	8.90862	2.04998	0.230112	-2.11959	-3.90504	9.42E-05	0.008119	yes	vanadium chloroperoxidase
MGG_00433T0	B157H2O2	RA6H2O2	34.3731	7.97167	0.231916	-2.10833	-3.9472	7.91E-05	0.007101	yes	omo
MGG_04736T0	B157H2O2	RA6H2O2	208.061	48.3294	0.232285	-2.10603	-5.17393	2.29E-07	5.15E-05	yes	NADH(P)_ binding
MGG_04036T0	B157H2O2	RA6H2O2	7.75668	1.80585	0.232812	-2.10276	-3.38131	0.000721	0.040536	yes	methyltransferase domain-containing protein

MGG_12468T0	B157H2O2	RA6H2O2	352.431	82.6784	0.234595	-2.09176	-4.57784	4.70E-06	0.000718	yes	CFEM SUPERFAM
MGG_17123T0	B157H2O2	RA6H2O2	162.417	38.3413	0.236067	-2.08273	-4.5943	4.34E-06	0.000669	yes	putative peptidase fam
MGG_07631T0	B157H2O2	RA6H2O2	4.96536	1.1727	0.236176	-2.08206	-3.41824	0.00063	0.036653	yes	fungal cellulose binding domain-containing protein
MGG_07227T0	B157H2O2	RA6H2O2	19.4171	4.628	0.238347	-2.06887	-4.2272	2.37E-05	0.002644	yes	PLAC8
MGG_03545T0	B157H2O2	RA6H2O2	7.39306	1.76267	0.238422	-2.06841	-4.27824	1.88E-05	0.002191	yes	*
MGG_07788T0	B157H2O2	RA6H2O2	6.79356	1.644	0.241994	-2.04696	-3.39433	0.000688	0.039023	yes	omo
MGG_17458T0	B157H2O2	RA6H2O2	33.9648	8.23435	0.242438	-2.04431	-3.65123	0.000261	0.018156	yes	*
MGG_05457T0	B157H2O2	RA6H2O2	12.4325	3.02083	0.242978	-2.0411	-4.56341	5.03E-06	0.000757	yes	Tau D
MGG_03464T0	B157H2O2	RA6H2O2	291.142	71.9083	0.246987	-2.01749	-4.98056	6.34E-07	0.000122	yes	*
MGG_10846T0	B157H2O2	RA6H2O2	64.2462	15.9453	0.248191	-2.01048	-4.50556	6.62E-06	0.000951	yes	omo
MGG_17594T0	B157H2O2	RA6H2O2	11.3466	2.83049	0.249457	-2.00314	-3.32733	0.000877	0.047	yes	omo

Down regulated genes under oxidative stress classified according to their putative functions

DUF proteins	**plant cell wall degrading enzymes**	**Secondary metabolism**	**General metabolism**	**Transporters / permeases**	**Transcription factors/ expression regulation protein**	**Peptidases & protein degrading enzymes**	**Light regulated**	**E1-E2 ATPase**	**Mitochondrial protein**	**Cell cycle**	**Miscellaneous**	**Others**		
MGG_03364T0	MGG_11608T0- laccase	MGG_09645T0- polyketide synthase	MGG_09376T0- FAD binding domain	MGG_04099T0- allantoate permease	MGG_07815T0 - Zn litaf domain	MGG_07404T0- tripeptyl petidase 1	MGG_00195T0- clock-controlled-9 protein	MGG_16361T0- H/K ATPase	MGG_02210T0- vanadium chloroperoxide	MGG_09383T1 NimA interacting protein TinC	MGG_12264T0 - Flavodoxin	MGG_12942T0	MGG_02814T0	MGG_10846T0
MGG_04632T0	MGG_11774T0- endoglucanase	MGG_09945T0- averantin oxidoreductase	MGG_02818T0- IAA oxidase	MGG_13107T0- HPP transporter	MGG_10422T0- Fungal transcription factor	MGG_08429T0- peptidase_s8	MGG_09015T0- Bacteriorhodopsin	MGG_10730T0 - K/Na ATPase	MGG_00771T0- oxoprolinase	MGG_09383T0- "	MGG_09107T0 - HET-C	MGG_02234T0	MGG_14269T0	MGG_17594T0
	MGG_13464T0- laccase	MGG_07219T0-	MGG_09647T0- Acyl	MGG_09941T0 nod	MGG_04036T0- methyl	MGG_00311T0-					MGG_00743T0 - Twin arginine	MGG_07577	MGG_16690T0	MGG_1

		conidial yellow pigment poly ketide synthase	CoA synthetase	factor-ABC transporter	transferase containg protein	peptidase_A4					signalling pathway	T0		4715T0
	MGG_17486T0- pectate lyase	MGG_08486T0- beta lactamase	MGG_10254T0- TAuD	MGG_04126T0- sulphate permease		MGG_09817T0- minor extracellular protease vpr					MGG_10252T0- cupin 1&2	MGG_17854T0	MGG_09763T0	MGG_16403T0
	MGG_13622T0- fungal cellulose binding	MGG_07227T0- PLAC8	MGG_04034T0- formate dehydrogenase	MGG_05595T0 - ABC transporter		MGG_17123T0- putative peptidase fam					MGG_02884T0- Beta Ig- H3 /Fascilin	MGG_17855T0	MGG_13908T0	MGG_00287T0
	MGG_14966T0- polysaccharide deacetylase		MGG_08589T0- A,b, hydrolase	MGG_05116T0- malic acid transporter							MGG_09762T0-vWFA Superfamily	MGG_07598T0	MGG_04939T0	MGG_15784T0
	MGG_05364T0- endoglucanase		MGG_04736T0- NADH(p) binding	MGG_07228T0- OPT							MGG_12468T0- CFEM SUPERFAM	MGG_08034T0	MGG_10244T0	MGG_09474T0
	MGG_07631T0- fungal cellulose binding		MGG_05457T0- TAU-D								MGG_12978T0- kynurenine 3-monooxygenase	MGG_08686T0	MGG_13716T0	MGG_02157T0
			MGG_00771T0- oxoprolinase									MGG_03365T0	MGG_00433T0	MGG_02082T0
			MGG_02543T0 - Lipase GDSL									MGG_03363T0	MGG_03545T0	MGG_15887T0
			MGG_14831T0- Fatty acid synthase S-acetyl transferase									MGG_09377T0	MGG_07788T0	MGG_10781T0
												MGG_05398	MGG_17458T0	MGG_0

												MGG_08962	MGG_03464T0	MGG_0
												MGG_17705	MGG_00787T0	
2	8	4	11	7	3	5	2	2	2	2	8	41		

Down regulated gene islands above cut off 4 fold B157 Vs RA6

test_id	**sample_1**	**sample_2**	**value_1**	**value_2**	**fold change**	**log2 (fold_change)**	**test_stat**	**p_value**	**q_value**	**significant**	**Putative Functions**
MGG_02814T0	B157H2O2	RA6H2O2	6.3046	1.18148	0.1874	-2.41581	-4.02208	5.77E-05	0.0056	yes	*
MGG_02818T0	B157H2O2	RA6H2O2	853.974	122.843	0.143849	-2.79738	-5.3307	9.78E-08	2.46E-05	yes	isoamyl alcohol oxidase
MGG_03363T0	B157H2O2	RA6H2O2	2.14536	0.205097	0.0956	-3.38684	-4.40671	1.05E-05	0.001385	yes	*
MGG_03364T0	B157H2O2	RA6H2O2	133.253	2.34987	0.017635	-5.82544	-10.4636	0	0	yes	DUF4360
MGG_04034T0	B157H2O2	RA6H2O2	4011.24	704.972	0.175749	-2.50841	-3.35191	0.000803	0.043989	yes	formate dehydrogenase
MGG_04036T0	B157H2O2	RA6H2O2	7.75668	1.80585	0.232812	-2.10276	-3.38131	0.000721	0.040536	yes	methyltransferase domain-containing protein
MGG_07227T0	B157H2O2	RA6H2O2	19.4171	4.628	0.238347	-2.06887	-4.2272	2.37E-05	0.002644	yes	PLAC8
MGG_07228T0	B157H2O2	RA6H2O2	4.06598	0.869093	0.213747	-2.22602	-3.80935	0.000139	0.011278	yes	OPT
MGG_09376T0	B157H2O2	RA6H2O2	2.76574	0.226616	0.081937	-3.60934	-4.72796	2.27E-06	0.000382	yes	FAD binding domain-containing protein (507 aa)
MGG_09377T0	B157H2O2	RA6H2O2	4.64912	0.480485	0.10335	-3.27439	-3.76404	0.000167	0.012938	yes	*

MGG_09383T0	B157H2O2	RA6H2O2	13.626	2.62086	0.192343	-2.37825	-3.93806	8.21E-05	0.007311	yes	NIMA-interacting protein TinC
MGG_09383T1	B157H2O2	RA6H2O2	11.6479	2.43737	0.209254	-2.25667	-3.32092	0.000897	0.047813	yes	NIMA-interacting protein TinC
MGG_09645T0	B157H2O2	RA6H2O2	79.2108	5.65632	0.071408	-3.80776	-8.62354	0	0	yes	polyketide synthase
MGG_09647T0	B157H2O2	RA6H2O2	59.7649	9.29319	0.155496	-2.68505	-6.14219	8.14E-10	3.39E-07	yes	acyl-CoA synthetase
MGG_09762T0	B157H2O2	RA6H2O2	6.31008	0.194793	0.03087	-5.01764	-7.22669	4.95E-13	4.63E-10	yes	vWFA uperfamily
MGG_09763T0	B157H2O2	RA6H2O2	3.9779	0.765412	0.192416	-2.3777	-3.56133	0.000369	0.023925	yes	*
MGG_09941T0	B157H2O2	RA6H2O2	446.637	81.898	0.183366	-2.4472	-4.42152	9.80E-06	0.001313	yes	nod factor export ATP-binding protein I
MGG_09945T0	B157H2O2	RA6H2O2	9.28816	1.25119	0.134708	-2.89209	-5.31908	1.04E-07	2.60E-05	yes	averantin oxidoreductase
MGG_10252T0	B157H2O2	RA6H2O2	237.194	30.7432	0.129612	-2.94773	-6.92348	4.41E-12	3.57E-09	yes	hypothetical protein
MGG_10254T0	B157H2O2	RA6H2O2	5.14373	0.864231	0.168016	-2.57333	-3.9794	6.91E-05	0.006445	yes	TAU D
MGG_17854T0	B157H2O2	RA6H2O2	63.7224	2.45585	0.03854	-4.69751	-8.64179	0	0	yes	*
MGG_17855T0	B157H2O2	RA6H2O2	32.2256	1.30029	0.04035	-4.6313	-7.28421	3.24E-13	3.34E-10	yes	*

7.3 Appendix 3: Primers and sequencing details

Table 1- Primers used in the study for construct preparations and expression analysis

Name of the	Sequence of the primers
MoHPT1F	5’ ATGGTACCGTACGGTTGTTTGATGTCGG 3’
MoHPT1R	5’ ATGGATCCAGCCTGTCTTTCGTTTGAAG 3’
MoHPT1 OF	5’ATGGGCCCTAAGCTTGTATTGCCTAGAGCAGTCCGA 3’
MoHPT1 OR	5’ ACGGGCCCTAAGCTTGTCTCCATATCCTTCTTG 3’
MoHPT1 NdeI F	5’ CGACATATGCAGTCCGATTCCGAAGAAAAC 3’
MoHPT1 XhoI R	5’ GCTCTCGAGAAGATCGATCACGAAAAACTCATTGAG 3’
MoHPT1q F	5’ AAGGGTTCATCCGCCACT 3’
MoHPT1qR	5’ ATAGCACACATCCTCGCTTG 3’
MoTUBqF	5’ GAGTCCAACATGAACGATCT 3’
MoTUBqR	5’ GTACTCCTCTTCCTCCTCGT 3’
Mossk1F	5’ GTTGGATCCATGGGAGATCTTGCTAGCAAACTC 3’
Mossk1R	5’ GTTCTCGAGTCATGGATCCTTGCCCATCTTGGTGTTAGC 3’
MoHog1qF	5’ AGCGACAGCCTCTCAAGAAC 3’
MoHog1qR	5’ CGAACTTCTCTCCGCTATG 3’
MoHik2qF	5’ TTTGGCCGGCAAGTCAACGGAA 3’
MoHik2qR	5’ AATCCCTCGGCGGTTTTCAGCT 3’
MoHik4qF	5’ ACTTCGCAAAGCCGGATGCA 3’
MoHik4qR	5’ ATTACCGACAGCCGCACGTT 3’
MoHik5qF	5’ ACATTCGCTTGCCCACCTTGCA 3’
MoHik5qR	5’ AAATCGGGGTTGCGCTTCTGGA 3’
MoHik7qF	5’ AGCGCAAAGGCATTGGCTACGA 3’
MoHik7qR	5’ TGCGATGTGTGTTGGACAGCGT 3’
MoHik8qF	5’ ATTTGAACGGAGCATCGCCGCA 3’
MoHik8qR	5’ TTGTTGCCGCACCTGACAAGCT 3’
MoHik9qF	5’ ACCAACAGGTCACGCGACGAAT 3’
MoHik9qR	5’ TGCAATCCCGTTGTGGCTACTG 3’

Table 2 - Primers used for Transcriptome validation.

Primers for validation of up regulated genes

Oligo Name	Sequence 5' to 3'
MGG_08802 F	5’ CCGCAAAGTACGGTGACTA 3’
MGG_08802 R	5’ GTTGACGATGTCGTGCTT 3’
MGG_09063 F	5’ CCAACATCCTCGTGTCTCT 3’
MGG_09063 R	5’ GGTATGAACCCAGTCAGTCA 3’
MGG_13793 F	5’ GTGGCATCACCTACTTCATC 3’
MGG_13793 R	5’ ATCATCACTAAGGGCACCAC 3’
MGG_00156 F	5’ GATGTTGGTGGACTTCAGG 3’
MGG_00156 R	5’ CTGGCTGAGCAGTTGTATGT 3’
MGG_02119 F	5’ CCTCACAGGAATCCAGTACA 3’
MGG_02119 R	5’ GGCGTAGTTCTTGACGAAG 3’
MGG_02124 F	5’ CCCCTACTTTGCCATCAAG 3’
MGG_02124 R	5’ GCATGGGTATGTGTAGGTCA 3’
MGG_08977 F	5’ GGTGGCCTACTTCATAATGCT 3’
MGG_08977 R	5’ ACAAACTGTCGCCTCCTT 3’
MGG_07980 F	5’ CCTGGTTTCTGTACAACTGG 3’
MGG_07980 R	5’ GAAGCAGTTGATGACGACTC 3’
MGG_09138 F	5’ TCATCCATCAAGCCCATC 3’
MGG_09138 R	5’ TTCACCTTTGTCAGGTACGG 3’
MGG_03823 F	5’ ATTCCTGTCCGAAACAACC 3’
MGG_03823 R	5’ GAAACCCTTCTCCTGGAACT 3’
MGG_02378 F	5’ ACTTTGAGGTCGAGGAGAAG 3’
MGG_02378 R	5’ CAGTGTAAGTAGTGCCGAGAA 3’
MGG_01569 F	5’ TACGCCGGTATCTTCATCTC 3’
MGG_01569 R	5’ ATGCCGAAGCACTTGGTGTA 3’
MGG_08519 F	5’ CATTCAAACGTCTCGGTCT 3’
MGG_08519 R	5’ ACGTCGTCTTCGATCTTTC 3’
MGG_05413 F	5’ GCGTCATGTACTTCCTCAAC 3’
MGG_05413 R	5’ CCGACAAACAGGATAGACAC 3’
MGG_01924 F	5’ ACTTTTCCAGCACCCTCTT 3’
MGG_01924 R	5’ GAAGAAACGGCTCATTGG 3’
MGG_05828 F	5’ TACGACTGCAACGACTTCA 3’
MGG_05828 R	5’ CCTCGTACAGCACATCAAAC 3’
MGG_01922 F	5’ TTCATCTTCCCCATCACC 3’
MGG_01922 R	5’ GTTCTTGCTCTTGAACTCGTC 3’

Primers for validation of down regulated genes

Oligo Name	Sequence 5' to 3'
MGG_11774 F	GCTAGGTTAGTATCTCCCTCCA
MGG_11774 R	GGCTGGGCTTCTTGTTAGTT
MGG_13622 F	CCATCAACTTTAGCGTCTGG
MGG_13622 R	GGTGGAAGAGGAAGAAGAAG
MGG_11608 F	CCATCGAGGAGAAGAATGA
MGG_11608 R	GTTGGTCTGCATGTTGTTG
MGG_13464 F	CACCTGCCTCGACATTATCA
MGG_13464 R	ACGTTGTTGACGGTCCAGTA
MGG_01912 F	TCGTTGGTGGAGGTCATGTA
MGG_01912 R	TCGGTGAAGTTTGACTGTGG
MGG_07219 F	TGACACCTTCCTCAACACCA
MGG_07219 R	GAGCACGTTGTGAAACCTCA
MGG_12214 F	CTGCATACGGGTGTTGCTTA
MGG_12214 R	CTATGGTTTTGCCCGTGACT
MGG_09645 F	TTGAGCTGGAGAGCTTTGGT
MGG_09645 R	TTCTGAACCTGGGGATCTTG
MGG_00195 F	GCAATTTCTGGCTCTCCTCA
MGG_00195 R	AATCTGTTGTGGCAGGGAAG
MGG_03002 F	CAGATACCAGAGCCCGAAAA
MGG_03002 R	AAGAAGTTGGCTGCGTTCTG
MGG_09015 F	CAAGCCCTCGAAATCAACTC
MGG_09015 R	TGAAGATGACGGCGGAAA
MGG_01041 F	TGCAACGAATCCTTTCCTC
MGG_01041 R	GCGCATGTCTTGAACCAAGT
MGG_00743 F	TTCCCCAGCTCGTCCTTTAT
MGG_00743 R	GGCCAGGTTTTGAAAGGTGT
MGG_09941 F	ATACCACGTTGCAGACACCA
MGG_09941 R	TCGTCAACATCCTTGGTGAG
MGG_14061 F	TTCAGCGACATTAGCGTGTC
MGG_14061 R	TGGCGGTCATGTTCTTGTT
MGG_05116 F	ACTTCACCTCGCAATGGTTC
MGG_05116 R	TGAGGCAGATGATTGTCAGG

Table 3-MoHPT1 Phosphorylation prediction by GPS phosphorylation prediction tool

position	code	kinase	peptide	score	cutoff
3	S	CK1	*****MYSVKDSEKS	21.694	5.872
3	S	CK1/CK1	*****MYSVKDSEKS	15.6	6.263
3	S	Other/PLK	*****MYSVKDSEKS	7	4.237
3	S	AGC/PKC	*****MYSVKDSEKS	0.747	0.236
7	S	CK1	*MYSVKDSEKSDSEE	14.549	5.872
7	S	Other/ULK	*MYSVKDSEKSDSEE	6.154	4.169
7	S	AGC/PKC	*MYSVKDSEKSDSEE	0.69	0.236
10	S	CMGC/CK2	SVKDSEKSDSEENAD	15.645	9.894
10	S	CK1	SVKDSEKSDSEENAD	14.076	5.872
10	S	CK1/CK1	SVKDSEKSDSEENAD	7.508	6.263
10	S	Atypical/TAF1	SVKDSEKSDSEENAD	7.375	4.681
10	S	Other/PLK	SVKDSEKSDSEENAD	4.831	4.237
10	S	CMGC	SVKDSEKSDSEENAD	1.266	0.963
12	S	CMGC/CK2	KDSEKSDSEENADKM	12.974	9.894
12	S	CK1/CK1	KDSEKSDSEENADKM	9.854	6.263
12	S	CK1	KDSEKSDSEENADKM	9.451	5.872
12	S	CAMK/CAMKL	KDSEKSDSEENADKM	8.945	8.942
12	S	STE/STE20	KDSEKSDSEENADKM	8.442	2.369
12	S	Atypical/TAF1	KDSEKSDSEENADKM	7.125	4.681
12	S	Other/ULK	KDSEKSDSEENADKM	4.692	4.169
12	S	CAMK/CAMK1	KDSEKSDSEENADKM	3.333	2.488
12	S	AGC/PKC	KDSEKSDSEENADKM	0.383	0.236
28	S	CK1	DFGAHVDSTTFEQIL	7.028	5.872
29	T	Other/TTK	FGAHVDSTTFEQILE	5.188	5.009
30	T	CK1	GAHVDSTTFEQILEM	7.562	5.872
61	T	Other/TTK	FFEQAEETFEKMDKA	5.062	5.009
87	S	AGC/NDR	LGHFLKGSSATLGFT	7.3	5.725
94	T	Other/PEK	SSATLGFTKVKDSCQ	14.682	9.43
94	T	STE	SSATLGFTKVKDSCQ	1.667	1.285
106	Y	Other/WEE	SCQVIQQYGNKLKLD	12	12
115	T	CMGC/CK2	NKLKLDGTEEPSEDV	10.226	9.894
115	T	Atypical/TAF1	NKLKLDGTEEPSEDV	6.125	4.681
115	T	Other/TTK	NKLKLDGTEEPSEDV	5.562	5.009
140	S	AGC/PKC	DAKKDMESLKKLLNE	0.41	0.236
154	S	Other/PEK	EFFVIDPSTP*****	16.727	9.43
154	S	Other/PLK	EFFVIDPSTP*****	5.149	4.237
154	S	AGC/PKC	EFFVIDPSTP*****	0.382	0.236
155	T	CMGC/MAPK	FFVIDPSTP******	57.384	35.046
155	T	Other/PEK	FFVIDPSTP******	10.636	9.43
155	T	AGC/PDK1	FFVIDPSTP******	10.093	2.257

155 T	CMGC/CDK	FFVIDPSTP******	7.001	5.656
155 T	CMGC/GSK	FFVIDPSTP******	2.583	1.8
155 T	CMGC	FFVIDPSTP******	2.12	0.963
155 T	CMGC/DYRK	FFVIDPSTP******	1.292	1.276
155 T	AGC/PKC	FFVIDPSTP******	0.372	0.236

Table 4. Amino acid variations in the Histidine Kinases of B157 *M. oryzae*

Histidine kinase	**Gene_id**	**Variations in protein sequence**
HiK1	MGG_11174	1 aa 84th aminoacid changed from H to Y
HiK2	MGG_01342	
HiK3	MGG_12530	25 aa missing(B157) (206- 231)aas is missing while 232nd aa is replaced from F to V, 233rd aa is replaced from P to G
HiK4	MGG_13891	
HiK5	MGG_11882	
HiK6	MGG_06696	
HiK7	MGG_12377	
HiK8	MGG_01227	1 aa 1189th aminoacid changed from L to P
HiK9	MGG_02665	
SLN1	MGG_07312	

Sequencing Details:

>RA6_LB3_XS-0025_A05_047.ab1

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>T1sense.ks_m13Forward_20686-1_7372,Trimmed Sequence(988 bp)

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>To.sense.ks_m13Forward_20686-2_7372,Trimmed Sequence(934 bp)

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