

A multi-omics analysis of the grapevine pathogen *Lasiodiplodia theobromae* reveals that temperature affects the expression of virulence- and pathogenicity-related genes

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Figure S1 Radial growth of *L. theobromae* LA-SOL3 after 48 h of incubation in PDB medium at different temperatures. Data is presented as average \pm standard error. Two-way ANOVA, followed by a Bonferroni multiple comparison test, was used to determine the statistical significance between the temperature of 30 °C and all the other temperatures (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$).

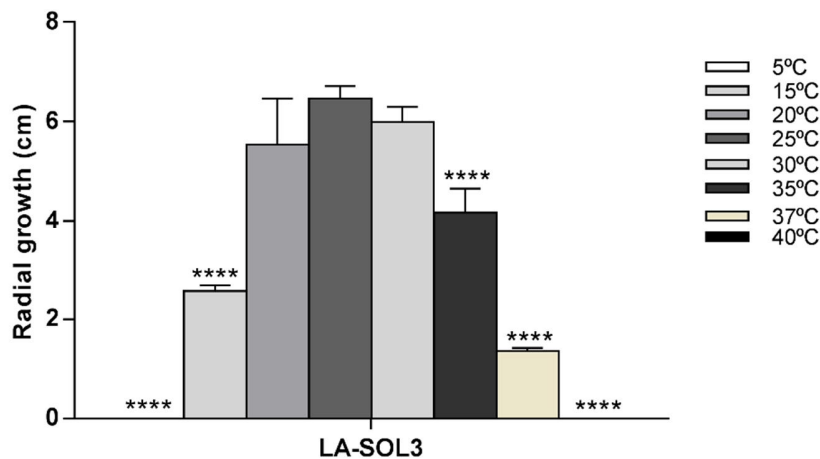


Figure S2 Volcano plot and hierarchical cluster analysis of the expression profiles of differentially expressed genes between 25 °C and 37 °C.

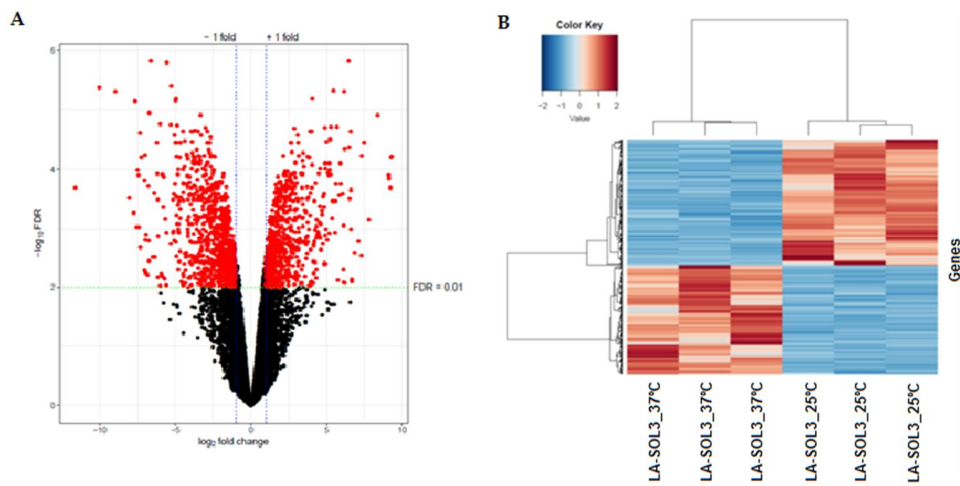


Figure S3 One-DE image of extracellular medium and mycelium of LA-SOL3 strain grown at 25 °C and 37 °C for 4 days, obtained from One-DE gels.

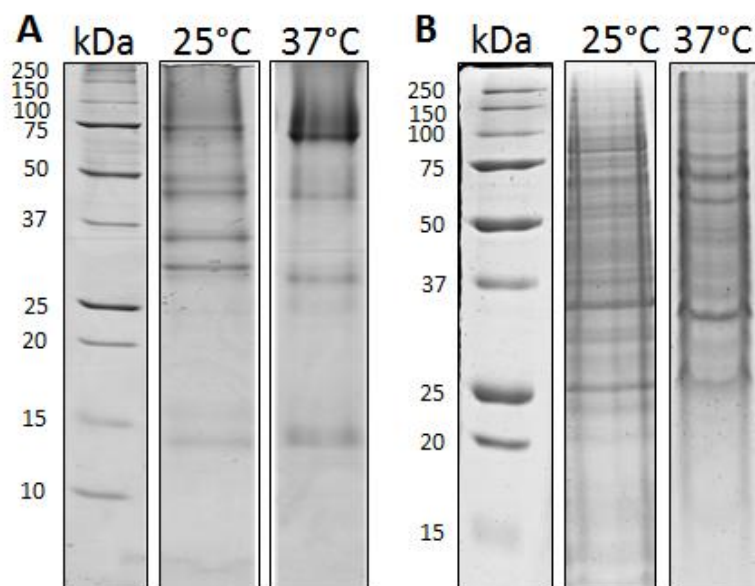


Table S1 Genes predicted to code for fungal peroxidases in the genome of *L. theobromae* LA-SOL3. Peroxidases were predicted with the web-based BLAST application of fPoxDB: Fungal Peroxidase Database.

Peroxidase	Genes (n)
New NoxA	6
Other class II peroxidase	6
Haloperoxidase (haem)	5
Linoleate diol synthase (PGHS like)	5
New NoxC	4
Atypical 2-Cysteine peroxiredoxin (type Q, BCP)	4
Cytochrome C peroxidase	4
Manganese peroxidase	4
New NoxB	4
1-Cysteine peroxiredoxin	3
Catalase	3
Hybrid Ascorbate-Cytochrome C peroxidase	3
Lignin peroxidase	3
Typical 2-Cysteine peroxiredoxin	3
Versatileperoxidase	3
Atypical 2-Cysteine peroxiredoxin (type II, type V)	2
Carboxymuconolactone decarboxylase (no peroxidase activity)	2
Prostaglandin H synthase (Cyclooxygenase)	1
New Rbohs	1
Fungi-Bacteria glutathione peroxidase	1
NoxR	1
New_Doux	0
DyP-type peroxidase D	0
No haem, Vanadium chloroperoxidase	0

Table S2 Fungal cytochrome P450 families predicted to be encoded by *L. theobromae* LA-SOL3.

Family	Genes (n)
CYP504	13
CYP505	2
CYP5080	1
CYP531	1
CYP532	2
CYP545	1
CYP547	1
CYP548	1
CYP56	3
CYP570	1
CYP573	1
CYP578	2
CYP586	1
CYP596	1
CYP6001	1
CYP617	1
CYP620	1
CYP626	2
CYP633	1
CYP65	1
CYP664	1
CYP671	2
CYP682	2

Table S3 Genes predicted to code for transporters in the genome of *L. theobromae* LA-SOL3.

Transporter Class	Genes (n)
Channels and pores	166
Electrochemical potential-driven transporters	857
Primary active transporters	737
Accessory factors involved in transport	44
Transmembrane electron carriers	29
Group translocators	20
Incompletely characterized transport systems	104
Total	1957

Table S4 Predicted heat shock proteins involved in responses to heat stress in the genome of *L. theobromae* LA-SOL3.

HSP name	HSP Family	Accession Code
Heat shock protein ST11	HSP 70	P15705
30 kDa heat shock protein	HSP 30	P40920
Heat shock protein hsp98	HSP clpA/clpB	P31540
12 kDa heat shock protein	HSP 20	P22943
Heat shock protein 78, mitochondrial	HSP clpA/clpB	Q96UX5
Heat shock protein 16	HSP20	O14368

Table S5 Proteins identified in the secretome of LA-SOL3 strain at 25 °C.

Table S6 Proteins identified in the intracellular proteome of LA-SOL3 strain at 25 °C.

Table S7 Proteins identified in the secretome of LA-SOL3 strain at 37 °C.

Table S8 Proteins identified in the intracellular proteome of LA-SOL3 strain at 37 °C.

Table S9 Up and down-regulated genes at 37 °C identified in LA-SOL3 strain and

correspondent GO biological process.

Table S10 Up and down-regulated proteins ($0.5 \geq FC \geq 2$) identified in the secretome of LA-SOL3 strain and correspondent GO biological process.

Table S11 Up and down-regulated proteins ($0.5 \geq FC \geq 2$) identified in the intracellular proteome of LA-SOL3 strain and correspondent GO biological process.

Table S12 Potentially relevant proteins identified in the secretome of strain LA-SOL3 grown at 25 °C and 37 °C.

GO Category	Accession code	Description	Gene names	Temperature (°C)
PATHOGENESIS	B8NM69	Peptidase S41 family protein ustP (EC 3.4.-.-)	ustP AFLA_095010	25
	C5FBW2	Tripeptidyl-peptidase SED2 (EC 3.4.14.10)	SED2 MCYG_00184	25
	C5FW30	Carboxypeptidase S1 homolog A (EC 3.4.16.6)	SCPA MCYG_06933	25
	C9SPU8	Probable zinc metalloprotease VDBG_06923 (EC 3.4.-.-)	VDBG_06923	25
	D4ALG0	LysM domain-containing protein ARB_05157	ARB_05157	25
	D4ALQ5	Probable extracellular glycosidase ARB_05253 (EC 3.2.-.-)	ARB_05253	25
	D4AP52	Carboxypeptidase S1 homolog B (EC 3.4.16.6)	SCPB ARB_06019	25
	D4APQ6	Probable thioredoxin reductase ARB_06224 (EC 1.8.1.9)	ARB_06224	25
	D4AQA7	Probable serine carboxypeptidase ARB_06414 (EC 3.4.16.-)	ARB_06414	25
	D4ARB1	Probable dipeptidyl-peptidase 5 (EC 3.4.14.-)	DPP5 ARB_06651	25
	D4AYB4	Antigenic thaumatin-like protein ARB_01183	ARB_01183	25
	D4AYS6	Probable extracellular serine carboxypeptidase (EC 3.4.-.-)	ARB_01345	25
	D4B327	Probable pathogenesis-related protein ARB_02861	ARB_02861	25
	D4B5N0	Metalloprotease A-like protein ARB_03789 (EC 3.4.17.-)	ARB_03789	25
	D7UQ40	Bifunctional solanapyrone synthase (EC 1.1.3.42) (Prosolanapyrone-II oxidase)	sol5	25
	G3XMD0	FAD-linked oxidoreductase azaL (EC 1.-.-.-)	azaL ASPNIDRAFT_132654	25
	M1W428	Thioredoxin reductase tcpT (EC 1.8.1.-)	tcpT CPUR_02681	25
	O42630	Vacuolar protease A (EC 3.4.23.25)	pep2 AFUA_3G11400	25

O42799	Allergen Asp f 7	AFUA_4G06670	25
O64411	Polyamine oxidase (EC 1.5.3.14) (EC 1.5.3.15)	PAO	25
O74238	Protein SnodProt1	SNOG_13722	25
P11838	Endothiapepsin (EC 3.4.23.22)	EAPA EPN-1	25
P24665	Aspergillopepsin-2 (EC 3.4.23.19)		25
P29717	Glucan 1,3-beta-glucosidase (EC 2.4.1.-) (EC 3.2.1.58)	XOG1 EXG EXG1 XOG CAALFM_C102990CA Ca49C10.05	25
P34946	Carboxypeptidase S1 (EC 3.4.16.6)		25/37
P36196	Acetylcholinesterase (EC 3.1.1.7)	ACHE	25
P39105	Lysophospholipase 1 (EC 3.1.1.5)	PLB1 YMR008C YM8270.10C	25
P42893	Endothelin-converting enzyme 1 (EC 3.4.24.71)	Ece1	25
P52719	Carboxypeptidase cpdS (EC 3.4.16.-)	cpdS	25
P58099	C5a peptidase (EC 3.4.21.110)	scpA SPy_2010 M5005_Spy1715	25
P64744	Sphingomyelinase (EC 3.1.4.12)	BQ2027_MB0912	25
P79085	Major allergen Alt a 1	ALTA1	25
P86325	Carboxylesterase (EC 3.1.1.1)		25
Q00668	Putative sterigmatocystin biosynthesis peroxidase stcC (EC 1.11.1.-)	stcC AN7823	25
Q03168	Lysosomal aspartic protease (EC 3.4.23.-)	AAEL006169	25
Q0D1P3	Multicopper oxidase terE (EC 1.-.-.-)	terE ATEG_00141	25
Q0V1D7	Neutral protease 2 homolog SNOG_02177 (EC 3.4.24.39)	SNOG_02177	25
Q4WFX9	Probable leucine aminopeptidase 2 (EC 3.4.11.-)	lap2 AFUA_3G00650	25
Q4WNV0	Aspartic-type endopeptidase ctsD (EC 3.4.23.-)	ctsD AFUA_4G07040	25
Q4WZS3	Putative aspergillopepsin A-like aspartic endopeptidase AFUA_2G15950 (EC 3.4.23.-)	AFUA_2G15950	25
Q5AZ42	Probable dipeptidyl peptidase 4 (EC 3.4.14.5)	dpp4 AN6438	25
Q70J59	Tripeptidyl-peptidase sed2 (EC 3.4.14.10)	sed2 sedB AFUA_4G03490	25
Q871C5	Extracellular metalloprotease NCU07200 (EC 3.4.24.-)	B8G12.220 NCU07200	25
Q8RJP2	Rhamnogalacturonate lyase (EC 4.2.2.23)	rhiE Dda3937_01465	25
Q92396	Tyrosinase (EC 1.14.18.1)	TYR	25
Q9DDE3	Acetylcholinesterase (EC 3.1.1.7)	ache	25

STRESS RESPONSE	Q9Y7F0	Peroxiredoxin TSA1-A (EC 1.11.1.15)	TSA1 TSA1A CAALFM_C306180CA CaO19.7417	25
	B0Y004	Cell wall protein phiA (Major allergen phiA)	phiA AFUB_045170	25
	B9W4V6	Aromatic peroxygenase (EC 1.11.2.1)	APO1	25
	C0IW58	Low-redox potential peroxidase (EC 1.11.1.7)	LnP	25
	D4AUF1	WSC domain-containing protein ARB_07867	ARB_07867	25
	D4AUF4	WSC domain-containing protein ARB_07870	ARB_07870	25
	G0Y276	Effector protein PevD1		25
	P29141	Minor extracellular protease vpr (EC 3.4.21.-)	vpr BSU38090 ipa-45r	25
	Q3HRQ2	Aldehyde oxidase GLOX (EC 1.2.3.1)	GLOX	25
	Q4WNS8	Protein ecm33	ecm33 AFUA_4G06820	25
	Q4WXZ5	Ribonuclease T2-like (EC 3.1.27.1)	my1 AFUA_3G11220	25
	Q86WA6	Valacyclovir hydrolase (EC 3.1.-.-)	BPHL MCNAA	25
	Q877A8	Catalase B (EC 1.11.1.6)	catB AO09012000068	25
	B5Y008	Oxygen-dependent choline dehydrogenase (EC 1.1.99.1) (EC 1.2.1.8)	betA KPK_3995	37
CELL WALL DEGRADATION	A1C4H2	Probable endo-beta-1,4-glucanase D (EC 3.2.1.4)	eglD ACLA_059790	25
	A1DBG6	Probable beta-glucosidase btgE (EC 3.2.1.21)	btgE NFIA_098360	25
	A1DBS6	Probable endo-beta-1,4-glucanase D (EC 3.2.1.4)	eglD NFIA_099510	25
	A1DME8	Probable endo-beta-1,4-glucanase B (EC 3.2.1.4)	eglB NFIA_053150	25
	A1DMR8	Probable beta-glucosidase F (EC 3.2.1.21)	bgIF NFIA_054350	25/37
	A1DMV3	Probable feruloyl esterase B-2 (EC 3.1.1.73)	faeB-2 NFIA_054700	25
	A2QT85	Probable arabinan endo-1,5-alpha-L-arabinosidase A (EC 3.2.1.99)	abnA An09g01190	25
	A2QYR9	Probable 1,4-beta-D-glucan cellobiohydrolase C (EC 3.2.1.91)	cbhC An12g02220	25
	B8MW97	probable endo-beta-1,4-glucanase B (EC 3.2.1.4)	eglB AFLA_087870	25
	B8MXJ7	Probable endo-beta-1,4-glucanase D (EC 3.2.1.4)	eglD AFLA_077840	25
	B8NJF4	Probable beta-glucosidase D (EC 3.2.1.21)	bgID AFLA_066750	25
	B8NMD3	Probable arabinan endo-1,5-alpha-L-arabinosidase C (EC 3.2.1.99)	abnC AFLA_123690	25
	B8NPT0	Probable feruloyl esterase B-2 (EC 3.1.1.73)	faeB-2 AFLA_001440	25

D4AJR9	Endo-1,3(4)-beta-glucanase ARB_04519 (EC 3.2.1.6)	ARB_04519	25
D4AV38	Probable secreted lipase ARB_00047 (EC 3.1.1.1)	ARB_00047	25
D4AZ24	Probable endo-1,3(4)-beta-glucanase ARB_01444 (EC 3.2.1.6)	ARB_01444	25
D4AZ78	Secreted lipase ARB_01498 (EC 3.1.1.3)	ARB_01498	25
P07982	Endoglucanase EG-II (EC 3.2.1.4)	egl2	25
P0C1A6	Pectate lyase L (EC 4.2.2.2)	pelL	25
P23360	Endo-1,4-beta-xylanase (EC 3.2.1.8)	XYNA	25/37
P23550	Endoglucanase B (EC 3.2.1.4)	celB	25
P41365	Lipase B (EC 3.1.1.3) (CALB)		25
P43317	Endoglucanase-5 (EC 3.2.1.4)	egl5	25
P45699	Putative endoglucanase type K (EC 3.2.1.4)		25
P53626	Glucan endo-1,3-beta-glucosidase BGN13.1 (EC 3.2.1.39)	bgn13.1	25
P55332	Endo-1,4-beta-xylanase A (EC 3.2.1.8)	xlnA AN3613	25
Q01738	Cellobiose dehydrogenase (EC 1.1.99.18)	CDH-1; CDH-2	25
Q0CEF3	Probable beta-glucosidase L (EC 3.2.1.21)	bglL ATEG_07931	25
Q0CMT2	Probable 1,4-beta-D-glucan cellobiohydrolase B (EC 3.2.1.91)	cbhB ATEG_05002	25
Q0CTD7	Probable beta-glucosidase A (EC 3.2.1.21)	bglA bglI ATEG_03047	25
Q2U7D2	Probable alpha-L-arabinofuranosidase axhA (EC 3.2.1.55)	axhA AO090701000885	25
Q45071	Arabinoxylan arabinofuranohydrolase (EC 3.2.1.55)	xynD BSU18160	25
Q5B9F2	Probable beta-glucosidase L (EC 3.2.1.21)	bglL AN2828	25
Q5ZNB1	Endo-1,4-beta-xylanase D (Xylanase D) (EC 3.2.1.8)	xynD	25
Q92194	Acetylxylan esterase A (EC 3.1.1.72)	axeA aceA	25
Q96VB6	Endo-1,4-beta-xylanase F3 (EC 3.2.1.8)	xynF3 xlnF3 AO090001000208	25
Q96WQ9	Probable endo-beta-1,4-glucanase D (EC 3.2.1.4)	eglD cel61A AKAW_08531	25
Q99034	Acetylxylan esterase (EC 3.1.1.72)	axe1	25

Table S13 Potentially relevant proteins identified in the intracellular proteome of strain LA-SOL3 grown at 25 °C and 37 °C.

GO Category	Accession	Description	Gene names	Temperature (°C)
PATHOGENESIS	A1CFL1	Alcohol dehydrogenase patD (EC 1.1.1.1)	patD ACLA_093590	25
	A1CFL2	Dehydrogenase patE (EC 1.1.-.-)	patE ACLA_093600	25
	A4GYZ0	Glutathione S-transferase gliG (EC 2.5.1.18)	gliG AFUA_6G09690	25
	A7UX13	Hercynylcysteine sulfoxide lyase (EC 4.4.1.-) (egt-2 NCU11365	25
	B2WKF1	Carboxypeptidase Y homolog A (EC 3.4.16.5)	cpyA PTRG_10461	25/37
	B6HJU2	Glandicoline B O-methyltransferase roqN (EC 3.1.1.-)	roqN gmt Pc21g15440	25
	B8N406	Secondary metabolism regulator laeA (EC 2.1.1.-)	laeA AFLA_033290	25
	B8NM69	Peptidase S41 family protein ustP (EC 3.4.-.-)	ustP AFLA_095010	25
	B9WYE6	Versiconal hemiacetal acetate reductase (EC 1.1.1.353)	vrda	25
	B9WZX1	Tryprostatin B 6-hydroxylase (EC 1.14.13.176)	ftmP450-1 ftmC	25
	C5FBW2	Tripeptidyl-peptidase SED2 (EC 3.4.14.10) (Sedolisin-B)	SED2 MCYG_00184	25
	C5P4Z8	Subtilisin-like protease CPC735_031240 (EC 3.4.21.-)	CPC735_031240	25
	D4ARB1	Probable dipeptidyl-peptidase 5 (EC 3.4.14.-) (Dipeptidyl-peptidase V) (DPP V) (DppV)	DPP5 ARB_06651	25
	D4B1R0	Probable glutamate carboxypeptidase ARB_02390 (EC 3.4.17.21)	ARB_02390	25
	D4B5N0	Metallo-carboxypeptidase A-like protein ARB_03789 (EC 3.4.17.-)	ARB_03789	25
	D7PHZ0	Aldolase vrtJ (EC 4.1.2.-)	vrtJ	25
	E9FCP6	Aldo-keto reductase dtxS3 (EC 1.1.1.-)	dtxS3 MAA_10045	25/37
	E9QUT3	Hydroxynaphthalene reductase arp2 (EC 1.1.-.-)	arp2 AFUA_2G17560	25
	J4UHQ8	Glutathione S-transferase-like protein OpS6 (EC 2.5.1.-)	OpS6 BBA_08184	25
	M1W428	Thioredoxin reductase tcpT (EC 1.8.1.-)	tcpT CPUR_02681	25
	M2SNN6	Secondary metabolism regulator LAE1 (EC 2.1.1.-)	LAE1 COCHEDRAFT_1197809	25
	N4WHA7	Reducing polyketide synthase PKS2 (EC 2.3.1.-)	PKS2 COCC4DRAFT_45941	25
	N4WQZ8	Probable esterase TOX9 (EC 3.1.2.-)	TOX9 COCC4DRAFT_155492	25
	N4WW42	Dehydrogenase RED3 (EC 1.1.1.1)	RED3 COCC4DRAFT_155403	25
	O42630	Vacuolar protease A (EC 3.4.23.25)	pep2 AFUA_3G11400	25/37
	O43301	Heat shock 70 kDa protein 12A	HSPA12A KIAA0417	25
	O74225	Heat shock protein hsp88	hsp88 NCU05269	25/37
	O74238	Protein SnodProt1	SNOG_13722	25
	O93806	Glucosamine 6-phosphate N-acetyltransferase (EC 2.3.1.4)	GNA1	25
	O93866	Heat shock 70 kDa protein	HSP70	25/37
	P11838	Endothiapepsin (EC 3.4.23.22)	EAPA EPN-1	25
	P14010	4-aminobutyrate aminotransferase (EC 2.6.1.19)	gatA AN2248	25/37

P15705	Heat shock protein STI1	STI1 YOR027W OR26.17	25
P29702	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha (EC 2.5.1.58) (EC 2.5.1.59alpha)	FNTA	25
P29717	Glucan 1,3-beta-glucosidase (EC 2.4.1.-) (EC 3.2.1.58)	XOG1 EXG EXG1 XOG CAALFM_C102990CA	25
P31540	Heat shock protein hsp98	hsp98 NCU00104	25
P34946	Carboxypeptidase S1 (EC 3.4.16.6)		25
P38624	Proteasome subunit beta type-1 (EC 3.4.25.1)	PRE3 YJL001W J1407	25/37
P38677	Carboxy-cis,cis-muconate cyclase (EC 5.5.1.5)	NCU04071	25
P39640	Dihydroantcapsin 7-dehydrogenase (EC 1.1.1.385)	bacC ywfD BSU37720 ipa-82d	25
P40108	Aldehyde dehydrogenase (EC 1.2.1.3)	CLAH10 CLAH3	25/37
P40850	Protein MKT1	MKT1 YNL085W N2302	25/37
P42059	Minor allergen Cla h 7	CLAH7 CLAH5	25/37
P54006	Protein TOXD	TOXD	25
P62998	Ras-related C3 botulinum toxin substrate 1 (p21-Rac1)	RAC1	25
P75863	Uncharacterized protein YcbX	ycbX b0947 JW5126	25
P78417	Glutathione S-transferase omega-1 (GSTO-1) (EC 2.5.1.18)	GSTO1 GSTTLP28	25
P79085	Major allergen Alt a 1	ALTA1	25
P86029	Catechol 1,2-dioxygenase (EC 1.13.11.1)	HQD2 CAALFM_C402230CA	25
P87017	5'-hydroxyaverantin dehydrogenase (EC 1.1.1.352)	afiH adhA P875_00052989-1	25
P87216	Protein vip1	vip1 SPAC10F6.06	25/37
Q00258	Norsolorinic acid reductase A (EC 1.1.1.-)	afiE norA P875_00052990	25/37
Q00278	Norsolorinic acid ketoreductase (EC 1.1.1.349)	afiD nor-1 P875_00052988	25
Q00455	Scytalone dehydratase (EC 4.2.1.94)	SCD1 Cob_03011	25
Q00859	Mitogen-activated protein kinase (EC 2.7.11.24)	MAPK	25/37
Q05533	Inositol monophosphatase 2 (EC 3.1.3.25)	INM2 IMP2 YDR287W	25
Q07505	Putative carboxymethylenebutenolidase (EC 3.1.1.45)	YDL086W	25/37
Q0CCX5	Questin oxidase (EC 1.-.-)	gedK ATEG_08459	25
Q0CJ62	6-methylsalicylic acid decarboxylase atA (EC 1.-.-)	atA ATEG_06272	25/37
Q12634	Tetrahydroxynaphthalene reductase (EC 1.1.1.252)	MGG_02252	25
Q2YDM1	ADP-ribosylation factor-like protein 1	ARL1	25
Q47317	N(6)-hydroxylysine O-acetyltransferase (EC 2.3.1.102)	iucB	25/37
Q49W60	Probable nitronate monooxygenase (EC 1.13.12.16)	SSP1854	25
Q4R7L8	Peroxisomal NADH pyrophosphatase NUDT12 (EC 3.6.1.22)	NUDT12 QtsA-14876	25/37
Q4V8V2	Nucleoside diphosphate-linked moiety X motif 17 (EC 3.6.1.-)	nudt17 zgc:114128	25
Q4W946	2-oxoglutarate-Fe(II) type oxidoreductase (EC 1.14.11.-)	encD AFUA_4G00230	25
Q4WHU1	Probable 4-hydroxyphenylpyruvate dioxygenase 1 (EC 1.13.11.27)	AFUA_2G04200	25/37
Q4WMJ1	N-methyltransferase gliN (EC 2.1.1.-)	gliN AFUA_6G09720	25

Q4WMJ5	O-methyltransferase gliM (EC 2.1.1.-)	gliM AFUA_6G09680	25
Q4WMJ7	Nonribosomal peptide synthetase gliP (EC 6.3.2.-)	gliP NRPS10 pesK AFUA_6G09660	25
Q4WMJ8	Dipeptidase gliJ (EC 3.4.13.19)	gliJ AFUA_6G09650	25
Q4WMJ9	Probable aminotransferase gliI (EC 2.6.1.-)	gliI AFUA_6G09640	25
Q4WQZ7	O-methyltransferase tpcA (EC 2.1.1.-)	tpcA tynA AFUA_4G14580	25/37
Q4WZB3	Heptaketide hydrolyase ayg1 (EC 3.7.1.-)	ayg1 AFUA_2G17550	25
Q4WZS3	Putative aspergillopepsin A-like aspartic endopeptidase AFUA_2G15950 (EC 3.4.23.-)	AFUA_2G15950	25
Q54DU5	von Willebrand factor A domain-containing protein DDB_G0292028	DDB_G0292028	25
Q5A599	Histidine protein kinase NIK1 (EC 2.7.13.3)	NIK1 COS1 HIK1 CAALFM_C702800WA	25
Q5AG40	Vacuolar protein sorting-associated protein 4	VPS4 CAALFM_C503090WA	25
Q5ANB1	White-opaque regulator 2	WOR2 CAALFM_C305170WA	25
Q6F4M7	Hydroxyquinol 1,2-dioxygenase (EC 1.13.11.37)	npcC	25
Q6Q875	Oxidoreductase sirO (EC 1.1.1.-)	sirO	25
Q6UEF0	NADH-dependent flavin oxidoreductase nadA (EC 1.-.-.-)	nadA P875_00053008	25/37
Q6UEF1	Oxidoreductase Afly (EC 1.-.-.-)	afly hypA P875_00053033	25
Q6WP50	Presilphiperfolan-8-beta-ol synthase (EC 4.2.3.74) (Botrydial synthesis protein 2)	BOT2 CND15	25
Q6Z965	12-oxophytodienoate reductase 7 (EC 1.3.1.42)	OPR7 OPR13 LOC_Os08g35740 OsJ_27573	25
Q88RC0	Glutarate-semialdehyde dehydrogenase DavD (EC 1.2.1.20)	davD PP_0213	25
Q8CG76	Aflatoxin B1 aldehyde reductase member 2 (EC 1.1.1.n11)	Akr7a2 Afar Akr7a5	25
Q92250	Farnesyl pyrophosphate synthase (EC 2.5.1.10)	fpp fpps 123A4.020 NCU01175	25
Q92398	Mitogen-activated protein kinase spm1 (EC 2.7.11.24)	spm1 pmk1 SPBC119.08	25/37
Q93XW5	Nitrile-specifier protein 5	NSP5 At5g48180 MIF21.7	25
Q96VN5	Triosephosphate isomerase (EC 5.3.1.1)	TPI1 TPI PAAG_02585	25/37
Q975C8	Acryloyl-coenzyme A reductase (EC 1.3.1.84)	STK_04800	25
Q9CA40	Nudix hydrolase 1 (EC 3.6.1.55)	NUDT1 NUDX1 At1g68760 F14K14.13	25
Q9N1F5	Glutathione S-transferase omega-1 (EC 2.5.1.18)	GSTO1	25
Q9P6C8	Alcohol dehydrogenase 1 (EC 1.1.1.1)	adh-1 B17C10.210 NCU01754	25/37
A9MYQ4	Gamma-aminobutyraldehyde dehydrogenase (EC 1.2.1.19)	prp SPAB_01688	25/37
Q9US47	Putative succinate-semialdehyde dehydrogenase C1002.12c [NADP(+)] (EC 1.2.1.16)	SPAC1002.12c	25
Q9UUN9	Aldehyde reductase 2 (EC 1.1.1.2)		25
Q9UW21	Oxysterol-binding protein-like protein OBPalph	OBPALPHA C5_01775C_B CaO19.10709/10710	25

STRESS RESPONSE

Q9Y885	Putative branched-chain-amino-acid aminotransferase TOXF (EC 2.6.1.42)	TOXF	25/37
S0EE84	Cytochrome P450 monooxygenase FUS8 (EC 1.-.-.-)	FUS8 FFUJ_10051	25
W7MLD7	Fusarin C synthetase (EC 2.3.1.-)	FUS1 FVEG_11086	25
W7MWX4	Putative aldehyde dehydrogenase FUS7 (EC 1.2.1.3)	FUS7 FVEG_11080	25
A1CNW6	Probable Xaa-Pro aminopeptidase ACLA_020440 (EC 3.4.11.9)	ACLA_020440	25/37
B8N4P0	Probable carboxypeptidase AFLA_037450 (EC 3.4.17.-)	AFLA_037450	37
B8N8Q9	NADPH dehydrogenase afvA (EC 1.6.99.1)	afvA AFLA_108540	25/37
G3XMB9	Ketoreductase azaE (EC 1.-.-.-)	azaE ASPNIDRAFT_212676	37
G3XMC4	Non-reducing polyketide synthase azaA (EC 2.3.1.-)	azaA ASPNIDRAFT_56946	37
J4UHQ6	Orsellinic acid synthase (EC 2.3.1.-)	OpS1 PKS9 BBA_08179	37
O65679	Probable pinoresinol-lariciresinol reductase 3 (EC 1.23.1.-)	PLR3 At4g34540 T4L20.120	37
O93868	NADP-dependent mannitol dehydrogenase (EC 1.1.1.138)	mtdH	37
O94246	Putative glutamate--cysteine ligase regulatory subunit	SPCC737.06c	25/37
P42893	Endothelin-converting enzyme 1 (EC 3.4.24.71)	Ece1	25/37
P53619	Coatomer subunit delta	ARCN1 COPD	25/37
Q01398	Haloacetate dehalogenase H-1 (EC 3.8.1.3)	dehH1	37
Q0DA50	Zinc finger CCCH domain-containing protein 45	Os06g0677700 LOC_Os06g46400	37
Q0U6E8	Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	mpd1 SNOG_12666	25/37
Q0U6G5	Probable Xaa-Pro aminopeptidase PEPP (EC 3.4.11.9)	PEPP SNOG_12649	25/37
Q10166	Hydrolase C26A3.11 (EC 3.5.-.-)	SPAC26A3.11	25/37
Q2UpZ7	Aspartyl aminopeptidase (EC 3.4.11.21)	dapA AO090005001447	37
Q59KZ1	Aminopeptidase 2 (EC 3.4.11.-)	APE2 CAALFM_C104400CA	37
Q5AK62	Virulence protein SSD1	SSD1 CAALFM_C504730CA	37
Q6ZXC1	Probable inactive dehydrogenase easA	easA cpoX3	25/37
A1VUV0	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.8)	bphD Pnap_4141	25
B0XPP3	Metacaspase-1A (EC 3.4.22.-)	casA AFUB_007090	25
B8N8R1	Aromatic peroxygenase (AaP) (EC 1.11.2.1)	AP01	25
B9W4V6	Low-redox potential peroxidase (EC 1.11.1.7)	LnP	25
C0IW58	Short chain dehydrogenase gsfK (EC 1.-.-.-)	gsfK	25
D7PI11	O-methyltransferase gsfB (EC 2.1.1.-)	gsfB	25
D7PI16	Short chain dehydrogenase gsfE (EC 1.-.-.-)	gsfE	25
D7PI19	E3 ubiquitin-protein ligase TRIP12 (EC 2.3.2.26)	trip12 si:ch211-272f3.4	25
F1RCR6	LanC-like protein GCR2	GCR2 GPCR At1g52920 F14G24.19	25
F4IEM5	Gibberellin 20-oxidase-like protein (EC 1.14.11.-)	At5g51310 MWD22.26	25
F4KBY0	Epoxide hydrolase A (EC 3.3.2.10)	ephA Rv3617 LH57_19705	25

I6YGS0	Putative monooxygenase Rv1533 (EC 1.13.12.-)	Rv1533	25
O06179	Putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 106 kDa subunit (EC 2.4.1.15)	SPAC2E11.16c SPACUNK4.16c	25
O14081	Peroxiredoxin Asp f3 (EC 1.11.1.15)	aspf3 AFUA_6G02280	25
O43099	Mitogen-activated protein kinase-binding protein 1	MAPKBP1 JNKBP1 KIAA0596	25
O60336	GTP-binding protein gtr2	gtr2 SPCC777.05	25
O74544	Mitochondrial protein import protein mas5	mas5 SPBC1734.11	25
O74752	GTP-binding protein rhb1	rhb1 SPBC428.16c	25/37
O94363	Serine/threonine-protein kinase srk1 (EC 2.7.11.1)	srk1 SPCC1322.08	25
O94524	Zeta-crystallin	CRYZ	25
O94547	Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)	SOD2 YHR008C	25
O97764	Exportin-1	xpo1 caf2 crm1	25
P00447	Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28)	Ddc	25/37
P14068	Granaticin polyketide synthase putative ketoacyl reductase 2 (EC 1.3.1.-)	gra-orf6	25/37
P14173	Allantoicase (EC 3.5.3.4)	alc-1 alc B8B8.070 NCU01816	25
P16543	Thioredoxin-1	TRX1 TRX2 YLR043C	25
P18407	Ubiquitin-activating enzyme E1 1 (EC 6.2.1.45)	UBA1 YKL210W	25
P22217	Fumarate reductase 1 (FRDS1) (EC 1.3.1.6)	FRD1 FRDS FRDS1 YEL047C SYGP-ORF35	25
P22515	Peroxiredoxin PRX1, mitochondrial (EC 1.11.1.15)	PRX1 YBL064C YBL0503 YBL0524	25
P32614	Bifunctional epoxide hydrolase 2 (EC 3.3.2.10)	EPHX2	25
P34227	Fatty acid repression mutant protein 2	FRM2 YCL026C-A YCLX08C YCLX8C	25/37
P34913	Probable quinone oxidoreductase (EC 1.6.5.5)	ZTA1 YBR046C YBR0421	25
P37261	6-phosphogluconate dehydrogenase, decarboxylating 1 (EC 1.1.1.44)	GND1 YHR183W	25/37
P38230	Dihydroxy-acid dehydratase, mitochondrial (EC 4.2.1.9)	ILV3 YJR016C J1450	25
P38720	Heat shock protein 90	hsp90 hsp1 AFUA_5G04170	25/37
P39522	scyllo-inositol 2-dehydrogenase (EC 1.1.1.370)	iolX yisS yucG yuxD BSU10850	25
P40292	Protein phosphatase 2C homolog 1 (EC 3.1.3.16)	ptc1 SPCC4F11.02	25/37
P40332	Thioredoxin	trx NCU05731	25
P40371	Cystathionine beta-synthase (EC 4.2.1.22)	cysB DDB_G0267386	25
P42115	Amine oxidase (EC 1.4.3.4)	mao	25/37
P46794	60S ribosomal protein L26-1	RPL26A At3g49910 F3A4.4 T16K5.260	25
P49253	Thioredoxin reductase (EC 1.8.1.9)	cys-9 NCU08352	25/37
P51414	Isoflavone reductase homolog P3 (EC 1.3.1.-)	At1g75280 F22H5.17	25
P51978	Zinc finger protein ZPR1	ZPR1 YGR211W	25/37

P53303	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (GFAT) (EC 2.6.1.16)	GFA1 CAALFM_C302280CA	25
P53373	26S proteasome non-ATPase regulatory subunit 4 homolog	RPN10 MBP1 MCB1 At4g38630 F20M13.190 T9A14.7	25/37
P53704	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial (EC 2.8.3.5)	OXCT1 OXCT SCOT	25
P55034	Aldo/keto reductase slr0942 (EC 1.1.1.184)	slr0942	25
P55809	Disulfide-bond oxidoreductase YfcG (EC 1.8.4.-)	yfcG b2302 JW2299	25
P74308	Bifunctional epoxide hydrolase 2 (EC 3.3.2.10)	Ephx2	25
P77526	Epoxide hydrolase B (EC 3.3.2.10)	MT1988	25
P80299	4-nitrophenylphosphatase (PNPPase) (EC 3.1.3.41)	pho2 SPBC15D4.15	25
P95276	O-methyltransferase MdmC (EC 2.1.1.-)	mdmC	25/37
Q00472	Calcium/calmodulin-dependent protein kinase cmkA (EC 2.7.11.17)	cmkA AN2412	25
Q00719	Nitronate monooxygenase (EC 1.13.12.16)	ncd-2 G17A4.200 NCU03949	25/37
Q00771	Glutamate decarboxylase (GAD) (EC 4.1.1.15)	GAD1 YMR250W YM9920.04	25
Q01284	DNA damage tolerance protein RHC31	AOS1 RHC31 YPR180W P9705.5	25/37
Q04792	Frataxin homolog, mitochondrial (EC 1.16.3.1)	YFH1 YDL120W	25
Q06624	Beta-lactamase domain-containing protein 2	lact-2 ZK945.1	25
Q07540	Phospholipase D1 (EC 3.1.4.4)	pld1 SPAC2F7.16c	25
Q09621	Probable peptide methionine sulfoxide reductase (EC 1.8.4.11)	mrx1 SPAC29E6.05c SPAC30.09c	25
Q09706	Catalase-peroxidase (EC 1.11.1.21)	katG ATEG_08422	25/37
Q09859	eIF-2-alpha kinase activator gcn1 (Translational activator gcn1)	gcn1 SPAC18G6.05c	25
Q0CD12	Damage response protein 1	DAP1 YPL170W P2515	25
Q10105	Small glutamine-rich tetratricopeptide repeat-containing protein 2	SGT2 YOR007C UNF346	25/37
Q12091	Nucleolar protein 56	NOP56 SIK1 YLR197W L8167.9	25
Q12118	Bleomycin hydrolase (EC 3.4.22.40)	BLMH	25
Q12460	Thiopurine S-methyltransferase (EC 2.1.1.67)	tpm NmUl_A2259	25
Q13867	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial (EC 1.3.3.3)	Cpox Cpo	25
Q2Y6S0	Survival factor 1	SVF1 FGRRES_05072 FGSG_05072	25
Q3B7D0	Cytochrome c peroxidase, mitochondrial (EC 1.11.1.5)	CCP1 FGRRES_01245 FGSG_01245	25
Q4IC16	Mitogen-activated protein kinase HOG1 (EC 2.7.11.24)	HOG1	25/37
Q4ING3	Ribonuclease T2-like (EC 3.1.27.1)	rny1 AFUA_3G11220	25/37
Q4W6D3	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase (EC 4.1.1.45)	acmsd DDB_G0286525	25
Q4WXZ5	Heat shock protein 60	hsp60 AN6089	25
Q54LN9	Heat shock 70 kDa protein	AN6010	25

Q5B041	Inorganic pyrophosphatase (EC 3.6.1.1)	ipp1 AN2968	25/37
Q5B0C0	Homoserine dehydrogenase (EC 1.1.1.3)	AN2882	25/37
Q5B912	Acyl-CoA ligase easD (EC 6.2.1.-)	easD AN2549	25/37
Q5B998	Quinone oxidoreductase (EC 1.6.5.5)	Cryz	25
Q5BA81	Translationally-controlled tumor protein homolog	NCU06464	25
Q6AYT0	Flavohemoprotein (EC 1.14.12.17)	hmp fhp BB3091	25
Q7RYV5	Glutathione reductase (EC 1.8.1.7)	gtr-1 glr1 B10C3.130 NCU03339	25
Q7WHW5	Catalase B (EC 1.11.1.6)	catB AO090120000068	25/37
Q873E8	2,4-dichlorophenol 6-monooxygenase (EC 1.14.13.20)	tfdB	25/37
Q877A8	cAMP-dependent protein kinase regulatory subunit	pkaR AFUA_3G10000	25
Q8KN28	O-acetyl-ADP-ribose deacetylase MACROD1 (EC 3.2.2.-) (EC 3.5.1.-)	MACROD1 LRP16	25
Q96UX3	Galactinol synthase 2 (EC 2.4.1.123)	GOLS2 At1g56600 F25P12.95	25/37
Q9BQ69	Nitronate monooxygenase (EC 1.13.12.16)	PA1024	25
Q9FXB2	Glycine-rich RNA-binding protein 4, mitochondrial	RBG4 GR-RBP4 GRP4 MRBP1B At3g23830 F14O13_2	25
Q9I4V0	Uncharacterized protein C1711.08	SPBC1711.08	25
Q9LIS2	Copper amine oxidase 1 (EC 1.4.3.21)	cao1 spao1 SPAC2E1P3.04	25
Q9P782	Glutathione S-transferase kappa 1 (EC 2.5.1.18) (GST 13-13) (GST class-kappa) (GSTK1-1) (hGSTK1) (Glutathione S-transferase subunit 13)	GSTK1 HDCMD47P	25/37
Q9P7F2	Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)	sod-2 18F11.030 NCU01213	25
Q9Y2Q3	Acyltransferase LovD (EC 2.3.1.238)	lovD	25
Q9Y783	Peroxiredoxin TSA1-A (EC 1.11.1.15)	TSA1 TSA1A CAALFM_C306180CA	25
Q9Y7D1	DnaJ homolog 1, mitochondrial	AN10778	25
Q9Y7F0	Thiamine thiazole synthase	sti35 FOXG_10428	25/37
C8V213	Glutathione hydrolase-like YwrD proenzyme (EC 2.3.2.2)	ywrD BSU36100	37
J9N5G7	30 kDa heat shock protein	hsp30 NCU09364	37
O05218	Mitochondrial FAD-linked sulfhydryl oxidase ERV1 (EC 1.8.3.2)	ERV1 YGR029W	25/37
O74180	Trehalose-phosphatase (EC 3.1.3.12)	TPS2 PFK3 YDR074W YD8554.07	37
P19752	Probable coatomer subunit gamma	sec21 SPAC57A7.10c	37
P27882	Formate dehydrogenase (EC 1.17.1.9)	aciA AN6525	37
P31688	Curved DNA-binding protein (42 kDa protein)	cdb4 SPAC23H4.09	37
P41751	ATP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.93)	SNOG_04206	37
P85978	Phosphatidylserine decarboxylase proenzyme 1, mitochondrial (EC 4.1.1.65)	PSD1 CAALFM_C100610WA	37
P87140	THO complex subunit 4D	ALY4 DIP2 THO4D At5g37720 K12B20.19	25/37

Q03134	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase (EC 3.1.4.54)	Napepld Mbldc1	25/37
Q09184	Heat shock protein 78, mitochondrial	HSP78 CAALFM_C203390CA	25/37
Q0UBT2	Stomatin-like protein 2, mitochondrial	STOML2 SLP2 HSPC108	25/37
Q0UVK8	ATP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.93)	SNOG_04206	37
Q5ABC5	Phosphatidylserine decarboxylase proenzyme 1, mitochondrial (EC 4.1.1.65)	PSD1 CAALFM_C100610WA	37
Q6NQ72	THO complex subunit 4D	ALY4 DIP2 THO4D At5g37720 K12B20.19	37
Q6ZQW0	Indoleamine 2,3-dioxygenase 2 (EC 1.13.11.-)	IDO2 INDOL1	37
Q8BH82	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D (EC 3.1.4.54)	Napepld Mbldc1	37
Q96UX5	Heat shock protein 78, mitochondrial	HSP78 CAALFM_C203390CA	37
Q9UJZ1	Stomatin-like protein 2, mitochondrial	STOML2 SLP2 HSPC108	37
