

## Appendix A. Supplementary material

**Supplementary Table 1.** The total number of *Heterobasidion* genes that were considered expressed<sup>a</sup> in each of the RNA samples.

Strain <sup>b</sup>	Time <sup>c</sup>	Interaction	Number of Expressed Genes (%)
A08-5	12	IS incompatible	11 855 (88.4)
A08-25	12	IS incompatible	11 841 (88.3)
A08-48	12	IS compatible	11 326 (84.5)
A08-73	12	IS compatible	11 154 (83.2)
A08-5	48	IS incompatible	11 375 (84.9)
A08-25	48	IS incompatible	11 872 (88.6)
A08-48	48	IS compatible	10 937 (81.6)
A08-73	48	IS compatible	11 292 (84.2)
A08-5	96	IS incompatible	10 359 (77.3)
A08-25	96	IS incompatible	11 628 (86.7)
A08-48	96	IS compatible	11 284 (86.7)
A08-73	96	IS compatible	11 157 (83.2)

<sup>a</sup> Genes were considered expressed if they were detected above had a threshold of 1 count per million (RPKM values  $\geq 0.1$ ) and at least 3 unique gene reads mapped to it (Wickramasinghe et al., 2012).

<sup>b</sup> The strains used in the pairing IS interactions with the tester strain S $\alpha$  16-4 (see Fig. 1).

<sup>c</sup> Time (hours) after hyphal fusion.

**Supplementary Table 2.** The differentially expressed (DE)<sup>a</sup> genes identified during pairwise comparisons across the various time points and between the IS compatible and incompatible interactions.

Prot. ID <sup>b</sup>	Cluster <sup>c</sup>	Putative product or domain <sup>d</sup>	E-Value <sup>e</sup>	Chromosome <sup>f</sup>	IS interactions <sup>g</sup>					
					Com 12h	Com 48h	Com 96h	Incom 12h	Incom 48h	Incom 96h
408198	1A	1 concanamycin induced protein c ( <i>G. trabeum</i> , EPQ59499)	2.65E-43	03:938349-938997	98242.00	29476.00	5838.00	164314.00	98242.00	5911.20
165066	1B	expansin-like protein ( <i>S. hirsutum</i> , EIM88869)	1.19E-46	14:272940-273625	4425.10	2860.00	2604.00	8309.00	4905.00	3655.20
326154	2B	No hit	No hit	09:1651048-1651399	76016.00	145928.00	77161.00	7140.10	76358.00	77554.00
436223	1A	No hit	No hit	10:917081-917420	4385.20	3386.50	1893.00	4205.50	4206.00	2118.70
408120	1C	aldo/keto reductase ( <i>S. hirsutum</i> , EIM88287)	0	03:675249-676688	2552.20	1596.70	4110.00	3278.80	3047.00	3221.60
55694	2C	hypothetical protein ( <i>T. terrestris</i> , XP003654187)	2.77E-43	09:1649577-1650521	5930.20	7984.10	26618.00	3054.00	7618.00	27471.00
155403	1A	hypothetical protein ( <i>P. carnosus</i> , EKM60008)	2.17E-22	03:1591124-1591648	3390.60	2979.00	1279.00	3022.40	2751.00	1550.60
449612	1A	cytochrome5 ( <i>S. hirsutum</i> , EIM88355)	1.67E-51	03:1165313-1166064	2212.20	2252.10	1252.00	2554.70	2358.00	1543.10
409622	1A	hypothetical protein ( <i>P. strigosozonata</i> , EIN12645)	1.30E-15	05:1626892-1627545	1441.80	1586.60	1462.00	1907.00	1707.00	903.38
148469	1C	aegerolysin aa-pri1 ( <i>P. ostreatus</i> , AAL57035)	3.07E-69	04:1415497-1416069	1275.30	268.35	1836.00	1869.80	723.50	3267.60
482007	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM79660)	4.13E-43	13:513747-514607	1633.90	1349.40	839.60	1452.20	1013.00	1091.70
156762	1C	hydrophobin 2 ( <i>H. annosum</i> , ABA46362)	3.64E-16	11:964831-965389	615.36	107.63	1354.00	1371.60	495.90	1876.10
455442	1B	predicted protein ( <i>L. bicolor</i> , XP 001881724)	1.86E-08	12:334962-335627	521.06	130.70	371.80	1298.30	385.50	594.46
329440	1A	40s ribosomal protein s26 ( <i>S. hirsutum</i> , EIM82046)	8.59E-57	12:519368-519950	1375.40	1274.00	962.60	1226.60	1176.00	1058.90
66455	1A	signal peptide protein ( <i>S. hirsutum</i> , EIM87680)	1.37E-37	12:1150787-1151460	1325.40	1170.00	258.10	1203.20	1178.00	314.22
441690	2B	delta-12 fatty acid desaturase protein ( <i>S. lacrymans</i> , EGN92175)	0	10:325003-327323	1475.40	2193.70	2262.00	1175.90	2074.00	2864.30
472133	1A	class i glutamine amidotransferase-like protein ( <i>S. hirsutum</i> , EIM87503)	3.58E-108	03:729006-730135	1049.00	1012.70	499.10	1147.60	1158.00	298.85
148682	1A	hypothetical protein ( <i>P. strigosozonata</i> , EIN08521)	3.35E-47	09:463117-464179	1109.60	902.18	421.10	1022.00	701.60	777.94
45002	1C	carotenoid ester lipase precursor ( <i>S. hirsutum</i> , EIM86239)	0	05:2480158-2482633	461.40	159.70	529.20	982.40	266.50	692.3
442873	1A	hypothetical protein ( <i>S. commune</i> , XP003026432)	1.88E-29	01: 625960-626486	412.27	426.4	510.5	916.08	672.2	114.07
412431	2C	helix-turn-helix domain-containing protein ( <i>S. hirsutum</i> , EIM83730)	2.97E-26	13:280828-281338	836.52	737.38	1453	914.71	993.20	1308.30
146178	2C	glycoside hydrolase family 16 protein ( <i>G. trabeum</i> , XP002472478)	5.01E-134	05:2364308-2366059	1041.30	1166.70	1828.00	888.85	1152.00	1995.30
388181	1A	aldo/keto reductase ( <i>S. hirsutum</i> , EIM88287)	0	09:1051666-1053180	879.03	731.11	442.00	884.34	686.60	478.66
479381	1C	hypothetical protein ( <i>C. cinerea</i> , XP001836190)	9.28E-81	09:1253638-1255194	346.19	86.42	491.10	843.10	242.10	541.55
458782	1A	cytochrome c ( <i>F. radiculosa</i> , CCM06772)	3.39E-66	04:2927844-2928507	940.11	857.16	381.60	842.03	831.80	480.05
63659	2C	glycoside hydrolase family 61 protein H ( <i>H. parvaporum</i> , AFO72237)	5.08E-138	07:1260362-1262045	1165.00	1285.30	2119.00	801.97	859.70	1881.90

**Supplementary Table 3.** Sequence description of the highly expressed *Heterobasidion* DE genes<sup>a</sup> identified in this study.

Prot. ID <sup>b</sup>	Putative product or domain <sup>c</sup>	E-Value <sup>d</sup>	Chromosome <sup>e</sup>	IS interactions <sup>f</sup>					
				Com 12h	Com 48h	Com 96h	Incom 12h	Incom 48h	Incom 96h
66455	signal peptide protein ( <i>S. hirsutum</i> , EIM87680)	1.37E-37	12:1150787-1151460	1325.40	1170.00	258.10	1203.20	1178.00	314.22
455442	predicted protein ( <i>L. bicolor</i> , XP 001881724)	1.86E-08	12:334962-335627	521.06	130.70	371.80	1298.30	385.50	594.46
436223	no hit	no hit	10:917081-917420	4385.20	3386.50	1893.00	4205.50	4206.00	2118.70
326154	no hit	no hit	09:1651048-1651399	76016.00	145928.00	77161.00	7140.10	76358.00	77554.00
55694	hypothetical protein ( <i>T. terrestris</i> , XP003654187)	2.77E-43	09:1649577-1650521	5930.20	7984.10	26618.00	3054.00	7618.00	27471.00
305913	hypothetical protein ( <i>S. hirsutum</i> , EIM92751)	8.64E-59	01: 2662103-2663036	320.82	367.97	2080.00	240.82	352.00	934.04
482007	hypothetical protein ( <i>S. hirsutum</i> , EIM79660)	4.13E-43	13:513747-514607	1633.90	1349.40	839.60	1452.20	1013.00	1091.70
409622	hypothetical protein ( <i>P. strigosozonata</i> , EIN12645)	1.30E-15	05:1626892-1627545	1441.80	1586.60	1462.00	1907.00	1707.00	903.38
148682	hypothetical protein ( <i>P. strigosozonata</i> , EIN08521)	3.35E-47	09:463117-464179	1109.60	902.18	421.10	1022.00	701.60	777.94
155403	hypothetical protein ( <i>P. camosa</i> , EKM60008)	2.17E-22	03:1591124-1591648	3390.60	2979.00	1279.00	3022.40	2751.00	1550.60
384154	hypothetical protein ( <i>F. mediterranea</i> , EJD06958)	5.48E-103	05:1298074-1299437	1088.00	1098.60	406.40	745.14	812.80	437.84
446505	hypothetical protein ( <i>C. subvermispora</i> , EMD32530)	1.12E-80	11:793291-794500	359.28	379.27	1082.00	575.57	479.50	1342.30
156762	hydrophobin 2 ( <i>H. annosum</i> , ABA46362)	3.64E-16	11:964831-965389	615.36	107.63	1354.00	1371.60	495.90	1876.10
33224	hydrophobin 2 ( <i>H. annosum</i> , ABA46362)	5.83E-40	06:277914-278512	437.73	336.89	1063.00	702.40	416.50	2477.70
437588	hlh domain-containing protein ( <i>F. radiculosa</i> , CCM03782)	2.63E-56	01: 1109903-1110932	713.77	780.22	1013.00	529.31	660.10	940.26
412431	helix-turn-helix domain-containing protein ( <i>S. hirsutum</i> , EIM83730)	2.97E-26	13:280828-281338	836.52	737.38	1453	914.71	993.20	1308.30
418675	heat shock protein 9 ( <i>D. squalens</i> , EJJ65505)	9.34E-33	06:1189110-1189661	210.46	111.46	1081.00	301.81	289.90	752.40
153951	glycoside hydrolase family 74 protein ( <i>T. versicolor</i> , EIW65405)	0	01: 2551222-2554556	1562.20	1551.60	1850.00	722.09	938.60	2203.80
63659	glycoside hydrolase family 61 protein H ( <i>H. parviporum</i> , AFO72237)	5.08E-138	07:1260362-1262045	1165.00	1285.30	2119.00	801.97	859.70	1881.90
181247	glycoside hydrolase family 5 protein ( <i>S. lacrymans</i> , EGO03450)	0	12:446511-448311	882.69	1024.00	921.30	455.60	607.30	1406.40
146178	glycoside hydrolase family 16 protein ( <i>G. trabeum</i> , XP002472478)	5.01E-134	05:2364308-2366059	1041.30	1166.70	1828.00	888.85	1152.00	1995.30
165066	expansin-like protein ( <i>S. hirsutum</i> , EIM88869)	1.19E-46	14:272940-273625	4425.10	2860.00	2604.00	8309.00	4905.00	3655.20
66839	endoglucanase ( <i>L. lacteus</i> , BAD67544)	3.96E-166	04:1605377-1607418	743.96	751.75	936.30	383.03	476.20	1201.30
154589	elongation factor 3 ( <i>S. hirsutum</i> , EIM90240)	0	02:906829-910413	747.60	813.40	1702.00	798.03	782.00	1243.20
441690	delta-12 fatty acid desaturase protein ( <i>S. lacrymans</i> , EGN92175)	0	10:325003-327323	1475.40	2193.70	2262.00	1175.90	2074.00	2864.30
449612	cytochrome5 ( <i>S. hirsutum</i> , EIM88355)	1.67E-51	03:1165313-1166064	2212.20	2252.10	1252.00	2554.70	2358.00	1543.10
472133	class i glutamine amidotransferase-like protein ( <i>S. hirsutum</i> , EIM87503)	3.58E-108	03:729006-730135	1049.00	1012.70	499.10	1147.60	1158.00	298.85

146426	carbohydrate-binding module family 12 protein ( <i>G. trabeum</i> , EPQ57167)	4.85E-100	06:1865149-1866529	487.73	507.25	1016.00	417.45	477.60	845.26
151850	carbohydrate-binding module family 1 protein ( <i>D. squalens</i> , EJF61065)	1.92E-126	05:1174701-1176194	1007	1103.80	1538.00	586.43	618.60	1477.10
408120	aldo/keto reductase ( <i>S. hirsutum</i> , EIM88287)	0	03:675249-676688	2552.20	1596.70	4110.00	3278.80	3047.00	3221.60
330758	aldehyde dehydrogenase ( <i>S. hirsutum</i> , EIM83734)	0	13:214835-216772	1163.10	1318.80	343.60	753.68	729.50	552.82
148469	aegerolysin aa-pri1 ( <i>P. ostreatus</i> , AAL57035)	3.07E-69	04:1415497-1416069	1275.30	268.35	1836.00	1869.80	723.50	3267.60
329440	40s ribosomal protein s26 ( <i>S. hirsutum</i> , EIM82046)	8.59E-57	12:519368-519950	1375.40	1274.00	962.60	1226.60	1176.00	1058.90
408198	1 concanamycin induced protein c ( <i>G. trabeum</i> , EPQ59499)	2.65E-43	03:938349-938997	98242.00	29476.00	5838.00	164314.00	98242.00	5911.20

<sup>a</sup> Genes were considered highly expressed if they had a Reads Per Kilobase per Million mapped reads (RPKM) value of more than 1000 (Burke et al., 2012). Genes were considered DE if they displayed a two-fold change in expression at a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e.,  $FDR\ q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995).

<sup>b</sup> JGI protein identity number.

<sup>c</sup> BLAST2GO (<http://www.blast2go.org>) was used to annotate the DE genes in each cluster.

<sup>d</sup> BLAST Expect values obtained with BLAST2GO. “No hit” indicated that no homologous sequences were detected in any of the databases searched.

<sup>e</sup> Genome location of the DE genes in the annotated *H. irregulare* reference genome (Olson et al., 2012; DOE Joint Genome Institute, JGI, <http://genome.jgi.doe.gov/>). The first two digits represent the chromosome on which the gene is located and the numbers following it indicates the nucleotide position on the chromosome.

<sup>f</sup> Expression value (indicated in RPKM).

**Supplementary Table 4.** Statistically significant GO terms<sup>a</sup> (Biological Process category) derived from the DE genes<sup>b</sup> involved in IS in *Heterobasidion*.

Gene Ontology ID: Term	P-Value <sup>c</sup>	
<b>Cluster 1A</b>		
GO:0071824: protein-DNA complex subunit organization	2.32E-05	Over <sup>d</sup>
GO:0006629: lipid metabolic process	0.001	Over
GO:0071840: cellular component organization or biogenesis	0.033	Over
GO:0044710: metabolic process	0.026	Over
GO:0006323: DNA packaging	2.87E-05	Over
GO:0071103: DNA conformation change	7.26E-05	Over
GO:0006996: organelle organization	0.005	Over
GO:0022607: cellular component assembly	0.006	Over
GO:0006527: arginine catabolic process	0.044	Over
GO:0018279: protein N-linked glycosylation via asparagine	0.044	Over
GO:0018196: peptidyl-asparagine modification	0.044	Over
GO:0042168: heme metabolic process	0.044	Over
GO:0006796: phosphate-containing compound metabolic process	0.029	Under
<b>Cluster 1B</b>		
GO:0006950: response to stress	0.039	Over
GO:0006914: autophagy	0.019	Over
GO:0006979: response to oxidative stress	0.020	Over
GO:0006066: alcohol metabolic process	6.13E-06	Over
GO:0006118: electron transport	0.00141	Over
GO:0044710: metabolic process	0.002	Over
GO:0009987: cellular process	0.014	Under
GO:0043170: macromolecule metabolic process	0.024	Under
GO:1901615: organic hydroxy compound metabolic process	1.08E-05	Over
GO:0006629: lipid metabolic process	0.005	Over
GO:0006720: isoprenoid metabolic process	0.005	Over
GO:0008299: isoprenoid biosynthetic process	0.005	Over
GO:0031668: cellular response to extracellular stimulus	0.007	Over
GO:0007033: vacuole organization	0.013	Over
GO:0006026: aminoglycan catabolic process	0.032	Over
<b>Cluster 1C</b>		
GO:0006118: electron transport	0.007	Over
GO:0022414: reproductive process	0.020	Over
GO:0006725: cellular aromatic compound metabolic process	0.026	Under
GO:1901576: organic substance biosynthetic process	0.026	Under
GO:0044238: primary metabolic process	0.034	Under
GO:0044267: cellular protein metabolic process	0.042	Under
GO:0006139: nucleobase-containing compound metabolic process	0.042	Under
GO:0044249: cellular biosynthetic process	0.043	Under
GO:0051715: cytolysis in other organism	0.005	Over
GO:0051701: interaction with host	0.005	Over
GO:0003006: developmental process involved in reproduction	0.005	Over

GO:0035821: modification of morphology or physiology of other organism	0.005	Over
GO:0001906: cell killing	0.005	Over
GO:0048608: reproductive structure development	0.005	Over
GO:0009987: cellular process	4.52E-06	Under
GO:0044237: cellular metabolic process	4.96E-05	Under
GO:0044260: cellular macromolecule metabolic process	0.002	Under
GO:0006807: nitrogen compound metabolic process	0.016	Under
GO:0034641: cellular nitrogen compound metabolic process	0.026	Under
GO:0008152: metabolic process	0.026	Under
GO:1901360: organic cyclic compound metabolic process	0.026	Under
GO:1901576: organic substance biosynthetic process	0.026	Under
GO:0019538: protein metabolic process	0.048	Under

### Cluster 2A

GO:0019538: protein metabolic process	0.010	Over
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### Cluster 2B

GO:0005975: carbohydrate metabolic process	0.005	Over
GO:0009987: cellular process	0.027	Under
GO:0051028: mRNA transport	0.007	Over
GO:0006403: RNA localization	0.013	Over
GO:0006308: DNA catabolic process	0.013	Over
GO:0071705: nitrogen compound transport	0.018	Over
GO:0009065: glutamine family amino acid catabolic process	0.026	Over
GO:0000272: polysaccharide catabolic process	0.033	Over

### Cluster 2C

GO:0008643: carbohydrate transport	0.002	Over
GO:0005975: carbohydrate metabolic process	1.29E-05	Over
GO:0051341: regulation of oxidoreductase activity	0.031	Over
GO:1901615: organic hydroxy compound metabolic process	0.023	Over
GO:0045229: external encapsulating structure organization	0.003	Over
GO:0006118: electron transport	3.93E-05	Over
GO:0043170: macromolecule metabolic process	1.07E-05	Under
GO:0006259: DNA metabolic process	0.010	Under
GO:0006412: translation	0.010	Under
GO:0044238: primary metabolic process	0.013	Under
GO:0071704: organic substance metabolic process	0.023	Under
GO:0071555: cell wall organization	0.003	Over
GO:0006066: alcohol metabolic process	0.015	Over
GO:0007040: lysosome organization	0.023	Over
GO:0032504: multicellular organism reproduction	0.046	Over
GO:0006665: sphingolipid metabolic process	0.046	Over
GO:0007033: vacuole organization	0.046	Over
GO:0006570: tyrosine metabolic process	0.046	Over
GO:0009987: cellular process	2.55E-10	Under
GO:0044237: cellular metabolic process	1.13E-08	Under
GO:0044267: cellular protein metabolic process	1.05E-04	Under
GO:0034641: cellular nitrogen compound metabolic process	0.001	Under

GO:0009058: biosynthetic process	0.003	Under
GO:0006725: cellular aromatic compound metabolic process	0.003	Under
GO:1901360: organic cyclic compound metabolic process	0.003	Under
GO:0006793: phosphorus metabolic process	0.034	Under
GO:0043412: macromolecule modification	0.048	Under
GO:0090304: nucleic acid metabolic process	0.028	Under
GO:0010467: gene expression	0.025	Under

<sup>a</sup> Statistical assessment of GO term enrichment was performed using BLAST2GO (Conesa et al., 2005).

<sup>b</sup> Genes were considered statistical significant differentially expressed if they displayed a two-fold change in expression and with a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e.,  $FDR\ q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995).

<sup>c</sup> The P-value for each GO term reflects the enrichment in frequency of that GO term in the input entity list relative to all entities in the background list.

<sup>d</sup> Over-represented (enriched) or under-represented (depleted) among genes in the set.

**Supplementary Table 5.** Statistically significant GO terms<sup>a</sup> (Molecular function category) derived from the DE genes<sup>b</sup> involved in IS in *Heterobasidion*.

Gene Ontology ID: Term		P-Value <sup>c</sup>	
<b>Cluster 1A</b>			
GO:0004452:	Isopentenyl-diphosphate delta-isomerase activity	0.002	Over <sup>d</sup>
GO:0050136:	NADH dehydrogenase (quinone) activity	0.008	Over
GO:0003913:	DNA photolyase activity	0.015	Over
GO:0018734:	butyrolactone hydrolase activity	0.018	Over
GO:0003954:	NADH dehydrogenase activity	0.023	Over
GO:0016655:	oxidoreductase activity, acting on NAD(P)H	0.039	Over
GO:0016614:	oxidoreductase activity, acting on CH-OH group of donors	0.010	Over
GO:0016491:	oxidoreductase activity	0.048	Over
GO:0033897:	ribonuclease T2 activity	0.030	Over
GO:0009703:	nitrate reductase (NADH) activity	0.030	Over
GO:0004088:	carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity	0.030	Over
GO:0008410:	CoA-transferase activity	0.030	Over
GO:0008891:	glycolate oxidase activity	0.030	Over
GO:0004408:	holocytochrome-c synthase activity	0.030	Over
GO:0004356:	glutamate-ammonia ligase activity	0.044	Over
GO:0003697:	single-stranded DNA binding	0.044	Over
GO:0004069:	L-aspartate:2-oxoglutarate aminotransferase activity	0.044	Over
GO:0004053:	arginase activity	0.044	Over
GO:0004030:	aldehyde dehydrogenase [NAD(P)+] activity	0.044	Over
GO:0032555:	purine ribonucleotide binding	0.003	Under
GO:0000166:	nucleotide binding	0.014	Under
GO:0043168:	anion binding	0.014	Under
GO:0016773:	phosphotransferase activity, alcohol group as acceptor	0.022	Under
<b>Cluster 1B</b>			
GO:0016209:	antioxidant activity	0.005	Over
GO:0004601:	peroxidase activity	0.002	Over
GO:0016746:	transferase activity, transferring acyl groups	0.044	Over
GO:0016491:	oxidoreductase activity	4.51E-08	Over
GO:0005199:	structural constituent of cell wall	0.005	Over
GO:0016298:	lipase activity	0.027	Over
GO:0004421:	hydroxymethylglutaryl-CoA synthase activity	0.006	Over
GO:0008471:	laccase activity	0.002	Over
GO:0016829:	lyase activity	0.011	Over
GO:0003824:	catalytic activity	0.002	Over
GO:0004192:	cathepsin D activity	0.032	Over
GO:0045551:	cinnamyl-alcohol dehydrogenase activity	0.038	Over
GO:0004337:	geranyltranstransferase activity	0.044	Over
GO:0018679:	dibenzothiophene-5,5-dioxide monooxygenase activity	0.044	Over
GO:0032555:	purine ribonucleotide binding	0.018	Under
GO:0008270:	zinc ion binding	0.030	Under
GO:0003676:	nucleic acid binding	0.034	Under
GO:0032559:	adenyl ribonucleotide binding	0.048	Under



**Cluster 1C**

GO:0005199:	structural constituent of cell wall	0.000	Over
GO:0016491:	oxidoreductase activity	0.001	Over
GO:0004497:	monooxygenase activity	0.004	Over
GO:0016682:	oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	0.005	Over
GO:0004856:	xylulokinase activity	0.010	Over
GO:0016616:	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	0.043	Over
GO:0004650:	polygalacturonase activity	0.045	Over
GO:0004553:	hydrolase activity, hydrolyzing O-glycosyl compounds	0.022	Over
GO:0050236:	pyridoxine:NADP 4-dehydrogenase activity	0.040	Over
GO:0004252:	serine-type endopeptidase activity	0.045	Over
GO:0072341:	modified amino acid binding	0.050	Over
GO:0016679:	oxidoreductase activity, acting on diphenols and related substances as donors	0.050	Over
GO:0004499:	N,N-dimethylaniline monooxygenase activity	0.050	Over
GO:0031177:	phosphopantetheine binding	0.050	Over
GO:0003676:	nucleic acid binding	0.031	Under

**Cluster 2A**

GO:0008233:	peptidase activity	0.003	Over
GO:0004351:	glutamate decarboxylase activity	0.002	Over
GO:0003960:	NADPH:quinone reductase activity	0.012	Over
GO:0004725:	protein tyrosine phosphatase activity	0.031	Over

**Cluster 2B**

GO:0030248:	cellulose binding	4.75E-06	Over
GO:0016787:	hydrolase activity	0.035	Over
GO:0070011:	peptidase activity, acting on L-amino acid peptides	0.050	Over
GO:0004177:	aminopeptidase activity	0.026	Over
GO:0016798:	hydrolase activity, acting on glycosyl bonds	5.91E-04	Over
GO:0008236:	serine-type peptidase activity	0.005	Over
GO:0004053:	arginase activity	0.020	Over
GO:0004187:	carboxypeptidase D activity	0.026	Over
GO:0051920:	peroxiredoxin activity	0.026	Over
GO:0050184:	phosphatidylcholine desaturase activity	0.033	Over
GO:0004559:	alpha-mannosidase activity	0.050	Over
GO:0004338:	glucan exo-1,3-beta-glucosidase activity	0.039	Over
GO:0016813:	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	0.039	Over
GO:0045551:	cinnamyl-alcohol dehydrogenase activity	0.039	Over
GO:0008810:	cellulase activity	0.039	Over
GO:0005509:	calcium ion binding	0.046	Over

**Cluster 2C**

GO:0016861:	intramolecular oxidoreductase activity, interconverting aldoses and ketoses	0.028	Over
GO:0016491:	oxidoreductase activity	1.14E-05	Over
GO:0010181:	FMN binding	2.23E-04	Over

GO:0004568:	chitinase activity	0.001	Over
GO:0005186:	pheromone activity	0.002	Over
GO:0030246:	carbohydrate binding	2.20E-06	Over
GO:1901476:	carbohydrate transporter activity	0.002	Over
GO:0030599:	pectinesterase activity	0.003	Over
GO:0004553:	hydrolase activity, hydrolyzing O-glycosyl compounds	3.94E-07	Over
GO:0008733:	L-arabinose isomerase activity	0.005	Over
GO:0005199:	structural constituent of cell wall	0.005	Over
GO:0030248:	cellulose binding	0.008	Over
GO:0008738:	L-fuculose-phosphate aldolase activity	0.023	Over
GO:0003824:	catalytic activity	0.014	Over
GO:0003959:	NADPH dehydrogenase activity	0.017	Over
GO:0008471:	laccase activity	0.021	Over
GO:0051213:	dioxygenase activity	0.021	Over
GO:0004348:	glucosylceramidase activity	0.023	Over
GO:0004328:	formamidase activity	0.023	Over
GO:0003857:	3-hydroxyacyl-CoA dehydrogenase activity	0.023	Over
GO:0047927:	gibberellin-44 dioxygenase activity (152691)	0.023	Over
GO:0008423:	bleomycin hydrolase activity	0.023	Over
GO:0008336:	gamma-butyrobetaine dioxygenase activity	0.023	Over
GO:0030729:	acetoacetate-CoA ligase activity	0.023	Over
GO:0005544:	calcium-dependent phospholipid binding	0.023	Over
GO:0004419:	hydroxymethylglutaryl-CoA lyase activity	0.023	Over
GO:0003676:	nucleic acid binding	4.12E-04	Under
GO:0016462:	pyrophosphatase activity	0.048	Under
GO:0032555:	purine ribonucleotide binding	0.002	Under
GO:0008270:	zinc ion binding	0.016	Under
GO:0016874:	ligase activity	0.030	Under
GO:0016740:	transferase activity	0.045	Under

<sup>a</sup> Statistical assessment of GO term enrichment was performed using BLAST2GO (Conesa et al., 2005).

<sup>b</sup> Genes were considered statistically significant differentially expressed if they displayed a two-fold change in expression and with a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e.,  $FDR\ q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995).

<sup>c</sup> The P-value for each GO term reflects the enrichment in frequency of that GO term in the input entity list relative to all entities in the background list.

<sup>d</sup> Over-represented (enriched) or under-represented (depleted) among genes in the set.

**Supplementary Table 6.** Statistically significant GO terms<sup>a</sup> (cellular components category) derived from the DE genes<sup>b</sup> involved in IS in *Heterobasidion*.

Gene Ontology ID: Term	P-Value <sup>c</sup>	
<b>Cluster 1A</b>		
GO:0032991: macromolecular complex	0.034	Over <sup>d</sup>
GO:0044444: cytoplasmic part	0.036	Over
<b>Cluster 1B</b>		
GO:0005618: cell wall	0.007	Over
GO:0030312: external encapsulating structure	0.009	Over
GO:0005622: intracellular	0.020	Under
<b>Cluster 1C</b>		
GO:0005618: cell wall	2.45E-06	Over
GO:0030312: external encapsulating structure	3.67E-06	Over
GO:0009326: formate dehydrogenase complex	0.015	Over
GO:0043229: intracellular organelle	0.026	Under
<b>Cluster 2A</b>		
<b>Cluster 2B</b>		
GO:0005576: extracellular region	7.49E-05	Over
GO:0016459: myosin complex	0.033	Over
<b>Cluster 2C</b>		
GO:0005576: extracellular region	1.17E-05	Over
GO:0005618: cell wall	7.13E-05	Over
GO:0030312: external encapsulating structure	1.17E-04	Over
GO:0016021: integral to membrane	9.80E-04	Over
GO:0071944: cell periphery	0.001	Over
GO:0005764: lysosome	0.023	Over
GO:0009339: glycolate oxidase complex	0.046	Over
GO:0005622: intracellular	2.72E-06	Under
GO:0032991: macromolecular complex	0.003	Under
GO:0005737: cytoplasm	0.009	Under
GO:0043229: intracellular organelle	0.009	Under
GO:0043234: protein complex	0.034	Under
GO:0030529: ribonucleoprotein complex	0.036	Under

<sup>a</sup> Statistical assessment of GO term enrichment was performed using BLAST2GO (Conesa et al., 2005).

<sup>b</sup> Genes were considered statistically significant differentially expressed if they displayed a two-fold change in expression and with a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e., FDR  $q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995).

<sup>c</sup> The P-value for each GO term reflects the enrichment in frequency of that GO term in the input entity list relative to all entities in the background list.

<sup>d</sup> Over-represented (enriched) or under-represented (depleted) among genes in the set.

**Supplementary Table 7.** Statistically significant GO terms<sup>a</sup> (Biological Process category) and the DE genes<sup>b</sup> they were derived from.

Prot. Name <sup>c</sup>	Cluster <sup>d</sup>	Putative product or domain <sup>e</sup>	E-Value <sup>f</sup>	Chromosome <sup>g</sup>	IS interactions <sup>h</sup>					
					Com 12h	Com 48h	Com 96h	Incom 12h	Incom 48h	Incom 96h
<b>Protein-DNA complex subunit organization and DNA conformational change (GO:0006259) Cellular component organization or biogenesis (GO:0071840)</b>										
428887	1A	histone H3 ( <i>L. bicolor</i> , XP001873642)	4.85E-81	08:1988863-1989541	320.33	282.03	157.7	309.51	245.4	174.13
318391	1A	histone H3	no hit	05:404792-405868	19.23	24.7	17.72	16.68	21.42	10.52
27951	1A	histone-fold-containing protein ( <i>C. subvermispora</i> , EMD35382)	1.58E-65	09:603609-604252	292.67	253.56	140.4	296.75	226.6	153.81
50608	1A	histone h4 ( <i>A. delicata</i> , EJD48157)	9.71E-58	08:1988084-1988576	414.83	384.52	188.7	442.88	341.7	234.99
445928	1A	histone H3 ( <i>S. hirsutum</i> , EIM86446)	8.99E-76	08:2052935-2053645	641.04	533.8	311.8	617.11	470.4	384.6
164342	1A	nucleotide excision repair, TFIIH, subunit TTDA	no hit	13:1164284-1164749	180.75	149.05	96.9	201.63	153.9	107.83
62555	1A	DNA photolyase (hypothetical protein, <i>S. hirsutum</i> , EIM92518)	0	03:889496-891715	26.06	25.41	10.72	12.48	11.8	9.29
<b>Lipid metabolism (GO:0006629)</b>										
407920	1A	isopentenylidiphosphate isomerase ( <i>S. hirsutum</i> , EIM83515)	1.27E-157	02:3076354-3077377	104.27	106.44	54.26	97.1	105.4	77.56
173594	1A	Lipase, class 3 <sup>b</sup> (No hit)	3.75E-144	05:1804791-1806014	14.19	13.24	3.38	11.77	11.94	5.82
36898	1A	cyclopropane-fatty-acyl-phospholipid synthase ( <i>S. commune</i> , XP003034568)	6.33E-162	05:1511102-1512932	57	44.41	15.57	54.51	43.35	13.57
431593	1A	delta 9-fatty acid desaturase protein ( <i>S. hirsutum</i> , EIM92883)	5.21E-168	01: 1898442-1900505	51.53	36.67	24.47	60.31	51.8	28.11
35715	1A	alpha beta-hydrolase (lipase, class 3) ( <i>S. hirsutum</i> , EIM80306)	2.17E-158	08:247728-249159	133.27	104.48	52.95	87.71	75.04	60.2
322385	1A	sgnh hydrolase ( <i>S. hirsutum</i> , EIM80236)	0	07:1838046-1839834	93.92	77.65	46.51	73.46	95.69	66.25
31013	1A	NUDIX hydrolase	no hit	01: 1964120-1965185	152.03	134.14	86.31	174.44	167.4	120.02
<b>Metabolism (GO:0044710)</b>										
330758	1A	aldehyde dehydrogenase ( <i>S. hirsutum</i> , EIM83734)	0	13:214835-216772	1163.1	1318.8	343.6	753.68	729.5	552.82
385801	1A	ferrochelatae ( <i>C. subvermispora</i> , EMD37920)	0	06:2217158-2218503	108.19	94.7	54.81	121.07	106.1	47.02
380456	1A	arginase ( <i>S. hirsutum</i> , EIM89805)	0	02:2907199-2908674	109.77	90.68	63.56	112.65	141	86.6
385108	1A	carbamoyl-phosphate synthase ( <i>F. radiculosa</i> , CCM03318)	0	06:833595-835187	227.64	193.97	97.55	215.49	203.8	106.5
306580	1A	atp synthase e chain domain-containing protein ( <i>P. carnosus</i> , EKM61435)	1.06E-43	01: 963603-964186	171.97	151.39	85.13	184.7	159.6	101.31
407920	1A	isopentenylidiphosphate isomerase ( <i>S. hirsutum</i> , EIM83515)	1.27E-157	02:3076354-3077377	104.27	106.44	54.26	97.1	105.4	77.56
173594	1A	Lipase, class 3 ( <i>S. hirsutum</i> , EIM81619)	3.75E-144	05:1804791-1806014	14.19	13.24	3.38	11.77	11.94	5.82
36898	1A	cyclopropane-fatty-acyl-phospholipid synthase ( <i>S. commune</i> , XP003034568)	6.33E-162	05:1511102-1512932	57	44.41	15.57	54.51	43.35	13.57
37439	1A	alcohol oxidase ( <i>F. mediterranea</i> , EJD00214)	0	10:264236-266713	104.78	59.58	36.13	87.35	56.86	52.46
431593	1A	delta 9-fatty acid desaturase protein ( <i>S. hirsutum</i> , EIM92883)	5.21E-168	01: 1898442-1900505	51.53	36.67	24.47	60.31	51.8	28.11
35715	1A	alpha beta-hydrolase ( <i>S. hirsutum</i> , EIM80306)	2.17E-158	08:247728-249159	133.27	104.48	52.95	87.71	75.04	60.2

322385	1A	sgnh hydrolase ( <i>S. hirsutum</i> , EIM80236)	0	07:1838046-1839834	93.92	77.65	46.51	73.46	95.69	66.25
31013	1A	NUDIX hydrolase	no hit	01: 1964120-1965185	152.03	134.14	86.31	174.44	167.4	120.02
172384	1B	alpha beta-hydrolase ( <i>S. lacrymans</i> , EGO01493)	5.61E-132	08:813860-815323	55.85	23.98	33.85	146.98	46.3	40.8
107764	1B	alcohol oxidase ( <i>S. hirsutum</i> , EIM82222)	0	09:1238659-1241329	24.94	16.6	17.17	35.27	24.04	15.3
442228	1B	alcohol oxidase ( <i>S. hirsutum</i> , EIM82222)	6.55E-126	12:329163-332048	150.42	45.09	69.87	299.78	95.77	134.64
50643	1B	alpha beta-hydrolase ( <i>G. trabeum</i> , EPQ55736)	1.80E-112	08:812068-813382	5.8	4.15	2.27	10.21	5.14	3.38
326305	1B	alcohol oxidase ( <i>S. hirsutum</i> , EIM82222)	0	09:1224614-1227167	31.66	15.19	9.07	53.66	25.28	32.52
103692	1B	aryl-alcohol oxidase-like protein ( <i>S. hirsutum</i> , EIM83224)	0	07:788111-790721	14.23	12.59	9.15	21.33	16.18	17.82
389280	1B	farnesyl-diphosphate synthase ( <i>C. subvermispora</i> , EMD31540)	7.76E-170	11:58824-60638	315.73	229.26	163.3	423.28	252.3	228.88
435998	1B	hydroxymethylglutaryl-synthase ( <i>S. hirsutum</i> , EIM88708)	0	09:1261763-1263627	305.28	183.36	107.3	393.07	238.3	197.02
151291	1B	alcohol oxidase ( <i>S. hirsutum</i> , EIM82222)	4.57E-88	07:1116342-1119327	24.09	8.28	12.34	55	19.59	26.35

### Reproductive processes (GO:0032504)

181241	1B	hydrophobin ( <i>S. lacrymans</i> , EGO03722)	1.19E-09	11:982325-983748	57.4	26.07	40.44	91.01	60.83	61.06
174682	1B	hydrophobin 2 ( <i>H. annosum</i> , ABA46362)	9.65E-14	11:968625-969535	32.25	9.47	15.21	210.76	100.5	61.24
65822	1C	hydrophobin fungal ( <i>F. mediterranea</i> , EJD00348)	1.41E-22	11:359293-360406	125.09	28.44	238.2	261.52	133.3	233.82
156762	1C	hydrophobin 2 ( <i>H. annosum</i> , ABA46362)	3.64E-16	11:964831-965389	615.36	107.63	1354	1371.6	495.9	1876.1
156763	1C	hydrophobin fungal ( <i>S. lacrymans</i> , EGN92731)	7.23E-11	11:965918-966483	46.94	23.5	78.87	80.75	55.19	76.9
181196	1C	hydrophobin 2 ( <i>M. perniciosus</i> , XP002390201)	1.38E-21	04:1864964-1867328	50.77	10.87	142.2	119.85	68.89	154.3
148469	1C	aegerolysin aa-pri1 ( <i>P. ostreatus</i> , AAL57035)	3.07E-69	04:1415497-1416069	1275.3	268.35	1836	1869.8	723.5	3267.6
38497	1C	erylysin ( <i>P. eryngii</i> , BAI45248)	0	04:1411975-1414021	220.1	82.93	279.1	336.35	163.4	532.1
156203	1C	fruit-body specific gene c ( <i>S. lacrymans</i> , EGN98565)	4.69E-80	05:440823-441637	129.07	64.77	181.2	184.02	97.89	272.7
426840	1C	fruit-body specific gene c ( <i>S. lacrymans</i> , EGN98565)	1.02E-68	05:439416-440272	17.19	8.56	22.42	26.08	16.1	43.58
454740	1C	thaumatin-like protein ( <i>S. commune</i> , XP003030993)	3.61E-24	10:1336937-1337436	14.41	6.8	27.61	32.34	42.24	66.48
412343	2A	phosphatases ii ( <i>S. hirsutum</i> , EIM87605)	5.90E-61	12:1672429-1673177	99.73	153.24	214.5	111.1	115.4	79.61
455911	2B	reductase akor2 ( <i>S. hirsutum</i> , EIM83757)	5.52E-151	13:408258-409807	8.96	12.37	24.8	7.09	9.63	10.59
411410	2B	sex-determining region y protein ( <i>S. hirsutum</i> , EIM91814)	6.79E-58	09:1987766-1988601	9.98	12.38	17.94	5.29	4.95	12.55
181126	2C	no hit (pheromone activity, GO:005186)	no hit	07:849217-849448	125.51	161.96	285.3	91.97	140.4	248.23
181275	2C	no hit (pheromone activity, GO:005186)	x	07:958757-958976	94.54	118.14	191.9	88.9	118.5	215.91
237963	2C	hmg1 protein ( <i>S. hirsutum</i> , EIM85725)	1.09E-144	03:1405832-1407078	85.62	111.76	200	108.28	110.5	145.02
460226	2C	hmg domain-containing protein ( <i>F. pinicola</i> , EIW54712)	9.19E-45	09:190411-192229	92.52	118.87	211.1	67.88	113.5	182.71
438733	2C	c6 transcription factor ( <i>C. subvermispora</i> , EMD40262)	1.85E-176	03:39068-41867	61.92	66.14	137.5	65.66	80.29	136.66
415132	2C	c6 transcription ( <i>R. solani</i> , CCO27576)	2.98E-12	02:2902354-2904013	11.95	9.95	39.67	16.17	12.58	31.15
316848	2C	von willebrand domain-containing protein ( <i>S. hirsutum</i> , EIM90572)	0	04:926698-929840	10.1	11.3	27.49	12.01	13.13	27.29
247090	2C	von willebrand factor ( <i>P. indica</i> , CCA66546)	6.19E-24	05:406388-407103	30.25	31.64	170.3	25.08	31.62	142.44
51894	2C	aquaporin ( <i>F. pinicola</i> , EKM51662)	9.84E-154	05:968216-969844	33.29	25.25	115.8	35.61	28.43	123.12

58543	2C	cgl3 lectin ( <i>L. amethystine</i> , BAJ72707)	0	01:439408-439999	94.25	47.3	947.5	104.44	76.94	1040
33224	2C	hydrophobin 2 ( <i>H. annosum</i> , ABA46362)	5.83E-40	06:277914-278512	437.73	336.89	1063	702.4	416.5	2477.7
104521	2C	hydrophobin fungal ( <i>F. radiculosa</i> , CCM03904)	3.38E-10	08:1919274-1919815	5.51	8.58	14.96	4.73	4.68	44.11
181114	2C	hydrophobin fungal ( <i>G. trabeum</i> , EGO28137)	4.07E-20	03:3245657-3246524	5.92	5.5	59.17	14.78	14.53	192.95

**Proteolysis (GO:0006508)**

67557	1A	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	09:1496495-1498705	77.13	85.84	27.84	40.42	40.16	49.61
453889	1C	Peptidase S9A ( <i>F. pinicola</i> , EGX45765)	1.04E-15	09:221135-224502	110.24	78.26	152.7	160.26	250.3	622.57
155109	2B	peptidase s28 ( <i>G. trabeum</i> , EPQ59204)	0	03:251163-253565	85.75	85.53	164	66.41	56.91	120.23
149096	2B	proline-specific peptidase ( <i>T. versicolor</i> , EIW57650)	3.95E-124	14:205224-206299	36.15	49.52	49.46	33.54	52.88	71.79
148451	2B	acid protease ( <i>G. trabeum</i> , EPQ52745)	0	04:1289530-1291515	526.9	537.09	775.7	368.06	444	537.43
155109	2B	peptidase s28 ( <i>G. trabeum</i> , EPQ59204)	0	03:251163-253565	85.75	85.53	164	66.41	56.91	120.23
44515	2C	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	02:189895-192254	50.29	71.53	220.2	31.46	39.91	103.56
156003	2C	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	08:1296630-1298969	24.19	23.72	45.58	32.25	32.19	44.42
411074	2C	peptidase c14 ( <i>S. hirsutum</i> , EIM89345)	4.08E-56	09:77243-78377	21.73	7.79	76.13	45.61	23.19	86.21
61505	2C	peptidase c1bleomycin hydrolase ( <i>S. hirsutum</i> , EIM82709)	0	06:513799-516147	69.86	73.16	150.1	74.91	84.09	134.11
127284	2A	family s53 protease ( <i>S. hirsutum</i> , EIM82265)	0	04:620130-622362	101.03	156.5	76.73	39.96	53.89	58.49
64560	2A	subtilisin-like proteases ( <i>S. hirsutum</i> , EIM86482)	0	08:1947169-1949597	252.38	310.7	227.6	202.01	158.9	136.82

**Stress (GO:0006950) and response to oxidative stress (GO:0006979)**

331089	1B	apg12-domain-containing protein ( <i>S. hirsutum</i> , EIM83856)	2.72E-63	13:328099-328876	107.29	99.82	67.97	141.36	110.6	91.46
64639	1B	catalase-like protein	no hit	08:2154270-2156882	16.52	17.43	8.34	20.41	25.99	21.82
155921	1B	linoleate diol synthase ( <i>S. hirsutum</i> , EIM86629)	0	08:650189-655077	234.75	70.29	151.8	352.02	166.6	229.13
107765	1B	cytochrome p450 ( <i>S. hirsutum</i> , EIM91248)	1.48E-180	09:1242813-1245113	96.07	34.59	49.85	168.81	61.45	67.35
420958	1B	cytochrome p450 ( <i>F. radiculosa</i> , CCM00085)	2.22E-126	09:1257970-1260405	25.17	15.01	12.62	45.81	25.55	13.11
67496	1B	cytochrome p450 ( <i>C. subvermispora</i> , EMD35209)	0	09:1221790-1223847	291.63	92.92	201	673.84	222.8	328.17
147966	1B	cytochrome p450 ( <i>H. annosum</i> , AAV83804)	0	10:473806-475868	155.96	106.35	145.3	279.41	153.4	203.67
156524	1B	cloroperoxidase ( <i>S. hirsutum</i> , EIM87381)	3.76E-133	10:1317021-1318295	155.64	68.93	106.2	249.74	141.1	154.49
419909	1B	cytochrome p450b	no hit	08:421524-423692	142.7	132.4	101	145.5	172.6	194.8
35202	1B	laccase ( <i>S. hirsutum</i> , EIM85733)	0	03:2845487-2847947	19.66	10.72	9.94	48.02	19.53	14.86
103190	1B	laccase ( <i>S. hirsutum</i> , EIM87621)	0	03:2685901-2688608	17.08	13.55	11.08	34.13	17.3	15
181064	1C	laccase 16 ( <i>S. hirsutum</i> , EIM86036)	0	10:1682568-1685382	56.86	32.96	56.96	104.69	64.63	130.69
151183	2C	cytochrome p450 ( <i>F. pinicola</i> , EPS95222)	0	03:2814908-2817239	39.2	57.32	78.08	40.03	41.12	85.54
317779	2C	cytochrome p450 ( <i>F. pinicola</i> , EPT03915)	1.83E-180	05:2288603-2290847	258.78	391.13	1109	241.13	246.5	731.09
169188	2C	cytochrome p450 ( <i>P. carnosus</i> , EKM61159)	0	06:569916-572105	43.23	52.25	94.1	36.37	52.93	122.29
56910	2C	cytochrome p450 ( <i>P. strigosozonata</i> , EIN09176)	0	14:218067-220325	17.52	21.6	42.63	17.04	19.68	41.71

321457	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM80175)	0	07:918098-920544	14.2	17.36	18.65	14.2	12.93	27.95
101388	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM81706)	2.59E-162	05:2261792-2264033	5.66	4.92	12.97	4.69	4.99	31.38
171924	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM81953)	0	07:406824-409305	11.3	13.45	35.87	13.9	11.63	25.2
171930	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM81953)	0	07:377650-380074	15.65	20.01	44.48	18.72	24.69	30.45
173740	2B	cytochrome p450 ( <i>S. hirsutum</i> , EIM82547)	1.00E-153	10:1781124-1783881	43.45	73.61	83.52	43.49	55.19	80.96
59406	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM92720)	0	01:2328172-2330993	40.18	55.52	164.5	32.4	42.25	72.3
51197	2C	cytochrome p450 ( <i>F. pinicola</i> , EPT03915)	0	06:158322-160526	25.92	23.17	83.05	23.58	23.04	84.93
61157	2C	cytochrome p450 monooxygenase cyp63 ( <i>P. carnos</i> , EKM50591)	0	02:80099-82626	42.34	49.04	84.28	42.65	46.1	56.67
152387	2C	alcohol oxidase (GMC oxidoreductase) ( <i>S. hirsutum</i> , EIM79352)	0	12:108041-111628	119.77	162.02	319	129.38	194.7	259.05
106092	2C	acetoin reductase family protein ( <i>F. mediterranea</i> , EJD00032)	5.29E-82	11:1024687-1025981	26.59	49.68	189.4	23.7	44.08	326.29
327285	2C	clavamate synthase-like protein (antimicrobial activity) ( <i>P. strigosozonata</i> , EIN14715)	2.71E-165	10:1797343-1798839	26.42	30.31	57.08	26.39	27.44	44.51
315329	2C	alpha-ketoglutarate-dependent sulfonate dioxygenase ( <i>P. strigosozonata</i> , EIN10030)	0	04:2673736-2675359	25.47	26.74	85.24	17.35	13.48	110.31
36460	2C	incomplete iron reductase ( <i>S. hirsutum</i> , EIM83963)	0	05:261673-263686	10.89	11.06	34.37	12.25	11.65	32.92
181240	2C	alcohol oxidase ( <i>S. hirsutum</i> , EIM84867)	0	11:1317694-1321133	59.75	44.9	180.1	42.5	58.06	329.09
422965	2C	fmn-linked oxidoreductase ( <i>S. hirsutum</i> , EIM83783)	2.16E-141	13:358971-360350	34.37	49.54	73.47	53.73	67.87	98.1
412581	2C	Aldo/keto reductase ( <i>S. hirsutum</i> , EIM83990)	3.65E-89	13:1128647-1129025	47.67	48.5	105.4	57.02	56.06	40.91
11764	2C	amine oxidase ( <i>E. lata</i> , EMR67970)	0	03:3278146-3279634	11.79	8.29	14.5	8.33	8.16	35.51
382250	2C	nadh-quinone oxidoreductase ( <i>S. hirsutum</i> , EIM87626)	3.42E-126	03:2436865-2438180	252.78	255.73	598.4	319.85	355.6	550.93
125828	2C	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM84866)	4.23E-101	11:1328371-1329819	18.48	33.13	74.83	24.8	25.46	58.52
157104	2C	Homogentisate 12-dioxygenase ( <i>G. trabeum</i> , EPQ53967)	0	04:1101471-1104247	20.77	22.85	40.6	19.91	21.15	30.13
124428	2C	alpha-ketoglutarate-dependent taurine dioxygenase ( <i>S. lacrymans</i> , EGN94276)	4.61E-163	07:729465-730908	4.64	4.49	25.81	5.82	6.5	46.59
457227	2C	FAD/NAD (P,-)binding domain-containing protein ( <i>S. hirsutum</i> , EIM81683)	0	02:105693-108289	73.39	64.23	364.8	87.2	77.14	174.7
154644	2C	sorbitol dehydrogenase (GroES-like protein) ( <i>S. hirsutum</i> , EIM82247)	0	02:104131-105480	29.23	27.31	50.2	35.76	46.08	73.14
35623	2C	iron reductase ( <i>T. versicolor</i> , EIW57052)	0	07:535187-537437	95.05	105.2	221.9	84.56	90.44	145.66
420140	2C	2-nitropropane dioxygenase ( <i>G. trabeum</i> , EPQ56409)	8.54E-116	08:1181837-1183203	81.04	88.96	157.6	90.33	108.6	147.58
165789	2C	laccase ( <i>L. edodes</i> , AET86511)	0	04:2963506-2966090	15.06	16.41	81.44	14.64	13.64	66.26
165788	2C	laccase ( <i>M. giganteus</i> , CBV46340)	0	04:2958641-2961296	30.55	15.17	150.3	55.33	18.71	221.35
181063	2C	laccase ( <i>M. giganteus</i> , CBV46340)	0	09:1927904-1930509	36.42	13.92	178.7	42.56	23.9	232.31
152691	2C	clavamate synthase-like protein (antimicrobial activity) ( <i>S. hirsutum</i> , EIM91457)	0	04:1696289-1697969	204.33	219.51	532.3	198.86	278.8	525.73
440215	2C	fmn-dependent alpha-hydroxy acid dehydrogenase ( <i>S. hirsutum</i> , EIM86179)	0	05:2588159-2590010	20.66	20.56	33.21	21.55	22.16	46.74
458375	2C	FAD/NAD (P)-binding domain-containing protein ( <i>S. hirsutum</i> , EIM80266)	3.93E-61	03:3318109-3320200	11.43	13.12	26.64	11.94	11.66	28.77
181069	2C	manganese peroxidase ( <i>P. ostreatus</i> , BAA33449)	1.06E-116	06:472294-474061	19.93	22.1	59.52	19.87	20.36	92.18
48370	2C	alcohol oxidase-like protein ( <i>S. hirsutum</i> , EIM87866)	0	03:294825-297988	33.31	19.1	73.51	60.32	39.03	119.02
431223	2C	glycoside hydrolase family 43 protein ( <i>T. versicolor</i> , EIW56188)	0	01:62344-65215	23.32	28.74	56.95	17.24	20.24	31
446181	2C	FMN-linked oxidoreductase ( <i>S. hirsutum</i> , EIM83783)	1.84E-174	09:1937521-1938915	19.73	29.96	40.85	21.1	19.75	60.06
420786	2C	fad nad-binding domain-containing protein ( <i>S. lacrymans</i> , EGN95517)	1.35E-122	09:783622-785183	49.53	66.89	96.18	41.49	46.66	79.31

<sup>a</sup> Statistical assessment of GO term enrichment was performed using BLAST2GO (Conesa & Götze, 2008)(Conesa et al., 2005).

<sup>b</sup> Genes were considered DE if they displayed a two-fold change in expression at a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e., FDR  $q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995).

<sup>c</sup> JGI protein identity number.

<sup>d</sup> The differentially expressed genes were clustered based on their expression profile using Gene Cluster version 3.0 identified 6 cluster (Hoon et al., 2004) and named according to Fig. 3.

<sup>e</sup> BLAST2GO (<http://www.blast2go.org>) was used to annotate the DE genes in each cluster.

<sup>f</sup> BLAST Expect values obtained with BLAST2GO. “No hit” indicated that no homologous sequences were detected in any of the databases searched.

<sup>g</sup> Genome location of the DE genes in the annotated *H. irregulare* reference genome (Olson et al., 2012; DOE Joint Genome Institute, JGI, <http://genome.jgi.doe.gov/>). The first two digits represent the chromosome on which the gene is located and the numbers following it indicates the nucleotide position on the chromosome.

<sup>h</sup> Expression value (indicated in RPKM).



**Supplementary Table 8.** DE genes<sup>a</sup> encoding proteins involved in Proteolysis (GO:0006508) involved in IS in *Heterobasidion*.

Prot. Name <sup>b</sup>	Cluster <sup>c</sup>	Putative product or domain <sup>d</sup>	E-Value <sup>e</sup>	Chromosome <sup>f</sup>	IS interactions <sup>g</sup>						
					Com 12h	Com 48h	Com 96h	Incom 12h	Incom 48h	Incom 96h	
<b>Family Aspartic</b>											
148451	2B	acid protease ( <i>G. trabeum</i> , EPQ52745)	0	04:1289530-1291515	526.9	537.09	775.7	368.06	444	537.43	
64456	1B	acid protease ( <i>S. hirsutum</i> , EIM86570)	2.61E-139	08:1665012-1666853	145.83	66.63	111.1	217.13	89.17	116.81	
<b>Family Cysteine</b>											
61505	2C	peptidase c1 bleomycin hydrolase ( <i>S. hirsutum</i> , EIM82709)	0	06:513799-516147	69.86	73.16	150.1	74.91	84.09	134.11	
411074	2C	peptidase c14 ( <i>S. hirsutum</i> , EIM89345)	4.08E-56	09:77243-78377	21.73	7.79	76.13	45.61	23.19	86.21	
<b>Family Serine</b>											
453889	1C	peptidase S9A ( <i>F. pinicola</i> , EGX45765)	1.04E-15	09:221135-224502	110.24	78.26	152.7	160.26	250.3	622.57	
155109	2B	peptidase s28 ( <i>G. trabeum</i> , EPQ59204)	0	03:251163-253565	85.75	85.53	164	66.41	56.91	120.23	
127284	2A	family s53 protease ( <i>S. hirsutum</i> , EIM82265)	0	04:620130-622362	101.03	156.5	76.73	39.96	53.89	58.49	
44515	2C	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	02:189895-192254	50.29	71.53	220.2	31.46	39.91	103.56	
156003	2C	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	08:1296630-1298969	24.19	23.72	45.58	32.25	32.19	44.42	
67557	1A	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	09:1496495-1498705	77.13	85.84	27.84	40.42	40.16	49.61	
64560	2A	family s53 protease ( <i>S. hirsutum</i> , EIM86482)	0	08:1947169-1949597	252.38	310.7	227.6	202.01	158.9	136.82	
<b>Family Proline</b>											
149096	2B	proline-specific peptidase ( <i>T. versicolor</i> , EIW57650)	3.95E-124	14:205224-206299	36.15	49.52	49.46	33.54	52.88	71.79	

<sup>a</sup> Genes were considered DE if they displayed a two-fold change in expression at a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e.,  $FDR\ q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995).

<sup>b</sup> JGI protein identity number.

<sup>c</sup> The differentially expressed genes were clustered based on their expression profile using Gene Cluster version 3.0 identified 6 cluster (Hoon et al., 2004) and named according to Fig. 3.

<sup>d</sup> BLAST2GO (<http://www.blast2go.org>) was used to annotate the DE genes in each cluster.

<sup>e</sup> BLAST Expect values obtained with BLAST2GO. “No hit” indicated that no homologous sequences were detected in any of the databases searched.

<sup>f</sup> Genome location of the DE genes in the annotated *H. irregulare* reference genome (Olson et al., 2012; DOE Joint Genome Institute, JGI, <http://genome.jgi.doe.gov/>). The first two digits represent the chromosome on which the gene is located and the numbers following it indicates the nucleotide position on the chromosome.

<sup>g</sup> Expression value (indicated in RPKM).

**Supplementary Table 9.** Carbohydrate active enzymes DE genes<sup>a</sup> involved in IS in *Heterobasidion*.

Prot ID <sup>b</sup>	Cluster <sup>c</sup>	Putative product or domain <sup>d</sup>	Chromosome <sup>e</sup>	IS interactions <sup>f</sup>						
				Com 12h	Com 48h	Com 96h	Incom 12h	Incom 48h	Incom 96h	
<b>Carbohydrate esterase family 8</b>										
45732	2C	pectin methylesterase (EC 3.1.1.11)	EIM83832, <i>S. hirsutum</i> , 2.29E-13	05:2447471-2448798	7.19	6.63	20.21	3.35	3.69	21.74
24532	2C	pectin methylesterase (EC 3.1.1.11)	EIM92036, <i>S. hirsutum</i> , 1.34E-14	01:3306926-3308207	34.62	38.89	57.9	21.64	28.7	84.89
<b>Carbohydrate esterase family 16</b>										
165050	2C	acetylerase (EC 3.1.1.6)	EIM80926, <i>S. hirsutum</i> , 1.42E-14	14:331157-332824	531.76	518.02	547.1	430.17	430.5	821.72
315263	2C	acetylerase (EC 3.1.1.6)	EGN93505, <i>S. lacrymans</i> , 2.10E-62	04:991582-992161	38.2	41.4	130.2	36.7	34.6	56.4
<b>Glycoside hydrolase 1 family (GH-A<sup>b</sup>)</b>										
52318	2C	Beta-glucosidase (EC 3.2.1.21)	EIM87182, <i>S. hirsutum</i> , 0	10:1467272-1469917	307.76	313.98	500	243.23	323.1	467.71
<b>Glycoside hydrolase 5 family (GH-A<sup>b</sup>)</b>										
66839	2B	Endoglucanase (EC:3.2.1.4)	BAD67544, <i>L. lacteus</i> , 3.96E-166	04:1605377-1607418	743.96	751.75	936.3	383.03	476.2	1201.3
<b>Glycoside hydrolase 12 family (GH-C)</b>										
56987	2B	Endocellulase	EJF57894, <i>D. squalens</i> , 1.68E-10	14:506929-508227	284.52	294.1	493.7	123.7	164.2	608.92
<b>Glycoside hydrolase 15 family (GH-L)</b>										
39327	1C	Glucoamylase (EC 3.2.1.3)	EIN06838, <i>P. strigosozonata</i> , 1.61E-13	13:1173670-1175714	56.93	20.98	82.12	111	41.66	147.04
157474	2C	Glucoamylase (EC 3.2.1.3)	EIN06838, <i>P. strigosozonata</i> , 4.97E-14	09:1250738-1252825	67.18	24.49	211.4	75.82	40.48	224.9
<b>Glycoside hydrolase 16 family (GH-B)</b>										
146178	2C	endo-1,3(4)- beta-glucanase (EC 3.2.1.6)	XP_002472478, <i>G. trabeum</i> , 5.01E-13	05:2364308-2366059	1041.3	1166.7	1828	888.85	1152	1995.3
<b>Glycoside hydrolase 17 family (GH-A)</b>										
476497	2C	Exo-beta-1,3-glucanase	EPQ57352, <i>G. trabeum</i> , 1.88E-17	06:1506351-1507982	54	75.14	944.9	56.59	56.86	442.58

<b>Glycoside hydrolase 18 family (GH-K)</b>										
62145	2C	Chitinase (EC 3.2.1.14)	EIN06697, <i>P. strigosozonata</i> , 4.77E-17	06:2267110-2268698	84.72	95.88	137	71.02	76.39	92.27
149771	2C	Chitinase (EC 3.2.1.14)	EJF66447, <i>D. squalens</i> , 0	01: 2826540-2829119	21.58	25.01	157.7	16.57	19.22	45.51
104184	2C	Chitinase (EC 3.2.1.14)	EIM86911, <i>S. hirsutum</i> , 2.71E-17	08:863224-864796	9.12	10.42	34.27	10.41	8.87	18.09
11431	1B	Chitinase (EC 3.2.1.14)	EIM88472, <i>S. hirsutum</i> , 7.46E-17	03:899898-901373	25.62	16.85	15.78	35.33	18.62	18.6
107336	2C	Chitinase (EC 3.2.1.14)	EIM91351, <i>S. hirsutum</i> , 0	04:2273069-2275310	10.55	10.34	36.87	9.25	7.95	25.45
<b>Glycoside hydrolase 20 family (GH-K)</b>										
33073	2C	N-acetylhexosaminidase (EC 3.2.1.-)	EPQ54821, <i>G. trabeum</i> , 0	05:2506266-2508269	39.08	48.91	170.8	45.97	44.04	114.1
<b>Glycoside hydrolase 28 family (GH-N)</b>										
174466	1C	Polygalacturonase (EC 3.2.1.15)	EJD03462, <i>F. mediterranea</i> , 1.34E-17	11:306877-308482	1.4	0.9	2	5.4	9.9	13.7
<b>Glycoside hydrolase 29 family (GH-none)</b>										
108369	2C	$\alpha$ -L-fucosidase (EC 3.2.1.51)	XP_003035417, <i>S. commune</i> , 0	14:919885-923846	46.42	69.77	381.7	49.28	56	168.54
<b>Glycoside hydrolase 30 family (GH-A)</b>										
474648	2C	GH30 protein	EIM91613, <i>S. hirsutum</i> , 5.97E-12	04:2943017-2944098	71.42	88.31	158.7	62.24	84.36	143.28
63706	2C	Glucosylceramidase (EC 3.2.1.45)	EIM84383, <i>S. hirsutum</i> , 0	07:1056768-1059505	8.65	11.6	85.87	6.76	7.62	40.46
<b>Glycoside hydrolase 31 family (GH-D)</b>										
153387	2C	$\alpha$ -glucosidase (EC 3.2.1.20)	EIM91808, <i>S. hirsutum</i> , 0	09:2100407-2104644	11.45	14.53	21.86	9.85	9.92	18.21
<b>Glycoside hydrolase 35 family (GH-A)</b>										
64765	2C	GH35 protein	EIM81437, <i>S. hirsutum</i> , 0	05:484481-488836	27.84	30	57.07	28.65	29.93	56.27
<b>Glycoside hydrolase 43 family (GH-F)</b>										
431223	2C	$\beta$ -galactosidase (EC 3.2.1.23)	EIW56188, <i>T. versicolor</i> , 0	01: 62344-65215	23.32	28.74	56.95	17.24	20.24	31

<b>Glycoside hydrolase 47 family (GH-none)</b>										
39061	2B	a-mannosidase (EC 3.2.1.113)	EIM88924, <i>S. hirsutum</i> , 0	09:757934-760448	42.09	49.53	56.16	21.79	34.16	52.25
67199	2C	GH47 protein	EIM88924, <i>S. hirsutum</i> , 0	09:371704-374209	10.33	9.88	61.01	11.05	9.36	24.43
<b>Glycoside hydrolase 5 family (GH-A)</b>										
39846	2C	endo-b-1,4-glucanase / cellulase (EC 3.2.1.4)	EIM80701, <i>S. hirsutum</i> , 0	14:379289-383752	97.2	107.67	182.1	83.36	88.86	136.22
181247	2B	endo-b-1,4-glucanase / cellulase (EC 3.2.1.4)	EGO03450, <i>S. lacrymans</i> , 0	12:446511-448311	882.69	1024	921.3	455.6	607.3	1406.4
<b>Glycoside hydrolase 61 family (GH-none)</b>										
181229	2B	GH61 protein A	AFO72232, <i>H. parviporum</i> , 1.60E-11	10:1078454-1079647	192.06	187.73	521.5	71.75	102.1	106.83
63659	2C	GH61 protein H	AFO72237, <i>H. parviporum</i> , 5.08E-14	07:1260362-1262045	1165	1285.3	2119	801.97	859.7	1881.9
<b>Glycoside hydrolase 74 family (GH-none)</b>										
153951	2B	xyloglucanase (EC 3.2.1.151)	EIW65405, <i>T. versicolor</i> , 0	01:2551222-2554556	1562.2	1551.6	1850	722.09	938.6	2203.8
<b>Glycoside hydrolase 79 family (GH-A)</b>										
163514	2C	GH79 protein	EKM58316, <i>P. carmosa</i> , 4.25E-11	04:1964943-1965958	12.79	10.96	20.19	9.3	11.54	26.44
163513	2C	GH79 protein	EIN04212, <i>P. strigosozonata</i> , 1.50E-39	04:1964147-1964818	8.54	6.71	17.7	4.79	5.2	18.1
37002	2C	GH79 protein	EIM91055, <i>S. hirsutum</i> , 0	06:115133-117418	63.93	63.92	130.5	72.93	66.45	86.15
50956	2C	GH79 protein	EGO01544, <i>S. lacrymans</i> , 0	06:175691-177579	19.22	21.12	29.67	15.51	14.95	32.52
<b>Glycoside hydrolase 92 family</b>										
123148	2C	GH92 protein	EMD37640, <i>C. subvermispora</i> , 0	06:1155083-1158989	12.07	13.48	30.12	8.36	8.86	25.36
<b>Glycosyltransferase family 2</b>										
410699	1A	glycosyltransferase family 2 protein	EIN05966, <i>P. strigosozonata</i> , 4.38E-137	08:563565-564903	70.12	64.85	34.58	70.2	63.85	44.22
47229	2B	glycosyltransferase family 2 protein	EIM88048, <i>S. hirsutum</i> , 0	03:575891-577972	18.18	19.63	31.84	10.68	16.75	17.17

<b>Glycosyltransferase family 20</b>										
126558	2C	glycosyltransferase family 20 protein	EIM89014, <i>S. hirsutum</i> , 0	09:361502-364954	89.39	64.03	97.46	53.87	67.45	143.45
<b>Polysaccharide lyase family 1</b>										
149208	2B	PL1 protein	EJD53916, <i>A. delicata</i> , 7.33E-10	09:1907844-1909462	116.39	190.1	107.1	59.03	109.7	336.18
<b>Polysaccharide lyase family 8</b>										
431647	2C	PL8 protein	EIM89219, <i>S. hirsutum</i> , 0	01: 2098007-2100736	24.96	21.79	55.31	28.41	24.41	47.15

<sup>a</sup> Genes were considered DE if they displayed a two-fold change in expression at a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e.,  $FDR\ q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995).

<sup>b</sup> JGI protein identity number.

<sup>c</sup> The differentially expressed genes were clustered based on their expression profile using Gene Cluster version 3.0 identified 6 cluster (Hoon et al., 2004) and named according to Fig. 3.

<sup>d</sup> BLAST2GO (<http://www.blast2go.org>) was used to annotate the DE genes in each cluster. GH = Glycoside hydrolases (EC 3.2.1.-), PL = Polysaccharide lyase (EC 4.2.2.-), CE = Carbohydrate esterase (EC=3.1.-.-) (Classification of these enzymes in families and subfamilies based on amino acid sequence similarities, <http://www.cazy.org/Carbohydrate-Binding-Modules.html>).

<sup>e</sup> Genome location of the DE genes in the annotated *H. irregulare* reference genome (Olson et al., 2012; DOE Joint Genome Institute, JGI, <http://genome.jgi.doe.gov/>). The first two digits represent the chromosome on which the gene is located and the numbers following it indicates the nucleotide position on the chromosome.

<sup>f</sup> Expression value (indicated in RPKM).

**Supplementary Table 10.** Secondary metabolite biosynthetic gene clusters identified in *H. irregulare*<sup>a</sup>.

Type	Chromosome	ClusterFinder probability
Terpene	2: 1200369 - 1224055	-
Terpene	2: 2983033 - 3003993	-
Terpene	3: 630731 - 652411	-
Other	4:31947- 476037	-
Putative	4:586174-756236	0.9497
Terpene	4:1041220-1073884	-
Terpene	4:1333428-1354547	-
Siderophore	4:1654538-1671055	-
Putative	4:1733304-1777559	0.8677
T1pks-terpene	5: 172413 - 364705	0.8424
Terpene	5: 823975 - 844679	-
Terpene	7: 336992 - 537245	0.9609
Putative	7: 767960 - 800584	0.8954
Other	7: 2256362 - 2299692	-
Terpene	8: 34816 - 56502	.
Terpene	9: 1051716 - 1270543	0.9698
Other	10: 1564154 - 1608183	-
Putative	10: 679505 - 724045	0.9831
Putative	11: 2437 - 63957	0.9869
Putative	12: 1428056 - 1618916	0.9418.
Other	12: 1374721 - 1418910	.
Other	12:450725 - 637420	0.9303
Putative	14:100248 - 222863	0.8230
Putative	14: 788691 - 887151	0.9845

<sup>a</sup> The online tool antiSMASH 2.0 (antibiotics and Secondary Metabolite Analysis SHell) were used to identify secondary metabolite biosynthesis gene clusters (Blin et al., 2013).

**Supplementary Table 11.** Cytochrome P450 (CYP) family members that displayed differential expression<sup>a</sup> during IS in *Heterobasidion*.

Name ID <sup>b</sup>	Cluster <sup>c</sup>	Clan <sup>d</sup>	Putative product or domain <sup>e</sup>	Chromosome <sup>f</sup>	IS interactions <sup>g</sup>					
					Com 12h	Com 48h	Com 96h	Incom 12h	Incom 48h	Incom 96h
59406	2C	63	<i>S. hirsutum</i> , EIM92720, 0	01:2328172-2330993	40.18	55.52	164.5	32.4	42.25	72.3
173740	2B	64	<i>S. hirsutum</i> , EIM82547, 1.00E-153	10:1781124-1783881	43.45	73.61	83.52	43.49	55.19	80.96
147966	1B	64	<i>H. annosum</i> , AAV83804, 0	10:473806-475868	155.96	106.35	145.3	279.41	153.4	203.67
327977	1C	64	<i>S. hirsutum</i> , EIM85912, 4.00E-140	11:335026-337353	17.35	9.23	32.54	29.82	15.2	36.23
148210	1A	64	<i>F. radiculosa</i> , CCM02682, 1.78E-156	12:80417-82739	50.45	61.86	9.12	24.47	27.32	14.67
67634	1C	64	<i>C. subvermispora</i> , EMD35209, 0	13:1123080-1125124	86.84	36.14	131.3	160.16	57.29	170.85
56910	2C	64	<i>P. strigosozonata</i> , EIN09176, 0	14:218067-220325	17.52	21.6	42.63	17.04	19.68	41.71
61157	2C	63	<i>P. carnososa</i> , EKM50591, 0	02:80099-82626	42.34	49.04	84.28	42.65	46.1	56.67
151183	2C	534	<i>F. pinicola</i> , EPS95222, 0	03:2814908-2817239	39.2	57.32	78.08	40.03	41.12	85.54
68311	1A	64	<i>S. hirsutum</i> , EIM90723, 0	04:743339-745585	340.44	303.66	193.1	373.55	283.4	186.98
101388	2C	64	<i>S. hirsutum</i> , EIM81706, 2.59E-162	05:2261792-2264033	5.66	4.92	12.97	4.69	4.99	31.38
317779	2C	64	<i>F. pinicola</i> , EPT03915, 1.83E-180	05:2288603-2290847	258.78	391.13	1109	241.13	246.5	731.09
51197	2C	64	<i>S. hirsutum</i> , EIM92720, 0	06:158322-160526	25.92	23.17	83.05	23.58	23.04	84.93
169188	2C	64	<i>P. carnososa</i> , EKM61159, 0	06:569916-572105	43.23	52.25	94.1	36.37	52.93	122.29
171930	2C	64	<i>S. hirsutum</i> , EIM81953, 0	07:377650-380074	15.65	20.01	44.48	18.72	24.69	30.45
171924	2C	64	<i>S. hirsutum</i> , EIM81953, 0	07:406824-409305	11.3	13.45	35.87	13.9	11.63	25.2
124408	1A	64	<i>S. hirsutum</i> , EIM84314, 5.32E-173	07:841649-843790	119.15	160.95	74.57	77.41	89.94	62.6
321457	2C	64	<i>S. hirsutum</i> , EIM80175, 0	07:918098-920544	14.2	17.36	18.65	14.2	12.93	27.95
419909	1B	64	no hit	08:421524-423692	142.7	132.4	101	145.5	172.6	194.8
388185	1A	534	<i>S. hirsutum</i> , EIM88819, 0	09:1057932-1060590	253.65	246.27	121.8	210.08	188.1	141.48
67496	1B	64	<i>C. subvermispora</i> , EMD35209, 0	09:1221790-1223847	291.63	92.92	201	673.84	222.8	328.17
107765	1B	64	<i>S. hirsutum</i> , EIM91248, 1.48E-180	09:1242813-1245113	96.07	34.59	49.85	168.81	61.45	67.35
55663	1C	63	<i>S. hirsutum</i> , EIM80594, 0	09:1255405-1257848	25.74	9.36	21.87	46.75	20.54	29.87

420958	1B	547	<i>F. radiculose</i> , CCM00085, 2.22E-126	09:1257970-1260405	25.17	15.01	12.62	45.81	25.55	13.11
163798	1C	64	<i>C. subvermispota</i> , EMD35209, 2.92E-180	09:385741-387743	22.91	8.54	24.28	44.75	18.52	31.72

<sup>a</sup> Genes were considered DE if they displayed a two-fold change in expression at a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e.,  $FDR\ q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995).

<sup>b</sup> JGI protein identity number.

<sup>c</sup> The differentially expressed genes were clustered based on their expression profile using Gene Cluster version 3.0 identified 6 cluster (Hoon et al., 2004) and named according to Fig. 3.

<sup>d</sup> Clans identified and named according to the cytochrome P450 monooxygenase (CYP) dendrogram generated using UPGMA (Unweighted Pair Group Method with Arithmetic mean) presented in Fig. 7.

<sup>e</sup> BLAST2GO (<http://www.blast2go.org>) was used to annotate the DE genes in each cluster.

<sup>f</sup> Genome location of the DE genes in the annotated *H. irregulare* reference genome (Olson et al., 2012; DOE Joint Genome Institute, JGI, <http://genome.jgi.doe.gov/>). The first two digits represent the chromosome on which the gene is located and the numbers following it indicates the nucleotide position on the chromosome.

<sup>g</sup> Expression value (indicated in RPKM).



154589	2C	elongation factor 3 ( <i>S. hirsutum</i> , EIM90240)	0	02:906829-910413	747.60	813.40	1702.00	798.03	782.00	1243.20
330758	1A	aldehyde dehydrogenase ( <i>S. hirsutum</i> , EIM83734)	0	13:214835-216772	1163.10	1318.80	343.60	753.68	729.50	552.82
384154	1A	hypothetical protein ( <i>F. mediterranea</i> , EJD06958)	5.48E-103	05:1298074-1299437	1088.00	1098.60	406.40	745.14	812.80	437.84
411721	1A	ribosomal protein L34e ( <i>S. hirsutum</i> , EIM87086)	6.55E-42	10:1646488-1647197	762.89	787.12	526.70	725.88	702.6	644.06
153951	2B	glycoside hydrolase family 74 protein ( <i>T. versicolor</i> , EIW65405)	0	01: 2551222-2554556	1562.20	1551.60	1850.00	722.09	938.60	2203.80
33224	2C	hydrophobin 2 ( <i>H. annosum</i> , ABA46362)	5.83E-40	06:277914-278512	437.73	336.89	1063.00	702.40	416.50	2477.70
409213	2C	No hit	No hit	04:2736877-2737258	500.49	604.68	952.20	690.40	620.40	677.46
67496	1B	cytochrome p450 ( <i>C. subvermispora</i> , EMD35209)	0	09:1221790-1223847	291.63	92.92	201.00	673.84	222.80	328.17
472277	1A	hypothetical protein ( <i>G. trabeum</i> , EIM88427)	8.92E-54	03:955176-955680	496.74	379.32	171.40	623.30	573.80	194.64
442522	1C	No hit	No hit	13:553661-554601	613.31	371.09	820.20	621.25	536.30	810.93
482307	1C	predicted protein ( <i>L. bicolor</i> , XP001884826)	4.61E-53	13:1255368-1256154	304.00	93.01	257.70	619.39	259.9	695.72
445928	1A	histone H3 ( <i>S. hirsutum</i> , EIM86446)	8.99E-76	08:2052935-2053645	641.04	533.80	311.80	617.11	470.40	384.60
435860	1B	no hit	No hit	09:655123-656608	398.70	289.70	574.60	609.20	381.10	282.90
418648	1A	OsmC-like protein ( <i>S. hirsutum</i> , EIM82790)	7.59E-73	06:1123392-1124177	290.40	232.16	23.94	603.00	402.80	22.32
326179	1C	hypothetical protein ( <i>S. hirsutum</i> , EIM79660)	2.18E-05	09:120939-121800	341.58	105.36	607.30	597.41	276.60	873.69
306015	1C	gpi-anchored small secreted protein ( <i>G. trabeum</i> , EPQ59019)	1.39E-24	01: 1725943-1726450	288.16	73.25	390.60	588.52	268.10	494.56
151850	2B	carbohydrate-binding module family 1 protein ( <i>D. squalens</i> , EJJF61065)	1.92E-126	05:1174701-1176194	1007	1103.80	1538.00	586.43	618.60	1477.10
446505	2C	hypothetical protein ( <i>C. subvermispora</i> , EMD32530)	1.12E-80	11:793291-794500	359.28	379.27	1082.00	575.57	479.50	1342.30
145292	1A	beta-flanking protein ( <i>T. versicolor</i> , EIW64298)	1.43E-52	01: 1601112-1602224	569.05	545.11	486.60	557.24	687.10	352.69
35909	2A	glutamate decarboxylase ( <i>S. hirsutum</i> , EIM86926)	0	08:800739-802904	526.90	453.30	912.10	550.80	505.10	348.20
437588	2C	hlh domain-containing protein ( <i>F. radiculosa</i> , CCM03782)	2.63E-56	01: 1109903-1110932	713.77	780.22	1013.00	529.31	660.10	940.26
382532	1A	argonaute-like protein ( <i>F. radiculosa</i> , CCM03176)	0	03:3300450-3304714	703.85	701.24	465.40	500.90	634.90	316.83
454193	1B	terpenoid synthase ( <i>A. gallica</i> , EIM91236)	0	09:1246392-1247746	226.62	62.42	71.35	493.98	153.50	158.06
332184	2C	No hit	No hit	14:226734-227127	431.17	442.54	870.80	480.87	588.90	712.06
423383	1A	hypothetical protein ( <i>R. solani</i> , CCO37402)	1.44E-61	14:345625-346350	400.38	506.72	199.20	480.31	536.40	424.35
181227	2C	esterase lipase ( <i>V. volvacea</i> , ABI63599)	3.79E-133	13:904173-905619	554.20	566.84	648.10	470.04	444.60	939.10
430720	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM79696)	1.12E-05	13:507814-508664	148.17	75.69	170.00	465.76	257.80	205.46
181247	2B	glycoside hydrolase family 5 protein ( <i>S. lacrymans</i> , EGO03450)	0	12:446511-448311	882.69	1024.00	921.30	455.60	607.30	1406.40
50608	1A	histone h4 ( <i>A. delicata</i> , EJD48157)	9.71E-58	08:1988084-1988576	414.83	384.52	188.70	442.88	341.70	234.99
408703	1A	No hit	No hit	03:3004366-3005620	508.76	520.51	148.10	435.30	445.40	157.49
165050	2C	carbohydrate esterase family 16 protein ( <i>S. hirsutum</i> , EIM80926)	1.42E-138	14:331157-332824	531.76	518.02	547.10	430.17	430.50	821.72

439831	1A	flagella accessory c family protein(A. woodii, YP005270316)	1.00E-20	05:95467-96217	567.11	599.98	287.70	429.29	578.90	274.06
449857	1B	glutathione s-transferase c-terminal-like protein (C. subvermispora, EMD40126)	1.79E-95	03:1888809-1889968	289.62	168.99	161.80	428.93	249.20	158.37
389280	1B	farnesyl-diphosphate synthase (C. subvermispora, EMD31540)	7.76E-170	11:58824-60638	315.73	229.26	163.30	423.28	252.30	228.88
418625	1A	hypothetical protein (F. mediterranea, EJD02639)	4.17E-52	06:1073148-1074676	421.29	416.71	418.00	420.90	405.10	210.70
146426	2C	carbohydrate-binding module family 12 protein (G. trabeum, EPQ57167)	4.85E-100	06:1865149-1866529	487.73	507.25	1016.00	417.45	477.60	845.26
142593	1B	No hit	No hit	07:1633348-1634826	305.56	233.93	238.70	394.01	449.50	429.31
435998	1B	hydroxymethylglutaryl- synthase (S. hirsutum, EIM88708)	0	09:1261763-1263627	305.28	183.36	107.30	393.07	238.30	197.02
61404	1A	alpha beta-hydrolase (S. hirsutum, EIM85821)	0	05:2001724-2003413	433.92	380.19	207.90	384.48	402.70	237.85
66839	2B	endoglucanase (L. lacteus, BAD67544)	3.96E-166	04:1605377-1607418	743.96	751.75	936.30	383.03	476.20	1201.30
68311	1A	cytochrome p450 (S. hirsutum, EIM90723)	0	04:743339-745585	340.44	303.66	193.10	373.55	283.40	186.98
325943	1A	hypothetical protein (S. hirsutum, EIM88980)	5.04E-06	09:375021-375893	376.20	449.88	160.70	371.91	539.50	152.64
148451	2B	acid protease (G. trabeum, EPQ52745)	0	04:1289530-1291515	526.90	537.09	775.70	368.06	444.00	537.43
477404	1A	endoplasmic reticulum protein (S. lacrymans, EGO03002)	2.65E-96	07:1050185-1051220	334.79	385.43	242.70	362.17	407.70	180.97
406919	1A	RTA1 like protein (P. strigosozonata, EIN13774)	1.96E-97	01: 1938100-1938979	396.24	297.70	199.40	357.95	356.00	188.89
155921	1B	linoleate diol synthase (S. hirsutum, EIM86629)	0	08:650189-655077	234.75	70.29	151.80	352.02	166.60	229.13
454198	1B	No hit	No hit	09:1264900-1265334	246.90	166.51	191.10	350.71	209.9	236.32
108168	1B	nad-binding protein (S. lacrymans, EGN94562)	8.00E-83	13:326254-327597	139.70	40.53	42.58	343.19	103.50	97.32
441440	1A	aldo/keto reductase (S. hirsutum, EIM89119)	4.57E-165	09:657502-658875	296.18	265.72	148.40	341.99	351.20	246.30
38497	1C	erylsin (P. eryngii, BAI45248)	0	04:1411975-1414021	220.10	82.93	279.10	336.35	163.40	532.10
430967	2C	rna-binding protein nrd1 (S. hirsutum, EIM80833)	0	14:227442-230090	337.02	350.34	766.10	324.09	365.70	546.36
382250	2C	nadh-quinone oxidoreductase (S. hirsutum, EIM87626)	3.42E-126	03:2436865-2438180	252.78	255.73	598.4	319.85	355.60	550.93
314168	1A	No hit	No hit	03:903842-904277	184.80	129.18	40.94	317.00	163.10	144.77
428887	1A	histone H3 (L. bicolor, XP001873642)	4.85E-81	08:1988863-1989541	320.33	282.03	157.70	309.51	245.40	174.13
418675	2C	heat shock protein 9 (D. squalens, EJJ65505)	9.34E-33	06:1189110-1189661	210.46	111.46	1081.00	301.81	289.90	752.40
442228	1B	alcohol oxidase (S. hirsutum, EIM82222)	6.55E-126	12:329163-332048	150.42	45.09	69.87	299.78	95.77	134.64
27951	1A	histone-fold-containing protein (C. subvermispora, EMD35382)	1.58E-65	09:603609-604252	292.67	253.56	140.40	296.75	226.60	153.81
410453	1A	RNA-binding domain-containing protein (S. hirsutum, EIM84397)	4.83E-55	07:1024816-1025909	286.62	222.84	139.10	292.57	259.20	137.10
168597	1A	expansin family protein (P. strigosozonata, EIN07546)	2.98E-52	02:391792-392586	213.31	163.47	76.76	285.46	159.40	104.60
438460	1A	3-oxoacid -transferase (S. hirsutum, EIM90116)	0	02:2076829-2079008	396.74	498.38	209.00	283.74	268.20	107.93
406682	1A	No hit	No hit	01: 988840-989158	426.70	388.68	177.70	282.10	312.10	243.65
146875	2B	cysteine peroxiredoxin (S. hirsutum, EIM88567)	1.40E-135	03:1937693-1938786	401.56	532.80	526.80	280.40	336.30	478.90

482290	1B	hypothetical protein ( <i>G. trabeum</i> , EPQ57165)	2.72E-50	13:1228482-1230142	263.06	245.91	97.93	279.62	396.50	337.41
147966	1B	cytochrome p450 ( <i>H. annosum</i> , AAV83804)	0	10:473806-475868	155.96	106.35	145.30	279.41	153.40	203.67
65822	1C	hydrophobin fungal ( <i>F. mediterranea</i> , EJD00348)	1.41E-22	11:359293-360406	125.09	28.44	238.20	261.52	133.30	233.82
314750	1A	nadh dehydrogenaseeata 18kda subunit ( <i>F. pinicola</i> , EPS94997)	1.85E-40	03:2641591-2642151	254.45	213.70	122.10	260.56	232.90	180.06
411342	1C	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM88722)	2.42E-152	09:1554536-1555838	127.44	95.82	164.30	256.37	150.40	166.17
62185	2C	hexose transporter ( <i>S. hirsutum</i> , EIM81067)	0	06:2397600-2401747	338.32	290.73	529.90	255.02	274.60	604.48
438899	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM88397)	2.19E-05	03:903140-903902	159.86	104.33	53.38	251.45	128.80	107.35
442648	1C	helicase SRCAP-like ( <i>D. rerio</i> , XP005173101)	8.09E-30	14:114221-115378	145.27	68.74	163.90	250.37	119.10	265.17
156524	1B	cloroperoxidase ( <i>S. hirsutum</i> , EIM87381)	3.76E-133	10:1317021-1318295	155.64	68.93	106.20	249.74	141.10	154.49
52318	2C	glycoside hydrolase family 1 protein ( <i>S. hirsutum</i> , EIM87182)	0	10:1467272-1469917	307.76	313.98	500.00	243.23	323.10	467.71
317779	2C	cytochrome p450 ( <i>F. pinicola</i> , EPT03915)	1.83E-180	05:2288603-2290847	258.78	391.13	1109.00	241.13	246.50	731.09
305913	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM92751)	8.64E-59	01: 2662103-2663036	320.82	367.97	2080.00	240.82	352.00	934.04
441964	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM84939)	1.34E-126	11:283126-285081	200.82	196.46	977.60	235.16	289.10	412.74
379225	1A	adenylate kinase 1 ( <i>S. hirsutum</i> , EIM82461)	2.33E-157	02:784648-785868	208.42	194.70	94.99	231.06	224.80	139.50
456139	1C	hypothetical protein ( <i>D. squalens</i> , EJJF59002)	8.48E-44	13:1264940-1265750	151.24	96.82	164.50	230.12	131.30	202.59
106513	1A	No hit	No hit	12:618884-619813	258.56	253.76	139.10	223.54	219.70	120.35
409659	1C	No hit	No hit	05:1928057-1928420	164.56	84.5	315.6	219.93	153.30	234.00
64456	1B	acid protease ( <i>S. hirsutum</i> , EIM86570)	2.61E-139	08:1665012-1666853	145.83	66.63	111.10	217.13	89.17	116.81
427791	1C	mismatchedase pair and cruciform dna recognition protein ( <i>C. subvermispora</i> , EMD35035)	1.47E-50	06:1853237-1853771	173.10	42.04	354.20	216.93	166.40	172.50
385108	1A	carbamoyl-phosphate synthase ( <i>F. radiculosa</i> , CCM03318)	0	06:833595-835187	227.64	193.97	97.55	215.49	203.80	106.50
442452	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM83735)	1.22E-128	13:217880-219322	396.28	449.85	152.70	211.28	235.90	242.5
174682	1B	hydrophobin 2 ( <i>H. annosum</i> , ABA46362)	9.65E-14	11:968625-969535	32.25	9.47	15.21	210.76	100.50	61.24
388185	1A	cytochrome p450 ( <i>S. hirsutum</i> , EIM88819)	0	09:1057932-1060590	253.65	246.27	121.80	210.08	188.10	141.48
447006	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM86344)	2.91E-159	13:1274587-1275785	261.21	195.07	100.40	209.64	196.00	161.39
419604	1B	no hit	No hit	07:1633092-1633353	144.00	106.40	95.90	207.90	233.60	210.60
313406	1A	nucleic acid-binding protein ( <i>S. lacrymans</i> , EGO27245)	6.88E-63	03:2142122-2142792	176.90	155.72	97.76	207.36	157.90	148.47
411851	2C	hesp-379-like protein (haustorially expressed secreted proteins) ( <i>T. versicolor</i> , EIW56411)	1.26E-37	11:437625-438689	205.67	161.19	320.10	205.85	154.70	379.53
64560	2A	subtilisin-like protein ( <i>S. hirsutum</i> , EIM86482)	0	08:1947169-1949597	252.38	310.70	227.60	202.01	158.90	136.82
164342	1A	No hit	No hit	13:1164284-1164749	180.75	149.05	96.90	201.63	153.90	107.83
152691	2C	clavamate synthase-like protein (antimicrobiol activity) ( <i>S. hirsutum</i> , EIM91457)	0	04:1696289-1697969	204.33	219.51	532.30	198.86	278.80	525.73

330694	1A	hypothetical protein ( <i>G. trabeum</i> , EPQ51676)	9.86E-49	13:1185906-1186604	187.43	188.42	68.62	198.00	258.80	76.09
248180	1A	hypothetical protein ( <i>S. lacrymans</i> , EGO01268)	5.44E-14	10:1644355-1644634	309.96	364.22	148.20	194.62	241.40	193.77
411679	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM88820)	1.07E-128	10:1433390-1435020	147.77	102.39	227.90	189.46	144.70	259.86
457659	1A	aminotransferase ( <i>S. lacrymans</i> , EMD38205)	0	02:2908929-2911550	248.75	213.62	102.10	187.74	191.8	114.72
324885	1B	nad-p-binding protein ( <i>C. subvermispora</i> , EMD40352)	6.93E-90	09:1248476-1249942	88.34	33.69	44.88	184.78	63.57	46.85
306580	1A	atp synthase e chain domain-containing protein ( <i>P. carnosae</i> , EKM61435)	1.06E-43	01: 963603-964186	171.97	151.39	85.13	184.70	159.60	101.31
156203	1C	fruit-body specific gene c ( <i>S. lacrymans</i> , EGN98565)	4.69E-80	05:440823-441637	129.07	64.77	181.20	184.02	97.89	272.70
472627	1A	Ndufa8 NADH-ubiquinone oxidoreductase complex I 19kd subunit ( <i>S. lacrymans</i> , EGN92038)	1.19E-87	03:1480308-1481213	150.68	144.41	92.05	179.17	155.20	129.81
169836	1A	cytochrome c peroxidase ( <i>S. hirsutum</i> , EIM81294)	0	06:2228660-2230403	196.40	197.83	77.67	177.98	194.40	175.82
66634	2B	No hit	No hit	04:2508628-2510684	210.72	242.77	324.20	176.45	170.20	175.51
40020	2C	DyP-type peroxidase ( <i>S. hirsutum</i> , EIM91696)	0	04:697214-699071	78.08	66.52	235.20	175.83	59.54	359.57
381995	1A	nad dehydrogenase ( <i>L. bicolor</i> , XP001886954)	5.64E-82	03:2094356-2095134	178.21	154.50	89.54	175.66	179.00	116.69
31013	1A	No hit	No hit	01: 1964120-1965185	152.03	134.14	86.31	174.44	167.40	120.02
435711	1A	HSP20-like chaperone ( <i>P. strigosozonata</i> , EIN11790)	2.01E-73	08:2089874-2090581	153.74	128.22	61.80	173.97	310.10	67.27
171688	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM84372)	8.30E-26	07:1039425-1039989	160.32	125.36	317.20	169.80	139.20	314.34
70138	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM84489)	2.35E-63	07:526990-527831	195.34	161.64	90.16	169.45	179.10	119.94
107765	1B	cytochrome p450 ( <i>S. hirsutum</i> , EIM91248)	1.48E-180	09:1242813-1245113	96.07	34.59	49.85	168.81	61.45	67.35
157210	1A	DnaJ-domain-containing protein ( <i>S. hirsutum</i> , EIM90788)	0	04:1867711-1869446	155.39	146.66	86.29	168.41	176.80	104.37
472015	2B	cytochrome P450 monooxygenase ( <i>S. hirsutum</i> , EIM88596)	0	03:505260-507571	219.14	562.09	797.30	167.02	224.50	343.56
415717	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM88110)	2.65E-48	03:1082276-1083476	96.74	62.66	87.55	164.71	115.60	102.32
441111	2C	No hit	No hit	08:1172414-1172935	185.08	193.94	310.20	160.37	182.80	270.95
453889	1C	peptidase S9A ( <i>F. pinicola</i> , EGX45765)	1.04E-15	09:221135-224502	110.24	78.26	152.70	160.26	250.30	622.57
452487	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM81098)	1.12E-106	06:2119494-2120680	122.11	118.53	219.4	161.70	100.5	197.44
67634	1C	cytochrome p450 ( <i>C. subvermispora</i> , EMD35209)	0	13:1123080-1125124	86.84	36.14	131.30	160.16	57.29	170.85
51706	1B	terpenoid synthase ( <i>A. gallica</i> , EIM91236)	2.61E-144	05:300390-301759	58.98	15.97	15.15	158.63	48.77	31.47
156748	2C	alpha beta-hydrolase ( <i>S. hirsutum</i> , EIM84924)	7.78E-122	11:810727-812113	108.73	131.00	250.90	152.45	155.30	198.01
44428	1A	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM89793)	2.67E-178	02:2886588-2888341	135.83	95.33	64.97	152.36	120.20	69.77
28617	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM88228)	7.49E-24	03:1816979-1817319	157.48	152.12	69.70	147.19	134.10	103.32
172384	1B	alpha beta-hydrolase ( <i>S. lacrymans</i> , EGO01493)	5.61E-132	08:813860-815323	55.85	23.98	33.85	146.98	46.30	40.80
440726	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM84585)	2.16E-133	07:583481-585238	278.33	300.11	90.96	146.00	176.10	90.76

419909	1B	no hit	No hit	08:421524-423692	142.70	132.40	101.00	145.50	172.60	194.80
37087	1A	4-hydroxybenzoate polyprenyl transferase ( <i>S. hirsutum</i> , EIM87162)	9.34E-161	10:1581033-1582459	180.85	149.75	83.90	144.99	159.30	67.61
331089	1B	apg12-domain-containing protein ( <i>S. hirsutum</i> , EIM83856)	2.72E-63	13:328099-328876	107.29	99.82	67.97	141.36	110.60	91.46
391411	2C	neutral alkaline nonlysosomal ceramidase ( <i>S. hirsutum</i> , EIM80776)	0	14:386472-391683	150.87	173.37	395.00	141.23	131.70	234.46
49340	2C	ctr copper uptake transporter ( <i>S. hirsutum</i> , EIM84484)	2.25E-60	07:539626-540369	139.53	152.44	529.70	141.20	145.70	280.54
156743	1C	copper radical oxidase ( <i>S. hirsutum</i> , EIM84975)	0	11:775943-779828	102.65	73.52	145.40	140.77	117.90	136.77
440110	1A	predicted protein ( <i>L. bicolor</i> , XP001888164)	2.14E-22	05:1589274-1590261	211.44	226.24	77.78	139.13	214.5	83.36
438993	1A	mitochondrial 50S ribosomal protein L22 ( <i>S. hirsutum</i> , EIM85631)	2.86E-92	03:1240917-1241775	123.43	104.40	71.17	138.92	112.00	89.45
445713	1B	No hit	No hit	08:611615-613250	123.89	76.26	63.81	138.11	102.9	111.81
453765	1B	hypothetical protein ( <i>P. carmosa</i> , EKM52506)	2.63E-08	08:2094771-2095585	95.55	56.88	23.79	137.06	57.73	56.87
442492	1A	hypothetical protein ( <i>D. squalens</i> , EJJ57077)	3.90E-75	13:437134-439032	158.82	160.35	72.44	135.29	103.10	137.99
106838	2C	receptor-activated ca2+-permeable cation channel ( <i>S. hirsutum</i> , EIM91141)	0	04:2362165-2367435	88.17	40.99	239.50	135.28	61.11	235.50
478777	1C	glutathione s-transferase ( <i>S. lacrymans</i> , EGN97111)	1.46E-109	08:2160242-2161157	120.30	94.60	158.80	134.40	175.20	199.40
24876	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM82827)	1.93E-91	06:609863-611138	134.44	132.78	89.64	134.35	126.2	106.75
305458	1A	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM92264)	1.35E-145	01: 1633296-1634591	101.65	70.52	30.33	132.97	105.80	23.30
408540	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM88391)	5.08E-85	03:2184815-2185514	150.22	133.01	81.97	132.45	110.40	68.56
440292	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM79946)	6.66E-05	06:276569-277235	91.14	73.95	177.6	131.52	96.49	114.38
100526	1A	p-loop containing nucleoside triphosphate hydrolase ( <i>G. trabeum</i> , EPQ58104)	1.30E-87	02:2289257-2290298	119.02	92.05	53.43	130.53	116.90	63.63
247266	1B	hypothetical protein ( <i>S. lacrymans</i> , EGO24949)	4.52E-58	01: 2158551-2159108	59.65	20.53	31.19	130.30	43.43	40.24
152387	2C	alcohol oxidase ( <i>S. hirsutum</i> , EIM79352)	0	12:108041-111628	119.77	162.02	319.00	129.38	194.70	259.05
18682	1A	No hit	No hit	04:2375773-2377139	108.4	98.66	56.84	129.17	120.60	74.56
157064	1A	Heat shock protein DnaJ ( <i>T. versicolor</i> , EIW57283)	6.09E-84	04:2475990-2477444	117.71	96.36	67.92	129.10	125.60	60.77
390723	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM83747)	9.07E-28	13:180129-180647	89.62	89.30	177.10	128.81	135.80	113.38
421788	1A	hypothetical protein ( <i>A. bisporus</i> , EKM76846)	1.30E-10	11:52596-53257	128.96	58.81	13.16	125.74	47.60	19.89
431119	1A	hypothetical protein ( <i>A. bisporus</i> , EKM77847)	1.29E-36	14:867288-867849	168.31	161.1	71.60	124.52	147.90	50.47
56987	2B	glycoside hydrolase family 12 protein ( <i>D. squalens</i> , EJJ57894)	1.68E-103	14:506929-508227	284.52	294.10	493.70	123.70	164.20	608.92
51672	1A	expansin family protein ( <i>F. mediterranea</i> , EJC97860)	5.00E-51	05:1498864-1499538	99.95	86.92	35.25	123.49	89.90	57.22
385801	1A	ferrochelataze ( <i>C. subvernispota</i> , EMD37920)	0	06:2217158-2218503	108.19	94.70	54.81	121.07	106.10	47.02
481675	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM87659)	0	12:1482430-1484219	157.87	118.70	62.74	120.96	123.60	195.71
104296	1A	No hit	No hit	08:1242573-1243366	113.08	98.10	44.49	119.98	128.70	37.54

181196	1C	<i>hydrophobin 2 (M. pernicioso, XP002390201)</i>	1.38E-21	04:1864964-1867328	50.77	10.87	142.20	119.85	68.89	154.30
156301	2C	hypothetical protein ( <i>C. subvermispora, EMD40107</i> )	6.74E-138	05:1060070-1061124	168.50	186.50	411.10	118.40	80.80	476.80
412478	1C	aldo/keto reductase ( <i>P. strigosozonata, EIN08741</i> )	0	13:492885-494807	89.33	44.80	263.30	117.92	67.64	149.85
49374	1A	hypothetical protein ( <i>S. hirsutum, EIM88429</i> )	5.50E-46	07:889888-890384	102.32	97.12	58.43	117.13	101.10	77.54
410468	1A	actin-like atpase domain-containing protein ( <i>S. hirsutum, EIM80152</i> )	2.53E-139	07:1108024-1109020	157.05	146.64	77.10	113.12	154.20	80.00
170409	1A	hypothetical protein ( <i>C. subvermispora, EMD40698</i> )	2.64E-23	03:978146-978747	137.70	108.83	64.91	113.05	95.93	109.35
380456	1A	arginase ( <i>S. hirsutum, EIM89805</i> )	0	02:2907199-2908674	109.77	90.68	63.56	112.65	141.00	86.60
482239	2C	aldo/keto reductase ( <i>S. hirsutum, EIM83990</i> )	2.07E-106	13:1127382-1128170	87.95	86.67	160.20	112.44	108.10	92.84
100583	1A	hypothetical protein ( <i>S. hirsutum, EIM90095</i> )	1.63E-21	02:2098124-2098510	95.72	85.13	56.98	111.94	95.37	74.83
105202	2C	S-adenosyl-L-methionine-dependent methyltransferase ( <i>S. hirsutum, EIM90620</i> )	1.66E-146	06:189693-191736	92.98	78.07	211.90	111.55	93.58	200.96
412343	2A	phosphatases ii ( <i>S. hirsutum, EIM87605</i> )	5.90E-61	12:1672429-1673177	99.73	153.24	214.50	111.10	115.40	79.61
39327	1C	glycoside hydrolase family 15 protein ( <i>P. strigosozonata, EIN06838</i> )	1.61E-132	13:1173670-1175714	56.93	20.98	82.12	111.00	41.66	147.04
237963	2C	hmg1 protein ( <i>S. hirsutum, EIM85725</i> )	1.09E-144	03:1405832-1407078	85.62	111.76	200.00	108.28	110.50	145.02
44857	2C	hypothetical protein ( <i>P. carosa, EKM60315</i> )	0	05:2004111-2006189	89.79	102.69	256.10	108.20	99.81	234.42
451809	2C	hypothetical protein ( <i>S. hirsutum, EIM86210</i> )	9.90E-130	05:2621129-2622419	141.90	127.02	418.40	106.74	110.80	325.77
181064	1C	laccase 16 ( <i>S. hirsutum, EIM86036</i> )	0	10:1682568-1685382	56.86	32.96	56.96	104.69	64.63	130.69
58543	2C	cgl3 lectin ( <i>L. amethystine, BAJ72707</i> )	0	01: 439408-439999	94.25	47.30	947.50	104.44	76.94	1040.00
459140	2C	hypothetical protein ( <i>S. hirsutum, EIM84596</i> )	6.11E-37	05:2396044-2397166	80.23	116.25	309.10	104.18	80.59	211.65
147736	1A	UAA transporter ( <i>D. squalens, EJJF63362</i> )	2.97E-164	05:1555815-1557383	107.95	100.79	48.70	103.76	123.60	60.52
445244	2C	hypothetical protein ( <i>T. versicolor, EIW62825</i> )	6.97E-76	06:1221750-1222854	48.77	55.59	142.60	102.92	68.73	54.17
460424	1C	NAD-P-binding protein ( <i>S. hirsutum, EIM88722</i> )	3.06E-151	09:1564197-1565488	50.24	40.29	75.91	102.88	64.78	70.37
314041	1B	hypothetical protein ( <i>S. lacrymans, EGO01877</i> )	0	03:1083564-1086122	52.73	30.00	39.42	101.90	62.22	53.34
330334	2A	hypothetical protein ( <i>G. trabeum, EPQ53120</i> )	8.33E-22	12:705221-705935	63.32	76.20	113.60	97.30	90.34	39.14
407920	1A	isopentenylidiphosphate isomerase ( <i>S. hirsutum, EIM83515</i> )	1.27E-157	02:3076354-3077377	104.27	106.44	54.26	97.10	105.4	77.56
308718	1A	c2-domain-containing protein ( <i>S. hirsutum, EIM82273</i> )	3.66E-25	02:274253-274595	72.78	75.83	40.52	96.83	78.68	77.54
414739	2C	hypothetical protein ( <i>S. hirsutum, EIM90166</i> )	1.05E-91	02:1919934-1921578	74.05	98.67	278.30	96.67	122.00	232.17
157976	2C	opt oligopeptide transporter ( <i>P. strigosozonata, EIN08007</i> )	0	03:3355335-3359116	122.98	148.25	202.20	95.27	111.50	202.49
440111	1A	hypothetical protein ( <i>S. hirsutum, EIM81424</i> )	4.41E-13	05:1591534-1592119	187.87	188.94	72.04	95.09	175.4	68.90
445021	2C	hypothetical protein ( <i>P. strigosozonata, EIN12488</i> )	6.19E-59	05:2346443-2348527	95.55	115.45	545.4	94.70	71.39	358.56
318153	1A	60s ribosomal protein 123 ( <i>P. placenta, XP002471959</i> )	4.42E-78	05:1061912-1063408	83.50	77.10	35.50	92.80	79.90	68.10
241658	1C	hypothetical protein ( <i>S. hirsutum, EIM82013</i> )	6.03E-86	09:1960392-1961369	70.97	55.44	114.70	92.53	68.95	102.10

430926	1A	3-carboxy- -mucoante lactonizing enzyme ( <i>S. hirsutum</i> , EIM80893)	1.48E-122	14:66824-68088	131.70	123.49	62.32	92.19	100.00	62.55
181126	2C	Protein with pheromone activity, GO:005186)	No hit	07:849217-849448	125.51	161.96	285.30	91.97	140.40	248.23
482815	2B	aliphatic nitrilase ( <i>R. solani</i> , CCO28557)	1.16E-175	14:1202875-1204587	209.97	293.37	490.70	91.90	232.20	357.91
181241	1B	hydrophobin ( <i>S. lacrymans</i> , EGO03722)	1.19E-09	11:982325-983748	57.40	26.07	40.44	91.01	60.83	61.06
121347	1C	pleiotropic drug resistance abc transporter ( <i>S. hirsutum</i> , EIM92405)	0	01: 927095-932955	69.55	45.02	64.81	90.50	62.22	77.52
433846	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM91349)	3.81E-42	04:2276564-2277098	95.24	92.88	148.4	90.42	94.17	111.9
420140	2C	2-nitropropane dioxygenase ( <i>G. trabeum</i> , EPQ56409)	8.54E-116	08:1181837-1183203	81.04	88.96	157.60	90.33	108.60	147.58
106207	1A	hmg-i hmg-y dna-binding conserved site protein ( <i>F. radiculosa</i> , CCM06252)	8.10E-35	11:1416171-1416699	30.86	31.86	19.20	90.14	105.30	4.25
37537	1A	sulfate anion transporter ( <i>S. hirsutum</i> , EIM84807)	0	11:302589-305936	95.50	81.74	45.67	89.37	85.89	57.54
181275	2C	Protein with pheromone activity, GO:005186)	no hit	07:958757-958976	94.54	118.14	191.90	88.90	118.50	215.91
165879	2C	No hit	No hit	03:3221770-3222084	55.76	55.19	155.60	88.73	76.34	109.44
471609	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM89736)	2.89E-82	02:3059340-3060642	59.73	50.77	42.81	88.55	58.89	58.18
442718	1A	No hit	No hit	14:539742-540177	103.18	102.54	42.80	88.17	98.56	74.93
474875	2C	6-hydroxy-d-nicotine oxidase ( <i>S. hirsutum</i> , EIM81536)	1.46E-90	05:574606-576316	100.84	110.60	175.80	88.17	87.89	141.77
35715	1A	alpha beta-hydrolase ( <i>S. hirsutum</i> , EIM80306)	2.17E-158	08:247728-249159	133.27	104.48	52.95	87.71	75.04	60.20
37439	1A	alcohol oxidase ( <i>F. mediterranea</i> , EJD00214)	0	10:264236-266713	104.78	59.58	36.13	87.35	56.86	52.46
457227	2C	FAD/NAD (P <sub>i</sub> )-binding domain-containing protein ( <i>S. hirsutum</i> , EIM81683)	0	02:105693-108289	73.39	64.23	364.80	87.20	77.14	174.70
52869	1A	nadh-ubiquinone oxidoreductase kda subunit ( <i>F. radiculosa</i> , CCM02711)	1.09E-30	11:215963-216541	64.39	67.19	37.22	87.01	91.98	65.80
316353	1A	hsp20-like chaperone ( <i>S. hirsutum</i> , EIM91039)	1.58E-55	04:1616942-1617503	77.70	82.70	57.39	86.89	78.52	44.50
408117	2C	stomatin family protein ( <i>S. hirsutum</i> , EIM88053)	0	03:658797-660250	65.75	81.06	137.90	86.35	88.92	126.63
436281	1B	hypothetical protein ( <i>T. versicolor</i> , EIW65002)	2.06E-73	10:1232627-1233841	62.70	27.98	52.93	86.26	40.52	59.80
437991	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM83463)	3.90E-50	01: 2819424-2820774	87.82	128.88	157.60	85.30	85.53	134.74
35623	2C	iron reductase ( <i>T. versicolor</i> , EIW57052)	0	07:535187-537437	95.05	105.20	221.90	84.56	90.44	145.66
106177	2C	No hit	No hit	11:1330021-1330684	56.34	85.89	185.60	84.08	79.04	67.60
149190	1A	No hit	No hit	09:1715978-1716407	107.65	96.12	47.15	83.44	72.27	64.18
39846	2C	glycoside hydrolase family 5 protein ( <i>S. hirsutum</i> , EIM80701)	0	14:379289-383752	97.20	107.67	182.10	83.36	88.86	136.22
481951	2C	phenylacetyl-CoA ligase ( <i>S. hirsutum</i> , EIM79727)	0	13:415642-419296	55.70	56.85	109.10	82.93	68.80	85.17
457467	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM90222)	2.53E-18	02:1844471-1845284	75.97	66.80	144.90	82.73	64.93	148.04
316228	1A	No hit	No hit	04:2925709-2926682	163.35	167.28	27.46	82.45	118.00	52.43
413677	1A	snf7-domain-containing protein ( <i>S. hirsutum</i> , EIM92730)	4.43E-88	01: 2365131-2366178	70.79	74.24	52.05	81.57	77.10	48.69

461146	1C	related to stress response protein rds1p ( <i>S. hirsutum</i> , EIM87668)	1.42E-94	12:1457296-1458593	45.85	19.93	56.47	81.22	43.96	60.78
156763	1C	<i>hydrophobin fungal</i> ( <i>S. lacrymans</i> , EGN92731)	7.23E-11	11:965918-966483	46.94	23.50	78.87	80.75	55.19	76.90
409369	2C	hypothetical protein ( <i>C. subvermispora</i> , EMD40024)	1.96E-04	05:508747-509144	57.75	50.88	99.18	80.59	66.15	119.12
115243	2C	expansin family protein ( <i>P. strigosozonata</i> , EIN07546)	3.82E-60	02:1275587-1277138	84.97	95.48	143.70	79.42	77.76	115.62
238463	1C	hypothetical protein ( <i>S. lacrymans</i> , EGN97899)	1.41E-75	05:1249075-1250438	50.41	16.62	68.27	79.13	44.32	84.93
446121	1B	terpenoid synthase ( <i>A. gallica</i> , AGR34199)	0	09:1234708-1236067	41.20	28.40	29.20	78.50	40.80	44.20
124408	1A	cytochrome p450 ( <i>S. hirsutum</i> , EIM84314)	5.32E-173	07:841649-843790	119.15	160.95	74.57	77.41	89.94	62.60
157474	2C	glycoside hydrolase family 15 protein ( <i>P. strigosozonata</i> , EIN06838)	4.97E-136	09:1250738-1252825	67.18	24.49	211.40	75.82	40.48	224.90
428719	2C	hypothetical protein ( <i>P. strigosozonata</i> , EIN12441)	1.41E-47	08:1300683-1301199	59.22	25.34	352.6	75.61	63.15	257.20
102262	1A	rab5-interacting protein ( <i>S. lacrymans</i> , EGO02134)	3.12E-46	03:66255-66812	70.18	70.10	35.47	75.42	64.25	69.78
61505	2C	peptidase c1bleomycin hydrolase ( <i>S. hirsutum</i> , EIM82709)	0	06:513799-516147	69.86	73.16	150.10	74.91	84.09	134.11
322385	1A	sgnh hydrolase ( <i>S. hirsutum</i> , EIM80236)	0	07:1838046-1839834	93.92	77.65	46.51	73.46	95.69	66.25
173387	1A	50s ribosomal protein l35 ( <i>G. trabeum</i> , EPQ54430)	2.79E-23	05:1201899-1202341	59.69	54.06	30.12	73.01	52.85	46.95
37002	2C	glycoside hydrolase family 79 protein ( <i>S. hirsutum</i> , EIM91055)	0	06:115133-117418	63.93	63.92	130.50	72.93	66.45	86.15
173066	1A	wim-domain-containing protein ( <i>P. carnosae</i> , EKM61412)	1.68E-120	05:360926-362407	75.10	96.98	35.77	72.77	95.39	39.48
469097	1A	hypothetical protein ( <i>A. bisporus</i> , EKV51381)	5.72E-66	01: 2073817-2074613	74.78	61.26	38.35	71.90	63.08	48.37
181229	2B	glycoside hydrolase family 61 protein A ( <i>H. parvaporum</i> , AFO72232)	1.60E-105	10:1078454-1079647	192.06	187.73	521.50	71.75	102.10	106.83
306773	1A	mitotic spindle checkpoint HORMA domain ( <i>S. commune</i> , XP003038822)	3.45E-89	01: 1629620-1630652	76.35	89.39	53.37	71.57	103.60	51.13
242628	1A	glucose-6-phosphate isomerase ( <i>S. hirsutum</i> , EIM86774)	7.33E-73	08:1869101-1869743	71.75	63.33	34.33	71.03	67.18	62.54
62145	2C	glycoside hydrolase family 18 protein ( <i>P. strigosozonata</i> , EIN06697)	4.77E-171	06:2267110-2268698	84.72	95.88	137.00	71.02	76.39	92.27
50287	2C	alpha beta-hydrolase ( <i>S. hirsutum</i> , EIM86754)	5.73E-106	08:482820-484097	132.41	108.12	149.60	70.96	73.90	277.88
240731	2C	staphylococcal nuclease domain-containing protein ( <i>S. hirsutum</i> , EIM81136)	4.43E-129	06:1996279-1997689	59.81	73.77	270.90	70.77	63.66	132.05
42095	1A	cytochrome c oxidase biogenesis protein cmc1-like ( <i>S. hirsutum</i> , EIM92658)	4.37E-28	01: 2258018-2258355	70.16	55.86	33.39	70.60	57.22	25.04
410699	1A	glycosyltransferase family 2 protein ( <i>P. strigosozonata</i> , EIN05966)	4.38E-137	08:563565-564903	70.12	64.85	34.58	70.20	63.85	44.22
418027	1B	homeobox kn domain-containing protein ( <i>S. hirsutum</i> , EIM85813)	2.33E-81	05:2009561-2011559	56.46	33.28	40.97	69.50	47.35	51.79
438103	1A	hypothetical protein ( <i>S. lacrymans</i> , EGN92715)	6.44E-34	01: 3364297-3365258	65.66	67.24	35.01	68.58	67.82	43.03
102028	1A	predicted protein ( <i>F. radiculosa</i> , CCM04376)	1.05E-09	06:1912023-1912484	66.12	52.50	40.79	66.64	52.51	24.36
460226	2C	hmg- protein ( <i>F. pinicola</i> , EIW54712)	9.19E-45	09:190411-192229	92.52	118.87	211.10	67.88	113.50	182.71
452833	1A	No hit	No hit	07:915096-915496	61.54	52.30	19.64	66.62	53.45	44.13
155109	2B	peptidase s28 ( <i>G. trabeum</i> , EPQ59204)	0	03:251163-253565	85.75	85.53	164.00	66.41	56.91	120.23



457678	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM89672)	6.59E-155	02:2996719-2998143	38.77	38.39	154.50	66.10	64.29	60.06
438733	2C	c6 transcription factor ( <i>C. subvermispora</i> , EMD40262)	1.85E-176	03:39068-41867	61.92	66.14	137.50	65.66	80.29	136.66
157466	2C	enolase c-terminal domain-like protein ( <i>S. hirsutum</i> , EIM88731)	0	09:1203867-1205879	85.78	93.86	133.30	65.61	82.34	125.24
451350	1C	No hit	No hit	05:925720-926547	48.16	27.64	48.21	65.57	43.53	56.19
170564	2C	No hit	No hit	03:1301381-1301639	48.77	31.45	212.30	65.48	47.51	95.80
427131	2C	predicted protein ( <i>L. bicolor</i> , XP 001877254)	1.16E-06	05:1618709-1619527	54.54	17.35	323.10	65.30	49.71	196.40
455697	1C	rcop c3 ( <i>S. hirsutum</i> , EIM87638)	4.49E-145	12:1369899-1372942	48.29	27.36	64.34	65.27	43.06	69.98
475223	1A	c-3 sterol dehydrogenase ( <i>S. hirsutum</i> , EIM81604)	0	05:1288607-1290151	72.99	61.90	34.39	65.12	59.95	49.42
319471	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM81248)	2.02E-35	06:1044466-1045018	50.98	74.07	181.3	64.83	59.87	137.81
156927	1A	nadp+-dependent d-mannitol dehydrogenase ( <i>C. subvermispora</i> , EMD34827)	0	12:564659-566316	81.11	78.52	46.44	64.56	93.47	58.38
456611	1C	hypothetical protein ( <i>S. hirsutum</i> , EIM83609)	0	01: 681302-683593	39.98	18.60	47.59	64.44	35.52	59.43
470555	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM90406)	2.76E-62	02:1292541-1293428	57.34	45.90	36.41	64.02	49.31	32.15
105151	2C	No hit	No hit	05:1615157-1616039	70.25	64.28	99.34	64.00	51.62	119.26
456720	2B	alpha beta-hydrolase ( <i>G. trabeum</i> , EJU01112)	0	01: 1226696-1229130	143.96	242.30	596.70	63.44	122.40	162.21
379105	1C	hypothetical protein ( <i>S. lacrymans</i> , EGN95739)	2.04E-35	02:383901-384721	38.58	26.66	50.98	62.69	46.25	45.41
122980	1A	cation efflux protein ( <i>S. hirsutum</i> , EIM82673)	4.94E-137	06:427292-428736	56.69	45.97	27.09	62.59	51.03	38.16
474648	2C	glycoside hydrolase family 30 protein ( <i>S. hirsutum</i> , EIM91613)	5.97E-120	04:2943017-2944098	71.42	88.31	158.70	62.24	84.36	143.28
382357	2A	No hit	No hit	03:2807423-2808073	50.51	47.66	90.34	61.94	86.39	35.16
409190	2C	No hit	No hit	04:2524587-2524911	54.89	63.47	102.70	61.92	57.57	70.53
446319	1C	hypothetical protein ( <i>S. hirsutum</i> , EIM87372)	7.17E-43	10:1228951-1230906	35.91	18.72	53.45	61.33	23.72	58.44
307623	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM92716)	8.09E-128	01: 2319476-2322278	65.19	57.29	127.8	61.22	59.89	113.59
426980	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM90508)	9.50E-09	05:997215-998891	43.09	47.06	58.64	61.14	47.23	82.89
48370	2C	alcohol oxidase-like protein ( <i>S. hirsutum</i> , EIM87866)	0	03:294825-297988	33.31	19.10	73.51	60.32	39.03	119.02
431593	1A	delta 9-fatty acid desaturase protein ( <i>S. hirsutum</i> , EIM92883)	5.21E-168	01: 1898442-1900505	51.53	36.67	24.47	60.31	51.80	28.11
61380	2C	related to ThiJ/Pfpl family protein ( <i>F. fujikuroi</i> , CCT74659)	3.99E-39	05:2247813-2248715	71.40	53.04	115.4	60.09	64.36	129.45
150109	2C	MFS general substrate transporter ( <i>S. hirsutum</i> , EIM90192)	0	02:1873145-1875229	71.03	56.66	102.80	59.63	50.81	109.46
241884	1A	duf298-domain-containing protein ( <i>S. hirsutum</i> , EIM90283)	6.35E-81	02:1016894-1017968	71.03	73.37	48.46	59.60	74.01	35.53
166543	1A	hypothetical protein ( <i>D. squalens</i> , EJF66861)	4.62E-56	01: 1574755-1576432	60.33	57.02	24.06	59.55	46.44	26.33
420076	1A	cytochrome c and c1 heme-lyase ( <i>S. hirsutum</i> , EIM86676)	1.17E-106	08:894887-895668	54.88	51.07	25.45	59.36	51.54	40.17
149208	2B	polysaccharide lyase family 1 protein ( <i>A. delicata</i> , EJD53916)	7.33E-102	09:1907844-1909462	116.39	190.10	107.10	59.03	109.70	336.18
56575	2A	zinc-binding oxidoreductase ( <i>S. hirsutum</i> , EIM83884)	7.42E-122	13:787116-788527	46.62	51.87	65.85	58.97	47.97	30.27

380619	2C	No hit	No hit	02:3220404-3221022	47.82	29.45	229.7	58.82	45.28	74.44
320366	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM81232)	1.05E-95	06:846592-847601	58.81	68.05	34.39	57.77	60.58	36.78
481195	2C	phospholipase C/P1 nuclease ( <i>S. hirsutum</i> , EIM81917)	2.30E-147	12:303445-304980	55.73	62.03	143.60	57.23	63.16	105.26
452226	1C	no hit	No hit	06:1164104-1164575	33.73	9.13	58.37	57.12	28.82	54.97
412581	2C	aldo/keto reductase ( <i>S. hirsutum</i> , EIM83990)	3.65E-89	13:1128647-1129025	47.67	48.50	105.40	57.02	56.06	40.91
424094	2B	No hit	No hit	01: 1928351-1929530	105.53	109.94	126.00	56.97	74.55	137.34
476497	2C	glycoside hydrolase family 17 protein ( <i>G. trabeum</i> , EPQ57352)	1.88E-173	06:1506351-1507982	54.00	75.14	944.90	56.59	56.86	442.58
243347	2A	hypothetical protein ( <i>S. lacrymans</i> , EGO02924)	4.21E-49	08:186034-186771	55.30	51.80	78.40	56.30	40.00	37.80
379299	1C	FAD/NAD (P,-)binding domain-containing protein ( <i>S. hirsutum</i> , EIM91768)	0	02:995276-997840	55.36	38.95	62.81	56.26	49.82	121.89
442189	1A	hypothetical protein ( <i>C. subvermispora</i> , EMD32502)	6.44E-54	12:43230-45623	93.88	90.41	43.54	56.15	56.10	41.77
436152	2B	ab-hydrolase ( <i>S. hirsutum</i> , EIM87587)	3.97E-110	10:321952-324902	79.74	123.78	138.30	55.84	94.03	231.02
475048	2C	predicted protein ( <i>P. placenta</i> , XP 002473771)	7.91E-161	05:956068-957335	79.26	66.27	282	55.79	67.13	156.68
410440	1A	No hit	No hit	07:958200-958595	46.50	39.22	20.94	55.68	48.18	34.53
165788	2C	laccase ( <i>M. giganteus</i> , CBV46340)	0	04:2958641-2961296	30.55	15.17	150.30	55.33	18.71	221.35
325408	2B	hypothetical protein ( <i>S. hirsutum</i> , EIM89036)	4.61E-55	09:931795-933621	72.61	96.33	122.80	55.24	70.06	87.23
308509	1A	Ribosomeio genesis proteinrx1 ( <i>S. lacrymans</i> , EGN95558)	1.20E-177	02:2816628-2817913	59.56	51.80	24.71	55.23	55.73	45.74
435843	1A	hypothetical protein ( <i>S. lacrymans</i> , EGO03903 )	5.90E-09	09:590743-591085	47.94	47.14	27.25	55.16	50.86	39.55
151291	1B	alcohol oxidase ( <i>S. hirsutum</i> , EIM82222)	4.57E-88	07:1116342-1119327	24.09	8.28	12.34	55.00	19.59	26.35
36898	1A	cyclopropane-fatty-acyl-phospholipid synthase ( <i>S. commune</i> , XP003034568)	6.33E-162	05:1511102-1512932	57.00	44.41	15.57	54.51	43.35	13.57
431496	1C	hypothetical protein ( <i>G. trabeum</i> , EPQ54493)	0	01: 1503902-1506053	23.72	9.64	23.37	54.48	19.27	25.19
126558	2C	glycosyltransferase family 20 protein ( <i>S. hirsutum</i> , EIM89014)	0	09:361502-364954	89.39	64.03	97.46	53.87	67.45	143.45
422965	2C	fmn-linked oxidoreductase ( <i>S. hirsutum</i> , EIM83783)	2.16E-141	13:358971-360350	34.37	49.54	73.47	53.73	67.87	98.10
326305	1B	alcohol oxidase ( <i>S. hirsutum</i> , EIM82222)	0	09:1224614-1227167	31.66	15.19	9.07	53.66	25.28	32.52
409415	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM91596)	8.08E-39	05:738893-740093	51.47	44.16	82.07	53.33	49.09	78.31
106475	1A	hypothetical protein ( <i>G. trabeum</i> , EIM82023)	4.79E-109	12:482030-483303	55.02	39.46	37.86	53.23	48.83	25.50
325458	1A	acyltransferase-domain-containing protein ( <i>G. trabeum</i> , EPQ53267)	1.31E-115	09:1565859-1567298	48.42	44.23	24.98	52.99	47.07	41.45
419923	1A	escrt-ii complex vps25 subunit ( <i>S. hirsutum</i> , EIM90833)	9.61E-109	08:468483-469406	45.01	38.67	25.00	52.97	54.91	35.95
459502	2C	acetoacetyl- synthetase ( <i>S. hirsutum</i> , EIM81306)	0	06:1937372-1940428	42.79	36.34	63.05	52.32	42.02	75.44
58654	2C	alpha beta-hydrolase ( <i>G. trabeum</i> , EPQ60247)	0	01: 738561-741082	57.15	61.38	129.40	52.13	57.00	90.20
416299	1A	mitochondrial carrier ( <i>P. strigosozonata</i> , EIN05961)	2.77E-127	03:2465373-2466835	44.74	44.45	25.37	50.93	44.01	26.84

319809	1B	ctg1 protein ( <i>S. hirsutum</i> , EIM90876)	3.20E-18	06:665304-665792	21.02	17.17	27.08	50.75	36.16	17.73
378076	1A	sm-like ribonucleo protein ( <i>C. puteana</i> , EIW86669)	2.01E-72	01: 2110723-2111511	40.48	36.33	25.53	50.72	47.41	33.97
476583	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM83052)	1.67E-92	06:1652522-1653689	45.91	37.78	71.14	50.34	50.53	68.75
428829	1B	actin-like atpase domain-containing protein ( <i>S. hirsutum</i> , EIM80433)	6.81E-26	08:1769290-1771212	52.82	56.42	33.04	49.85	72.70	54.54
390525	1A	glutamine synthetase/guanido kinase ( <i>S. hirsutum</i> , EIM91588)	5.97E-174	12:1418568-1420214	48.85	37.28	24.52	49.59	47.65	39.91
147254	1A	predicted protein ( <i>L. bicolor</i> , XP 001874555)	1.15E-04	08:383979-384468	53.00	47.85	22.71	49.41	47.08	36.34
108369	2C	glycoside hydrolase family 29 protein ( <i>S. commune</i> , XP003035417)	0	14:919885-923846	46.42	69.77	381.70	49.28	56.00	168.54
316216	2B	ThiJ/Pfpl family protein ( <i>M. acridum</i> , Efy84268)	4.72E-41	04:1959435-1960309	64.48	82.03	112.30	49.21	69.77	83.84
173037	1A	nad-p-binding protein ( <i>G. trabeum</i> , EPQ50952)	3.99E-114	05:269281-270285	57.6	53.57	52.80	49.20	47.42	29.96
452516	2A	No hit	No hit	06:2211772-2212473	37.42	54.98	77.21	49.15	38.33	14.52
156970	2C	MFS general substrate transporter ( <i>S. hirsutum</i> , EIM90062)	0	12:897711-900504	61.62	74.49	93.55	49.03	60.95	89.48
424395	1A	dienelactone hydrolase ( <i>G. trabeum</i> , EPQ61022)	9.50E-09	01: 3168865-3170347	35.16	43.35	27.44	48.91	54.02	26.49
419147	1A	No hit	No hit	07:26515-26873	57.96	50.81	18.87	48.43	39.14	24.89
428514	1A	No hit	No hit	08:347382-348653	38.92	25.33	13.74	48.34	34.13	33.56
442060	2B	hypothetical protein ( <i>S. hirsutum</i> , EIM84062)	2.88E-05	11:877222-877943	63.09	79.99	145.30	48.19	63.66	62.11
156207	2C	duf323 domain-containing protein ( <i>S. hirsutum</i> , EIM81474)	0	05:470970-474602	54.51	60.22	120.90	48.06	60.93	87.01
35202	1B	laccase ( <i>S. hirsutum</i> , EIM85733)	0	03:2845487-2847947	19.66	10.72	9.94	48.02	19.53	14.86
65718	1A	mfs general substrate transporter ( <i>S. lacrymans</i> , EGO00981)	2.96E-141	10:99292-101063	52.15	67.97	30.62	47.93	55.53	51.23
174386	2B	predicted protein ( <i>F. radiculosa</i> , CCM02530)	7.29E-58	11:89860-93744	47.52	56.17	70.70	47.82	35.97	49.72
406591	1A	No hit	No hit	01: 607699-608000	50.85	60.66	21.57	47.74	73.12	36.37
227973	1A	had-like protein ( <i>A. bisporus</i> , EKM80995)	4.15E-103	06:306581-307677	28.49	10.16	1.47	47.61	17.78	4.43
307509	2C	marvel-like domain protein ( <i>S. hirsutum</i> , EIM83567)	4.44E-43	01: 603681-604352	35.56	30.72	81.26	46.97	58.41	46.21
55663	1C	cytochrome p450 ( <i>S. hirsutum</i> , EIM80594)	0	09:1255405-1257848	25.74	9.36	21.87	46.75	20.54	29.87
313698	1A	embryonic polyadenylate-binding protein 2 ( <i>T. versicolor</i> , EIW61854)	3.25E-10	03:1876376-1877437	62.37	58.69	42.18	46.66	56.19	31.33
323021	2C	hypothetical protein ( <i>D. squalens</i> , EJJF64154)	5.95E-67	08:1574337-1575060	39.65	50.14	65.80	46.56	58.97	86.11
475616	1B	NAD-P-binding protein ( <i>T. versicolor</i> , EIW52371)	1.14E-98	05:2360574-2361774	35.11	26.97	14.10	46.38	36.47	39.96
457281	1A	Dolichyl-diphosphooligosaccharide-protein ( <i>S. hirsutum</i> , EIM82457)	4.37E-176	02:692726-694579	44.51	42.84	37.73	46.25	43.64	21.99
449702	1A	protein serine threonine phosphatase 2c ( <i>S. lacrymans</i> , EGO27656)	0	03:1427212-1429072	52.71	51.21	26.47	46.05	47.41	30.56
33073	2C	glycoside hydrolase family 20 protein ( <i>G. trabeum</i> , EPQ54821)	0	05:2506266-2508269	39.08	48.91	170.80	45.97	44.04	114.10
420958	1B	cytochrome p450 ( <i>F. radiculosa</i> , CCM00085)	2.22E-126	09:1257970-1260405	25.17	15.01	12.62	45.81	25.55	13.11
429241	1B	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM88722)	3.61E-143	09:1236384-1237706	21.84	10.96	12.86	45.66	16.08	22.85

411074	2C	peptidase c14 ( <i>S. hirsutum</i> , EIM89345)	4.08E-56	09:77243-78377	21.73	7.79	76.13	45.61	23.19	86.21
409992	2C	No hit	No hit	06:1022110-1022374	29.68	30.22	55.30	45.57	38.47	57.81
61766	2B	hypothetical protein ( <i>S. hirsutum</i> , EIM82767)	6.52E-57	06:1144702-1145443	48.18	66.78	86.77	45.36	46.83	57.18
439691	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM90873)	7.69E-89	04:2182699-2184103	36.47	32.96	84.32	45.17	59.82	65.77
121927	2C	opt oligopeptide transporter ( <i>S. hirsutum</i> , EIM92929)	0	01: 2947469-2950398	61.12	89.26	184.40	45.14	85.72	134.97
442717	2C	No hit	No hit	14:534510-535269	53.38	63.77	103.80	45.09	59.80	96.01
163798	1C	cytochrome p450 ( <i>C. subvermispora</i> , EMD35209)	2.92E-180	09:385741-387743	22.91	8.54	24.28	44.75	18.52	31.72
120415	1B	hypothetical protein ( <i>P. carmosa</i> , EKM51718)	1.82E-15	13:52080-53153	30.74	23.17	20.5	44.44	38.41	42.64
410050	1A	had-like protein ( <i>S. lacrymans</i> , EGN99735)	0	06:1327529-1329396	50.07	59.28	24.45	44.14	41.30	32.59
147857	2C	No hit	No hit	10:1330503-1331164	50.67	49.85	101.40	44.08	42.29	123.62
118433	1C	acyl- n-acyltransferase ( <i>S. hirsutum</i> , EIM87385)	8.33E-27	10:1239918-1241460	35.82	26.82	48.66	44.01	36.88	80.91
243529	1B	predicted protein ( <i>L. bicolor</i> , XP 001878385)	1.72E-16	02:296598-297171	15.73	5.51	3.83	43.83	11.16	7.04
121827	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM83362)	1.79E-46	01: 2586791-2587265	34.76	27.31	15.83	43.67	34.91	27.99
115725	1A	hypothetical protein ( <i>S. lacrymans</i> , EGN99841 )	1.41E-53	06:345385-346054	34.76	27.31	15.83	43.67	34.91	27.99
173740	2B	cytochrome p450 ( <i>S. hirsutum</i> , EIM82547)	1.00E-153	10:1781124-1783881	43.45	73.61	83.52	43.49	55.19	80.96
305690	1A	hypothetical protein ( <i>T. versicolor</i> , EIW53052)	1.69E-45	01: 1199999-1200835	37.82	32.34	18.24	43.28	34.90	26.18
311400	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM89643)	1.62E-27	02:3113833-3114442	51.06	83.05	32.54	42.80	63.84	37.16
320207	1A	hypothetical protein ( <i>P. carmosa</i> , EKM52244)	8.46E-24	06:863088-863704	44.52	31.88	16.76	42.72	32.93	15.29
436431	1A	peroxiredoxin ( <i>S. hirsutum</i> , EIM80687)	4.81E-99	11:129992-131161	51.52	60.41	25.09	42.65	34.53	23.77
61157	2C	cytochrome p450 monooxygenase cyp63 ( <i>P. carmosa</i> , EKM50591)	0	02:80099-82626	42.34	49.04	84.28	42.65	46.10	56.67
181063	2C	laccase ( <i>M. giganteus</i> , CBV46340)	0	09:1927904-1930509	36.42	13.92	178.70	42.56	23.90	232.31
181240	2C	alcohol oxidase ( <i>S. hirsutum</i> , EIM84867)	0	11:1317694-1321133	59.75	44.90	180.10	42.50	58.06	329.09
165026	1A	No hit	No hit	14:423132-423893	35.37	33.80	17.96	41.92	34.17	21.21
27404	1A	nadh:ubiquinone subunit ( <i>F. radiculosa</i> , CCM03270)	8.64E-25	09:755646-756076	39.07	31.68	21.60	41.55	37.58	17.91
245547	2B	rds1 protein ( <i>S. hirsutum</i> , EIM92371)	4.69E-156	07:1215362-1216820	47.84	62.50	104.80	41.51	43.69	43.22
420786	2C	fad nad -binding domain-containing protein ( <i>S. lacrymans</i> , EGN95517)	1.35E-122	09:783622-785183	49.53	66.89	96.18	41.49	46.66	79.31
147294	1A	No hit	No hit	08:666586-666916	36.05	41.93	21.67	41.47	43.31	32.55
317252	1A	duf2205 domain-containing protein ( <i>S. hirsutum</i> , EIM81643)	7.99E-35	05:1265556-1266031	36.76	29.12	20.82	41.30	35.84	26.67
307924	1A	alpha beta-hydrolase ( <i>C. subvermispora</i> , EMD32541)	3.68E-98	01:22345-23602	49.78	70.11	24.80	41.23	48.25	48.20
322707	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM84204)	0	07:1607567-1610525	46.16	60.54	79.22	40.90	46.43	78.35
67557	1A	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	09:1496495-1498705	77.13	85.84	27.84	40.42	40.16	49.61

418029	1A	magnesium-dependent phosphatase-1 ( <i>G. trabeum</i> , EPQ52962)	7.50E-100	05:2029348-2030540	32.89	30.12	11.87	40.36	42.56	21.30
244542	2B	transcriptional regulator prz1 ( <i>S. hirsutum</i> , EIM91502)	1.19E-47	04:2523445-2523858	37.36	49.02	70.73	40.10	45.02	50.09
151183	2C	cytochrome p450 ( <i>F. pinicola</i> , EPS95222)	0	03:2814908-2817239	39.2	57.32	78.08	40.03	41.12	85.54
127284	2A	family s53 protease ( <i>S. hirsutum</i> , EIM82265)	0	04:620130-622362	101.03	156.50	76.73	39.96	53.89	58.49
430054	1B	hypothetical protein ( <i>L. bicolor</i> , EDR05813)	1.16E-05	11:1142618-1144788	48.37	72.66	40.35	39.94	56.91	31.82
68211	2C	plp-dependent transferase ( <i>C. subvermispora</i> , EMD32985)	2.03E-180	14:122377-124598	24.03	18.82	70.33	39.79	30.70	69.33
411690	1A	hypothetical protein ( <i>C. puteana</i> , EIW79636)	9.66E-05	10:1498433-1498958	31.05	27.67	16.64	39.55	33.37	25.15
34584	2C	membrane protein ( <i>P. carnososa</i> , EKM59491)	0	03:1364258-1367668	46.27	52.90	72.97	39.03	47.33	55.37
439710	1A	tpr-like protein ( <i>P. strigosozonata</i> , EIN10949)	4.66E-92	04:2338805-2341263	55.80	64.87	37.32	38.75	50.28	29.47
246092	2C	tpr-like protein ( <i>S. hirsutum</i> , EIM83322)	0	01: 3090988-3092606	50.37	53.52	77.63	38.67	44.41	68.93
103680	1B	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM84803)	7.44E-84	07:823846-825243	23.39	18.73	28.08	38.61	34.11	25.41
436614	2C	No hit	No hit	11:1282305-1283285	31.86	38.88	92.80	38.43	29.98	77.97
146116	2C	alpha beta-hydrolase ( <i>S. hirsutum</i> , EIM91454)	0	02:86370-89724	41.90	47.29	113.80	38.28	37.82	99.19
410753	1C	No hit	No hit	08:792060-792645	20.47	7.77	45.49	38.26	21.41	43.87
442094	2B	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM87945)	4.32E-95	11:1063604-1065070	57.35	175.69	190.20	38.21	66.29	113.67
434304	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM85764)	1.60E-178	05:1818032-1820224	26.19	17.76	63.74	37.49	24.41	68.74
146884	2C	No hit	No hit	03:1972192-1973056	35.28	28.21	65.28	37.31	32.54	81.94
145408	1B	proline-rich protein ( <i>G. trabeum</i> , EPQ60758)	4.13E-50	01: 2156035-2157321	22.49	10.47	10.69	37.25	17.54	14.28
477949	2C	hypothetical protein ( <i>S. lacrymans</i> , EGN93930)	3.31E-75	08:463510-465033	43.33	42.70	76.55	36.91	40.30	64.55
439893	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM81454)	6.26E-106	05:506678-508614	34.56	28.84	64.81	36.91	35.5	68.71
456021	2C	hypothetical protein ( <i>G. trabeum</i> , EPQ52355)	6.73E-58	13:875785-877762	46.19	52.58	131.40	36.87	44.15	76.45
315263	2C	carbohydrate esterase family 16 protein ( <i>S. lacrymans</i> , EGN93505)	2.10E-62	04:991582-992161	38.20	41.40	130.20	36.70	34.60	56.40
169188	2C	cytochrome p450 ( <i>P. carnososa</i> , EKM61159)	0	06:569916-572105	43.23	52.25	94.10	36.37	52.93	122.29
451672	1A	No hit	No hit	05:2027226-2028116	29.81	20.38	8.27	36.21	24.46	13.27
461150	1A	predicted protein ( <i>P. placenta</i> , XP002468905)	2.64E-45	12:1478870-1479628	39.55	42.16	14.35	36.19	38.39	16.32
432303	2C	fas1 domain-containing protein ( <i>S. hirsutum</i> , EIM82540)	3.99E-83	02:1598906-1601288	25.82	23.81	62.60	36.06	38.65	32.49
443382	1A	hypothetical protein ( <i>P. indica</i> , CCA72793)	5.05E-45	02:54612-56023	29.99	29.65	17.93	36.02	29.51	28.39
449746	1C	nad-dependent formate dehydrogenase ( <i>C. subvermispora</i> , BAF98207)	0	03:1557871-1559648	21.98	10.97	25.55	35.99	14.91	47.91
154644	2C	sorbitol dehydrogenase (GroES-like protein) ( <i>S. hirsutum</i> , EIM82247)	0	02:104131-105480	29.23	27.31	50.20	35.76	46.08	73.14
101911	1A	No hit	No hit	06:1546794-1547577	32.92	28.9	12.89	35.63	35.18	19.75
51894	2C	aquaporin ( <i>F. pinicola</i> , EKM51662)	9.84E-154	05:968216-969844	33.29	25.25	115.80	35.61	28.43	123.12

460997	1B	hypothetical protein ( <i>A. delicata</i> , EJD41680)	6.52E-06	12:332469-333085	6.74	2.62	3.66	35.42	7.12	18.89
11431	1B	glycoside hydrolase family 18 protein ( <i>S. hirsutum</i> , EIM88472)	7.46E-171	03:899898-901373	25.62	16.85	15.78	35.33	18.62	18.60
107764	1B	alcohol oxidase ( <i>S. hirsutum</i> , EIM82222)	0	09:1238659-1241329	24.94	16.60	17.17	35.27	24.04	15.30
455051	1A	No hit	No hit	11:652787-653527	44.19	51.43	38.30	35.14	39.18	22.70
47313	1B	compass-shg1 domain-containing protein ( <i>G. trabeum</i> , EPQ59615)	5.25E-42	03:2077785-2078345	26.27	22.05	17.64	35.00	25.48	28.72
389554	1A	RCC1/BLIP-II ( <i>S. hirsutum</i> , EIM86894)	0	11:718491-720662	33.59	27.33	17.42	34.71	32.42	22.51
328280	1C	plant expansin ( <i>S. hirsutum</i> , EIM82407)	3.53E-39	11:139101-139832	8.86	7.73	8.09	34.67	59.50	76.90
434290	2C	No hit	No hit	05:1701579-1702089	23.68	23.49	59.27	34.65	29.69	49.17
456226	1A	hypothetical protein ( <i>B. assiana</i> , EJP66168)	1.03E-54	14:163190-164064	35.12	40.72	17.33	34.57	33.54	23.85
324730	2B	chitin binding ( <i>A. delicata</i> , EJD46113)	1.16E-79	08:454457-455495	62.91	52.84	95.54	34.39	39.01	90.80
454290	1A	SET domain-containing protein ( <i>S. hirsutum</i> , EIM91996)	1.73E-58	09:1671025-1672594	31.68	40.45	28.13	34.22	34.92	15.59
152933	2C	hypothetical protein ( <i>F. mediterranea</i> , EJD05897)	1.01E-08	09:1208580-1209783	37.91	40.87	105.40	34.19	42.32	91.33
103190	1B	laccase ( <i>S. hirsutum</i> , EIM87621)	0	03:2685901-2688608	17.08	13.55	11.08	34.13	17.30	15.00
458434	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM90791)	2.42E-34	04:582739-584195	15.13	7.70	9.38	34.07	15.38	18.67
156610	2B	MFS general substrate transporter ( <i>S. hirsutum</i> , EIM82651)	0	10:728943-731313	46.28	71.60	76.45	33.77	44.89	111.31
473550	1A	No hit	No hit	03:3108784-3109276	33.80	34.46	19.23	33.76	33.89	15.95
385524	1A	d-lactaldehyde dehydrogenase ( <i>S. hirsutum</i> , EIM85307)	1.80E-154	06:1716612-1718153	46.85	53.23	27.52	33.74	35.52	22.53
149096	2B	proline-specific peptidase ( <i>T. versicolor</i> , EIW57650)	3.95E-124	14:205224-206299	36.15	49.52	49.46	33.54	52.88	71.79
322797	2C	No hit	No hit	07:1149330-1149657	19.63	24.64	41.84	33.54	29.47	42.7
106900	1A	No hit	No hit	04:2551612-2551988	35.3	45.32	6.91	33.43	43.05	15.44
39076	2C	glutathione S-transferase ( <i>S. hirsutum</i> , EIM92344)	3.43E-163	09:796335-797844	41.43	75.27	149.70	33.28	36.95	84.65
434918	2C	duf803-domain-containing protein ( <i>S. hirsutum</i> , EIM81323)	0	06:2319551-2322622	28.43	34.31	52.92	33.22	32.93	37.01
328975	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM80655)	2.63E-20	11:364404-364755	31.13	26.26	9.12	32.99	27.96	21.7
148835	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM84970)	1.39E-96	13:1192009-1193657	23.96	13.67	62.51	32.84	20.98	103.11
243603	1C	developmental regulator medusa ( <i>S. hirsutum</i> , EIM82854)	1.25E-55	06:1022773-1023286	22.17	16.95	41.17	32.64	24.46	34.90
440636	1A	fungal zn -cysinuclear domain-containing protein ( <i>P. strigosozonata</i> , EIN11228)	7.31E-17	06:2335312-2337093	30.42	21.75	12.61	32.55	27.34	24.99
59406	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM92720)	0	01: 2328172-2330993	40.18	55.52	164.50	32.40	42.25	72.30
454740	1C	thaumatin-like protein ( <i>S. commune</i> , XP003030993)	3.61E-24	10:1336937-1337436	14.41	6.80	27.61	32.34	42.24	66.48
477119	2C	NAD-P-binding protein ( <i>T. versicolor</i> , EIW58515)	6.50E-47	07:373065-374084	26.74	22.21	46.03	32.28	34.19	33.60
156003	2C	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	08:1296630-1298969	24.19	23.72	45.58	32.25	32.19	44.42
445342	2C	related to proteophosphoglycan ppg4-leishmaniaraziliensis ( <i>S. hirsutum</i> ,	8.51E-49	06:1965898-1967759	30.34	32.46	59.71	32.23	31.62	55.35

EIM81268)

429158	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM85885)	3.23E-10	09:883938-884621	35.49	21.78	60.05	32.22	30.54	46.11
166634	1A	ribonuclease T1 ( <i>H. erinaceum</i> , BAG15896)	9.20E-45	01: 1773584-1774157	57.86	51.93	4.16	32.15	35.72	8.56
153833	1A	e3 ubiquitin-protein ligase Uhrf1 ( <i>S. hirsutum</i> , EIM92451)	2.97E-108	01: 2086559-2088118	32.77	27.90	17.74	32.00	22.46	16.35
460782	2B	immunomodulatory protein ( <i>F. mediterranea</i> , EJD00474)	1.84E-17	11:399645-400730	38.44	52.68	52.46	31.97	45.89	101.35
454655	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM87318)	7.14E-16	10:1006967-1008660	37.10	40.04	17.59	31.89	31.26	26.70
157732	2C	oligopeptide transporter ( <i>S. hirsutum</i> , EIM85116)	0	14:547467-551325	35.70	43.67	59.33	31.72	35.46	49.45
461401	1A	n2227-domain-containing protein ( <i>C. gloeosporioides</i> , EQB59359)	1.76E-78	14:161063-162628	26.12	24.49	13.38	31.60	27.10	20.18
321340	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM83983)	6.61E-78	06:1707402-1708568	19.41	9.71	14.11	31.47	15.79	21.00
44515	2C	family s53 protease ( <i>S. hirsutum</i> , EIM82266)	0	02:189895-192254	50.29	71.53	220.20	31.46	39.91	103.56
156655	2B	FAD/NAD (P <sub>i</sub> )-binding domain-containing protein ( <i>S. hirsutum</i> , EIM80609)	0	11:8014-10249	38.87	58.77	70.46	31.44	39.85	61.26
144228	1A	No hit	No hit	04:1987171-1987591	27.57	23.68	11.64	30.92	25.34	14.56
331517	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM91931)	6.84E-40	13:929478-930624	35.43	29.39	20.13	30.65	27.12	17.59
384935	2B	huwe1 protein ( <i>S. hirsutum</i> , EIM82707)	0	06:529359-541596	43.45	47.98	61.66	30.61	46.00	53.11
437243	1C	No hit	No hit	14:107176-108268	17.05	12.03	21.36	30.6	26.47	28.82
434783	1A	NmrA family protein ( <i>S. hirsutum</i> , EIM83982)	0	06:1704700-1705934	38.24	39.24	18.85	30.16	30.27	16.49
119119	1C	No hit	No hit	12:334081-334710	17.95	8.34	29.45	30.04	22.36	30.74
327977	1C	cytochrome p450 ( <i>S. hirsutum</i> , EIM85912)	4.00E-140	11:335026-337353	17.35	9.23	32.54	29.82	15.20	36.23
479494	1A	No hit	No hit	09:1716327-1718379	40.97	33.91	17.86	29.51	25.80	25.32
146885	1C	No hit	No hit	03:1984103-1984835	14.41	6.95	16.00	29.48	7.68	25.51
107456	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM88963)	9.31E-04	09:337771-338937	28.69	23.83	13.55	29.34	23.90	22.35
447732	1B	hypothetical protein ( <i>D. squalens</i> , EJF67266)	3.11E-07	01: 1869096-1869517	27.28	18.03	14.04	29.30	21.96	16.27
477447	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM87253)	7.43E-14	07:1148938-1149385	19.04	20.10	41.06	29.19	28.53	41.79
64765	2C	glycoside hydrolase family 35 protein ( <i>S. hirsutum</i> , EIM81437)	0	05:484481-488836	27.84	30.00	57.07	28.65	29.93	56.27
327286	1B	phosphoglycerate mutase-like protein ( <i>S. hirsutum</i> , EIM86685)	0	10:1264341-1266133	12.27	13.28	5.49	28.43	21.52	54.21
431647	2C	polysaccharide lyase family 8 protein ( <i>S. hirsutum</i> , EIM89219)	0	01: 2098007-2100736	24.96	21.79	55.31	28.41	24.41	47.15
37102	2C	pleiotropic drug resistance abc transporter ( <i>S. hirsutum</i> , EIM87167)	0	10:1553158-1558598	24.11	17.21	55.77	28.36	34.37	53.49
414046	1A	ring u-box ( <i>P. strigosozonata</i> , EIN13137)	8.45E-52	01:3299093-3299680	29.85	26.69	12.99	28.06	22.83	14.52
458388	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM87399)	6.54E-12	03:3414253-3414853	23.18	20.17	10.83	28.05	25.25	25.7
148438	2C	general substrate transporter ( <i>P. carmosa</i> , EKM53797)	0	04:1077772-1080058	35.94	38.88	63.50	27.84	28.84	75.33
432387	2B	ARM repeat-containing protein ( <i>P. strigosozonata</i> , EIN07478)	1.40E-125	02:1922703-1926095	29.40	41.45	56.10	27.81	29.56	27.80

104518	1A	No hit	No hit	08:1913795-1914380	26.43	20.88	9.88	27.70	24.97	14.18
107369	1C	No hit	No hit	09:98412-99461	20.36	7.40	41.67	27.51	18.48	33.93
474626	2C	hypothetical protein ( <i>P. strigosozonata</i> , EIN10084)	0	04:2897804-2902323	26.69	30.1	76.27	27.31	28.43	55.65
55110	2C	general substrate transporter ( <i>S. lacrymans</i> , EGN98602)	0	04:1601753-1604897	31.47	33.69	86.59	27.24	40.42	96.68
473759	2C	hypothetical protein ( <i>S. lacrymans</i> , EGN99336)	7.62E-06	04:657335-657977	29.50	32.04	51.32	27.24	33.90	44.48
157044	2C	kinase-like protein ( <i>S. hirsutum</i> , EIM91142)	0	04:2360108-2361860	28.67	34.06	56.01	27.07	29.96	49.67
148791	1B	terpenoid synthase ( <i>A. gallica</i> , AGR34199)	0	09:1215593-1216952	12.92	8.43	4.40	26.96	14.70	16.38
165917	1A	No hit	No hit	03:3057855-3058234	30.18	34.76	10.30	26.82	29.77	6.70
412617	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM87399)	3.46E-10	13:1320597-1321173	20.45	17.40	12.14	26.82	22.70	25.12
409911	2C	No hit	No hit	06:664196-664938	22.75	23.7	40.79	26.81	26.73	52.33
415863	1C	hypothetical protein ( <i>S. hirsutum</i> , EIM90791)	6.08E-42	03:1458119-1459619	16.05	10.40	21.10	26.79	16.76	21.84
57251	1A	acetyl- synthetase-like protein ( <i>S. lacrymans</i> , EGO18816)	0	14:788641-792992	26.35	45.26	12.00	26.78	39.07	8.74
46877	1A	polyketide cyclase dehydrase and lipid transport domain ( <i>S. lacrymans</i> , EGN93078)	4.34E-79	03:200575-201430	22.39	24.30	13.19	26.64	25.65	18.50
2786.1	1A	xap5-domain-containing protein ( <i>S. lacrymans</i> , EGN93284)	7.98E-154	02:2611904-2613323	26.14	21.54	12.47	26.47	25.16	15.06
327285	2C	clavamate synthase-like protein (antimicrobiol activity) ( <i>P. strigosozonata</i> , EIN14715)	2.71E-165	10:1797343-1798839	26.42	30.31	57.08	26.39	27.44	44.51
453887	1C	cytochrome c oxidase assembly protein ( <i>F. pinicola</i> , EPT04847)	6.21E-94	09:217087-218504	24.60	19.70	30.70	26.20	31.30	81.40
426840	1C	fruit-body specific gene c ( <i>S. lacrymans</i> , EGN98565)	1.02E-68	05:439416-440272	17.19	8.56	22.42	26.08	16.10	43.58
421637	2A	predicted protein ( <i>L. bicolor</i> , XP 001877463)	5.63E-05	10:1518310-1519707	26.03	32.86	48.94	26.06	30.87	14.39
452225	1C	no hit	No hit	06:1163465-1163840	14.05	3.06	29.99	25.63	18.49	26.40
108448	1A	no hit	No hit	14:659548-660747	41.5	46.60	15.30	25.60	22.10	29.50
165939	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM85598)	0	01: 50251-53313	17.36	13.74	65.20	25.26	22.83	30.85
247090	2C	von willebrand factor ( <i>P. indica</i> , CCA66546)	6.19E-24	05:406388-407103	30.25	31.64	170.30	25.08	31.62	142.44
451052	1A	No hit	No hit	04:2884575-2885303	23.98	18.11	7.55	24.98	18.86	12.80
148402	2C	MFS general substrate transporter ( <i>F. mediterranea</i> , EJD00211)	9.26E-117	04:2452547-2454708	24.11	31.91	42.07	24.87	40.73	53.01
125828	2C	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM84866)	4.23E-101	11:1328371-1329819	18.48	33.13	74.83	24.80	25.46	58.52
413871	2B	No hit	No hit	01: 2846351-2847022	46.06	44.67	46.65	24.79	41.06	49.05
319827	2B	nuclease le1 ( <i>S. hirsutum</i> , EIM79942)	1.27E-135	06:94548-96313	44.93	49.04	56.20	24.68	31.28	36.52
65769	2C	six-hairpin glycosidase ( <i>S. lacrymans</i> , EGN97365)	1.22E-149	11:191581-193534	23.58	23.81	44.62	24.65	27.47	49.52
410823	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM92834)	2.14E-24	08:1230315-1231152	17.92	18.69	132.80	24.62	18.66	126.05
312991	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM88621)	4.25E-68	03:1493538-1494458	21.17	19.79	9.27	24.61	21.95	14.99



148210	1A	cytochrome p450 ( <i>F. radiculosa</i> , CCM02682)	1.78E-156	12:80417-82739	50.45	61.86	9.12	24.47	27.32	14.67
312506	2C	hypothetical protein ( <i>C. subvermispora</i> , EMD40889)	1.89E-96	03:1639206-1640445	21.39	20.65	47.57	24.45	27.80	38.16
50111	1A	fmn-dependent alpha-hydroxy acid dehydrogenase ( <i>S. lacrymans</i> , EGO01300)	0	08:1236785-1238759	14.95	15.89	8.75	24.41	20.21	7.50
446436	1A	hypothetical protein ( <i>P. carmosa</i> , EKM61872)	2.01E-102	11:206889-208763	27.82	25.64	13.88	24.33	25.12	14.63
482450	1A	hypothetical protein ( <i>A. bisporus</i> , EKM81182)	2.68E-49	14:221483-222085	18.81	15.71	7.02	24.32	20.66	7.58
320971	1A	No hit	No hit	06:362570-365655	31.16	35.79	22.27	24.16	30.97	17.84
448126	2C	protein tyrosine phosphatase ( <i>S. hirsutum</i> , EIM92437)	1.12E-67	01: 3122231-3127522	22.74	26.73	56.96	23.83	28.45	23.56
106092	2C	acetoin reductase family protein ( <i>F. mediterranea</i> , EJD00032)	5.29E-82	11:1024687-1025981	26.59	49.68	189.40	23.70	44.08	326.29
436026	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM85293)	6.98E-21	09:1599533-1600251	19.78	19.89	46.24	23.66	22.74	31.23
439855	2B	hypothetical protein ( <i>S. hirsutum</i> , EIM85935)	2.57E-27	05:258131-260217	26.49	36.79	62.33	23.65	37.27	44.24
384394	1C	No hit	No hit	05:1798491-1798764	11.61	15.64	21.23	23.62	23.84	33.58
51197	2C	cytochrome p450 ( <i>F. pinicola</i> , EPT03915)	0	06:158322-160526	25.92	23.17	83.05	23.58	23.04	84.93
314211	2A	No hit	No hit	03:2839913-2840222	30.08	23.21	35.95	23.05	36.23	15.16
101642	1A	No hit	No hit	06:704651-705086	30.02	35.56	5.90	22.51	25.81	9.45
64180	2C	dihydroxyacetone kinase 1 ( <i>S. hirsutum</i> , EIM86916)	0	08:883490-886007	18.3	17.05	45.10	22.44	20.87	37.02
145098	2C	hypothetical protein ( <i>T. versicolor</i> , EIW63855)	1.63E-11	01: 510190-511003	26.68	25.26	45.65	22.43	28.62	44.33
320867	2C	predicted protein ( <i>L. bicolor</i> , XP001873675)	4.69E-64	06:46275-49280	26.13	30.50	49.92	22.42	24.11	45.59
417699	1C	rgs domain-containing protein ( <i>S. hirsutum</i> , EIM85899)	9.67E-141	05:922234-924567	19.21	11.19	33.29	22.32	19.06	23.64
418857	2C	related toluene-light-inducibleli-3 protein ( <i>F. pinicola</i> , EPT04536)	2.84E-95	06:1807501-1808433	15.03	14.19	62.63	22.15	26.00	31.20
440186	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM82329)	2.14E-41	05:2399891-2400889	20.88	26.47	39.57	21.86	21.11	48.99
39061	2B	glycoside hydrolase family 47 protein ( <i>S. hirsutum</i> , EIM88924)	0	09:757934-760448	42.09	49.53	56.16	21.79	34.16	52.25
99048	1A	No hit	No hit	01: 477130-477886	19.60	20.03	7.30	21.72	17.98	12.37
101506	1C	No hit	No hit	06:304284-305320	12.02	5.38	21.19	21.69	9.47	25.00
24532	2C	carbohydrate esterase family 8 protein ( <i>S. hirsutum</i> , EIM92036)	1.34E-141	01: 3306926-3308207	34.62	38.89	57.90	21.64	28.70	84.89
379059	1A	opa3-domain-containing protein ( <i>S. hirsutum</i> , EIM82339)	8.98E-72	02:224032-225170	17.57	18.01	9.57	21.56	18.72	14.67
440215	2C	fmn-dependent alpha-hydroxy acid dehydrogenase ( <i>S. hirsutum</i> , EIM86179)	0	05:2588159-2590010	20.66	20.56	33.21	21.55	22.16	46.74
448449	1B	histone acetyltransferase gcn5 ( <i>F. pinicola</i> , EPT05008)	8.76E-32	02:801755-802215	18.11	11.10	6.77	21.55	17.24	18.18
40579	1A	ribonuclease T2 ( <i>D. squalens</i> , EJF66828)	1.38E-156	01: 1664962-1666259	18.96	13.97	6.42	21.49	16.63	13.6
163075	1A	No hit	No hit	04:2417204-2417523	26.31	18.56	9.36	21.38	21.99	11.33
390472	1A	No hit	No hit	12:1180227-1180551	18.47	16.02	8.03	21.35	16.53	14.15

103692	1B	aryl-alcohol oxidase-like protein ( <i>S. hirsutum</i> , EIM83224)	0	07:788111-790721	14.23	12.59	9.15	21.33	16.18	17.82
169504	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM81282)	5.79E-17	06:1332216-1332830	24.60	20.59	10.3	21.27	20.02	14.2
446181	2C	FMN-linked oxidoreductase ( <i>S. hirsutum</i> , EIM83783)	1.84E-174	09:1937521-1938915	19.73	29.96	40.85	21.10	19.75	60.06
150371	2C	carotenoid ester lipase precursor ( <i>S. lacrymans</i> , EGN97919)	0	05:2493008-2495553	22.58	13.58	458.30	21.08	18.29	387.77
147022	2B	alpha beta-hydrolase ( <i>D. squalens</i> , EJJF60058)	0	03:2919727-2922449	32.18	46.26	57.29	20.99	27.62	41.40
411748	2C	4-oxalocrotonate tautomerase ( <i>C. fuscus</i> , WP002630507)	3.33E-11	10:1836598-1837182	29.52	62.34	122.40	20.85	29.05	79.70
108660	2C	plasma-membrane proton-e ( <i>S. lacrymans</i> , EGN91849)	0	14:14636-19662	18.58	23.25	66.52	20.80	22.08	13.94
172906	1C	wd40 repeat-like protein ( <i>C. subvermispora</i> , EMD30819)	3.03E-159	08:2137127-2141326	23.05	18.55	19.47	20.66	22.04	38.56
415096	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM89817)	3.59E-119	02:2814318-2816040	27.55	31.56	14.66	20.64	23.42	13.79
100036	2C	No hit	No hit	01: 3273848-3275240	23.30	26.47	38.38	20.50	22.03	29.95
64639	1B	No hit	No hit	08:2154270-2156882	16.52	17.43	8.34	20.41	25.99	21.82
461406	2C	hypothetical protein ( <i>S. lacrymans</i> , EGO26162)	7.16E-91	14:183350-186926	21.66	24.45	60.84	20.27	21.92	51.08
442815	2C	hypothetical protein ( <i>R. solani</i> , ELU40704)	7.39E-08	14:1249149-1250519	16.81	25.83	50.65	20.26	31.85	40.01
430508	1A	No hit	No hit	12:1367780-1368694	14.15	17.34	11.28	20.24	16.86	4.92
328172	2C	predicted protein ( <i>F. radiculosa</i> , CCM02015)	2.60E-21	11:137249-138451	15.55	14.74	26.68	20.18	17.21	33.57
429320	1A	No hit	No hit	09:1696329-1697439	21.79	20.82	6.16	20.04	16.34	10.61
60386	1A	aquaporin-like protein ( <i>S. hirsutum</i> , EIM91284)	6.00E-126	02:2360848-2362402	30.83	19.68	11.98	19.99	22.19	19.37
157104	2C	homogentisate 12-dioxygenase ( <i>G. trabeum</i> , EPQ53967)	0	04:1101471-1104247	20.77	22.85	40.60	19.91	21.15	30.13
181069	2C	manganese peroxidase ( <i>P. ostreatus</i> , BAA33449)	1.06E-116	06:472294-474061	19.93	22.10	59.52	19.87	20.36	92.18
480661	1A	No hit	No hit	11:727305-727656	12.64	10.42	3.30	19.74	14.95	12.63
446810	2C	S-adenosyl-L-methionine-dependent methyltransferase ( <i>S. hirsutum</i> , EIM91130)	3.23E-115	12:1430887-1432939	16.48	19.54	27.63	19.67	18.06	33.49
149346	1C	No hit	No hit	01: 285314-286947	13.20	8.33	35.61	19.29	14.67	24.36
449940	2C	No hit	No hit	03:2165981-2167205	22.00	23.48	70.85	19.15	20.86	57.10
321671	1A	transcription factor Rst2 ( <i>S. pombe</i> , NP593288)	9.52E-06	07:228973-229588	27.13	29.50	15.42	18.86	20.89	9.20
447205	2C	No hit	No hit	01: 78915-79686	23.89	24.58	52.98	18.85	24.42	44.16
148861	2C	MFS general substrate transporter ( <i>P. strigosozonata</i> , EIN07491)	9.00E-154	13:878753-881331	19.36	26.46	79.43	18.78	19.29	62.00
171930	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM81953)	0	07:377650-380074	15.65	20.01	44.48	18.72	24.69	30.45
459530	2C	mfs general substrate transporter ( <i>S. hirsutum</i> , EIM81131)	5.39E-174	06:2069918-2072834	15.16	20.04	30.49	18.65	17.67	24.45
166801	1C	No hit	No hit	01: 2133173-2135358	15.80	5.95	13.25	18.56	7.84	19.80
479514	2C	p-loop containing nucleoside triphosphate hydrolase protein ( <i>C. subvermispora</i> , EMD41416)	0	09:1806333-1814783	24.57	31.91	47.32	18.52	23.42	46.50

145724	2C	calcium proton exchanger ( <i>G. trabeum</i> , EPQ57950)	1.48E-178	02:2855420-2857745	20.32	24.52	37.09	18.52	21.44	24.72
315694	2B	No hit	No hit	04:496474-497644	18.74	36.79	37.03	18.16	17.65	17.69
439360	1A	No hit	No hit	03:3075288-3076062	15.92	18.53	16.53	18.15	24.04	8.01
331093	2C	clavaminase synthase-like protein (antimicrobiol activity) ( <i>S. hirsutum</i> , EIM91457)	9.34E-49	13:550598-551190	20.78	14.24	46.41	18.05	14.78	34.85
324683	2B	regulation of carbohydrate metabolism-related protein ( <i>S. hirsutum</i> , EIM86779)	6.56E-112	08:508396-511873	20.97	25.25	33.07	17.99	22.28	25.99
248092	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM80597)	4.94E-26	14:679216-679785	14.95	15.46	34.35	17.71	22.86	29.52
319002	1B	No hit	No hit	05:2533517-2533828	13.50	7.35	5.84	17.62	17.62	14.21
450365	1A	No hit	No hit	04:427816-428726	17.98	13.34	5.81	17.60	13.01	7.27
433932	2C	peroxisomal enoyl-CoA-hydratase ( <i>S. hirsutum</i> , EIM91526)	1.66E-105	04:2845623-2846994	12.88	16.79	32.28	17.54	14.75	36.16
126495	2B	agmatinase( <i>S. lacrymans</i> , EGN97034)	0	09:55064-56659	24.21	32.03	36.94	17.47	21.79	48.98
315329	2C	alpha-ketoglutarate-dependent sulfonate dioxygenase ( <i>P. strigosozonata</i> , EIN10030)	0	04:2673736-2675359	25.47	26.74	85.24	17.35	13.48	110.31
431223	2C	glycoside hydrolase family 43 protein ( <i>T. versicolor</i> , EIW56188)	0	01: 62344-65215	23.32	28.74	56.95	17.24	20.24	31.00
117862	1C	hypothetical protein ( <i>S. hirsutum</i> , EIM86402)	4.61E-08	08:2179884-2181710	14.56	9.24	17.25	17.19	10.66	23.38
56910	2C	cytochrome p450 ( <i>P. strigosozonata</i> , EIN09176)	0	14:218067-220325	17.52	21.60	42.63	17.04	19.68	41.71
246221	2C	hypothetical protein ( <i>F. mediterranea</i> , EJC98082)	3.08E-109	05:1752806-1753813	21.51	25.75	34.32	16.88	23.09	36.64
165326	2C	MFS general substrate transporter ( <i>A. delicata</i> , EJD50788)	0	04:448775-451424	19.82	20.75	34.17	16.86	19.45	53.11
222332	1B	hypothetical protein ( <i>C. subvermispota</i> , EMD34819)	1.49E-24	12:1223889-1224882	9.10	6.61	5.80	16.80	13.97	13.66
320591	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM91156)	2.80E-23	06:265545-267016	12.50	12.34	38.75	16.71	19.53	40.85
244485	2B	regulatory protein cys-3 ( <i>S. hirsutum</i> , EIM92802)	7.94E-29	01: 2910381-2910733	20.44	21.52	37.81	16.68	12.06	28.30
318391	1A	No hit	No hit	05:404792-405868	19.23	24.70	17.72	16.68	21.42	10.52
149771	2C	glycoside hydrolase family 18 protein ( <i>D. squalens</i> , EJJ66447)	0	01: 2826540-2829119	21.58	25.01	157.70	16.57	19.22	45.51
472692	2C	MFS general substrate transporter ( <i>S. hirsutum</i> , EIM88009)	0	03:1572983-1575560	15.76	18.99	47.05	16.25	17.51	39.28
415132	2C	c6 transcription ( <i>R. solani</i> , CCO27576)	2.98E-12	02:2902354-2904013	11.95	9.95	39.67	16.17	12.58	31.15
51087	2C	vwa domain-containing protein ( <i>F. pinicola</i> , XP570901)	1.29E-47	05:270762-275153	14.30	14.95	37.04	16.12	18.06	74.84
313750	2B	ferric reductase transmembrane component 5 ( <i>S. hirsutum</i> , EIM88523)	0	03:2393337-2395631	43.50	50.60	96.50	16.10	24.10	91.90
328204	1B	predicted protein ( <i>L. bicolor</i> , XP 001883307)	5.58E-07	11:1011982-1012270	10.92	8.78	5.75	16.03	11.56	7.91
418419	2C	No hit	No hit	06:474150-474534	13.53	21.43	41.08	15.90	13.38	67.14
321839	1A	gastrula zinc finger protein ( <i>B. maydis</i> , EMD86086)	1.50E-04	07:200826-202108	21.21	20.85	6.70	15.84	18.46	6.76
49391	2C	arad-like aldolase/epimerase ( <i>S. hirsutum</i> , EIM80361)	4.98E-150	07:1020495-1021887	17.80	20.75	48.85	15.76	17.13	49.26
52983	2C	vacuolar calcium ion transporter ( <i>S. hirsutum</i> , EIM84946)	2.63E-177	11:286068-288284	13.62	15.26	40.61	15.64	13.94	24.32

148374	2C	general substrate transporter ( <i>D. squalens</i> , EJF55996)	0	12:1692196-1723258	23.54	27.83	54.15	15.57	16.73	46.41
107006	1A	hypothetical protein ( <i>A. bisporus</i> , EKM77847)	2.53E-26	04:1291823-1292363	16.50	10.14	6.35	15.57	13.20	7.54
50956	2C	glycoside hydrolase family 79 protein ( <i>S. lacrymans</i> , EGO01544)	0	06:175691-177579	19.22	21.12	29.67	15.51	14.95	32.52
11797	2C	MFS general substrate transporter ( <i>S. hirsutum</i> , EIM92326)	1.16E-133	01:3064321-3066640	11.05	5.83	20.15	15.03	9.93	25.08
157171	2C	galactan -beta-galactosidase ( <i>F. mediterranea</i> , EJD04256)	0	04:1666293-1668546	15.97	16.39	27.18	14.96	17.07	34.46
436926	1C	wd40 repeat-like protein ( <i>S. lacrymans</i> , EGN94934)	1.59E-73	12:1412242-1415785	16.52	11.90	15.24	14.86	15.43	29.34
181114	2C	hydrophobin fungal ( <i>G. trabeum</i> , EGO28137)	4.07E-20	03:3245657-3246524	5.92	5.50	59.17	14.78	14.53	192.95
474219	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM84417)	4.15E-98	04:1884463-1886100	25.79	25.46	7.02	14.76	13.59	11.30
165789	2C	laccase ( <i>L. edodes</i> , AET86511)	0	04:2963506-2966090	15.06	16.41	81.44	14.64	13.64	66.26
423795	1A	hypothetical protein <i>S. hirsutum</i> , EIM90730 )	6.55E-42	01:754240-758858	15.94	10.72	5.48	14.42	12.27	7.52
237830	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM80136)	0	07:1142906-1144685	12.45	10.47	44.8	14.35	14.39	24.74
321457	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM80175)	0	07:918098-920544	14.20	17.36	18.65	14.20	12.93	27.95
322995	2B	pkinaase-domain-containing protein ( <i>T. versicolor</i> , EIW56823)	4.39E-177	07:1122192-1123340	22.88	23.94	29.27	14.15	18.18	27.14
412619	1B	hypothetical protein ( <i>G. trabeum</i> , EPQ57139)	6.89E-112	13:1330366-1331515	8.08	7.10	4.50	14.06	13.41	12.58
418272	2C	p-loop containing nucleoside triphosphate hydrolase protein ( <i>S. hirsutum</i> , EIM91903)	8.33E-38	06:40690-42075	16.08	16.02	31.98	13.97	15.86	22.97
460551	2B	hypothetical protein ( <i>S. hirsutum</i> , EIM87477)	3.85E-69	10:741936-743320	14.30	22.31	26.89	13.97	19.79	30.67
101001	1A	abc transporter ( <i>D. squalens</i> , EJF62714)	1.09E-16	02:818011-828329	10.87	7.77	3.94	13.95	10.78	8.44
327415	2C	hydroxymethylglutaryl- lyase ( <i>F. mediterranea</i> , EJD02005)	2.80E-120	10:284348-285798	10.17	13.06	23.19	13.95	15.58	19.48
171924	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM81953)	0	07:406824-409305	11.30	13.45	35.87	13.90	11.63	25.20
247165	2C	hypothetical protein ( <i>S. lacrymans</i> , EGN98316 )	1.72E-40	11:199130-200052	11.71	12.03	22.34	13.77	16.58	27.95
60846	2C	MFS general substrate transporter ( <i>S. hirsutum</i> , EIM90472)	0	02:1329564-1332059	13.07	16.66	30.53	13.15	11.28	23.44
173543	2C	No hit	No hit	05:1599248-1599855	9.70	11.12	39.36	13.15	13.55	31.13
147950	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM87597)	5.33E-37	10:710845-711715	15.32	13.80	34.84	13.00	24.04	30.83
322938	2C	coq5 family (stres,) ( <i>S. lacrymans</i> , EGO04041)	1.56E-156	07:2122585-2124310	13.74	17.18	25.94	12.94	14.94	22.77
428722	2C	FAD/NAD (P,-)binding domain-containing protein ( <i>P. strigosozonata</i> , EIN13002)	4.27E-72	08:1321516-1322281	10.05	8.76	22.11	12.91	9.47	13.29
439366	1C	No hit	No hit	03:3210266-3211373	6.51	2.89	13.50	12.82	6.41	13.16
62555	1A	hypothetical protein ( <i>S. hirsutum</i> , EIM92518)	0	03:889496-891715	26.06	25.41	10.72	12.48	11.80	9.29
422466	2C	zinc-finger-containing protein ( <i>S. lacrymans</i> , EGO29239)	6.66E-28	12:495423-496560	10.42	9.00	29.14	12.26	12.08	13.18
36460	2C	incomplete iron reductase ( <i>S. hirsutum</i> , EIM83963)	0	05:261673-263686	10.89	11.06	34.37	12.25	11.65	32.92
157680	2C	mfs general substrate transporter ( <i>C. subvermispota</i> , EMD33116)	0	14:890364-893235	11.00	10.80	29.62	12.09	14.90	30.47

124191	2C	predicted protein ( <i>L. bicolor</i> , XP001874758)	2.22E-64	03:2966952-2968080	8.77	8.17	30.93	12.09	11.93	30.08
107454	1B	hypothetical protein ( <i>S. hirsutum</i> , EIM88968)	5.60E-14	09:334631-335608	3.84	2.37	1.80	12.06	13.02	5.65
417746	2C	hypothetical protein ( <i>G. trabeum</i> , EPQ54467)	1.18E-41	05:1076919-1079555	13.72	15.04	29.98	12.05	12.77	23.86
316848	2C	von willebrand domain-containing protein( <i>S. hirsutum</i> , EIM90572)	0	04:926698-929840	10.10	11.30	27.49	12.01	13.13	27.29
458375	2C	FAD/NAD (P,-)-binding domain-containing protein ( <i>S. hirsutum</i> , EIM80266)	3.93E-61	03:3318109-3320200	11.43	13.12	26.64	11.94	11.66	28.77
62517	2C	protein kinase response regulator receiver domain-containing protein ( <i>S. hirsutum</i> , EIM88484)	0	03:809695-815527	14.60	16.34	27.55	11.79	14.68	19.81
173594	1A	alpha beta-hydrolase ( <i>S. hirsutum</i> , EIM81619)	3.75E-144	05:1804791-1806014	14.19	13.24	3.38	11.77	11.94	5.82
162919	2B	high affinity methionine permease ( <i>S. hirsutum</i> , EIM87629)	0	12:1450741-1452880	13.83	24.02	48.40	11.70	24.16	29.82
315982	2C	acetamidase formamidase ( <i>F. mediterranea</i> , EJD06687)	0	04:846380-849564	8.93	8.90	34.20	11.69	11.24	27.86
473535	1A	No hit	No hit	03:3053953-3055051	17.25	19.98	11.40	11.59	16.73	7.15
309285	1A	hypothetical protein ( <i>S. lacrymans</i> , EGN92462)	1.26E-26	02:2401420-2401809	11.04	7.66	2.80	11.59	7.54	10.50
156836	2C	No hit	No hit	11:1696314-1706067	11.66	12.91	27.84	11.15	15.14	24.16
67199	2C	glycoside hydrolase family 47 protein ( <i>S. hirsutum</i> , EIM88924)	0	09:371704-374209	10.33	9.88	61.01	11.05	9.36	24.43
449337	2A	proline-rich protein ( <i>G. trabeum</i> , EPQ58291)	1.49E-83	03:369275-370452	17.29	25.24	35.91	10.93	31.46	8.72
479355	1A	No hit	No hit	09:1220947-1221208	12.34	7.42	1.57	10.91	8.19	8.33
387972	2C	carboxymuconolactone decarboxylase ( <i>S. hirsutum</i> , EIM89135)	3.76E-67	09:654126-655077	11.59	13.70	43.05	10.91	10.37	14.45
422092	2C	small secreted protein ( <i>S. hirsutum</i> , EIM79124)	2.69E-40	11:1101756-1102444	6.54	6.89	23.40	10.91	9.02	30.36
330567	1C	No hit	No hit	13:882708-883065	6.27	4.30	14.98	10.9	12.02	18.40
47229	2B	glycosyltransferase family 2 protein ( <i>S. hirsutum</i> , EIM88048)	0	03:575891-577972	18.18	19.63	31.84	10.68	16.75	17.17
109309	1A	No hit	No hit	03:3058138-3058652	13.07	14.88	1.60	10.61	11.53	6.07
434492	2B	hypothetical protein ( <i>S. hirsutum</i> , EIM87966)	5.56E-29	06:250270-252048	12.39	19.69	20.51	10.56	13.53	23.57
104184	2C	glycoside hydrolase family 18 protein ( <i>S. hirsutum</i> , EIM86911)	2.71E-173	08:863224-864796	9.12	10.42	34.27	10.41	8.87	18.09
315947	2C	clavamate synthase-like protein ( <i>H. annosum</i> , ACB69808)	1.22E-109	04:1698890-1700240	12.24	8.46	61.07	10.29	10.91	55.09
50643	1B	alpha beta-hydrolase ( <i>G. trabeum</i> , EPQ55736)	1.80E-112	08:812068-813382	5.80	4.15	2.27	10.21	5.14	3.38
436311	1C	No hit	No hit	10:1376453-1376833	10.30	5.14	14.07	10.20	10.78	26.55
243345	2C	hypothetical protein ( <i>G. trabeum</i> , EPQ52589)	1.68E-27	13:178942-179544	4.62	5.75	22.44	10.19	9.64	7.56
170814	1A	No hit	No hit	03:1803274-1803585	5.37	6.07	1.78	10.17	9.04	5.34
66544	2B	general substrate transporter ( <i>L. bicolor</i> , XP001885131)	1.65E-130	12:1599503-1600883	17.23	19.43	31.40	10.15	10.38	35.25
153387	2C	glycoside hydrolase family 31 protein ( <i>S. hirsutum</i> , EIM91808)	0	09:2100407-2104644	11.45	14.53	21.86	9.85	9.92	18.21
429324	1A	No hit	No hit	09:1710686-1711844	12.14	11.96	3.43	9.80	11.42	3.28

319888	2C	No hit	No hit	06:662591-663305	12.13	10.75	18.86	9.76	11.39	24.91
154814	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM92273)	8.68E-131	06:696660-698398	9.29	11.31	19.42	9.56	12.22	30.09
451269	1C	hypothetical protein ( <i>G. trabeum</i> , EPQ55936)	2.89E-44	05:652184-653166	6.11	5.00	7.05	9.53	7.38	15.82
163514	2C	glycoside hydrolase family 79 protein ( <i>P. camosa</i> , EKM58316)	4.25E-113	04:1964943-1965958	12.79	10.96	20.19	9.30	11.54	26.44
107336	2C	glycoside hydrolase ( <i>S. hirsutum</i> , EIM91351)	0	04:2273069-2275310	10.55	10.34	36.87	9.25	7.95	25.45
420743	2C	No hit	No hit	09:682730-683195	7.66	8.28	27.93	9.07	8.87	23.39
67689	2B	aryl-alcohol oxidase-like protein ( <i>F. mediterranea</i> , EJD00209)	0	13:872487-875269	20.60	32.80	31.60	9.00	13.70	12.30
106901	1A	phosphotransferase family protein ( <i>Z. tritici</i> , XP003849307)	1.11E-06	04:2551998-2553383	10.71	11.90	5.53	8.97	13.35	6.81
383960	2C	atypical pikp trrap protein kinase (te doen met tor.) ( <i>S. lacrymans</i> , EGO01921)	0	05:927018-938889	13.60	14.67	21.38	8.92	13.34	20.47
170624	2B	c2h2 type zinc finger domain protein ( <i>F. radiculosa</i> , CCM00658)	1.01E-22	03:1423229-1424421	14.23	18.99	13.94	8.75	13.77	20.72
452058	2C	hypothetical protein ( <i>P. camosa</i> , EKM54064)	2.29E-48	06:653848-654640	5.76	4.57	19.3	8.66	13.19	11.12
123148	2C	glycoside hydrolase family 92 protein ( <i>C. subvermispora</i> , EMD37640)	0	06:1155083-1158989	12.07	13.48	30.12	8.36	8.86	25.36
11764	2C	amine oxidase ( <i>E. lata</i> , EMR67970)	0	03:3278146-3279634	11.79	8.29	14.50	8.33	8.16	35.51
325922	1A	zinc finger protein isoform crab ( <i>C. teleata</i> , ELT92398)	7.35E-06	09:1708066-1708627	10.14	9.14	3.69	8.27	8.79	1.00
173894	2C	predicted protein ( <i>L. bicolor</i> XP001881106, )	3.08E-28	10:1373526-1376112	8.63	7.59	27.15	8.23	10.34	27.66
101092	2B	No hit	No hit	02:437527-437845	18.55	33.42	80.77	8.16	11.16	15.81
318834	2C	predicted protein ( <i>P. placenta</i> , XP002475924)	2.48E-18	05:175822-176502	8.35	14.48	24.81	8.16	19.16	39.87
325498	1A	early growth response 2B ( <i>M. iheringi</i> , AFR58517)	6.07E-04	09:1722192-1722747	11.93	10.48	1.73	8.04	9.44	1.50
449514	2A	glutaminase GtaA ( <i>G. trabeum</i> , EPQ59419)	0	03:894431-897652	16.59	18.11	13.38	7.90	7.50	6.44
428080	2C	hypothetical protein ( <i>P. camosa</i> , EKM52498)	3.11E-17	07:510061-512139	8.26	8.72	40.88	7.6	7.48	13.6
225844	2C	p-loop containing nucleoside triphosphate hydrolase protein ( <i>C. subvermispora</i> , EMD41416)	0	06:42668-46207	11.17	12.18	24.41	7.56	10.42	20.24
454178	2C	zinc-finger-containing protein ( <i>P. camosa</i> , EKM56502)	5.75E-43	09:1192463-1193582	6.29	5.40	15.72	7.49	7.02	10.66
384845	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM91156)	7.50E-41	06:264519-265389	4.10	5.20	20.19	7.49	5.21	18.76
315818	2A	other 1 protein kinase ( <i>G. trabeum</i> , EPQ53938)	2.01E-13	04:765491-765956	8.6	11.51	20.31	7.44	5.71	4.31
322937	1A	No hit	No hit	07:232669-233942	7.73	7.75	1.39	7.40	9.42	5.47
409394	2C	hypothetical protein ( <i>G. trabeum</i> , EPQ55935)	5.30E-28	05:654235-655207	7.34	6.20	18.27	7.40	6.35	16.83
243873	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM80502)	3.24E-48	08:1518647-1519195	8.42	11.91	25.63	7.24	8.93	19.67
415413	2B	hypothetical protein ( <i>S. hirsutum</i> , EIM81970)	4.74E-04	03:301578-302582	11.22	9.33	18.87	7.21	14.23	14.12
455911	2B	reductase akor2 ( <i>S. hirsutum</i> , EIM83757)	5.52E-151	13:408258-409807	8.96	12.37	24.80	7.09	9.63	10.59
28304	1A	hypothetical protein ( <i>F. pinicola</i> , EPT01447)	1.72E-26	06:2257665-2258046	8.91	5.21	5.23	7.05	3.78	1.49

63706	2C	glycoside hydrolase ( <i>S. hirsutum</i> , EIM84383)	0	07:1056768-1059505	8.65	11.60	85.87	6.76	7.62	40.46
379364	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM90295)	4.64E-19	02:1099293-1099943	4.38	2.89	20.25	6.74	6.34	20.56
104716	2C	No hit	No hit	05:265025-266355	6.08	4.00	10.53	6.61	3.61	13.47
324192	2C	dihydroxyacetone kinase ( <i>P. carnosus</i> , EKM50436)	4.12E-08	08:878067-878524	5.17	5.25	15.44	6.55	5.17	9.39
124428	2C	alpha-ketoglutarate-dependent taurine dioxygenase ( <i>S. lacrymans</i> , EGN94276)	4.61E-163	07:729465-730908	4.64	4.49	25.81	5.82	6.50	46.59
326073	2C	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM84014)	6.49E-140	09:1013659-1014987	9.81	10.48	100.30	5.67	7.32	41.71
319489	2C	hypothetical protein ( <i>C. subvermispora</i> , EMD37740)	0	06:365993-367518	7.01	6.71	43.37	5.54	6.33	10.11
118857	2B	hypothetical protein ( <i>A. bisporus</i> , EKV41818)	1.42E-09	11:937028-937782	11.11	19.21	36.78	5.51	12.47	10.63
106234	2C	No hit	No hit	11:1479847-1480288	8.81	14.42	602.20	5.40	9.95	313.23
174466	1C	glycoside hydrolase family 28 protein ( <i>F. mediterranea</i> , EJD03462)	1.34E-169	11:306877-308482	1.40	0.90	2.00	5.40	9.90	13.70
411410	2B	sex-determining region y protein ( <i>S. hirsutum</i> , EIM91814)	6.79E-58	09:1987766-1988601	9.98	12.38	17.94	5.29	4.95	12.55
426943	2C	hypothetical protein ( <i>S. hirsutum</i> , EIM83396)	1.18E-63	05:865282-866497	5.07	5.28	19.83	4.96	4.78	20.56
163513	2C	glycoside hydrolase family 79 protein ( <i>P. strigosozonata</i> , EIN04212)	1.50E-39	04:1964147-1964818	8.54	6.71	17.70	4.79	5.20	18.10
104521	2C	hydrophobin fungal ( <i>F. radiculosa</i> , CCM03904)	3.38E-10	08:1919274-1919815	5.51	8.58	14.96	4.73	4.68	44.11
101388	2C	cytochrome p450 ( <i>S. hirsutum</i> , EIM81706)	2.59E-162	05:2261792-2264033	5.66	4.92	12.97	4.69	4.99	31.38
451895	2C	predicted protein ( <i>F. radiculosa</i> , CCM01101)	1.35E-37	06:89015-89681	4.11	3.42	18.51	4.60	4.86	25.38
438214	2B	predicted protein ( <i>L. bicolor</i> , XP001887743)	1.14E-60	02:658252-659494	5.02	13.92	23.55	3.88	9.65	13.64
45732	2C	carbohydrate esterase family 8 protein ( <i>S. hirsutum</i> , EIM83832)	2.29E-133	05:2447471-2448798	7.19	6.63	20.21	3.35	3.69	21.74
416354	2B	No hit	No hit	03:2761093-2761375	5.08	5.60	15.54	3.18	4.99	4.88
482531	2B	u3 snornp protein utp20 ( <i>P. placenta</i> , XP002471821)	3.18E-143	14:410355-411941	7.37	6.04	14.68	2.92	7.38	9.72
473974	2C	NAD-P-binding protein ( <i>S. hirsutum</i> , EIM81244)	2.26E-84	04:1416245-1417443	3.10	2.46	7.720	2.36	2.13	10.84
103357	2B	acyl- n-acyltransferase ( <i>S. hirsutum</i> , EIM80260)	8.66E-33	07:2055605-2056412	6.06	9.06	10.03	2.17	4.00	4.17
442064	2B	hypothetical protein ( <i>P. strigosozonata</i> , EIN08989)	2.93E-05	11:916443-917165	8.75	13.6	25.9	1.73	3.67	6.11
436435	2C	zgc:162509 protein ( <i>F. radiculosa</i> , CCM02016)	6.20E-77	11:141791-142805	2.45	3.17	26.81	1.53	2.23	13.42
448317	2B	hypothetical protein ( <i>G. trabeum</i> , EPQ50841)	2.24E-45	02:251487-252993	3.97	4.93	8.73	1.43	1.62	2.85
310038	2B	predicted protein ( <i>P. placenta</i> , XP002471919)	8.82E-25	02:700001-700755	3.92	10.77	9.62	1.05	3.80	7.56
389963	2A	hypothetical protein ( <i>S. hirsutum</i> , EIM86336)	4.97E-07	11:1781869-1783428	5.36	7.53	11.74	0.69	0.29	0.30
101051	2B	vacuolar (h+)-atpase subunit ( <i>G. trabeum</i> , EPQ58682)	1.79E-48	02:589958-590482	5.92	6.72	14.96	0.41	1.93	2.09
422186	2C	No hit	No hit	11:104435-104771	1.02	1.63	4.37	0.00	0.00	0.00

<sup>a</sup> Genes were considered DE if they displayed a two-fold change in expression at a Benjamini-Hochberg false discovery rate (FDR) cutoff value of 0.05 (i.e.,  $FDR\ q \leq 0.05$ ; and at a 2.0 fold change) (Benjamini and Hochberg, 1995.)

<sup>b</sup> JGI protein identity number.

<sup>c</sup> The differentially expressed genes were clustered based on their expression profile using Gene Cluster version 3.0 identified 6 cluster (Hoon et al., 2004) and named according to Fig. 3.

<sup>d</sup> BLAST2GO (<http://www.blast2go.org>) was used to annotate the DE genes in each cluster.

<sup>e</sup> BLAST Expect values obtained with BLAST2GO. “No hit” indicated that no homologous sequences were detected in any of the databases searched.

<sup>f</sup> Genome location of the DE genes in the annotated *H. irregulare* reference genome (Olson et al., 2012; DOE Joint Genome Institute, JGI, <http://genome.jgi.doe.gov/>). The first two digits represent the chromosome on which the gene is located and the numbers following it indicates the nucleotide position on the chromosome.

<sup>g</sup> Expression value (indicated in Reads Per Kilobase per Million mapped reads, or RPKM).