

Table S3. Identified overexpressed DEGs (according to the DESeq2 results) in strain 385cyc8⁺.

ID	Potential gene product	BLAST results			
		Biological process	Organism	E-value	Identity (%)
KX517841	MFS multidrug resistance transporter	Transmembrane transport	<i>Fusarium fujikuroi</i>	1.8 E-76	62
KX517842	Drug: H ⁺ antiporter	Transmembrane transport	<i>Cryptococcus gattii</i>	2.0 E-122	44
KX517843	High affinity glucose transporter ght2	Transmembrane transport	<i>Rhizoctonia solani</i>	1.8 E-146	53
KX517844	Oligopeptide transporter OPT/MTD1	Transmembrane transport	<i>Rhodosporidium toruloides</i>	2.2 E-98	61
KX517845	OPT oligopeptide transporter	Transmembrane transport	<i>Rhizoctonia solani</i>	0.0	53
KX517846	AAT family aminoacid transporter	Transmembrane transport	<i>Laccaria bicolor</i>	3.0 E-83	54
KX517847	Neutral amino acid transporter	Transmembrane transport	<i>Aspergillus flavus</i>	2.1 E-128	44
KX517848	Aminoacid permease	Transmembrane transport	<i>Punctularia strigosozonata</i>	9.3 E-28	38
KX517849	MFS transporter/Nicotinic acid transporter Tna1	Transmembrane transport	<i>Rhizoctonia solani</i>	5.3 E-122	44
KX517850	Major facilitator superfamily transporter/ Pantotenate transporter	Transmembrane transport	<i>Penicillium roqueforti</i>	0.0	69
KX517851	MFS general substrate transporter	Transmembrane transport	<i>Colletotrichum fiorinae</i>	5.8 E-19	48
KX517852	MFS general substrate transporter	Transmembrane transport	<i>Auricularia delicata</i>	0.0	57
KX517853	MFS general substrate transporter	Transmembrane transport	<i>Cryptococcus neoformans</i>	1.7 E-139	62
KX517854	MFS general substrate transporter	Transmembrane transport	<i>Melanopsichium pennsylvanicum</i>	6.3 E-139	47
KX517855	MFS protein/DUF895 domain membrane protein	Transmembrane transport	<i>Rhodosporidium toruloides</i>	7.6 E-15	41
KX517856	Mitochondrial carrier protein, tricarboxylate/iron carrier	Transmembrane transport	<i>Cryptococcus neoformans</i>	1.8 E-125	57
KX384930	Siderophore-iron transporter Str1	Transmembrane transport/ iron homeostasis	<i>Cryptococcus gattii</i>	4.0 E-95	70
KX517857	MOSC domain containing protein/ molybdenum cofactor sulfurase	Transmembrane transport	<i>Pseudozyma antarctica</i>	8.3 E-53	35
KX384901	PLP-dependent transferase/aminotransferase	Amino acid metabolism	<i>Fomitiporia mediterranea</i>	1.5 E-109	43
KX517858	GNAT family acetyltransferase/Acyl CoA acyltransferase	Protein/Histone modification	<i>Rhizoctonia solani</i>	3.0 E-50	40
KX517859	Acyl CoA N acyltransferase,GNAT family	Protein/Histone modification	<i>Glarea lozoyensis</i>	3.14 E-20	33
KX517860	Acyl CoA N acyltransferase	Protein modification	<i>Punctularia strigosozonata</i>	7.5 E-41	38
KX517861	Glycosyl transferase family 8 protein/ glycogenin	Protein modification	<i>Gloeophyllum trabeum</i>	4.9 E-98	50
KX517862	GNAT family acetyltransferase/Acyl CoA N-acetyltransferase	Protein/Histone modification	<i>Rhizoctonia solani</i>	1.5 E-49	40
KX517863	Aspartic peptidase, endopeptidase	Proteolysis	<i>Cryptococcus neoformans</i>	1.6 E-60	42
KX517864	Imidazoleglycerol phosphate synthase/HisHF	Amino acid biosynthesis	<i>Cryptococcus gattii</i>	0.0	63

KX517865	Polisaccharide lyase family 1 protein/pectin lyase	Polysaccharide catabolic process	<i>Bipolaris zeicola</i>	1.8 E-22	69
KX517904	Six hairpin glycosidase/glycoside hydrolase family 125 protein	Carbohydrate metabolism	<i>Penicillium italicum</i>	8.9 E-115	44
KX517866	Glycoside hydrolase family 16 protein	Carbohydrate metabolism	<i>Rhizoctonia solani</i>	0.0	57
KX517867	Phosphoenolpyruvate carboxykinase	Gluconeogenesis	<i>Cryptococcus gattii</i>	0.0	83
KX517868	Fructose biphosphate aldolase	Glycolysis	<i>Rhizoctonia solani</i>	0.0	79
KX517869	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	phenylacetate catabolism	<i>Aspergillus kawachii</i>	5.4 E-144	75
KX384910	Alpha -beta hydrolase	Lipid metabolism	<i>Heterobasidion irregulare</i>	5.1 E-81	42
KX517870	SGNH hydrolase/ GDSL like lipase	Lipid metabolism	<i>Auricularia subglabra</i>	1.0 E-51	44
KX384927	Mevalonate kinase	Isoprenoid metabolism	<i>Cryptococcus gattii</i>	0.0	60
KX517871	Nitrilase	Nitrogen compound metabolism	<i>Paxillus involutus</i>	4.0 E-74	48
KX517872	NADP-dependent dehydrogenase acting on 3-hydroxy acids/malonic semialdehyde reductase	Nitrogen utilization/pyrimidine nucleobase catabolism	<i>Piriformospora indica</i>	7.4 E-110	59
KX517873	2-nitropropane dioxygenase	Pyrimidine nucleobase biosynthesis	<i>Cryptococcus gattii</i>	1.0 E-64	72
KX517874	2-Oxoglutarate-Fe (II) dependent oxygenase	DNA repair	<i>Trametes versicolor</i>	2.8 E-31	48
KX517875	DNA repair protein rev1	DNA repair	<i>Moniliophthora roreri</i>	9.0 E-5	40
KX517876	Transcriptional regulator	Transcription regulation	<i>Cryptococcus gattii</i>	1.4 E-97	59
KX517877	PacC, Ph response transcription factor	Transcription regulation	<i>Rhizoctonia solani</i>	0.0	43
KX517878	HMG-box transcription factor/mating type protein MAT1-2	Transcription regulation	<i>Melanopsichium pennsylvanicum</i>	8.1 E-10	35
KX517879	Nitrogen assimilation transcription factor/ nit-4	Transcription regulation	<i>Rhodosporidium toruloides</i>	1.4 E-9	32
KX517880	Stress response protein rds1p	Stress response	<i>Piriformospora indica</i>	1.1 E-84	54
KX517881	Sporulation specific protein spo7	Sporulation/stress response	<i>Postia placenta</i>	2.7 E-27	49
KX517882	Meiotic recombination protein SPO11	Sporulation/ stress response	<i>Cryptococcus gattii</i>	1.3 E-4	50
KX517883	RIO/RIO1 protein kinase	Cell cycle and Ribosome biogenesis	<i>Rhizoctonia solani</i>	5.64 E-9	64
KX384909	G1/S specific cyclin Pcl1	Cell cycle	<i>Cryptococcus neoformans</i>	4.0 E-61	49

ID: accession number of the identified DEG