

Table captions

Table. S1: Primers used in RT-qPCR (*M. guilliermondii*).

Gene ID	Gene Name	Forward primer (5' to 3')
		Reverse primer (5' to 3')
PGUG_00994	<i>NOP53</i>	TCACAGTCACACTCGTGCCAAAG TGCCACCCACCACCTCATCATC
PGUG_01741	<i>MRR1</i>	AACCCATACCGCAACCACAACG ACAAGCCCAAATCTCGCCTCATG
PGUG_01881	<i>SPCC24B10.20</i>	TGGTCAATCGAAGGCTGCTCT TCGTGGCCCATATCGGTTCC
PGUG_05287	<i>YML131W</i>	TCTGCTGCTTCTGGGGCTACC GACGCAAACATCGGCACCAATAC
PGUG_01077	<i>SPCC663.08c</i>	CACCGCAGCACACACCATCC GACCAATTCCACGAGAAGCACCAG
PGUG_04552	<i>GRP2</i>	AAGGCAGCGTGCGGAGTTTGTTG TCAGCGGTCATGTTGAGCGTTC
PGUG_05192	<i>YPR022C</i>	GGTGTTTCGTGGCCTGATTGTGG TGGTTCTGTCTTGTTCTCGTGCTG
PGUG_04009	<i>YJR096W</i>	GATCCACTCGCCTCAATCGAACAG TCCAATCCGTCCCATTCCAACAAC
PGUG_05193	<i>SPCC663.09c</i>	CTGATTGCGGCTCGTTAAACTTGG GCTCCAACGTCTCGCCAACTC
PGUG_01005	<i>GSH2</i>	TTCGGAACCTGCTCGTGGTCTTG CGCTCGCCAGGTTGAACAATTAC
PGUG_03271	<i>MDR1</i>	GGTCAATGGCAGCAAACTCTTCG CTTCGGCACCAGGAGTGTAGATTG
PGUG_00888	<i>YHK8</i>	GACGACGGCAACGACAAGGAG AAGCTAGGGACCATGCTGAGGAG
PGUG-05383	β -tublin	CCAATTCCTGGCTCCGCTTACG CTGTCCTACTTCCGCACCCTTTTC

Table. S2: Comparison of clean data and reference genome.

Treatment	samlpes	reads aligned (%)	exonic (%)	intronic (%)	intergenic (%)
CK	CK-1	96.69	85.09	0.02	14.89
	CK-2	96.58	84.87	0.02	15.11
	CK-3	96.29	84.37	0.02	15.62
Pat	Pat-1	96.46	85.70	0.02	14.28
	Pat-2	96.44	85.09	0.02	14.89
	Pat-3	96.78	84.90	0.02	15.09

Table. S3: Number of annotated DEGs.

DEG Set	DEGs Number	Swiss-Prot	GO	KEGG	COG	KOG	Pfam	NR
CK_vs_Pat	348	281	275	160	105	194	279	323