

Supplementary **Table S1**. Primer sequences used in qRT-PCR verification.

Gene	Annotation	Primer sequences
<i>GAP1</i>	Putative Ras GTPase-activating protein	F: GAACTTGTGGGTTTGGCAGC R: AGTGGCATCGACGGAAGAAG
<i>MEP2</i>	Ammonium permease involved in regulation of pseudohyphal growth	F: TGCCACGCTCATTGTTG R: AATAGCGACAAGACCGGCAA
<i>DIP5</i>	Dicarboxylic amino acid permease	F: CAATGGCAAGGCTCCCAAGA R: CGTTGAGGTACGCAAGAGCA
<i>UGA4</i>	A gamma-aminobutyrate (GABA) transport protein involved in the utilization of GABA as a nitrogen source	F: TGGCGTTCCCATTAGAGCAG R: GCAACAGCCATGCAAGAGAG
<i>SFC1</i>	Mitochondrial succinate-fumarate transporter	F: AAGTACAGAAATGCCGCCCA R: GTTTGCCACGAAGGAAGCTG
<i>ECM33</i>	GPI-anchored protein	F: CTACCGCGTCTTGTCGATGT R: ACGGTACGGAGATCAAAGCC
<i>TOS1</i>	Covalently-bound cell wall protein	F: GATGCCCCCTTGATCCCGATT R: GACATCAAACCTCACCGCAGC
<i>GAS5</i>	1,3-beta-glucanosyltransferase	F: CAGGCGATCATTCCGAGTGT R: TGTCGATTGTGGCAAACACG
<i>FDH1</i>	NAD(+)-dependent formate dehydrogenase	F: CTCACTTGTCTGGCACGTCT R: CTTGTCTCTCTGGCCGTAGG
<i>DSE4</i>	Daughter cell-specific secreted protein with similarity to glucanases	F: TGCTCAAGGCGGTGATACTG R: CACGAACGAGCGAATTGACC
<i>CTS1</i>	Endochitinase	F: TCACAAGCGTCCAAGCGTTA R: TAGCCGTTGTCGGGATTGAC
<i>IRA2</i>	GTPase-activating protein that negatively regulates RAS by converting it from the GTP-to the GDP-bound inactive form	F: CCGAAACAACCTCAACTCGCC R: GAAATGAACGCCACGAAGCA
<i>FBA1</i>		F: CATTGCCGGTGGTATTGCTG

	Fructose 1,6-bisphosphate aldolase	R: TGAAGTAAGCCTCATCGGCG
<i>PDC1</i>	Major of three pyruvate decarboxylase isozymes	F: TTGGCATTTCGCAGGTGTTG R: GTTCAGGTTCCAGCGGATCA
<i>ATG22</i>	Vacuolar integral membrane protein required for efflux of amino acids during autophagic body breakdown in the vacuole	F: TGCCTAGGTCTTTATGCGT R: GTTGCGTCGTAGGATTGCAC
<i>GRE2</i>	NADPH-dependent methylglyoxal reductase	F: GCAACCTCAACACGTCTGAAC R: TTGTCAAGCTCAGCCGATGT
<i>ALD4</i>	Mitochondrial aldehyde dehydrogenase	F: CTCCCACCGTCTTTGCTGAT R: AGCCTTGTTGACATCCTGGG
<i>ALDH3A1</i>	Putative fatty aldehyde dehydrogenase	F: ACAAACATGCGTTGCTCCTG R: TACCGCCGACAACAATGGTA
<i>SDH2</i>	Iron-sulfur protein subunit of succinate dehydrogenase	F: TTGTTGTCCGCGATCTGGTT R: TCCACCAATATGACGGGCAG
<i>gatA</i>	4-aminobutyrate aminotransferase	F: TGCTGATGGCCTACTTGCAG R: GGGTGTCTATAACCACGCTCT
<i>β-actin</i>	A highly conserved cytoskeletal protein involved in cell motility, structure, and integrity.	F: ACGGACTGGGACGATATGGA R: TGCTCGTGGATTGAGAGGTG

* *β -actin* was used as the reference gene.