

Supplementary Material to “Transcriptome sequencing and screening of genes related to glucose availability in *Schizosaccharomyces pombe* by RNA-seq analysis”

Table S1. The quantitative change in the expression of individual genes depending on the glucose concentration.

Systematic ID / Gene name	Fold change in gene expression according to the glucose concentration		
	Expression in 3% compare to %5	Expression in 8% compare to 3%	Expression in %8 compare to 5%
SPAPB24D3.10c (maltose alpha-glucosidase Agl1)	-2,15	-2,09	-4,24
SPCC548.07c (hexose transmembrane transporter Ght1)		-3,00	-4,07
SPCC1235.14 (hexose transmembrane transporter Ght5)			-2,26
SPBPB2B2.13 (galactokinase Gal1)		-2,37	-2,65
SPBPB2B2.10c (galactose-1-phosphate uridylyltransferase Gal7)		-2,21	-2,62
SPBPB2B2.12c (UDP-glucose 4-epimerase/aldose 1-epimerase Gal10)			-2,71
SPCC1223.03c (glycerol-3-phosphate dehydrogenase Gut2 (predicted))		-3,07	-3,43
SPAC13F5.03c (mitochondrial glycerol dehydrogenase Gld1)		-3,78	-4,66
SPCC794.01c (glucose-6-phosphate 1-dehydrogenase Zwf2 (predicted))			-2,61
SPBPB2B2.11			-2,61
SPCC191.11 (external invertase, beta-fructofuranosidase)			-2,88
Systematic ID / Gene name	Fold change in gene expression according to the glucose concentration in SD medium		
	Expression in 3% compare to %5	Expression in 8% compare to 3%	Expression in %8 compare to 5%
SPAPB15E9.03c (retrotransposable element/transposon Tf2-type)	-9,71		
SPAC26A3.13c (retrotransposable element/transposon Tf2-type)			+2,24
SPBC3E7.02c (heat shock protein Hsp16)		-3,17	-2,06
SPBC16D10.08c		-2,13	

(heat shock protein Hsp104)			
SPAC13G7.02c (heat shock protein Ssa1 (predicted))		-2,75	-2,29
SPBC23G7.09, mat1-Mc (mating type m specific polypeptide)	+8,64		
SPCC965.07c (glutathione S-transferase Gst2)		+2,68	+ 2,03
SPAP11E10.02c (cell agglutination protein Mam3)		+2,33	+1,52
SPBC685.02 (mitochondrial single stranded DNA specific 5'-3' exodeoxyribonuclease Exo5 (predicted))		+2,51	
SPCC61.02 (SAGA complex subunit Spt3)		+2,45	
aes1 enhancer of RNA-mediated gene silencing)			-2,29
SPAC823.06 (transcription factor TFIID complex subunit Taf3 (predicted))		+ 2,43	
SPBC1718.05 (TRAPP complex subunit Trs31 (predicted))		+2,41	
SPBP4H10.09 (transcription factor Rsv1)			-2,82
SPAC1071.04c (signal peptidase subunit Spc2 (predicted))		+2,40	
SPBP4H10.10 (rhomboid family protease)			-2,40
Systematic ID / Gene name		Fold change in gene expression according to the glucose concentration in SD medium	
		Expression in 3% compare to %5	Expression in 8% compare to 3%
SPCC63.03 (DNAJ domain protein, DNAJC11 family)		+2,40	
SPAC5H10.06c (aldo/keto reductase, predicted calcium channel regulator)		+2,34	
SPBC29A3.03c (GID complex ubiquitin-protein ligase E3 subunit Gid2/Rmd5 (predicted))		+2,27	
SPCC663.08c (short chain dehydrogenase)		+2,17	
SPAC869.02c (nitric oxide dioxygenase Yhb1)		+2,15	
SPBC887.06c (sorting nexin Snx3 (predicted))		+2,14	
SPCC1020.01c (P-type proton ATPase, P3-type Pma)		+2,08	
SPAC12G12.09 (conserved fungal protein associated with stress granule)		+2,01	
SPBC359.04c		-3,45	

(cell surface glycoprotein (predicted), DIPSY family)			
SPBPB2B2.05 (peptidase family C26 protein)		-2,32	
SPBC21C3.19 (SBDS family protein Rtc3 (predicted))		-2,18	
SPBC725.12 (Borealin homolog Nbl1)		+4,32	
SPBC28E12.01c (anaphase-promoting complex TPR lobe accessory factor Apc13)		+3,13	
SPCC1902.02 (Meiotically Upregulated Gene, mug72)		+2,5	
SPCC1223.15c (DASH complex subunit Spc19)		+2,34	
Systematic ID / Gene name	Fold change in gene expression according to the glucose concentration in SD medium		
	Expression in 3% compare to %5	Expression in 8% compare to 3%	Expression in %8 compare to 5%
SPBC1604.20c (kinesin family plus-end microtubule motor Tea2)		+2,27	
SPAC1687.20c (kinetochore protein, CENP-I ortholog Mis6)		+2,05	
SPCC970.12 (kinetochore protein Mis18)		+2,02	
SPAC589.02c (mediator complex subunit Med13)		+2,00	
SPBP22H7.09c (kinetochore protein, CENP-N ortholog Mis15)		-2,64	
SPAC750.04c (<i>S. pombe</i> specific 5Tm protein family)	-2,54		
SPAC959.06c (conserved fungal protein)		+2,95	+2,02
SPBC660.05 (WW domain containing conserved fungal protein)		-4,44	-4,40
SPAC977.18 (conserved fungal protein)	-2,41		-2,23
SPCC576.19c (dubious)			+2,29
SPBPB2B2.18 (<i>Schizosaccharomyces</i> specific protein)	-2,75		
SPBPB21E7.04c (human COMT ortholog 2)	-2,10		
SPCC1235.18 (dubious)		-2,32	
SPCP20C8.02c (<i>S. pombe</i> specific UPF0321 family protein 1)			+2,01
SPAC959.11 (<i>Schizosaccharomyces</i> specific protein)			-12,44

SPAC2F3.07c (<i>Schizosaccharomyces pombe</i> specific protein)	-2,05		
SPAC4F8.08 (<i>Schizosaccharomyces pombe</i> specific protein Mug114)	-2,69		