

Web Table C: Genes induced in response to starvation/pheromone (continuous).

Continuous genes are induced immediately upon nitrogen starvation and remain activated throughout the experiment.

Metabolic response		
	SPBC1289.16C	putative amine oxidase
	SPBPB2B2.10C	putative galactose-1-phosphate uridylyltransferase
	SPCC417.11C	putative glutamate-1-semialdehyde aminotransferase
	SPAC3G9.11C	pyruvate decarboxylase
	SPAC1F8.04C	putative chlorohydrolase/deaminase
	SPCC306.08C	malate dehydrogenase, mitochondrial precursor
	SPAC18B11.09C	putative acetyltransferase
	SPAC3C7.13C	glucose-6-phosphate 1-dehydrogenase
	SPAC4D7.02C	putative glycerophosphoryl diester phosphodiesterase
Transporters		
	SPAC2G11.13	MFS transporter of unknown specificity
Mating		
<i>isp6</i>	SPAC4A8.04	sexual differentiation process protein; putative subtilase-type proteinase
<i>gpa1</i>	SPBC24C6.06	guanine nucleotide-binding protein alpha-1 subunit; required for mating and sporulation
<i>ste7</i>	SPAC23E2.03C	required for mating and meiosis
Sequence orphans		
	SPCC576.01C	hypothetical protein; sequence orphan
	SPAC6B12.03C	hypothetical protein; sequence orphan
	SPCC338.18	hypothetical protein; sequence orphan
	SPBC428.10	hypothetical protein; sequence orphan
	SPBC56F2.06	hypothetical protein; sequence orphan
	SPCC70.04C	hypothetical protein; sequence orphan; 4 predicted transmembrane helices
	SPBC8E4.02C	hypothetical protein; sequence orphan
	SPAC4D7.11	hypothetical protein; sequence orphan
	SPAC25B8.18	hypothetical protein; sequence orphan
	SPAC29B12.13	hypothetical protein; sequence orphan
	SPAC637.03	hypothetical protein; sequence orphan; 8 predicted transmembrane segments; predicted N-term signal sequence
	SPCC63.14	hypothetical protein; sequence orphan; coiled-coil region
	SPBC11C11.06C	hypothetical protein; sequence orphan
Stress response		
<i>hsp9</i>	SPAP8A3.04C	heat shock protein
<i>gpx1</i>	SPBC32F12.03C	glutathione peroxidase
	SPCC63.13	hypothetical DNAJ domain protein
	SPBC106.13	conserved hypothetical protein; similar to <i>S. cerevisiae</i> YIL097W, involved in stress response
<i>ntp1</i>	SPBC660.07	neutral trehalase
Others		
	SPBC18H10.05	WD repeat protein
	SPAC589.07C	WD domain protein; highly similar to <i>S. cerevisiae</i> YFR021W
	SPCC1322.08	putative serine/threonine protein kinase
<i>pim1 ptr2</i>	SPBC557.03C	pim1 GTPase protein
	SPCC338.12	putative proteinase precursor
	SPAP14E8.04	putative zinc metallopeptidase

	SPAPJ691.02	hypothetical zinc binding protein yipee-like
<i>isp4</i>	SPBC29B5.02C	sexual differentiation process protein
	SPBC1271.05C	zinc finger zf-AN1 protein
	SPAC1039.10	putative translation initiation inhibitor
	SPBC1652.01	may bind Pst1 histone deacetylase B; by similarity to <i>S. cerevisiae</i> SIN complex protein (transcriptional regulator of RNA polymerase II)
	SPAPB8E5.04C	putative phosphatidylglycerol/phosphatidylinositol transfer
	SPCC1739.08C	short chain dehydrogenase; putative sorbitol utilization
	SPCC736.13	short chain dehydrogenase
	SPAC19G12.09	putative aldose reductase
	SPBC16A3.02C	putative quinone oxidoreductase; zinc binding oxidoreductase
	SPBC725.10	similar to peripheral-type benzodiazepine receptor
	SPAC26F1.14C	putative flavoprotein; similar to human Mitochondrial apoptosis-inducing factor; flavoprotein inducing chromatin condensation and DNA fragmentation
	SPAC630.05	TBC domain protein; putative GTPase activating protein of Rab-like GTPase
	SPCP31B10.06	C2-domain protein; synaptotagmin family
<i>vps27</i>	SPAC19A8.05C	putative vacuolar sorting protein
	SPAC19B12.08	putative Protein that mediates attachment of autophagosomes to microtubules, by similarity to <i>S. cerevisiae</i> <i>AUT2</i>
	SPAC4H3.04C	hypothetical protein; similar to <i>S. cerevisiae</i> YJR008W; UPF0103 FAMILY
	SPBC365.12C	hypothetical protein; similar to <i>S. cerevisiae</i> YML128C (low)
	SPAC10F6.11C	hypothetical protein; similar to <i>S. cerevisiae</i> <i>APG17</i> ; contains Pfam-B_36869; putative coiled-coil
	SPAC31G5.18C	conserved hypothetical protein
	SPAC12B10.13	conserved hypothetical protein; contains Pfam-B_8841
	SPAC688.03C	conserved hypothetical protein
	SPCC622.11	hypothetical protein; contains Pfam-B_37204
	SPCC285.11	hypothetical protein with UBX, Domain present in ubiquitin-regulatory proteins
	SPCC1020.05	hypothetical protein; Pfam-B_7731 domain
	SPAC3C7.05C	hypothetical protein; contains Pfam-B_11461 domain
	SPBC660.05	hypothetical protein; pombe specific domain Pfam-B_15930
	SPAC20G4.05C	hypothetical protein; UPF0061 family
	SPAC167.06C	hypothetical protein
	SPBC16E9.16C	pseudogene
	SPCC1450.01C	putative pseudogene
	SPAC186.04C	putative pseudogene, has similarity to transmembrane channels