

Table S5 Genes significantly regulated in response to *MSS11* over-expression or deletion in Σ 1278b (indicated as Σ 1278b *MSS11* and Σ 1278b *mss11* respectively) or over-expression in S288c (S288c *MSS11*). Shown are the degree of regulation (\log_2 fold), the open reading frame (ORF), the gene name if applicable as well as a short description as obtained from the *Saccharomyces genome database* (SGD).

| \log_2 fold | ORF | Gene name | Short description |
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| S288c <i>MSS11</i> | | | |
| -2.738 | YJL170C | <i>ASG7</i> | Protein that regulates signaling from a G protein beta subunit Ste4p and its relocalization within the cell |
| -2.307 | YIL015W | <i>BAR1</i> | Aspartyl protease secreted into the periplasmic space of mating type a cells, helps cells find mating partners, cleaves and inactivates alpha factor allowing cells to recover from alpha-factor-induced cell cycle arrest |
| -1.87 | YCL026C-A | <i>FRM2</i> | Protein of unknown function, involved in the integration of lipid signaling pathways with cellular homeostasis |
| -1.148 | YMR279C | | Putative protein of unknown function |
| -1.066 | YJL160C | | Putative protein of unknown function |
| -1.061 | YDL127W | <i>PCL2</i> | G1 cyclin, associates with Pho85p cyclin-dependent kinase (Cdk) to contribute to entry into the mitotic cell cycle, essential for cell morphogenesis |
| -0.919 | YBR019C | <i>GAL10</i> | UDP-glucose-4-epimerase, catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism |
| -0.919 | YOR114W | | Putative protein of unknown function |
| -0.887 | YPL130W | <i>SPO19</i> | Meiosis-specific protein of unknown function, involved in completion of nuclear divisions |
| -0.85 | R0020C | <i>REP1</i> | Master regulator that acts in concert with Rep2p to regulate transcript levels of the FLP1 gene that promotes plasmid copy amplification |
| -0.849 | YGR131W | | Protein of unknown function |
| -0.807 | YDR106W | <i>ARP10</i> | Component of the dynactin complex, localized to the pointed end of the Arp1p filament |
| -0.7 | YJR112W | <i>NNF1</i> | Essential component of the MIND kinetochore complex (Mtw1p Including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules |
| -0.655 | YPR106W | <i>ISR1</i> | Predicted protein kinase, overexpression causes sensitivity to staurosporine, which is a potent inhibitor of protein kinase C |

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| -0.651 | YKL089W | <i>MIF2</i> | Kinetochore protein with homology to human CENP-C, required for structural integrity of the spindle during anaphase spindle elongation, interacts with histones H2A, H2B, and H4, phosphorylated by Ipl1p |
| -0.647 | YJL196C | <i>ELO1</i> | Elongase I, medium-chain acyl elongase, catalyzes carboxy-terminal elongation of unsaturated C12-C16 fatty acyl-CoAs to C16-C18 fatty acids |
| -0.627 | YDR179W-A | | Putative protein of unknown function |
| -0.626 | YHR063C | <i>PAN5</i> | 2-dehydropantoate 2-reductase, part of the pantothenic acid pathway, structurally homologous to E. coli panE |
| -0.569 | YFL046W | <i>FMP32</i> | Putative protein of unknown function |
| -0.513 | YML023C | <i>NSE5</i> | Essential subunit of the Mms21-Smc5-Smc6 complex |
| 0.5 | YNR018W | | Putative protein of unknown function |
| 0.746 | YLR216C | <i>CPR6</i> | Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues |
| 0.783 | YHR112C | | Putative protein of unknown function |
| 0.859 | YPL024W | <i>RM11</i> | Subunit of the RecQ (Sgs1p) - Topo III (Top3p) complex |
| 0.904 | YNL191W | <i>DUG3</i> | Probable glutamine amidotransferase, forms a complex with Dug1p and Dug2p to degrade glutathione (GSH) and other peptides containing a gamma-glu-X bond in an alternative pathway to GSH degradation by gamma-glutamyl transpeptidase (Ecm38p) |
| 0.966 | YER042W | <i>MXR1</i> | Methionine-S-sulfoxide reductase, involved in the response to oxidative stress |
| 1.039 | YGL010W | | Putative protein of unknown function |
| 1.162 | YPR196W | | Putative maltose activator |
| 1.225 | YAL012W | <i>CYS3</i> | Cystathionine gamma-lyase, catalyzes one of the two reactions involved in the transsulfuration pathway that yields cysteine from homocysteine with the intermediary formation of cystathionine |
| 1.249 | YNL276C | | |
| 1.249 | YNL277W | <i>MET2</i> | L-homoserine-O-acetyltransferase, catalyzes the conversion of homoserine to O-acetyl homoserine which is the first step of the methionine biosynthetic pathway |

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| 1.465 | YDL059C | <i>RAD59</i> | Protein involved in the repair of double-strand breaks in DNA during vegetative growth via recombination and single-strand annealing |
| 1.501 | YDR044W | <i>HEM13</i> | Coproporphyrinogen III oxidase, an oxygen requiring enzyme that catalyzes the sixth step in the heme biosynthetic pathway |
| 1.521 | YHL036W | <i>MUP3</i> | Low affinity methionine permease, similar to Mup1p |
| 1.528 | YKL109W | <i>HAP4</i> | Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression |
| 1.599 | YDL245C | <i>HXT15</i> | Protein of unknown function with similarity to hexose transporter family members, expression is induced by low levels of glucose and repressed by high levels of glucose |
| 1.599 | YJR158W | <i>HXT16</i> | Protein of unknown function with similarity to hexose transporter family members, expression is repressed by high levels of glucose |
| 1.655 | YOR009W | <i>TIR4</i> | Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins |
| 1.658 | YLL061W | <i>MMP1</i> | High-affinity S-methylmethionine permease, required for utilization of S-methylmethionine as a sulfur source |
| 1.719 | YKL201C | <i>MNN4</i> | Putative positive regulator of mannosylphosphate transferase (Mnn6p), involved in mannosylphosphorylation of N-linked oligosaccharides |
| 1.719 | YKL202W | | |
| 1.755 | YMR244W | | Putative protein of unknown function |
| 1.808 | YLR364W | <i>GRX8</i> | Glutaredoxin that employs a dithiol mechanism of catalysis |
| 1.881 | YDR253C | <i>MET32</i> | Zinc-finger DNA-binding protein, involved in transcriptional regulation of the methionine biosynthetic genes, similar to Met31p |
| 1.898 | YMR081C | <i>ISF1</i> | Serine-rich, hydrophilic protein with similarity to Mbr1p |
| 1.931 | YJL212C | <i>OPT1</i> | Proton-coupled oligopeptide transporter of the plasma membrane |
| 1.961 | YFL051C | | Putative protein of unknown function |
| 1.968 | YEL070W | <i>DSF1</i> | Deletion suppressor of mpt5 mutation |
| 1.968 | YNR073C | | Putative mannitol dehydrogenase |
| 2.1 | YGR055W | <i>MUP1</i> | High affinity methionine permease, integral membrane protein with 13 putative membrane-spanning regions |

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| 2.374 | YAR064W | | Putative protein of unknown function |
| 2.374 | YHR213W-B | | Putative protein of unknown function |
| 2.458 | YER011W | <i>TIR1</i> | Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins |
| 2.47 | YDR342C | <i>HXT7</i> | High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt6p, expressed at high basal levels relative to other HXTs, expression repressed by high glucose levels |
| 2.47 | YDR343C | <i>HXT6</i> | High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt7p, expressed at high basal levels relative to other HXTs, repression of expression by high glucose requires SNF3 |
| 2.522 | YKL068W-A | | Putative protein of unknown function |
| 2.629 | YJL218W | | Putative protein of unknown function, similar to bacterial galactoside O-acetyltransferases |
| 2.951 | YAL063C | <i>FLO9</i> | Lectin-like protein with similarity to Flo1p, thought to be expressed and involved in flocculation |
| 2.951 | YAL064W-B | | Fungal-specific protein of unknown function |
| 2.951 | YAR050W | <i>FLO1</i> | Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers flocculating ability that is chymotrypsin sensitive and heat resistant |
| 2.951 | YHR211W | <i>FLO5</i> | Lectin-like cell wall protein (flocculin) involved in flocculation, binds to mannose chains on the surface of other cells, confers flocculating ability that is chymotrypsin resistant but heat labile |
| 2.966 | YHR092C | <i>HXT4</i> | High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high levels of glucose |
| 3.052 | YMR317W | | Putative protein of unknown function with some similarity to sialidase from Trypanosoma |
| 3.172 | YMR164C | <i>MSS11</i> | Transcription factor involved in regulation of invasive growth and starch degradation |
| 3.214 | YDL039C | <i>PRM7</i> | Pheromone-regulated protein, predicted to have one transmembrane segment |
| 3.23 | YIL011W | <i>TIR3</i> | Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins |
| 3.319 | YMR011W | <i>HXT2</i> | High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by |

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| | | | high levels of glucose |
| 3.732 | YDL039C | <i>PRM7</i> | Pheromone-regulated protein, predicted to have one transmembrane segment |
| 3.747 | YAL065C | | Putative protein of unknown function |
| 3.822 | YOR010C | <i>TIR2</i> | Putative cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins |
| 3.853 | YJR150C | <i>DAN1</i> | Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p |
| 3.876 | YHR213W-A | | Putative protein of unknown function |
| 4.818 | YJL116C | <i>NCA3</i> | Protein that functions with Nca2p to regulate mitochondrial expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase |
| 4.991 | YIR019C | <i>MUC1</i> | GPI-anchored cell surface glycoprotein (flocculin) required for pseudohyphal formation, invasive growth, flocculation, and biofilms |
| 5.373 | YAR062W | | Hypothetical protein |
| 5.373 | YHR213W | | Putative protein of unknown function |
| 5.798 | YAR050W | <i>FLO1</i> | Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers flocc-forming ability that is chymotrypsin sensitive and heat resistant |
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| Σ1278b <i>MSS11</i> | | | |
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| -0.857 | YOL147C | <i>PEX11</i> | Peroxisomal membrane protein required for peroxisome proliferation and medium-chain fatty acid oxidation, most abundant protein in the peroxisomal membrane, regulated by Adr1p and Pip2p-Oaf1p, promoter contains ORE and UAS1-like elements |
| -0.855 | YHR143W | <i>DSE2</i> | Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother |
| 0.916 | YNL036W | <i>NCE103</i> | Carbonic anhydrase |
| 1.086 | YGR213C | <i>RTA1</i> | Protein involved in 7-aminocholesterol resistance |
| 1.204 | YOR032C | <i>HMS1</i> | Basic helix-loop-helix (bHLH) protein with similarity to myc-family transcription factors |
| 1.321 | YMR317W | | Putative protein of unknown function with some similarity to sialidase from Trypanosoma |
| 1.321 | YIL013C | <i>PDR11</i> | ATP-binding cassette (ABC) transporter, multidrug transporter involved in multiple drug resistance |

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| 1.403 | YHR213W-A | | Putative protein of unknown function |
| 1.437 | YAL063C | <i>FLO9</i> | Lectin-like protein with similarity to Flo1p, thought to be expressed and involved in flocculation |
| 1.437 | YAL064W-B | | Fungal-specific protein of unknown function |
| 1.437 | YAR050W | <i>FLO1</i> | Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers flocculating ability that is chymotrypsin sensitive and heat resistant |
| 1.437 | YHR211W | <i>FLO5</i> | Lectin-like cell wall protein (flocculin) involved in flocculation, binds to mannose chains on the surface of other cells, confers flocculating ability that is chymotrypsin resistant but heat labile |
| 1.494 | YDL039C | <i>PRM7</i> | Pheromone-regulated protein, predicted to have one transmembrane segment |
| 1.528 | YNR002C | <i>ATO2</i> | Putative transmembrane protein involved in export of ammonia, a starvation signal that promotes cell death in aging colonies |
| 1.571 | YHL043W | <i>ECM34</i> | Putative protein of unknown function |
| 1.66 | YOR009W | <i>TIR4</i> | Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins |
| 1.892 | YMR081C | <i>ISF1</i> | Serine-rich, hydrophilic protein with similarity to Mbr1p |
| 2.206 | YAR050W | <i>FLO1</i> | Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers flocculating ability that is chymotrypsin sensitive and heat resistant |
| 2.229 | YJL116C | <i>NCA3</i> | Protein that functions with Nca2p to regulate mitochondrial expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase |
| 2.452 | YAR062W | | Hypothetical protein |
| 2.452 | YHR213W | | Putative protein of unknown function |
| 2.49 | YIR019C | <i>MUC1</i> | GPI-anchored cell surface glycoprotein (flocculin) required for pseudohyphal formation, invasive growth, flocculation, and biofilms |
| 2.586 | YIL011W | <i>TIR3</i> | Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins |
| 2.791 | YDL039C | <i>PRM7</i> | Pheromone-regulated protein, predicted to have one transmembrane segment |
| 4.329 | YMR164C | <i>MSS11</i> | Transcription factor involved in regulation of invasive growth and starch degradation |
| 4.497 | YOR010C | <i>TIR2</i> | Putative cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins |

Σ1278b *mss11*

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| -3.171 | YIR019C | <i>MUC1</i> | GPI-anchored cell surface glycoprotein (flocculin) required for pseudohyphal formation, invasive growth, flocculation, and biofilms |
| -2.962 | YMR164C | <i>MSS11</i> | Transcription factor involved in regulation of invasive growth and starch degradation |
| -2.426 | YOR032C | <i>HMS1</i> | Basic helix-loop-helix (bHLH) protein with similarity to myc-family transcription factors |
| -2.199 | YDR259C | <i>YAP6</i> | Putative basic leucine zipper (bZIP) transcription factor |
| -1.683 | YIL011W | <i>TIR3</i> | Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins |
| -1.656 | YHL043W | <i>ECM34</i> | Putative protein of unknown function |
| -1.21 | YPR013C | | Putative zinc finger protein |
