

Genes that are Sty1p- and/or Atf1p-dependent in unstressed cells

Genes that require Sty1p for basal level of expression in unstressed cells:

SPBPB10D8.01	putative allantoate permease of the major facilitator superfamily (MFS)
SPBC713.11C	UPF0057 family protein; possible stress response protein
SPBC23G7.10C	putative nadh-dependent flavin oxidoreductase
SPBC16A3.02C	putative quinone oxidoreductase; zinc binding oxidoreductase
frp1	ferric reductase transmembrane component
SPBPB2B2.01	putative amino-acid permease
fip1	iron permease
rec15	meiotic recombination protein rec15.
SPCC622.12C	nadp-specific glutamate dehydrogenase
SPAC23C4.05C	hypothetical protein; sequence orphan; predicted N-terminal signal sequence
SPCC736.15	hypothetical protein; similar to <i>S. cerevisiae</i> YGR086C
SPBC14F5.13C	putative vacuolar alkaline phosphatase; dephosphorylation of phosphopeptides
SPBPB2B2.13	putative galactokinase
SPAC922.04	sequence orphan; contains predicted N-term signal sequence
exg3	glucan 1,3-beta-glucosidase
vip1	vip1 protein
chol	phospholipid methyltransferase
SPAC26A3.16	yeast dsk2 homolog, ubiquitin-like protein
SPAC4D7.02C	putative glycerophosphoryl diester phosphodiesterase; hydrolyses deacylated phospholipids to G3p and the corresponding alcohols
mae2	malate oxidoreductase [nad]
SPCC1884.01	possibly pseudogene telomeric and has 2 non-consensus branch sites
SPAC212.09C	pseudogene; malic enzyme with 2 frameshifts
SPAC23D3.11	putative short chain dehydrogenase
SPCC338.12	putative proteinase precursor
SPAC19G12.09	putative aldose reductase
SPACUNK4.15	hypothetical protein; sequence orphan
SPAC750.08C	NAD-dependent malic enzyme- homologue 2
grx1	thioltransferase
SPBC2A9.02	putative dyhydroflavanol-4-reductase
SPCC63.14	hypothetical protein; sequence orphan; possible coiled-coil region
SPBC21H7.06C	conserved hypothetical protein
SPAC26F1.07	probable oxidoreductase
SPAC9E9.04	conserved protein; putative ER transmembrane protein; similar to <i>S. cerevisiae</i> YET1; predicted N-term signal sequence and transmembrane helices
SPBPB10D8.02C	putative arylsulfatase; contains sulphatase domain
SPAC22F8.05	putative alpha,alpha-trehalose-phosphate synthase
SPBC11C11.06C	hypothetical protein; sequence orphan
pyp1	protein-tyrosine phosphatase 1 (EC 3.1.3.48)
SPBC21C3.19	hypothetical protein; similar to <i>S. cerevisiae</i> YHR087W
cta1	catalase
gpx1	glutathione peroxidase
rds1	stress response protein rds1p
gpd1	NADH-dependent glycerol-3-phosphate dehydrogenase, involved in the production of glycerol in response to high osmolarity
SPBC725.10	similar to peripheral-type benzodiazepine receptor
hsp9	heat shock protein hsp9

Genes that require *Atflp* for basal level of expression in unstressed cells:

SPAC1786.04	very hypothetical protein
SPACUNK4.10	putative 2-hydroxyacid dehydrogenase
SPAC977.08	putative short chain dehydrogenase
cdt2	target of <i>cdc10</i> transcription factor: coupling START with cytokinesis
SPAC1687.16C	sterol desaturase
mae1	malic acid transport protein (malate permease)
SPBC887.17	putative uracil permease
SPBC1683.10C	similar to <i>S. coelicolor</i> glutamate synthase large subunit and plant nodulin-21 which may be important for nitrogen fixation; has 8 predicted transmembrane domains
SPBC1271.05C	Zinc finger zf-AN1 protein
SPAC922.04	hypothetical protein; sequence orphan; contains predicted N-term signal sequence; has transcript
SPAPJ695.01C	hypothetical protein; possibly <i>S. pombe</i> specific; similar to SPCC569.02 and SPCC20C8.02 Predicted N-terminal signal sequence
SPAC11D3.13	conserved hypothetical protein; contains ThiJ domain
SPAC17H9.18C	hypothetical protein; sequence orphan
SPBC1289.16C	putative amine oxidase
SPAC2E1P3.01	putative dehydrogenase by similarity
SPAC1348.05	putative membrane transporter
SPAC1786.02	putative lysophospholipase precursor
vip1	vip1 protein
SPAC513.05	probable alpha-mannosidase
SPBC1347.01C	putative deoxycytidyl transferase; possibly involved in mutagenic translesion DNA synthesis by similarity to <i>S. cerevisiae</i> rev1; similarity to damage inducible proteins; contains BRCA1 C Terminus (BRCT) d
mei3	21 kd protein inducing meiosis and sporulation
SPAC977.15	putative hydrolase
SPCC663.14C	hypothetical protein; similar to <i>S. cerevisiae</i> YPL221W; contains predicted N-terminal signal sequence; contains 8 predicted transmembrane helices
SPAC2F3.05C	aldo/keto reductase family oxidoreductase
SPBC8E4.04	probable oxidoreductase
misc_RNA_1.1.38.RC	MEIRNA D31852 Fission yeast DNA for meiRNA, complete sequence
SPCC550.11	putative RanBP7/importin-beta/Cse1p superfamily RanGTP-binding protein
SPAC186.03	l-asparaginase precursor
misc_RNA_2.2.48.RC	RNA associated with spc02611 spc02031, possible cellular RNA as no obvious open reading frame or spliced gene in this region
SPAPB24D3.08C	putative NADP dependent oxidoreductase
SPAC977.14C	putative oxidoreductase
SPBC947.04	hypothetical serine/threonine rich repeat protein; similar to <i>S. pombe</i> SPBC1289.15, SPBC21D10.06, SPCC188.09C SPAP11E10.02C SPBC21D10.06C SPAC1348.08C SPAC977.07C; possibly <i>S. pombe</i> specific; serine/threonine-rich low similarity to cell surface glycoproteins
SPAC27D7.12C	hypothetical protein; sequence orphan
SPBC16A3.02C	putative quinone oxidoreductase; zinc binding oxidoreductase
SPCC622.12C	nadp-specific glutamate dehydrogenase
SPBC19C7.04C	similar to <i>S. cerevisiae</i> Ymr295p; possibly fungal specific
SPBC215.11C	putative oxidoreductase; aldo-keto family
SPBC582.06C	hypothetical protein; sequence orphan; predicted coiled-coil protein
SPBC1347.11	hypothetical protein; sequence orphan

SPBC409.08	putative membrane transport protein
tRNA	tRNA
SPAC139.05	probable succinate semialdehyde dehydrogenase
SPBPB10D8.01	putative allantoin permease of the major facilitator superfamily (MFS)
SPCC550.07	acetamidase
SPAC26F1.04C	hypothetical protein; similar to <i>S. cerevisiae</i> YBR026
SPAC4D7.02C	putative glycerophosphoryl diester phosphodiesterase; hydrolyses deacylated phospholipids to G3p and the corresponding alcohols
git5	G-protein beta subunit git5p.
SPAC750.01	pseudogene; oxidoreductase; no initiator methionine
SPCC584.02	putative metal-binding regulatory protein
SPAC26F1.14C	putative flavoprotein; similar to human mitochondrial apoptosis-inducing factor; inducing chromatin condensation and DNA fragmentation
SPBC4C3.08	unknown function, with Pfam-B_20341; predicted N-term signal sequence
SPAC23D3.11	putative short chain dehydrogenase
rec8	meiotic cohesin; similar to <i>S. cerevisiae</i> REC8
SPAC343.20	hypothetical protein; sequence orphan; has transcript profile on microarray
SPBC8D2.19	serine/threonine protein kinase; putative positive regulator of meiotic genes; similar to <i>S. cerevisiae</i> IME2; meiosis specific transcription
SPBC713.11C	UPF0057 family protein; possible stress response protein
SPBC1861.01C	hypothetical protein; sequence orphan
SPAC212.09C	pseudogene; malic enzyme with 2 frameshifts
obr1	brefeldin A resistance protein
SPAC27D7.10C	hypothetical protein; pombe specific; contains Pfam-B_10631 and a putative signal peptide
SPAC869.09	hypothetical protein; similar to <i>N. crassa</i> conidiation protein 6
SPAPB24D3.07C	hypothetical protein; sequence orphan; predicted N-terminal signal sequence
mae2	malate oxidoreductase [nad]
SPCC338.18	hypothetical protein; sequence orphan
SPAC750.08C	NAD-dependent malic enzyme- homologue 2
SPBC11C11.06C	hypothetical protein; sequence orphan
SPAC27D7.09C	hypothetical protein; pombe specific; contains Pfam-B_10631 and a putative signal peptide
dak2	dihydroxyacetone kinase
pyp1	protein-tyrosine phosphatase 1 (EC 3.1.3.48)
SPCC338.12	putative proteinase precursor
SPAC3H1.11	C2H2 TYPE Zinc finger protein
SPAC15A10.05C	hypothetical protein; similar to <i>S. cerevisiae</i> YNL200C
SPAC9E9.04	conserved hypothetical protein; putative endoplasmic reticulum transmembrane protein; similar to <i>S. cerevisiae</i> YET1; contains predicted N-term signal sequence; contains 2 predicted transmembrane helices; contains predicted C-term coiled-coil
SPAC31G5.19	tat-binding homolog 7, AAA ATPase family protein
SPBC1271.09	MFS transporter of unknown specificity
SPBPB2B2.01	putative amino-acid permease
SPAC22H10.13	putative metallothionein; possibly not real; may be spurious Pfam due to CYS
SPAC2F7.06C	DNA polymerase X family; involved in repair
SPBPB2B2.13	putative galactokinase
SPCC1884.01	possibly pseudogene telomeric and has 2 non-consensus branch sites
SPAC1002.19	putative GTP cyclohydrolase; riboflavin biosynthesis

SPAC26F1.07	probable oxidoreductase (EC 1.-.-)
pex7	peroxisomal targeting signal 2 receptor 2
SPBC11B10.08	hypothetical protein; similar to <i>S. cerevisiae</i> YFL010C (cell wall protein); but with pombe specific domain Pfam-B_15930
exg3	glucan 1,3-beta-glucosidase
abp2	ars binding protein 2
cta1	catalase
SPBC21C3.19	hypothetical protein; similar to <i>S. cerevisiae</i> YHR087W
isp4	sexual differentiation process protein isp4
grx1	thioltransferase
I22_pex7	peroxisomal targeting signal 2 receptor 2
SPAC1002.17C	probable uracil phosphoribosyltransferase
SPAC19G12.09	putative aldose reductase
SPBC23G7.10C	putative nadh-dependent flavin oxidoreductase
SPAC2H10.01	hypothetical fungal binuclear cluster domain protein
SPBC2A9.02	putative dyhydroflavanol-4-reductase
gpd1	NADH-dependent glycerol-3-phosphate dehydrogenase, involved in the production of glycerol in response to high osmolarity
rds1	stress response protein rds1p
gpx1	glutathione peroxidase
hsp9	heat shock protein 9

Genes that are de-repressed in unstressed *sty1* deletion cells:

SPAC3C7.08C	member of the non-transporter group of the ATP-binding cassette (ABC) superfamily; similar to <i>S. cerevisiae</i> NEW1
SPAPB15E9.01C	hypothetical protein; sequence orphan; low complexity protein; similar to cell surface proteins
SPAC186.05C	hypothetical protein;UPF0016 family
pfk1	6-phosphofructokinase beta subunit
SPAC16E8.01	putative cytoskeleton assembly control protein; SRC homology domain
SPCC584.01C	putative sulfite reductase
SPCC18B5.02C	cinnamoyl-coa reductase pseudogene
SPBC1271.07C	acetyltransferase
app1	actin binding protein with SH3 domains
SPBC56F2.08C	RNA binding protein with pumilio domains; may be associated with cell structure (microtubules) by similarity to yeast <i>jsn1</i>
SPAC20G8.06	putative CCR4-Not complex; similar to <i>S. cerevisiae</i> carbon catabolite repressor protein 4 component CDC39
misc_RNA_2.2.51.RC	potential RNA gene
SPBC27B12.12C	MIT family metal ion transporter PI066
SPBC36.03C	MSF drug efflux transporter of unknown specificity
SPCC550.11	putative RanBP7/importin-beta/Cse1p superfamily RanGTP-binding protein
SPBC119.17	putative zinc metalloprotease
SPAC1348.13	similar to fragment of <i>cox1</i> intron protein; pseudogene
eng1	endo-1,3-beta-glucanase
SPBC18H10.02	putative long-chain-fatty-acid--coa ligase
SPBC1D7.03	cyclin-like protein
SPBC359.02	putative alanine racemase
ura4	orotidine 5'-phosphate decarboxylase; similar to <i>S. cerevisiae</i> URA3
kap104	putative importin beta-2 subunit (transportin), beta-karyopherin involved in nuclear transport of mRNA-binding proteins
SPCC23B6.04C	conserved CRAL/TRIO domain; SEC14 cytosolic factor family; possibly involved in lipid movement between membranes by similarity to yeast <i>pdr16</i>
SPCC663.08C	putative short chain dehydrogenase
isp7	sexual differentiation process protein <i>isp7</i>
SPBC354.10	agglutinin-like protein; serine-rich protein; putative glucoamylase; predicted cell surface protein
SPCC965.07C	glutathione-S-transferase
SPBC19C2.09	putative transcription factor; similar to <i>S. cerevisiae</i> YOR032C
SPAC1B3.16C	MFS transporter of unknown specificity
SPAC29A4.16	putative serine/threonine protein kinase
wsp1	Wiskott-Aldrich syndrome protein homolog; implicated in stress-response pathways; implicated in control of the actin cytoskeleton; involved in actin patch assembly and localization; promoter contains <i>homo1D</i> box
SPBC146.13C	putative myosin I protein
pi021	hypothetical protein located in cell periphery and cytoplasm; sequence orphan
SPAC1B3.10C	putative regulatory protein; SEL repeats; extracellular by similarity to <i>C. elegans sel-1</i>
SPBC30B4.05	putative karyopherin-beta involved in the nuclear export of karyopherin-alpha, possible kinetochore protein that interacts with centromeric element

	CDEII; putative chromosomal segregation/apoptosis susceptibility protein- by similarity to <i>S. cerevisiae</i> CSE1
P22190	mitochondrial protein
SPCC63.03	hypothetical DNAJ domain protein
SPCC663.06C	putative short chain dehydrogenase protein
SPBC660.15	RNA-binding protein
SPCC1742.01	hypothetical protein; sequence orphan; large repeated threonine-rich region; contains 4 Trp mucin, mucin-like glycoprotein repeat; contains predicted N-terminal signal sequence
SPAC1039.02	membrane protein; similar to <i>S. cerevisiae</i> YHR202W; putative esterase; contains Pfam-B_34335; contains Pfam-B_34336; which co-occur in 5' nucleotidase
tea2/klp4	kinesin-like protein; KIP2 subfamily
SPAC1F5.11C	putative transcriptional regulatory complex protein; yeast tra1 homologue
SPAC212.11	DNA helicase possibly pseudo
hmg1	3-hydroxy-3-methylglutaryl-coenzyme a reductase
aro1	pentafunctional arom polypeptide [includes 3-dehydroquinate synthase](ec 4.6.1.3); 3-dehydroquinate dehydratase
spt3	transcriptional regulator; putative SAGA complex (Spt-Ada-Gcn5- Acetyltransferase); similar to <i>S. cerevisiae</i> SPT3
SPAC1A6.04C	putative lysophospholipase precursor
SPAC31F12.01	related to yeast zds family proteins
SPBPB2B2.05	putative gmp synthase [glutamine-hydrolyzing] (ec 6.3.5.2) (glutamineamidotransferase) (gmp synthetase)
SPAC22A12.06C	similar to <i>S. pombe</i> dihydrofolate reductase Dfr1p
SPAC1002.17C	probable uracil phosphoribosyltransferase
SPBPB2B2.06C	putative 5' nucleotidase family protein; possibly involved in the degradation of external UDP-glucose by similarity
rRNA	5S ribosomal RNA
SPBC336.03	centromere-associated spindle component; possibly involved in chromosome segregation; putative guanine nucleotide exchange factor; similar to <i>S. cerevisiae</i> SPC24
SPCC320.06	hypothetical protein; sequence orphan
SPCC1322.06	Putative member of the RanBP7-importin-beta-Cse1p superfamily; similar to human RAN binding protein 11
SPBC3H7.03C	2-oxoglutarate dehydrogenase e1 component
hsp16	heat shock protein 16
SPCC1235.05C	helicase of the Snf2p family with a DNA-dependent ATPase domain, possibly involved in resistance to UV radiation; by similarity to yeast snf2
wee1	dual specificity mitosis inhibitor protein kinase; CDK tyrosine kinase; negatively regulates G2/M transition; similar to <i>S. cerevisiae</i> SWE1
SPAC1006.01	putative subtilase-type peptidase
SPAC212.06C	pseudogene; truncated C terminal of DNA helicase in rearranged telomeric region
SPAC19G12.16C	Hypothetical serine/threonine-rich protein.
SPBPB7E8.02	putative RNA pol II specific subunit C82/hRPC62
SPBC19C7.06	prolyl-trna synthetase, cytoplasmic
SPCC70.05C	putative serine/threonine protein kinase
SPAC1399.01C	putative purine permease
SPCC417.12	putative carboxylesterase-lipase family member
SPAC12G12.09	hypothetical protein; sequence orphan

SPBC21C3.08C	ornithine aminotransferase (EC 2.6.1.13)
msh6	mutS family DNA mismatch repair protein msh6
SPBC713.12	squalene epoxidase; ergosterol biosynthesis
SPBC20F10.10	similarity to yeast Pho85p-associated PCL6 Cyclin
SPAC57A10.02	serine/threonine protein kinase; regulation of cell cycle progression; nim1 family
P21547	mitochondrial protein
SPAC24H6.11C	putative SulP sulfate transporter
SPCC965.14C	putative Cytidine and deoxycytidylate deaminase zinc-binding protein
cdc28/prp8	Putative ATP-dependent RNA helicase involved in cell cycle progression and mRNA splicing
SPCC70.08C	probable methyltransferase
rad22	DNA repair and recombination protein; involved in mating type switching; similar to <i>S. cerevisiae</i> RAD52
P05511	mitochondrial protein
SPAPB21F2.02	Protein with similarity to <i>Aspergillus nidulans</i> dopA which causes delayed and asynchronous morphogenesis during asexual reproduction and <i>S. cerevisiae</i> DOP1 (which is lethal)
SPBC1685.12C	very hypothetical protein
SPAC26F1.09	TBC domain protein; putative GTPase activating protein of Rab-like GTPase
pyr1	pyruvate carboxylase (EC 6.4.1.1)
pgak	P-type calcium ATPase
SPAC6C3.09	hypothetical protein; with similarity to ribonuclease p protein subunit p40
SPCC285.05	purine transporter
SPBC215.08C	carbamoyl-phosphate synthase
SPAC1142.08	similar to N-term of yeast FhlI transcriptional activator of the forkhead/HNF3 family
SPBC530.11C	putative transcriptional regulator
bfr1/hba2	MFS brefeldin A efflux transporter

Genes that are de-repressed in unstressed *atf1* deletion cells:

SPBC359.02	putative alanine racemase
SPAC1F8.03C	MFS efflux transporter of unknown specificity
SPACUNK4.19	hypothetical protein; sequence orphan
SPBC359.06	putative class II aldolase and adducin N terminal domain
SPCC1322.07C	hypothetical protein; sequence orphan; has transcript pattern on microarray
SPAPB24D3.03	putative agmatinase precursor
SPAC186.05C	hypothetical protein;UPF0016 family
SPAC11D3.09	arginase family protein; putative agmatinase precursor
SPBC359.03C	putative amino acid permease
SPAC4H3.03C	putative family 15 glycosyl hydrolase
SPBC21C3.08C	ornithine aminotransferase (EC 2.6.1.13)
ipk1	inositol 1,3,4,5,6-pentakisphosphate (IP5) kinase
SPBPB2B2.06C	putative 5' nucleotidase family protein; possibly involved in the degradation of external UDP-glucose by similarity
SPBC359.01	putative amino acid permease
SPAC869.05C	SulP sulfate transporter
SPAC1039.02	membrane protein; similar to <i>S. cerevisiae</i> YHR202W; putative esterase; contains Pfam-B_34335; contains Pfam-B_34336; which co-occur in 5' nucleotidase
SPAC9E9.09C	putative aldehyde dehydrogenase
SPBC1683.12	MFS transporter of unknown specificity
map1	pheromone receptor transcription activator
SPBC1683.06C	putative inosine-uridine preferring nucleoside hydrolase
SPBC359.05	ABC multidrug or ion efflux transporter
mfm2	M-factor precursor 2
SPBC32H8.02c	hypothetical protein located in cell periphery and cytoplasm; sequence orphan
SPAC26F1.05	hypothetical protein; sequence orphan; has transcript from microarray
fbp1	fructose-1,6-bisphosphatase
SPCC757.12	putative alpha-amylase
car1	arginase, catalyzes the first step in arginine degradation, the hydrolysis of arginine to urea and ornithine in the urea cycle
aru1	arginase
isp3/meu4	sexual differentiation process protein isp3; meiotic expression upregulated
SPAC1399.02	MFS drug transporter of unknown specificity
SPCC1739.08C	short chain dehydrogenase; putative sorbitol utilization
SPAC3H1.06C	MFS drug efflux transporter of unknown specificity
SPCC1235.01	hypothetical T/N-rich protein; contains ~37 copies of a 7-10 repeat consensus 'PMEEITMTI' and a S/N rich C terminal region
SPAC11D3.01C	protein with similarity to neurospora conidiation specific protein
fip1	iron permease
SPBC29A3.11C	MC transporter of unknown specificity
SPCC569.07	putative aromatic aminotransferase
SPBC660.05	hypothetical glycine-rich protein; pombe specific domain Pfam-B_15930
SPBC4F6.09	MFS efflux transporter of unknown specificity
ste11/aff1/stex	transcription factor; HMG box; regulates genes required for mating
SPCC2H8.02	MFS inorganic phosphate transporter
SPBC3H7.05C	hypothetical protein; sequence orphan; contains 7 predicted transmembrane helices contains predicted N-term signal sequence
SPAC22A12.06C	similar to <i>S. pombe</i> dihydrofolate reductase Dfr1p

SPCC1322.08	putative serine/threonine protein kinase
misc RNA 1.1.7.RC	RNA not associated with an ORF
SPAC13F5.07C	very hypothetical protein
SPBPB2B2.09C	putative ketopantoate reductase (2-dehydropantoate 2-reductase), has similarity to Cbs2p and yeast YHR063C
SPCC1020.03	CDF metal cation transporter
ght4	putative glucose transporter protein
SPAC11D3.06	MATE family transporter of unknown specificity
SPCC569.05C	MFS drug efflux transporter of unknown specificity
SPBC1271.07C	acetyltransferase
SPAC13G7.12C	putative choline kinase
SPCC306.08C	malate dehydrogenase, mitochondrial precursor
SPBC660.15	RNA-binding protein
SPCC285.05	purine transporter
mam2	pheromone p-factor receptor
mvp1	putative vacuolar protein sorting protein
SPAC17G6.02C	putative cell wall protein; S cerevisiae has many paralogs which confer resistance to a variety of substances
ght3	MFS glucose transporter
SPBC8E4.02C	hypothetical protein; sequence orphan
SPCC2H8.03	very hypothetical protein
SPCC965.14C	putative cytidine and deoxycytidylate deaminase zinc-binding protein