

## Clusters from Figure 5A

### Cluster 1:

vip1	vip1 protein
SPBC215.11C	putative oxidoreductase; aldo-keto family
SPCC965.06	putative potassium channel subunit
SPBC23G7.10C	putative nadh-dependent flavin oxidoreductase
SPCC736.15	hypothetical protein; similar to <i>S. cerevisiae</i> YGR086C
exg3	glucan 1,3-beta-glucosidase
SPBC2A9.02	putative dyhydroflavanol-4-reductase
gpx1	glutathione peroxidase
SPAC26F1.07	probable oxidoreductase
SPAC23D3.11	putative short chain dehydrogenase
hsp9	heat shock protein 9
rds1	stress response protein rds1p
gpd1	NADH-dependent glycerol-3-phosphate dehydrogenase, involved in production of glycerol in response to high osmolarity
SPAC9E9.04	conserved hypothetical protein; putative endoplasmic reticulum transmembrane protein; similar to <i>S. cerevisiae</i> YET1; contains N-term signal sequence; contains transmembrane helices; contains C-term coiled-coil
SPAC19G12.09	putative aldose reductase
SPAC4D7.02C	putative glycerophosphoryl diester phosphodiesterase; hydrolyses deacylated phospholipids to G3p and the corresponding alcohols
git5	G-protein beta subunit git5p.
grx1	thioltransferase
SPBC21C3.19	hypothetical protein; similar to <i>S. cerevisiae</i> YHR087W
SPBC11C11.06C	hypothetical protein; sequence orphan
SPCC338.12	putative proteinase precursor
SPBC16A3.02C	putative quinone oxidoreductase; zinc binding oxidoreductase
SPAC57A10.09C	nonhistone chromosomal protein 6b
SPAC26F1.14C	putative flavoprotein; similar to human mitochondrial apoptosis-inducing factor; flavoprotein inducing chromatin condensation and DNA fragmentation

**Cluster 2:**

SPAC27D7.09C	hypothetical protein; pombe specific; contains Pfam-B_10631 and a putative signal peptide
SPAC27D7.10C	hypothetical protein; pombe specific; contains Pfam-B_10631 and a putative signal peptide
SPAC27D7.11C	hypothetical protein; pombe specific; contains Pfam-B_10631 and a putative signal peptide; contains low-complexity threonine-rich region
SPAC4H3.08	putative short chain dehydrogenase
SPAC22H10.13	putative metallothionein; may be spurious Pfam due to CYS
SPAC22G7.11C	hypothetical protein; similar to N. crassa conidiation -specific protein 6
SPAC869.09	hypothetical protein; similar to N. crassa conidiation protein 6
SPAC23D3.05C	alcohol dehydrogenase pseudogene
SPBC1773.06C	alcohol dehydrogenase
SPCC16A11.15C	hypothetical protein; sequence orphan
SPAC22A12.17C	short chain dehydrogenase; possible sorbitol utilization
SPBC1289.14	adducin N terminal domain protein
SPBC12C2.04	conserved hypothetical protein
isp6	sexual differentiation process protein; putative subtilase-type proteinase
SPBC56F2.06	hypothetical protein; sequence orphan
SPAC3C7.05C	hypothetical protein; contains Pfam-B_11461 domain
SPBC428.10	hypothetical protein; sequence orphan
SPAC16A10.01	hypothetical protein; similar to S. cerevisiae YJL108C which is regulated by pheromone; contains 9 predicted transmembrane helices
gut2	glycerol-3-phosphate dehydrogenase, mitochondrial precursor(ec 1.1.99.5)
SPAC3C7.13C	glucose-6-phosphate 1-dehydrogenase
SPCP31B10.06	C2-domain protein; synaptotagmin family
SPAC15E1.02C	hypothetical protein; sequence orphan; 3 predicted transmembrane helices
SPCC1393.12	hypothetical protein; sequence orphan
SPAC139.05	probable succinate semialdehyde dehydrogenase
SPCC757.03C	conserved hypothetical protein
SPBC725.03	hypothetical protein; similar to S. cerevisiae YGR017W
SPAC167.06C	hypothetical protein
SPACUNK4.17	putative sugar oxidoreductase; possible sorbitol utilisation
SPAC23H3.15C	hypothetical serine-rich protein; sequence orphan
SPAC637.03	hypothetical protein; sequence orphan; contains 8 predicted transmembrane segments contains predicted N-term signal sequence
SPAC23C11.06C	hypothetical protein; similar to S. cerevisiae YNL115C; contains 5 predicted transmembrane helices
SPAC688.04C	glutathione S transferase 3
SPBC365.12C	hypothetical protein; low similarity to S. cerevisiae YML128C
ptc4	protein phosphatase 2c isoform
SPAC513.02	protein with similarity to phosphoglycerate mutases
SPBC24C6.09C	similarity to transketolase; contains Pfam-B_53149 and Pfam-B_17168; high similarity to Synechocystis Sp SW:P74690; putative phosphotransacetylase;
SPBC16E9.16C	pseudogene
SPCC61.03	conserved hypothetical protein
pyp2	protein-tyrosine phosphatase 2; nuclear/cytoplasmic
SPBC660.05	hypothetical glycine-rich protein; pombe specific domain Pfam-B_15930
pcr1/mts2	B-zip transcription factor pcr1
SPCC1183.11	protein with DUF0003, Pfb_28723 and ehand
SPBC1105.14	putative Zinc-finger transcriptional activator for genes involved in the

	multistress response by similarity to yeast msn2
SPAC22E12.03C	THIJ/PFPI family protein; putative thiamine biosynthesis enzyme
SPAC25H1.02	JOR domain; possibly chromatin associated; Koonin et al
tms1	putative sorbitol dehydrogenase
SPAPB1A11.03	putative FMN dependent dehydrogenase; similar to lactate dehydrogenase
SPAC5H10.02C	hypothetical protein; similar to <i>S. cerevisiae</i> YPL280W
cmb1	HMG box mismatch binding protein; binds to cytosines in base mismatches and opposite chemically altered guanines
SPAC11D3.13	conserved hypothetical protein; contains ThiJ domain
SPAC2E1P3.01	putative dehydrogenase by similarity
SPAC2F3.05C	aldo/keto reductase family oxidoreductase
SPAC26F1.04C	hypothetical protein; similar to <i>S. cerevisiae</i> YBR026
SPAC977.13C	putative hydrolase pseudogene

**Cluster 3:**

cgs1	CAMP-dependent protein kinase regulatory chain; similar to S. cer. BCY1
mpr1/spy1	stress response regulator phosphotransmitter; response regulator phosphotransferase; similar to S. cerevisiae YPD1
mvp1	putative vacuolar protein sorting protein
SPAC607.08C	conserved hypothetical protein; similar to YFL034W
SPAC1348.12	zinc finger protein; pseudo
SPAC31A2.12	hypothetical protein; similar to S. cerevisiae ROD; similar to S. pombe SPCC584.15C
SPBC20F10.10	similarity to yeast Pho85p-associated PCL6 Cyclin
SPAC19B12.08	putative Protein that mediates attachment of autophagosomes to microtubules, by similarity to yeast aut2
SPAC57A7.05	hypothetical protein; similar to S. cerevisiae YDL231C at the C-term; contains 11 predicted transmembrane helices; leucine-serine rich
SPCC1494.03	hypothetical protein; sequence orphan
SPCC576.04	putative receptor-associated protein
SPBC23G7.06C	hypothetical protein; similar to S. cerevisiae YPR091c; similar to A. thaliana t18k17.13 protein; all 3 contain predicted N-terminal signal sequence
pka1/tpk/git6	CAMP-dependent protein kinase catalytic subunit
SPAC1E11.03	serine/threonine protein kinase; yeast yak1 homolog
ntp1	neutral trehalase; subcellular localization of GFP fusion- Cytoplasm
SPAC2C4.17C	hypothetical protein; contains DUF0003 Pfb_28723 and ehand
SPBC660.06	hypothetical glycine rich protein; pombe specific domain Pfam-B_15930
SPCC1322.08	putative serine/threonine protein kinase
SPCC306.08C	malate dehydrogenase, mitochondrial precursor
SPAC4H3.03C	putative family 15 glycosyl hydrolase
SPBP4H10.10	membrane protein of unknown function, possibly involved in respiration by similarity to YGR101W; rhomboid family
SPBC20F10.03	hypothetical protein; contains Pfam-B_11425; similarity to mouse and rat interferon-related developmental regulator 1- nerve growth factor; also conserved in C. elegans
atf1/mts1/sss1/gad7	transcription factor atf1; heterodimeric transcriptional activator; binds M26 recombination hotspot; stimulated by the stress-activated Sty1p MAP kinase cascade
ptc1	protein phosphatase 2c homolog
SPCC191.01	hypothetical protein; sequence orphan
SPCC417.05C	putative involvement in chitin biosynthesis; by similarity
SPCC4G3.03	hypothetical protein similar to S. cerevisiae YLR149C; putative apoptotic protease activating factor, by low similarity to human spaf1 (conserved catalytic residues)

**Cluster 4:**

SPBC1773.17C	putative glycerate- and formate-dehydrogenase
SPBC1271.08C	very hypothetical protein
SPAC2C4.15C	ubiquitin regulatory domain (UBX) protein
SPBC30D10.14	putative hydrolase
tps1	alpha,alpha-trehalose-phosphate synthase
psi1	DNAJ domain protein
SPACUNK4.16C	putative alpha-trehalose-phosphate synthase
hsp16	heat shock protein 16
SPAC22H12.01C	hypothetical protein; sequence orphan
SPCC338.18	hypothetical protein; sequence orphan
SPBC119.03	putative catechol o-methyltransferase
SPBC1105.13C	hypothetical protein; sequence orphan; low correlation score; shows expression on microarray
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
SPAC521.03	putative short chain dehydrogenase
plr1	pyridoxal reductase
SPBC1539.04	hypothetical protein; similar to <i>S. cerevisiae</i> YLL023C
SPCC576.03C	thioredoxin peroxidase
trx2	thioredoxin II; alternative C terminal reported
SPAC513.07	putative cinnamoyl-coa reductase

**Cluster 5:**

SPCC24B10.11C	hypothetical protein; predicted coiled-coil region; sequence orphan
ura3	dihydroorotate dehydrogenase precursor
ade8	adenylosuccinate lyase
SPCC1223.14	chorismate synthase
SPCC297.04C	SET domain protein
SPAC23A1.03	putative adenine phosphoribosyltransferase (APRT); similar to <i>S. cerevisiae</i> APT1; member of the phosphoribosyl transferases family
SPBC8D2.18C	putative adenosylhomocysteinase
SPBC8D2.10C	putative arginine n-methyltransferase
SPBC1778.01C	zuotin like protein; putative zdna binding; dnaj domain containing protein
tef5	elongation factor 1 beta
gln1	glutamine synthetase
SPBC1198.02	adenosine deaminase
SPBC1734.01C	hypothetical protein; similar to <i>S. cerevisiae</i> YDR365C which is null lethal
SPAC1F7.02C	probable ATP-dependent RNA helicase
ade9	C-1-tetrahydrofolate synthase, mitochondrial; Includes: methylenetetrahydrofolate dehydrogenase; methylenetetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase
rpc34	DNA-directed rna polymerase III subunit
SPBC776.17	putative protein involved in pre-rRNA processing and ribosome assembly; by similarity to yeast rrp7
SPAC823.08C	putative atp-dependent RNA helicase
SPCC1183.07	putative rRNA biogenesis protein; rrp5 homolog; multiple S1 RNA binding domain protein
kap123	putative importin beta-4 subunit; Karyopherin-beta involved in nuclear import of ribosomal proteins
SPCC1827.01C	hypothetical helicase
SPBC16D10.01C	homolog of yeast tc1; Protein that interacts with protein phosphatase 2C
SPBC1711.07	WD repeat protein; possible nuclear pore complex associated
SPAC926.08C	hypothetical protein; similar to <i>S. cerevisiae</i> YKR081C; contains Pfam-B_20446
SPBC83.15	conserved hypothetical protein; similar to <i>S. cerevisiae</i> YGL111W
SPBC29A3.06	WD repeat protein
SPAC8F11.04	hypothetical protein; similar to <i>S. cerevisiae</i> YKR060W
SPAC683.02C	hypothetical zinc-finger protein
rpa49	DNA-directed RNA polymerase I 49 kd polypeptide
SPAC23H4.15	hypothetical protein; similar to <i>S. cerevisiae</i> YDL060W- which is null lethal; contains Pfam-B_1475 and Pfam-B_6211
rpl24-3	60S ribosomal protein L24C (L30)
SPAC6G9.02C	RNA binding protein
SPBC4F6.14	RNA binding ribonucleoprotein
SPBC106.14C	possibly required for actin cytoskeletal organisation by similarity to yeast sda1
SPAC19A8.07C	U3 snoRNP component; required for pre-18S rRNA processing; similar to <i>S. cerevisiae</i> IMP4
SPCP1E11.11	conserved hypothetical protein; pumilio-like
SPBC11G11.03	putative 60S acidic ribosomal protein
SPBC9B6.07	Protein involved in maturation of 25S rRNA; by similarity to yeast rrp1
SPBC16C6.12C	Protein possibly involved in cell morphogenesis, cytoskeletal regulation; establishment of cell polarity; by similarity to yeast LAS1
SPAC1486.09	Protein that may associates with the 26S proteasome; by similarity to yeast

	nob1
SPAC222.06	putative Nuclear protein with HMG-like acidic region, required for propagation of M1 double-stranded RNA; by similarity to yeast mak16
SPBC19F5.05C	pescadillo-like hypothetical protein; yeast homolog YGR103W purifies as part of nuclear pore complex
SPCC320.11C	putative protein involved in 60S ribosome subunit biogenesis
mis3	strong similarity to yeast cell division and spore germination protein Krr1p
SPBC800.06	protein required for biogenesis of the 60S ribosomal subunit; possibly localized to the nucleolus; similar to <i>S. cerevisiae</i> BRX1
SPAC890.05	conserved hypothetical protein with G-patch domain
SPCC18.12C	tRNA synthetase class II (D K N), cytoplasmic
SPBC14F5.06	putative RNase L inhibitor
SPAC10F6.03C	probable CTP synthase
SPBC23E6.05	conserved hypothetical protein
fkbp39	peptidyl prolyl cis-trans isomerase
gar1	pre-mrna processing protein Gar1p
SPBC32H8.05	hypothetical protein; similar to <i>S. cerevisiae</i> YBL028C
SPBC215.06C	protein with a putative zinc finger domain, has similarity to mouse LYAR cell growth regulating nucleolar protein
SPAC18B11.06	putative U3 snoRNP component; required for pre-18S rRNA processing; similar to <i>S. cerevisiae</i> LCP5
SPBC29A3.16	putative regulator of ribosome synthesis by similarity to yeast rrs1
SPAC1B9.03C	similarity to yeast mating protein SSF1
SPCC613.08	putative cdk inhibitor by similarity to human tok1
SPAC30C2.02	hypothetical protein; similar to <i>S. cerevisiae</i> YJR070C
dbp2	DEAD/DEAH box helicase; putative pre-mRNA splicing factor; human p68-like protein; similar to <i>S. cerevisiae</i> DPB2; large 3' intron as in <i>S. cerevisiae</i>
SPAC1142.04	possible nuclear pore complex by similarity to yeast YOR206W; putative coiled-coil regions
rpl7-3	60S ribosomal protein L7
SPAC56F8.09	possibly involved in cleavage at site A2 in pre-rRNA; ribosomal RNA processing pathway; similar to <i>S. cerevisiae</i> RRP8
SPAPB1A10.14	hypothetical protein; sequence orphan
SPAC6G9.10C	DNA2/NAM family DEAD-box RNA helicase; putative positive effector of tRNA-splicing endonuclease; required for intron cleavage of tRNAs; possibly involved in snRNA/snoRNA maturation; similar to <i>S. cerevisiae</i> SEN1
SPAC19B12.01	similar to <i>S. cerevisiae</i> YNL313C Protein of unknown function, YNL313C has tetratricopeptide (TPR) repeats
SPCC584.13	APC amino acid transporter
SPBC17D1.06	putative atp-dependent rna helicase
SPBC16E9.10C	AAA ATPase
SPBP8B7.20C	putative nucleolar protein; NOL1/NOP2/sun family
SPAC20G8.09C	hypothetical protein; similar to <i>S. cerevisiae</i> YNL132W/KRE33 Killer toxin resistant which is null lethal- and induced by glucose repression; highly conserved
SPAC17H9.04C	RNA-binding / Ran zinc finger protein
SPAC23C4.17	putative methyltransferase that methylates cytidine to 5-methyl-cytidine (m5C) at several positions in different tRNAs; by similarity to yeast ncl1

**Cluster 6:**

SPBP23A10.11C	serine-rich protein; putative cell wall; possible septation and/or ageing, by similarity
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
SPBC887.17	putative uracil permease
SPBC1683.01	MFS inorganic phosphate transporter
SPBC8E4.01C	MFS inorganic phosphate transporter
SPBC839.07	rhodanase domain protein
SPBC23E6.09	tpr domain protein; putative $\beta$ General repressor of RNA polymerase II transcription that is brought to target promoters by sequence-specific DNA-binding proteins by similarity to yeast ssn6
SPBPB7E8.01	hypothetical protein; sequence orphan; predicted N-term signal sequence
pho4	thiamine-repressible acid phosphatase precursor
SPAC6G10.12C	hypothetical zinc-finger protein; possibly involved in metallothionein expression
prh1	probable atp-dependent rna helicase prh1
SPCC965.13	MFS amiloride efflux transporter; car1 homologue
SPBC25B2.09C	arginyl-trna synthetase, putative cytoplasmic
lps1	pseudouridylate synthase



**Cluster 7:**

SPBC776.08C	hypothetical protein; similar to <i>S. cerevisiae</i> YGR090W
SPBC21C3.08C	ornithine aminotransferase (EC 2.6.1.13)
SPBC36.03C	MSF drug efflux transporter of unknown specificity
sou1	sorbitol utilization protein sou1; short chain dehydrogenase
SPAC13G7.13C	putative Protein required for sporulation and formation of meiotic spindle; by similarity to yeast rim4; has two RNA recognition motif (RRM) domains