Supplemental Methods

Description of GOnet. We have constructed a database with a Web interface that integrates genomic and proteomic information across several other existing databases. Information about yeast ORFs and their annotations, GO terms, and protein interactions are stored, and periodically refreshed, in an open-source relational database—implemented using MySQL (http://www.mysql.com/) and other publicly available, open source, tools. The database retrieves information about ORFs (description, mutant phenotype, gene product, etc.) from the SGD available at http://www.yeastgenome.org/.

SGD provides an anonymous FTP site (ftp://genome-ftp.stanford.edu/pub/yeast/) which allows users to download a gene registry file that has detailed information of named genes (ftp://genome-ftp.stanford.edu/pub/yeast/data_download/gene_registry/registry.genenames.tab), and another file (ftp://genome-ftp.stanford.edu/pub/yeast/data_download/chromosomal_feature/chromosomal_feature.tab) which includes information about dubious ORFs.

We run a redundancy check on these data and whenever an ORF is present in both files we retain the more informative version contained in the registry.genenames.tab file as input. The GO term files are downloaded from the Gene Ontology Consortium's website (http://www.geneontology.org/). The GO hierarchy is retrieved and analyzed by parsing the corresponding XML tags. A suite of Perl scripts (http://www.perl.org) is used to parse the ORF information files, extract useful information, and link each ORF with the corresponding GO information, if available.

The General Repository for Interaction Datasets (GRID), which is available at http://biodata.mshri.on.ca/grid/servlet/Index, provides genetic and physical interactions information. Registered users of their website can download a text file which contains information about protein-protein interactions, the experimental methods by which the information was derived (e.g. yeast two-hybrid) information, and related resources. Interactions included in this file are not fully symmetric. For example, in the current version, *YHR151C* interacts with *YNL193W*, but *YNL193W* does not interact with *YHR151C*. This is an experimental and data-entry artifact that we correct by adding all the missing symmetric interactions to the file to produce a final symmetric set of interactions, as reflected in the online version of the GRID database

Based on the interactions from GRID, we link each gene in an interacting pair to their SGD and GO information. For each pair of genes, the levels of relatedness of the GO terms are also computed, to determine how closely these terms are related in the GO tree hierarchy. For instance, in Molecular Function GO terms, "molecular_function" is at level 1, "kinase activity" is at level 2, and "amino acid kinase activity" and "carbohydrate kinase activity" are at level 3. Because "amino acid kinase activity" and "carbohydrate kinase activity" share the same immediate upper level —"kinase activity" (level 2), these two terms are considered to be related at level 2.

The Web interface to the database is developed using JavaScript and PHP, which is a widely used general-purpose, open-source scripting language that is especially suited for Web development (http://www.php.net), and has built-in interface for MySQL. Its basic functionality is to allow users to rapidly cluster genes by using interaction and GO hierarchy information. More precisely, the query form allows users to:

(1) Enter a list of genes;

(2) Enter GO terms or possible keywords in GO terms for each category—Molecular Function, Biological Process, and/or Cellular Component;

(3) Enter GO terms or possible keywords without specifying which category they belong to;

(4) Select different levels of relatedness within the GO hierarchy for Function, Process, and/or Component;

(5) Select the experimental method(s) used to establish interactions (e.g. yeast two-hybrid versus all methods);

(6) Limit the results to those ORFs which appear both in the input (query) list and in the output (interaction) list.

Users can sort the results by ORF names or by the three categories of GO terms. Results can also be downloaded as tab-delimited text files which can be opened in Excel. We provide the text files with a variety of sorting options such as by ORF name, by interacting gene's name, and by Function GO term. If a user chooses to limit the results to ORFs appearing both in the input (query) and output (interaction) list but stills want to see which ones are present in the input only, he/she can do so by following a link on the result page.

Submission of a query immediately produces a list of genes satisfying the corresponding criteria. Each hit provides not only the names of the interacting genes GO terms, and gene details, but also automatically provides an hyperlink to the corresponding information in the SGD database. It allows users to rapidly and fairly exhaustively (up to errors in the original data) explore small clusters of interacting genes with similar GO classifications and therefore find those genes which are likely to participate in the same processes, functions, or pathways.

On the website, genes are also grouped according to their GO terms. The grouping is based on GO information stored in the database and their relative positions in the GO hierarchy. For each category of GO terms (Function, Process and Component), different levels of specificity are used. For example, in the category of Molecular Function, at level 1 there is a link to genes grouped by "binding", which includes genes participating in all the bindings in all of its sub-levels—not only level 2, but also 3, 4, etc., such as amino acid binding, cellulose binding, and peptide antigen binding; at level 2, there is a link to genes grouped by "nucleic acid binding" which includes genes participating in all the sub-levels of nucleic acid binding; at level 3, there is a link to genes grouped by "RNA binding"; at level 4, there is a link to genes grouped by "mRNA binding". Users can also find details of each gene, such as the names of interacting genes, phenotype, function, process and component GO terms, etc.

We also provide a function that allows users to automatically retrieve sequences and blast them against the mouse or human genome using the Blastp program and the NCBI Blast servers. This function is particularly useful when applied to multiple ORFs. It is implemented using Perl LWP (http://lwp.linpro.no/lwp/) and the URLAPI package (http://www.ncbi.nlm.nih.gov/BLAST/Doc/urlapi.html) from NCBI. If the "Generate a summary" option is not selected, then the result page lists the relevant ORFs with links to each blast results on the NCBI server. If the "Generate a summary" option is selected, then a summary report is generated within typically a few minutes. The report displays information such as total number of hits (or no hits) and the details of each hit (P value, E value, and links) for each ORF.

Supplemental Figure Legends

Fig. 1. Ty3 Gag3, IN and cDNA intermediates in 66 knockout mutants. Mutants representing nine of the functional categories of genes recovered in the screen were assayed as described in Materials and Methods in two independent transformants for Ty3 proteins (Gag3, p27, CA, and IN) and cDNA (with the exception of three mutants). Cells were initially induced in mid-log phase cultures and were grown under inducing conditions for 24 h. Eight independent wt transformants were used as controls. On each of the Western and Southern blots pools of three different transformants were used on each side of the blot. For Western analysis blots have been reconstructed here (as indicated by dividing lines) to better group similar functions and include cases where individual samples were reprepared due to technical problems. The original blots are available upon request. Blots shown were exposed so that the wt CA, IN and PGK controls were similar intensity among the blots, but these results are considered qualitative rather than quantitative. cDNA levels are expressed in the bar graph as the ratio of Ty3 cDNA to plasmid. The wt control value (0.57 +/- 0.31) represents an average of eight independent transformants. The mutant values represent the average of two independent transformants. In three cases, protein and Southern analysis is based on one rather than two mutants as it appeared the mutant had little or no Ty3 plasmid present. Results from these blots are summarized in Fig. 3 and Supplemental Table 3.

Reference List

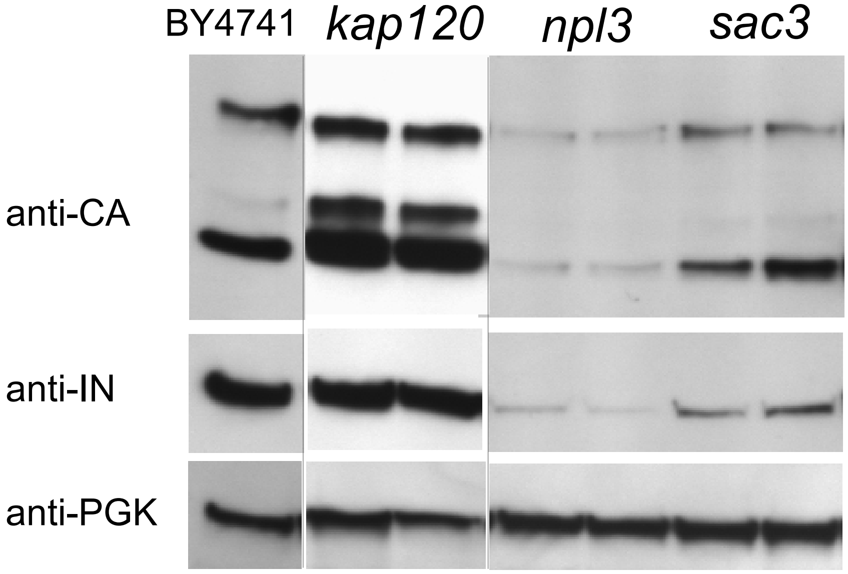
1. Scholes, D. T., Banerjee, M., Bowen, B. & Curcio, M. J. (2001) *Genetics* **159**, 1449-1465.

2. von Schwedler, U. K., Stuchell, M., Muller, B., Ward, D. M., Chung, H. Y., Morita, E., Wang, H. E., Davis, T., He, G. P., Cimbora, D. M. *et al.* (2003) *Cell* **114**, 701-713.

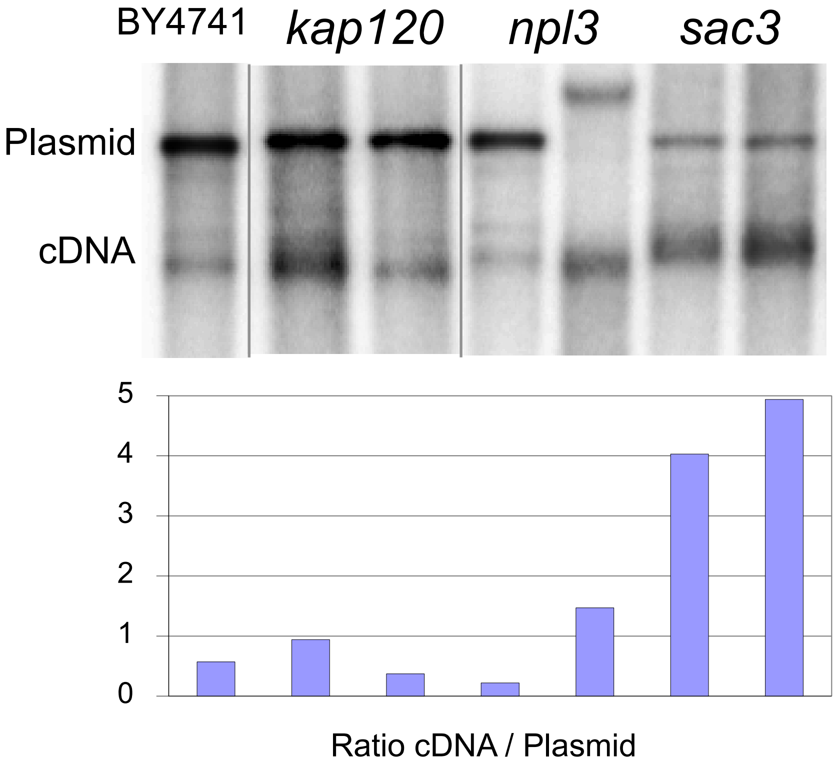
3. Odorizzi, G., Katzmann, D. J., Babst, M., Audhya, A. & Emr, S. D. (2003) *Journal of Cell Science* **116**, 1893-1903.

Nuclear Transport

Western

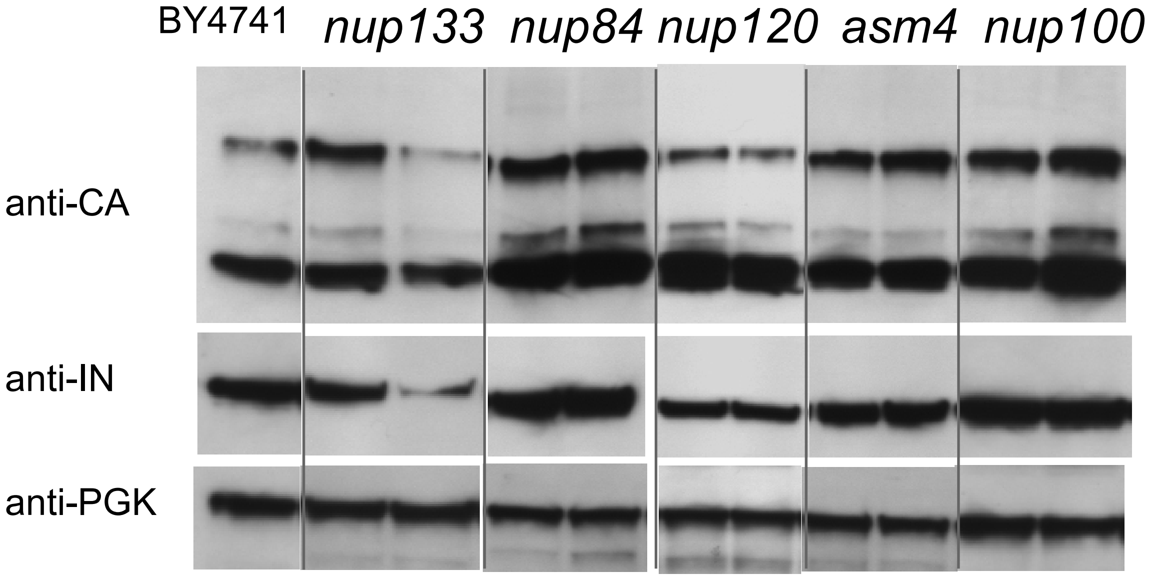


Southern



Nuclear Transport

Western



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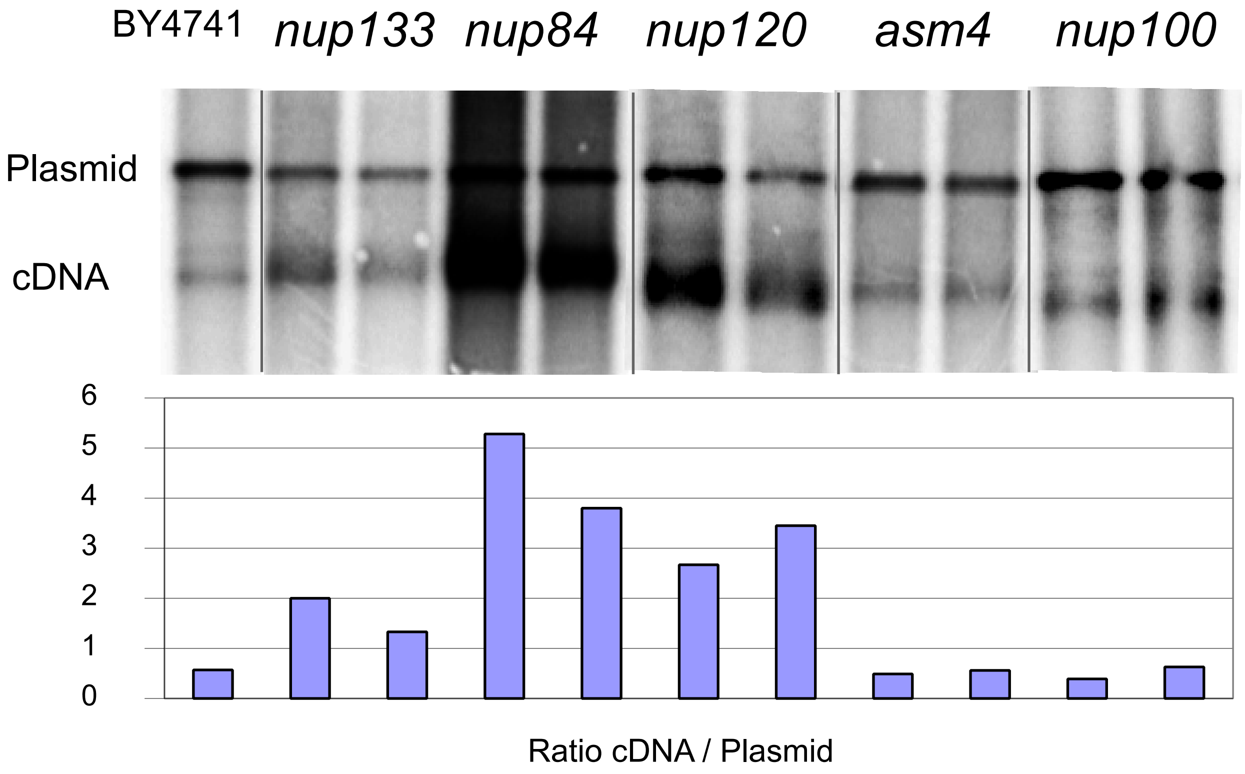
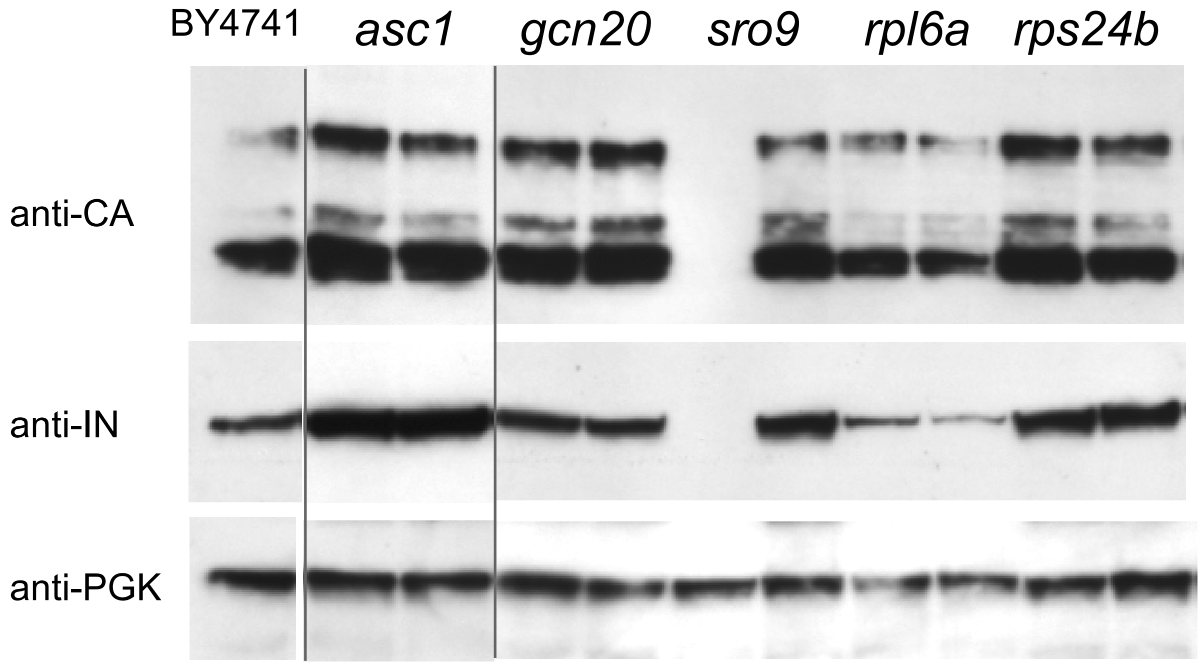


Translation

Western



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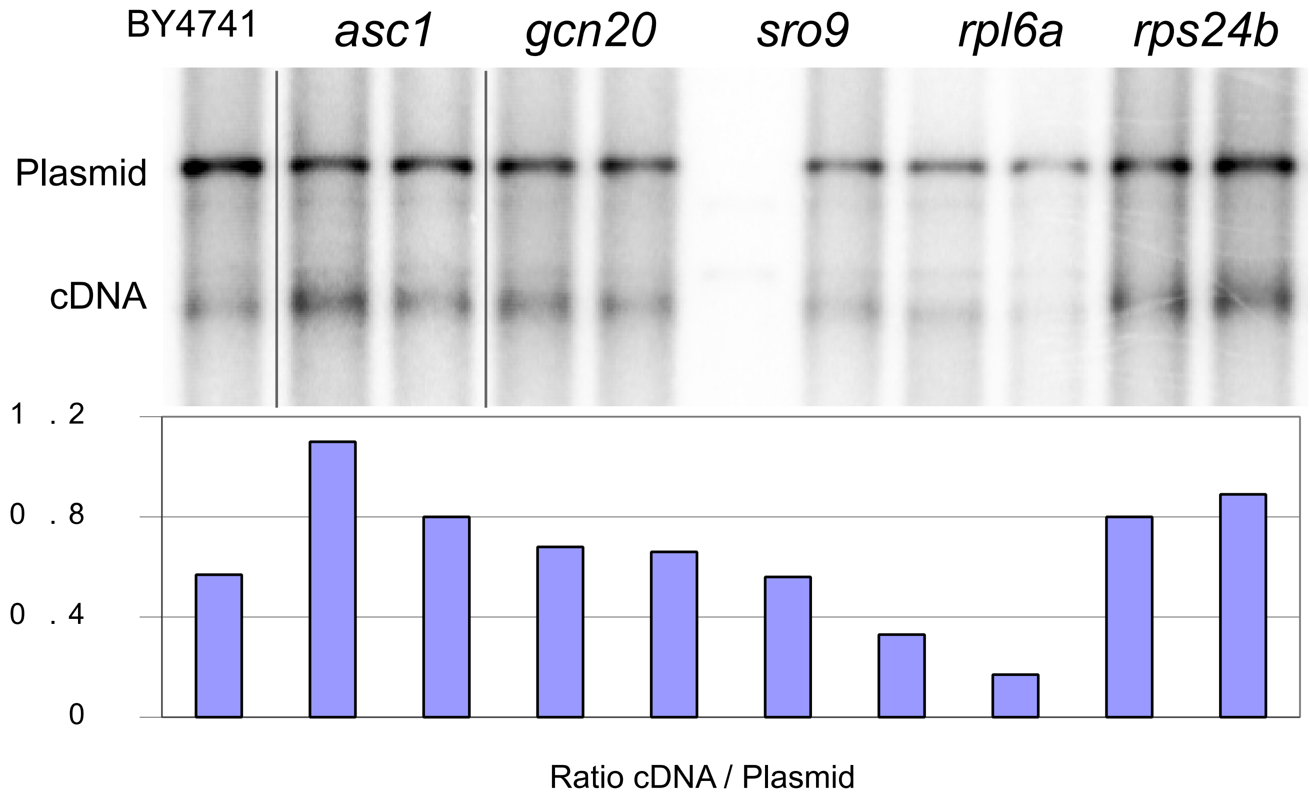
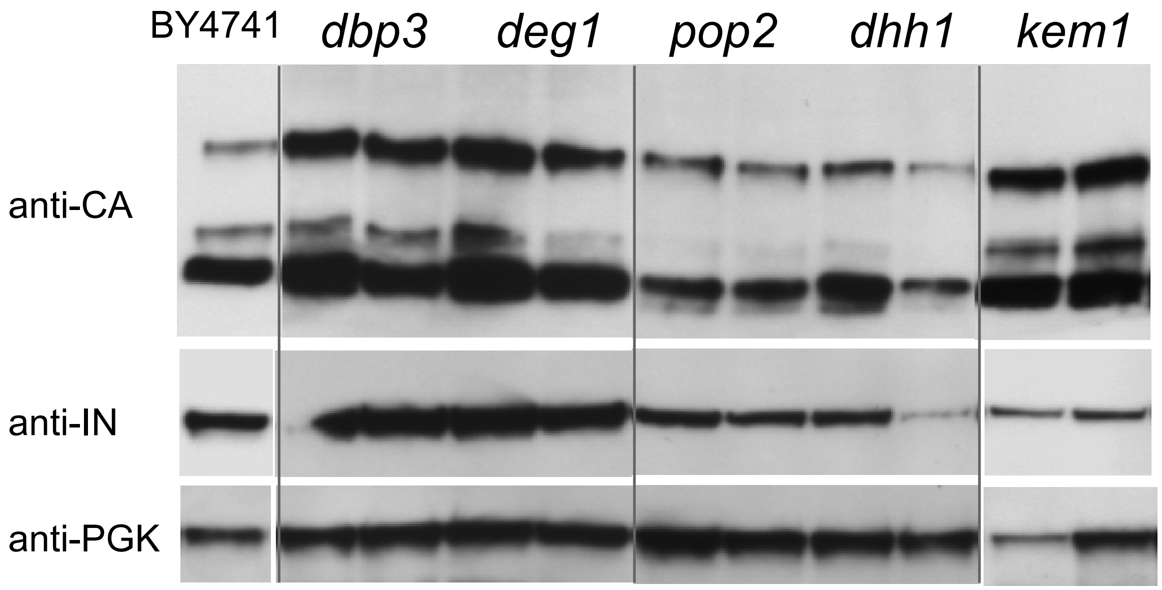


RNA Processing

Western



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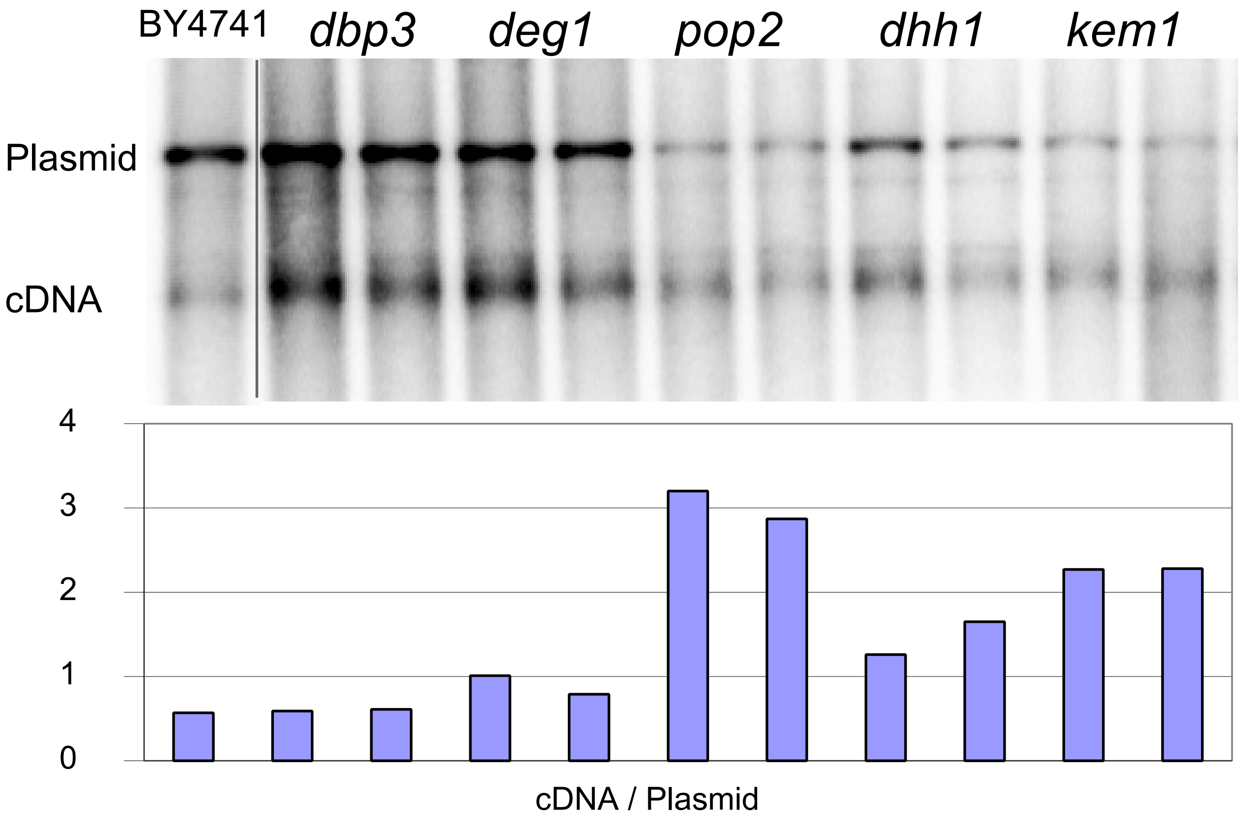
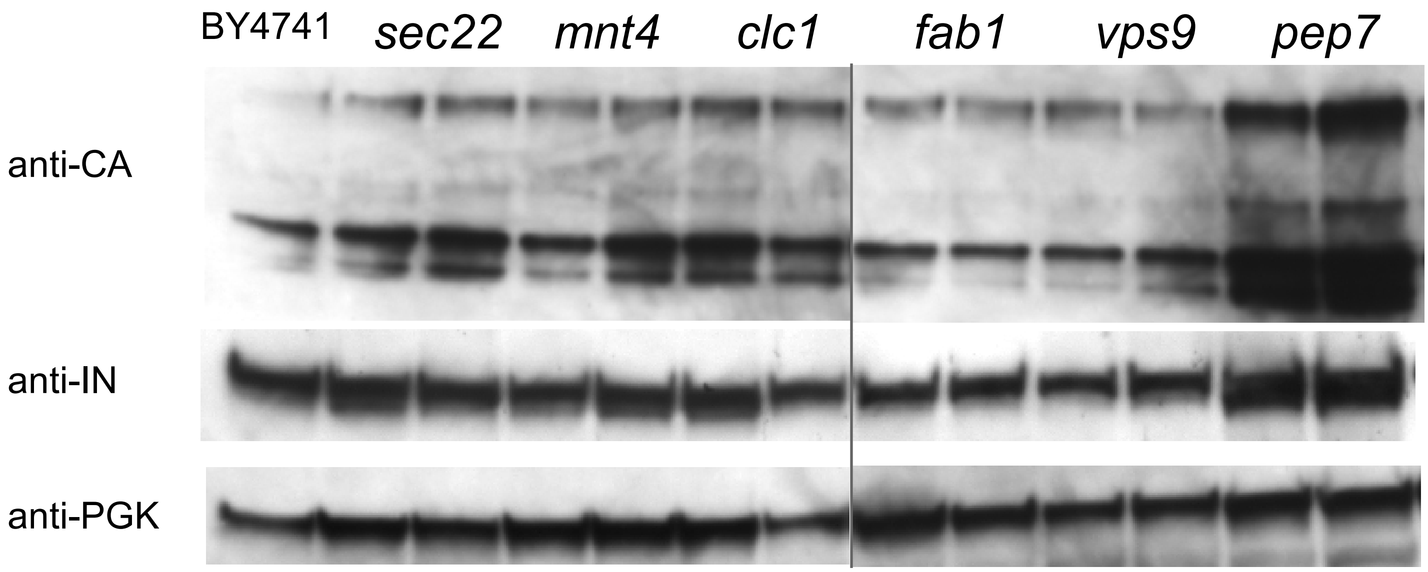


Secretion / Vesicular Trafficking / Vacuolar

Western



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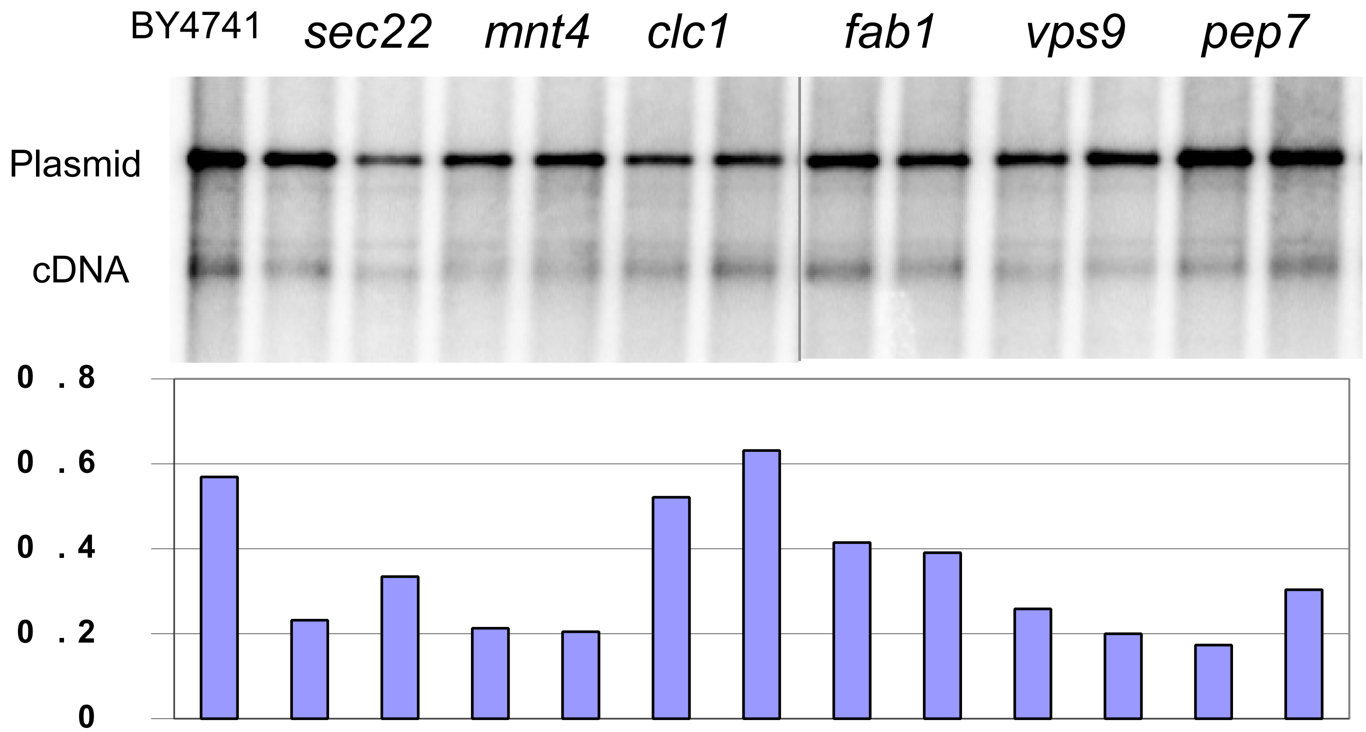
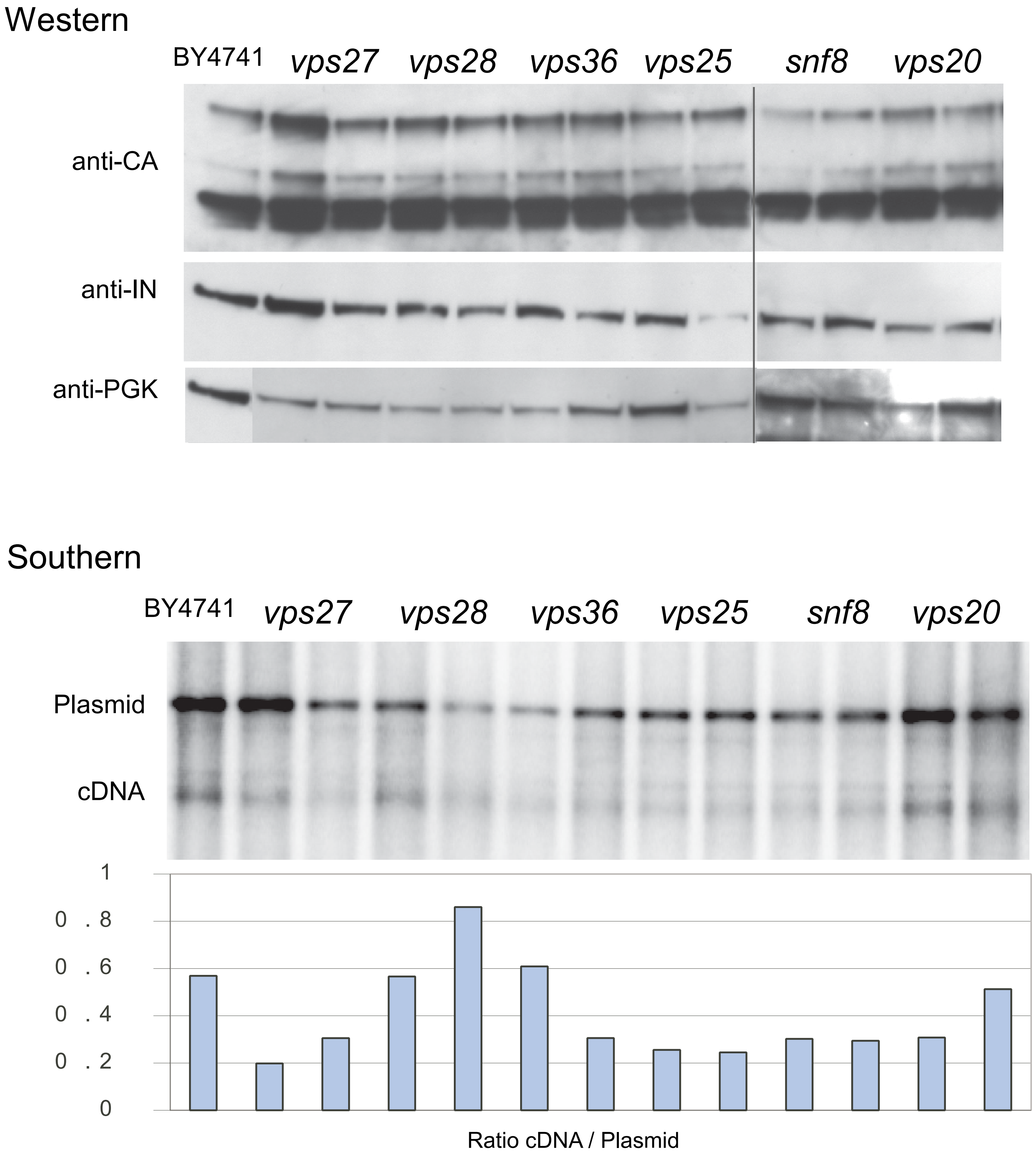


Ratio cDNA / Plasmid

Secretion / Vesicular Trafficking / Vacuolar



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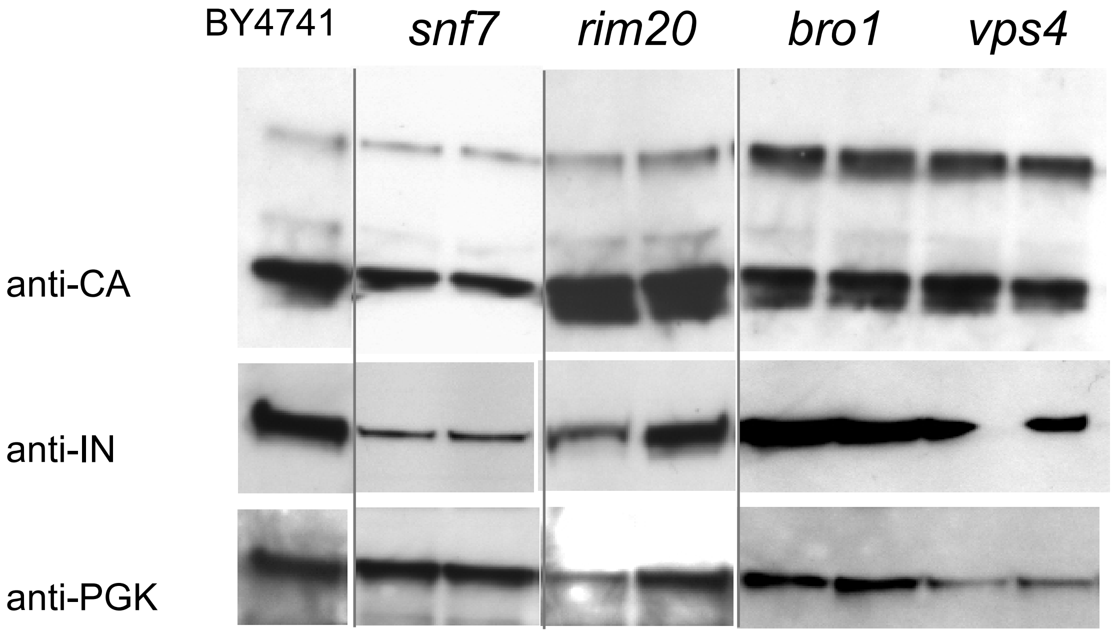
Western



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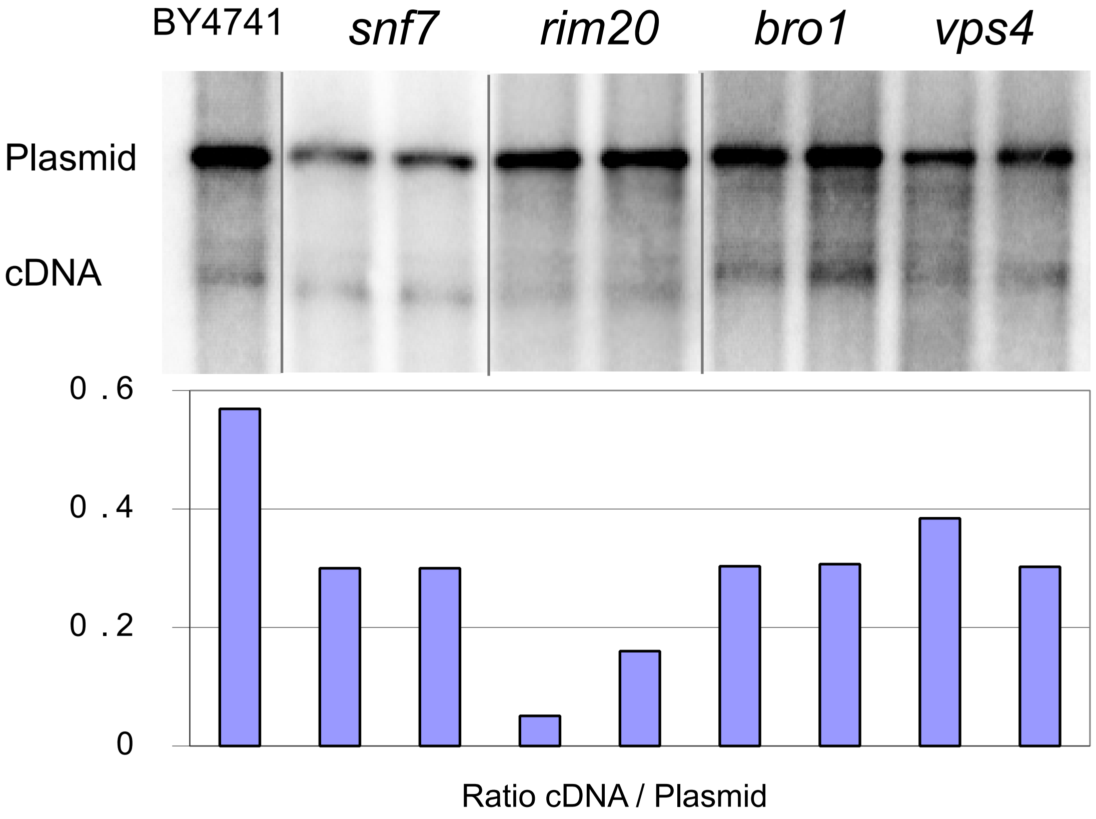
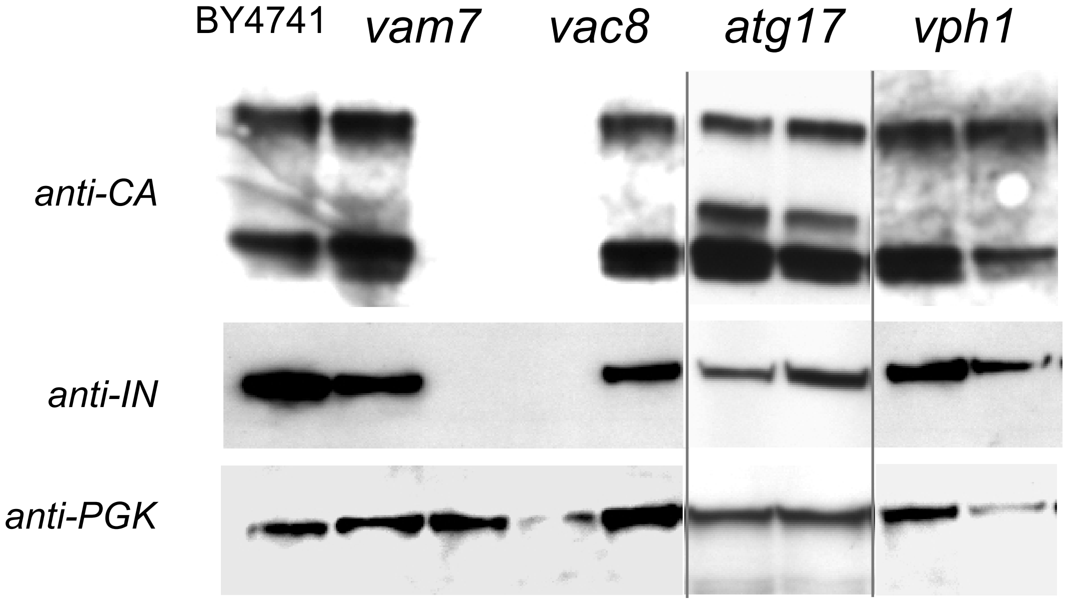


Secretion / Vesicular Trafficking / Vacuolar

Western



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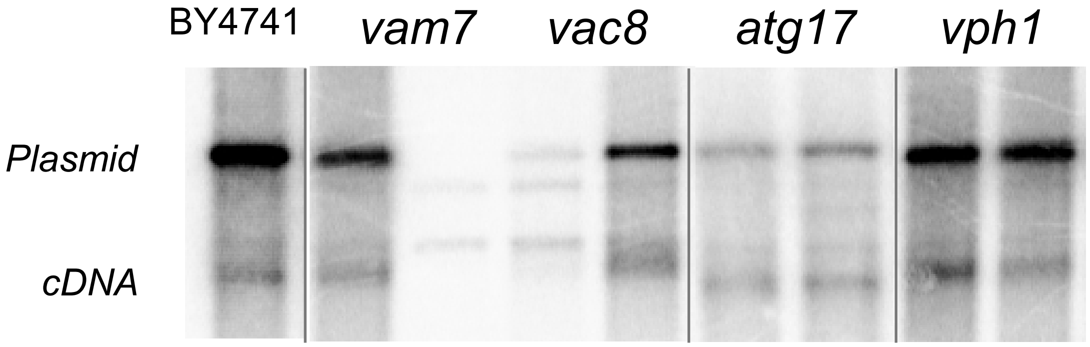
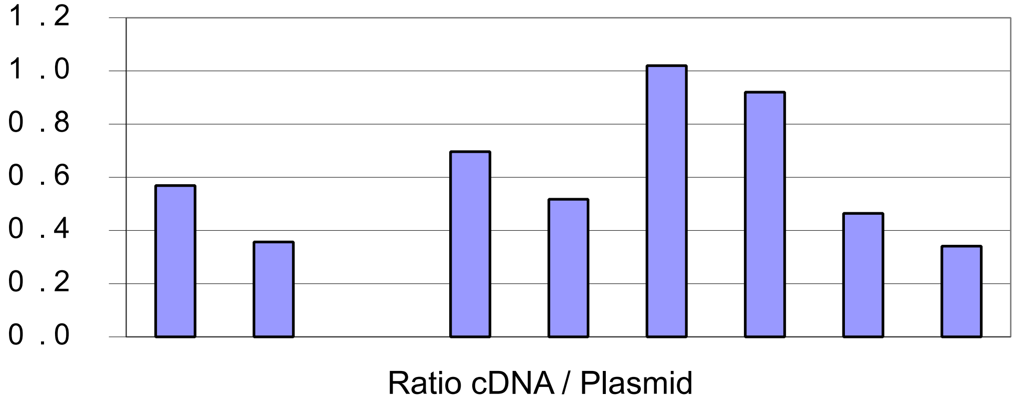
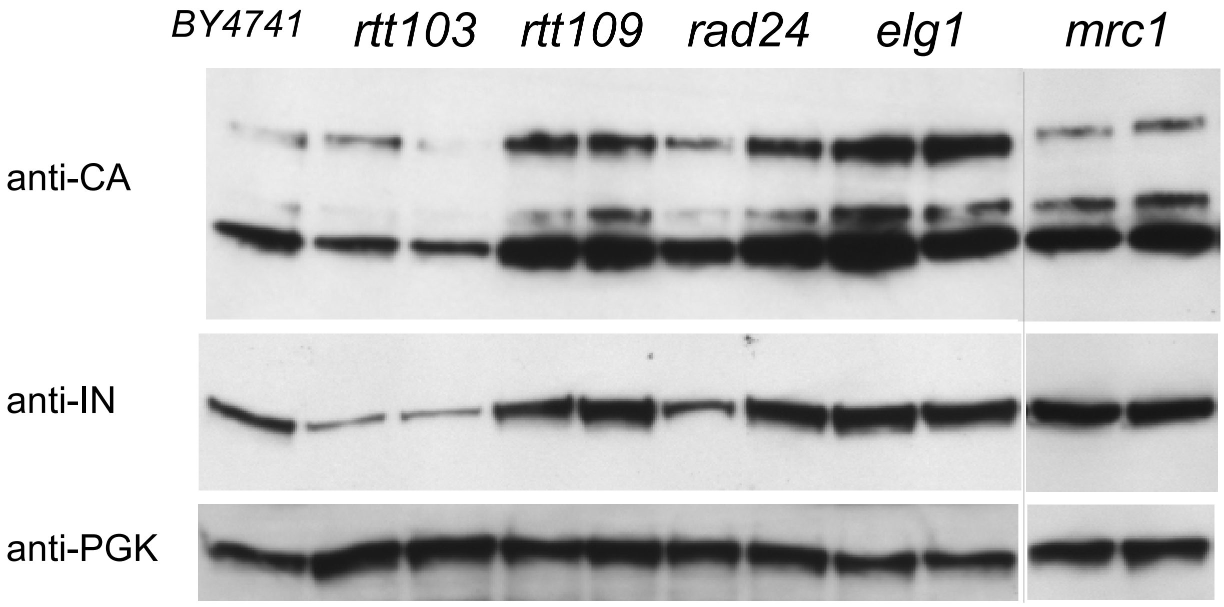




Ty1 and DNA Maintenance

Western



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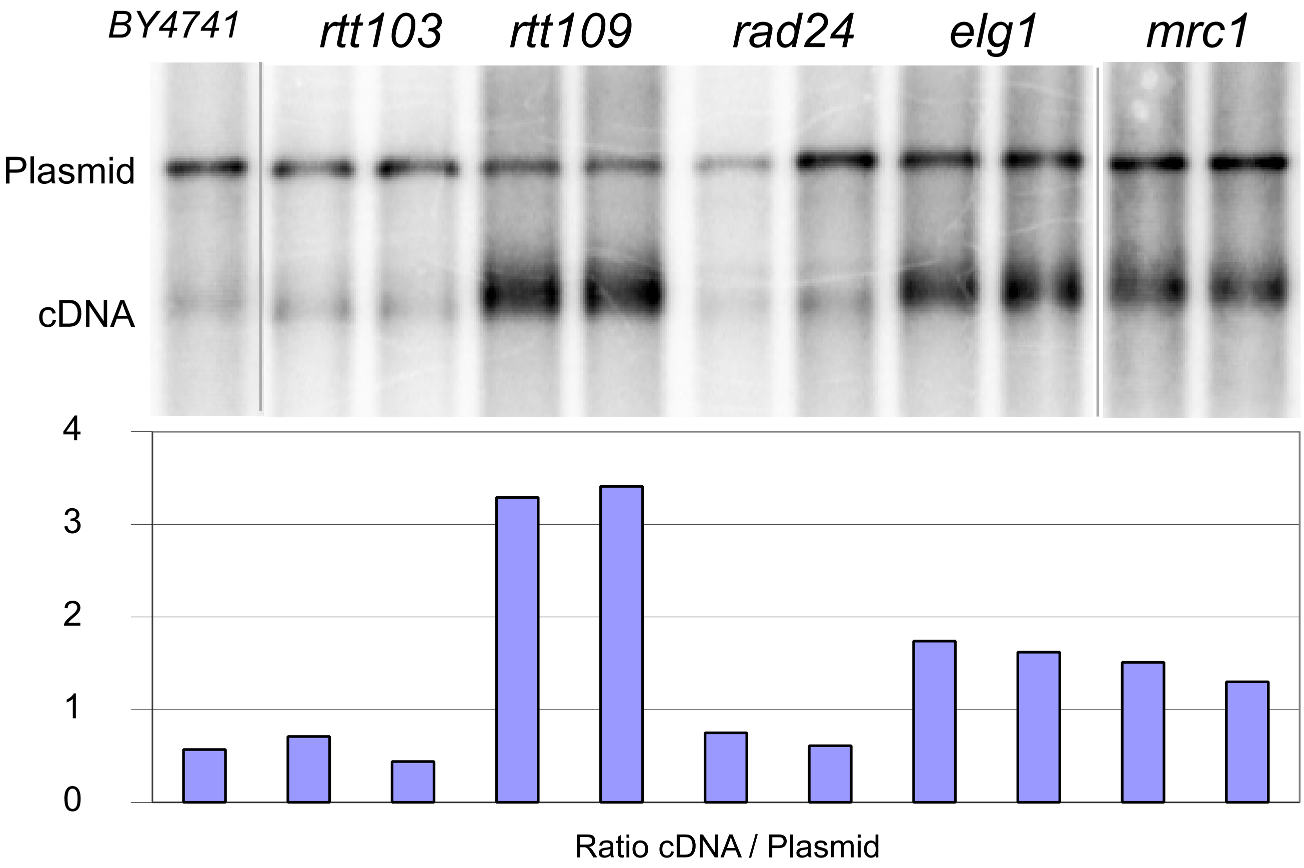
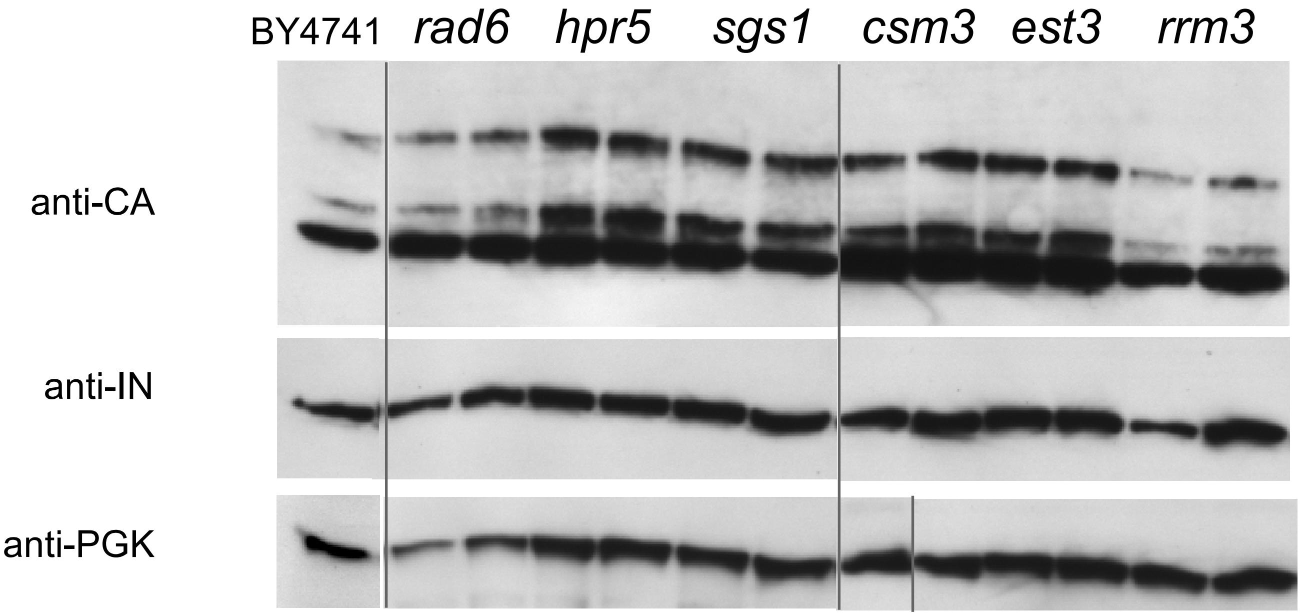


DNA Maintenance

Western



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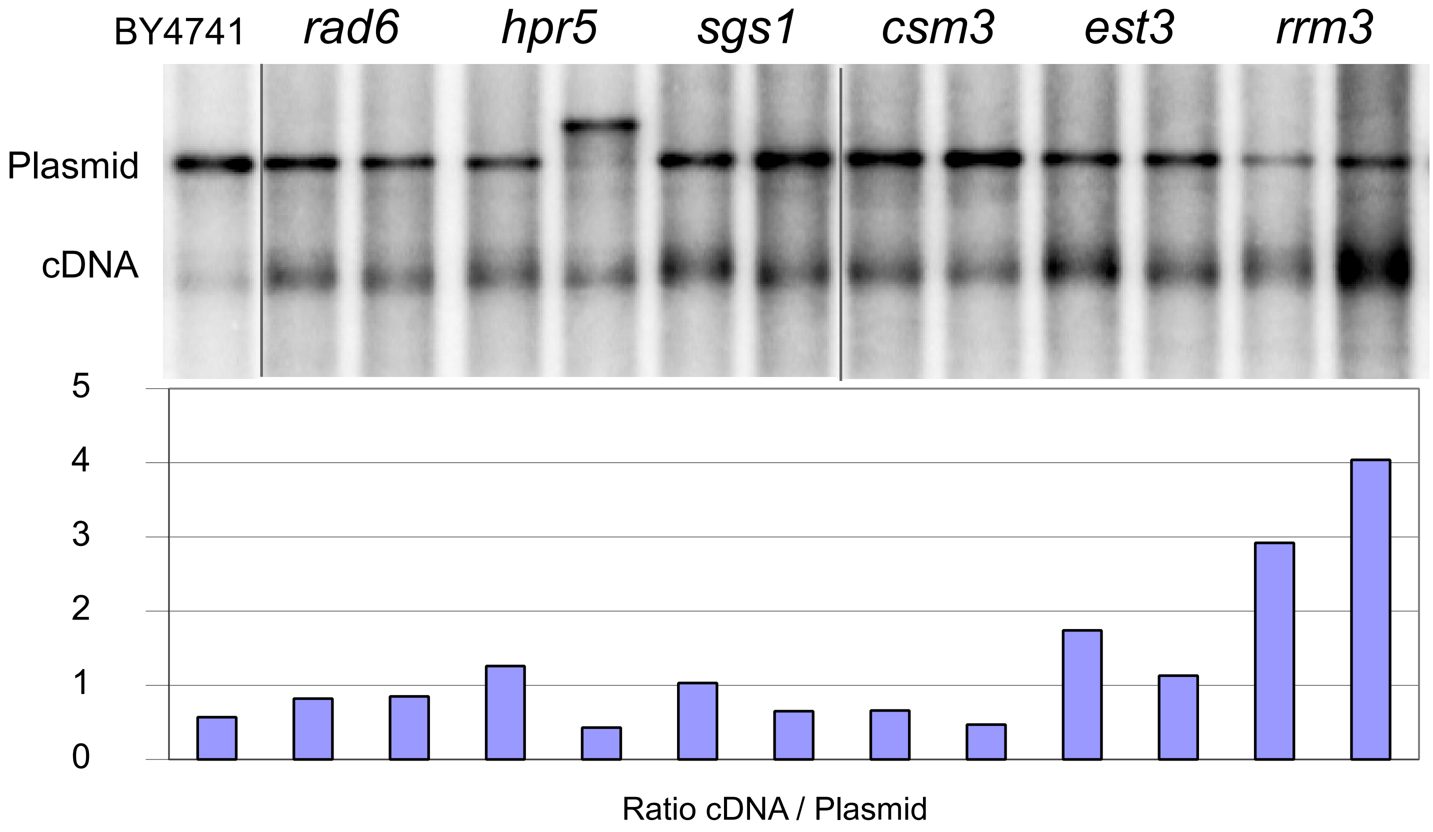
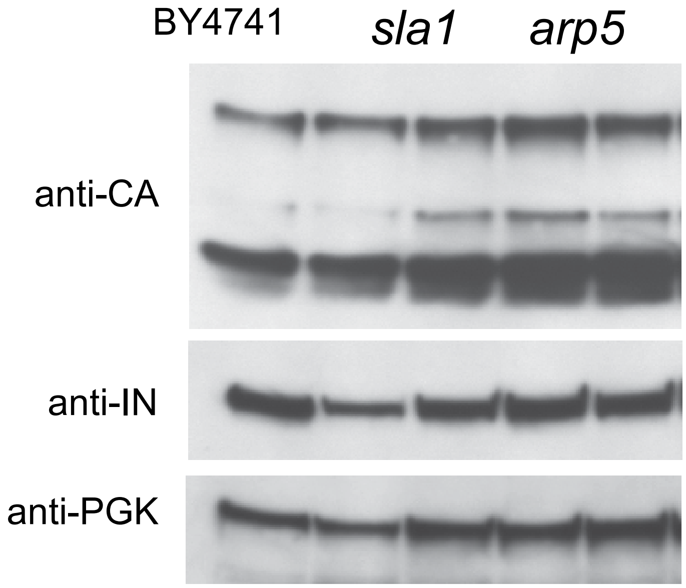
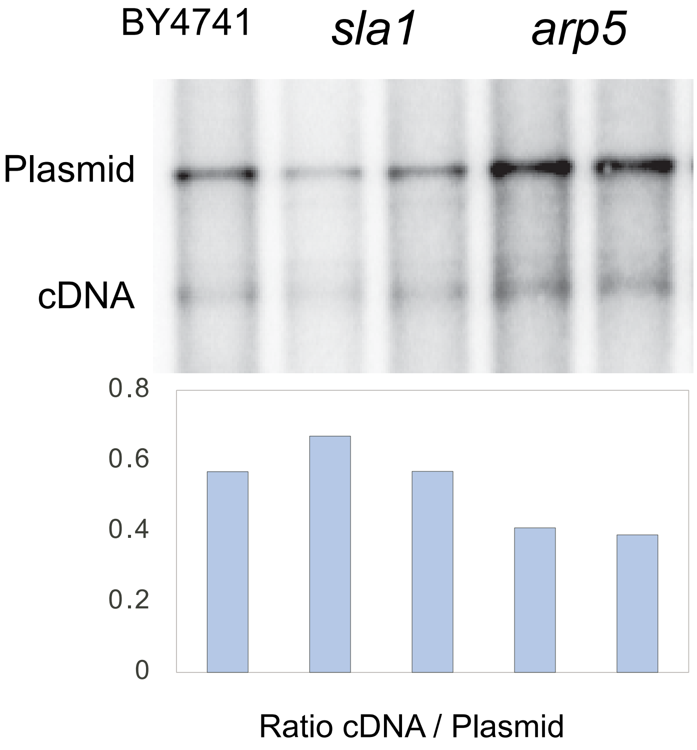


Cytoskeleton

Western

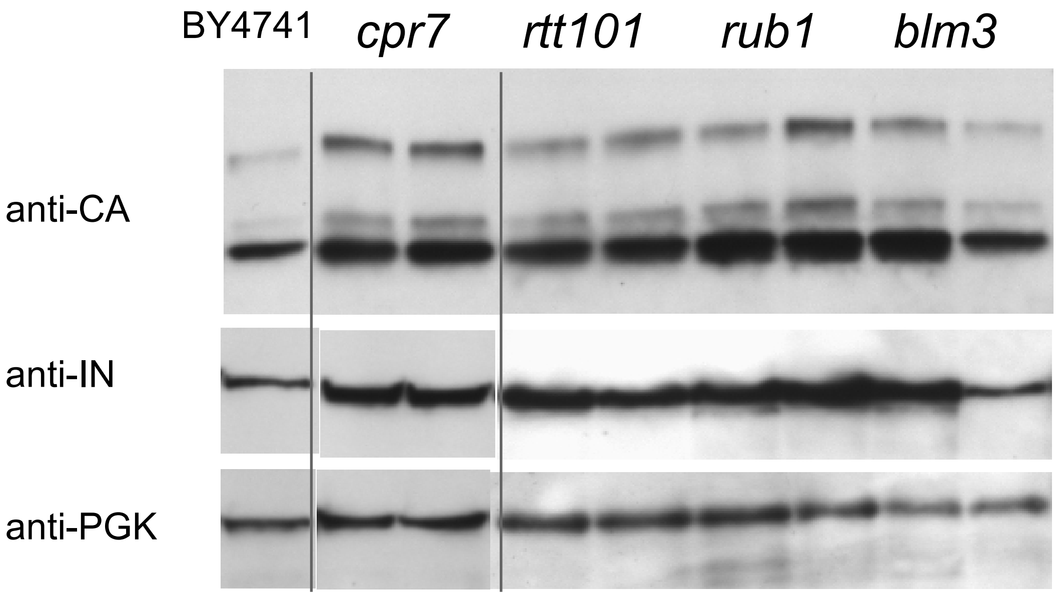


Southern



Stress / Chaperone / Modification

Western



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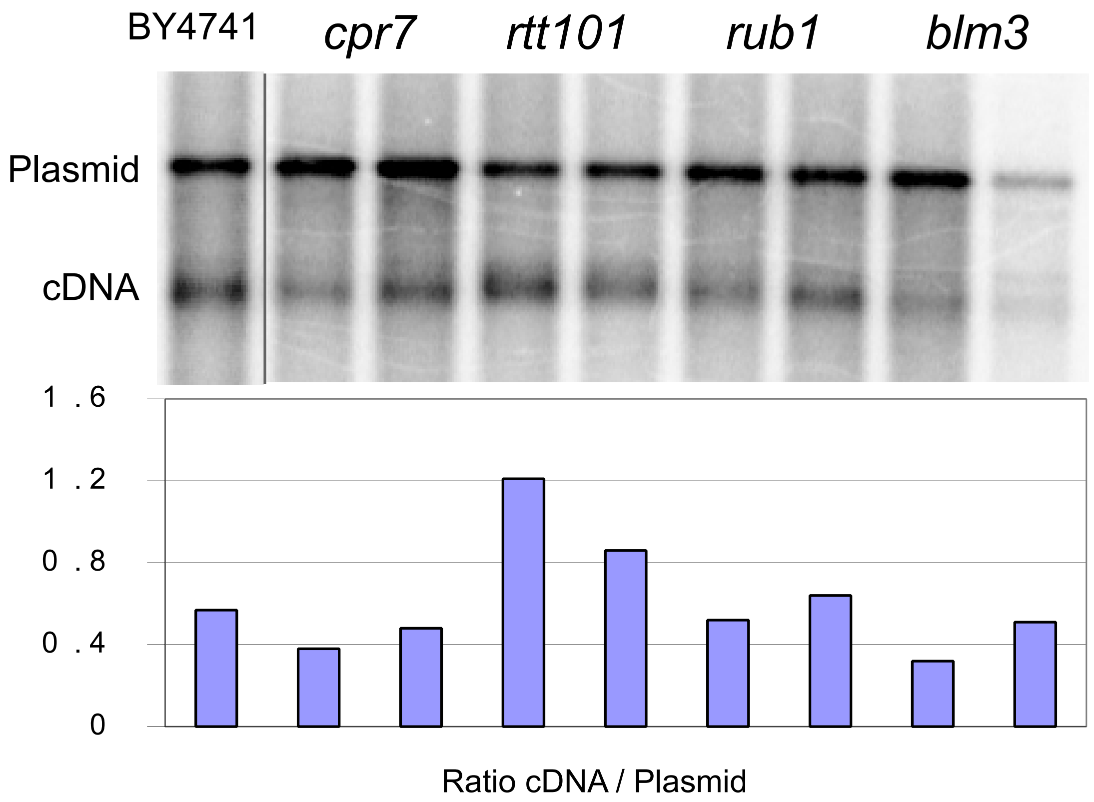
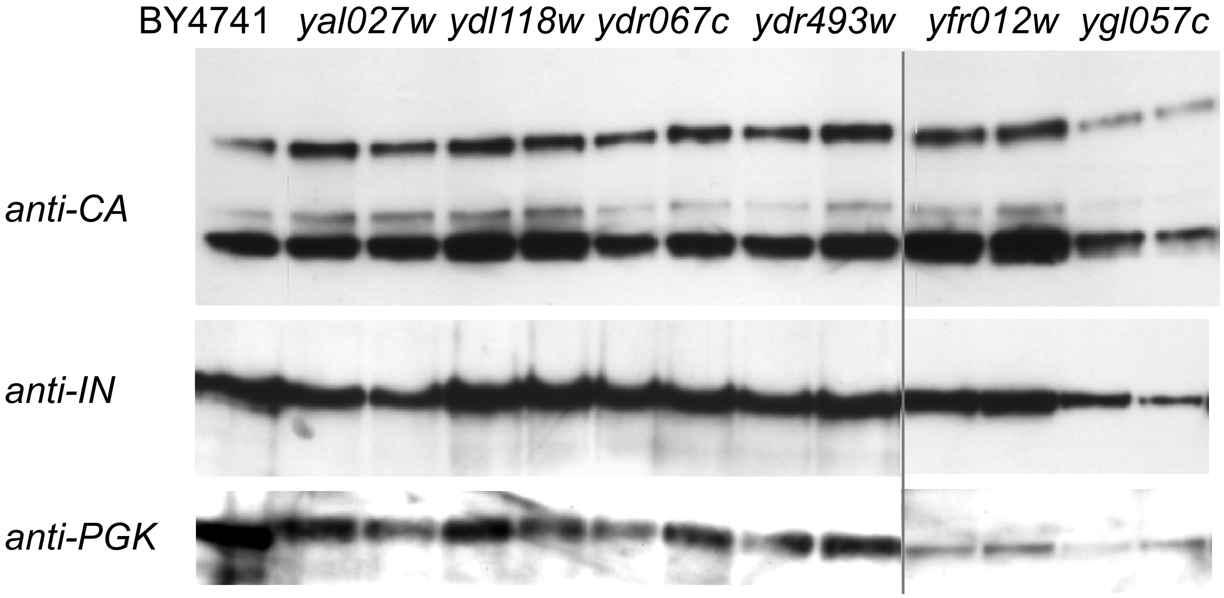


Unknowns

Western



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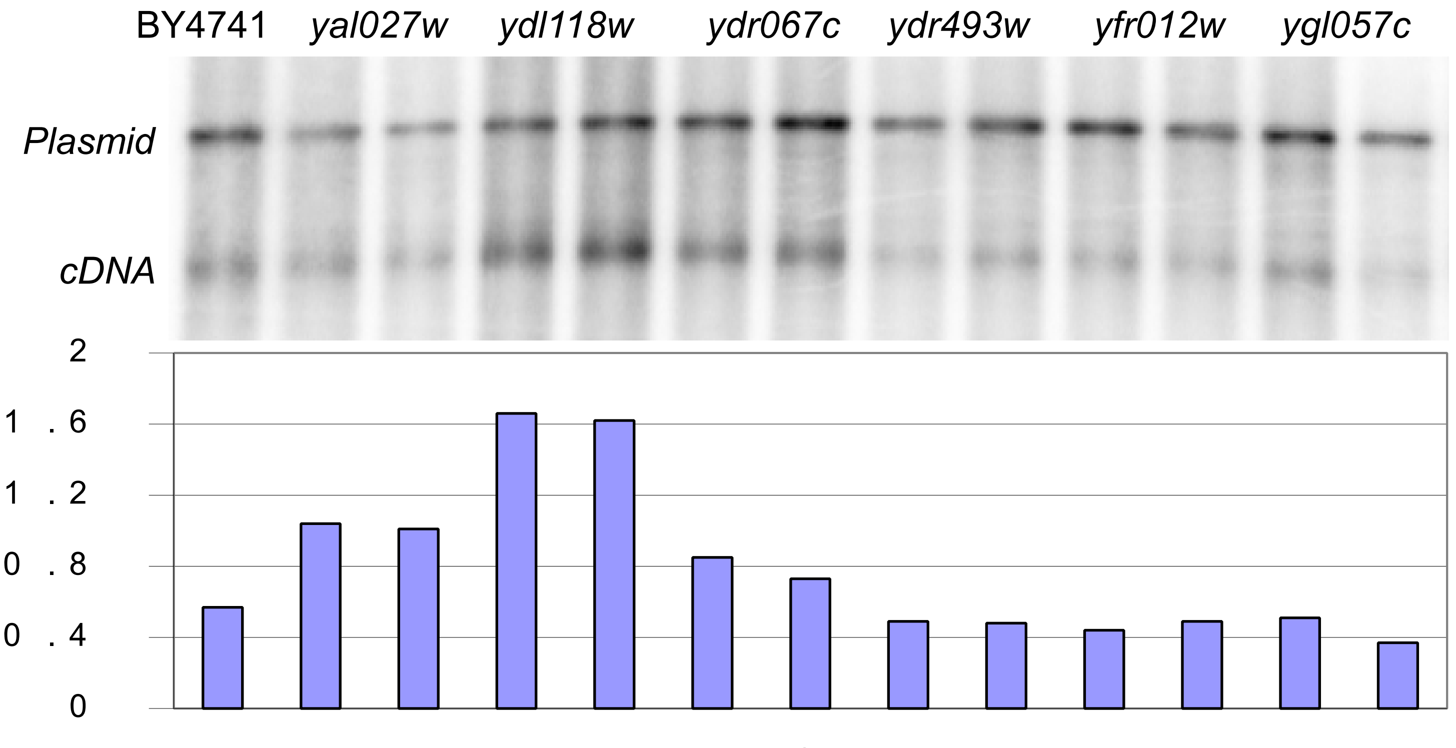
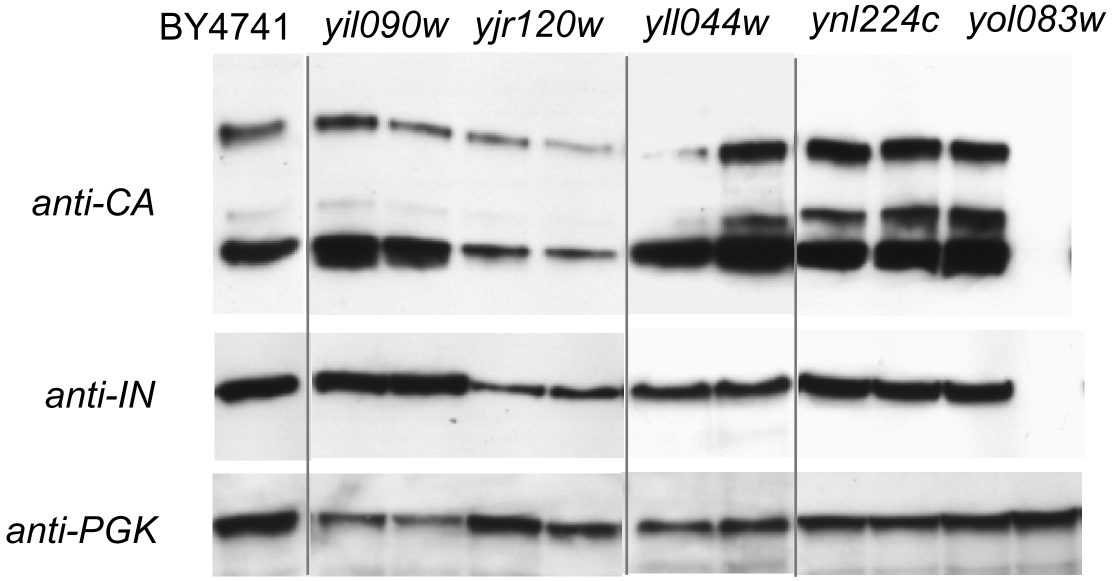


Ratio cDNA / Plasmid

Unknowns

Western



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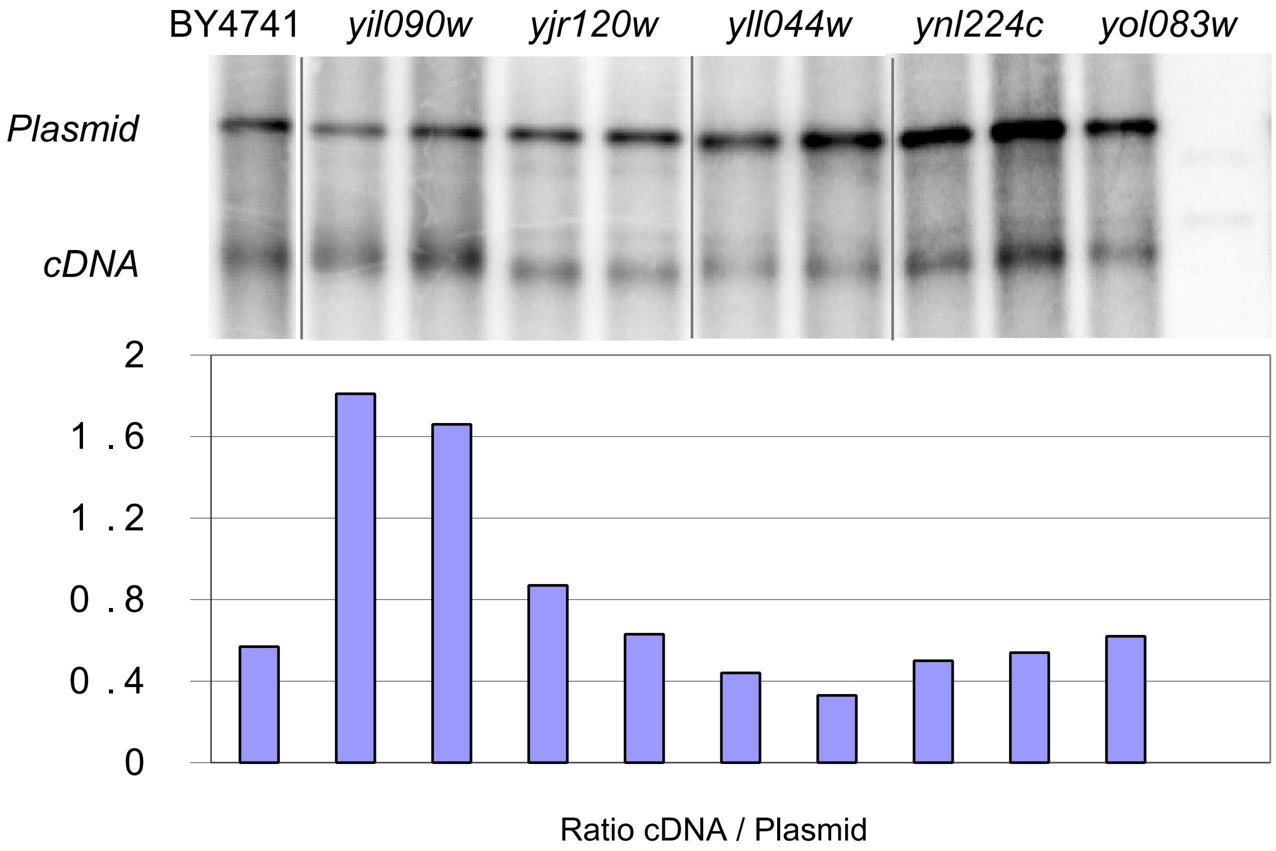

Sup. Table 1. Mutants that were not assayed because of poor growth

Collection ID	ORF	Gene Name	Description[1]
398	YAL010C	*MDM10*	YAL010C Mitochondrial outer membrane protein involved in mitochondrial morphology and inheritance
6866	YAL016W	*TPD3*	YAL016W protein phosphatase 2A regulatory subunit A
3026	YBL002W	*HTB2*	YBL002W Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
3038	YBL012C	0	questionable ORF, Dubious
3047	YBL021C	*HAP3*	transcriptional activator protein of CYC1
3048	YBL022C	*PIM1*	YBL022C mitochondrial ATP-dependent protease
3051	YBL025W	*RRN10*	Upstream activation factor subunit
3059	YBL033C	*RIB1*	YBL033C GTP cyclohydrolase II
3064	YBL038W	*MRPL16*	Mitochondrial ribosomal protein MRPL16
3070	YBL044W	0	hypothetical protein, uncharacterized
3071	YBL045C	*COR1*	YBL045C 44 kDa core protein of yeast coenzyme QH2 cytochrome c reductase
3078	YBL052C	*SAS3*	SAS3 for Something about silencing, gene 3. Influences silencing at HMR.
3106	YBL080C	*PET112*	YBL080C 62-kDa protein
3125	YBL099W	*ATP1*	mitochondrial F1F0-ATPase alpha subunit
3126	YBL100C	0	questionable ORF, dubious
3138	YBR003W	*COQ1*	hexaprenyl pyrophosphate synthetase
3155	YBR018C	*GAL7*	galactose-1-phosphate uridyl transferase
3156	YBR019C	*GAL10*	YBR019C UDP-glucose 4-epimerase
3163	YBR026C	*MRF1'*	YBR026C Nuclear protein that binds to T-rich strand of core consensus sequence of autonomously replicating sequence
3172	YBR035C	*PDX3*	YBR035C pyridoxine (pyridoxiamine) phosphate oxidase
3174	YBR037C	*SCO1*	inner mitochondrial membrane protein
3206	YBR069C	*VAP1*	Probable amino acid transport protein
3236	YBR097W	*VPS15*	Myristoylated Serine\/threonine protein kinase involved in vacuolar protein sorting
7161	YBR112C	*CYC8*	YBR112C Transcription regulatory protein
3261	YBR122C	*MRPL36*	YBR122C Mitochondrial ribosomal protein MRPL36 (YmL36)
3271	YBR132C	*AGP2*	YBR132C Amino acid permease
3303	YBR163W	*DEM1*	weak similarity ot pre-tRNA processing protein
3324	YBR184W	0	ORF, uncharacterized
3366	YBR226C	0	ORF, dubious
3386	YBR246W	0	ORF, uncharacterized
3388	YBR248C	*HIS7*	glutamine amidotransferase:cyclase
3391	YBR251W	*MRPS5*	YBR251W Probable mitochondrial ribosomal protein S5
3399	YBR259W	0	ORF, uncharacterized
3407	YBR267W	0	ORF, uncharacterized
3408	YBR268W	*MRPL37*	Probable mitochondrial protein L37
5730	YBR282W	*MRPL27*	Mitochondrial ribosomal protein MRPL27 (YmL27)
3410	YCL002C	0	ORF, uncharacterized
3415	YCL007C	*CWH36*	YCL007C Calcofluor White Hypersensitivity
3437	YCL030C	*HIS4*	YCL030C histidinol dehydrogenase
3483	YCR003W	*MRPL32*	Mitochondrial ribosomal protein MRPL32 (YmL32)
3484	YCR004C	*YCP4*	YCR004C FMN-binding protein
5752	YCR024C	0	ORF, uncharacterized
7179	YCR028C-A	*RIM1*	Single-stranded DNA-binding protein that is essential for mitochondrial genome maintenance
7183	YCR046C	*IMG1*	YCR046C required for respiration and maintenance of mitochondrial genome
7184	YCR047C	*BUD23*	bud site selection
7198	YCR084C	*TUP1*	YCR084C glucose repression regulatory protein, exhibits similarity to beta subunits of G proteins
3698	YDL002C	*NHP10*	YDL002C HMG1-box containing protein
3728	YDL032W	0	ORF, dubious
3729	YDL033C	0	ORF, uncharacterized
3736	YDL040C	*NAT1*	YDL040C N-terminal acetyltransferase
3740	YDL044C	*MTF2*	Necessary for the stability and\/or processing of some large mitochondrial transcripts
3742	YDL045W-A	*MRP10*	Mitochondrial ribosomal protein of the small subunit
3744	YDL047W	*SIT4*	SIT4 suppress mutations in DBF2
3746	YDL049C	*KNH1*	YDL049C KRE9 homolog
3754	YDL057W	0	ORF, uncharacterized
3759	YDL062W	0	ORF, dubious
3764	YDL067C	*COX9*	Subunit VIIa of cytochrome c oxidase
3765	YDL068W	0	ORF, dubious
3766	YDL069C	*CBS1*	translational activator of cytochrome b
3801	YDL104C	*QRI7*	YDL104C similarity to H.influenzae sialoglycoprotease (gcp)
3804	YDL107W	*MSS2*	YDL107W cox1 pre-mRNA splicing factor
3810	YDL113C	*ATG20*	Protein required for the transport of aminopeptidase I (Lap4p) through the cytoplasm-to-vacuole targeting pathway
3844	YDL146W	0	ORF, uncharacterized
3865	YDL167C	*NRP1*	YDL167C Asparagine-rich protein

3879	YDL181W	*INH1*	YDL181W ATPase inhibitor
3900	YDL202W	*MRPL11*	Mitochondrial ribosomal protein MRPL11 (YmL11)
3929	YDL232W	*OST4*	YDL232W 3.6-kDa protein, probably membrane-located
3949	YDR009W	*GAL3*	YDR009W galactokinase
3956	YDR017C	*KCS1*	YDR017C Shows homology to basic leucine zipper family of transcription factors
3966	YDR027C	*VPS54*	Loss Upsets Vacuole; Golgi to vacuole transport; in Garp complex, Golgi apparatus
3967	YDR028C	*REG1*	YDR028C regulatory subunit for protein phosphatase Glc7p
3978	YDR042C	0	ORF, uncharacterized
3993	YDR057W	*YOS9*	Appears to play a direct role in the transport of GPI-anchored proteins to the Golgi apparatus. ER ot Golgi transport, in the ER
4000	YDR065W	0	ORF, uncharacterized
4013	YDR078C	*SHU2*	Suppressor of HydroxyUrea sensitivity
4014	YDR079W	*PET100*	YDR079W cytochrome c oxidase-specific assembly factor
4048	YDR114C	0	ORF, dubious
4049	YDR115W	0	mitochondrial large ribosomal subunit
3516	YDR158W	*HOM2*	aspartic beta semi-aldehyde dehydrogenase
3553	YDR194C	*MSS116*	YDR194C Mitochondrial RNA helicase of the DEAD box family
3556	YDR197W	*CBS2*	cytochrome b translational activator
3563	YDR204W	*COQ4*	YDR204W Involved in ubiquinone biosynthesis
3585	YDR226W	*ADK1*	YDR226W cytosolic adenylate kinase
3590	YDR231C	*COX20*	Mitochondrial inner membrane protein, required for proteolytic processing of Cox2p and its assembly into cytochrome c oxidase
3596	YDR237W	*MRPL7*	YDR237W Mitochondrial ribosomal protein MRPL7 (YmL7)
3627	YDR268W	*MSW1*	mitochondrial tryptophanyl-tRNA synthetase
3655	YDR296W	*MHR1*	Mitochondrial Homologous DNA Recombination
3659	YDR300C	*PRO1*	YDR300C gamma-glutamyl kinase
3681	YDR322W	*MRPL35*	YDR322W Mitochondrial ribosomal protein MRPL35 (YmL35)
4184	YDR347W	*MRP1*	37 kDa mitochondrial ribosomal protein
4187	YDR350C	*TCM10*	YDR350C protein of unknown function
4201	YDR364C	*CDC40*	Member of the beta transducin family
4211	YDR375C	*BCS1*	Mitochondrial protein of the CDC48/PAS1 /SEC18 ATPase family, required for expression of functional Rieske iron-sulfur protein
4236	YDR400W	*URH1*	Uridine RiboHydrolase, pyrimidine salvage
4241	YDR405W	*MRP20*	YDR405W 263-amino acid mitochondrial ribosomal large subunit protein\; similar to L23 family of ribosomal proteins
4304	YDR470C	*UGO1*	outer membrane protein required for for mitochondrial fusion
4318	YDR484W	*SAC2*	YDR484W May interact with actin as a component or controller of the assembly or stability of the actin cytoskeleton
4341	YDR507C	*GIN4*	YDR507C putative serine\/threonine kinase
4343	YDR509W	0	ORF, dubious
4346	YDR512C	*EMI1*	Early Meiotic Induction
4352	YDR518W	*EUG1*	Protein disulfide isomerase homolog
4355	YDR521W	0	ORF, dubious
4357	YDR523C	*SPS1*	YDR523C serine\/threonine kinase homologous to Ste20p\; expressed in middle\/late meiosis
4363	YDR529C	*QCR7*	YDR529C ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)
4366	YDR532C	0	ORF, uncharacterized
265	YEL024W	*RIP1*	YEL024W Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex
268	YEL027W	*CUP5*	YEL027W Vacuolar ATP synthase 17-kDa proteolipid C subunit of VO sector\; dicyclohexylcarbodiimide binding subunit
277	YEL036C	*ANP1*	Mannan 8; Protein of the endoplasmic reticulum with a role in retention of glycosyltransferases in the Golgi, also involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol
286	YEL045C	0	ORF, dubious
287	YEL046C	*GLY1*	YEL046C Threonine Aldolase
291	YEL050C	*RML2*	YEL050C Mitochondrial ribosomal protein L2 of the large subunit
292	YEL051W	*VMA8*	YEL051W Vacuolar H-ATPase D subunit of the V1 catalytic sector
145	YER014C-A	*BUD25*	bud site selection
148	YER017C	*AFG3*	YER017C ATP-dependent metalloprotease
173	YER040W	*GLN3*	positive nitrogen regulatory protein
177	YER044C	*ERG28*	Endoplasmic reticulum membrane protein, may facilitate protein-protein interactions between the Erg26p dehydrogenase and the Erg27p 3-ketoreductase and/or tether these enzymes to the ER
185	YER050C	*RSM18*	Ribosomal Small subunit in Mitochondria
190	YER055C	*HIS1*	YER055C ATP phosphoribosyltransferase
194	YER058W	*PET117*	cytochrome c oxidase assembly factor
198	YER061C	*CEM1*	Protein homologous to beta-keto-acyl synthase
207	YER068W	*MOT2*	YER068W putative zinc finger protein
210	YER070W	*RNR1*	YER070W ribonucleotide reductase
6101	YER103W	*SSA4*	YER103W member of 70 kDa heat shock protein family
6108	YER110C	*KAP123*	YER110C Karyopherin beta 4
6121	YER122C	*GLO3*	YER122C Zinc-finger-containing protein with similarity to Gcs1p and Sps18p
6139	YER141W	*COX15*	cytochrome oxidase assembly factor
6150	YER153C	*PET122*	YER153C translational activator of cytochrome c oxidase subunit III
6151	YER154W	*OXA1*	YER154W Required for correct assembly of the cytochrome c oxidase and the ATP synthase complex
6165	YER169W	*RPH1*	Repressor of PHR1 transcription; binds to PHR1 URS
7280	YFL016C	*MDJ1*	YFL016C DnaJ homolog involved in mitochondrial biogenesis and protein folding

5657	YFL036W	*RPO41*	YFL036W mitochondrial RNA polymerase II
7082	YFR025C	*HIS2*	YFR025C Histidinolphosphatase
4406	YGL038C	*OCH1*	YGL038C membrane-bound mannosyltransferase
4431	YGL064C	*MRH4*	mitochondrial DEAD box RNA helicase
4437	YGL070C	*RPB9*	YGL070C RNA polymerase II subunit
4438	YGL071W	*RCS1*	YGL071W Putative transcription factor that binds the consensus site PyPuCACCCPu
4443	YGL076C	*RPL7A*	Ribosomal protein L7A (L6A) (rp11) (YL8)
4462	YGL095C	*VPS45*	YGL095C cytosolic and peripheral membrane protein
4474	YGL107C	*RMD9*	Required for Meiotic nuclear Division
4496	YGL129C	*RSM23*	Ribosomal Small subunit in Mitochondria
4498	YGL131C	*SNT2*	Name reserved, Daniel Schaft
4502	YGL135W	*RPL1B*	Ribosomal Protein of the Large subunit
4510	YGL143C	*MRF1*	Mitochondrial polypeptide chain release factor
4515	YGL148W	*ARO2*	YGL148W Chorismate synthase
4572	YGL206C	*CHC1*	YGL206C presumed vesicle coat protein
6884	YGL218W	*SRF1*	Stress Resistance during Fermentation, name reserved
4586	YGL220W	0	ORF, uncharacterized
4589	YGL223C	*COG1*	Conserved Oligomeric Golgi complex; intra-Golgi transport; retrograde (vesicle recycling within Golgi) transport
4604	YGL237C	*HAP2*	transcriptional activator protein of CYC1
4607	YGL240W	*DOC1*	Doc1p and Cdc26p are associated with the anaphase-promoting complex and are involved in the degradation of Clb2p
4613	YGL246C	*RAI1*	processing of 27S pre-rRNA, in nucleus
4636	YGR006W	*PRP18*	YGR006W RNA splicing factor associated with U5 snRNP
4650	YGR020C	*VMA7*	Vacuolar H-ATPase 14 kDa subunit (subunit F) of the catalytic (V1) sector
4666	YGR036C	*CWH8*	YGR036C Cwh8p contains 3 short stretches of amino acids that are characteristic for a wide variety of phosphatases, including lipid phosphatases and a protein phosphatase.
4692	YGR062C	*COX18*	YGR062C Cytochrome OXidase gene 18
4706	YGR076C	*MRPL25*	Mitochondrial ribosomal protein MRPL25 (YmL25)
4715	YGR085C	*RPL11B*	YGR085C 60S ribosomal protein L11B (L16B) (rp39B) (YL22)
4731	YGR101W	*PCP1*	processing of cytochrome c peroxidase
4732	YGR102C	0	ORF, uncharacterized
4742	YGR112W	*SHY1*	YGR112W mitochondrial protein with homology to the mammalian SURF-1 gene
4765	YGR135W	*PRE9*	YGR135W proteasome component Y13
4780	YGR150C	0	ORF, uncharacterized
6696	YGR155W	*CYS4*	YGR155W Cystathionine beta-synthase
4795	YGR165W	*MRPS35*	Mitochondrial Ribosomal Protein, Small subunit
4804	YGR174C	*CBP4*	YGR174C Essential for the expression and activity of ubiquinol-cytochrome c reductase
4810	YGR180C	*RNR4*	YGR180C Ribonucleotide Reductase
4813	YGR183C	*QCR9*	YGR183C 7.3 kDa subunit 9 of the ubiquinol cytochrome c oxidoreductase complex
6591	YGR204W	*ADE3*	encodes the cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase
4845	YGR215W	*RSM27*	Mitochondrial Ribosomal Protein, Small subunit
5872	YGR219W	0	ORF, dubious
5873	YGR220C	*MRPL9*	YGR220C Mitochondrial ribosomal protein MRPL9 (YmL9) (E. coli L3) (human MRL3)
5875	YGR222W	*PET54*	YGR222W translational activator of cytochrome c oxidase subunit III
7287	YGR255C	*COQ6*	YGR255C COQ6 monooxygenase
7288	YGR257C	*MTM1*	Manganese Trafficking factor for Mitochondrial SOD2
5914	YGR262C	*BUD32*	bud site selection
5937	YGR285C	*ZUO1*	YGR285C Zuotin, putative Z-DNA binding protein
946	YHL017W	0	ORF, uncharacterized
925	YHL038C	*CBP2*	YHL038C Cytochrome B pre-mRNA processing protein
6608	YHR025W	*THR1*	YHR025W homoserine kinase
6609	YHR026W	*PPA1*	proteolipid protein of the proton ATPase
5948	YHR039C-B		ORF, merged
1879	YHR051W	*COX6*	subunit VI of cytochrome c oxidase
1888	YHR060W	*VMA22*	YHR060W required for V-ATPase activity
6414	YHR064C	*PDR13*	YHR064C Hsp70 Protein
6615	YHR067W	*RMD12*	Required for Meiotic nuclear Division
1919	YHR091C	*MSR1*	YHR091C Arginyl-tRNA synthetase
1928	YHR100C	0	ORF, uncharacterized
1932	YHR104W	*GRE3*	YHR104W Aldo-keto reductase
1944	YHR116W	0	ORF, uncharacterized
1948	YHR120W	*MSH1*	mutS homolog involved in mitochondrial DNA repair
1952	YHR124W	*NDT80*	YHR124W meiosis-specific gene, mRNA is sporulation-specific
2841	YHR147C	*MRPL6*	YHR147C Mitochondrial ribosomal protein MRPL6 (YmL6)
2851	YHR157W	*REC104*	mRNA is induced early in meiosis
6417	YHR168W	0	ORF, uncharacterized
2872	YHR178W	*STB5*	YHR178W Zinc finger (6-Cys)
2877	YHR183W	*GND1*	YHR183W Phosphogluconate Dehydrogenase (Decarboxylating)

6634	YHR185C	*PFS1*	Prospore Formation at Selected spindle poles
1413	YIL020C	*HIS6*	phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase
2275	YIL116W	*HIS5*	histidinol-phosphate aminotransferase
1377	YJL046W	0	ORF, uncharacterized
1371	YJL052W	*TDH1*	YJL052W Glyceraldehyde-3-phosphate dehydrogenase 1
1367	YJL056C	*ZAP1*	YJL056C Metalloregulatory protein involved in zinc-responsive transcriptional regulation
1328	YJL095W	*BCK1*	YJL095W putative 163 kDa protein kinase
1327	YJL096W	*MRPL49*	Mitochondrial Ribosomal Protein, Large subunit
7097	YJL101C	*GSH1*	gamma-glutamylcysteine synthetase
1321	YJL102W	*MEF2*	mitochondrial elongation factor G-like protein
1304	YJL120W	0	ORF, dubious
1305	YJL121C	*RPE1*	D-ribulose-5-Phosphate 3-epimerase
1295	YJL130C	*URA2*	YJL130C carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase
7002	YJL136C	*RPS21B*	Ribosomal protein S21B (S26B) (YS25)
1285	YJL140W	*RPB4*	YJL140W fourth-largest subunit of RNA polymerase II
1245	YJL180C	*ATP12*	YJL180C essential for assembly of a functional F1-ATPase
1237	YJL188C	*BUD19*	bud site selection
1236	YJL189W	*RPL39*	Ribosomal protein L39 (L46) (YL40)
7018	YJL189W	*RPL39*	Ribosomal protein L39 (L46) (YL40)
2551	YJR073C	*OPI3*	YJR073C Methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipid N-methyltransferase)
6902	YJR090C	*GRR1*	F box protein with several leucine rich repeats
2583	YJR105W	*ADO1*	adenosine kinase
6918	YJR113C	*RSM7*	mitochondrial ribosome small subunit
6921	YJR118C	*ILM1*	weak similarity to Helicobacter pylori UreD protein
6925	YJR122W	*CAF17*	YJR122W CCR4 associated factor
6937	YJR144W	*MGM101*	mitochondrial genome maintenance
4850	YKL002W	*DID4 (VPS2)*	class E vacuolar-protein sorting and endocytosis factor; late endosome to vacuole transport
4851	YKL003C	*MRP17*	Mitochondrial ribosomal protein MRP17
4865	YKL016C	*ATP7*	YKL016C ATP synthase d subunit
4881	YKL032C	*IXR1*	intrastrand crosslink recognition protein
4984	YKL134C	*OCT1*	iron ion homeostasis; in mitochondrion
4990	YKL140W	*TGL1*	triglyceride lipase-cholesterol esterase
4993	YKL143W	*LTV1*	YKL143W low temperature viability protein
5005	YKL155C	*RSM22*	mitochondrial small ribosomal subunit
5009	YKL159C	*RCN1*	calcium-dependent protein serine/threonine phosphatase; in calcineurin complex
5010	YKL160W	*ELF1*	name reserved by Fred Winston
5019	YKL169C	0	ORF, dubious
5020	YKL170W	*MRPL38*	mitochondrial ribosomal protein L14
5034	YKL184W	*SPE1*	YKL184W Ornithine decarboxylase
5062	YKL212W	*SAC1*	YKL212W integral membrane protein localizing to the ER and Golgi
5066	YKL216W	*URA1*	YKL216W dihydroorotate dehydrogenase
5070	YKL221W	*MCH2*	monocarboxylate permease homologue
5077	YKR006C	*MRPL13*	Mitochondrial ribosomal protein YmL13
7102	YKR085C	*MRPL20*	22.3 kDa mitochondrial ribosomal large subunit protein YmL20; homologous to L17 of E. coli
6006	YKR090W	*PXL1*	name reserved by Scott Erdman
1494	YLL006W	*MMM1*	mitochondrial outer membrane protein
6022	YLL018C-A	*COX19*	Protein required for cytochrome c oxidase assembly, located in the cytosol and mitochondrial intermembrane space
1515	YLL027W	*ISA1*	iron ion transport, in mitochondrial matrix
1582	YLR027C	*AAT2*	aspartate aminotransferase, cytosolic
6436	YLR038C	*COX12*	subunit VIb of cytochrome c oxidase
2667	YLR056W	*ERG3*	YLR056W C-5 sterol desaturase
2678	YLR067C	*PET309*	YLR067C Involved in expression of mitochondrial COX1 by regulating translation of COX1 mRNA and by affecting transcription or stability of COX1 mRNAs
2685	YLR074C	*BUD20*	bud site selection
2698	YLR087C	*CSF1*	Protein required for fermentation at low temperature
2700	YLR089C	0	alanine degradation and biosynthesis
2725	YLR114C	0	ORF, uncharacterized
4096	YLR139C	*SLS1*	YLR139C 73 kDa mitochondrial integral membrane protein
4105	YLR148W	*PEP3*	YLR148W vacuolar membrane protein
4150	YLR201C	0	ORF, uncharacterized
4151	YLR202C	0	ORF, dubious
4152	YLR203C	*MSS51*	YLR203C Protein involved in maturation of COX1 and COB mRNA
4167	YLR218C	0	ORF, uncharacterized
5149	YLR240W	*VPS34*	YLR240W phosphatidylinositol 3-kinase
5153	YLR244C	*MAP1*	YLR244C methionine aminopeptidase
5179	YLR270W	*DCS1*	deadenylation-dependent decapping; hydrolase in the HIT superfamily
5198	YLR288C	*MEC3*	involved in checkpoint control and DNA repair

5221	YLR312W-A	*MRPL15*	Mitochondrial Ribosomal Protein, Large subunit
5233	YLR324W	0	ORF, uncharacterized
5278	YLR369W	*SSQ1*	Hsp70 family protein; DNA dependent DNA replication
5282	YLR373C	*VID22*	vacuole import and degradation, integral to plasma membrane
6715	YLR382C	*NAM2*	mitochondrial leucyl tRNA synthetase
5305	YLR396C	*VPS33*	YLR396C Vacuolar sorting protein essential for vacuolar morphogenesis and function
5312	YLR403W	*SFP1*	YLR403W split zinc finger protein
7109	YLR439W	*MRPL4*	Mitochondrial 60S ribosomal protein L4
561	YML013C-A	*YML012C-A*	ORF, dubious
6719	YML022W	*APT1*	Adenine phosphoribosyltransferase
482	YML088W	*UFO1*	ubiquitin-protein ligase activity, F-box protein; response to DNA damage stimulus
6506	YML106W	*URA5*	YML106W Orotate phosphoribosyltransferase 1
6510	YML110C	*DBI56*	YML110C DBF2 Interacting Protein
6512	YML112W	*CTK3*	YML112W CTD kinase-I gamma subunit
6532	YML131W	0	ORF, uncharacterized
599	YMR024W	*MRPL3*	Mitochondrial ribosomal protein MRPL3 (YmL3)
611	YMR035W	*IMP2*	YMR035W Inner membrane protease (mitochondrial protein)
618	YMR042W	*ARG80*	YMR042W Regulator of arginine-responsive genes with ARG81 and ARG82
6188	YMR054W	*STV1*	YMR054W vacuolar proton pumping ATPase, 110-kDa subunit\; not in vacuole membrane
6197	YMR064W	*AEP1*	basic, hydrophilic protein of 59 kDa
6199	YMR066W	*SOV1*	Synthesis Of Var, name reserved Marie Sanchirico
6204	YMR071C	*TVP18*	Tlg2-Vesicle Protein, integral membrane protein
6205	YMR072W	*ABF2*	YMR072W HMG-1 homolog, mitochondrial
6217	YMR083W	*ADH3*	alcohol dehydrogenase isoenzyme III
6218	YMR084W	0	ORF, uncharacterized
6224	YMR089C	*YTA12*	YMR089C mitochondrial membrane ATPase of the CDC48\/PAS1\/SEC18 (AAA) family
6538	YMR098C	0	ORF, uncharacterized
722	YMR141C	0	ORF, dubious
732	YMR150C	*IMP1*	YMR150C Inner membrane protease (mitochondrial protein)
731	YMR151W	*YIM2*	YMR151W hypothetical protein
6444	YMR158W	*MRPS8*	Mitochondrial Ribosomal Protein, Small subunit
814	YMR228W	*MTF1*	YMR228W Mitochondrial RNA polymerase specificity factor
842	YMR256C	*COX7*	subunit VII of cytochrome c oxidase
843	YMR257C	*PET111*	YMR257C translational activator of cytochrome c oxidase subunit II
853	YMR267W	*PPA2*	YMR267W mitochondrial inorganic pyrophosphatase
869	YMR283C	*RIT1*	YMR283C Initiator methionine tRNA 2'-O-ribosyl phosphate transferase
872	YMR286W	*MRPL33*	Mitochondrial ribosomal protein MRPL33 (YmL33) (E. coli L30)
873	YMR287C	*MSU1*	YMR287C Protein essential for mitochondrial biogenesis
880	YMR293C	0	amidase activity, in mitochonddrion
5333	YNL005C	*MRP7*	YNL005C Mitochondrial ribosomal protein MRP7 (YmL2) (E. coli L27)
7210	YNL052W	*COX5A*	YNL052W Cytochrome-c oxidase chain Va
7220	YNL073W	*MSK1*	mitochondrial lysine-tRNA synthetase
2995	YNL081C	*SWS2*	Sick Without Securin; name reserved Orna Cohen-Fix
2052	YNL160W	*YGP1*	YNL160W YGP1 encodes gp37, a glycoprotein synthesized in response to nutrient limitation which is homologous to the sporulation-specific SPS100 gene
2035	YNL177C	*MRPL22*	Mitochondrial Ribosomal Protein, Large subunit
1999	YNL213C	0	mitochondrion organization and biogenesis
1987	YNL225C	*CNM67*	YNL225C chaotic nuclear migration\; predicted mass is 67kDa
6465	YNL252C	*MRPL17*	Mitochondrial Ribosomal Protein, Large subunit
7386	YNL284C	*MRPL10*	YNL284C Mitochondrial ribosomal protein MRPL10 (YmL10)
1140	YNL304W	*YPT11*	acts positively on mitochondrial distribution toward the bud; mitochondrion inheritance
7387	YNL315C	*ATP11*	essential for assembly of a functional F1-ATPase
5411	YNR036C	0	strong similarity to ribosomal protein S12
5412	YNR037C	0	ORF, uncharacterized
5416	YNR041C	*COQ2*	para hydroxybenzoate: polyprenyl transferase
5420	YNR045W	*PET494*	YNR045W translational activator of cytochrome c oxidase
1697	YOL006C	*TOP1*	YOL006C topoisomerase I
1700	YOL009C	*MDM12*	YOL009C Mdm12p is a mitochondrial outer membrane protein. An Mdm12p homolog exists in S. Pombe which confers a dominant negative phenotype when expressed in S. cerevisiae
1703	YOL012C	*HTA3*	An evolutionarily conserved member of the histone H2A FVZ family of histone variants
1714	YOL023W	*IFM1*	YOL023W mitochondrial initiation factor 2
1740	YOL049W	*GSH2*	YOL049W Glutathione Synthetase
1764	YOL072W	*THP1*	RNA-nucleus export; in nuclear envelope-ER network, nuclear pore
1771	YOL080C	*REX4*	RNA EXonuclease; member of 3'->5' exonuclease family; ribosome assembly
1772	YOL081W	*IRA2*	YOL081W encodes a GTPase activating protein, highly homologous to Ira1p, homologue of neurofibromin
6246	YOL096C	*COQ3*	YOL096C 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
6250	YOL100W	*PKH2*	MAPKKK cascade; in nucleus
6288	YOL138C	0	ORF, uncharacterized

6652	YOL143C	*RIB4*	YOL143C 6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase)
7390	YOL148C	*SPT20*	YOL148C transcription factor, member of the histone acetyltransferase SAGA complex
6659	YOL150C	0	ORF, dubious
1811	YOR035C	*SHE4*	Required for mother cell-specific HO expression
1812	YOR036W	*PEP12*	YOR036W integral membrane protein\; c-terminal TMD\; located in endosome
1829	YOR053W	0	ORF, dubious
1831	YOR055W	0	ORF, dubious
1856	YOR080W	*DIA2*	Digs Into Agar, invasive growth
1868	YOR092W	*ECM3*	YOR092W ExtraCellular Mutant
2381	YOR125C	*CAT5*	YOR125C may encode a protein involved in one or more monoxygenase or hydroxylase steps of ubiquinone biosynthesis
2406	YOR150W	*MRPL23*	ribosomal protein of the large subunit, mitochondrial
2414	YOR158W	*PET123*	YOR158W Mitochondrial ribosomal protein of small subunit
2440	YOR184W	*SER1*	YOR184W phosphoserine transaminase
2441	YOR185C	*GSP2*	YOR185C GTP binding protein, almost identical to Gsp1p
2455	YOR199W	0	ORF, dubious
2456	YOR200W	0	ORF, dubious
2457	YOR201C	*PET56*	YOR201C Ribose methyltransferase for mitochondrial 21S rRNA
2461	YOR205C	*FMP38*	Found in Mitochondrial Proteome; name reserved by Reter Rehling
2467	YOR211C	*MGM1*	YOR211C encodes protein with GTP-binding domain related to dynamin
2477	YOR221C	*MCT1*	malonyl-CoA:ACP transferase; in mitochondrion
2485	YOR229W	*WTM2*	YOR229W Transcriptional modulator
2497	YOR241W	*MET7*	tetrahydrofolylpolyglutamate synthase
1586	YOR290C	*SNF2*	YOR290C transcriptional regulator
1602	YOR305W	0	ORF, uncharacterized
1627	YOR330C	*MIP1*	YOR330C catalytic subunit of mitochondrial DNA polymerase
1631	YOR334W	*MRS2*	YOR334W splicing factor
1634	YOR337W	*TEA1*	YOR337W Mutants are defective in Ty1 Enhancer-mediated Activation
1647	YOR350C	*MNE1*	weak similarity to Esp1p and mitochondrial L.illustris cytochrome oxidase I
1655	YOR358W	*HAP5*	Component, along with Hap2p and Hap3p, of CCAAT-binding transcription factor
1672	YOR375C	*GDH1*	YOR375C NADP-specific glutamate dehydrogenase
2823	YPL005W	0	ORF, uncharacterized
2815	YPL013C	*MRPS16*	ribosomal protein S16, mitochondrial
7339	YPL017C	0	Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family
2799	YPL029W	*SUV3*	YPL029W putative ATP-dependent helicase
2769	YPL059W	*GRX5*	Member of glutaredoxin subfamily together w/GRX3, GRX4. Significant sequence diff. from other glutaredoxin subfamily, GRX1 & GRX2. Part of mt machinery involved in synthesis/assembly of iron/sulfur
7343	YPL078C	*ATP4*	YPL078C F(1)F(0)-ATPase complex delta subunit, mitochondrial
2749	YPL079W	*RPL21B*	YPL079W Ribosomal protein L21B
2157	YPL095C	0	ORF, uncharacterized
2155	YPL097W	*MSY1*	YPL097W Tyrosyl-tRNA synthetase
2148	YPL104W	*MSD1*	Aspartyl-tRNA synthetase, mitochondrial
2134	YPL118W	*MRP51*	YPL118W Component of small subunit of the mitochondrial ribosome
6479	YPL132W	*COX11*	YPL132W Putative heme A biosynthetic enzyme involved in forming the formyl group at position 8 of the porphyrin ring
7344	YPL137C	0	ORF, uncharacterized
2080	YPL172C	*COX10*	YPL172C Putative farnesyl transferase required for heme A synthesis
2079	YPL173W	*MRPL40*	YPL173W Mitochondrial ribosomal protein MRPL40 (YmL40)
1104	YPL188W	*POS5*	YPL188W similarity to Utr1p and YEL041w
1098	YPL194W	*DDC1*	YPL194W DNA damage checkpoint gene
1058	YPL234C	*TFP3*	YPL234C 17-kDa subunit C of vacuolar membrane H(+)-ATPase
1044	YPL248C	*GAL4*	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
1038	YPL254W	*HFI1*	YPL254W transcription factor, member of Ada\/Gcn5 protein complex
7135	YPL268W	*PLC1*	phosphoinositide-specific phospholipase C
1022	YPL270W	*MDL2*	YPL270W ATP-binding cassette (ABC) transporter family member
1021	YPL271W	*ATP15*	YPL271W nuclear gene for ATP synthase epsilon subunit
7144	YPR024W	*YME1*	YPR024W Mitochondrial protein of the CDC48\/PAS1\/SEC18 family of ATPases
5449	YPR030W	*CSR2*	Nuclear protein with a potential regulatory role in utilization of galactose and nonfermentable carbon sources; in nucleus
7151	YPR067W	*ISA2*	iron ion transport, in mitochondrial intermembrane space
5491	YPR072W	*NOT5*	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription
5516	YPR099C	0	ORF, dubious
5517	YPR100W	*MRPL51*	Mitochondrial Ribosomal Protein, Large subunit
5532	YPR116W	0	ORF, uncharacterized
5606	YPR191W	*QCR2*	YPR191W 40 kDa ubiquinol cytochrome-c reductase core protein 2
5613	YPR198W	*SGE1*	multi-copy suppressor of gal11 null\; member of drug-resistance protein family

[1] Description from SGD

Sup. Table 2A. Mutants affected in high-copy Ty3-*HIS3* transposition

ORF	Gene Name	Description[1]	High copy tpn	Low tpn	Other Ty screens[2]
YAL013W	*DEP1*	Transcriptional modulator involved in the regulation of structural genes involved in phospholipid biosynthesis, also participates in regulation of metabolically unrelated genes as well as maintenance of mating efficiency	2	2	SD
YAL021C	*CCR4*	carbon catabolite repression; transcriptional regulator for some glucose-repressed genes including ADH2; 95 kDa containng leucine rich tandem repeats	5	3	
YAL023C	*PMT2*	Transfers mannosyl residues from dolichyl phosphate-D-mannose to seryl and threonyl residues in proteins; acts in complex with Pmt1p; dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase	4	3	
YAL027W	*0*	0	2	2	
YAL029C	*MYO4*	Required for mother-specific HO expression, for the bud tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p; myosin	4	2	
YAR003W	*SWD1*	Subunit of the COMPASS complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres	4	4	MA
YAR030C	*0*	0	4	2	
YAR043C	*0*	0	4	2	
YBL006C	*LDB7*	Protein of unknown function; null mutant shows a reduced affinity for the alcian blue dye suggesting a decreased net negative charge of the cell surface	5	5	
YBL007C	*SLA1*	Protein involved in assembly of the cortical actin cytoskeleton, contains 3 SH3 domains, interacts with Bee1p	1	1	

YBL024W	*NCL1*	Nuclear protein 1, similar to NOP2 and human proliferation associated nucleolar protein p120; Probable proliferating-cell nucleolar antigen (human p120)	5	2	MA
YBL094C	*0*	0	4	4	
YBL103C	*RTG3*	Basic helix-loop-helix-leucine zipper (bHLH/Zip) transcription factor that forms a complex with another bHLH/Zip protein, Rtg1p, to activate the retrograde (RTG) and TOR pathways	5	3	
YBR021W	*FUR4*	Uracil permease, localized to the plasma membrane; expression is tightly regulated by uracil levels and environmental cues	1	1	
YBR044C	*TCM62*	mitochondrial protein; (putative) chaperone	2	2	
YBR062C	*0*	0	4	2	
YBR077C	*0*	0	5	2	SD
YBR105C	*VID24*	also involved in vacuolar protein targeting; peripheral vesicle membrane protein	5	2	
YBR114W	*RAD16*	Protein that recognizes and binds damaged DNA in an ATP-dependent manner (with Rad7p) during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 4 (NEF4); member of the SWI/SNF family	2	3	
YBR182C	*SMP1*	Transcription factor of the MADS (Mcm1p, Agamous, Deficiens, SRF) box family; closely related to RLM1; Probable DNA-binding transcription factor, Homolog to SRF/SL-2	5	3	
YBR269C	*FMP21*	The authentic, non-tagged protein was localized to the mitochondria	4	4	
YBR277C	*0*	0	4	4	

YBR281C	*0*	0	4	3	
YBR284W	*0*	0	4	4	MA
YBR297W	*MAL33*	MAL-activator protein, part of complex locus MAL3; nonfunctional in genomic reference strain S288C	4	3	
YBR298C	*MAL31*	Maltose permease, high-affinity maltose transporter (alpha-glucoside transporter); encoded in the MAL3 complex locus; member of the 12 transmembrane domain superfamily of sugar transporters; functional in	4	3	
YCL037C	*SRO9*	Associates with translating ribosomes; may function in the cytoplasm to modulate mRNA translation; may be involved in organization of actin filaments; RNA binding protein with La motif	5	4	
YCL061C	*MRC1*	S-phase checkpoint protein found at replication forks, required for DNA replication; also required for Rad53p activation during DNA replication stress, where it forms a replication-pausing complex with Tof1p and is	4	4	
YCR020W-B	*HTL1*	High-Temperature Lethal; high-temperature lethal	4	4	
YCR045C	*0*	0	4	3	
YCR050C	*0*	0	4	3	
YDL013W	*HEX3*	Ring finger protein involved in the DNA damage response with possible recombination role; genetically identified by synthetic lethality with SGS1 (DNA helicase) and TOP3 (DNA topoisomerase); sporulation role; interacts	4	3	
YDL021W	*GPM2*	Similar to GPM1 (phosphoglycerate mutase); converts 3-phosphoglycerate to 2-phosphoglycerate in glycolysis; phosphoglycerate mutase, involved in glycolysis	4	3	
YDL056W	*MBP1*	transcription factor	4	4	

YDL074C	*BRE1*	E3 ubiquitin ligase for Rad6p, required for the ubiquitination of histone H2B, recruitment of Rad6p to promoter chromatin and subsequent methylation of histone H3 (on L4 and L79), contains RING finger domain	4	4	
YDL088C	*ASM4*	Nuclear pore complex subunit, part of a subcomplex also containing Nup53p, Nup170p, and Pse1p	1	1	
YDL116W	*NUP84*	Subunit of the nuclear pore complex (NPC), forms a subcomplex with Nup85p, Nup120p, Nup145p-C, Sec13p, and Seh1p that plays a role in nuclear mRNA export and NPC biogenesis	4	4	SD
YDL118W	*0*	0	1	2	
YDL135C	*RDI1*	Rho GDP dissociation inhibitor with activity toward Rho1p; Rho GDP dissociation inhibitor	4	3	
YDL151C	*BUD30*	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 96% of ORF overlaps the verified gene RPC53; diploid mutant displays a weak budding pattern phenotype in	1	4	SD
YDL160C	*DHH1*	Cytoplasmic DExD/H-box helicase, stimulates mRNA decapping, coordinates distinct steps in mRNA function and decay, interacts with both the decapping and deadenylase complexes, may have a role in mRNA	2	2	
YDL162C	*0*	0	5	3	
YDR049W	*0*	0	4	3	
YDR067C	*0*	0	2	2	
YDR074W	*TPS2*	Trehalose-6-phosphate phosphatase	4	4	SD
YDR139C	*RUB1*	Related to ubiquitin (53% identical). Homolog of mammalian ubiquitin-like protein NEDD8. Matures by proteolytic removal of C-terminal asparagine (ASN) residue. Requires the proteins ULA1 & UBA3 for activation; ubiquitin-	2	2	

YDR159W	*SAC3*	A component of the nuclear pore that is involved in the nuclear export of both mRNA and protein; Leucine permease transcriptional regulator	5	5	
YDR176W	*NGG1*	Involved in glucose repression of GAL4p-regulated transcription; transcription factor; genetic and mutant analyses suggest that Ngg1p (Ada3p) is part of two transcriptional adaptor/HAT (histone acetyltransferase	4	4	
YDR255C	*RMD5*	Cytosolic protein required for sporulation; also required for the ubiquitination of the gluconeogenetic enzyme fructose-1,6-bisphosphatase, which is degraded rapidly after the switch from gluconeogenesis to glycolysis	4	1	
YDR272W	*GLO2*	Cytoplasmic glyoxalase II, catalyzes the hydrolysis of S-D-lactoylglutathione into glutathione and D-lactate	4	2	
YDR289C	*RTT103*	Regulator of Ty1 Transposition; regulator of Ty1 Transposition	5	5	JC
YDR290W	*0*	Sick Without Securin; HU sensitive mutant; name reserved Orna Cohen-Fix	5	5	
YDR293C	*SSD1*	Protein with a role in maintenance of cellular integrity, interacts with components of the TOR pathway; ssd1 mutant of a clinical S. cerevisiae strain displays elevated virulence	5	3	
YDR323C	*PEP7*	Multivalent adaptor protein that facilitates vesicle-mediated vacuolar protein sorting by ensuring high-fidelity vesicle docking and fusion, which are essential for targeting of vesicles to the endosome; required for vacuole	2	2	
YDR392W	*SPT3*	Subunit of the SAGA and SAGA-like transcriptional regulatory complexes, interacts with Spt15p to activate transcription of some RNA polymerase II-dependent genes, also functions to inhibit trancription at some promoters	4	3	
YDR410C	*STE14*	farnesyl cysteine-carboxyl methyltransferase	4	3	
YDR425W	*SNX41*	Sorting nexin that mediates retrieval from endosomes	4	2	
YDR432W	*NPL3*	RNA-binding protein that carries poly(A)+ mRNA from the nucleus into the cytoplasm; phosphorylation by Sky1p in the cytoplasm may promote release of mRNAs	4	5	

YDR448W	*ADA2*	transcription factor, member of ADA and SAGA, two transcriptional adaptor/HAT (histone acetyltransferase)complexes	4	5	
YDR486C	*VPS60*	vacuolar protein sorting (putative)	2	3	
YDR493W	*FMP36*	The authentic, non-tagged protein was localized to the mitochondria	2	2	
YEL003W	*GIM4*	Prefoldin subunit 2; putative homolog of subunit 2 of bovine prefoldin, a chaperone comprised of six subunits; bovine prefoldin subunit 2 homolog (putative)	4	2	
YEL004W	*YEA4*	Shows sequence similarity to GOG5, a gene involved in vanadate resistance; similar to Gog5, which is involved in vanadate resistance	4	4	
YEL013W	*VAC8*	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions	5	4	JC
YEL044W	*IES6*	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions	1	2	
YER057C	*HMF1*	Member of the p14.5 protein family with similarity to Mmf1p, functionally complements Mmf1p function when targeted to mitochondria; heat shock inducible; high-dosage growth inhibitor; forms a homotrimer in vitro	4	4	
YER060W-A	*FCY22*	Putative purine-cytosine permease, very similar to Fcy2p but cannot substitute for its function	4	4	
YER145C	*FTR1*	High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron	2	2	
YER155C	*BEM2*	Rho GTPase activating protein (RhoGAP) involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence	4	4	
YER173W	*RAD24*	Checkpoint protein, involved in the activation of the DNA damage and meiotic pachytene checkpoints; subunit of a clamp loader that loads Rad17p-Mec3p-Ddc1p onto DNA; homolog of human and S. pombe Rad17 protein	2	2	

YFL001W	*DEG1*	Non-essential tRNA:pseudouridine synthase, introduces pseudouridines at position 38 or 39 in tRNA, important for maintenance of translation efficiency and normal cell growth, localizes to both the nucleus and cytoplasm	2	2
YFL007W	*BLM3*	Protein involved in assembly of proteasomal core particles in the nucleus; required for normal resistance to bleomycin, may be involved in protection against oxidative damage	2	2
YFL034W	*0*	0	4	2
YFL043C	*0*	0	4	3
YFR009W	*GCN20*	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA	2	2
YFR010W	*UBP6*	Ubiquitin-specific protease situated in the base subcomplex of the 26S proteasome, releases free ubiquitin from branched polyubiquitin chains; deletion causes hypersensitivity to cycloheximide and other toxic	4	2
YFR012W	*0*	0	2	2
YFR019W	*FAB1*	1-phosphatidylinositol-3-phosphate 5-kinase; vacuolar membrane kinase that generates phosphatidylinositol (3,5)P2, which is involved in vacuolar sorting and homeostasis	2	2
YGL016W	*KAP122*	Karyopherin beta, responsible for import of the Toa1p-Toa2p complex into the nucleus; binds to nucleoporins Nup1p and Nup2p; may play a role in regulation of pleiotropic drug resistance	2	4
YGL057C	*0*	0	2	2
YGL058W	*RAD6*	Ubiquitin-conjugating enzyme (E2), involved in postreplication repair (with Rad18p), sporulation, telomere silencing, and uniquitin-mediated N-end rule protein degradation (with Ubr1p)	5	5
YGL066W	*SGF73*	SaGa associated Factor 73kDa; Probable 73KkDa Subunit of SAGA histone acetyltransferase complex	5	4

YGL078C	*DBP3*	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis	1	1	
YGL154C	*LYS5*	Phosphopantetheinyl transferase involved in lysine biosynthesis; converts inactive apo-form of Lys2p (alpha-aminoadipate reductase) into catalytically active holo-form by posttranslational addition of phosphopantetheine	4	3	SD
YGL170C	*SPO74*	Component of the meiotic outer plaque of the spindle pole body, involved in modifying the meiotic outer plaque that is required prior to prospore membrane formation	4	3	
YGL173C	*KEM1*	5'-3' exonuclease involved in mRNA decay, evolutionarily conserved component of cytoplasmic processing (P) bodies, plays a role in microtubule-mediated processes, filamentous growth, and ribosomal RNA maturation	2	1	
YGL174W	*BUD13*	Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern	4	4	
YGL212W	*VAM7*	Regulator of vacuolar morphogenesis; hydrophilic protein, heptad repeat motif	2	2	
YGL243W	*TAD1*	tRNA-specific adenosine deaminase, deaminates adenosine-37 to inosine in tRNA-Ala	4	2	
YGR056W	*RSC1*	RSC1 is a member of RSC complex, which remodels the structure of chromatin; Member of RSC complex	5	4	
YGR069W	*0*	0	5	2	
YGR125W	*0*	0	4	2	
YGR167W	*CLC1*	Clathrin light chain	1	2	
YGR188C	*BUB1*	checkpoint gene involved in permitting entry into mitosis depending upon the assembly state of microtubules; Serine/threonine protein kinase required for cell cycle arrest in response to loss of microtubule function	2	2	

YGR270W	*YTA7*	Protein of unknown function, member of CDC48/PAS1/SEC18 family of ATPases, potentially phosphorylated by Cdc28p	4	4	
YHL003C	*LAG1*	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lac1p	4	5	
YHL011C	*PRS3*	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes	1	3	
YHL029C	*0*	0	4	2	
YHL030W	*ECM29*	Major component of the proteasome; tethers the proteasome core particle to the regulatory particle, and enhances the stability of the proteasome	5	4	
YHR008C	*SOD2*	Manganese-containing superoxide dismutase	2	2	
YHR031C	*RRM3*	involved in rDNA replication and Ty1 transposition; DNA helicase	5	5	JC
YHR048W	*0*	0	4	3	
YHR154W	*RTT107*	Regulator of Ty1 Transposition; Establishes Silent Chromatin; involved in silencing	4	3	JC
YHR167W	*THP2*	affects transcription elongation	5	3	SD
YHR177W	*GON3*	unknown	4	4	
YIL009C-A	*EST3*	Component of the telomerase holoenzyme, involved in telomere replication	5	4	

YIL011W	*TIR3*	TIP1-related	4	5
YIL015W	*BAR1*	Aspartyl protease secreted into the periplasmic space of mating type a cells, cleaves and inactivates alpha factor allowing cells to recover from alpha-factor-induced cell cycle arrest	5	5
YIL044C	*AGE2*	ADP-ribosylation factor (ARF) GTPase activating protein (GAP) effector ; ARF GAP with effector function(s)	4	2
YIL069C	*RPS24B*	Protein component of the small (40S) ribosomal subunit; identical to Rps24Ap and has similarity to rat S24 ribosomal protein	4	5
YIL073C	*SPO22*	Meiosis-specific protein with similarity to phospholipase A2, involved in completion of nuclear divisions during meiosis; induced early in meiosis	2	1
YIL090W	*0*	0	4	4
YIL121W	*QDR2*	Multidrug transporter responsible for resistance to quinidine and barban; member of a family of drug:proton antiporters; plasma membrane transporter	5	2
YIL125W	*KGD1*	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA	4	3
YIL134W	*FLX1*	Protein required for transport of flavin adenine dinucleotide (FAD) from mitochondria, where it is synthesized from riboflavin, to the cytosol	2	2
YIR009W	*MSL1*	U2B component of U2 snRNP, involved in splicing, binds the U2 snRNA stem-loop IV in vitro; does not contain the conserved C-terminal RNA binding domain found in other family members	4	3
YIR021W	*MRS1*	Protein required for the splicing of two mitochondrial group I introns (BI3 in COB and AI5beta in COX1); forms a splicing complex, containing four subunits of Mrs1p and two subunits of the BI3-encoded maturase, that binds	4	4
YIR037W	*HYR1*	Thiol peroxidase that functions as a hydroperoxide receptor to sense intracellular hydroperoxide levels and transduce a redox signal to the Yap1p transcription factor	4	2

YIR038C	*GTT1*	ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; functional overlap with Gtt2p, Grx1p, and Grx2p	4	3	
YJL006C	*CTK2*	Beta subunit of C-terminal domain kinase I (CTDK-I), which phosphorylates the C-terminal repeated domain of the RNA polymerase II large subunit (Rpo21p) to affect both transcription and pre-mRNA 3' end processing; has	1	2	
YJL047C	*RTT101*	Cullin family member; subunit of a complex containing ubiquitin ligase activity; binds HRT1 and is modified by the ubiquitin like protein, RUB1; Regulator of Ty1 Transposition; Regulator of Ty1 Transposition	4	4	JC
YJL092W	*HPR5*	DNA helicase and DNA-dependent ATPase involved in DNA repair, required for proper timing of commitment to meiotic recombination and the transition from Meiosis I to Meiosis II; potential Cdc28p substrate	4	4	
YJL132W	*0*	0	5	2	
YJR032W	*CPR7*	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; binds to Hsp82p and contributes to chaperone activity	2	1	SD
YJR040W	*GEF1*	Chloride channel localized to late- or post-Golgi vesicles, involved in iron metabolism; highly homologous to voltage-gated chloride channels in vertebrates	4	2	
YJR054W	*0*	0	4	3	
YJR056C	*0*	0	4	3	
YJR102C	*VPS25*	vacuolar protein sorting (putative)	1	2	
YJR120W	*0*	0	2	2	
YJR121W	*ATP2*	Beta subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis	2	2	

YKL006W	*RPL14A*	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Bp and has similarity to rat L14 ribosomal protein; rpl14a csh5 double null mutant exhibits synthetic slow growth	4	2	SD
YKL023W	*0*	0	5	3	
YKL027W	*0*	0	4	2	
YKL038W	*RGT1*	transcriptional repressor and activator	4	2	
YKL039W	*PTM1*	Putative membrane protein	4	2	
YKL041W	*VPS24*	involved in secretion	4	4G	
YKL043W	*PHD1*	protein similar to StuA of Aspergillus nidulans; putative transcription factor	4	2	
YKL047W	*0*	0	5	2	
YKL053W	*0*	0	4	2	
YKL054C	*DEF1*	RNAPII degradation factor, forms a complex with Rad26p in chromatin, enables ubiquitination and proteolysis of RNAPII	1	4G	
YKL055C	*OAR1*	Mitochondrial 3-oxoacyl-[acyl-carrier-protein] reductase, may comprise a type II mitochondrial fatty acid synthase along with Mct1p	4	1	
YKL057C	*NUP120*	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), required for even distribution of NPCs around the nuclear envelope, involved in establishment of a normal nucleocytoplasmic concentration	5	5	

YKL062W	*MSN4*	Zinc finger transcription factor, key regulator of stress-responsive gene expression; multicopy suppressor of snf1 mutation	4	2	
YKL068W	*NUP100*	Subunit of the nuclear pore complex (NPC) that is localized to both sides of the pore; contains a repetitive GLFG motif that interacts with mRNA export factor Mex67p and with karyopherin Kap95p; homologous to Nup116p	4	4	
YKL072W	*STB6*	binds Sin3p in two-hybrid assay; involved in transcription	4	3	
YKL101W	*HSL1*	Nim1p-related protein kinase that regulates the morphogenesis and septin checkpoints; associates with the assembled septin filament; required along with Hsl7p for bud neck recruitment, phosphorylation, and degradation of	5	3	MA
YKL106W	*AAT1*	Mitochondrial aspartate aminotransferase, catalyzes the conversion of oxaloacetate to aspartate in aspartate and asparagine biosynthesis	4	1	
YKL113C	*RAD27*	5' to 3' exonuclease, 5' flap endonuclease, required for Okazaki fragment processing and maturation as well as for long-patch base-excision repair; member of the S. pombe RAD2/FEN1 family	4	3	
YKL129C	*MYO3*	One of two class-I myosins; localizes to actin cortical patches; deletion of MYO3 has little affect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeletion organization; myosin I	4	2	
YKL135C	*APL2*	Beta-adaptin, large subunit of the clathrin-associated protein (AP-1) complex	5	5	
YKL149C	*DBR1*	RNA lariat debranching enzyme, involved in intron turnover; required for efficient Ty1 transposition	1	2	SD
YKL161C	*0*	0	4	2	
YKL168C	*KKQ8*	Putative serine/threonine protein kinase with unknown cellular role	4	3	
YKR020W	*VPS51*	whiskey (whi) mutant; forms a tetramer with VPS52, VPS53, and VPS54	1	2	

YKR035W-A	*DID2*	Class E protein of the vacuolar protein-sorting (Vps) pathway, associates reversibly with the late endosome, has human ortholog that may be altered in breast tumors	5	2	
YKR054C	*DYN1*	Cytoplasmic heavy chain dynein, microtubule motor protein, required for anaphase spindle elongation; involved in spindle assembly, chromosome movement, and spindle orientation during cell division, targeted to	4	3	
YKR069W	*MET1*	S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in sulfate assimilation, methionine metabolism, and siroheme biosynthesis	4	3	
YKR082W	*NUP133*	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p	5	4	SD
YKR091W	*SRL3*	Cytoplasmic protein that, when overexpressed, suppresses the lethality of a rad53 null mutation; potential Cdc28p substrate	4	2	
YKR099W	*BAS1*	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways	2	2	
YLL002W	*RTT109*	Regulator of Ty1 Transposition; Regulation of mitochondrial network; Killed in Mutagen, sensitive to diepoxybutane and/or mitomycin C; diepoxybutane and mitomycin C resistance	5	4	JC
YLL030C	*0*	0	5	4	
YLL044W	*0*	0	5	4	
YLR015W	*BRE2*	Subunit of the COMPASS complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; has similarity to ASH2L member of trithorax proteins	5	4	
YLR025W	*SNF7* *VPS32*	Involved in derepression of SUC2 in response to glucose limitation; involved in glucose derepression	1	2	
YLR031W	*0*	0	4	3	

YLR081W	*GAL2*	Galactose permease, required for utilization of galactose; also able to transport glucose	2	4	
YLR118C	*APT1*	hydrolase acting on ester bonds	2	3	
YLR177W	*0*	0	4	3	
YLR181C	*VTA1*	Protein involved in endosomal protein sorting; binds to Vps20 and Vps4 and may regulate Vps4function; has coiled-coil domains; mutants show class E vacuolar-protein sorting defects	4	2	
YLR183C	*TOS4*	Transcription factor that binds to a number of promoter regions, particularly promoters of some genes involved in pheromone response and cell cycle; potential Cdc28p substrate; expression is induced in G1 by bound SBF	4	2	
YLR235C	*0*	0	5	4	
YLR242C	*ARV1*	Protein with similarity to Nup120p and C.elegans R05H5.5 protein	1	1	
YLR268W	*SEC22*	Identified in a screen for dense cells that accumulated invertase at the non-permissive temperature, SEC22 encodes a v-SNARE present on ER to Golgi vesicles and is involved in anterograde and retrograde transport	4	5	SD
YLR384C	*IKI3*	Subunit of RNA polymerase II elongator complex, which is a histone acetyltransferase; involved in maintaining structural integrity of the complex; iki3 mutations confer resistance to the K. lactis toxin zymocin	2	3	SD
YLR399C	*BDF1*	Protein involved in transcription initiation at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1;	4	5	
YLR417W	*VPS36*	Protein involved in vacuolar protein sorting	1	2	
YLR423C	*ATG17*	required for activation of Apg1 protein kinase; involved in autophagy	1	1	SD

YLR436C	*ECM30*	Non-essential protein of unknown function	4	2	MA
YML051W	*GAL80*	Transcriptional regulator involved in the repression of GAL genes in the absence of galactose; inhibits transcriptional activation by Gal4p; inhibition relieved by Gal3p or Gal1p binding	5	5	
YML063W	*RPS1B*	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Ap and has similarity to rat S3a ribosomal protein	1	L	
YML073C	*RPL6A*	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA	2	1	SD
YML081C-A	*ATP18*	Subunit of the mitochondrial F1F0 ATP synthase, which is a large enzyme complex required for ATP synthesis; termed subunit I or subunit j; does not correspond to known ATP synthase subunits in other organisms	2	2	
YML090W	*0*	0	2	4	
YML097C	*VPS9*	Protein required for Golgi to vacuole trafficking, has similarity with mammalian ras inhibitors	1	1	SD
YMR014W	*BUD22*	Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern	1	5	
YMR039C	*SUB1*	Suppressor of TFIIB mutations; transcriptional coactivator	2	3	SD
YMR048W	*CSM3*	Protein required for accurate chromosome segregation during meiosis	4	4	
YMR058W	*FET3*	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases	2	2	
YMR070W	*MOT3*	Nuclear transcription factor with two Cys2-His2 zinc fingers; involved in repression of a subset of hypoxic genes by Rox1p, repression of several DAN/TIR genes during aerobic growth, and repression of ergosterol	4	3	

YMR077C	*VPS20*	vaculolar protein sorting (putative)	1	1	
YMR085W	*0*	0	4	3	
YMR088C	*0*	0	4	3	
YMR116C	*ASC1*	WD repeat protein (G-beta like protein) that interacts with the translational machinery; G-beta like protein	1	1	
YMR123W	*PKR1*	Pichia farinosa Killer toxin Resistance; Pichia farinosa killer toxin resistance	2	2	
YMR143W	*RPS16A*	Protein component of the small (40S) ribosomal subunit; identical to Rps16Bp and has similarity to E. coli S9 and rat S16 ribosomal proteins	1	4	
YMR154C	*RIM13*	Regulator of IME2 (RIM); Cysteine protease similar to E. nidulans palB	2	2	MA
YMR158W-B	*0*	0	2	2	
YMR190C	*SGS1*	Nucleolar DNA helicase of the RecQ family, involved in maintenance of genome integrity; has similarity to human BLM and WRN helicases implicated in Bloom and Werner syndromes	5	4	JC
YMR201C	*RAD14*	Protein that recognizes and binds damaged DNA during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); contains zinc finger motif; homolog of human XPA protein	4	3	
YMR206W	*0*	0	4	2	
YMR242C	*RPL20A*	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp and has similarity to rat L18a ribosomal protein	2	3	

YMR258C	*0*	0	4	2	
YNL059C	*ARP5*	Actin-related protein, involved in the carboxypeptidase Y pathway	1	2	
YNL136W	*EAF7*	Subunit of the NuA4 histone acetyltransferase complex	2	1	
YNL138W	*SRV2*	Adenylyl cyclase-associated protein; N-terminal domain appears to be involved in cellular responsiveness to RAS	5	5	
YNL153C	*GIM3*	Prefoldin subunit 4; putative homolog of subunit 4 of bovine prefoldin, a chaperone comprised of six subunits; bovine prefoldin subunit 4 homolog (putative)	1	3	
YNL212W	*VID27*	Vacuole import and degradation	5	3	
YNL224C	*0*	0	1	1	
YNL236W	*SIN4*	involved in positive and negative regualtion of transcription, possibly via changes in chromatin structure; regulation of YGP1 expression; component of RNA polymerase II holoenzyme/mediator complex	1	2	SD MA
YNL242W	*ATG2*	Defective in autophagy; required for sporulation; Required for sporulation.	4	4	
YNL250W	*RAD50*	Subunit of MRX complex, with Mre11p and Xrs2p, involved in processing double-strand DNA breaks in vegetative cells, initiation of meiotic DSBs, telomere maintenance, and nonhomologous end joining	4	3	JC
YNL283C	*WSC2*	cell wall integrity and stress response component 2; Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC3 and WSC4	4	3	
YNL285W	*0*	0	4	3	

YNL293W	*MSB3*	GTPase-activating protein for Sec4p and several other Rab GTPases, regulates exocytosis via its action on Sec4p, also required for proper actin organization; similar to Msb4p; both Msb3p and Msb4p localize to sites of	4	3	
YNL321W	*0*	0	4	3	
YNR006W	*VPS27*	hydrophilic protein; has cysteine rich putative zinc finger esential for function	1	2	
YNR052C	*POP2*	RNase of the DEDD superfamily, subunit of the Ccr4-Not complex that mediates 3' to 5' mRNA deadenylation	5	5	SD
YNR059W	*MNT4*	Putative alpha-1,3-mannosyltransferase, not required for protein O-glycosylation	2	2	
YOL007C	*0*	0	4	3	
YOL041C	*NOP12*	Nucleolar protein, required for pre-25S rRNA processing; contains an RNA recognition motif (RRM) and has similarity to Nop13p, Nsr1p, and putative orthologs in Drosophila and S. pombe	2	5	SD
YOL060C	*MAM3*	Protein required for normal mitochondrial morphology, has similarity to hemolysins	4	3	
YOL083W	*0*	0	2	2	
YOL141W	*PPM2*	Putative carboxyl methyl transferase, has similarity to Ppm1p but biochemical activity not yet demonstrated	4	2	
YOL159C	*0*	0	4	3	SD
YOR006C	*0*	0	5	3	

YOR009W	*TIR4*	0	4	3	
YOR039W	*CKB2*	protein kinase CK2, beta' subunit	5	4	
YOR051C	*0*	0	4	2	
YOR144C	*ELG1*	Protein required for S phase progression and telomere homeostasis, forms an alternative replication factor C complex important for DNA replication and genome integrity; mutants are sensitive to DNA damage	4	4	JC
YOR270C	*VPH1*	vacuolar ATPase V0 domain subunit a (100 kDa)	1	1	SD
YOR275C	*RIM20*	Regulator of IME2	2	2	
YOR293W	*RPS10A*	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps10Bp and has similarity to rat ribosomal protein S10	2	5	SD
YOR321W	*PMT3*	Transfers mannose residues from dolichyl phosphate-D-mannose to specific serine/threonine residues of proteins in the secretory pathway; dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase	4	2	
YOR364W	*0*	0	4	3	
YPL002C	*SNF8*	appears to be functionally related to SNF7; involved in glucose derepression	1	2	
YPL024W	*NCE4*	involved in cell separation	4	5	
YPL042C	*SSN3*	Component of RNA polymerase II holoenzyme, involved in RNA pol II carboxy-terminal domain phosphorylation	1	1	

YPL065W	*VPS28*	soluble, hydrophilic protein involved in transport of precursors for soluble vauolar hydrolases from the late endosome to the vacuole; involved in vacuolar protein targeting	1	2	
YPL084W	*BRO1*	BCK1-like resistance to osmotic shock	1	2	MA
YPL119C	*DBP1*	Putative ATP-dependent RNA helicase of the DEAD-box protein family; mutants show reduced stability of the 40S ribosomal subunit scanning through 5' untranslated regions of mRNAs	4	3	
YPL125W	*KAP120*	Karyopherin with a role in the assembly or export of 60S ribosomal subunits	1	1	
YPL129W	*TAF14*	Subunit (30 kDa) of TFIID, TFIIF, and SWI/SNF complexes, involved in RNA polymerase II transcription initiation and in chromatin modification	4	3	
YPL152W	*RRD2*	Resistant to Rapamycin Deletion 2; similar to hosphotyrosyl phosphatase activator (PTPA) from several organisms	4	3	JC
YPL225W	*0*	0	2	2	
YPL240C	*HSP82*	Cytoplasmic chaperone (Hsp90 family) required for pheromone signaling and negative regulation of Hsf1p; docks with the mitochondrial import receptor Tom70p for preprotein delivery; interacts with co-chaperones	4	2	
YPL256C	*CLN2*	role in cell cycle START; G(sub)1 cyclin	4	4	
YPL269W	*KAR9*	Karyogamy protein required for correct positioning of the mitotic spindle and for orienting cytoplasmic microtubules, localizes at the shmoo tip in mating cells and at the tip of the growing bud in small-budded cells through	4	3	
YPR119W	*CLB2*	Involved in mitotic induction; G(sub)2-specific B-type cyclin	4	4	
YPR135W	*CTF4*	Chromatin-associated protein, required for sister chromatid cohesion; interacts with DNA polymerase alpha (Pol1p) and may link DNA synthesis to sister chromatid cohesion	4	1	

YPR164W	*MMS1*	sensitive to methyl methanesulfonate (MMS), diepoxybutane, and mitomycin C; sensitive to diepoxybutane and mitomycin C	4	1	JC
YPR173C	*VPS4*	Defective in vacuolar protein sorting; homologous to mouse SKD1 and to human hVPS4; AAA-type ATPase	1	1	

[1] Description downloaded as described under GOnet in Materials and Methods

[2] Other screens are: Ty1, Scholes et al. (JC); Ty1, Griffith et al. (SD); and Ty3, Aye et al. (MA)

Sup. Table 2B. Pairs of closely spaced ORFs among the genes affecting high-copy Ty3-*HIS3* transposition

ORF	Name	Description[1]	High-copy tpn	Low-copy tpn
YBL006C	*LDB7*	Protein of unknown function; null mutant shows a reduced affinity for the alcian blue dye suggesting a decreased net negative charge of the cell surface	5	5
YBL007C	*SLA1*	Protein involved in assembly of the cortical actin cytoskeleton, contains 3 SH3 domains, interacts with Bee1p	1	1
YBR297W	*MAL33*	MAL-activator protein, part of complex locus MAL3; nonfunctional in genomic reference strain S288C	4	3
YBR298C	*MAL31*	Maltose permease, high-affinity maltose transporter (alpha-glucoside transporter); encoded in the MAL3 complex locus; member of the 12 transmembrane domain superfamily of sugar transporters; functional in genomic	4	3
YCL061C/YCL060C	*MRC1*	S-phase checkpoint protein found at replication forks, required for DNA replication; also required for Rad53p activation during DNA replication stress, where it forms a replication-pausing complex with Tof1p and is phosphorylated	4	4
YDR289C	*RTT103*	Regulator of Ty1 Transposition; regulator of Ty1 Transposition	5	5
YDR290W	*0*	Sick Without Securin; HU sensitive mutant; name reserved Orna Cohen-Fix	5	5
YEL003W	*GIM4*	Prefoldin subunit 2; putative homolog of subunit 2 of bovine prefoldin, a chaperone comprised of six subunits; bovine prefoldin subunit 2 homolog (putative)	4	2
YEL004W	*YEA4*	Shows sequence similarity to GOG5, a gene involved in vanadate resistance; similar to Gog5, which is involved in vanadate resistance	4	4
YFR009W	*GCN20*	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA	2	2

YFR010W	*UBP6*	Ubiquitin-specific protease situated in the base subcomplex of the 26S proteasome, releases free ubiquitin from branched polyubiquitin chains; deletion causes hypersensitivity to cycloheximide and other toxic compounds	4	2
YGL057C	*0*	0	2	2
YGL058W	*RAD6*	Ubiquitin-conjugating enzyme (E2), involved in postreplication repair (with Rad18p), sporulation, telomere silencing, and uniquitin-mediated N-end rule protein degradation (with Ubr1p)	5	5
YGL173C	*KEM1*	5'-3' exonuclease involved in mRNA decay, evolutionarily conserved component of cytoplasmic processing (P) bodies, plays a role in microtubule-mediated processes, filamentous growth, and ribosomal RNA maturation	2	1
YGL174W	*BUD13*	Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern	4	4
YIR037W	*HYR1*	Thiol peroxidase that functions as a hydroperoxide receptor to sense intracellular hydroperoxide levels and transduce a redox signal to the Yap1p transcription factor	4	2
YIR038C	*GTT1*	ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; functional overlap with Gtt2p, Grx1p, and Grx2p	4	3
YJR120W	*0*	0	2	2
YJR121W	*ATP2*	Beta subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis	2	2
YKL038W	*RGT1*	transcriptional repressor and activator	4	2
YKL039W	*PTM1*	Putative membrane protein	4	2
YKL054C	*DEF1*	RNAPII degradation factor, forms a complex with Rad26p in chromatin, enables ubiquitination and proteolysis of RNAPII	1	4

Sup. Table 3. Mutants affected in high- and low-copy Ty3*HIS3* transposition

ORF	Name	Table 1 designation	Sup. Fig. 1[1]	CA:Gag3[2]	Gag3:PGK[3]	IN:PGK[3]	plasmid trans 1[4]	plasmid trans 2[4]	cDNA/ plasmid[5]	Description[6]	Gene Product[6]	Function[6]	Process[6]	Component[6]	High-copy tpn	Low-copy tpn	Other Screens[7]
YJR032W	*CPR7*	stress/chaperone/ modification	L	3	3	3	3	3	0.43	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; binds to Hsp82p and contributes to chaperone activity	cyclophilin 40|peptidyl-prolyl cis-trans isomerase (PPIase)	unfolded protein binding*	response to stress	cytosol	2	1	SD
YJL047C	*RTT101*	stress/chaperone/ modification	L	3	3	3	3	3	1.04	Cullin family member; subunit of a complex containing ubiquitin ligase activity; binds HRT1 and is modified by the ubiquitin like protein, RUB1; Regulator of Ty1 Transposition; Regulator of Ty1 Transposition	0	protein binding*	ubiquitin-dependent protein catabolism*	cytoplasm*	4	4	JC
YDR139C	*RUB1*	stress/chaperone/ modification	L	3	3	3	3	3	0.58	Related to ubiquitin (53% identical). Homolog of mammalian ubiquitin-like protein NEDD8. Matures by proteolytic removal of C-terminal asparagine (ASN) residue. Requires the proteins ULA1 & UBA3 for activation; ubiquitin-like protein	ubiquitin-like protein	protein binding	NEDD8 class-dependent protein catabolism	cytoplasm	2	2	
YFL007W	*BLM3*	stress/chaperone/ modification	L	3	3	?	3	1	0.42	Protein involved in assembly of proteasomal core particles in the nucleus; required for normal resistance to bleomycin, may be involved in protection against oxidative damage	involved in protecting the cell against bleomycin damage	molecular_function unknown	biological_process unknown	membrane	2	2	
YBL007C	*SLA1*	cytoskeleton	K	3	3	3	2	2	0.62	Protein involved in assembly of the cortical actin cytoskeleton, contains 3 SH3 domains, interacts with Bee1p	cytoskeletal protein binding protein	protein binding, bridging*	cell wall organization and biogenesis*	actin cortical patch (sensu Fungi)	1	1	
YNL059C	*ARP5*	cytoskeleton	K	3	3	3	3	3	0.40	Actin-related protein, involved in the carboxypeptidase Y pathway	actin related protein	molecular_function unknown	protein-vacuolar targeting	nucleus	1	2	
YGL212W	*VAM7*	trafficking	H	3	3	3	2	0	0.36*	Regulator of vacuolar morphogenesis; hydrophilic protein, heptad repeat motif	heptad repeat motif|hydrophilic protein	v-SNARE activity	vesicle fusion*	vacuolar membrane (sensu Fungi)	2	2	
YEL013W	*VAC8*	trafficking	H	3	3	3	1	2	0.61	Phosphorylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions	0	protein binding	protein-vacuolar targeting*	vacuole (sensu Fungi)	5	4	JC
YLR423C	*ATG17*	trafficking	H	3	3	3	2	2	0.97	required for activation of Apg1 protein kinase; involved in autophagy	0	kinase activator activity	autophagy	cytoplasm	1	1	SD
YOR270C	*VPH1*	trafficking	H	3	3	3	3	3	0.46	vacuolar ATPase V0 domain subunit a (100 kDa)	V0 sector subunit|essential for vacuolar acidification and vacuolar H-ATPase activity|vacuolar ATPas	hydrogen-transporting ATPase activity, rotational mechanism	vacuolar acidification*	vacuole*	1	1	SD
YNR006W	*VPS27*	trafficking	F	3	3	3	3	2	0.25	hydrophilic protein; has cysteine rich putative zinc finger esential for function	cysteine rich putative zinc finger essential for function|hydrophilic protein	protein binding	protein-Golgi retention*	endosome	1	2	
YPL065W	*VPS28*	trafficking	F	3	3	3	2	1	0.71	soluble, hydrophilic protein involved in transport of precursors for soluble vauolar hydrolases from the late endosome to the vacuole; involved in vacuolar protein targeting	0	molecular_function unknown	protein-vacuolar targeting*	endosome*	1	2	
YLR417W	*VPS36*	trafficking	F	3	3	3	1	2	0.46	Protein involved in vacuolar protein sorting	0	regulator of G-protein signaling activity	protein-vacuolar targeting*	ESCRT II complex	1	2	
YJR102C	*VPS25*	trafficking	F	3	3	3	2	2	0.25	vacuolar protein sorting (putative)	0	molecular_function unknown	protein-vacuolar targeting*	ESCRT II complex	1	2	
YPL002C	*SNF8*	trafficking	F	3	3	3	2	2	0.30	appears to be functionally related to SNF7; involved in glucose derepression	0	molecular_function unknown	protein-vacuolar targeting*	ESCRT II complex	1	2	
YMR077C	*VPS20*	trafficking	F	3	3	3	3	3	0.41	vaculolar protein sorting (putative)	0	molecular_function unknown	late endosome to vacuole transport	cytoplasm*	1	1	
YLR025W	*SNF7* *VPS32*	trafficking	G	3	1	1	3	3	0.30	Involved in derepression of SUC2 in response to glucose limitation; involved in glucose derepression	0	molecular_function unknown	late endosome to vacuole transport	cytoplasm*	1	2	
YOR275C	*RIM20*	trafficking	G	3	3	3	3	3	0.11	Regulator of IME2	Unknown function	molecular_function unknown	proteolysis and peptidolysis*	cytoplasm*	2	2	
YPL084W	*BRO1*	trafficking	G	2	3	3	3	3	0.31	BCK1-like resistance to osmotic shock	0	intracellular transporter activity	ubiquitin-dependent protein catabolism*	cytoplasm*	1	2	MA
YPR173C	*VPS4*	trafficking	G	2	3	3	2	2	0.34	Defective in vacuolar protein sorting; homologous to mouse SKD1 and to human hVPS4; AAA-type ATPase	AAA ATPase	ATPase activity	late endosome to vacuole transport*	cytoplasm*	1	1	
YLR268W	*SEC22*	trafficking	E	3	3	3	3	3	0.28	Identified in a screen for dense cells that accumulated invertase at the non-permissive temperature, SEC22 encodes a v-SNARE present on ER to Golgi vesicles and is involved in anterograde and retrograde transport between the ER and Golgi; Synaptobrev	0	v-SNARE activity	ER to Golgi transport*	endoplasmic reticulum*	4	5	SD
YNR059W	*MNT4*	trafficking	E	3	3	3	3	3	0.21	Putative alpha-1,3-mannosyltransferase, not required for protein O-glycosylation	mannosyltransferase (putative)	alpha-1,3-mannosyltransferase activity	O-linked glycosylation	cellular_component unknown	2	2	
YGR167W	*CLC1*	trafficking	E	3	3	3	2	2	0.58	Clathrin light chain	clathrin light chain	structural molecule activity	vesicle-mediated transport	clathrin vesicle coat	1	2	
YFR019W	*FAB1*	trafficking	E	3	3	3	3	3	0.40	1-phosphatidylinositol-3-phosphate 5-kinase; vacuolar membrane kinase that generates phosphatidylinositol (3,5)P2, which is involved in vacuolar sorting and homeostasis	1-phosphatidylinositol-3-phosphate 5-kinase	1-phosphatidylinositol-3-phosphate 5-kinase activity	response to stress*	vacuolar membrane	2	2	
YML097C	*VPS9*	trafficking	E	3	3	3	3	3	0.23	Protein required for Golgi to vacuole trafficking, has similarity with mammalian ras inhibitors	0	guanyl-nucleotide exchange factor activity	protein-vacuolar targeting	cytosol	1	1	SD
YDR323C	*PEP7*	trafficking	E	3	5	5	4	4	0.24	Multivalent adaptor protein that facilitates vesicle-mediated vacuolar protein sorting by ensuring high-fidelity vesicle docking and fusion, which are essential for targeting of vesicles to the endosome; required for vacuole inheritance	three zinc fingers; cysteine rich regions of amino acids are essential for function	molecular_function unknown	vesicle fusion*	cytoplasm*	2	2	
YGL078C	*DBP3*	RNA processing	D	3	4	4	3	3	wt	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis	ATP dependent RNA helicase|dead/deah box protein CA3	ATP-dependent RNA helicase activity	35S primary transcript processing*	nucleolus	1	1	SD
YFL001W	*DEG1*	RNA processing	D	3	4	4	3	3	0.90	Non-essential tRNA:pseudouridine synthase, introduces pseudouridines at position 38 or 39 in tRNA, important for maintenance of translation efficiency and normal cell growth, localizes to both the nucleus and cytoplasm	0	pseudouridylate synthase activity	RNA processing	cytoplasm*	2	2	
YNR052C	*POP2*	RNA processing	D	3	2		2	2	3.04	RNase of the DEDD superfamily, subunit of the Ccr4-Not complex that mediates 3' to 5' mRNA deadenylation	transcription factor (putative)	3'-5'-exoribonuclease activity	regulation of transcription from Pol II promoter*	cytoplasm*	5	5	SD
YDL160C	*DHH1*	RNA processing	D	3	2	2	3	2	1.46	Cytoplasmic DExD/H-box helicase, stimulates mRNA decapping, coordinates distinct steps in mRNA function and decay, interacts with both the decapping and deadenylase complexes, may have a role in mRNA export and translation	0	protein binding	deadenylylation-dependent decapping*	cytoplasm*	2	2	
YGL173C	*KEM1*	RNA processing	D	1	3	3	2	2	2.28	5'-3' exonuclease involved in mRNA decay, evolutionarily conserved component of cytoplasmic processing (P) bodies, plays a role in microtubule-mediated processes, filamentous growth, and ribosomal RNA maturation	5'-3' exonuclease	recombinase activity*	35S primary transcript processing*	cytoplasm*	2	1	
YAL027W	*0*	unknown	M	3	3	3	2	2	0.56	0	0	0	0	0	2	2	
YDL118W	*0*	unknown	M	3	3	3	3	3	1.64	0	0	0	0	0	1	2	

YDR067C	*0*	unknown	M	3	3	3	3	3	0.79	0	0	0	0	0	2	2	
YDR493W	*FMP36*	unknown	M	3	3	3	3	3	0.49	The authentic, non-tagged protein was localized to the mitochondria	0	molecular_function unknown	biological_process unknown	mitochondrion	2	2	
YFR012W	*0*	unknown	M	3	3	3	3	3	0.47	0	0	0	0	0	2	2	
YGL057C	*0*	unknown	M	3	3	3	3	3	0.44	0	0	0	0	0	2	2	
YIL090W	*0*	unknown	N	3	3	3	3	3	1.74	0	0	0	0	0	4	4	
YJR120W	*0*	unknown	N	2	3	3	3	3	0.75	0	0	0	0	0	2	2	
YLL044W	*0*	unknown	N	3	3	?	3	3	0.41	0	0	0	0	0	5	4	
YNL224C	*0*	unknown	N	3	3	3	3	3	0.52	0	0	0	0	0	1	1	
YOL083W	*0*	unknown	N	3	3	3	3	0	0.62*	0	0	0	0	0	2	2	
YMR116C	*ASC1*	translation	C	3	4	5	3	3	0.95	WD repeat protein (G-beta like protein) that interacts with the translational machinery; G-beta like protein	G-beta like protein	molecular_function unknown	biological_process unknown	cytoplasm	1	1	
YFR009W	*GCN20*	translation	C	3	3	3	3	3	0.67	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA	ATP-binding cassette (ABC) family	molecular_function unknown	regulation of translational elongation	cytosol*	2	2	
YCL037C	*SRO9*	translation	C	3	3	4	0	3	0.56	Associates with translating ribosomes; may function in the cytoplasm to modulate mRNA translation; may be involved in organization of actin filaments; RNA binding protein with La motif	0	RNA binding	protein biosynthesis	polysome	5	4	
YML073C	*RPL6A*	translation	C	3	2	2	2	2	0.25	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA	ribosomal protein L6A (L17A) (rp18) (YL16)	structural constituent of ribosome*	protein biosynthesis*	cytosolic large ribosomal subunit (sensu Eukarya)	2	1	SD
YIL069C	*RPS24B*	translation	C	3	3	4	3	3	0.85	Protein component of the small (40S) ribosomal subunit; identical to Rps24Ap and has similarity to rat S24 ribosomal protein	ribosomal protein S24B	structural constituent of ribosome	protein biosynthesis	cytosolic small ribosomal subunit (sensu Eukarya)	4	5	
YPL125W	*KAP120*	nuclear transport	A	3	3	3	3	3	0.66	Karyopherin with a role in the assembly or export of 60S ribosomal subunits	karyopherin	structural constituent of nuclear pore	protein-nucleus import	cytoplasm*	1	1	
YDR432W	*NPL3*	nuclear transport	A	2	1	1	3	2	0.85	RNA-binding protein that carries poly(A)+ mRNA from the nucleus into the cytoplasm; phosphorylation by Sky1p in the cytoplasm may promote release of mRNAs	contains RNA recognition motif|nuclear shuttling protein	mRNA binding*	mRNA-nucleus export	cytoplasm*	4	5	
YDR159W	*SAC3*	nuclear transport	A	2	1	1	2	2	4.49	A component of the nuclear pore that is involved in the nuclear export of both mRNA and protein; Leucine permease transcriptional regulator	0	protein binding	mRNA-nucleus export*	nuclear pore	5	5	
YKR082W	*NUP133*	nuclear transport	B	3	3	3	3	2	1.67	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p	nuclear pore complex subunit	structural molecule activity	mRNA-nucleus export*	nuclear pore	5	4	SD
YDL116W	*NUP84*	nuclear transport	B	3	4	4	4	4	4.54	Subunit of the nuclear pore complex (NPC), forms a subcomplex with Nup85p, Nup120p, Nup145p-C, Sec13p, and Seh1p that plays a role in nuclear mRNA export and NPC biogenesis	nuclear pore complex subunit|similar to mammalian Nup107p	structural molecule activity	mRNA-nucleus export*	nuclear pore	4	4	SD
YKL057C	*NUP120*	nuclear transport	B	3	3	3	3	3	3.06	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), required for even distribution of NPCs around the nuclear envelope, involved in establishment of a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p	100 kDa protein (predicted molecular weight is 120 kDa) with two leucine zipper motifs, coiled-coil	structural molecule activity	mRNA-nucleus export*	nuclear pore	5	5	
YDL088C	*ASM4*	nuclear transport	B	3	3	3	3	3	0.53	Nuclear pore complex subunit, part of a subcomplex also containing Nup53p, Nup170p, and Pse1p	nuclear pore complex subunit	structural molecule activity	mRNA-nucleus export*	nuclear pore	1	1	
YKL068W	*NUP100*	nuclear transport	B	3	4	4	3	3	0.51	Subunit of the nuclear pore complex (NPC) that is localized to both sides of the pore; contains a repetitive GLFG motif that interacts with mRNA export factor Mex67p and with karyopherin Kap95p; homologous to Nup116p	nuclear pore complex subunit	structural molecule activity	mRNA-nucleus export*	nuclear pore	4	4	
YDR289C	*RTT103*	Ty1 related	I	3	1	1	3	3	0.58	Regulator of Ty1 Transposition; regulator of Ty1 Transposition	0	molecular_function unknown	negative regulation of DNA transposition	cellular_component unknown	5	5	JC
YLL002W	*RTT109*	Ty1 related	I	3	3	3	3	3	3.35	Regulator of Ty1 Transposition; Regulation of mitochondrial network; Killed in Mutagen, sensitive to diepoxybutane and/or mitomycin C; diepoxybutane and mitomycin C resistance	0	molecular_function unknown	negative regulation of DNA transposition	nucleus	5	4	JC
YER173W	*RAD24*	DNA maintenance	I	3	3	3	2	3	0.68	Checkpoint protein, involved in the activation of the DNA damage and meiotic pachytene checkpoints; subunit of a clamp loader that loads Rad17p-Mec3p-Ddc1p onto DNA; homolog of human and S. pombe Rad17 protein	cell cycle exonuclease (putative)	DNA clamp loader activity	meiotic recombination*	nucleus*	2	2	
YOR144C	*ELG1*	DNA maintenance	I	3	4	4	3	3	1.68	Protein required for S phase progression and telomere homeostasis, forms an alternative replication factor C complex important for DNA replication and genome integrity; mutants are sensitive to DNA damage	0	molecular_function unknown	DNA replication*	cytoplasm*	4	4	JC
YCL061C	*MRC1*	DNA maintenance	I	3	3	3	3	3	1.41	S-phase checkpoint protein found at replication forks, required for DNA replication; also required for Rad53p activation during DNA replication stress, where it forms a replication-pausing complex with Tof1p and is phosphorylated by Mec1p; protein in	0	molecular_function unknown	chromatin silencing at telomere*	nucleus*	4	4	
YGL058W	*RAD6*	DNA maintenance	J	3	3	3	3	3	0.84	Ubiquitin-conjugating enzyme (E2), involved in postreplication repair (with Rad18p), sporulation, telomere silencing, and uniquitin-mediated N-end rule protein degradation (with Ubr1p)	ubiquitin-conjugating enzyme	ubiquitin conjugating enzyme activity	ubiquitin-dependent protein catabolism*	cytoplasm*	5	5	
YJL092W	*HPR5*	DNA maintenance	J	2	4	4	3	3	0.85	DNA helicase and DNA-dependent ATPase involved in DNA repair, required for proper timing of commitment to meiotic recombination and the transition from Meiosis I to Meiosis II; potential Cdc28p substrate	DNA helicase	DNA helicase activity	DNA repair*	nucleus	4	4	
YMR190C	*SGS1*	DNA maintenance	J	2	4	4	3	3	0.84	Nucleolar DNA helicase of the RecQ family, involved in maintenance of genome integrity; has similarity to human BLM and WRN helicases implicated in Bloom and Werner syndromes	0	ATP-dependent DNA helicase activity	mitotic sister chromatid segregation*	nucleolus	5	4	JC
YMR048W	*CSM3*	DNA maintenance	J	2	4	4	3	3	0.57	Protein required for accurate chromosome segregation during meiosis	0	molecular_function unknown	DNA replication checkpoint*	nucleus	4	4	
YIL009C-A	*EST3*	DNA maintenance	J	2	4	4	3	3	1.44	Component of the telomerase holoenzyme, involved in telomere replication	20.5 kDa 181aa protein	telomerase activity	telomerase-dependent telomere maintenance	nucleus*	5	4	
YHR031C	*RRM3*	DNA maintenance	J	3	3	3	3	3	3.48	involved in rDNA replication and Ty1 transposition; DNA helicase	DNA helicase	DNA helicase activity*	DNA replication	nuclear telomeric heterochromatin	5	5	JC
YBR021W	*FUR4*	cell wall, membrane								Uracil permease, localized to the plasma membrane; expression is tightly regulated by uracil levels and environmental cues	uracil permease	uracil permease activity	uracil transport	plasma membrane	1	1	
YER145C	*FTR1*	cell wall, membrane								High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron	iron permease	iron ion transporter activity	high affinity iron ion transport	plasma membrane	2	2	

YMR058W	*FET3*	cell wall, membrane	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases	multicopper oxidase	ferroxidase activity	high affinity iron ion transport*	plasma membrane	2	2	
YMR123W	*PKR1*	cell wall, membrane	Pichia farinosa Killer toxin Resistance; Pichia farinosa killer toxin resistance	0	molecular_function unknown	biological_process unknown	endoplasmic reticulum	2	2	
YBL006C	*LDB7*	cell wall, membrane	Protein of unknown function; null mutant shows a reduced affinity for the alcian blue dye suggesting a decreased net negative charge of the cell surface	0	molecular_function unknown	cell wall mannoprotein biosynthesis	cellular_component unknown	5	5	
YHL030W	*ECM29*	cell wall, membrane	Major component of the proteasome; tethers the proteasome core particle to the regulatory particle, and enhances the stability of the proteasome	0	protein binding	protein catabolism	cytoplasm*	5	4	
YIL011W	*TIR3*	cell wall, membrane	TIP1-related	cell wall mannoprotein	molecular_function unknown	biological_process unknown	cell wall (sensu Fungi)	4	5	
YER155C	*BEM2*	cytoskeleton	Rho GTPase activating protein (RhoGAP) involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence	rho GTPase activating protein (GAP)	signal transducer activity*	cell wall organization and biogenesis*	intracellular	4	4	
YGL174W	*BUD13*	cytoskeleton	Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern	0	molecular_function unknown	bud site selection	nucleus	4	4	
YNL138W	*SRV2*	cytoskeleton	Adenylyl cyclase-associated protein; N-terminal domain appears to be involved in cellular responsiveness to RAS	70 kDa adenylyl cyclase-associated protein	cytoskeletal protein binding*	cytoskeleton organization and biogenesis*	actin cortical patch (sensu Fungi)	5	5	
YGR188C	*BUB1*	cytoskeleton	checkpoint gene involved in permitting entry into mitosis depending upon the assembly state of microtubules; Serine/threonine protein kinase required for cell cycle arrest in response to loss of microtubule function	0	protein binding*	protein amino acid phosphorylation*	nucleus*	2	2	
YPL256C	*CLN2*	DNA maintenance	role in cell cycle START; G(sub)1 cyclin	G1 cyclin	cyclin-dependent protein kinase regulator activity	regulation of cyclin dependent protein kinase activity*	cytoplasm*	4	4	
YPR119W	*CLB2*	DNA maintenance	Involved in mitotic induction; G(sub)2-specific B-type cyclin	B-type cyclin	cyclin-dependent protein kinase regulator activity	G2/M transition of mitotic cell cycle*	cytoplasm*	4	4	
YBR044C	*TCM62*	mitochondrial related	mitochondrial protein; (putative) chaperone	chaperone (putative)	unfolded protein binding	protein complex assembly	mitochondrial inner membrane	2	2	
YHR008C	*SOD2*	mitochondrial related	Manganese-containing superoxide dismutase	Mn-containing superoxide dismutase	manganese superoxide dismutase activity	oxygen and reactive oxygen species metabolism	mitochondrion*	2	2	
YIL134W	*FLX1*	mitochondrial related	Protein required for transport of flavin adenine dinucleotide (FAD) from mitochondria, where it is synthesized from riboflavin, to the cytosol	FAD carrier protein	flavin-adenine dinucleotide transporter activity	flavin-adenine dinucleotide transport	mitochondrion	2	2	
YIR021W	*MRS1*	mitochondrial related	Protein required for the splicing of two mitochondrial group I introns (BI3 in COB and AI5beta in COX1); forms a splicing complex, containing four subunits of Mrs1p and two subunits of the BI3-encoded maturase, that binds to the BI3 RNA	0	RNA binding*	Group I intron splicing	mitochondrion	4	4	
YJR121W	*ATP2*	mitochondrial related	Beta subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis	F(1)F(0)-ATPase complex beta subunit	hydrogen-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport*	soluble fraction*	2	2	
YML081C-A	*ATP18*	mitochondrial related	Subunit of the mitochondrial F1F0 ATP synthase, which is a large enzyme complex required for ATP synthesis; termed subunit I or subunit j; does not correspond to known ATP synthase subunits in other organisms	ATP synthase associated protein	hydrogen-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	proton-transporting ATP synthase complex,	2	2	
YBR269C	*FMP21*	mitochondrial related	The authentic, non-tagged protein was localized to the mitochondria	0	molecular_function unknown	biological_process unknown	mitochondrion	4	4	
YER057C	*HMF1*	stress/chaperone/ modification	Member of the p14.5 protein family with similarity to Mmf1p, functionally complements Mmf1p function when targeted to mitochondria; heat shock inducible; high-dosage growth inhibitor; forms a homotrimer in vitro	0	molecular_function unknown	biological_process unknown	cytoplasm*	4	4	
YDR074W	*TPS2*	stress/chaperone/ modification	Trehalose-6-phosphate phosphatase	trehalose-6-phosphate phosphatase	trehalose-phosphatase activity	response to stress*	alpha,alpha-trehalose-phosphate	4	4	SD
YAL013W	*DEP1*	metabolic	Transcriptional modulator involved in the regulation of structural genes involved in phospholipid biosynthesis, also participates in regulation of metabolically unrelated genes as well as maintenance of mating efficiency and sporulation	0	molecular_function unknown	regulation of transcription from Pol II promoter*	cellular_component unknown	2	2	SD
YHL003C	*LAG1*	metabolic	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lac1p	0	sphingosine N-acyltransferase activity	replicative cell aging*	endoplasmic reticulum	4	5	
YLR242C	*ARV1*	metabolic	Protein with similarity to Nup120p and C.elegans R05H5.5 protein	Protein involved in sterol distribution	molecular_function unknown	sterol transport*	endoplasmic reticulum*	1	1	
YER060W-A	*FCY22*	metabolic	Putative purine-cytosine permease, very similar to Fcy2p but cannot substitute for its function	purine-cytosine permease	cytosine-purine permease activity	biological_process unknown	integral to membrane	4	4	
YDL074C	*BRE1*	DNA maintenance	E3 ubiquitin ligase for Rad6p, required for the ubiquitination of histone H2B, recruitment of Rad6p to promoter chromatin and subsequent methylation of histone H3 (on L4 and L79), contains RING finger domain	0	ubiquitin-protein ligase activity	chromatin silencing at telomere*	nucleus	4	4	
YIL015W	*BAR1*	other	Aspartyl protease secreted into the periplasmic space of mating type a cells, cleaves and inactivates alpha factor allowing cells to recover from alpha-factor-induced cell cycle arrest	protease|synthesized in a-cells; cleaves and inactivates alpha factor	aspartic-type endopeptidase activity	protein catabolism	periplasmic space (sensu Fungi)	5	5	
YIL073C	*SPO22*	metabolic	Meiosis-specific protein with similarity to phospholipase A2, involved in completion of nuclear divisions during meiosis; induced early in meiosis	meiosis-specific phospholipase A2 homolog	molecular_function unknown	meiosis	cellular_component unknown	2	1	
YKL149C	*DBR1*	RNA processing	RNA lariat debranching enzyme, involved in intron turnover; required for efficient Ty1 transposition	RNA lariat debranching enzyme	RNA lariat debranching enzyme activity	RNA catabolism*	nucleus	1	2	SD
YKL135C	*APL2*	trafficking	Beta-adaptin, large subunit of the clathrin-associated protein (AP-1) complex	beta-adaptin|clathrin associated protein complex large subunit	clathrin binding	vesicle-mediated transport	AP-1 adaptor complex	5	5	
YEL004W	*YEA4*	trafficking	Shows sequence similarity to GOG5, a gene involved in vanadate resistance; similar to Gog5, which is involved in vanadate resistance	0	UDP-N-acetylglucosamine transporter activity	cell wall chitin biosynthesis*	endoplasmic reticulum	4	4	
YGR270W	*YTA7*	trafficking	Protein of unknown function, member of CDC48/PAS1/SEC18 family of ATPases, potentially phosphorylated by Cdc28p	0	ATPase activity	protein catabolism	nucleus	4	4	
YNL242W	*ATG2*	trafficking	Defective in autophagy; required for sporulation; Required for sporulation.	peripheral membrane protein	molecular_function unknown	protein-vacuolar targeting*	extrinsic to membrane	4	4	
YKL041W	*VPS24*	trafficking	involved in secretion	0	molecular_function unknown	late endosome to vacuole transport	cytoplasm*	4	4	
YMR154C	*RIM13*	trafficking	Regulator of IME2 (RIM); Cysteine protease similar to E. nidulans palB	calpain-like protease involved in proteolytic processing of Rim1p/Rim101p|cysteine protease|similar	cysteine-type endopeptidase activity	protein processing	cellular_component unknown	2	2	MA
YKR020W	*VPS51*	trafficking	whiskey (whi) mutant; forms a tetramer with VPS52, VPS53, and VPS54		protein binding	protein-vacuolar targeting	Golgi apparatus	1	2	

YDR290W	*0*	unknown	Sick Without Securin; HU sensitive mutant; name reserved Orna Cohen-Fix; overlaps 42% with *RTT103*	0	0	0	0	5	5	
YBL094C	*0*	unknown	0	0	0	0	0	4	4	
YBR277C	*0*	unknown	0	0	0	0	0	4	4	
YBR284W	*0*	unknown	0	0	0	0	0	4	4	MA
YHR177W	*0*	unknown	0	0	0	0	0	4	4	
YLL030C	*0*	unknown	0	0	0	0	0	5	4	
YLR235C	*0*	unknown	0	0	0	0	0	5	4	
YMR158W-B	*0*	unknown	0	0	0	0	0	2	2	
YPL225W	*0*	unknown	0	0	0	0	0	2	2	
YDR176W	*NGG1*	chromatin modification and transcription	Involved in glucose repression of GAL4p-regulated transcription; transcription factor; genetic and mutant analyses suggest that Ngg1p (Ada3p) is part of two transcriptional adaptor/HAT (histone acetyltransferase complexes, the 0.8 MD ADA complex and	genetic and mutant analyses suggest that Ngg1p (Ada3p) is part of two transcriptional adaptor/HAT (h	transcription cofactor activity	histone acetylation*	SAGA complex*	4	4	
YEL044W	*IES6*	chromatin modification and transcription	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions	0	molecular_function unknown	metabolism	nucleus	1	2	
YGL066W	*SGF73*	chromatin modification and transcription	SaGa associated Factor 73kDa; Probable 73KkDa Subunit of SAGA histone acetyltransferase complex	Probable 73KkDa Subunit of SAGA histone acetyltransferase complex	molecular_function unknown	histone acetylation	SAGA complex	5	4	
YGR056W	*RSC1*	chromatin modification and transcription	RSC1 is a member of RSC complex, which remodels the structure of chromatin; Member of RSC complex	RSC complex member	molecular_function unknown	chromatin remodeling	nucleosome remodeling complex	5	4	
YJL006C	*CTK2*	chromatin modification and transcription	Beta subunit of C-terminal domain kinase I (CTDK-I), which phosphorylates the C-terminal repeated domain of the RNA polymerase II large subunit (Rpo21p) to affect both transcription and pre-mRNA 3' end processing; has similarity to cyclins	RNA polymerase II C-terminal domain kinase beta subunit, similar to cyclin	cyclin-dependent protein kinase regulator activity	protein amino acid phosphorylation*	nucleus	1	2	
YLR015W	*BRE2*	chromatin modification and transcription	Subunit of the COMPASS complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; has similarity to ASH2L member of trithorax proteins	compass (complex proteins associated with Set1p) component	chromatin binding*	chromatin silencing at telomere*	nuclear chromatin*	5	4	
YNL236W	*SIN4*	chromatin modification and transcription	involved in positive and negative regualtion of transcription, possibly via changes in chromatin structure; regulation of YGP1 expression; component of RNA polymerase II holoenzyme/mediator complex	RNA polymerase II holoenzyme/mediator subunit	RNA polymerase II transcription mediator activity	transcription from Pol II promoter	mediator complex	1	2	SD MA
YPL042C	*SSN3*	chromatin modification and transcription	Component of RNA polymerase II holoenzyme, involved in RNA pol II carboxy-terminal domain phosphorylation	cyclin (SSN8)-dependent serine/threonine protein kinase	general RNA polymerase II transcription factor activity*	protein amino acid phosphorylation*	transcription factor complex	1	1	
YNL136W	*EAF7*	chromatin modification and transcription	Subunit of the NuA4 histone acetyltransferase complex	0	molecular_function unknown	biological_process unknown	nucleus	2	1	
YOR039W	*CKB2*	chromatin modification and transcription	protein kinase CK2, beta' subunit	protein kinase CK2, beta' subunit	protein kinase CK2 activity	protein amino acid phosphorylation*	protein kinase CK2 complex	5	4	
YCR020W-B	*HTL1*	chromatin modification and transcription	High-Temperature Lethal; high-temperature lethal	0	molecular_function unknown	regulation of cell cycle*	RSC complex	4	4	
YDL056W	*MBP1*	chromatin modification and transcription	transcription factor	transcription factor	DNA binding*	regulation of cell cycle*	nucleus	4	4	
YDR448W	*ADA2*	chromatin modification and transcription	transcription factor, member of ADA and SAGA, two transcriptional adaptor/HAT (histone acetyltransferase)complexes	transcription factor	transcription coactivator activity	histone acetylation*	SAGA complex*	4	5	
YKR099W	*BAS1*	chromatin modification and transcription	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways	transcription factor	RNA polymerase II transcription factor activity	transcription from Pol II promoter*	nucleus	2	2	
YLR399C	*BDF1*	chromatin modification and transcription	Protein involved in transcription initiation at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p	0	transcription regulator activity	chromatin remodeling*	nucleus	4	5	
YML051W	*GAL80*	chromatin modification and transcription	Transcriptional regulator involved in the repression of GAL genes in the absence of galactose; inhibits transcriptional activation by Gal4p; inhibition relieved by Gal3p or Gal1p binding	transcriptional regulator	transcription corepressor activity	regulation of transcription, DNA-dependent*	cytoplasm*	5	5	
YPL024W	*NCE4*	chromatin modification and transcription	involved in cell separation	0	molecular_function unknown	biological_process unknown	cytoplasm*	4	5	
YAR003W	*SWD1*	chromatin modification and transcription	Subunit of the COMPASS complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres	compass (complex proteins associated with Set1p) component	transcriptional activator activity*	chromatin silencing at telomere*	nuclear chromatin*	4	4	MA

[1] Mutants presented in the Westerns and Southerns of Sup. Fig. 1 are in the order indicated here. This was not the order in the original gels which have been repositioned here in order to better compare mutants with related functions. The original blots are available upon request.

2 Ratio of CA:Gag3 visually estimated in order to identify strong processing phenotypes based on Westerns in Sup. Fig. 1; 3=wt

[3] Amt of CA/IN relative to wt based on PGK signal in the same sample; 3=wt

[4] Sample loading was compared by ethidium staining of genomic DNA. These scores are based on visual comparison between amt of plasmid in mutant transformant to amt in wt sample on the same Southern.

[5] Ratio of cDNA:plasmid was determined by scanning both transformants, averaging the cDNA:plasmid intensity ratio and comparing it to the wt ratio. The wt ratio was determined by averaging the ratio of eight independent transformants. The average was 0.57 and the Std.Dev. was 0.31. Mutants were considered to have high or low cDNA if they differed by more than one Std.Dev.

[6] Database information on genes was downloaded from SGD and accessed using GOnet as described in Materials and Methods.

[7] Other screens are: Ty1, Scholes et al. (JC) (Scholes et al. 2001); Ty1, Griffith et al. (SD)(Griffith et al. 2003); and Ty3, Aye et al. (MA)(Aye et al. 2004).

Sup. Table 4. Human homologs of yeast mutants (Table 1 genes only)

Yeast ORF	Yeast Gene	Human Gene[1]	BLAST *p* value[2]
YGL173C	*KEM1*	5'-3' exoribonuclease 1 [Homo sapiens]	0
YJR121W	*ATP2*	ATP synthase, H+ transporting, mitochondri...	0
YMR190C	*SGS1*	Bloom syndrome protein [Homo sapiens]	1.00E-115
YKL135C	*APL2*	adaptor-related protein complex 2, beta 1 ...	1.00E-126
YGR270W	*YTA7*	two AAA domain containing protein [Homo sa...	1.00E-134
YPR173C	*VPS4*	vacuolar protein sorting factor 4B [Homo s...	1.00E-146
YFR009W	*GCN20*	ATP-binding cassette, sub-family F (GCN20)...	1.00E-157
YDL160C	*DHH1*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 [...	1.00E-162
YOR270C	*VPH1*	ATPase, H+ transporting, lysosomal V0 subu...	1.00E-177
YHL030W	*ECM29*	PREDICTED: KIAA0368 protein [Homo sapiens]	5.00E-97
YMR116C	*ASC1*	guanine nucleotide binding protein (G prot...	8.00E-96
YPL125W	*KAP120*	Ran binding protein 11 [Homo sapiens]	7.00E-85
YGL078C	*DBP3*	DEAD box polypeptide 17 isoform p82 [Homo ...	1.00E-84
YFR019W	*FAB1*	phosphatidylinositol-3-phosphate/phosphati...	5.00E-78
YNL138W	*SRV2*	adenylyl cyclase-associated protein 2 [Hom...	1.00E-74
YKL149C	*DBR1*	debranching enzyme homolog 1 [Homo sapiens]	8.00E-68
YFL001W	*DEG1*	pseudouridylate synthase 3 [Homo sapiens]	1.00E-67
YPL042C	*SSN3*	cyclin-dependent kinase 8 [Homo sapiens]	2.00E-67
YBR284W	*YBR284W*	adenosine monophosphate deaminase 2 (isofo...	8.00E-62
YGL058W	*RAD6*	ubiquitin-conjugating enzyme E2A isoform 1...	1.00E-61

YKL068W	*NUP100*	nucleoporin 98kD isoform 3 [Homo sapiens]	6.00E-56
YPR119W	*CLB2*	cyclin B2 [Homo sapiens]	1.00E-53
YOR039W	*CKB2*	casein kinase 2, beta polypeptide [Homo sa...	8.00E-53
YDR448W	*ADA2*	transcriptional adaptor 2-like isoform a [...	1.00E-51
YNR052C	*POP2*	CCR4-NOT transcription complex, subunit 8 ...	1.00E-50
YHR008C	*SOD2*	superoxide dismutase 2, mitochondrial [Hom...	3.00E-48
YOR275C	*RIM20*	programmed cell death 6 interacting protei...	1.00E-45
YJR032W	*CPR7*	peptidylprolyl isomerase D [Homo sapiens]	4.00E-43
YGR188C	*BUB1*	BUB1 budding uninhibited by benzimidazoles...	1.00E-41
YEL004W	*YEA4*	solute carrier family 35, member B4 [Homo ...	1.00E-40
YNL059C	*ARP5*	ARP5 actin-related protein 5 homolog [Homo...	1.00E-40
YIL134W	*FLX1*	mitochondrial folate transporter/carrier [...	4.00E-40
YPL084W	*BRO1*	programmed cell death 6 interacting protei...	6.00E-39
YLR268W	*SEC22*	vesicle trafficking protein sec22b [Homo s...	9.00E-39
YPL002C	*SNF8*	EAP30 subunit of ELL complex [Homo sapiens]	1.00E-38
YIL069C	*RPS24B*	ribosomal protein S24 isoform c [Homo sapi...	6.00E-38
YLR399C	*BDF1*	bromodomain-containing protein 4 isoform l...	1.00E-37
YDR159W	*SAC3*	minichromosome maintenance protein 3 assoc...	1.00E-35
YML073C	*RPL6A*	ribosomal protein L6 [Homo sapiens]	1.00E-35
YLR025W	*SNF7*	Snf7 homologue associated with Alix 2 [Hom...	9.00E-33
YDL074C	*BRE1*	ring finger protein 20 [Homo sapiens]	1.00E-28
YPL225W	*YPL225W*	chromosome X open reading frame 26 [Homo s...	8.00E-27

YPL065W	*VPS28*	vacuolar protein sorting 28 isoform 1 [Hom...	1.00E-26
YNR006W	*VPS27*	hepatocyte growth factor-regulated tyrosin...	2.00E-26
YGR056W	*RSC1*	polybromo 1 [Homo sapiens]	9.00E-26
YIL015W	*BAR1*	progastricsin (pepsinogen C) [Homo sapiens]	9.00E-26
YML097C	*VPS9*	RAB guanine nucleotide exchange factor (GE...	2.00E-25
YER155C	*BEM2*	PREDICTED: Rho GTPase activating protein 2...	4.00E-24
YKL041W	*VPS24*	vacuolar protein sorting 24 isoform 1 [Hom...	5.00E-24
YEL013W	*VAC8*	armadillo repeat containing 3 [Homo sapiens]	3.00E-23
YER057C	*HMF1*	heat-responsive protein 12 [Homo sapiens]	5.00E-21
YDR139C	*RUB1*	neural precursor cell expressed, developme...	8.00E-21
YMR077C	*VPS20*	hypothetical protein FLJ11749 [Homo sapiens]	2.00E-20
YDR432W	*NPL3*	heterogeneous nuclear ribonucleoprotein R ...	5.00E-20
YJR102C	*VPS25*	hypothetical protein MGC10540 [Homo sapiens]	5.00E-20
YKR099W	*BAS1*	small nuclear RNA activating complex, poly...	5.00E-19
YIL011W	*TIR3*	PREDICTED: chromosome 6 open reading frame...	6.00E-19
YHL003C	*LAG1*	LAG1 longevity assurance homolog 2 isoform...	6.00E-17
YER173W	*RAD24*	RAD17 homolog isoform 2 [Homo sapiens]	9.00E-17
YDL116W	*NUP84*	nuclear pore complex protein [Homo sapiens]	5.00E-16
YNL242W	*ATG2*	chromosome 14 open reading frame 103 [Homo...	7.00E-16
YCL061C	*MRC1*	KIAA1212 [Homo sapiens]	6.00E-15
YDR323C	*PEP7*	FYVE-finger-containing Rab5 effector prote...	2.00E-14
YDR289C	*RTT103*	chromosome 20 open reading frame 77 [Homo ...	3.00E-14

YBR044C	*TCM62*	chaperonin [Homo sapiens]	1.00E-13
YCL037C	*SRO9*	FLJ10378 protein isoform 2 [Homo sapiens]	2.00E-12
YNL136W	*YNL136W*	splicing factor, arginine/serine-rich 12 [...	3.00E-12
YJL006C	*CTK2*	cyclin K [Homo sapiens]	2.00E-11
YFL007W	*BLM3*	proteasome (prosome, macropain) activator ...	1.00E-10
YLR242C	*ARV1*	ARV1 homolog [Homo sapiens]	2.00E-10
YMR154C	*RIM13*	calpain 7 [Homo sapiens]	4.00E-10
YGL066W	*SGF73*	forkhead box P2 isoform I [Homo sapiens]	1.00E-09
YBL007C	*SLA1*	mucin 17 [Homo sapiens]	8.00E-09
YEL044W	*IES6*	chromosome 18 open reading frame 37 [Homo ...	6.00E-08
YMR048W	*CSM3*	timeless-interacting protein [Homo sapiens]	8.00E-08
YGL174W	*BUD13*	hypothetical protein MGC13125 [Homo sapiens]	9.00E-08
YAL013W	*DEP1*	Snf2-related CBP activator protein [Homo s...	1.00E-07
YDL056W	*MBP1*	death-associated protein kinase 1 [Homo sa...	1.00E-06
YNL224C	*YNL224C*	angiogenic factor VG5Q [Homo sapiens]	2.00E-06
YIL073C	*SPO22*	testis expressed sequence 11 isoform 2 [Ho...	3.00E-06
YDL088C	*ASM4*	dentin sialophosphoprotein preproprotein [...	7.00E-06
YJL047C	*RTT101*	cullin 2 [Homo sapiens]	9.00E-06
YLR423C	*ATG17*	centromere protein E [Homo sapiens]	9.00E-06
YOR144C	*ELG1*	hypothetical protein FLJ12735 [Homo sapiens]	2.00E-05
YPL256C	*CLN2*	cyclin A [Homo sapiens]	5.00E-05
YGR167W	*CLC1*	clathrin, light polypeptide A isoform a [H...	7.00E-05

YGL212W	*VAM7*	syntaxin 6 [Homo sapiens]	9.00E-05
YBR269C	*YBR269C*	chromosome 6 open reading frame 57 [Homo s...	2.00E-04
YDR176W	*NGG1*	transcriptional adaptor 3-like isoform a [...	3.00E-04
YHR177W	*GON3*	nuclear factor of activated T-cells 5 isof...	3.00E-04
YKR020W	*VPS51*	kinectin 1 [Homo sapiens]	3.00E-03
YLR417W	*VPS36*	CGI-145 protein [Homo sapiens]	5.00E-03
YMR058W	*FET3*	PREDICTED: similar to hephaestin [Homo sap...	7.00E-03
YKR020W	*VPS51*	kinectin 1 [Homo sapiens]	3.00E-03

[1] Description downloaded as described under GOnet in Materials and Methods

[2] Homologs were identified using NCBI BLAST and batch searching through GOnet;

The e-value measures the probability of the given alignment score under a random sequence model.