

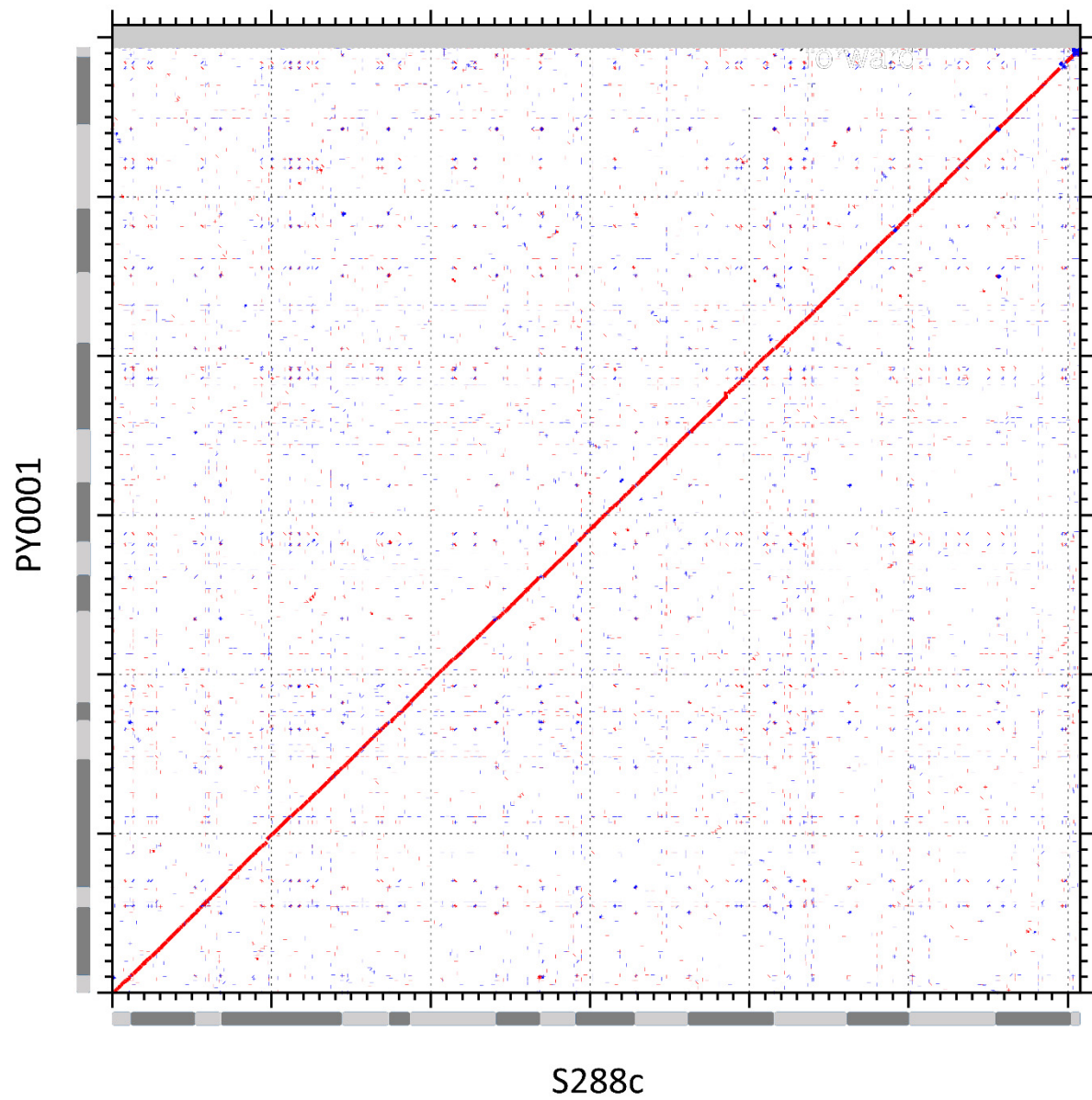
Supplementary file S1.

Comparative genomic results of the probiotic isolates used in this study.

Features of the assembled genome of the PY0001 isolate: length of chromosomes compared with the *S. cerevisiae* S288c reference genome, and the number of the annotated protein coding genes. The mitochondrial genome of the strain CIM was used as it was not assembled for PY0001.

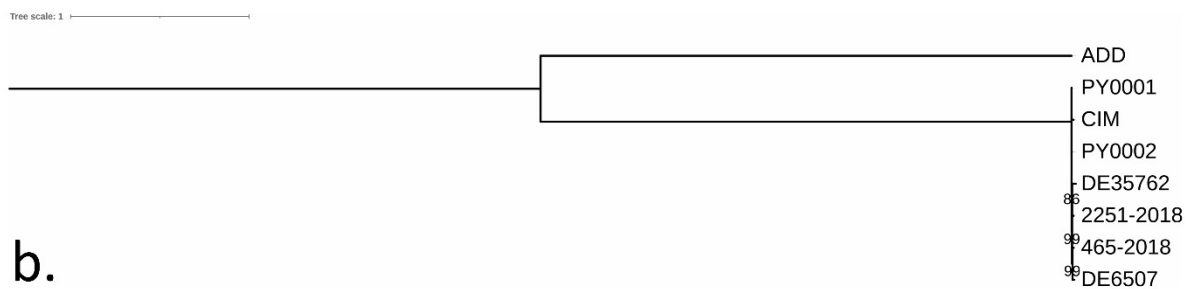
| Chromosome | S288c reference genome | PY0001 reference (this study) |
|------------|------------------------|-------------------------------|
| Chr. I. | 230218 bp | 210 734 bp, 95 genes |
| Chr. II. | 813 184 bp | 793 175 bp, 397 genes |
| Chr. III. | 316 620 bp | 315 973 bp, 159 genes |
| Chr. IV. | 1 531 933 bp | 1 510 005 bp, 743 genes |
| Chr. V. | 576 874 bp | 565 474 bp, 273 genes |
| Chr. VI. | 270 161 bp | 245 370 bp, 122 genes |
| Chr. VII. | 1 090 940 bp | 1 058 692 bp, 503 genes |
| Chr. VIII. | 562 643 bp | 523 461 bp, 271 genes |
| Chr. IX. | 439 888 bp | 420 152 bp, 208 genes |
| Chr. X. | 745 751 bp | 730 649 bp, 354 genes |
| Chr. XI. | 666 816 bp | 668 834 bp, 321 genes |
| Chr. XII. | 1 078 177 bp | 1 051 807 bp, 472 genes |
| Chr. XIII. | 924 431 bp | 909 758 bp, 450 genes |
| Chr. XIV. | 784 333 bp | 790 714 bp, 382 genes |
| Chr. XV. | 1 091 291 bp | 1 054 797 bp, 511 genes |
| Chr. XVI. | 948 066 bp | 931 421 bp, 456 genes |
| mtDNA | 85 779 bp | 87 321 bp, 20 genes |
| plasmid | none | not assembled |

Whole genome alignment of the S288c reference *S. cerevisiae* and PY0001 reference genomes. Chromosomes are shown with grey bars on the axes.

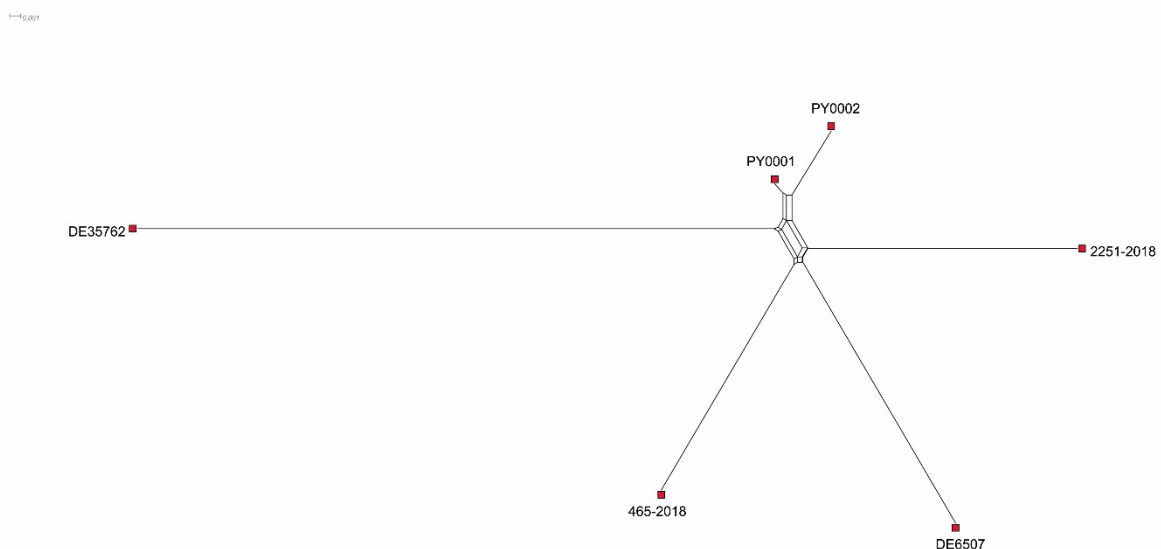


Phylogenetic relationships of the 6 strains used in this study. a) Maximum Likelihood dendrogram based on the identified polymorphisms. Support for branches with a higher than 80% bootstrap approximation support is indicated. ADD represents the Y-prime amplification subclade of the Win/European clade, and it is used as an outgroup. b) Network based on whole genome SNPs and considering heterozygous positions (by averaging the uncorrected P distance of the two haplotypes).

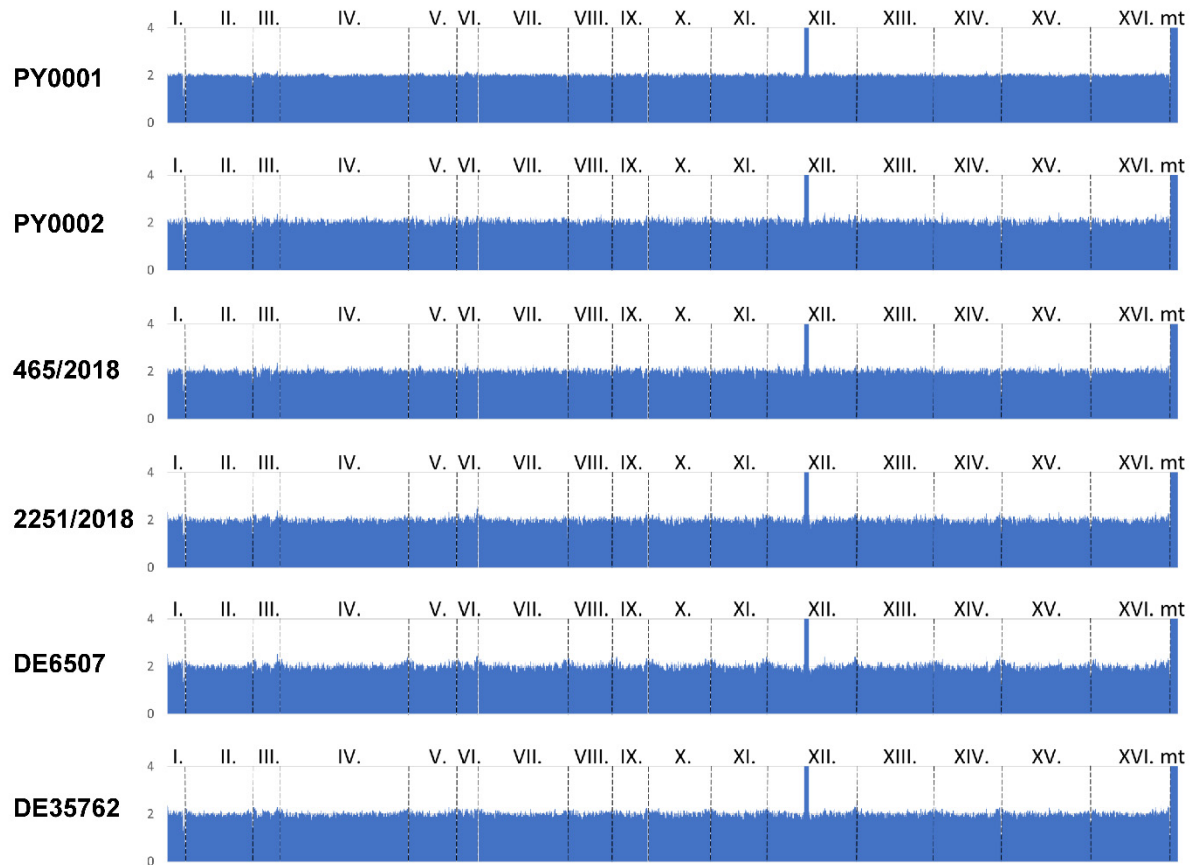
a.



b.



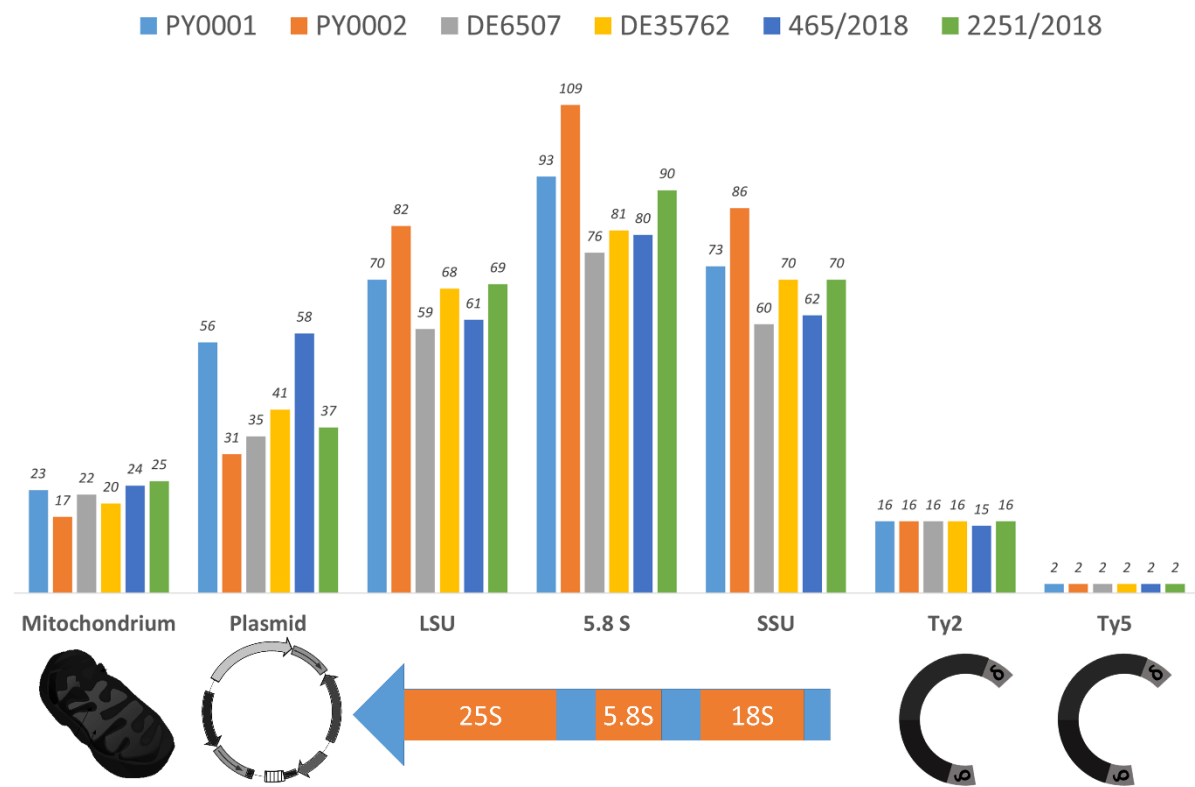
Coverage data for each sequenced isolate with 10 000 bp sliding windows (sliding every 5 000 bp). Disomy can be observed for all 16 chromosomes, and the peak caused by ribosomal DNA repeats can be seen on chr. XII. Mitochondrial coverage is higher due to high copy number. The x-axis shows the chromosomes and the y-axis shows the number of copies calculated from coverage.



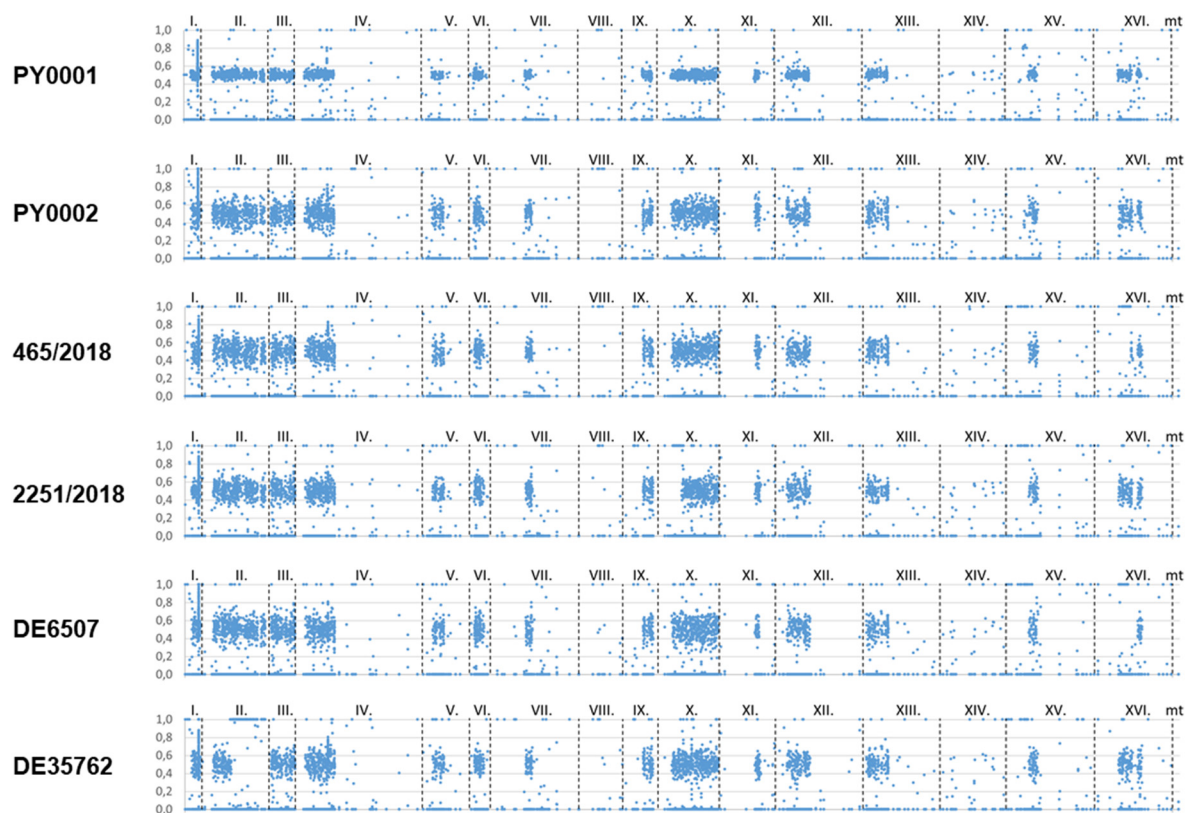
Differences in gene copy numbers observed between isolates. Copy number differences were identified in only 10 genes on 8 different chromosomes based on coverage data. Copy numbers are ranging from 1 to 2 per haploid genome.

| Gene name | Description | PY0001 | PY0002 | 465/2018 | 2251/2018 | DE6507 | DE35762 |
|-------------------------|--|--------|--------|----------|-----------|--------|---------|
| <i>G0000950</i> | dubious telomeric | 1 | 1 | 1 | 2 | 2 | 1 |
| <i>YBR196C-A</i> | uncharacterized | 1 | 1 | 1 | 2 | 1 | 1 |
| <i>YER188C-A</i> | uncharacterized | 2 | 1 | 2 | 2 | 2 | 2 |
| <i>YDL069C</i> | mitochondrial respiratory chain complex III assembly | 1 | 2 | 1 | 1 | 1 | 1 |
| <i>YDL009C</i> | uncharacterized | 1 | 2 | 1 | 1 | 1 | 1 |
| <i>G0021860</i> | dubious | 1 | 1 | 1 | 2 | 1 | 1 |
| <i>G0025660</i> | dubious | 1 | 1 | 1 | 1 | 2 | 2 |
| <i>YLR211C</i> | involved in macroautophagy | 1 | 1 | 1 | 1 | 2 | 1 |
| <i>G0039200</i> | dubious telomeric | 1 | 1 | 1 | 2 | 1 | 1 |
| <i>YPR166C</i> | involved in mitochondrial translation | 1 | 2 | 1 | 1 | 1 | 1 |

Copy number differences between sequenced isolates in mitochondrial and plasmid copy number, and copy numbers of rDNA elements and retrotransposons relative to haploid genome. Isolates are color-coded on the bar chart.



Ratio of AD values (y-axis) of variants (insertion / deletion and SNP variants) identified on the chromosomes (x-axis) of the sequenced isolates. Each data point shows the AD ratios of individual variants. The difference in the number of heterozygous variants on each chromosome is notable.



Heterozygosity (percentage of heterozygous nucleotides) along each chromosome in the six sequenced isolates.

| | PY0001 | PY0002 | 465/2018 | 2251/2018 | DE6507 | DE35762 |
|-------------------|---------------|---------------|-----------------|------------------|---------------|----------------|
| Chr. I. | 0.14810% | 0.13670% | 0.14280% | 0.14140% | 0.13810% | 0.14620% |
| Chr. II. | 0.05420% | 0.05360% | 0.05410% | 0.05300% | 0.05400% | 0.02030% |
| Chr. III. | 0.07150% | 0.07180% | 0.07030% | 0.06740% | 0.07180% | 0.07090% |
| Chr. IV. | 0.02020% | 0.01980% | 0.02070% | 0.02000% | 0.02050% | 0.02050% |
| Chr. V. | 0.01500% | 0.01540% | 0.01490% | 0.01470% | 0.01520% | 0.01500% |
| Chr. VI. | 0.04690% | 0.04690% | 0.04120% | 0.04650% | 0.04650% | 0.04610% |
| Chr. VII. | 0.00760% | 0.00740% | 0.00720% | 0.00700% | 0.00710% | 0.00720% |
| Chr. VIII. | 0.00060% | 0.00020% | 0.00040% | 0.00060% | 0.00110% | 0.00080% |
| Chr. IX. | 0.02280% | 0.02170% | 0.02140% | 0.02190% | 0.02170% | 0.02120% |
| Chr. X. | 0.05980% | 0.05870% | 0.05940% | 0.04780% | 0.05980% | 0.06010% |
| Chr. XI. | 0.00990% | 0.00960% | 0.00960% | 0.00990% | 0.00750% | 0.01000% |
| Chr. XII. | 0.01630% | 0.01570% | 0.01610% | 0.01630% | 0.01600% | 0.01610% |
| Chr. XIII. | 0.01580% | 0.01490% | 0.01550% | 0.01590% | 0.01570% | 0.01600% |
| Chr. XIV. | 0.00240% | 0.00230% | 0.00230% | 0.00270% | 0.00240% | 0.00230% |
| Chr. XV. | 0.00780% | 0.00700% | 0.00650% | 0.00640% | 0.00610% | 0.00670% |
| Chr. XVI. | 0.01670% | 0.01630% | 0.00700% | 0.01600% | 0.00460% | 0.01650% |

Locations of longer (minimum 10 variant positions) tracts of heterozygosity losses and gains when the sequence isolates are compared to PY0001.

| Chromosome | start | end | PY0002 | 465/2018 | 2251/2018 | DE6507 | DE35762 |
|-------------------|--------------|------------|---------------|-----------------|------------------|---------------|----------------|
| chr. I. | 169 499 | 169 588 | loss | | | | |
| chr. II. | 349 630 | 750 382 | | | | | loss |
| chr. IV. | 390 373 | 390 430 | | gain | | gain | gain |
| chr. VI. | 125 779 | 128 246 | | loss | | | |
| chr. X. | 84 809 | 284 582 | | | loss | | |
| chr. XI. | 478 095 | 486 704 | | | | loss | |
| chr. XVI. | 290 756 | 425 832 | | loss | | | |
| chr. XVI. | 290 756 | 489 943 | | | | loss | |

List of genes affected by high effect mutations in the genomes of each isolate, including description of the genes. Gene names beginning with 'G' are dubious ORFs found during annotation, without determined homologies.

| List of affected strains | Affected genes | Description of affected genes |
|---|-----------------|--|
| PY0002, 465/2018, 2251/2018, DE6507, DE35762 | <i>G0005430</i> | not characterized during annotation |
| | <i>G0005510</i> | not characterized during annotation |
| | <i>G0005990</i> | not characterized during annotation |
| | <i>G0008480</i> | not characterized during annotation |
| | <i>G0008490</i> | not characterized during annotation |
| | <i>G0008580</i> | not characterized during annotation |
| | <i>G0008590</i> | not characterized during annotation |
| | <i>G0008670</i> | not characterized during annotation |
| | <i>G0027120</i> | not characterized during annotation |
| | <i>G0028660</i> | not characterized during annotation |
| | <i>G0028710</i> | not characterized during annotation |
| | <i>G0028750</i> | not characterized during annotation |
| | <i>G0028760</i> | not characterized during annotation |
| | <i>G0029600</i> | not characterized during annotation |
| | <i>YCL014W</i> | Guanine nucleotide exchange factor (GEF) for Cdc42p |
| | <i>YCL024W</i> | Protein kinase of the bud neck involved in the septin checkpoint |
| | <i>YCR014C</i> | DNA polymerase IV |
| | <i>YDL003W</i> | Essential alpha-kleisin subunit of the cohesin complex |
| | <i>YDL009C</i> | Protein of unknown function |
| | <i>YDL013W</i> | Subunit of the Slx5-Slx8 SUMO-targeted Ub ligase (STUbL) complex |
| | <i>YDL030W</i> | Subunit of the SF3a splicing factor complex |
| | <i>YEL016C</i> | Nucleotide pyrophosphatase/phosphodiesterase |
| | <i>YJL002C</i> | Alpha subunit of the oligosaccharyltransferase complex of the ER lumen |
| | <i>YJL005W</i> | Adenylate cyclase |
| | <i>YJL023C</i> | Protein of unknown function |
| | <i>YJL070C</i> | Putative metallo-dependent hydrolase superfamily protein |
| | <i>YJL071W</i> | Acetylglutamate synthase (glutamate N-acetyltransferase) |
| | <i>YJL076W</i> | Core subunit of the RENT complex |
| | <i>YJR050W</i> | Member of the NineTeen Complex (NTC) |
| | <i>YJR053W</i> | Subunit of a two-component GTPase-activating protein, Bfa1p-Bub2p |
| | <i>YPL105C</i> | Protein of unknown function that influences nuclear pore distribution |

| | | |
|--|------------------|--|
| | <i>YPL116W</i> | Trichostatin A-insensitive homodimeric histone deacetylase (HDAC) |
| | <i>YPL119C-A</i> | Putative protein of unknown function |
| PY0001, PY0002, 465/2018, 2251/2018, DE6507 | <i>YBR132C</i> | Plasma membrane regulator of polyamine and carnitine transport |
| | <i>YER083C</i> | Subunit of the GET complex |
| PY0001, PY0002, 2251/2018, DE35762, DE6507 | <i>YDL039C</i> | Pheromone-regulated protein |
| | <i>YFR028C</i> | Protein phosphatase required for mitotic exit |
| PY0001, 2251/2018, DE35762 | <i>G0029090</i> | dubious/partial |
| PY0001, 2251/2018 | <i>YOR305W</i> | Protein of unknown function |
| 2251/2018 | <i>YEL013W</i> | Vacuole-specific Myo2p receptor |
| DE6507 | <i>YHR080C</i> | Sterol-binding protein that localizes to puncta in the cortical ER |
| | <i>YMR127C</i> | Histone acetyltransferase (HAT) catalytic subunit of the SAS complex |
| DE35762 | <i>YKR101W</i> | Protein involved in silencing at mating-type loci HML and HMR |
| All 6 isolates | <i>G0000760</i> | not characterized during annotation |
| | <i>G0002090</i> | not characterized during annotation |
| | <i>G0002480</i> | not characterized during annotation |
| | <i>G0006270</i> | not characterized during annotation |
| | <i>G0008130</i> | not characterized during annotation |
| | <i>G0008160</i> | not characterized during annotation |
| | <i>G0008510</i> | not characterized during annotation |
| | <i>G0016810</i> | not characterized during annotation |
| | <i>G0017310</i> | not characterized during annotation |
| | <i>G0017400</i> | not characterized during annotation |
| | <i>G0029090</i> | not characterized during annotation |
| | <i>G0029890</i> | not characterized during annotation |
| | <i>G0031090</i> | not characterized during annotation |
| | <i>G0034190</i> | not characterized during annotation |
| | <i>G0036200</i> | not characterized during annotation |
| | <i>G0040610</i> | not characterized during annotation |
| | <i>G0048920</i> | not characterized during annotation |
| | <i>YAR027W</i> | Putative integral membrane protein of unknown function |
| | <i>YBR058C</i> | Ubiquitin-specific protease |
| | <i>YBR148W</i> | Protein required for normal prospore membrane formation |
| | <i>YBR260C</i> | GTPase-activating protein (RhoGAP) for Rho3p and Rho4p |
| | <i>YCL049C</i> | Protein of unknown function |

| | | |
|--|----------------|--|
| | <i>YCL051W</i> | Protein involved in control of cell wall structure and stress response |
| | <i>YCR091W</i> | Putative serine/threonine protein kinase |
| | <i>YCR100C</i> | Protein involved in protein sorting |
| | <i>YCR106W</i> | Putative zinc cluster transcription factor |
| | <i>YCL049C</i> | Protein of unknown function |
| | <i>YDL109C</i> | Putative lipase |
| | <i>YDL171C</i> | NAD(+)-dependent glutamate synthase (GOGAT) |
| | <i>YER093C</i> | Subunit of TORC2 (Tor2p-Lst8p-Avo1-Avo2-Tsc11p-Bit61p) |
| | <i>YFL018C</i> | Dihydrolipoamide dehydrogenase |
| | <i>YFR047C</i> | Quinolate phosphoribosyl transferase |
| | <i>YIR003W</i> | Subunit of a complex that associates with actin filaments |
| | <i>YJL050W</i> | RNA duplex-sensing translocase |
| | <i>YJR040W</i> | Voltage-gated chloride channel |
| | <i>YJR131W</i> | Alpha-1,2-mannosidase |
| | <i>YJR134C</i> | Protein of unknown function |
| | <i>YJR148W</i> | Cytosolic branched-chain amino acid (BCAA) aminotransferase |
| | <i>YKR002W</i> | Poly(A) polymerase |
| | <i>YLR006C</i> | Cytoplasmic phosphorelay intermediate osmosensor and regulator |
| | <i>YLR078C</i> | v-SNARE (vesicle specific SNAP receptor) |
| | <i>YLR145W</i> | Subunit of RNase MRP |
| | <i>YNL113W</i> | RNA polymerase subunit AC19 |
| | <i>YNL317W</i> | Integral subunit of the pre-mRNA CPF complex |
| | <i>YOR032C</i> | bHLH protein with similarity to myc-family transcription factors |
| | <i>YOR037W</i> | Mitochondrial peripheral inner membrane protein |
| | <i>YOR043W</i> | Negative regulator of TORC1 in response to limiting leucine |

List of genes affected by moderate effect mutations in the genomes of each isolate, including description of the genes.

| List of affected strains | Affected genes | Description of affected genes |
|---|-----------------|---|
| PY0001, 465/2018, 2251/2018, DE6507, DE35762 | <i>YLR086W</i> | Subunit of the condensin complex |
| PY0001, PY0002, 2251/2018, DE6507, DE35762 | <i>YFR003C</i> | Regulatory subunit of the type I protein phosphatase (PP1) Glc7p |
| | <i>YPL061W</i> | Cytosolic aldehyde dehydrogenase |
| | <i>YPL064C</i> | Component of a complex containing Cef1p |
| | <i>YPL065W</i> | Component of the ESCRT-I complex |
| | <i>YPL085W</i> | COPII vesicle coat protein required for ER transport vesicle budding |
| | <i>YPL101W</i> | Subunit of hexameric RecA-like ATPase Elp456 Elongator subcomplex |
| | <i>YPL104W</i> | Mitochondrial aspartyl-tRNA synthetase |
| | <i>YPL105C</i> | Protein of unknown function that influences nuclear pore distribution |
| | <i>YPL106C</i> | ATPase component of heat shock protein Hsp90 chaperone complex |
| | <i>YPL108W</i> | Cytoplasmic protein of unknown function |
| | <i>YPL110C</i> | Glycerophosphocholine (GroPCho) phosphodiesterase |
| | <i>YPL113C</i> | Glyoxylate reductase |
| PY0001, PY0002, 465/2018, DE6507, DE35762 | <i>G0028750</i> | not characterized during annotation |
| | <i>G0028770</i> | not characterized during annotation |
| | <i>YBR036C</i> | Endoplasmic reticulum membrane protein |
| | <i>YBR037C</i> | Copper-binding protein of mitochondrial inner membrane |
| | <i>YCR045C</i> | Probable subtilisin-family protease |
| | <i>YJL092W</i> | DNA helicase and DNA-dependent ATPase |
| | <i>YJL106W</i> | Serine/threonine protein kinase involved in activation of meiosis |
| | <i>YJL111W</i> | Subunit of the cytosolic chaperonin Cct ring complex |
| | <i>YJL115W</i> | Nucleosome assembly factor |
| | <i>YJL123C</i> | Protein of unknown function that may interact with ribosomes |
| PY0001, PY0002, 465/2018, 2251/2018, DE35762 | <i>YKR023W</i> | Subunit of ribosome-associated quality control trigger complex (RQT) |
| | <i>YKR024C</i> | Putative ATP-dependent RNA helicase of the DEAD-box family |
| | <i>YPL083C</i> | Subunit of the tRNA splicing endonuclease |

| | | |
|--|-----------------|--|
| | <i>YPL084W</i> | Cytoplasmic class E vacuolar protein sorting (VPS) factor |
| | <i>YPL126W</i> | U3 snoRNP protein |
| | <i>YPL130W</i> | Meiosis-specific prospore protein |
| | <i>YPL133C</i> | Transcription factor involved in regulating gluconeogenesis |
| PY0001, PY0002, 465/2018, 2251/2018, DE6507 | <i>G0004120</i> | not characterized during annotation |
| | <i>YBR078W</i> | GPI-anchored protein involved in efficient glucose uptake |
| | <i>YBR081C</i> | Subunit of the SAGA transcriptional regulatory complex |
| | <i>YBR084W</i> | Mitochondrial C1-tetrahydrofolate synthase |
| | <i>YBR094W</i> | Putative tubulin tyrosine ligase associated with P-bodies |
| | <i>YBR097W</i> | Serine/threonine protein kinase involved in vacuolar protein sorting |
| | <i>YBR098W</i> | Subunit of structure-specific Mms4p-Mus81p endonuclease |
| | <i>YBR103W</i> | WD40 repeat-containing subunit of Set3C histone deacetylase complex |
| | <i>YBR115C</i> | Alpha aminoadipate reductase |
| | <i>YBR122C</i> | Mitochondrial ribosomal protein of the large subunit |
| | <i>YBR136W</i> | Genome integrity checkpoint protein and PI kinase superfamily member |
| | <i>YBR141C</i> | Nucleolar S-adenosylmethionine-dependent rRNA methyltransferase |
| | <i>YBR156C</i> | Subunit of the conserved chromosomal passenger complex (CPC) |
| | <i>YBR222C</i> | Oxalyl-CoA synthetase |
| | <i>YBR225W</i> | Putative protein of unknown function |
| | <i>YBR260C</i> | GTPase-activating protein (RhoGAP) for Rho3p and Rho4p |
| | <i>YBR272C</i> | Evolutionarily conserved 19S regulatory particle assembly-chaperone |
| PY0001, PY0002, DE35762 | <i>G0049070</i> | not characterized during annotation |
| PY0001, 2251/2018, DE35762 | <i>G0029600</i> | not characterized during annotation |
| PY0001, PY0002 | <i>YOL016C</i> | Calmodulin-dependent protein kinase |
| | <i>YOL023W</i> | Mitochondrial translation initiation factor 2 |
| | <i>YOL025W</i> | Protein that negatively regulates the SCF E3-ubiquitin ligase |
| | <i>YOL036W</i> | Protein of unknown function |
| | <i>YOL040C</i> | Protein component of the small (40S) ribosomal subunit |
| | <i>YOL044W</i> | Tail-anchored type II integral peroxisomal membrane protein |
| PY0001 | <i>YDL014W</i> | Histone glutamine methyltransferase |
| PY0002 | <i>G0047510</i> | not characterized during annotation |
| 2251/2018 | <i>G0039660</i> | not characterized during annotation |

| | | |
|-----------------------|-----------------|---|
| | <i>YDR101C</i> | Nuclear export factor for the ribosomal pre-60S subunit |
| | <i>YDR513W</i> | Cytoplasmic glutaredoxin |
| DE6507 | <i>YGL113W</i> | Protein involved in the initiation of DNA replication |
| | <i>YHR074W</i> | Glutamine-dependent NAD(+) synthetase |
| | <i>YKL062W</i> | Stress-responsive transcriptional activator |
| DE35762 | <i>G0029090</i> | not characterized during annotation |
| | <i>YHR098C</i> | Component of the Sec23p-Sfb3p heterodimer of the COPII vesicle coat |
| | <i>YIL088C</i> | Vacuolar amino acid transporter |
| | <i>YJR111C</i> | Peroxisomal matrix protein with naturally active promoter |
| | <i>YKR101W</i> | Protein involved in silencing at mating-type loci HML and HMR |
| | <i>YLR383W</i> | Subunit of the SMC5-SMC6 complex |
| | <i>YLR398C</i> | Ski complex component and putative RNA helicase |
| | <i>YNL055C</i> | Mitochondrial porin (voltage-dependent anion channel) |
| | <i>YOR307C</i> | Protein involved in ER-to-Golgi transport |
| All 6 isolates | <i>G0000750</i> | not characterized during annotation |
| | <i>G0000760</i> | not characterized during annotation |
| | <i>G0000770</i> | not characterized during annotation |
| | <i>G0000800</i> | not characterized during annotation |
| | <i>G0001840</i> | not characterized during annotation |
| | <i>G0002090</i> | not characterized during annotation |
| | <i>G0005430</i> | not characterized during annotation |
| | <i>G0005450</i> | not characterized during annotation |
| | <i>G0006190</i> | not characterized during annotation |
| | <i>G0006260</i> | not characterized during annotation |
| | <i>G0007310</i> | not characterized during annotation |
| | <i>G0007670</i> | not characterized during annotation |
| | <i>G0008160</i> | not characterized during annotation |
| | <i>G0008510</i> | not characterized during annotation |
| | <i>G0008670</i> | not characterized during annotation |
| | <i>G0020230</i> | not characterized during annotation |
| | <i>G0026820</i> | not characterized during annotation |
| | <i>G0029590</i> | not characterized during annotation |
| | <i>G0029930</i> | not characterized during annotation |
| | <i>G0035540</i> | not characterized during annotation |
| | <i>G0049200</i> | not characterized during annotation |
| | <i>G0049350</i> | not characterized during annotation |
| | <i>YAL007C</i> | Member of the p24 family involved in ER to Golgi transport |
| | <i>YAL008W</i> | Integral mitochondrial outer membrane (MOM) protein |
| | <i>YAL010C</i> | Subunit of both the ERMES and the SAM complex |
| | <i>YAL011W</i> | Protein of unknown function |
| | <i>YAL013W</i> | Component of the Rpd3L histone deacetylase complex |
| | <i>YAL014C</i> | Endosomal SNARE related to mammalian syntaxin 8 |

| | | |
|--|----------------|--|
| | <i>YAL018C</i> | Protein Involved in spore wall assembly |
| | <i>YAL019W</i> | Snf2p family member with ATP-dependent chromatin remodeling activity |
| | <i>YAL021C</i> | Component of the CCR4-NOT transcriptional complex |
| | <i>YAR002W</i> | FG-nucleoporin component of central core of the nuclear pore complex |
| | <i>YAR003W</i> | Subunit of the COMPASS (Set1C) complex |
| | <i>YAR007C</i> | Subunit of heterotrimeric Replication Protein A (RPA) |
| | <i>YAR014C</i> | Protein involved in bud-site selection |
| | <i>YAR018C</i> | Nonessential serine/threonine protein kinase |
| | <i>YAR027W</i> | Putative integral membrane protein of unknown function |
| | <i>YAR042W</i> | Protein similar to mammalian oxysterol-binding protein |
| | <i>YBL007C</i> | Cytoskeletal protein binding protein |
| | <i>YBL008W</i> | Subunit of the HIR complex |
| | <i>YBL009W</i> | Atypical protein kinase |
| | <i>YBL010C</i> | Clathrin adaptor (adaptin) accessory protein |
| | <i>YBL014C</i> | Component of the core factor (CF) rDNA transcription factor complex |
| | <i>YBL017C</i> | Type I transmembrane sorting receptor for multiple vacuolar hydrolases |
| | <i>YBL019W</i> | Class II abasic (AP) endonuclease involved in repair of DNA damage |
| | <i>YBL022C</i> | ATP-dependent Lon protease |
| | <i>YBL023C</i> | Protein involved in DNA replication |
| | <i>YBL024W</i> | S-adenosyl-L-methionine-dependent tRNA: m5C-methyltransferase |
| | <i>YBL032W</i> | RNA binding protein involved in asymmetric localization of ASH1 mRNA |
| | <i>YBL033C</i> | GTP cyclohydrolase II |
| | <i>YBL034C</i> | Microtubule plus-end-tracking non-motor protein |
| | <i>YBL035C</i> | B subunit of DNA polymerase alpha-primase complex |
| | <i>YBR001C</i> | Putative neutral trehalase, required for thermotolerance |
| | <i>YBR015C</i> | Alpha-1,2-mannosyltransferase |
| | <i>YBR020W</i> | Galactokinase |
| | <i>YBR021W</i> | Plasma membrane localized uracil permease |
| | <i>YBR023C</i> | Chitin synthase III |
| | <i>YBR033W</i> | Putative zinc cluster protein, predicted to be a transcription factor |
| | <i>YBR040W</i> | Integral membrane protein required for efficient mating |
| | <i>YBR043C</i> | Multidrug transporter of the major facilitator superfamily |
| | <i>YBR049C</i> | RNA polymerase I enhancer binding protein |
| | <i>YBR050C</i> | Regulatory subunit of the Glc7p type-1 protein phosphatase |
| | <i>YBR052C</i> | Protein of unknown function |
| | <i>YBR053C</i> | Putative protein of unknown function |
| | <i>YBR058C</i> | Ubiquitin-specific protease |

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| | YBR059C | Ser/Thr protein kinase |
| | YBR065C | Pre-mRNA splicing factor |
| | YBR074W | Multi-spanning vacuolar membrane protease |
| | YBR079C | eIF3a subunit of the eukaryotic translation initiation factor 3 (eIF3) |
| | YBR080C | AAA ATPase and SNARE disassembly chaperone |
| | YBR086C | Cortical ER protein involved in ER-plasma membrane (PM) tethering |
| | YBR093C | Repressible acid phosphatase |
| | YBR101C | Hsp70 (Ssa1p) nucleotide exchange factor |
| | YBR102C | Exocyst subunit with dual roles in exocytosis and spliceosome assembly |
| | YBR112C | General transcriptional co-repressor |
| | YBR138C | Cytoplasmic protein of unknown function |
| | YBR140C | GTPase-activating protein |
| | YBR148W | Protein required for normal prospore membrane formation |
| | YBR150C | Protein of unknown function |
| | YBR152W | mRNA splicing factor, component of U4/U6.U5 tri-snRNP |
| | YBR153W | Diaminohydroxyphosphoribosylaminopyrimidine deaminase |
| | YBR163W | Mitochondrial 5'-3' exonuclease and sliding exonuclease |
| | YBR169C | Member of Hsp110 subclass of the heat shock protein 70 (HSP70) family |
| | YBR172C | GYF domain protein |
| | YBR175W | Essential subunit of the COMPASS (Set1C) complex |
| | YBR176W | Ketopantoate hydroxymethyltransferase |
| | YBR180W | Putative dityrosine transporter of the major facilitator superfamily |
| | YBR182C | MADS-box transcription factor involved in osmotic stress response |
| | YBR186W | Hexameric ring ATPase that remodels chromosome axis protein Hop1p |
| | YBR187W | Calcium and manganese transporter with higher affinity for Ca ²⁺ |
| | YBR196C | Glycolytic enzyme phosphoglucose isomerase |
| | YBR196C-A | Putative protein of unknown function |
| | YBR199W | Glycosyltransferase involved in protein glycosylation |
| | YBR204C | Serine hydrolase |
| | YBR207W | Putative high affinity iron transporter |
| | YBR208C | Urea amidolyase |
| | YBR229C | Glucosidase II catalytic subunit |
| | YBR253W | Subunit of the RNA polymerase II mediator complex |
| | YBR255W | Protein of unknown function |
| | YBR267W | Cytoplasmic pre-60S factor |
| | YBR270C | Subunit of TORC2 membrane-associated complex |

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| | <i>YBR271W</i> | S-adenosylmethionine-dependent methyltransferase |
| | <i>YBR274W</i> | Serine/threonine kinase and DNA damage checkpoint effector |
| | <i>YBR275C</i> | Protein involved in control of DNA replication |
| | <i>YBR280C</i> | F-Box protein involved in proteasome-dependent degradation of Aah1p |
| | <i>YBR281C</i> | Component of glutamine amidotransferase (GATase II) |
| | <i>YCL004W</i> | Phosphatidylglycerolphosphate synthase |
| | <i>YCL014W</i> | Guanine nucleotide exchange factor (GEF) for Cdc42p |
| | <i>YCL018W</i> | Beta-isopropylmalate dehydrogenase (IMDH) |
| | <i>YCL024W</i> | Protein kinase of the bud neck involved in the septin checkpoint |
| | <i>YCL025C</i> | Broad-specificity, low-affinity amino acid permease |
| | <i>YCL027W</i> | Membrane protein localized to the shmoo tip |
| | <i>YCL029C</i> | Microtubule-associated protein |
| | <i>YCL030C</i> | Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase |
| | <i>YCL036W</i> | Protein of unknown function |
| | <i>YCL039W</i> | Subunit of GID Complex that binds directly to central component Vid30p |
| | <i>YCL043C</i> | Protein disulfide isomerase |
| | <i>YCL048W-A</i> | Putative protein of unknown function |
| | <i>YCL052C</i> | Component of glycosylphosphatidylinositol-mannosyltransferase I |
| | <i>YCL054W</i> | AdoMet-dependent methyltransferase |
| | <i>YCR003W</i> | Mitochondrial ribosomal protein of the large subunit |
| | <i>YCR011C</i> | Putative ATP-dependent permease of the ABC transporter family |
| | <i>YCR014C</i> | DNA polymerase IV |
| | <i>YCR015C</i> | Protein required for cold tolerance |
| | <i>YCR017C</i> | GPI lipid remodelase |
| | <i>YCR032W</i> | Protein homologous to Chediak-Higashi syndrome and Beige proteins |
| | <i>YCR042C</i> | TFIID subunit (150 kDa) |
| | <i>YCR047C</i> | Ribosome biogenesis factor |
| | <i>YCR059C</i> | Negative regulator of eIF2 kinase Gcn2p |
| | <i>YCR065W</i> | Forkhead transcription factor |
| | <i>YCR075C</i> | Protein involved in cystine transport |
| | <i>YCR077C</i> | Deadenylation-dependent mRNA-decapping factor |
| | <i>YCR079W</i> | Mitochondrial type 2C protein phosphatase (PP2C) |
| | <i>YCR083W</i> | Mitochondrial thioredoxin |
| | <i>YCR089W</i> | Cell wall adhesin, expressed specifically during mating |
| | <i>YCR092C</i> | Mismatch repair protein |
| | <i>YCR093W</i> | Subunit of the CCR4-NOT1 core complex |
| | <i>YCR106W</i> | Putative zinc cluster transcription factor |

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| | <i>YDL010W</i> | Cis-Golgi localized monothiol glutaredoxin, binds Fe-S cluster |
| | <i>YDL015C</i> | Enoyl reductase |
| | <i>YDL019C</i> | Member of an oxysterol-binding protein family with seven members |
| | <i>YDL024C</i> | Protein of unknown function |
| | <i>YDL025C</i> | Putative protein kinase, potentially phosphorylated by Cdc28p |
| | <i>YDL030W</i> | Subunit of the SF3a splicing factor complex |
| | <i>YDL033C</i> | tRNA-specific 2-thiouridylase |
| | <i>YDL035C</i> | Plasma membrane G protein coupled receptor (GPCR) |
| | <i>YDL036C</i> | Mitochondrial tRNA:pseudouridine synthase |
| | <i>YDL039C</i> | Pheromone-regulated protein |
| | <i>YDL044C</i> | Mitochondrial protein that interacts with mitochondrial RNA polymerase |
| | <i>YDL049C</i> | Protein with similarity to Kre9p |
| | <i>YDL052C</i> | 1-acyl-sn-glycerol-3-phosphate acyltransferase |
| | <i>YDL055C</i> | GDP-mannose pyrophosphorylase (mannose-1-phosphate guanylttransferase) |
| | <i>YDL056W</i> | Transcription factor |
| | <i>YDL058W</i> | Essential protein involved in vesicle-mediated ER to Golgi transport |
| | <i>YDL065C</i> | Chaperone and import receptor for newly-synthesized class I PMPs |
| | <i>YDL070W</i> | Protein involved in transcription initiation |
| | <i>YDL073W</i> | Scaffold protein in the HKR1 sub-branch of the Hog1p-signaling pathway |
| | <i>YDL074C</i> | E3 ubiquitin ligase |
| | <i>YDL086W</i> | Putative carboxymethylenebutenolidase |
| | <i>YDL089W</i> | Protein involved in regulation of mitotic exit |
| | <i>YDL095W</i> | Protein O-mannosyltransferase of the ER membrane |
| | <i>YDL097C</i> | Essential, non-ATPase regulatory subunit of the 26S proteasome lid |
| | <i>YDL098C</i> | Component of the U4/U6.U5 snRNP complex |
| | <i>YDL099W</i> | Cis-golgi localized protein involved in ER to Golgi transport |
| | <i>YDL100C</i> | Guanine nucleotide exchange factor for Gpa1p |
| | <i>YDL102W</i> | Catalytic subunit of DNA polymerase delta |
| | <i>YDL104C</i> | Protein involved in threonylcarbamoyl adenosine biosynthesis |
| | <i>YDL106C</i> | Homeobox transcription factor |
| | <i>YDL109C</i> | Putative lipase |
| | <i>YDL113C</i> | Sorting nexin family member |
| | <i>YDL117W</i> | SH3-domain protein located in the bud neck and cytokinetic actin ring |
| | <i>YDL123W</i> | Protein of unknown function |

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| | <i>YDL124W</i> | NADPH-dependent alpha-keto amide reductase |
| | <i>YDL134C</i> | Catalytic subunit of protein phosphatase 2A, PP2A |
| | <i>YDL136W</i> | Ribosomal 60S subunit protein L35B |
| | <i>YDL138W</i> | Plasma membrane high glucose sensor that regulates glucose transport |
| | <i>YDL139C</i> | Nonhistone component of centromeric chromatin |
| | <i>YDL140C</i> | RNA polymerase II largest subunit B220 |
| | <i>YDL143W</i> | Subunit of the cytosolic chaperonin Cct ring complex |
| | <i>YDL145C</i> | Alpha subunit of COPI vesicle coatomer complex |
| | <i>YDL149W</i> | Transmembrane protein involved in forming Cvt and autophagic vesicles |
| | <i>YDL154W</i> | Protein of the MutS family |
| | <i>YDL155W</i> | B-type cyclin involved in cell cycle progression |
| | <i>YDL171C</i> | NAD(+)-dependent glutamate synthase (GOGAT) |
| | <i>YDL174C</i> | Major mitochondrial D-lactate dehydrogenase |
| | <i>YDL186W</i> | Putative protein of unknown function |
| | <i>YDL193W</i> | Forms dehydrodolichyl diphosphate synthase complex with RER2 or SRT1 |
| | <i>YDR005C</i> | Highly conserved negative regulator of RNA polymerase III |
| | <i>YDR006C</i> | Protein of unknown function |
| | <i>YDR009W</i> | Transcriptional regulator |
| | <i>YDR390C</i> | Subunit of heterodimeric nuclear SUMO activating enzyme E1 with Aos1p |
| | <i>YEL007W</i> | Transcriptional regulator of pseudohyphal growth |
| | <i>YEL011W</i> | Glycogen branching enzyme, involved in glycogen accumulation |
| | <i>YER004W</i> | Protein of unknown function |
| | <i>YER007W</i> | Microtubule effector required for tubulin heterodimer formation |
| | <i>YER008C</i> | Subunit of the exocyst complex |
| | <i>YER022W</i> | Subunit of the RNA polymerase II mediator complex |
| | <i>YER033C</i> | Protein of unknown function |
| | <i>YER034W</i> | Protein of unknown function |
| | <i>YER039C</i> | Protein of unknown function |
| | <i>YER040W</i> | Transcriptional activator in nitrogen catabolite repression system |
| | <i>YER041W</i> | Holliday junction resolvase |
| | <i>YER042W</i> | Methionine-S-sulfoxide reductase |
| | <i>YER044C-A</i> | Meiosis-specific protein involved in forming DSBs |
| | <i>YER045C</i> | ATF/CREB family basic leucine zipper (bZIP) transcription factor |
| | <i>YER047C</i> | Putative ATPase of the AAA family |
| | <i>YER050C</i> | Mitochondrial ribosomal protein of the small subunit |
| | <i>YER051W</i> | JmjC domain family histone demethylase specific for H3-K36 |

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| | <i>YER054C</i> | Putative regulatory subunit of protein phosphatase Glc7p |
| | <i>YFL001W</i> | tRNA:pseudouridine synthase |
| | <i>YFL002C</i> | Putative ATP-dependent RNA helicase |
| | <i>YFL003C</i> | Protein involved in meiotic recombination |
| | <i>YFL012W</i> | Putative protein of unknown function |
| | <i>YFL013C</i> | Subunit of the INO80 chromatin remodeling complex |
| | <i>YFL017W-A</i> | Core Sm protein Sm G |
| | <i>YFL021W</i> | Transcriptional activator of nitrogen catabolite repression genes |
| | <i>YFL023W</i> | Unconventional prefoldin protein involved in translation initiation |
| | <i>YFL024C</i> | Subunit of NuA4, an essential histone H4/H2A acetyltransferase complex |
| | <i>YFL025C</i> | GPI inositol deacylase of the endoplasmic reticulum (ER) |
| | <i>YFL027C</i> | GTPase-activating protein for yeast Rab family members |
| | <i>YFR002W</i> | Linker nucleoporin component of the nuclear pore complex (NPC) |
| | <i>YFR005C</i> | Conserved zinc-finger domain protein involved in pre-mRNA splicing |
| | <i>YFR006W</i> | Putative X-Pro aminopeptidase |
| | <i>YFR015C</i> | Glycogen synthase |
| | <i>YFR019W</i> | 1-phosphatidylinositol-3-phosphate 5-kinase |
| | <i>YFR022W</i> | Alpha-arrestin involved in ubiquitin-dependent endocytosis |
| | <i>YFR040W</i> | Protein required for function of the Sit4p protein phosphatase |
| | <i>YGL006W</i> | Vacuolar Ca ²⁺ ATPase involved in depleting cytosol of Ca ²⁺ ions |
| | <i>YGL008C</i> | Plasma membrane P2-type H ⁺ -ATPase |
| | <i>YGL009C</i> | Isopropylmalate isomerase |
| | <i>YGL013C</i> | Transcription factor that regulates the pleiotropic drug response |
| | <i>YGL014W</i> | Member of the PUF protein family |
| | <i>YGL015C</i> | Formin inhibitor |
| | <i>YGL016W</i> | Karyopherin beta |
| | <i>YGL023C</i> | Phosphatidylinositol 3-phosphate binding protein |
| | <i>YGL027C</i> | Processing alpha glucosidase I |
| | <i>YGL028C</i> | Cell wall protein with similarity to glucanases |
| | <i>YGL035C</i> | Transcription factor involved in glucose repression |
| | <i>YGL039W</i> | Aldehyde reductase |
| | <i>YGR014W</i> | Mucin family member involved in various signaling pathways |
| | <i>YHR211W</i> | Lectin-like cell wall protein (flocculin) involved in flocculation |
| | <i>YIL001W</i> | Putative protein of unknown function |
| | <i>YIL005W</i> | ER protein with chaperone and co-chaperone activity |

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| | <i>YIL007C</i> | Evolutionarily conserved 19S regulatory particle assembly-chaperone |
| | <i>YIL017C</i> | GID Complex subunit, serves as adaptor for regulatory subunit Vid24p |
| | <i>YIL019W</i> | Protein required for pre-rRNA processing |
| | <i>YIL023C</i> | Zinc transporter |
| | <i>YIL036W</i> | Basic leucine zipper (bZIP) transcription factor from ATF/CREB family involved in stress-responsive regulatory network |
| | <i>YIL037C</i> | Pheromone-regulated protein |
| | <i>YIL038C</i> | Component of the CCR4-NOT core complex, involved in mRNA decapping |
| | <i>YIL041W</i> | BAR domain protein that localizes to early and late Golgi vesicles |
| | <i>YIL042C</i> | Mitochondrial protein kinase |
| | <i>YIR001C</i> | Cytoplasmic RNA-binding protein |
| | <i>YIR003W</i> | Subunit of a complex that associates with actin filaments |
| | <i>YIR006C</i> | Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p |
| | <i>YIR007W</i> | Steryl-beta-glucosidase with broad specificity for aglycones |
| | <i>YIR008C</i> | Subunit of DNA primase |
| | <i>YIR010W</i> | Essential component of the outer kinetochore MIND complex |
| | <i>YIR018W</i> | Basic leucine zipper (bZIP) iron-sensing transcription factor |
| | <i>YJL001W</i> | Beta 1 subunit of the 20S proteasome |
| | <i>YJL002C</i> | Alpha subunit of the oligosaccharyltransferase complex of the ER lumen |
| | <i>YJL010C</i> | Essential subunit of U3-containing 90S preribosome |
| | <i>YJL025W</i> | Component of the core factor (CF) rDNA transcription factor complex |
| | <i>YJL027C</i> | Putative protein of unknown function |
| | <i>YJL029C</i> | Component of the GARP (Golgi-associated retrograde protein) complex |
| | <i>YJL042W</i> | Microtubule-associated protein involved in microtubule organization |
| | <i>YJL052W</i> | Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), isozyme 1 |
| | <i>YJL054W</i> | Component of the mitochondrial TIM22 complex |
| | <i>YJL056C</i> | Zinc-regulated transcription factor |
| | <i>YJL057C</i> | Protein kinase of unknown cellular role |
| | <i>YJL058C</i> | Subunit of TORC2 membrane-associated complex |
| | <i>YJL060W</i> | Kynurenine aminotransferase |
| | <i>YJL063C</i> | Mitochondrial ribosomal protein of the large subunit |

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| | <i>YJL073W</i> | DnaJ-like chaperone required for nuclear membrane fusion during mating |
| | <i>YJL074C</i> | Subunit of the multiprotein cohesin complex |
| | <i>YJL078C</i> | GPI-anchored cell wall protein involved in export of sterols |
| | <i>YJL080C</i> | Essential RNA-binding G protein effector of mating response pathway |
| | <i>YJL082W</i> | Protein required for clearance of inclusion bodies |
| | <i>YJL083W</i> | EH domain-containing protein |
| | <i>YJL089W</i> | C6 zinc cluster transcriptional activator |
| | <i>YJL094C</i> | Putative K ⁺ /H ⁺ antiporter |
| | <i>YJL095W</i> | MAPKKK acting in the protein kinase C signaling pathway |
| | <i>YJL098W</i> | Protein that forms a complex with the Sit4p protein phosphatase |
| | <i>YJL099W</i> | Member of the ChAPs (Chs5p-Arf1p-binding proteins) family |
| | <i>YJL100W</i> | Type II phosphatidylinositol 4-kinase |
| | <i>YJL102W</i> | Mitochondrial elongation factor involved in translational elongation |
| | <i>YJL128C</i> | MAP kinase kinase of the HOG signaling pathway |
| | <i>YJL129C</i> | Component of the Trk1p-Trk2p potassium transport system |
| | <i>YJL130C</i> | Bifunctional carbamoylphosphate synthetase/aspartate transcarbamylase |
| | <i>YJR002W</i> | Component of the SSU processome and 90S preribosome |
| | <i>YJR005W</i> | Beta-adaptin |
| | <i>YJR008W</i> | Protein of unknown function |
| | <i>YJR013W</i> | Glycosylphosphatidylinositol-alpha 1,4 mannosyltransferase I |
| | <i>YJR016C</i> | Dihydroxyacid dehydratase |
| | <i>YJR017C</i> | Peptidylprolyl-cis/trans-isomerase (PPIase) |
| | <i>YJR024C</i> | 5'-methylthioribulose-1-phosphate dehydratase |
| | <i>YJR031C</i> | Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs) |
| | <i>YJR032W</i> | Peptidyl-prolyl cis-trans isomerase (cyclophilin) |
| | <i>YJR033C</i> | Subunit of RAVE complex (Rav1p, Rav2p, Skp1p) |
| | <i>YJR035W</i> | Protein involved in transcription-coupled nucleotide excision repair |
| | <i>YJR039W</i> | Mitochondrial protein of unknown function |
| | <i>YJR041C</i> | Protein required for normal metabolism of the rRNA primary transcript |
| | <i>YJR043C</i> | Third subunit of DNA polymerase delta |
| | <i>YJR051W</i> | Fumarate reductase, catalyzes the reduction of fumarate to succinate |
| | <i>YJR054W</i> | Potassium transporter that mediates K ⁺ influx |
| | <i>YJR061W</i> | Protein required for N-glycan mannosylphosphorylation |

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| | <i>YJR062C</i> | Amidase |
| | <i>YJR066W</i> | PIK-related protein kinase and rapamycin target |
| | <i>YJR076C</i> | Component of the septin ring that is required for cytokinesis |
| | <i>YJR077C</i> | Mitochondrial phosphate carrier |
| | <i>YJR078W</i> | Tryptophan 2,3-dioxygenase or indoleamine 2,3-dioxygenase |
| | <i>YJR083C</i> | Protein of unknown function |
| | <i>YJR089W</i> | Subunit of chromosomal passenger complex (CPC) |
| | <i>YJR094C</i> | Master regulator of meiosis that is active only during meiotic events |
| | <i>YJR094W-A</i> | Ribosomal 60S subunit protein L43B |
| | <i>YJR106W</i> | Protein involved in calcium homeostasis and exit from quiescence |
| | <i>YJR107W</i> | Putative lipase |
| | <i>YJR109C</i> | Large subunit of carbamoyl phosphate synthetase |
| | <i>YJR117W</i> | Highly conserved zinc metalloprotease |
| | <i>YJR121W</i> | Beta subunit of the F1 sector of mitochondrial F1F0 ATP synthase |
| | <i>YJR125C</i> | Protein containing an N-terminal epsin-like domain |
| | <i>YJR132W</i> | Karyopherin |
| | <i>YJR134C</i> | Protein of unknown function |
| | <i>YJR136C</i> | Subunit of the ASTRA complex, involved in chromatin remodeling |
| | <i>YJR137C</i> | Sulfite reductase beta subunit |
| | <i>YJR138W</i> | GTPase-activating protein (GAP) subunit of the Iml1p/SEACIT complex |
| | <i>YJR139C</i> | Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase) |
| | <i>YJR149W</i> | Putative protein of unknown function |
| | <i>YJR151C</i> | Cell wall mannoprotein |
| | <i>YJR152W</i> | Allantoate permease |
| | <i>YJR153W</i> | Endo-polygalacturonase |
| | <i>YJR154W</i> | Putative protein of unknown function |
| | <i>YJR155W</i> | Putative aryl-alcohol dehydrogenase |
| | <i>YKR002W</i> | Poly(A) polymerase |
| | <i>YKR008W</i> | Component of the RSC chromatin remodeling complex |
| | <i>YKR009C</i> | 3-hydroxyacyl-CoA dehydrogenase and enoyl-CoA hydratase |
| | <i>YKR011C</i> | Protein of unknown function |
| | <i>YKR018C</i> | Protein of unknown function |
| | <i>YKR019C</i> | EH domain-containing protein |
| | <i>YKR021W</i> | Alpha arrestin, substrate of calcineurin |
| | <i>YKR022C</i> | Essential protein that forms a dimer with Ntr1p |
| | <i>YKR029C</i> | Defining member of the SET3 histone deacetylase complex |

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| | <i>YKR054C</i> | Cytoplasmic heavy chain dynein |
| | <i>YLL019C</i> | Protein kinase involved in negative regulation of PolIII transcription |
| | <i>YLL021W</i> | Component of the polarisome |
| | <i>YLR002C</i> | Subunit of a nuclear complex with Noc2p and pre-replicative complexes |
| | <i>YLR006C</i> | Cytoplasmic phosphorelay intermediate osmosensor and regulator |
| | <i>YLR014C</i> | Zinc finger transcription factor |
| | <i>YLR015W</i> | Subunit of COMPASS (Set1C) complex |
| | <i>YLR020C</i> | Steryl ester hydrolase |
| | <i>YLR021W</i> | Component of a heterodimeric Poc4p-Irc25p chaperone |
| | <i>YLR024C</i> | Cytoplasmic ubiquitin-protein ligase (E3) |
| | <i>YLR027C</i> | Cytosolic aspartate aminotransferase involved in nitrogen metabolism |
| | <i>YLR032W</i> | DNA helicase/Ubiquitin ligase |
| | <i>YLR039C</i> | Protein involved in retrograde transport to the cis-Golgi network |
| | <i>YLR059C</i> | 3'-5' RNA exonuclease |
| | <i>YLR068W</i> | Nucleolar protein required for maturation of 18S rRNA |
| | <i>YLR069C</i> | Mitochondrial elongation factor involved in translational elongation |
| | <i>YLR082C</i> | Protein of unknown function |
| | <i>YLR084C</i> | Protein required for the maintenance of bud site selection |
| | <i>YLR087C</i> | Protein with structural similarity to lipid transport protein Vps13p |
| | <i>YLR106C</i> | Huge dynein-related AAA-type ATPase (midasin) |
| | <i>YLR108C</i> | Protein of unknown function |
| | <i>YLR113W</i> | Mitogen-activated protein kinase involved in osmoregulation |
| | <i>YLR114C</i> | Conserved protein involved in exocytic transport from the Golgi |
| | <i>YLR115W</i> | Subunit of the mRNA cleavage and polyadenylation factor (CPF) |
| | <i>YLR116W</i> | Component of commitment complex |
| | <i>YLR119W</i> | Component of the ESCRT-I complex |
| | <i>YLR120C</i> | Aspartic protease |
| | <i>YLR121C</i> | Aspartic protease |
| | <i>YLR126C</i> | Putative glutamine amidotransferase |
| | <i>YLR129W</i> | Nucleolar protein |
| | <i>YLR131C</i> | Transcription factor required for septum destruction after cytokinesis |
| | <i>YLR136C</i> | mRNA-binding protein expressed during iron starvation |
| | <i>YLR138W</i> | Na ⁺ /H ⁺ antiporter |
| | <i>YLR144C</i> | Intracellular beta-1,3-endoglucanase |

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| | <i>YLR145W</i> | Subunit of RNase MRP |
| | <i>YLR146C</i> | Spermine synthase |
| | <i>YLR148W</i> | Component of CORVET membrane tethering complex |
| | <i>YML017W</i> | Asn rich cytoplasmic protein that contains RGG motifs |
| | <i>YML018C</i> | Protein of unknown function |
| | <i>YML043C</i> | Component of the core factor (CF) rDNA transcription factor complex |
| | <i>YML046W</i> | U1 snRNP protein involved in splicing |
| | <i>YML059C</i> | Serine esterase |
| | <i>YML061C</i> | DNA helicase, potent G-quadruplex DNA binder/unwinder |
| | <i>YML064C</i> | GTPase involved in initiation of Mitotic Exit Network (MEN) |
| | <i>YML065W</i> | Largest subunit of the origin recognition complex |
| | <i>YML068W</i> | Protein that modulates the efficiency of translation termination |
| | <i>YML071C</i> | Component of the conserved oligomeric Golgi complex |
| | <i>YML074C</i> | Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase) |
| | <i>YML076C</i> | Homodimeric Zn2Cys6 zinc finger transcription factor |
| | <i>YML091C</i> | Protein subunit of mitochondrial RNase P |
| | <i>YML093W</i> | Subunit of U3-containing Small Subunit (SSU) processome complex |
| | <i>YML097C</i> | Guanine nucleotide exchange factor (GEF) and ubiquitin receptor |
| | <i>YML099C</i> | Zinc finger transcription factor involved in arginine-responsive genes |
| | <i>YML102W</i> | Subunit of chromatin assembly factor I (CAF-1), with Rlf2p and Msi1p |
| | <i>YML103C</i> | Subunit of the inner ring of the nuclear pore complex (NPC) |
| | <i>YNL108C</i> | Protein phosphatase |
| | <i>YNL271C</i> | Formin |
| | <i>YNR006W</i> | Endosomal protein that forms a complex with Hse1p |
| | <i>YNR013C</i> | Low-affinity vacuolar phosphate transporter |
| | <i>YMR020W</i> | Polyamine oxidase |
| | <i>YMR086W</i> | Component of eisosome required for proper eisosome assembly |
| | <i>YMR152W</i> | Aldehyde reductase |
| | <i>YOL001W</i> | Cyclin |
| | <i>YOL004W</i> | Component of both the Rpd3S and Rpd3L histone deacetylase complexes |
| | <i>YOR005C</i> | DNA ligase required for nonhomologous end-joining (NHEJ) |
| | <i>YOR011W</i> | Plasma membrane sterol transporter of the ATP-binding cassette family |
| | <i>YOR014W</i> | B-type regulatory subunit of protein phosphatase 2A (PP2A) |

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| | <i>YOR019W</i> | Protein of unknown function |
| | <i>YOR032C</i> | bHLH protein with similarity to myc-family transcription factors |
| | <i>YOR038C</i> | Subunit of HIR nucleosome assembly complex |
| | <i>YPL001W</i> | Catalytic subunit of the Hat1p-Hat2p histone acetyltransferase complex |
| | <i>YPL004C</i> | Eisosome core component |
| | <i>YPL009C</i> | Component of the Ribosome Quality Control (RQC) complex |
| | <i>YPL043W</i> | Nucleolar protein |
| | <i>YPL054W</i> | Zinc-finger protein of unknown function |
| | <i>YPL055C</i> | Protein involved in histone H2B ubiquitination |
| | <i>YPL057C</i> | Mannosylinositol phosphorylceramide (MIPC) synthase catalytic subunit |
| | <i>YPL078C</i> | Subunit b of the stator stalk of mitochondrial F1F0 ATP synthase |
| | <i>YPR003C</i> | Putative sulfate permease |
| | <i>YPR005C</i> | Cytoplasmic protein involved in halotolerance |
| | <i>YPR006C</i> | 2-methylisocitrate lyase of the mitochondrial matrix |
| | <i>YPR011C</i> | Mitochondrial transporter |