Phenotypic and genomic differences among *S. cerevisiae* strains in nitrogen requirements during wine fermentations

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Abstract

Nitrogen requirements by *S. cerevisiae* during wine fermentation are highly strain-dependent. Different approaches were applied to explore the nitrogen requirements of 28 wine yeast strains. Based on the growth and fermentation behaviour displayed at different nitrogen concentrations, high and low nitrogen-demanding strains were selected and further verified by competition fermentation. Biomass production with increasing nitrogen concentrations in the exponential fermentation phase was analysed by chemostat cultures. Low nitrogen-demanding (LND) strains produced a larger amount of biomass in nitrogen-limited synthetic grape musts, whereas high nitrogen-demanding (HND) strains achieved a bigger biomass yield when the YAN concentration was above 100 mg/L. Constant rate fermentation was carried out with both strains to determine the amount of nitrogen required to maintain the highest fermentation rate. Large differences appeared in the analysis of the genomes of low and high-nitrogen demanding strains showed for heterozygosity and the amino acid substitutions between orthologous proteins, with nitrogen recycling system genes showing the widest amino acid divergences. The CRISPR/Cas9-mediated genome modification method was used to validate the involvement of *GCN1* in the yeast strain nitrogen needs. However, the allele swapping of gene *GCN1* from low nitrogen-demanding strains to high nitrogen-demanding strains did not significantly influence the fermentation rate.

Keywords

S. cerevisiae, nitrogen requirement, genetic basis, biomass production, competition experiments, CRISPR/Cas9

1. Introduction

In modern oenology, a common practice followed to conduct wine fermentation is inoculating commercial wine yeast to grape must to ensure wine quality. Specific yeast strains are selected by experienced oenologists to serve difference fermentation purposes. Some of the most substantial features to be considered in yeast selection are their fermentation ability, aroma production, stress tolerance and nutrition requirements. The climate of each vintage, viticulture management and degree of ripeness largely determine the quality of grapes and, subsequently, wine quality (Henschke and Jiranek, 1993; Alexandre and Charpentier, 1998; Bell and Henschke, 2005). The right yeast strains can help oenologists to compensate any defects and enhance the merits of grape must. Nitrogen is one of the most important nutrients for yeast, and its availability in grape must is a key parameter for the wine fermentation progress. Grape-must contains a wide variety of nitrogen sources, including ammonium, amino acids, and small peptides (Kevvai et al., 2016). The nitrogen sources that can be utilised by yeast to support growth and fermentation are defined as yeast assimilable nitrogen (YAN). A sufficient amount of YAN is crucial for the fermentation process to be successful. It regulates yeast biomass formation which, in turn, impacts fermentation kinetics and fermentation duration (Bell and Henschke, 2005; Martínez-Moreno et al., 2012; Mendes- Ferreira et al., 2004; Varela et al., 2004). Previous studies reveal that a minimum of 140 mg/L of YAN is required for yeast to complete alcoholic fermentation (Bell and Henschke, 2005; Bely et al., 1990; Butzke, 1998). Deficient YAN in grape-must may cause stuck or stopped fermentation, which can diminish wine quality or lead to wine becoming completely spoiled (Bisson, 1999; Bell and Henschke, 2005). Moreover, many nitrogen sources provide important precursors for aroma compounds. Therefore, the availability and quality of nitrogen sources directly determine wine quality (Barbosa et al., 2009, 2012; Bell and Henschke,

2005; Seguinot et al., 2018). Winemakers regulate the grape-must nitrogen concentration by adding external nitrogen sources, such as di-ammonium phosphate. However, this practice is not easy to control, and may lead to microbial instability and an undesirable organoleptic profile in the final product (Ough and Amerine, 1988). Consequently, it is relevant to understand the nitrogen requirement of yeast strains in order to choose a suitable candidate to match the nitrogen condition of grape must.

Despite belonging to the same species, the ability of different *S. cerevisiae* strains to carry out fermentations at different nitrogen concentrations is highly strain-dependent (Bely et al., 1990; Gutiérrez et al., 2012; Su et al., 2019a). Some yeast strains are able to conduct fermentations with a limited amount of YAN, whereas others may need more to accomplish the process. Many studies have been carried out to determine yeast nitrogen requirements by analysing their growth and fermentation characters at different nitrogen concentrations (García-Ríos et al., 2014, 2019; Gutiérrez et al., 2012, 2013). Competition fermentations under nitrogen-limited (60 mg/L YAN), standard (140 or 180 mg/L YAN) and excessive (300 mg/L YAN) conditions were performed by García-Ríos et al. (2014) and Su et al. (2019a) to compare the nitrogen demands of two yeast strains. Manginot et al. (1997; 1998) firstly described a creative nitrogen requirement analysis method, which involves maintaining a stable fermentation rate by adding nitrogen in the stationary fermentation phase, and the amount of nitrogen supplied during fermentation was used as a criterion to quantify a certain yeast strain's nitrogen requirement. This method was later applied by Brice et al. (2014a) to assess the nitrogen requirements of different *S. cerevisiae* wine yeasts.

In *S. cerevisiae*, nitrogen metabolism is regulated by a series of interconnected processes (Gobert et al., 2019), such as the Ssy1-Ptr3-Ssy5 (SPS) signalling sensor system (Forsberg and Ljungdahl, 2001; Ljungdahl and Daignan-Fornier, 2012), the target of

rapamycin (TOR) regulatory pathway (Conrad et al., 2014), nitrogen catabolite repression
 (NCR) (Hofman-Bang, 1999; Beltran et al. 2004), the general amino acid control (GAAC)
 pathway (Hinnebusch and Natarajan, 2002; Hinnebusch, 2005), and other related
 regulatory mechanisms. These pathways form a complicated and sophisticated system
 (Reviewed by Zhang et al., 2018), which sets challenges to understand the underlying
 genetic basis of nitrogen requirement differences. Brice et al. (2014a) compared various
 physiological traits between high and low nitrogen-demanding strains and conducted a
 transcriptomic analysis. Their results revealed an overexpression of stress genes in high
 nitrogen requirement strains and a higher expression of biosynthetic genes in low nitrogen
 requirement strains. Quantitative trait loci (QTL) and RNA-seq analyses were carried out
 to identify the genetic variants between strains with different nitrogen requirements
 (Brice et al. 2014b; Cubillos et al. 2017; Jara et al., 2014; Kessi-Pérez et al., 2020).
 Depending on allelic variations, several nitrogen sensing and metabolising genes, namely
GCN1, *ARG81*, *MDS3* (Brice et al., 2014b) and *CPS1*, *LYP1*, *ALP1* and *ASI2* (Cubillos
 et al., 2017), were identified, and their function in the difference of nitrogen requirements
 was verified. The confluence of these genes may compose molecular mechanisms that
 influence nitrogen utilisation by yeast.

In the present study, we comprehensively determined the nitrogen requirements of a set
 of industrial wine yeast strains by applying different approaches. The growth and
 fermentation characters of yeast strains were determined under three nitrogen conditions.
 The strains of high and low nitrogen requirements were selected and their phenotypic
 features were further confirmed by competition fermentation, chemostat fermentation and
 constant rate fermentation. The genome sequences of two representative high and low
 nitrogen demanding strains were obtained. The genetic differences between strains were
 analysed and the gene function was studied by the CRISPR/Cas9-mediated genome

editing method. New insights are introduced to understand yeast nitrogen requirements both phenotypically and genetically.

2. Material and Methods

2.1 Strains and media

In our study, 28 industrial wine yeast strains provided by Lallemmand Inc. (Canada) were used. The strain codes and their corresponding commercial names are showed in Table S1. The oenological features of these strains can be obtained from the company's website (<http://www.lallemmandwine.com>).

The derivative strains of P12, P13, P17, P20 and P26 were constructed by introducing geneticin resistance gene *KanMX4*. One copy of the open reading frame (ORF) of gene *GAL1* was replaced with deletion cassette *KanMX4* by the short flanking homology (SFH) method. Plasmid pUG6 (Güldener et al, 1996) was used as a template to obtain this deletion cassette. Yeast transformation was carried out by the lithium acetate method (Gietz and Woods, 2002). Transformants were selected by resistance to geneticin and later confirmed by PCR. Primers used for gene deletion and transformants verification is listed in Table S2.

Yeast propagation was carried out firstly in yeast extract peptone dextrose (YPD) medium, which contains 20 g/L glucose, 20 g/L peptone and 10 g/L yeast extract. It was then transferred to SD media (2% glucose, 0.017% yeast nitrogen base) with 230.8 mg/L NH₄Cl (corresponding to 60 mg/L YAN) to eliminate the influence of YPD nitrogen-rich media. YPD with 200 mg/L G418 disulphate salt (Formedium, UK) was used as geneticin resistance selective medium.

Synthetic grape must (SM) was used for the growth and fermentation experiments. The recipe was modified based on Bely et al. (1990), which contains 100 g/L glucose, 100 g/L

fructose, 5 g/L malic acid, 0.5 g/L citric acid and 3 g/L tartaric acid. Minerals and vitamins were supplied at the same concentration as those described by Su et al. (2019a). Nitrogen sources were supplied as a mixture of 40% ammonium chloride and 60% amino acids. The composition of amino acids in the 1-litre stock was 1.5 g L-tyrosine, 13.4 g L-tryptophan, 2.5 g L-isoleucine, 3.4 g L-aspartic acid, 9.2 g L-glutamic acid, 28.3 g L-arginine, 3.7 g L-leucine, 5.8 g L-threonine, 1.4 g glycine, 38.4 g L-glutamine, 11.2 g L-alanine, 3.4 g L-valine, 2.4 g L-methionine, 2.9 g L-phenylalanine, 6 g L-serine, 2.6 g L-histidine, 1.3 g L-lysine, 1.5 g L-cysteine and 46.1 g L-proline, which corresponded to 22.15 g/L of YAN. The nitrogen source concentration in SM was adjusted according to the requirements of different experiments.

2.2 Determination of growth parameter at different nitrogen concentrations

The growth parameters of the various strains were determined at three different nitrogen concentrations: 60, 140, and 300 mg/L YAN. Growth characters were determined by the microtiter plate screening method described by Warringer and Blomberg (2003) and Su et al. (2019a). 96 well-microtiter plates were used. Each well was filled with 250 µL of synthetic must and inoculated with 10⁶ yeast cells/mL. Growth curves were monitored by recording the increase in optical density (OD) at wavelength 600 nm. Microtiter plates were incubated in a SPECTROstar Nano® microplate reader (BGM Labtech, Offenburg, Germany) at 28°C with 500 rpm orbital shaking. The optical density of each well was measured every 30 min until the growth reached the stationary phase. All the nitrogen conditions were assayed in triplicate. The growth characters of each strain at different nitrogen conditions was calculated by directly fitting OD measurements *versus* time to the Gompertz equation proposed by Zwietering et al. (1990), which has the following expression:

$$y = D * \exp \{ -\exp [((\mu_{\max} * e) / D) * (\lambda - t) + 1] \}$$

where $y = \ln (OD_t/OD_0)$, OD_0 is the initial OD and OD_t is the OD at time t ; $D = \ln (OD_\infty / OD_0)$ is the OD value reached with OD_∞ as the asymptotic maximum, $\mu_{\max}$ is the maximum specific growth rate (h^{-1}) and λ is the lag phase period (h). Phenotypic data were fitted to the Gompertz model by non-linear least-squares fitting using the Gauss-Newton algorithm as implemented in the nls function in the R statistical software, v.3.0.

2.3 Determination of fermentation characters at different nitrogen concentrations

The fermentation characters at the different nitrogen concentrations were screened by microscale fermentation. Fermentations were carried out in 15 mL tubes with 10 mL of synthetic must. The screw caps of tubes were loosened to allow CO_2 to release. SM was modified with three different nitrogen concentrations: 60, 140 and 300 mg/L of YAN. These values correspond to nitrogen limited, standard and excessive conditions (Bely et al., 1990). Around 2×10^6 cells/mL were inoculated. Fermentations were followed by CO_2 production, which was represented by the weight loss of fermentation tubes. The tubes filled with 10 mL SM without inoculation were used as the controls for evaporation weight loss (EWL). The weight of fermentation tubes was determined around every 12 h. Fermentations were considered completed when tube weight stopped lowering. Fermentation curves was obtained by plotting weight loss against time. Data were fitted to the Gompertz model as described in 2.2. The maximum fermentation rates ($V_{\max}$) were obtained by applying a similar equation to the calculation with $\mu_{\max}$, but by changing only the OD value to the weight loss value. The fermentation experiment was carried out in triplicate.

2.4 Laboratory-scale fermentation

Fermentations were carried out in 100 mL bottles with 80 mL of SM at two nitrogen concentrations (60 and 300 mg/L YAN) at 28 °C with continuous orbital shaking at 120

rpm. SM was inoculated with 2×10^6 cells/mL. Fermentation kinetics was followed by measuring the density of SM with a portable densitometer (Densito 30PX, Mettler Toledo, Switzerland). Samples were centrifuged to remove yeast cells before density measurements. Fermentation was considered finished when density reached 998 g/L (Gutiérrez et al., 2012).

2.5 Competition fermentation

In order to determine the competitiveness of the different yeast strains at certain nitrogen concentrations, one-to-one competition fermentation was carried out between different pairs of *S. cerevisiae* strains. Fermentations were performed in 80 mL SM as described in 2.3. In all, 2×10^6 cells/mL were inoculated with 50% of each strain. One of the strains in the competition pairs was labelled with geneticin (G418) resistance marker *KanMX4*. The yeast cell population was determined by plating on YPD and counting colony-forming units (CFU). The percentage of each strain throughout fermentation was monitored by replica plating from YPD to YPD-G418.

2.6 Chemostat fermentation and dry weight measurements

Chemostat cultures were carried out to determine the influence of nitrogen concentration on yeast biomass production. Continuous cultures were performed at 28°C in a 0.5 L reactor (MiniBio, Applikon Biotechnology) with a working volume of 0.35 L. The operation parameters in the bioreactor were temperature 28°C, pH 3.3 and 300 rpm stirring. The dilution rate (D) was set at 0.2 h^{-1} , which corresponds to the exponential growth phase. pH at 3.3 was controlled by the automatic addition of 2 M NaOH and 2×10^6 cells/mL yeast were inoculated. Prior to starting the continuous culture, cells were allowed to grow in a batch culture under the same condition as the continuous culture in SM with 60 mg/L of YAN to achieve enough biomass in a batch phase. The continuous culture started when the batch culture entered the stationary phase. Steady states were

sampled only after all the continuous cultures had been running for at least five residence times and the biomass values were constant. The continuous cultures were fed with the SM of the high YAN concentration. Every time the steady state was achieved, the introduced SM was changed to an SM with a higher YAN concentration. The continuous culture was started by introducing SM with 60 mg/L of YAN before being increased to 80, 100, 140, 160, 180, and finally to 200 mg/L of YAN. For the biomass dry weight analysis, 5 ml of samples were collected in a pre-weighed tube and centrifuged at 4000 rpm for 5 minutes to remove the supernatant. The cell pellet was washed 3 times with distilled water and dried in a 70°C oven for 2 days until constant weight.

2.7 Constant rate fermentation by nitrogen addition

Nitrogen requirements during fermentations were also determined by constant rate fermentation as described by Manginot et al. (1997, 1998). Batch fermentations were carried out at 28°C in a 0.5 L bioreactor (MiniBio, Applikon, the Netherlands) with a working volume of 0.35 L. 2×10^6 cells/mL were inoculated in SM at the initial nitrogen concentration of 140 mg/L of YAN. The CO₂ production rate was monitored by a gas monitor (Multi-Gas Monitors INNOVA 1316, LumaSense Technologies) throughout fermentation. When the CO₂ production rate reached the peak value, the automatic addition of nitrogen compounds (40% NH₄Cl and 60% amino acids) was activated to maintain the CO₂ production rate at the maximum value until the residual sugar become limiting. Residual nitrogen was determined by HPLC as described by Su et al. (2019b). The amount of nitrogen added to fermentation throughout this process was considered to be the nitrogen required to maintain a constant fermentation rate.

2.8 Genome sequencing and analysis of two *S. cerevisiae* strains.

Two of the selected strains, P17 and P20, were sequenced by Illumina HiSeq with 150 bp paired-ends reads. Trimmomatic v.0.33 (Bolger, Lohse, and Usadel 2014) was used to remove adapters, while Sickle (version 1.33, available at <https://github.com/najoshi/sickle>) was run to read trimming by quality. *De novo* genome assemblies were obtained using SPAdes v.3.1.0 (Bankevich et al. 2012). Annotation was done by transferring the annotation from the *S. cerevisiae* S288c reference strain (R64-2-1) to our assemblies using RATT (Otto et al. 2011). Then a *de novo* gene prediction with Augustus (Stanke and Waack 2003) was performed. Finally, both annotations were merged and manually corrected.

Phylogeny reconstruction was performed using the genome sequencing data from 90 representative strains of different *S. cerevisiae* lineages (Peter et al., 2018). In all, 1732 orthologous genes were translated into proteins, aligned with MAFFT v.7.2 (Kato and Standley, 2013) and backtranslated into codons. The concatenated codon alignment was carried out for maximum-likelihood phylogeny reconstruction using RAxML v.8.2 (Stamatakis, 2014) with 100 rapid bootstraps and the GTRGAMMA model.

To perform a chromosome copy number variation analysis, reads were mapped against the reference assembly of *S. cerevisiae* S288C (version R64-2-1) using bowtie2 v2.3.0 (Langmead and Salzberg, 2012). The position read depth was computed using an in-house Python script of a sliding-window method in which the mean mapping reads was calculated and represented in 10 kb windows along each chromosome.

A variant calling analysis was performed using FreeBayes v1.2. (Garrison and Marth 2012) with default parameters. Low quality SNPs were removed with vcftools (Danecek et al. 2011).

To analyse the differences between genomes of P17 and P20 at the coding sequence level, pair-wise amino acid substitutions were calculated using aligned pairs of orthologous proteins between P17 and P20. In this way, a total number of 6035 orthologs were found and analysed using an in-house Python script.

2.9 CRISPR/Cas9-mediated allele swapping

CRISPR/Cas9-mediated genomic editing was performed to explore the genetic basis for the differences in nitrogen requirement. CRISPR/Cas9 plasmid pWS174 (Addgene plasmid # 90961; <http://n2t.net/addgene:90961>; RRID: Addgene 90961) was used in our study. This plasmid contains *NatR* as a yeast marker, *KanR* as an *E. coli* marker and GFP, which is replaced with the designed guide RNA (gRNA). The 20 bp gRNA target was designed by following the instructions described in Benchling (<https://www.benchling.com>). A *BsmBI* restriction site (GACT overhang at the 5' and GTTT at the 3', and an additional TT included between the 5' overhang and the gRNA sequence) was added to the target sequence. The oligonucleotides were assembled into pWS174 as described by Shaw et al., (2019). They were firstly phosphorylated by T4 PNK, annealed and then assembled to the vector in a 10 µL *BsmBI* golden gate assembly using T4 DNA ligase (Thermo Fisher Scientific). The reaction mix was transformed into *E. coli* and plated on LB medium with kanamycin. In the successfully constructed plasmids, GFP should be replaced with gRNA. Therefore, the *E. coli* colonies without florescent were selected, and plasmids were extracted and verified by PCR and sequencing. The gRNA sequences and primers are shown in Table S2. To accomplish a precise genome modification, the homology directed repair (HRD) method was applied for double strand break (DSB) repair. Donor DNA was transformed into yeast cells together with CRISPR plasmids. Yeast transformation was carried out by the lithium acetate method (Gietz and

Woods, 2002). For each transformation, around 100-200 ng of CRISPR plasmid and more than 2 µg of donor DNA were used as illustrated by Shaw et al. (2019).

Two successive CRISPR events were carried out with the gene *GCN1* of P17 to achieve allele swapping as described by Biot-Pelletier et al. (2016). In the first step, the CRISPR-Cas 9 system introduced DSB in *GCN1* and the *KanMX4* cassette obtained from the pUG6 plasmid (Güldener et al, 1996) with 40 bp homology arms of the target was used as donor DNA to repair DSB. 628 bp of the target gene were replaced with *KanMX4*. Transformants were selected by double resistance of G418 and nourseothricin. Primers up- and down-stream of the *KanMX4* was designed and the insertion was verified by sequencing. In the second step, the new gRNA that targeted the inserted *KanMX4* was designed. CRISPR plasmid introduced the DSB in the *KanMX4* gene, and part of *GCN1* gene including the mutation sites (762 bp) from P20 was used as the donor DNA for DSB repairing. Transformants were selected by replicate plate from YPD-clonNAT to YPD-G418. The transformants without resistance to G418 were further confirmed by sequencing. The newly constructed strain was named P17m.

Laboratory-scale fermentations (80 mL, 28°C) were carried out with SM of 60 mg/L of YAN to check the fermentative ability of P17 modified with the P20-*GCN1* allele (P17m) in a nitrogen-limited environment. P17 and P20 were used as the control strains. Fermentations were monitored by measuring density throughout the fermentation process and were considered completed when density went below 998 g/L.

2.10 Statistical analysis

All the growth and fermentation experiments were carried out in triplicate. Parameters of fermentation kinetics was calculated by fitting the density data to the 4-parameter logistic model. The time needed to consume 5% (T5), 50% (T50) and 100% sugars (T100) was

extracted from the smoothed data. A one-way analysis of variance (ANOVA) was conducted with version 7.0 of the Statistica software package. The statistical level of significance was set at $p \leq 0.05$ with a Tukey HSD test.

3. Results

3.1 Growth performance of the different strains in SM at three concentrations

The 28 commercial wine yeasts showed different growth performances in SM with 60, 140 and 300 mg/L of YAN (Fig. 1). As expected, the strains grown in SM with 60 and 300 mg/L of YAN (SM60 and SM300) obtained the lowest and highest maximum growth rate, respectively. Surprisingly, the SM with 140 mg/L of YAN (SM140) did not promote significantly higher $\mu_{\max}$ than SM60, which suggests that higher nitrogen concentrations are needed to speed up cell duplication. The Area Under the Curve (AUC; Fig. S1) was also calculated, which represents the three main growth parameters: lag phase, $\mu_{\max}$ and maximum population (yield). The AUC values showed clear differences in all three nitrogen conditions, and SM140 had the highest value and SM60 had the lowest one. Thus the highest nitrogen content (SM300) promoted the highest growth rate, but prolonged the lag phase (Fig. S1).

On the Y-axis of Figure 1, strains were ranked from high to low by their $\mu_{\max}$ under each growth condition. Strains P11, P13 and P21 showed the best growth performance for all three conditions. On the contrary, strains P12, P16 and P24 were among the worst ones regardless of the nitrogen concentration. Most strains maintained their ranking position within three nitrogen concentrations. Some representative exceptions were P1 and P26, which the $\mu_{\max}$ showed lower ranking at a low nitrogen concentration, but their $\mu_{\max}$ substantially increased with SM300 and their ranking consequently went up on the Y-axis. Conversely, the ranking position of P2 and P18 dropped with increased nitrogen

concentrations. This indicates that a higher nitrogen concentration significantly influences the growth performance of these strains. P1 and P26 may need a higher amount of nitrogen to obtain better growth, whereas the strains P2 and P18 seemed to grow better than other tested strains when nitrogen concentration is limited.

3.2 Fermentation performance of different strains at three nitrogen concentrations

Similarly to the growth performances, the same wine yeast strains showed distinct fermentation behaviours with SM60, SM140 and SM300. An overlook of the maximum fermentation rate clearly demonstrated that a higher nitrogen concentration in the SM resulted in higher fermentation rates (Fig. 2). The maximum fermentation rate of each strain was ranked high to low on the Y-axis. Different ranking pictures were observed for each nitrogen concentration. Unlike that observed for the growth rate, the ranking positions of many strains changed at three nitrogen concentrations, which indicated the significant influence that nitrogen availability had on the fermentation rates. Several representative strains were selected. Strains P9, P11, P13 and P20 showed good fermentation performance with limited nitrogen. However, when carrying out the fermentations with higher nitrogen concentrations, fermentation rates were not as promoted as other strains, which resulted in lower rankings. Conversely, strains P12, P17 and P26 showed poor fermentation performance with SM60, but their fermentation rates dramatically increased with higher nitrogen concentrations, therefore, ranked higher on the Y-axis. In our study, strains P9, P11, P13, and P20 were considered as low nitrogen-demanding strains (LND) for their outstanding fermentation performance with low nitrogen concentration, and their average to poor performance with a high nitrogen concentration; *vice versa*, strains P12, P17 and P26 were considered as high nitrogen-demanding strains (HND) as their fermentation performance clearly enhanced only by a high nitrogen concentration.

3.3 Laboratory-scale fermentation to confirm the selected strains

The fermentation performances of seven strains selected as high or low nitrogen-demanding strains were further evaluated by carrying out microvinification in 80 mL of SM with 60, 140 and 300 mg/L of YAN. Fermentation kinetics were determined more precisely by measuring density reduction. Strains P13 and P20, which were selected as low nitrogen-demanding strains, finished fermentations (T100) in a significantly shorter time in SM60 than the strains selected as high nitrogen-demanding P17 and P26 (Fig. 3). With SM300, P13, P17, P20 and P26 finished fermentation almost at the same time. Strains P9 and P12 did not show the same features as observed in the fermentations done with 10 mL of SM. Depending on the results obtained with the 10 mL fermentation, P12 was classified as high nitrogen-demanding. However, in 80 mL of SM, it was the first strain to finish fermentation with SM60, and the last strain to finish the fermentation with SM300, which correspond to the features of a low nitrogen-demanding strain. Strain P9 required a longer time to finish fermentations at all three nitrogen concentrations. Strain P11 displayed an average behaviour for all three conditions. According to our results, candidates were narrowed down to P12, P13 and P20 as LND strains, and to P17 and P26 as HND strains.

3.4 Competition fermentation

Competition fermentations were carried out with pairs of strains under the nitrogen-limited (SM60) and excess nitrogen (SM300) conditions. Five competition pairs were analysed: P17(HND) vs. P20(LND), P17(HND) vs. P12(LND), P17(HND) vs. P13(LND), P26(HND) vs. P20(LND) and P26(HND) vs. P12(LND). The percentage of each strain was monitored during fermentation (Fig. 4). In four of the five analysed pairs, one strain always outcompeted the another one regardless of the nitrogen concentration in SM: P13(LND) outcompeted P17(HND); P26(HND) outcompeted P12(LND);

P20(LND) outcompeted P26(HND); P17 (HND) outcompeted P12 (LND). These results suggest that the outcome of the competition between these pair of strains was not dependent on nitrogen concentration. Conversely, pair P17(HND) vs. P20(LND) exhibited different competition behaviours. When fermentation was carried out with SM60, the percentage of P20 gradually increased from 50% to 62% at the end of fermentation, whereas the percentage of P17 dropped to around 37%. P17 showed a growth advantage with SM300, and its percentage increased to 64% at the end of fermentation, which left only 36% of P20 in fermentation. Nitrogen concentration clearly determined the dominant population in fermentation. This competition pair perfectly matched our assumption, and further confirmed that P17 was LND and P20 was HND.

3.5 Influence of nitrogen concentration on biomass production

Nitrogen availability significantly influences yeast biomass production. A continuous culture with an increased nitrogen concentration was carried out to determine the influence of nitrogen concentration on biomass production in the exponential fermentation stage. The selected HND P17 and LND P20 strains were evaluated. Overall for both strains, biomass production increased with nitrogen concentration until YAN reached 140 mg/L (Fig. 5A). Then the biomass remained stable with a nitrogen concentration higher than 140 mg/L. Interestingly when SM with 60 and 80 mg/L of YAN was supplied to the continuous culture, the LND strain P20 produced more biomass than P17. When YAN exceeded 100 mg/L, the biomass production by HND strain P17 rapidly increased and was significantly higher than that of P20. When the nitrogen concentration continued to increase to 140 mg/L of YAN, both strains reached their maximum carrying capacity. SM with more than 140 mg/L of YAN triggered flocculation formation with P17, which consequently resulted in a lower unstable biomass production. The biomass formation by P20 remained stable with SM from 140 to 200 mg/L of YAN. By way of

conclusion, when the nitrogen concentration was limited (SM60 and SM80), the LND strain produced more biomass than the HND strain. The HND strain started to produce more biomass than LND with SM100. Biomass formation stopped increasing when the nitrogen concentration reached 140 mg/L, which can be considered the nitrogen-limiting concentration to reach the maximum biomass.

3.6 Determining yeast nitrogen requirement by constant rate fermentation

Constant rate fermentation was carried out to evaluate the amount of nitrogen required by yeast strains to maintain the fermentation rate (CO₂ production) at the same level throughout fermentation. In a normal batch fermentation of SM140, P20 required some 15 h less than P17 to complete fermentation (Fig. 5B). When the fermentation rate was controlled and remained constant by supplying nitrogen to SM, the two strains finished fermentation almost at the same time (Fig. 5C). This indicates that the availability of nitrogen sources could be the limiting factor for the differences found in the fermentation times between two strains. Nitrogen sources were added in the form of a mixture containing amino acids and ammonium. The result showed that P17 required twice as much nitrogen as P20 to maintain a constant fermentation rate (109.1 vs. 48.1 mg/L YAN; Fig. 5D).

3.7 Genome sequencing and comparison between LND and HND strains

The genomes of P17 and P20 were sequenced and analysed, and 6161 genes were annotated for P17, as were 6145 genes for P20. The sequencing data are available at NCBI database under bioproject accession number PRJNA625869. The phylogenetic analysis using representative genomes of the different described *S. cerevisiae* lineages (Peter et al., 2018) (Table S3) showed that strains P17 and P20 were grouped into the Wine/European clade (Fig. 6).

The chromosome copy number analysis did not show any signal of aneuploidy in either of the two strains. Interestingly, the variant calling analysis evidenced that P17 was completely homozygous along the genome, but P20 presented higher heterozygosity levels with some patterns of loss of heterozygosity in specific chromosome regions (Fig. 7). Position read depth is shown in Figure S2. Another major difference between the two strains was that strain P20 had a region of 35 genes in chromosome XV duplicated. The genes contained in this region are shown in Table S4. Neither gene ontology (GO) nor pathway enrichment was found for this set of genes.

The proportions of amino acid substitutions were calculated between the pair-wise orthologous proteins from the annotation of genomes P17 and P20 (Table S5). Higher values indicate a higher proportion of amino acid positions in which amino acid residues differ compared to the orthologous aligned proteins of P17 and P20. The genes encoding the proteins with the highest values were: YLR255C, a protein of unknown function, but one that is conserved across *S. cerevisiae* strains; *VPS61*, a dubious ORF whose deletion causes a vacuolar protein sorting defect (Fisk et al., 2006); *EHD3*, a 3-hydroxyisobutyryl-CoA hydrolase whose deletion affects fluid-phase endocytosis (Wiederkehr et al., 2001) and is related to the proteome of *S. cerevisiae* mitochondria (Sickmann et al., 2003).

3.8 CRISPR/Cas9-mediated allele swapping and the gene function analysis

Of all the genes showing amino acid divergence, *GCN1* was identified as our gene of interest. This gene has been previously connected to nitrogen metabolism regulation (Brice et al., 2014b) and we considered that it was worth evaluating the different alleles in both strains. This gene is a positive regulator of the Gcn2p kinase and forms a complex with Gcn20p (Garcia-Barrio, et al., 2000; Kubota et al., 2001). It is involved in nitrogen sensing and signalling in response to nitrogen availability (Hinnebusch, 2005). Four non-synonymous mutations were found between *GCN1* of P17 and P20 (Fig. 8A). Allele

swapping was performed to investigate the influence of mutations on nitrogen requirement. As *GCN1* is a relatively large gene of 8kb, it is difficult to make modifications with the entire gene. Therefore, a 762-bp piece, including three mutation points at amino acid positions 377, 556 and 585 in P17, was replaced with the allele of P20 by the CRISPR/Cas9-mediated genomic editing method. Fermentations were carried out with P17, P20 and modified strain P17m in SM60. SM60 is nitrogen-limited medium and our previous data showed large differences in fermentation performance in both strains under this condition. However, the result demonstrated that the fermentation behaviour of P17m was similar to that of P17 (Fig. 8B). No significant differences in T5, T50 and T100 were observed between P17 and P17m, unlike those between P17m and P20 (Fig. 8C). Partial modification of *GCN1* gene by introducing three out of four mutation points of the allele showing a better fitness (P20) did not improve the fermentation performance of the strain that was more affected by nitrogen limitation (P17).

4. Discussion

Nitrogen concentration is one of the most important nutrients for yeast that has a substantial impact on the wine fermentation process. The nitrogen requirement of yeast is highly strain-dependent. Understanding the nitrogen demand of yeast strains is of significant importance for a successful winemaking process. A set of *S. cerevisiae* wine strains was herein assessed for their growth and fermentation activities in SMs with different nitrogen concentrations. HND and LND strains were selected and the corresponding genetic evidence was explored.

Our first aim was to assess the impact of nitrogen concentration on yeast growth and fermentation activity in a set of 28 *S. cerevisiae* industrial wine yeast strains. In growth behaviour terms, we focused on the influence of nitrogen on the maximum growth rate

($\mu_{\max}$), lag phase and the maximum OD ($OD_{\max}$). AUC was used as a complex parameter summarising the all three independent variables. Surprisingly both $\mu_{\max}$ and AUC did not show any direct correlation with nitrogen concentration. The maximum growth rate increased only with the highest concentration, whereas the highest AUC value was obtained for SM140. In a similar study, Gutierrez et al. (2012) reported that the nitrogen-limiting concentration required to reach the $\mu_{\max}$ value was much lower than the nitrogen concentration to obtain the maximum area. This perfectly matches our results when SM300 was excluded (this high nitrogen concentration was not tested in Gutierrez et al. (2012)). In any case, this indicates that SM140 did increase the final cell population and the lag phase time was relatively shorter, but the concentration was not high enough to improve the maximum growth rate. SM300 promoted the maximum growth rate, but the highest nitrogen concentration may have some inhibiting effect for yeast to start growing because a much longer lag phase was observed (Fig. S1). As expected, we observed a positive correlation between $\mu_{\max}$ and $OD_{\max}$ and a negative correlation between $OD_{\max}$ and the lag phase time regardless of nitrogen concentration (Fig S3). However, both the positive and negative correlations were stronger for SM140 than for SM300. Ibstedt et al. (2015), who exhaustively evaluated the lag, rate and efficiency of *S. cerevisiae* in a wide variety of nitrogen-limited environments, concluded that growth components were well correlated under nitrogen restriction and pointed out a concerted evolution of yeast nitrogen use.

When we compared the growth and fermentation performance among strains at the different nitrogen concentrations, we observed that nitrogen concentration clearly determined the fermentation fitness of most strains, as seen from the changing ranking orders under different conditions. These changes in strain ranking were not so evident for growth performance. The yeast fermentation rate can be influenced by either glycolytic

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505 flux per cell or the yeast population. Several previous studies have concluded that in
506 nitrogen-deficient fermentation, the fermentation rate is driven by yeast cell population
507 rather than by specific flux per cell (Albertin et al., 2011; Valera et al., 2004). However,
508 Gutiérrez et al. (2012) provided evidence for the non-correlation between biomass
509 production and nitrogen requirement. Similarly, Barbosa et al. (2014) compared growth
510 and fermentation performance at two different concentrations, and concluded that the
511 highest fermentation rates were observed under high nitrogen conditions due to the higher
512 final yeast cell biomass. However, at the same nitrogen concentration when comparing
513 yeast strains, the same correlation between the yeast cell final biomass and better
514 fermentative performance was not established.

515 The first screening based on miniaturised systems for determining the growth and
516 fermentation activity of the different strains allowed us to select several strains to be
517 categorized as HND and LND. Pair-wise combinations of strains (LND vs. HND) were
518 used to ferment SMs with a limiting (SM60) and non-limiting (SM300) nitrogen
519 concentration to determine the competitiveness of each strain according to nitrogen
520 availability. During the fermentation process many species and strains are competing for
521 the resources and the absolute numerical presence, and persistence over time, of these
522 species/strains are affected by parameters such as temperature, sulphur dioxide (SO₂), pH,
523 osmotic pressure, oxygen and nutrient availability (Bagheri et al., 2020; Garcia-Rios et
524 al., 2014; Pérez-Torrado et al., 2017; Su et al., 2019b). In our experiment of competitions,
525 only the fitness of one pair of strains was clearly determined by nitrogen concentration.
526 In the other strain combinations, other abiotic or biotic factors had to determine the
527 capacity to outcompete other strains. So the fermentation tests provided us with valuable
528 information to select the best candidates as LND and HND strains.

After selecting the most promising candidates with different nitrogen requirements, we assessed the influence of increasing nitrogen concentration on biomass production and fermentation rate in a more controlled and accurate system. For biomass production, we used different continuous cultures with increasing nitrogen concentrations in the feed medium, which ensured a strict control of the fermentation conditions (Vázquez-Lima et al., 2014). The results clearly showed that the LND strain was more efficient in producing biomass at low nitrogen concentrations whereas it was the other way around at a high nitrogen concentration. We also determined the measurement of the nitrogen supply required to maintain the fermentation rate constant in the stationary phase (constant rate fermentation method). This method has been previously proposed to quantify the nitrogen needs of yeast strains (Julien et al. 2000; Manginot et al. 1997; Manginot et al. 1998). As expected, strain HND needed the addition of 2-fold nitrogen to keep a constant fermentation rate. When combining the results of biomass production and fermentation rate in SM140, we concluded that the HND strain yielded a higher biomass, but needed more available nitrogen to keep a constant fermentation rate in the stationary phase. As previously mentioned, these data revealed a possible decoupling between the biomass yield and the fermentation rate.

Many questions are undisclosed about what determines the ability of strains to carry out fermentation in low nitrogen-containing media and the molecular mechanisms underlying these differences. Some authors conclude that these differences in nitrogen demand correlate with the nitrogen uptake rate (Gutiérrez et al., 2012; Jara et al., 2014), nitrogen sensing (Brice et al., 2014a; Tesnière et al., 2015; Kessi-Pérez et al., 2020) or the nitrogen recycling system, through autophagy and the ubiquitin–proteasome-associated system (Piggott et al., 2011; Walker et al., 2014). To explore the genetic background that supports the differences in nitrogen requirements, the selected LND and HND strains were whole-

genome sequenced and analysed. One of the striking results disclosed that P17 is completely homozygous as most cases industrial strains are heterozygous (Gallone et al., 2018; Peter et al., 2018). Industrial strains tend to display higher levels heterozygosity due to their facultative asexual reproduction, while homozygous strains are efficient sporulators (Magwene et al., 2011). At times of nutritional stress, such as carbon or nitrogen starvation, diploid yeasts cells tend to undergo the sporulation process. Cells were observed during fermentation to check whether the sporulation of P17 at a low nitrogen concentration was the reason for a slower fermentation speed. However, the result did not support this hypothesis because no strain sporulated during the fermentation of SM60 (data not shown). It is not clear whether the homozygosity of P17 had any impact on its nitrogen requirement. However, it shed light on some possible future explorations.

As many of the genes showed different amino acid position between P17 and P20, determining which genes were responsible for nitrogen requirement differences was complicated. Regarding the genes with the highest amino acid divergences, most were related to the nitrogen recycling system, which underscores the importance of autophagy and the proteasome system for yeast fitness under wine fermentation conditions. However, Brice et al. (2014b) carried out the QTL analysis with a population of F2 segregants generated from a cross between one HND and one LND, to find that most genes were involved in sensing and signalling nitrogen. These authors pointed out that *GCN1* was an allele with a direct effect on the fermentation rate. *GCN1* is known to be a positive regulator of general amino acid control (GAAC), and one required for *GCN2* activity, which triggers the preferential translation of the *GCN4* transcription factor which, in turn, controls the expression of the genes encoding the proteins involved in amino acid biosynthesis (Hinnebusch, 2005). In our study, four non-synonymous differences between P17 and P20 were found in *GCN1*. However, these SNPs differed from the

mutation positions described by Brice et al. (2014b). In their study, the *GCN1* allele from the LND strain showed a negative effect on the fermentation rate. However, the allele swapping between P20 and P17 did not significantly influence fermentation activities under the nitrogen-limited condition. As illustrated in many studies and reviews (Forsberg and Ljungdahl, 2001; Ljungdahl and Daignan-Fornier, 2012; Hofman-Bang, 1999; Beltran et al. 2004; Hinnebusch and Natarajan, 2002; Hinnebusch, 2005; Zhang et al., 2018), nitrogen metabolism in *S. cerevisiae* is regulated by several complicated and sophisticated systems. Thus the nitrogen requirement of different yeast strains can be expected to result from the collaboration of a group or many groups of genes. A further in-depth analysis with more LND and HND strains should be conducted to decipher the general genetic pattern that determines yeast nitrogen requirements.

5. Conclusions

This study combined different methods to phenotypically explore the nitrogen requirement of a set of commercial *S. cerevisiae* strains. LND and HND strains were selected based on the alteration in growth and fermentation behaviour at different nitrogen concentrations. Their nitrogen requirements were further verified by competition fermentation, biomass production and constant rate fermentation at different nitrogen concentrations. The genome information of these two strains revealed large differences in heterozygosity terms and in the amino acid substitutions between orthologous proteins, which stresses the importance of the cell recycling system under nitrogen restriction conditions. The allele swapping of the *GCN1* gene from the LND strain to the HND strain did not show any significant impact on fermentation behaviour in nitrogen-limited fermentation. Our study provides a guideline for the comprehensive analysis of nitrogen requirements by yeast during fermentation. Further genetic analyses are still required to gain a better understanding of this complex yeast feature.

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Figure legends

Figure 1. Maximum growth rate ($\mu_{\max}$) of 28 strains in SM60 (A), SM140 (B) and SM300 (C). Box plot summaries the $\mu_{\max}$ of all the strains at three nitrogen concentrations (D).

Figure 2. Maximum fermentation rate ($V_{\max}$) of 29 strains in SM60 (A), SM140 (B) and SM300 (C). The selected high nitrogen-demanding strains are marked in red, and the low nitrogen-demanding strains are marked in blue. Box plot summaries the $V_{\max}$ of all the strains at three nitrogen concentrations (D).

Figure 3. Time (hours) required to consume the 5% (T5), 50% (T50) and 100% (T100) of the sugar content in SM60, SM140 and SM300.

Figure 4. The percentage of each strain during fermentation within each competition pair of strains HND and LHD in SM60 and SM300.

Figure 5. A. Biomass production of P17 (HND) and P20 (LND) in a chemostat with increasing nitrogen concentrations. *indicates a significant difference between two strains (HSD Tukey test $p < 0.05$). (B) CO_2 production during batch fermentation of strain P17 (HND) and P20 (LND). (C) CO_2 production of P17 (HND) and P20 (LND) during constant rate fermentation as consequence of nitrogen addition. (D) Amount of nitrogen added during constant rate fermentation.

Figure 6. Phylogenetic tree with 90 strains from different *S. cerevisiae* lineages.

Figure 7. Herozygotic positions along chromosomes P17 (blue) and P20 (orange).

Figure 8. (A) Mutation positions of *GCN1* between P17 and P20. (B) Fermentation kinetics in SM60 with modified strain P17m. (C) T5, T50 and T100 of fermentation in SM60. Different letters above bars indicate significant differences (HSD; Tukey test $p < 0.05$).

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878 **Supplementary Figure 1.** Ranking of the AUC value of the different strains with SM60
879 (A), SM140 (B) and SM300 (C). Box plot summarises AUC (D), Lag phase (E) and
880 OD_{max} (F) of all the strains at three nitrogen concentrations.

881 **Supplementary Figure 2.** Position read depth along P17 (blue) and P20 (orange)
882 chromosomes.

883 **Supplementary Figure 3.** Pearson correlation analysis between the maximum growth
884 rate ($\mu_{\max}$), the maximum biomass yield (OD_{max}) and the lag phase time (Lag) for each
885 nitrogen concentration. Linear regression (black line) is displayed. The correlation
886 coefficient (R) is also shown.

887

Figure 1

[Click here to access/download;Figure;Fig. 1.tif](#)

Figure 2

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Figure 3

Figure 4

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Figure 5

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Figure 6

GCN1 (8019bp)

A Non-synonymous mutations

Position nucleotide	Position AA	P17	P20
1129	377	L	F
1668	556	A	S
1755	585	I	M
4145	1382	P	L

B

C

Figure S3

[Click here to access/download;Figure;Fig. S3.tif](#)

Table S1. Strains used in this study

Code Name	Commercial Name
P1	Lalvin®ICVD254
P2	Uvaferm®WAM
P3	Lalvin®ICVD80
P4	Lalvin® Rhone2056
P5	Lalvin®ICVGRE
P6	Lalvin®EC1118
P7	Lalvin®ICVD47
P8	Uvaferm®CEG
P9	Lalvin®Rhone2323
P10	Uvaferm®BC
P11	Uvaferm®VRB
P12	Uvaferm®43
P13	CrossEvolution®
P14	Lalvin®71B
P15	Lalvin®BM45
P16	Enoferm®M1
P17	Enoferm®M2
P18	Uvaferm®BDX
P19	Uvaferm®CM
P20	Lalvin®ICVD21
P21	Lalvin®Rhone2226
P22	Lalvin®CY3079
P23	*
P24	*
P25	*
P26	*
P27	*
P28	T73

*The commercial names are not available for these strains, since they are still under development.

Table S2. Primers used in this work

Primer	Sequence 5'-3'	purpose
galKanMX F	AAAATTGTTAATATACCTCTATACT TTAACGTCAAGGAGAAAAAACTAT Acagctgaagcttcgtacgc	To amplify <i>KanMX4</i> cassette as donor DNA to replace <i>GAL1</i>
galKanMX R	ATTATCATAACAATCATTTATTAAGT AGTTGAAGCATGTATGAACTATAA Agcataggccactagtggatc	To amplify <i>KanMX4</i> cassette as donor DNA to replace <i>GAL1</i>
Galcp-F	CGTTCCTGAAACGCAGATG	To check the deletion of <i>GAL1</i>
Galcp-R	CTCCTCGCGCTTGTCTACTAA	To check the deletion of <i>GAL1</i>
gcnKanMX donor F	GGTAGTTAGATCCGTCTCGCTTCAG TCTATGATAATCTTAcagctgaagcttcgtac gc	To amplify KanMX4 cassette as donor DNA to replace part of <i>GCN1</i>
gcnKanMX donor R	TCTTGGACACGCATTCTCCTTTCAA TTGCATCAATCACGCgcataggccactagt gatc	To amplify KanMX4 cassette as donor DNA replace part of <i>GCN1</i>
GCN1 gRNA F	gactttATCATACATTATCAGACTCA	gRNA for CRISPR targeted at <i>GCN1</i>
GCN1 gRNA R	aaacTGAGTCTGATAATGTATGATaa	gRNA for CRISPR targeted at <i>GCN1</i>
GCN1 gRNA F2	gactttTGTTTTGCCGGGGATCGCAG	gRNA for CRISPR targeted at <i>KanMX4</i>
GCN1 gRNA R2	aaacCTGCGATCCCCGGCAAACAAa	gRNA for CRISPR targeted at <i>KanMX4</i>
K2	GGGACAATTCAACGCGTCTG	Internal primer to check the integration of KanMX4 cassette
GCN1 swap F	GCCTTTGCTTCCTCGAAACT	To amplify the GCN1 allele from P20
GCN1 swap R	CCAGTAGTACAGAAGTGACA	To amplify the GCN1 allele from P20
Crispr cp F	ATCAACAACAGAGGACATAT	To check gRNA integration and sequencing
Crispr cp R	ATCCTGCACTCATCTACTAC	To check gRNA integration and sequencing

GCN1 seq F	GCAACCAGCTCTGCACTCCGTT	To check the integration by sequencing
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GCN1 seq R	AGCTGGATCAAGCCTTGACGT	To check the integration by sequencing
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Table S3. Genomes used for phy

Isolate name	Standardized name
Enorferm M2	P17
Lalvin ICVD21	P20
HE020	BCQ
CEY651	BNB
CEY650	BNA
CEY652	BNC
CLIB227	ASH
DBVPG6693	BSI
CBS1230	AQT
CBS2165a	AAC
AY529516	ANN
MTF2555	CQM
MTF2553	CQK
MTF2549	CQF
FTPW3	CPT
Dji2-2A(a)	CFA
FTPW32	CQA
YPS1009_b	ADF
UWOPS03-429.1	BMA
UWOPS03-433.3	BMB
UWOPS03-459.1	BMC
YJM1447	SACE_YCY
CECT10171-5B	CDT
1560	CPG
UCD_09-448	CGD
DBVPG6302	BRK
CLQCA_20-156	CCC
CLQCA_20-221	CCE
CLQCA_20-246	CCF
CLQCA_20-259	CCG
YPS163_1b	ACD
YPS129	ANC
YPS143	ANI
YPS128	AKN
CBS1593	ARI
S11F3-6B	CCT
S8BM-32-4D(a)	CDA
CBS1594	AGR
RIB1014	CMB
RIB1016	CMD
RIB1017	CME
RIB6005	CMK
BMQ557	CGL
IFO_0289:4-3(b)	CEV
SGB1	CGN
TayTa	CGG
SA.1.5.	CNK
SA.9.4.BR2	CNP
SM.8.8.CVR1	CNI

TableSx_phyloStrains

SM.9.4.BL2	BVG
sample 33	CLD
EXF-7197	BFP
ZP_567	BTG
sample 40	CLB
EXF-7145	BFN
EXF-5871	BFH
CLIB552	BGD
CLQCA_13-023	ALD
N26-1-10:7-5(a)	CES
CBS4454	AEN
CBS4456	AFL
N34:2-4(a)	CER
CBS1398	ARE
6.2_WLP570	CFF
DBVPG6590	BRM
CLIB272_2	AAQ
CBS1236-a	AAL
CCY_21-4-97	BBD
CBS1252	AFF
646-3B	CHI
RB3-7Sc2	CRA
DBVPG1126	BIQ
D-1	CAH
AGME_5I	CRI
DBVPG1708	BNL
L-319	CRH
EXF-4126	BEQ
A-14	CBA
DBVPG1626	BLH
DBVPG4651	BRA
DBVPG1656	BLM
DBVPG1976	BPV
DBVPG1339	BKC
DBVPG1975	BLS
DBVPG3022	BLV
DBVPG1712	BNN
DBVPG1595	BKS
DBVPG1661	BLP
Lib73	CHF
L-958	BSR

References

Peter, Jackson, Matteo De Chiara, Anr

TableSx_phyloStrains

Phylogeny reconstruction

Isolation	Ecological origins
Wine	Wine
Wine	Wine
Human	Human
Fruits	Fruit
Agouti paca (RO)	Nature
Fruits	Fruit
Beer holland	Beer
Beer	Beer
Beer	Beer
Brewers	Beer
Cocoa bean fermentation	Fermentation
Cocoa bean fermentation	Fermentation
Cocoa bean fermentation	Fermentation
Cocoa bean fermentation	Fermentation
Palm wine	Palm wine
Palm wine	Palm wine
Palm wine	Palm wine
Exudate from Quercus sp.	Tree
Nectar, bertam palm	Tree
Nectar, bertam palm	Tree
Nectar, bertam palm	Tree
Bertam Palm	Tree
Larvae of Dacus oleae	Insect
Manzanilla-Alorena, olive (Noe), 2003	Nature
Olives from Middle of season 1. on RBCA 11.25.09 Streaked onto PDA 11/30/09	Fruit
Alpechin (waste from olive oil production)	Industrial
Flower (Gesneriaceae sp.)	Flower
Flower from Heliconia sp.	Flower
Termite mound	Insect
Decaying fruit	Fruit
Exudate from Quercus sp.	Tree
Flux from Quercus alba	Tree
Soil beneath(q.rubra)	Soil
Soil beneath Quercus alba	Soil
Fermenting cacao	Fermentation
Phloem sap of Caryota urens	Tree
Phloem sap of Caryota urens	Tree
Plant	Nature
Sake	Sake
Sake	Sake
Sake	Sake
Sake	Sake
Unknown	Unknown
Moromi of Chinese wine kaoliangchiu	Distillery
Rice fermentation starter culture	Fermentation
Unknown	Unknown
Bioethanol	Bioethanol
Bioethanol	Bioethanol
Bioethanol	Bioethanol

TableSx_phyloStrains

Bioethanol	Bioethanol
Flower	Flower
Quercus sp.	Tree
Quercus pyrenaica	Tree
Tree leaves	Tree
Quercus robur	Tree
Homemade cheese	Dairy
Dairy, cheese (camembert)	Dairy
Wax on rock surface	Nature
Maize dough	Bakery
Kaffir beer	Beer
Kaffir beer	Beer
Maize dough	Bakery
Leaf of Eucalyptus sp.	Tree
Carlsberg Beer	Beer
Alcohol production tank	Distillery
Beer	Beer
Bakery	Bakery
Fish pond water	Water
Bakery	Bakery
Bakery	Bakery
Wine	Wine
Grape must	Wine
Wine conserved in amphora	Wine
Wine	Wine
Soil	Soil
Wine	Wine
Dry wine-berry selection	Wine
Wine conserved in amphora	Wine
Grape must	Wine
Surface of Tuber magnatum	Nature
Grape must treated with sulfur dioxide	Wine
Wine	Wine
Grape must	Wine
Wine	Wine
Grape must	Wine
Grape must	Wine
Grape must	Wine
Grape must	Wine
Fermenting grape must (red wine)	Wine
Wine	Wine

ie Friedrich, Jia-Xing Yue, David Pflieger, Anders Bergström, Anastasie Sigwalt, et al. 2018. “C

TableSx_phyloStrains

Geographical origins	Ploidy	Aneuploidies	Zygosity
NA	2	euploid	homozygous
NA	2	euploid	heterozygous
French Guiana	2	euploid	heterozygous
French Guiana	2	euploid	heterozygous
French Guiana	2	euploid	heterozygous
French Guiana	2	euploid	heterozygous
Netherlands	4	aneu;-1*1;-1*5;-1*7;-1*8;+1*9;-1*14;+1*16;	heterozygous
Belgium	4	aneu;+1*1;+1*9;-1*14;	heterozygous
Belgium	3	aneu;+1*6;	heterozygous
England	2	euploid	heterozygous
Ghana	2	euploid	heterozygous
West Africa	2	euploid	heterozygous
West Africa	2	euploid	heterozygous
West Africa	2	euploid	heterozygous
Burkina Faso	2	aneu;+1*9;	heterozygous
Djibouti	2	euploid	homozygous
Burkina Faso	2	euploid	heterozygous
USA	1	euploid	homozygous
Malaysia	2	euploid	homozygous
Malaysia	2	euploid	homozygous
Malaysia	2	euploid	homozygous
Malaysia	2	euploid	homozygous
Spain	2	euploid	homozygous
Aceituna, Spain	2	euploid	homozygous
Davis, CA, UCD	2	euploid	homozygous
Spain	2	euploid	homozygous
Yasuni, Orellana	2	euploid	homozygous
Yasuni, Orellana	2	euploid	homozygous
Yasuni, Orellana	2	euploid	homozygous
Yasuni, Orellana	2	euploid	homozygous
USA	1	euploid	homozygous
Pennsylvania, USA	2	euploid	homozygous
Pennsylvania, USA	2	euploid	homozygous
Pennsylvania, USA	2	euploid	homozygous
Java, Indonesia	2	aneu;+2*1;+1*2;	heterozygous
Sri Lanka	2	euploid	homozygous
Sri Lanka	1	euploid	homozygous
NA	1	euploid	homozygous
Japan	2	aneu;+1*11;	heterozygous
Japan	2	aneu;+1*3;+1*9;	heterozygous
Japan	2	aneu;+1*9;	heterozygous
Japan	2	euploid	heterozygous
Hai Phong, North Vietnam	2	euploid	heterozygous
China	1	euploid	homozygous
Saigon, South Vietnam	2	euploid	heterozygous
Long An, South Vietnam	2	euploid	heterozygous
Brazil	2	euploid	heterozygous
Brazil	2	euploid	heterozygous
Brazil	2	euploid	heterozygous

TableSx_phyloStrains

Brazil	2	euploid	heterozygous
Bordeaux, France	2	aneu;+2*3;	homozygous
Montenegro	2	euploid	homozygous
Portugal, Castelo de Vide,	2	euploid	homozygous
Bordeaux, France	2	euploid	homozygous
Serbia	2	aneu;+1*10;	heterozygous
Slovenia	2	euploid	heterozygous
Normandy, France	2	euploid	heterozygous
Bolivar, Ecuador	2	euploid	heterozygous
Ghana	2	aneu;-1*1;	homozygous
South Africa	2	aneu;+1*1;+1*3;+1*4;	heterozygous
South Africa	1	aneu;+1*8;	homozygous
Ghana	2	euploid	homozygous
NA	2	aneu;+1*2;+1*3;+1*6;+4*9;+1*12;+1*14;+1*15;	heterozygous
Belgium	2	euploid	heterozygous
Brazil	1	euploid	homozygous
USA	1	euploid	homozygous
France	2	aneu;-1*6;	heterozygous
Jakubov, Slovakia	2	aneu;+1*8;	heterozygous
France	1	euploid	homozygous
USA	2	euploid	heterozygous
Italy	2	aneu;-1*1;	heterozygous
Aquila, Italy	1	aneu;+1*3;	homozygous
Georgia	2	aneu;+1*4;	heterozygous
Italy	2	aneu;+1*4;+1*8;+1*15;	homozygous
Ultura, Sweden	2	euploid	heterozygous
Chile	2	euploid	heterozygous
Ljubljana, Slovenia	2	euploid	heterozygous
Georgia	2	euploid	heterozygous
La Mancha, Spain	2	euploid	homozygous
Italy	2	euploid	homozygous
Los Campillos, La Mancha, Spain	2	euploid	homozygous
Slovakia	2	euploid	homozygous
Netherlands	2	euploid	heterozygous
Greece	2	euploid	heterozygous
Squinzano, Italy	2	euploid	homozygous
Pedrejon, Rioja, Spain	2	euploid	homozygous
La Mancha, Spain	2	euploid	heterozygous
Los Polos, La Mancha, Spain	2	euploid	heterozygous
Lebanon	2	euploid	heterozygous
Mendoza area, Argentina	2	euploid	heterozygous

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Strains according to Peter et al.	Reference
1. Wine/European	This study
1. Wine/European	This study
10. French Guiana human	Peter et al., 2018
10. French Guiana human	Peter et al., 2018
10. French Guiana human	Peter et al., 2018
10. French Guiana human	Peter et al., 2018
11. Ale beer	Peter et al., 2018
11. Ale beer	Peter et al., 2018
11. Ale beer	Peter et al., 2018
11. Ale beer	Peter et al., 2018
12. West African cocoa	Peter et al., 2018
12. West African cocoa	Peter et al., 2018
12. West African cocoa	Peter et al., 2018
12. West African cocoa	Peter et al., 2018
13. African palm wine	Peter et al., 2018
13. African palm wine	Peter et al., 2018
13. African palm wine	Peter et al., 2018
13. African palm wine	Peter et al., 2018
19. Malaysian	Peter et al., 2018
19. Malaysian	Peter et al., 2018
19. Malaysian	Peter et al., 2018
19. Malaysian	Peter et al., 2018
2. Alpechin	Peter et al., 2018
2. Alpechin	Peter et al., 2018
2. Alpechin	Peter et al., 2018
2. Alpechin	Peter et al., 2018
21. Ecuadorean	Peter et al., 2018
21. Ecuadorean	Peter et al., 2018
21. Ecuadorean	Peter et al., 2018
21. Ecuadorean	Peter et al., 2018
23. North American oak	Peter et al., 2018
23. North American oak	Peter et al., 2018
23. North American oak	Peter et al., 2018
23. North American oak	Peter et al., 2018
24. Asian islands	Peter et al., 2018
24. Asian islands	Peter et al., 2018
24. Asian islands	Peter et al., 2018
24. Asian islands	Peter et al., 2018
25. Sake	Peter et al., 2018
25. Sake	Peter et al., 2018
25. Sake	Peter et al., 2018
25. Sake	Peter et al., 2018
26. Asian fermentation	Peter et al., 2018
26. Asian fermentation	Peter et al., 2018
26. Asian fermentation	Peter et al., 2018
26. Asian fermentation	Peter et al., 2018
3. Brazilian bioethanol	Peter et al., 2018
3. Brazilian bioethanol	Peter et al., 2018
3. Brazilian bioethanol	Peter et al., 2018

TableSx_phyloStrains

[illegible]

thing Group: 339–44. doi:10.1038/s41586-018-0030-5.

Table S4. Genes in the d

Systematic gene name	Standard gene name
YOR138C	RUP1
YOR140W	SFL1
YOR141C	ARP8
YOR142W	LSC1
YOR143C	THI80
YOR144C	ELG1
YOR145C	PN01
YOR147W	MDM32
YOR148C	SPP2
YOR149C	SMP3
YOR150W	MRPL23
YOR151C	RPB2
YOR152C	ATG40
YOR153W	PDR5
YOR154W	SLP1
YOR155C	ISN1
YOR156C	NFI1
YOR157C	PUP1
YOR158W	PET123
YOR159C	SME1
YOR160W	MTR10
YOR161C	PNS1
YOR162C	YRR1
YOR163W	DDP1
YOR164C	GET4
YOR165W	SEY1
YOR166C	SWT1
YOR167C	RPS28A
YOR168W	GLN4
YOR171C	LCB4
YOR172W	YRM1
YOR173W	DCS2
YOR174W	MED4
YOR175C	ALE1
YOR176W	HEM15

uplicated region of chromosome XV of P20

Description

Rsp5-Ubp2 interacting Protein
Suppressor gene for Flocculation
Actin-Related Protein
Ligase of Succinyl-CoA
THIamine metabolism
Enhanced Level of Genomic instability
Partner of NOB1
Mitochondrial Distribution and Morphology
Suppressor of PrP
Stable Maintenance of pSRI
Mitochondrial Ribosomal Protein, Large subunit
RNA Polymerase B
AuTophaGy related
Pleiotropic Drug Resistance
SUN-Like Protein
IMP-Specific 5'-Nucleotidase
Neck Filament Interacting
PUTative Proteasome subunit
PETite colonies
Sm protein E
Mrna TRANsport defective
pH Nine Sensitive
Yeast Reveromycin-A Resistant
Diadenosine and Diphosphoinositol Polyphosphate
Guided Entry Tail-anchored proteins
Synthetic Enhancement of YOP1
Synthetically lethal With Trex
Ribosomal Protein of the Small subunit
GLutamiNe metabolism
Long-Chain Base
Yeast Reveromycin resistance Modulator
DeCapping Scavenger
MEDiator complex
Acyltransferase for Lyso-phosphatidylEthanolamine
HEMe biosynthesis

P20_P17

Table S5. Pairwise genetic distance between P17 and P20

YLR255C			0.20391
YDR136C	VPS61	Vacuolar Protein Sorting	0.1315
YDR036C	EHD3		0.10759
YML032C	RAD52	RADiation sensitive	0.07722
YHL048W	COS8	COnserved Sequence	0.06506
YJL077W-B			0.06454
YJL077C	ICS3	Increased Copper Sensitivity	0.06301
YMR304C-A			0.05311
YGR240C-A			0.04652
YDR094W			0.04609
YLR349W			0.04581
YOL086C	ADH1	Alcohol DeHydrogenase	0.04406
YMR084W			0.04256
YOR010C	TIR2	Tlp1-Related	0.04256
YGL007W	BRP1		0.03637
YJL195C			0.03449
YPR192W	AQY1	AQuaporin from Yeast	0.03106
YKL088W	CAB3	Coenzyme A Biosynthesis	0.03022
YER006C-A			0.02899
YMR272W-B			0.02899
YHR007C-A			0.02857
YOL160W			0.02691
YOR044W	IRC23	Increased Recombination Centers	0.02581
YKL037W	AIM26	Altered Inheritance rate of Mitochondria	0.02575
YDR015C			0.02564
YHL043W	ECM34	ExtraCellular Mutant	0.025
YER011W	TIR1	Tlp1-Related	0.02457
YIL059C			0.02449
YLR171W			0.02353
YHL008C			0.0224
YNL331C	AAD14	Aryl-Alcohol Dehydrogenase	0.02151
YGR051C			0.02128
YHR056W-A			0.02105
YNL130C-A	DGR1	2-Deoxy-Glucose Resistant 1	0.02105
YPL257W			0.02094
YHL041W			0.02034
YLR030W			0.02028
YER107W-A			0.01905
YKL044W	MMO1	Mini Mitochondria ORF	0.01905
YDR068W	DOS2		0.01899
YHL050W-A			0.01893
YDR014W-A	HED1	High copy suppressor of rED1	0.01869
YFL014W	HSP12	Heat Shock Protein	0.01852
YDR201W	SPC19	Spindle Pole Component	0.01835
YHR050W-A			0.01802
YLR285C-A			0.01802
YMR169C	ALD3	ALdehyde Dehydrogenase	0.01795
YJL119C			0.01786
YCL022C			0.0177
YAL066W			0.01709

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YJR099W	YUH1	Yeast Ubiquitin Hydrolase	0.01709
YBR119W	MUD1	Mutant U1 Die	0.01692
YDL034W			0.01681
YJR018W			0.01681
YLR108C			0.01663
YOR380W	RDR1	Repressor of Drug Resistance	0.01662
YAL016C-B			0.01653
YGR102C	GTF1	Glutaminy Transamidase subunit F	0.01653
YOL052C-A	DDR2	DNA Damage Responsive	0.01653
YJR083C	ACF4	Assembly Complementing Factor	0.01631
YMR230W-A			0.01626
YMR325W	PAU19	seriPAUperin	0.01626
YNL134C			0.01609
YFL041W-A			0.016
YLR402W			0.016
YML122C			0.016
YKL040C	NFU1	NifU-like protein	0.01575
YNL146C-A			0.01575
YIL141W			0.01563
YKL036C			0.0155
YOR139C			0.0155
YDR066C	RTR2	Regulator of TRanscription	0.01542
YBR264C	YPT10	Yeast Protein Two	0.01519
YIR036W-A			0.01515
YPL062W			0.01504
YLR007W	NSE1	Non-SMC Element	0.01499
YLR341W	SPO77	SPOrulation	0.01478
YKL183C-A			0.01439
YLR296W			0.01439
YML100W-A			0.01439
YDR079C-A	TFB5		0.01399
YMR170C	ALD2	ALdehyde Dehydrogenase	0.01393
YDL092W	SRP14	Signal Recognition Particle	0.01379
YDR037W	KRS1	Lysyl (K) tRNA Synthetase	0.01363
YOR008C-A			0.01361
YDR063W	AIM7	Altered Inheritance rate of Mitochondria	0.01351
YDR273W	DON1	DONut	0.0135
YFL061W	DDI2	DNA Damage Inducible	0.01342
YKL023C-A	MIN9	mitochondrial MINi protein of 9 kDa	0.01342
YDR534C	FIT1	Facilitator of Iron Transport	0.01311
YFL017W-A	SMX2		0.01307
YCR006C			0.01282
YLR286C	CTS1	ChiTinaSe	0.01276
YMR175W	SIP18	Salt Induced Protein	0.01274
YGL194C-A			0.01258
YMR324C			0.01258
YIL063C	YRB2	Yeast Ran Binder	0.01231
YOR394W	PAU21	seriPAUperin	0.01227
YPL282C	PAU22	seriPAUperin	0.01227
YEL016C	NPP2	ecto-Nucleotide Pyrophosphatase/Phosphodiesterase	0.01225
YDR073W	SNF11	Sucrose NonFermenting	0.0122

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YFL010W-A	AUA1	Amino acid Uptake Activation	0.01198
YPL108W			0.01198
YPR012W			0.01198
YDL007C-A			0.01183
YJR017C	ESS1	ESSential	0.01183
YLR114C	AVL9	Apl2 Vps1 Lethal	0.01183
YLR363W-A			0.01183
YHL033C	RPL8A	Ribosomal Protein of the Large subunit	0.01179
YJL215C			0.0117
YOL028C	YAP7	Yeast AP-1	0.01165
YLR366W			0.01156
YPL119C-A			0.01156
YBR122C	MRPL36	Mitochondrial Ribosomal Protein, Large subunit	0.01136
YJR101W	RSM26	Ribosomal Small subunit of Mitochondria	0.01134
YAL037W			0.0113
YBR062C			0.01117
YKL069W			0.01117
YLR046C			0.01117
YCR107W	AAD3	Aryl-Alcohol Dehydrogenase	0.01108
YHR093W	AHT1		0.01105
YIR020C			0.01105
YLR199C	PBA1	Proteasome Biogenesis-Associated	0.01093
YOR053W			0.01093
YGR052W	FMP48	Found in Mitochondrial Proteome	0.0109
YGR108W	CLB1	CycLin B	0.01067
YLR254C	NDL1	NuDeL homolog	0.01064
YNL033W			0.01062
YDL045W-A	MRP10	Mitochondrial Ribosomal Protein	0.01058
YFR034W-A			0.01058
YGR236C	SPG1	Stationary Phase Gene	0.01058
YOL043C	NTG2	eNdonuclease Three-like Glycosylase	0.01058
YPL250W-A			0.01058
YDR259C	YAP6	Yeast homolog of AP-1	0.0105
YGL228W	SHE10	Sensitivity to High Expression	0.01045
YAL034W-A	MTW1	Mis TWelve-like	0.01043
YOR069W	VPS5	Vacuolar Protein Sorting	0.01042
YDR220C			0.01036
YJL056C	ZAP1	Zinc-responsive Activator Protein	0.01028
YEL041W	YEF1		0.01015
YLL056C			0.01012
YBL072C	RPS8A	Ribosomal Protein of the Small subunit	0.01005
YDL016C			0.01005
YDR114C			0.01005
YER102W	RPS8B	Ribosomal Protein of the Small subunit	0.01005
YPL102C			0.01005
YPL278C			0.01005
YGL083W	SCY1		0.01
YFR035C			0.00995
YHR125W			0.00995
YLR346C	CIS1	Cltrinin Sensitive knockout	0.00995
YML118W	NGL3		0.00993

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YLR055C	SPT8	SuPpressor of Ty	0.00992
YAL031W-A			0.00985
YGR242W			0.00985
YIL086C			0.00985
YKL024C	URA6	URAcil requiring	0.00985
YNL086W	SNN1	SNapiN	0.00985
YCL014W	BUD3	BUD site selection	0.00983
YBL073W			0.00976
YDL026W			0.00976
YGR039W			0.00976
YOR387C			0.00976
YNL296W			0.00966
YOR235W	IRC13	Increased Recombination Centers	0.00966
YPL178W	CBC2	Cap Binding Complex	0.00966
YBR268W	MRPL37	Mitochondrial Ribosomal Protein, Large subunit	0.00957
YDR115W	MRX14	Mitochondrial oRganization of gene eXpression (MIOREX)	0.00957
YDR278C			0.00957
YER149C	PEA2	PEAnut shmoo mutant	0.00957
YFL015W-A			0.00957
YIL054W			0.00957
YJL135W			0.00957
YPL142C			0.00957
YDR072C	IPT1	InositolPhosphoTransferase	0.00953
YBL028C			0.00948
YKR032W			0.00948
YKR073C			0.00948
YPR087W	VPS69	Vacuolar Protein Sorting	0.00948
YIL132C	CSM2	Chromosome Segregation in Meiosis	0.00943
YDL011C			0.00939
YER058W	PET117	PETite colonies	0.00939
YER181C			0.00939
YIR023C-A			0.00939
YMR133W	REC114	RECombination	0.00939
YGR269W			0.0093
YJL009W			0.0093
YOL131W			0.0093
YJL076W	NET1	Nucleolar silencing Establishing factor and Telophase regulator	0.00929
YJR074W	MOG1	Multicopy suppressor Of ts Gsp1	0.00922
YLR111W			0.00922
YLR123C			0.00922
YNR061C			0.00917
YBR027C			0.00913
YEL068C			0.00913
YIL007C	NAS2	Non-ATPase Subunit	0.00913
YMR319C	FET4	FErrous Transport	0.0091
YER018C	SPC25	Spindle Pole Component	0.00909
YKR044W	UIP5	Ulp1 Interacting Protein	0.00907
YLL007C	LMO1	eLMO homolog	0.00906
YDR226W	ADK1	ADenylate Kinase	0.00905
YOL135C	MED7	MEDiator complex	0.00905
YFR025C	HIS2	HIStidine requiring	0.009

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YHR101C	BIG1	Bad In Glucose	0.009
YKL041W	VPS24	Vacuolar Protein Sorting	0.00897
YOR012W			0.00893
YDL209C	CWC2	Complexed With Cef1p	0.00889
YLR118C	TML25	acyl-protein Thioesterase with Multiple Localizations, protein of 2	0.00885
YDL065C	PEX19	PEroXisome related	0.00881
YGR228W			0.00881
YLR200W	YKE2	Yeast ortholog of mouse KE2	0.00881
YOR068C	VAM10	VAcuolar Morphogenesis	0.00881
YOR232W	MGE1	Mitochondrial GrpE	0.00881
YPL205C			0.00881
YGR232W	NAS6	Non-ATPase Subunit 6	0.00877
YDR183W	PLP1	Phosducin-Like Protein	0.00873
YER076W-A			0.00873
YIL100W			0.00873
YLL033W	IRC19	Increased Recombination Centers	0.00873
YBR276C	PPS1	Protein Phosphatase S phase	0.00871
YER002W	NOP16	Nucleolar Protein	0.0087
YER004W	FMP52	Found in Mitochondrial Proteome	0.0087
YLR298C	YHC1	Yeast Homolog of human U1C	0.0087
YGL157W	ARI1	Aldehyde Reductase Intermediate, subclass of SDR	0.00868
YBR051W			0.00866
YKL084W	HOT13	Helper Of Tim	0.00866
YLR280C			0.00866
YAL034C-B			0.00858
YCR085W			0.00858
YER010C			0.00858
YGR035W-A			0.00851
YGR050C			0.00851
YJR108W	ABM1	Aberrant Microtubules	0.00851
YJR128W			0.00844
YLR116W	MSL5	Mud Synthetic-Lethal	0.00844
YJR089W	BIR1	Baculoviral IAP Repeat-containing protein	0.00842
YMR318C	ADH6	Alcohol DeHydrogenase	0.00837
YJL123C	MTC1	Maintenance of Telomere Capping	0.00835
YBR272C	HSM3	enhanced Spontaneous Mutability	0.00833
YDR196C	CAB5		0.00833
YGL250W	RMR1	Reduced Meiotic Recombination	0.00833
YLR394W	CST9	Chromosome STability	0.00833
YBR105C	VID24	Vacuolar Import and Degradation	0.00832
YDR031W	MIX14	Mitochondrial Intermembrane space CX(n)C motif protein	0.0083
YDR506C	GMC1	Grand Meiotic recombination Cluster	0.00826
YDR065W	RRG1	Required for Respiratory Growth	0.00825
YLR137W	RKM5	Ribosomal lysine (K) Methyltransferase 5	0.00821
YCR033W	SNT1	SaNT domains	0.00819
YIL115W-A			0.00816
YJL184W	GON7		0.00816
YPR015C			0.00813
YHR163W	SOL3	Suppressor Of Los1-1	0.00806
YNL142W	MEP2		0.00805
YIR001C	SGN1	Slower Growth on Non-fermentable carbon sources	0.00803

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YKR012C			0.00803
YLL027W	ISA1	Iron Sulfur Assembly	0.00803
YLR122C			0.00803
YLR331C	JIP3	Jumonji domain Interacting Protein	0.00803
YML057C-A			0.00803
YOL126C	MDH2	Malate DeHydrogenase	0.00799
YKL161C	KDX1	Kinase Dead X-talker	0.00797
YHR056C	RSC30	Remodel the Structure of Chromatin	0.00796
YBR099C			0.00791
YER001W	MNN1	MaNNosyltransferase	0.00791
YGL127C	SOH1	Suppressor Of Hpr1	0.00791
YJR037W			0.00791
YBR157C	ICS2	Increased Copper Sensitivity	0.00787
YOL044W	PEX15	PEroXisome related	0.00786
YNR015W	SMM1	Suppressor of Mitochondrial Mutation	0.00784
YBR155W	CNS1	Cyclophilin Seven suppressor	0.00782
YDR504C	SPG3	Stationary Phase Gene	0.00778
YLR297W			0.00778
YDR442W			0.00772
YBR250W	SPO23	SPOrulation	0.00768
YDL204W	RTN2	ReTiculoN-like	0.00766
YLR101C			0.00766
YLR104W	LCL2	Long Chronological Lifespan 2	0.00766
YDR496C	PUF6	PUMilio-homology domain Family	0.00765
YML007W	YAP1	Yeast AP-1	0.00762
YJR146W			0.0076
YKL136W			0.0076
YOR268C			0.0076
YDL111C	RRP42	Ribosomal RNA Processing	0.00758
YBL012C			0.00755
YDR511W	SDH7	Succinate DeHydrogenase	0.00755
YIL156W-A			0.00755
YKR083C	DAD2	Duo1 And Dam1 interacting	0.00755
YLR110C	CCW12	Covalently linked Cell Wall protein	0.00755
YNL294C	RIM21	Regulator of IME2	0.00753
YLR128W	DCN1	Defective in Cullin Neddylation	0.00746
YIL119C	RPI1	Ras-cAMP Pathway Inhibitor	0.00743
YDR076W	RAD55	RADiation sensitive	0.00742
YGR042W	MTE1	Mph1-associated TElomere maintenance protein	0.00741
YGR280C	PXR1	PinX1-Related gene	0.00741
YBR086C	IST2	Increased Sodium Tolerance	0.0074
YKL219W	COS9	COnserved Sequence	0.0074
YGR265W			0.00738
YHR070C-A			0.00738
YBR073W	RDH54	RaD54 Homolog	0.00734
YBR213W	MET8	METHionine requiring	0.00733
YDR209C			0.00733
YGL087C	MMS2	Methyl MethaneSulfonate sensitivity	0.00733
YMR178W	FPY1	FAD PYrophosphatase	0.00733
YLL057C	JLP1	dnaJ-Like Protein	0.00731
YDR317W	HIM1	High Induced Mutagenesis	0.00727

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YIL040W	APQ12	APical growth revealed by Quantitative morphological analysis	0.00727
YJL075C	APQ13		0.00727
YKL006W	RPL14A	Ribosomal Protein of the Large subunit	0.00727
YGL019W	CKB1	Casein Kinase Beta subunit	0.00722
YHR192W	LNP1	LuNaPark family member	0.00722
YLR112W			0.00722
YFL055W	AGP3	high-Affinity Glutamine Permease	0.00721
YBR167C	POP7	Processing Of Precursor RNAs	0.00717
YDL123W	SNA4	Sensitivity to NA+	0.00717
YHR067W	HTD2	Hydroxyacyl-Thioester Dehydratase	0.00717
YGL090W	LIF1	Ligase Interacting Factor	0.00715
YEL009C	GCN4	General Control Nonderepressible	0.00714
YBL058W	SHP1	Suppressor of High-copy PP1	0.00712
YIL027C	EMC5	ER Membrane protein Complex	0.00712
YJR067C	YAE1		0.00712
YMR302C	YME2	Yeast Mitochondrial Escape	0.00708
YOL156W	HXT11	HeXose Transporter	0.00708
YDR106W	ARP10	Actin-Related Protein	0.00707
YER159C	BUR6	Bypass UAS Requirement	0.00707
YOL040C	RPS15	Ribosomal Protein of the Small subunit	0.00707
YFR038W	IRC5	Increased Recombination Centers	0.00706
YDR100W	TVP15	Tlg2-Vesicle Protein	0.00702
YOR041C			0.00702
YPR082C	DIB1	S. pombe DIm1+ in Budding yeast	0.00702
YBR095C	RXT2		0.007
YPL168W	MRX4	Mitochondrial oRganization of gene eXpression (MIOREX)	0.007
YMR085W			0.00697
YBL106C	SRO77	Suppressor of rho3	0.00695
YDR284C	DPP1	Diacylglycerol Pyrophosphate Phosphatase	0.00694
YER035W	EDC2	Enhancer of mRNA DeCapping	0.00692
YJR106W	ECM27	ExtraCellular Mutant	0.00692
YGR259C			0.00687
YMR074C	SDD2	Suppressor of Degenerative Death	0.00687
YNL232W	CSL4	Cep1 Synthetic Lethal	0.00687
YNL319W			0.00687
YNL328C	MDJ2	Mitochondrial DnaJ homolog	0.00687
YHR062C	RPP1	Ribonuclease P Protein	0.00685
YDR462W	MRPL28	Mitochondrial Ribosomal Protein, Large subunit	0.00683
YPR109W	GLD1	Golgi/endosome Localized Dsc protein	0.00683
YBR007C	DSF2	Deletion Suppressor of mptFive/pufFive mutation	0.00682
YNL329C	PEX6	PEroXin	0.00682
YHR058C	MED6	MEDIator complex	0.0068
YMR148W	LDO16	LD Organization protein of 16kD	0.00678
YMR216C	SKY1	SRPK1-like Kinase in Yeast	0.00676
YDL093W	PMT5	Protein O-MannosylTransferase	0.00675
YDR096W	GIS1	Glg1-2 Suppressor	0.00673
YFL015C			0.00673
YJR150C	DAN1	Delayed ANaerobic	0.00673
YKL027W	TCD2	tRNA ThreonylCarbamoyladenine Dehydratase	0.00673
YER175C	TMT1	Trans-aconitate MethylTransferase	0.00671
YGL162W	SUT1	Sterol UpTake	0.00671

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YPR031W	NTO1	NuA Three Orf	0.00671
YDR288W	NSE3	Non SMC Element	0.00662
YPL158C	AIM44	Altered Inheritance rate of Mitochondria	0.00662
YDR393W	SHE9	Sensitivity to High Expression	0.0066
YDR374C	PHO92	PHOsphate metabolism	0.00656
YIL062C	ARC15	ARp2/3 Complex subunit	0.00651
YML005W	TRM12	TRna Methyltransferase	0.00651
YBR199W	KTR4	Kre Two Related	0.00649
YCR099C			0.00647
YFR003C	YPI1	Yeast Phosphatase Inhibitor	0.00647
YPR178W	PRP4	Pre-mRNA Processing	0.00647
YPL200W	CSM4	Chromosome Segregation in Meiosis	0.00643
YPR193C	HPA2	Histone and other Protein Acetyltransferase	0.00643
YGR096W	TPC1	Thiamine Pyrophosphate Carrier	0.00639
YOL132W	GAS4	Glycophospholipid-Anchored Surface protein	0.00639
YPR168W	NUT2	Negative regulation of URS Two	0.00639
YOR066W	MSA1	Mbf and Sbf Associated	0.00638
YDL125C	HNT1	Histidine triad NucleoTide-binding	0.00635
YKL201C	MNN4	MaNNosyltransferase	0.00634
YMR048W	CSM3	Chromosome Segregation in Meiosis	0.00633
YBL030C	PET9	PETite	0.00631
YDL103C	QRI1		0.00631
YGR117C			0.00631
YIL016W	SNL1	Suppressor of Nup116-C Lethal	0.00631
YPR034W	ARP7	Actin-Related Protein	0.00631
YJL054W	TIM54	Translocase of the Inner Mitochondrial membrane	0.0063
YMR094W	CTF13	Chromosome Transmission Fidelity	0.0063
YBR265W	TSC10	Temperature-sensitive Suppressors of Csg2 mutants	0.00627
YLR257W			0.00625
YCR052W	RSC6	Remodel the Structure of Chromatin	0.00623
YPR098C	TMH18	TMem205 Homolog of 18 kDa	0.00623
YMR287C	DSS1	Deletion of SUV3 Supressor	0.00621
YBR120C	CBP6	Cytochrome B Protein synthesis	0.00619
YOL071W	SDH5	Succinate DeHydrogenase	0.00619
YLR429W	CRN1	CoRoNin	0.00616
YHR180W			0.00615
YDR435C	PPM1	Protein Phosphatase Methyltransferase	0.00612
YGR256W	GND2	6-phosphoGlucoNateDehydrogenase	0.00612
YBL105C	PKC1	Protein Kinase C	0.0061
YER145C-A			0.00608
YJR054W	KCH1	Potassium (K) regulator of CcH1	0.00605
YEL035C	UTR5	Unidentified TRanscript	0.00604
YER161C	SPT2	SuPpressor of Ty's	0.00602
YKL026C	GPX1	Glutathione PeroXidase	0.00601
YKL122C	SRP21	Signal Recognition Particle	0.00601
YPL223C	GRE1	Genes de Respuesta a Estres (spanish for stress responsive ge	0.00601
YOR072W			0.00597
YMR317W			0.00595
YKL153W			0.00593
YMR081C	ISF1	Increasing Suppression Factor	0.00593
YOL143C	RIB4	RIBoflavin biosynthesis	0.00593

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YJR129C	EFM3	Elongation Factor Methyltransferase	0.00592
YJR015W			0.0059
YGL158W	RCK1	Radiation sensitivity Complementing Kinase	0.00588
YGR163W	GTR2	GTP binding protein Resemblance	0.00588
YIL001W			0.00587
YBL060W	YEL1	Yeast EFA6-Like	0.00584
YMR285C	NGL2		0.00584
YGR071C	ENV11	late ENdosome and Vacuole interface function	0.00583
YJL124C	LSM1	Like SM	0.00583
YPL118W	MRP51	Mitochondrial Ribosomal Protein	0.00583
YPR175W	DPB2	DNA Polymerase B subunit 2	0.00582
YLR372W	ELO3	fatty acid ELongation	0.00581
YMR014W	BUD22	BUD site selection	0.0058
YDR009W	GAL3	GALactose metabolism	0.00579
YJR141W	IPA1	Important for cleavage and PolyAdenylation	0.00578
YPL174C	NIP100	Nuclear ImPort	0.00578
YLR035C	MLH2	MutL Homolog	0.00577
YMR215W	GAS3	Glycophospholipid-Anchored Surface protein	0.00574
YDR279W	RNH202	RNase H	0.00573
YJL122W	ALB1	Arx1 Little Brother	0.00573
YPR101W	SNT309	Synthetic lethal to prp NineTeen mutation	0.00573
YPR194C	OPT2	OligoPeptide Transporter	0.00572
YDL107W	MSS2	Mitochondrial Splicing	0.00571
YJL074C	SMC3	Stability of MiniChromosomes	0.00571
YPL138C	SPP1	Set1c, Phd finger Protein	0.00568
YCL034W	LSB5	Las Seventeen Binding protein	0.00567
YDL100C	GET3	Guided Entry of Tail-anchored proteins	0.00567
YMR042W	ARG80	ARGinine requiring	0.00567
YNL160W	YGP1	Yeast GlycoProtein	0.00567
YGL235W			0.00563
YOR252W	TMA16	Translation Machinery Associated	0.00563
YHR025W	THR1	THReonine requiring	0.00562
YJR036C	HUL4	Hect Ubiquitin Ligase	0.00562
YNL187W	SWT21	Synthetic With Tgs1	0.00562
YDR185C	UPS3	UnProceSsed	0.0056
YNR044W	AGA1	a-AGglutinin	0.00559
YPR028W	YOP1	YIP One Partner	0.00557
YER007C-A	TMA20	Translation Machinery Associated	0.00554
YLR065C	SND2	SRP-iNDependent targeting	0.00554
YOL081W	IRA2	Inhibitory Regulator of the RAS-cAMP pathway	0.00554
YDR235W	PRP42	Pre-mRNA Processing	0.00553
YDL116W	NUP84	NUclear Pore	0.00552
YFR018C			0.00552
YLR141W	RRN5	Regulation of RNA polymerase I	0.00552
YBR065C	ECM2	ExtraCellular Mutant	0.00551
YPL099C	INA17	INner membrane Assembly 17 kDa	0.00551
YBR018C	GAL7	GALactose metabolism	0.00548
YHR050W	SMF2	Suppressor of Mitochondria import Function	0.00548
YLR339C			0.00548
YER042W	MXR1	peptide Methionine sulfoXide Reductase	0.00545
YLL019C	KNS1	Kinase Next to SPA2	0.00544

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YDR191W	HST4	Homolog of SIR Two (SIR2)	0.00542
YER034W			0.00542
YEL058W	PCM1	Phosphoacetylglucosamine Mutase	0.0054
YER075C	PTP3	Protein Tyrosine Phosphatase	0.0054
YNL301C	RPL18B	Ribosomal Protein of the Large subunit	0.00539
YPL165C	SET6	SET domain-containing	0.00538
YHR121W	LSM12	Like SM	0.00536
YNR075W	COS10	COnserved Sequence	0.00536
YPR197C			0.00536
YOL128C	YGK3	Yeast homolog of Glycogen synthase Kinase	0.00535
YIL120W	QDR1	QuiniDine Resistance	0.00534
YER152W-A			0.00533
YHR052W	CIC1	Core Interacting Component	0.00533
YLR306W	UBC12	UBiquitin-Conjugating	0.00533
YPL010W	RET3	RETrieval from ER	0.00531
YGR241C	YAP1802	Yeast Assembly Polypeptide	0.0053
YKR015C			0.0053
YOR014W	RTS1	Rox Three Suppressor	0.0053
YCR086W	CSM1	Chromosome Segregation in Meiosis	0.00528
YGL160W	AIM14	Altered Inheritance rate of Mitochondria	0.00528
YHR189W	PTH1	Peptidyl-Trna Hydrolase	0.00528
YOL036W			0.00527
YGL082W			0.00526
YGL209W	MIG2	Multicopy Inhibitor of GAL gene expression	0.00525
YGL067W	NPY1	NADH PYrophosphatase	0.00522
YLR152C			0.00522
YMR086W	SEG1	Stability of Eisosomes Guaranteed	0.00522
YMR167W	MLH1	MutL Homolog	0.00522
YDR532C	KRE28		0.00521
YGR046W	TAM41	Translocator Assembly and Maintenance	0.00521
YLR131C	ACE2	Activator of CUP1 Expression	0.00521
YOR067C	ALG8	Asparagine-Linked Glycosylation	0.00521
YCL026C-A	FRM2	Fatty acid Repression Mutant	0.00519
YIR023W	DAL81	Degradation of Allantoin	0.00519
YBR246W	RRT2	Regulator of rDNA Transcription	0.00518
YOL146W	PSF3	Partner of Sld Five	0.00517
YMR288W	HSH155	Human Sap Homolog	0.00516
YGR250C	RIE1	Restoration of Impaired growths of ERMES-lacking cells	0.00513
YDR022C	ATG31	AuTophagy related	0.00512
YGR251W	NOP19	Nucleolar Protein	0.00512
YML028W	TSA1	Thiol-Specific Antioxidant	0.00512
YMR295C		Ilm1p Binding	0.00512
YGR077C	PEX8	PEroXin	0.00511
YNL130C	CPT1	CholinePhosphoTransferase	0.0051
YHL004W	MRP4	Mitochondrial Ribosomal Protein	0.00509
YIL157C	COA1	Cytochrome Oxidase Assembly	0.00509
YLR251W	SYM1	Stress-inducible Yeast Mpv17	0.00509
YNL056W	OCA2	Oxidant-induced Cell cycle Arrest	0.00509
YJL069C	UTP18	U Three Protein	0.00506
YBR042C	CST26	Chromosome STability	0.00505
YLR019W	PSR2	Plasma membrane Sodium Response	0.00505

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YMR017W	SPO20	SPOrulation	0.00505
YBR089W			0.00504
YER169W	RPH1	Regulator of PHR1	0.00504
YIL133C	RPL16A	Ribosomal Protein of the Large subunit	0.00504
YDR042C			0.00501
YEL034C-A			0.00501
YPR172W			0.00501
YJL193W			0.00499
YLR179C			0.00499
YMR263W	SAP30	Sin3-Associated Polypeptide	0.00499
YOL148C	SPT20	SuPpressor of Ty	0.00499
YDR018C			0.00498
YJR013W	GPI14	GlycosylPhosphatidylinositol anchor biosynthesis	0.00498
YER050C	RSM18	Ribosomal Small subunit of Mitochondria	0.00496
YJR149W			0.00496
YLR107W	REX3	Rna EXonuclease	0.00496
YNR021W			0.00496
YLR036C			0.00494
YDL104C	QRI7		0.00493
YIL158W	AIM20	Altered Inheritance rate of Mitochondria	0.00491
YLR016C	PML1	Pre-mRNA Leakage	0.00491
YMR052W	FAR3	Factor ARrest	0.00491
YNL152W	INN1	required for INgression	0.0049
YDL112W	TRM3	Transfer RNA Methyltransferase	0.00489
YLR435W	TSR2	Twenty S rRNA accumulation	0.00489
YEL012W	UBC8	UBiquitin-Conjugating	0.00487
YOL083W	ATG34	AuTophagy related	0.00487
YDR085C	AFR1	Alpha-Factor Receptor regulator	0.00485
YJR092W	BUD4	BUD site selection	0.00485
YDL080C	THI3	THlamine metabolism	0.00484
YFL046W	FMP32	Found in Mitochondrial Proteome	0.00484
YOL008W	COQ10	COenzyme Q	0.00484
YOR016C	ERP4	Emp24p/Erv25p Related Protein	0.00484
YCL024W	KCC4		0.00483
YOR227W	HER1	Hmg2p ER Remodeling	0.00483
YBL057C	PTH2	Peptidyl-Trna Hydrolase	0.00482
YMR132C	JLP2	dnaJ-Like Protein	0.00482
YKR048C	NAP1	Nucleosome Assembly Protein	0.00481
YIL038C	NOT3	Negative On TATA	0.0048
YLR027C	AAT2	Aspartate AminoTransferase	0.0048
YKL062W	MSN4	Multicopy suppressor of SNF1 mutation	0.00477
YNL066W	SUN4	Sim1 Uth1 Nca3	0.00477
YNR049C	MSO1	Multicopy suppressor of Sec One	0.00477
YER183C	FAU1	Folinic Acid Utilization	0.00475
YLR130C	ZRT2	Zinc-Regulated Transporter	0.00475
YPL166W	ATG29	AuTophagy related	0.00475
YDR298C	ATP5	ATP synthase	0.00473
YBR005W	RCR1	Resistance to Congo Red	0.00471
YMR012W	CLU1	CLUstered mitochondria	0.00471
YGR244C	LSC2	Ligase of Succinyl-CoA	0.00469
YNL095C			0.00468

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YBR294W	SUL1	SULfate	0.00467
YER003C	PMI40	PhosphoMannose Isomerase	0.00467
YPR186C	PZF1	Putative Zinc Finger	0.00467
YAL007C	ERP2	Emp24p/Erv25p Related Protein	0.00466
YCR020C	PET18	PETite colonies	0.00466
YDL001W	RMD1	Required for Meiotic nuclear Division	0.00466
YIL010W	DOT5	Disruptor Of Telomeric silencing	0.00466
YJL073W	JEM1	DnaJ-like protein of the ER Membrane	0.00466
YDR014W	RAD61	RADiation sensitive	0.00465
YIR012W	SQT1	Suppressor of QSR1 Truncations	0.00465
YHR137C-A			0.00464
YIR024C	INA22	INner membrane Assembly 22 kDa	0.00464
YDR277C	MTH1	MSN Three Homolog	0.00463
YOR110W	TFC7		0.00461
YOR301W	RAX1	Revert to Axial	0.00461
YDR236C	FMN1	FMN biosynthesis	0.0046
YGL033W	HOP2	HOmologous Pairing	0.0046
YGL079W	KXD1	KxDL homolog	0.0046
YPR190C	RPC82	RNA Polymerase C	0.0046
YHR001W	OSH7	OxySterol binding protein Homolog	0.00459
YPR179C	HDA3	Histone DeAcetylase	0.00459
YDR246W	TRS23	TRapp Subunit	0.00458
YJR098C			0.00458
YLR085C	ARP6	Actin-Related Protein	0.00458
YMR008C	PLB1	PhosphoLipase B	0.00457
YBR066C	NRG2	Negative Regulator of Glucose-controlled genes	0.00456
YCR018C	SRD1		0.00454
YDR140W	MTQ2	Methyltransferase	0.00454
YFL001W	DEG1	DEpressed Growth rate	0.00454
YKL198C	PTK1	Putative serine/Threonine protein Kinase	0.00454
YML038C	YMD8		0.00454
YMR243C	ZRC1	Zinc Resistance Conferring	0.00454
YPR174C			0.00454
YKL090W	CUE2	Coupling of Ubiquitin conjugation to ER degradation	0.00452
YBR081C	SPT7	SuPpressor of Ty's	0.00451
YCR051W			0.00451
YJL010C	NOP9	NucleOlar Protein	0.00451
YMR202W	ERG2	ERGosterol biosynthesis	0.00451
YFL048C	EMP47		0.0045
YDL139C	SCM3	Suppressor of Chromosome Missegregation	0.00449
YDR078C	SHU2	Suppressor of HydroxyUrea sensitivity	0.00449
YPL133C	RDS2	Regulator of Drug Sensitivity	0.00449
YDR074W	TPS2	Trehalose-6-Phosphate Synthase/phosphatase	0.00447
YER119C	AVT6	Amino acid Vacuolar Transport	0.00447
YHR022C			0.00447
YMR095C	SNO1	SNZ proximal Open reading frame	0.00447
YPR030W	CSR2	Chs5 Spa2 Rescue	0.00447
YBR055C	PRP6	Pre-mRNA Processing	0.00446
YDR295C	HDA2	Histone DeAcetylase	0.00446
YMR210W	MGL2	MonoacylGlycerol Lipase	0.00446
YBL009W	ALK2		0.00445

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YDL018C	ERP3	Emp24p/Erv25p Related Protein	0.00445
YEL001C	IRC22	Increased Recombination Centers	0.00445
YKL106W	AAT1	Aspartate AminoTransferase	0.00444
YML097C	VPS9	Vacuolar Protein Sorting	0.00444
YPL151C	PRP46	Pre-mRNA Processing	0.00444
YBR182C	SMP1	Second MEF2-like Protein 1	0.00443
YDR296W	MHR1	Mitochondrial Homologous Recombination	0.00443
YER139C	RTR1	Regulator of TRanscription	0.00443
YKL179C	COY1	CASP Of Yeast	0.00443
YPL049C	DIG1	Down-regulator of Invasive Growth	0.00443
YHR177W	ROF1	Regulator Of Fluffy	0.00442
YLR431C	ATG23	AuTophagy related	0.00442
YOR295W	UAF30	Upstream Activation Factor subunit	0.0044
YJL044C	GYP6	Gtpase-activating protein of Ypt6 Protein	0.00438
YOL102C	TPT1	tRNA 2'-PhosphoTransferase	0.00436
YOR283W			0.00436
YJL093C	TOK1		0.00435
YLR396C	VPS33	Vacuolar Protein Sorting	0.00435
YPL201C	YIG1	Yeast protein Interacting with Glycerol 3-phosphatase	0.00435
YDL010W	GRX6	GlutaRedoXin	0.00434
YIL118W	RHO3	Ras HOMolog	0.00434
YOL149W	DCP1	mRNA DeCaPping	0.00434
YPL003W	ULA1	Ubiquitin-Like protein Activation	0.00434
YBL061C	SKT5		0.00432
YKL002W	DID4	Doa4-Independent Degradation	0.00432
YMR293C	HER2	Hmg2p ER Remodeling	0.00432
YOR111W			0.00432
YGR235C	MIC26	Mitochondrial contact site and Cristae organizing system	0.0043
YLR266C	PDR8	Pleiotropic Drug Resistance	0.00429
YIR038C	GTT1	GlutaThione Transferase	0.00428
YJL192C	SOP4	Suppressor Of Pma1-7	0.00428
YKL038W	RGT1	Restores Glucose Transport	0.00428
YEL011W	GLC3	GLyCogen	0.00427
YBL035C	POL12	POLymerase	0.00426
YGL198W	YIP4	Ypt-Interacting Protein	0.00426
YGR233C	PHO81	PHOSphate metabolism	0.00426
YOL060C	MAM3		0.00426
YJR056C			0.00425
YKL033W-A			0.00425
YBR070C	ALG14	Asparagine Linked Glycosylation	0.00423
YBR293W	VBA2	Vacuolar Basic Amino acid transporter	0.00423
YFR043C	IRC6	Increased Recombination Centers	0.00423
YIL123W	SIM1	Start Independent of Mitosis	0.00423
YMR134W	ERG29	ERGosterol biosynthesis	0.00423
YMR188C	MRPS17	Mitochondrial Ribosomal Protein, Small subunit	0.00423
YNR057C	BIO4	BIOtin	0.00423
YOR391C	HSP33	Heat-Shock Protein	0.00423
YPL280W	HSP32	Heat-Shock Protein	0.00423
YEL025C			0.00422
YMR044W	IOC4	Iswi One Complex	0.00422
YJL063C	MRPL8	Mitochondrial Ribosomal Protein, Large subunit	0.00421

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YJL112W	MDV1	Mitochondrial DiVision	0.00421
YKL028W	TFA1	Transcription Factor a, subunit 1	0.00421
YPL213W	LEA1	Looks Exceptionally like U2A	0.00421
YMR280C	CAT8	CATabolite repression	0.0042
YCR007C			0.00419
YGL022W	STT3	STaurosporine and Temperature sensitive	0.00419
YGR255C	COQ6	COenzyme Q	0.00418
YLR326W			0.00418
YNL261W	ORC5	Origin Recognition Complex	0.00418
YPL066W	RGL1	Rho1 GEF Localizing	0.00418
YLR411W	CTR3	Copper TRansport	0.00416
YNL010W	PYP1	PolYol Phosphatase	0.00416
YBR097W	VPS15	Vacuolar Protein Sorting	0.00414
YHR127W			0.00412
YOR043W	WHI2	WHIskey	0.00412
YBR153W	RIB7	RIBoflavin biosynthesis	0.00411
YPL078C	ATP4	ATP synthase	0.00411
YLR442C	SIR3	Silent Information Regulator	0.0041
YNR045W	PET494	PETite colonies	0.0041
YOL030W	GAS5	Glycophospholipid-Anchored Surface protein	0.0041
YDL048C	STP4	protein with similarity to Stp1p	0.00409
YGL098W	USE1	Unconventional SNARE in the ER	0.00409
YJL055W	LOG1	LOnely Guy	0.00409
YML064C	TEM1	TErmination of M phase	0.00409
YLR106C	REA1	Ribosome Export/Assembly	0.00408
YML002W			0.00408
YAL049C	AIM2	Altered Inheritance rate of Mitochondria	0.00407
YGR001C	EFM5	Elongation Factor Methyltransferase	0.00407
YNL119W	NCS2	Needs Cla4 to Survive	0.00407
YPL097W	MSY1	Mitochondrial aminoacyl-tRNA Synthetase, tyrosine (Y)	0.00407
YCL076W			0.00406
YDR082W	STN1	Suppressor of cdc ThirteenN	0.00406
YGR091W	PRP31	Pre-mRNA Processing	0.00406
YDR080W	VPS41	Vacuolar Protein Sorting	0.00404
YGR172C	YIP1	Ypt-Interacting Protein	0.00404
YDR097C	MSH6	MutS Homolog	0.00403
YOR351C	MEK1	MEiotic Kinase	0.00403
YEL036C	ANP1	ANP and osmotic sensitive	0.00402
YER039C	HVG1	Homologous to VRG4	0.00402
YKL068W	NUP100	NUclear Pore	0.00402
YLL046C	RNP1	RiboNucleoProtein	0.00402
YNR009W	NRM1	Negative Regulator of MBF targets	0.00402
YGL240W	DOC1	Destruction Of Cyclin B	0.00401
YKL099C	UTP11	U Three Protein	0.00401
YIL011W	TIR3	Tlp1-Related	0.00399
YNL283C	WSC2	cell Wall integrity and Stress response Component	0.00399
YLL036C	PRP19	Pre-RNA Processing	0.00398
YMR221C	FMP42	Found in Mitochondrial Proteome	0.00398
YBL034C	STU1	Suppressor of TUBulin	0.00397
YGR229C	SMI1	Suppressor of MAR Inhibitor	0.00397
YAL023C	PMT2	Protein O-MannosylTransferase	0.00396

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YAL031C	GIP4	Glc7 Interacting Protein	0.00396
YGL021W	ALK1		0.00396
YPL124W	SPC29	Spindle Pole Component	0.00396
YMR020W	FMS1	Fenpropimorph-resistance Multicopy Suppressor	0.00394
YNL148C	ALF1	ALpha tubulin Folding	0.00394
YMR177W	MMT1	Mitochondrial Metal Transporter	0.00393
YNL314W	DAL82	Degradation of Allantoin	0.00393
YDR371W	CTS2	ChiTinaSe	0.00392
YOR140W	SFL1	Suppressor gene for FLocculation	0.00392
YCL027W	FUS1	cell FUSion	0.00391
YDR169C	STB3	Sin Three Binding protein	0.00391
YOR060C	SLD7	Synthetic Lethality with Dpb11-24	0.0039
YDR323C	PEP7	carboxyPEPTidase Y-deficient	0.00389
YPR002W	PDH1	prpD Homolog	0.00388
YPR032W	SRO7	Suppressor of rho3	0.00388
YCL010C	SGF29	SaGa associated Factor	0.00387
YLR144C	ACF2	Assembly Complementing Factor	0.00386
YAL027W	SAW1	Single-strand Annealing Weakened	0.00384
YDR428C	BNA7	Biosynthesis of NAD	0.00384
YHR167W	THP2	THO2 - HPR1 Phenotype	0.00384
YDL223C	HBT1	HuB1 Target	0.00383
YER021W	RPN3	Regulatory Particle Non-ATPase	0.00383
YGL218W			0.00382
YCL002C			0.00381
YDR405W	MRP20	Mitochondrial Ribosomal Protein	0.00381
YNL138W	SRV2	Suppressor of RasVal19	0.00381
YER052C	HOM3	HOMoserine requiring	0.0038
YIL093C	RSM25	Ribosomal Small subunit of Mitochondria	0.0038
YKR023W	RQT4	Ribosome-Quality control Trigger factor	0.00378
YLR102C	APC9	Anaphase Promoting Complex	0.00378
YOL076W	MDM20	Mitochondrial Distribution and Morphology	0.00378
YLL041C	SDH2	Succinate DeHydrogenase	0.00377
YML010W	SPT5	SuPpressor of Ty's	0.00377
YER056C	FCY2	FluoroCYtosine resistance	0.00376
YBR103W	SIF2	Sir4p-Interacting Factor	0.00375
YDR147W	EKI1	Ethanolamine KInase	0.00375
YEL021W	URA3	URAcil requiring	0.00375
YER157W	COG3	Conserved Oligomeric Golgi complex	0.00375
YER177W	BMH1	Brain Modulosignalin Homolog	0.00375
YPR183W	DPM1	Dolichol Phosphate Mannose synthase	0.00375
YOL033W	MSE1	Mitochondrial aminoacyl-tRNA Synthetase, Glutamate (E)	0.00374
YOR062C			0.00374
YPL241C	CIN2	Chromosome INstability	0.00374
YAR002W	NUP60	NUclear Pore	0.00372
YGR220C	MRPL9	Mitochondrial Ribosomal Protein, Large subunit	0.00372
YGR261C	APL6	clathrin Adaptor Protein complex Large chain	0.00372
YHR134W	WSS1	Weak Suppressor of Smt3	0.00372
YHR135C	YCK1	Yeast Casein Kinase I homolog	0.00372
YJR144W	MGM101	Mitochondrial Genome Maintenance	0.00372
YLR059C	REX2	Rna EXonuclease	0.00372
YBR049C	REB1	RNA polymerase I Enhancer Binding protein	0.00371

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YNL210W	MER1	MEiotic Recombination	0.00371
YNL318C	HXT14	HeXose Transporter	0.00371
YGR119C	NUP57	NUclear Pore	0.0037
YHR006W	STP2	protein with similarity to Stp1p	0.0037
YKR043C	SHB17	SedoHeptulose 1,7-Bisphosphatase	0.0037
YDR227W	SIR4	Silent Information Regulator	0.00369
YLR023C	IZH3	Implicated in Zinc Homeostasis	0.00369
YLR305C	STT4	STaurosporine and Temperature sensitive	0.00369
YBR270C	BIT2	Binding partner of Tor2p	0.00368
YML003W			0.00368
YNR068C			0.00368
YDL086W			0.00367
YGL229C	SAP4	Sit4 Associated Protein	0.00367
YHR028C	DAP2	Dipeptidyl AminoPeptidase	0.00367
YMR199W	CLN1	CycLiN	0.00367
YPL162C			0.00367
YPL256C	CLN2	CycLiN	0.00367
YCL061C	MRC1	Mediator of the Replication Checkpoint	0.00366
YKR060W	UTP30	U Three Protein	0.00366
YLR271W	CMG1	Cytoplasmic and Mitochondrial G-patch protein 1	0.00366
YOR145C	PNO1	Partner of NOb1	0.00366
YOR241W	MET7	METHionine requiring	0.00366
YHR205W	SCH9		0.00365
YIL140W	AXL2	AXiaL 2 bud site selection	0.00365
YAR008W	SEN34	Splicing ENdonuclease	0.00364
YEL015W	EDC3	Enhancer of mRNA DeCapping	0.00364
YOL019W			0.00364
YER026C	CHO1	CHOline requiring	0.00363
YGL096W	TOS8	Target Of Sbf	0.00363
YDL186W			0.00362
YIR031C	DAL7	Degradation of Allantoin	0.00362
YOL088C	MPD2	Multicopy suppressor of PDI1 deletion	0.00362
YDR387C	CIN10	Chromosome INstability	0.00361
YGL027C	CWH41	Calcofluor White Hypersensitive	0.00361
YDR087C	RRP1	Ribosomal RNA Processing	0.0036
YGR026W			0.0036
YKL095W	YJU2		0.0036
YOR255W	OSW1	Outer Spore Wall	0.0036
YLL023C	POM33	POre Membrane, 33 kDa	0.00359
YMR296C	LCB1	Long-Chain Base	0.00359
YOR011W	AUS1	ABC protein involved in Uptake of Sterols	0.00359
YFR002W	NIC96	Nucleoporin-Interacting Component of 96 kDa	0.00358
YGL179C	TOS3	Target Of Sbf	0.00358
YHR045W			0.00358
YFR027W	ECO1	Establishment of COhesion	0.00357
YMR088C	VBA1	Vacuolar Basic Amino acid transporter	0.00357
YNR056C	BIO5	BIOfin	0.00357
YGR087C	PDC6	Pyruvate DeCarboxylase	0.00356
YEL005C	VAB2	VAc8p Binding	0.00355
YDL142C	CRD1	CaRDiolipin synthase	0.00354
YMR053C	STB2	Sin Three Binding protein	0.00354

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YMR087W	PDL32	Protein of Dual Localization of 32 kDa	0.00353
YPL030W	TRM44	TRna Methyltransferase	0.00353
YPL156C	PRM4	Pheromone-Regulated Membrane protein	0.00353
YDR536W	STL1	Sugar Transporter-Like protein	0.00352
YKL127W	PGM1	PhosphoGlucoMutase	0.00351
YMR069W	NAT4	N-AcetylTransferase	0.00351
YBR002C	RER2	Retention in the Endoplasmic Reticulum	0.0035
YDL201W	TRM8	Transfer RNA Methyltransferase	0.0035
YER013W	PRP22	Pre-mRNA Processing	0.0035
YMR149W	SWP1	Suppressor of a WbP1 mutation	0.0035
YNL270C	ALP1		0.0035
YFL034C-B	MOB2	Mps One Binder	0.00349
YGR055W	MUP1	Methionine UPtake	0.00349
YJL071W	ARG2	ARGinine requiring	0.00349
YPR105C	COG4	Conserved Oligomeric Golgi complex	0.00349
YDR326C	YSP2	Yeast Suicide Protein	0.00348
YGR171C	MSM1	Mitochondrial aminoacyl-tRNA Synthetase, Methionine	0.00348
YJR155W	AAD10	Aryl-Alcohol Dehydrogenase	0.00348
YFL028C	CAF16	CCR4 Associated Factor	0.00347
YGL232W	TAN1	Trna Acetylation	0.00347
YGR070W	ROM1	RhO1 Multicopy suppressor	0.00347
YNL159C	ASI2	Amino acid Sensor-Independent	0.00347
YOL080C	REX4	Rna EXonuclease	0.00347
YIL066C	RNR3	RiboNucleotide Reductase	0.00346
YKL124W	SSH4	Suppressor of SHR3 deletion	0.00346
YCR016W			0.00345
YNR064C			0.00345
YOL153C			0.00345
YOR385W			0.00345
YHR014W	SPO13	SPOrulation	0.00344
YKR055W	RHO4	Ras HOmolog	0.00344
YOL077C	BRX1	Xenopus laevis Brix (Biogenesis of Ribosomes in Xenopus) hom	0.00344
YDR285W	ZIP1	molecular ZIPper	0.00343
YDR287W	INM2	INositol Monophosphatase	0.00343
YJR088C	EMC2	ER Membrane protein Complex	0.00343
YKL052C	ASK1	Associated with Spindles and Kinetochores	0.00343
YNL221C	POP1	Processing Of Precursor RNAs	0.00343
YBR163W	EXO5	EXOnuclease V	0.00342
YBR281C	DUG2	Deficient in Utilization of Glutathione	0.00342
YGR222W	PET54	PETite colonies	0.00342
YHR108W	GGA2	Golgi-localized, Gamma-adaptin ear homology, Arf-binding prote	0.00342
YLL028W	TPO1	Transporter of POLyamines	0.00342
YDL076C	RXT3		0.00341
YDR489W	SLD5	Synthetic Lethality with Dpb11-1	0.00341
YHR029C	YHI9		0.00341
YPL149W	ATG5	AuTophagy related	0.00341
YPL248C	GAL4	GALactose metabolism	0.00341
YBR037C	SCO1	Suppressor of Cytochrome Oxidase deficiency	0.0034
YDR233C	RTN1	ReTiculoN-like	0.0034
YDR294C	DPL1	Dihydrosphingosine Phosphate Lyase	0.0034
YMR227C	TAF7	TATA binding protein-Associated Factor	0.0034

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YOR073W	SGO1	ShuGOshin (Japanese for "guardian spirit")	0.0034
YFL033C	RIM15	Regulator of IME2	0.00339
YOL066C	RIB2	RIBoflavin biosynthesis	0.00339
YIL124W	AYR1	1-Acyldihydroxyacetone-phosphate Reductase	0.00337
YPL173W	MRPL40	Mitochondrial Ribosomal Protein, Large subunit	0.00337
YLR348C	DIC1	Dlcarboxylate Carrier	0.00336
YNL333W	SNZ2	SNooZe	0.00336
YDL145C	COP1	COat Protein	0.00334
YDL154W	MSH5	MutS Homolog	0.00334
YDL198C	GGC1	GDP/GTP Carrier	0.00334
YGR044C	RME1	Regulator of MEiosis	0.00334
YLR146C	SPE4	SPERmidine auxotroph	0.00334
YKR039W	GAP1	General Amino acid Permease	0.00333
YPL054W	LEE1		0.00333
YPL167C	REV3	REVersionless	0.00333
YPR160W	GPH1	Glycogen PHosphorylase	0.00333
YDR446W	ECM11	ExtraCellular Mutant	0.00332
YER106W	MAM1	Monopolar microtubule Attachment during Meiosis I	0.00332
YBR231C	SWC5	SWr Complex	0.00331
YDL052C	SLC1	SphingoLipid Compensation	0.00331
YFL002C	SPB4	Suppressor of PAB1	0.00331
YHL019C	APM2	clathrin Adaptor Protein complex Medium chain	0.00331
YOR238W			0.00331
YPR018W	RLF2	Rap1 protein Localization Factor	0.00331
YNR063W	PUL4	PULcherrimin	0.0033
YDR123C	INO2	INOsitol requiring	0.00329
YLR455W	PDP3	PWWP Domain-containing Protein	0.00329
YOL091W	SPO21	SPOrulation	0.00329
YDR280W	RRP45	Ribosomal RNA Processing	0.00328
YLR248W	RCK2	Radiation sensitivity Complementing Kinase	0.00328
YDL045C	FAD1	FAD synthetase	0.00327
YMR055C	BUB2	Budding Uninhibited by Benzimidazole	0.00327
YMR098C	ATP25	ATPase	0.00327
YPL177C	CUP9		0.00327
YBR147W	RTC2	Restriction of Telomere Capping	0.00326
YDL119C	HEM25	HEME synthesis by SLC25 family member	0.00326
YJL126W	NIT2	NITrilase superfamily	0.00326
YKR075C			0.00326
YMR092C	AIP1	Actin Interacting Protein	0.00326
YDL114W			0.00325
YDL127W	PCL2	Pho85 CycLin	0.00325
YLL004W	ORC3	Origin Recognition Complex	0.00325
YPL119C	DBP1	Dead Box Protein	0.00325
YCL009C	ILV6	IsoLeucine Valine	0.00324
YHR187W	IKI1	Insensitive to KIller toxin	0.00324
YIL145C	PAN6	PANtothenate biosynthesis	0.00324
YKL107W			0.00324
YNL177C	MRPL22	Mitochondrial Ribosomal Protein, Large subunit	0.00324
YOR065W	CYT1	CYTochrome c1	0.00324
YDL025C	RTK1	Ribosome biogenesis and TRNA synthetase-associated Kinase	0.00323
YHR199C	AIM46	Altered Inheritance rate of Mitochondria	0.00323

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YOL152W	FRE7	Ferric REductase	0.00323
YPL134C	ODC1	OxoDicarboxylate Carrier	0.00323
YAL047C	SPC72	Spindle Pole Component	0.00322
YDR104C	SPO71	SPOrulation	0.00322
YGL146C	RRT6	Regulator of rDNA Transcription	0.00322
YJR077C	MIR1	Mitochondrial Import Receptor	0.00322
YML050W	AIM32	Altered Inheritance rate of Mitochondria	0.00322
YDL124W			0.00321
YEL029C	BUD16	BUD site selection	0.00321
YFR034C	PHO4	PHOsphate metabolism	0.00321
YGR089W	NNF2		0.00321
YKR008W	RSC4	Remodel the Structure of Chromatin	0.00321
YML087C	AIM33	Altered Inheritance rate of Mitochondria	0.00321
YMR119W	ASI1	Amino acid Sensor-Independent	0.00321
YLR409C	UTP21	U Three Protein	0.0032
YMR206W			0.0032
YNL322C	KRE1	Killer toxin REsistant	0.0032
YBR108W	AIM3	Altered Inheritance rate of Mitochondria	0.00319
YHR061C	GIC1	GTPase Interactive Component	0.00319
YLR283W			0.00319
YNL063W	MTQ1	Methyltransferase	0.00319
YCR073W-A	SOL2	Suppressor Of Los1-1	0.00318
YER005W	YND1	Yeast Nucleoside Diphosphatase	0.00318
YNR038W	DBP6	Dead Box Protein	0.00318
YPL157W	TGS1	TrimethylGuanosine Synthase	0.00318
YDR492W	IZH1	Implicated in Zinc Homeostasis	0.00317
YGL212W	VAM7	VACuolar Morphogenesis	0.00317
YDL218W			0.00316
YCR017C	CWH43	Calcofluor White Hypersensitive	0.00315
YGL023C	PIB2	Phosphatidylinositol(3)-phosphate Binding	0.00315
YNL127W	FAR11	Factor ARrest	0.00315
YGL227W	VID30	Vacuolar Import and Degradation	0.00314
YLR439W	MRPL4	Mitochondrial Ribosomal Protein, Large subunit	0.00314
YOL063C	CRT10	Constitutive RNR Transcription regulators	0.00314
YOR342C			0.00314
YBR045C	GIP1	Glc7-Interacting Protein	0.00313
YDL113C	ATG20	AuTophagy related	0.00313
YDL183C			0.00313
YGL099W	LSG1	Large-Subunit Gtpase	0.00313
YIL056W	VHR1	VHt1 Regulator	0.00313
YMR180C	CTL1	Capping enzyme mRNA Triphosphatase-Like	0.00313
YER037W	PHM8	PHosphate Metabolism	0.00312
YLR139C	SLS1	Synthetic Lethal with SSM4	0.00312
YNL299W	TRF5	Topoisomerase one-Related Function	0.00312
YPL206C	PGC1	Phosphatidyl Glycerol phospholipase C	0.00312
YDR093W	DNF2	Drs2 Neo1 Family	0.00311
YEL030W	ECM10	ExtraCellular Mutant	0.00311
YIL164C	NIT1	NITrilase superfamily	0.00311
YLR316C	TAD3	tRNA-specific Adenosine Deaminase	0.00311
YOL073C	DSC2	Defective for SREBP Cleavage	0.00311
YDL109C			0.0031

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YNL025C	SSN8	Suppressor of SNf1	0.0031
YLL062C	MHT1	S-Methylmethionine-Homocysteine methylTransferase	0.00309
YLR098C	CHA4	Catabolism of Hydroxy Amino acids	0.00309
YML082W			0.00309
YAL018C	LDS1	Lipid Droplets in Sporulation	0.00308
YBR074W	PFF1	Protease in FXNA-related Family	0.00308
YGR009C	SEC9	SECretry	0.00308
YNL271C	BNI1	Bud Neck Involved	0.00308
YPR176C	BET2	Blocked Early in Transport	0.00308
YDR118W	APC4	Anaphase Promoting Complex	0.00307
YML004C	GLO1	GLyOxalase	0.00307
YOR340C	RPA43	RNA Polymerase A	0.00307
YJR093C	FIP1	Factor Interacting with Poly(A) polymerase	0.00306
YMR060C	SAM37	Sorting and Assembly Machinery	0.00306
YKR062W	TFA2	Transcription Factor a, subunit 2	0.00305
YPL104W	MSD1	Mitochondrial aminoacyl-tRNA Synthetase, Aspartate (D)	0.00304
YDR307W	PMT7		0.00303
YHL009C	YAP3	Yeast AP-1	0.00303
YHR027C	RPN1	Regulatory Particle Non-ATPase	0.00303
YOR246C	ENV9	late ENdosome and Vacuole interface function	0.00303
YDR194C	MSS116	Mitochondrial Splicing System	0.00302
YDR508C	GNP1	GlutamiNe Permease	0.00302
YOR350C	MNE1		0.00302
YPL055C	LGE1	LarGE cells	0.00302
YBR260C	RGD1	Related GAP Domain	0.00301
YNR070W	PDR18	Pleiotropic Drug Resistance	0.00301
YBR121C	GRS1	Glycyl-tRNA Synthase	0.003
YNL316C	PHA2	PHenylAlanine requiring	0.003
YDL230W	PTP1	Protein Tyrosine Phosphatase	0.00299
YDR204W	COQ4	COenzyme Q	0.00299
YEL006W	YEA6		0.00299
YGL236C	MTO1	Mitochondrial Translation Optimization	0.00299
YGL241W	KAP114	KAryoPherin	0.00299
YLR278C			0.00299
YML042W	CAT2	Carnitine AcetylTransferase	0.00299
YHR080C	LAM4	Lipid transfer protein Anchored at Membrane contact sites	0.00298
YHR143W	DSE2	Daughter Specific Expression	0.00298
YDR495C	VPS3	Vacuolar Protein Sorting	0.00297
YKR088C	TVP38	Tlg2-Vesicle Protein	0.00297
YOR087W	YVC1	Yeast Vacuolar Conductance	0.00297
YPL183C	RTT10	Regulator of Ty1 Transposition	0.00297
YBL031W	SHE1	Sensitivity to High Expression	0.00296
YKL193C	SDS22	homolog of S. pombe SDS22	0.00296
YOR243C	PUS7	PseudoUridine Synthase	0.00296
YOR261C	RPN8	Regulatory Particle Non-ATPase	0.00296
YOR313C	SPS4	SPorulation Specific transcript	0.00296
YBR050C	REG2	REsistance to Glucose repression	0.00295
YGR084C	MRP13	Mitochondrial Ribosomal Protein	0.00295
YJR033C	RAV1	Regulator of (H+)-ATPase in Vacuolar membrane	0.00295
YLR151C	PCD1	Peroxisomal Coenzyme A Diphosphatase	0.00295
YBR117C	TKL2	TransKetoLase	0.00294

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YDL099W	BUG1	Binder of USO1 and GRH1	0.00294
YEL055C	POL5	POLymerase	0.00294
YML049C	RSE1	RNA Splicing and ER-to-Golgi transport	0.00294
YPL004C	LSP1	Long chain bases Stimulate Phosphorylation	0.00294
YEL004W	YEA4		0.00293
YJR142W			0.00293
YKL210W	UBA1	UBiquitin Activating	0.00293
YMR144W	FDO1	Forkhead one interacting protein involved in DOnor preference	0.00293
YHR076W	PTC7	Phosphatase type Two C	0.00292
YJR107W	LIH1	LIpase Homolog	0.00292
YLR375W	STP3	protein with similarity to Stp1p	0.00292
YMR231W	PEP5	carboxyPEPtidase Y-deficient	0.00292
YOL089C	HAL9	HALotolerance	0.00292
YOR249C	APC5	Anaphase Promoting Complex	0.00292
YOR352W	TFB6		0.00292
YBR259W			0.00291
YIL128W	MET18	METHionine requiring	0.00291
YPR004C	AIM45	Altered Inheritance rate of Mitochondria	0.00291
YKL057C	NUP120	NUclear Pore	0.0029
YCL032W	STE50	STERile	0.00289
YGR101W	PCP1	Processing of Cytochrome c Peroxidase	0.00289
YHR034C	PIH1	Protein Interacting with Hsp90	0.00289
YIL154C	IMP2'	Independent of Mitochondrial Particle	0.00289
YJR154W			0.00289
YML015C	TAF11	TATA binding protein-Associated Factor	0.00289
YML016C	PPZ1	Protein Phosphatase Z	0.00289
YPR180W	AOS1	Activation Of Smt3p	0.00289
YLR377C	FBP1	Fructose-1,6-BisPhosphatase	0.00288
YBR156C	SLI15	Synthetically Lethal with Ipl1	0.00287
YGL100W	SEH1	SEc13 Homolog	0.00287
YMR315W			0.00287
YDL077C	VAM6	VACuolar Morphogenesis	0.00286
YDR017C	KCS1	pKC1 Suppressor	0.00286
YDR214W	AHA1	Activator of Heat shock protein 90 ATPase	0.00286
YGL145W	TIP20	SEC20 (Twenty) Interacting Protein	0.00286
YGR266W			0.00286
YNL231C	PDR16	Pleiotropic Drug Resistance	0.00285
YOR365C			0.00285
YKL051W	SFK1	Suppressor of Four Kinase	0.00284
YKR001C	VPS1	Vacuolar Protein Sorting	0.00284
YKR070W			0.00284
YLR039C	RIC1	RIbosome Control	0.00284
YMR006C	PLB2	PhosphoLipase B	0.00284
YMR163C	INP2	INheritance of Peroxisomes	0.00284
YNL132W	KRE33	Killer toxin RESistant	0.00284
YOL104C	NDJ1	NonDisJunction	0.00284
YOR107W	RGS2	Regulator of heterotrimeric G protein Signaling	0.00284
YPL264C			0.00284
YJL109C	UTP10	U Three Protein	0.00283
YLR424W	SPP382	Suppressor of PrP38 #2	0.00283
YMR207C	HFA1		0.00283

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YCR044C	PER1	protein Processing in the ER	0.00281
YML119W			0.00281
YOL047C	LDS2	Lipid Droplets in Sporulation	0.00281
YBR053C			0.0028
YGL013C	PDR1	Pleiotropic Drug Resistance	0.0028
YJR147W	HMS2	High-copy Mep Suppressor	0.0028
YPL152W	RRD2	Resistant to Rapamycin Deletion	0.0028
YER033C	ZRG8	Zinc Regulated Gene	0.00279
YHR069C	RRP4	Ribosomal RNA Processing	0.00279
YCR091W	KIN82	protein KINase	0.00278
YHR102W	KIC1	Kinase that Interacts with Cdc31p	0.00278
YDR414C	ERD1	Endoplasmic reticulum Retention Defective	0.00277
YKR066C	CCP1	Cytochrome c Peroxidase	0.00277
YCR019W	MAK32	MAintenance of Killer	0.00276
YIR021W	MRS1	Mitochondrial RNA Splicing	0.00276
YKL135C	APL2	clathrin Adaptor Protein complex Large chain	0.00276
YOL042W	NGL1		0.00276
YDL215C	GDH2	Glutamate DeHydrogenase	0.00275
YER111C	SWI4	SWItching deficient	0.00275
YJR119C	JHD2	JmjC domain-containing Histone Demethylase	0.00275
YMR154C	RIM13	Regulator of IME2	0.00275
YPL236C	ENV7	late ENdosome and Vacuole interface function	0.00275
YDL102W	POL3	POLymerase	0.00274
YER107C	GLE2	GLFG LEthal	0.00274
YIL083C	CAB2	Coenzyme A Biosynthesis	0.00274
YKL112W	ABF1	ARS-Binding Factor 1	0.00274
YLR063W	BMT6	Base Methyltransferase of Twenty five S rRNA 6	0.00274
YML131W			0.00274
YNL080C	EOS1	ER-localized and Oxidants Sensitive	0.00274
YDR531W	CAB1	Coenzyme A Biosynthesis	0.00273
YER118C	SHO1	Synthetic, High Osmolarity-sensitive	0.00273
YIR025W	MND2	Meiotic Nuclear Divisions	0.00273
YMR218C	TRS130	TRapp Subunit	0.00273
YOL010W	RCL1	Rna 3'-terminal phosphate Cyclase Like	0.00273
YCR102C			0.00272
YDR318W	MCM21	MiniChromosome Maintenance	0.00272
YMR166C	MME1	Mitochondrial Magnesium Exporter	0.00272
YPR185W	ATG13	AuTophagy related	0.00272
YGL248W	PDE1	PhosphoDiEsterase	0.00271
YKR076W	ECM4	ExtraCellular Mutant	0.00271
YML066C	SMA2	Spore Membrane Assembly	0.00271
YNL144C			0.00271
YCR026C	NPP1	ecto-Nucleotide Pyrophosphatase/Phosphodiesterase	0.0027
YLR383W	SMC6	Structural Maintenance of Chromosomes	0.0027
YOR242C	SSP2	Sporulation SPecific	0.0027
YIL035C	CKA1	Casein Kinase Alpha subunit	0.00269
YLR430W	SEN1	Splicing ENdonuclease	0.00269
YBL067C	UBP13	UBiquitin-specific Protease	0.00268
YBR235W	VHC1	Vacuolar protein Homologous to CCC family	0.00268
YIL006W	YIA6		0.00268
YMR289W	ABZ2	para-AminoBenZoic acid (PABA) biosynthesis	0.00268

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YMR294W	JNM1	Just Nuclear Migration	0.00268
YNL288W	CAF40	CCR4 Associated Factor	0.00268
YOR299W	BUD7	BUD site selection	0.00268
YDL193W	NUS1	Nuclear Undecaprenyl pyrophosphate Synthase	0.00267
YGR264C	MES1	MEthionyl-tRNA Synthetase	0.00267
YOR390W	FEX1		0.00267
YPL279C	FEX2		0.00267
YBR094W	PBY1	P-BodY associated protein	0.00266
YKR004C	ECM9	ExtraCellular Mutant	0.00266
YLR332W	MID2	Mating pheromone-Induced Death	0.00266
YMR214W	SCJ1	S. Cerevisiae DnaJ	0.00266
YPR003C			0.00266
YBR204C	LDH1	Lipid Droplet Hydrolase	0.00265
YHR112C			0.00265
YCL016C	DCC1	Defective in sister Chromatid Cohesion	0.00264
YGL126W	SCS3	Suppressor of Choline Sensitivity	0.00264
YJL053W	PEP8	carboxyPEPTidase Y-deficient	0.00264
YNL230C	ELA1	ELongin A	0.00264
YER129W	SAK1	Snf1 Activating Kinase	0.00263
YLR069C	MEF1	Mitochondrial Elongation Factor	0.00263
YPL193W	RSA1	RiboSome Assembly	0.00263
YDR264C	AKR1	AnKyrin Repeat containing	0.00262
YGR097W	ASK10	Activator of SKn7	0.00262
YHR197W	RIX1	Ribosome eXport	0.00262
YJL090C	DPB11	DNA Polymerase B (II)	0.00262
YJR090C	GRR1	Glucose Repression-Resistant	0.00262
YDR502C	SAM2	S-AdenosylMethionine requiring	0.00261
YNL224C	SQS1	SQuelch of Splicing suppression	0.00261
YPR184W	GDB1	Glycogen DeBranching	0.00261
YJL033W	HCA4	Helicase CA	0.0026
YKR010C	TOF2	TOpoisomerase I-interacting Factor	0.0026
YLL022C	HIF1	Hat1 Interacting Factor	0.0026
YOL006C	TOP1	TOPOisomerase	0.0026
YDL168W	SFA1	Sensitive to FormAldehyde	0.00259
YDR161W	ACL4	Assembly Chaperone of RpL4	0.00259
YEL046C	GLY1	GLYcine requiring	0.00259
YKL134C	OCT1	OCTapeptidyl aminopeptidase	0.00259
YKR092C	SRP40	Serine Rich Protein	0.00259
YLR244C	MAP1	Methionine AminoPeptidase	0.00259
YLR422W	DCK1	DoCK1 homolog	0.00259
YML006C	GIS4	Glg1-2 Suppressor	0.00259
YMR203W	TOM40	Translocase of the Outer Mitochondrial membrane	0.00259
YOR084W	LPX1	Lipase of PeroXisomes	0.00259
YHR158C	KEL1	KELch repeat	0.00258
YNL054W	VAC7	VACuolar segregation	0.00258
YPR054W	SMK1		0.00258
YDR197W	CBS2	Cytochrome B Synthesis	0.00257
YGL009C	LEU1	LEUcine biosynthesis	0.00257
YLR277C	YSH1	Yeast Seventy-three Homolog	0.00257
YMR024W	MRPL3	Mitochondrial Ribosomal Protein, Large subunit	0.00257
YOR328W	PDR10	Pleiotropic Drug Resistance	0.00256

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YPL176C	TRE1	Transferrin REceptor like	0.00256
YBR125C	PTC4	Phosphatase Two C	0.00255
YDR245W	MNN10	MaNNosyltransferase	0.00255
YHR182W			0.00255
YLR449W	FPR4	FKBP Proline Rotamase (isomerase)	0.00255
YML018C			0.00255
YNR048W			0.00255
YOR099W	KTR1	Kre Two Related	0.00255
YPL230W	USV1	Up in StarVation	0.00255
YBL017C	PEP1	carboxyPEPtidase Y-deficient	0.00254
YPL112C	PEX25	PEroXisome related	0.00254
YLR453C	RIF2	Rap1p-Interacting Factor	0.00253
YOL053W	AIM39	Altered Inheritance rate of Mitochondria	0.00253
YDR485C	VPS72	Vacuolar Protein Sorting	0.00252
YEL037C	RAD23	RADiation sensitive	0.00252
YFR016C			0.00252
YHL022C	SPO11	SPOrulation	0.00252
YKR096W	ESL2	EST/SMG-like	0.00252
YNL242W	ATG2	AuTophagy related	0.00252
YOL136C	PFK27	6-PhosphoFructo-2-Kinase	0.00252
YDR021W	FAL1	eukaryotic translation initiation factor Four A Like	0.00251
YER109C	FLO8	FLOcculation	0.00251
YGR234W	YHB1	Yeast flavoHemogloBin	0.00251
YMR026C	PEX12	PEroXin	0.00251
YGL234W	ADE5,7	ADEnine requiring	0.0025
YMR257C	PET111	PETite colonies	0.0025
YOR017W	PET127	PETite colonies	0.0025
YPL171C	OYE3	Old Yellow Enzyme	0.0025
YER144C	UBP5	UBiquitin-specific Protease	0.00249
YGL181W	GTS1	Glycine Threonine Serine repeat protein	0.00249
YLR182W	SWI6	SWItching deficient	0.00249
YDL122W	UBP1	UBiquitin-specific Protease	0.00248
YKL195W	MIA40	Mitochondrial intermembrane space Import and Assembly	0.00248
YKR053C	YSR3	Yeast Sphingolipid Resistance	0.00248
YMR049C	ERB1	Eukaryotic Ribosome Biogenesis	0.00248
YNL051W	COG5	Conserved Oligomeric Golgi complex	0.00248
YNL292W	PUS4	PseudoUridine Synthase	0.00248
YJR126C	VPS70	Vacuolar Protein Sorting	0.00247
YGR217W	CCH1	Calcium Channel Homolog	0.00246
YJL080C	SCP160	S. cerevisiae protein involved in the Control of Ploidy	0.00246
YLR095C	IOC2	Iswi One Complex	0.00246
YDR289C	RTT103	Regulator of Ty1 Transposition	0.00245
YER044C-A	MEI4	MEIosis-specific	0.00245
YIR008C	PRI1	DNA PRImase	0.00245
YNL064C	YDJ1	Yeast dnaJ	0.00245
YOR134W	BAG7		0.00245
YBR036C	CSG2	Calcium Sensitive Growth	0.00244
YOR042W	CUE5	Coupling of Ubiquitin conjugation to ER degradation	0.00244
YOR303W	CPA1	Carbamyl Phosphate synthetase A	0.00244
YLL032C			0.00243
YDR282C	MRX10	Mitochondrial oRganization of gene eXpression (MIOREX)	0.00242

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YFL004W	VTC2	Vacuolar Transporter Chaperone	0.00242
YGL206C	CHC1	Clathrin Heavy Chain	0.00242
YJL089W	SIP4	SNF1-Interacting Protein	0.00242
YLR263W	RED1	REDuctional division	0.00242
YMR219W	ESC1	Establishes Silent Chromatin	0.00242
YDR222W			0.00241
YGL208W	SIP2	SNF1-Interacting Protein	0.00241
YOL082W	ATG19	AuTophagy related	0.00241
YDR207C	UME6	Unscheduled Meiotic gene Expression	0.0024
YML083C			0.0024
YMR102C			0.0024
YNL304W	YPT11	Yeast Protein Two	0.0024
YPL255W	BBP1	Bfr1 Binding Protein	0.00239
YDL027C	MRX9	Mitochondrial oRganization of gene eXpression (MIOREX)	0.00238
YDR255C	RMD5	Required for Meiotic nuclear Division	0.00238
YJR136C	TTI2	Two Tel2-Interacting protein	0.00238
YLL054C			0.00238
YNL309W	STB1	Sin Three Binding protein	0.00238
YOL031C	SIL1	Suppressor of the Ire1/Lhs1 double mutant	0.00238
YJL183W	MNN11	MaNNosyltransferase	0.00237
YOR266W	PNT1	PeNTamidine resistance	0.00237
YBR130C	SHE3	Swi5p-dependent HO Expression	0.00236
YGR202C	PCT1	Phosphocholine CytidylylTransferase	0.00236
YKL129C	MYO3	MYOsin	0.00236
YNL136W	EAF7	Esa1-Associated Factor	0.00236
YDR160W	SSY1	Sulfonylurea Sensitive on YPD	0.00235
YLL006W	MMM1	Maintenance of Mitochondrial Morphology	0.00235
YMR076C	PDS5	Precocious Dissociation of Sisters	0.00235
YNL234W			0.00235
YBR287W			0.00234
YGL196W	DSD1		0.00234
YDR263C	DIN7	DNA Damage INducible	0.00233
YEL002C	WBP1	Wheat germ agglutinin-Binding Protein	0.00233
YKL209C	STE6	STERile	0.00233
YLR398C	SKI2	SuperKiller	0.00233
YDL090C	RAM1	RAS protein and A-factor Maturation	0.00232
YER172C	BRR2	Bad Response to Refrigeration	0.00232
YGR150C	CCM1	COB and COX1 mRNA maturation	0.00232
YHR169W	DBP8	Dead Box Protein	0.00232
YIR004W	DJP1	DnaJ Protein	0.00232
YCR032W	BPH1	Beige Protein Homolog	0.00231
YDR448W	ADA2	transcriptional ADaptor	0.00231
YKL082C	RRP14	Ribosomal RNA Processing	0.00231
YNL128W	TEP1	TEnsin-like Phosphatase	0.00231
YNL330C	RPD3	Reduced Potassium Dependency	0.00231
YOR237W	HES1	Homologous to kES1	0.00231
YAR018C	KIN3	protein KINase	0.0023
YBR289W	SNF5	Sucrose NonFermenting	0.0023
YMR091C	NPL6	Nuclear Protein Localization	0.0023
YNL049C	SFB2	Sed Five Binding	0.00229
YNL082W	PMS1	PostMeiotic Segregation	0.00229

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YNR011C	PRP2	Pre-mRNA Processing	0.00229
YPR173C	VPS4	Vacuolar Protein Sorting	0.00229
YDL216C	RRI1	Regulator of Rub1 specific Isopeptidase	0.00228
YER132C	PMD1	Paralog of MDS3	0.00228
YGL092W	NUP145	NUclear Pore	0.00228
YGL164C	YRB30	Yeast Ran Binder	0.00228
YHR111W	UBA4	UBiquitin-Activating	0.00228
YLR113W	HOG1	High Osmolarity Glycerol response	0.00228
YML099C	ARG81	ARGinine requiring	0.00228
YOR316C	COT1	COalt Toxicity	0.00228
YPL085W	SEC16	SECretory	0.00228
YCR079W	PTC6	Phosphatase Two C	0.00227
YDR206W	EBS1	Est1-like Bcy1 Suppressor	0.00227
YDR329C	PEX3	PEroXin	0.00227
YER061C	CEM1	Condensing Enzyme with Mitochondrial function	0.00227
YCR073C	SSK22	Suppressor of Sensor Kinase	0.00226
YDR303C	RSC3	Remodel the Structure of Chromatin	0.00226
YDR027C	VPS54	Vacuolar Protein Sorting	0.00225
YER008C	SEC3	SECretory	0.00225
YHR190W	ERG9	ERGosterol biosynthesis	0.00225
YIL071C	PCI8	Proteasome-COP9 signalosome (CSN)-eIF3	0.00225
YLR045C	STU2	Suppressor of TUBulin	0.00225
YLR080W	EMP46		0.00225
YMR268C	PRP24	Pre-mRNA Processing	0.00225
YOR250C	CLP1	CLeavage/Polyadenylation factor Ia subunit	0.00225
YPR089W			0.00225
YDR515W	SLF1	SuLFide production	0.00224
YHR004C	NEM1	Nuclear Envelope Morphology	0.00224
YLR382C	NAM2	Nuclear Accommodation of Mitochondria	0.00224
YNL233W	BNI4	Bud Neck Involved	0.00224
YNR047W	FPK1	FliPase Kinase 1	0.00224
YOL016C	CMK2	CalModulin dependent protein Kinase	0.00224
YOR025W	HST3	Homolog of SIR Two (SIR2)	0.00224
YER047C	SAP1	Sin1 Associated Protein	0.00223
YJR065C	ARP3	Actin-Related Protein	0.00223
YNL166C	BNI5	Bud Neck Involved	0.00223
YLR373C	VID22	Vacuolar Import and Degradation	0.00222
YOR059C	LPL1	LD phospholipase	0.00222
YPR021C	AGC1	Aspartate-Glutamate Carrier	0.00222
YBR166C	TYR1	TYRosine	0.00221
YDR312W	SSF2	Suppressor of ste4 (Four)	0.00221
YGL194C	HOS2	Hda One Similar	0.00221
YHR066W	SSF1	Suppressor of ste4 (Four)	0.00221
YLR014C	PPR1	Pyrimidine Pathway Regulation	0.00221
YNL074C	MLF3	Multicopy suppressor of LeFlunomide sensitivity	0.00221
YDR375C	BCS1	ubiquinol-cytochrome c reductase (bc1) Synthesis	0.0022
YMR135C	GID8	Glucose Induced Degradation deficient	0.0022
YPL101W	ELP4	ELongator Protein	0.0022
YPR084W			0.0022
YBL082C	ALG3	Asparagine Linked Glycosylation	0.00219
YDL233W	MFG1	Morphogenetic regulator of Filamentous Growth	0.00219

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YJR062C	NTA1	N-Terminal Amidase	0.00219
YMR238W	DFG5	Defective for Filamentous Growth	0.00219
YBL089W	AVT5	Amino acid Vacuolar Transport	0.00218
YDR103W	STE5	STERile	0.00218
YFR024C-A	LSB3	Las Seventeen Binding protein	0.00218
YGL219C	MDM34	Mitochondrial Distribution and Morphology	0.00218
YML111W	BUL2	Binds Ubiquitin Ligase	0.00218
YNL237W	YTP1	Yeast putative Transmembrane Protein	0.00218
YPL139C	UME1	Unscheduled Meiotic gene Expression	0.00218
YDL036C	PUS9	PseudoUridine Synthase	0.00217
YDL220C	CDC13	Cell Division Cycle	0.00217
YDR247W	VHS1	Viable in a Hal3 Sit4 background	0.00217
YMR265C			0.00217
YCL048W	SPS22	SPorulation Specific 2 too (2)	0.00216
YDR069C	DOA4	Degradation Of Alpha	0.00216
YDR081C	PDC2	Pyruvate DeCarboxylase	0.00216
YER038C	KRE29	Killer toxin RESistant	0.00216
YKL143W	LTV1	Low Temperature Viability	0.00216
YOR123C	LEO1	LEft Open reading frame	0.00216
YEL040W	UTR2	Unidentified TRanscript	0.00215
YHL021C	AIM17	Altered Inheritance rate of Mitochondria	0.00215
YHR146W	CRP1	Cruciform DNA-Recognizing Protein	0.00215
YPL083C	SEN54	Splicing ENdonuclease	0.00215
YDL024C	DIA3	Digs Into Agar	0.00214
YDR223W	CRF1	Co-Repressor with FHL1	0.00214
YHL030W	ECM29	ExtraCellular Mutant	0.00214
YPL082C	MOT1	Modifier of Transcription	0.00214
YDR473C	PRP3	Pre-mRNA Processing	0.00213
YGR019W	UGA1	Utilization of GAba	0.00213
YLL021W	SPA2	Spindle Pole Antigen	0.00213
YLR058C	SHM2	Serine HydroxyMethyltransferase	0.00213
YMR027W			0.00213
YPR196W			0.00213
YDR356W	SPC110	Spindle Pole Component	0.00212
YGL012W	ERG4	ERGosterol biosynthesis	0.00212
YIL002C	INP51	INositol polyphosphate 5-Phosphatase	0.00212
YIL075C	RPN2	Regulatory Particle Non-ATPase	0.00212
YKL221W	MCH2	MonoCarboxylate transporter Homolog	0.00212
YLL003W	SFI1	Suppressor of Fermentation Induced loss of stress resistance	0.00212
YMR211W	DML1	Drosophila melanogaster Misato-Like protein	0.00211
YCR081W	SRB8	Suppressor of RNA polymerase B	0.0021
YER093C	TSC11	Temperature-sensitive Suppressors of Csg2 mutants	0.0021
YJL002C	OST1	OligoSaccharylTransferase	0.0021
YKL157W	APE2	AminoPEptidase	0.0021
YPR189W	SKI3	SuperKiller	0.0021
YDR198C	RKM2	Ribosomal protein lysine (K) Methyltransferase	0.00209
YLR378C	SEC61	SECretory	0.00209
YMR205C	PFK2	PhosphoFructoKinase	0.00209
YDR181C	SAS4	Something About Silencing	0.00208
YGL097W	SRM1	Suppressor of Receptor Mutations	0.00208
YNL071W	LAT1		0.00208

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YBR247C	ENP1	Essential Nuclear Protein	0.00207
YBR288C	APM3	clathrin Adaptor Protein complex Medium chain	0.00207
YDR514C			0.00207
YKL211C	TRP3	TRyPtophan	0.00207
YNL026W	SAM50	Sorting and Assembly Machinery	0.00207
YPL091W	GLR1	GLutathione Reductase	0.00207
YBR083W	TEC1	Transposon Enhancement Control	0.00206
YFR053C	HXK1	HeXoKinase	0.00206
YGL104C	VPS73	Vacuolar Protein Sorting	0.00206
YMR070W	MOT3	Modifier of Transcription	0.00206
YMR080C	NAM7	Nuclear Accommodation of Mitochondria	0.00206
YNL137C	NAM9	Nuclear Accommodation of Mitochondria	0.00206
YNL277W	MET2	METHionine requiring	0.00206
YPR001W	CIT3	CITrate synthase	0.00206
YDL238C	GUD1	GUanine Deaminase	0.00205
YER045C	ACA1	ATF/CREB Activator	0.00205
YNL053W	MSG5	Multicopy Suppressor of GPA1	0.00205
YPL254W	HFI1	Histone H2A Functional Interactor	0.00205
YBR283C	SSH1	Sec Sixty-one Homolog	0.00204
YCR045C	RRT12	Regulator of rDNA Transcription	0.00204
YIL088C	AVT7	Amino acid Vacuolar Transport	0.00204
YIL090W	ICE2	Inheritance of Cortical ER	0.00204
YIL130W	ASG1	Activator of Stress Genes	0.00204
YML126C	ERG13	ERGosterol biosynthesis	0.00204
YAL010C	MDM10	Mitochondrial Distribution and Morphology	0.00203
YER051W	JHD1	JmjC domain-containing Histone Demethylase	0.00203
YER122C	GLO3	GLyOxalase	0.00203
YLR227C	ADY4	Accumulation of DYads	0.00203
YNL124W	NAF1	Nuclear Assembly Factor	0.00203
YNL223W	ATG4	AuTophagy related	0.00203
YOR346W	REV1	REVersionless	0.00203
YPR169W	JIP5	Jumonji domain Interacting Protein	0.00203
YDR132C			0.00202
YLR256W	HAP1	Heme Activator Protein	0.00202
YDR348C	PAL1	Pears And Lemons	0.00201
YFL018C	LPD1	LiPoamide Dehydrogenase	0.00201
YFL027C	GYP8	Gtpase-activating protein for Ypt Proteins	0.00201
YGL122C	NAB2	Nuclear polyAdenylated RNA-Binding	0.00201
YHR070W	TRM5	tRNA Methyltransferase	0.00201
YJR122W	IBA57	Iron-sulfur cluster assembly factor for Biotin synthase and Aconit	0.00201
YKL035W	UGP1	UDP-glucose pyrophosphorylase	0.00201
YNL123W	NMA111	Nuclear Mediator of Apoptosis	0.00201
YPL026C	SKS1	Suppressor Kinase of SNF3	0.00201
YDL079C	MRK1	Mds1p Related Kinase	0.002
YJR051W	OSM1	OSMotic sensitivity	0.002
YNR012W	URK1	URidine Kinase	0.002
YPL040C	ISM1	Isoleucyl tRNA Synthetase of Mitochondria	0.002
YPL061W	ALD6	ALdehyde Dehydrogenase	0.002
YAL058W	CNE1	CalNExin and calreticulin homolog	0.00199
YFR040W	SAP155	Sit4 Associated Protein	0.00199
YGL017W	ATE1	Arginyl-tRNA-protein transfErase	0.00199

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YOR048C	RAT1	Ribonucleic Acid Trafficking	0.00199
YER064C	VHR2	VHt1 Regulator	0.00198
YMR290C	HAS1	Helicase Associated with Set1	0.00198
YNL241C	ZWF1	ZWischenFerment	0.00198
YPL140C	MKK2	Mitogen-activated Kinase Kinase	0.00198
YPL181W	CTI6	Cyc8-Tup1 Interacting protein	0.00198
YEL052W	AFG1	ATPase Family Gene	0.00197
YGR093W	DRN1	Debranching enzyme-associated RiboNuclease	0.00197
YIL104C	SHQ1	Small nucleolar RNAs of the box H/ACA family Quantitative accu	0.00197
YLR345W			0.00197
YOR231W	MKK1	Mitogen-activated protein Kinase-Kinase	0.00197
YFL016C	MDJ1	Mitochondrial DnaJ	0.00196
YMR004W	MVP1	Multi-copy suppressor of vps1	0.00196
YOL004W	SIN3	Switch INdependent	0.00196
YDL101C	DUN1	DNA-damage UNinducible	0.00195
YDR060W	MAK21	MAintenance of Killer	0.00195
YFL021W	GAT1		0.00195
YHR048W	YHK8		0.00195
YHR137W	ARO9	AROMATIC amino acid requiring	0.00195
YJL194W	CDC6	Cell Division Cycle	0.00195
YML128C	MSC1	Meiotic Sister-Chromatid recombination	0.00195
YMR093W	UTP15	U Three Protein	0.00195
YMR283C	RIT1	Ribosylation of Initiator tRNA	0.00195
YCR072C	RSA4	RiboSome Assembly	0.00194
YDR256C	CTA1	CaTalase A	0.00194
YJL013C	MAD3	Mitotic Arrest-Deficient	0.00194
YKL047W	ANR2	Avl Nine Related family 2	0.00194
YNR051C	BRE5	BREfeldin A sensitivity	0.00194
YOR149C	SMP3	Stable Maintenance of pSRI	0.00194
YEL042W	GDA1	Guanosine DiphosphatAse	0.00193
YER007W	PAC2	Perish in the Absence of Cin8p	0.00193
YHR168W	MTG2	MiTochondrial Gtpase 2	0.00193
YKL033W	TTI1	Two Tel2-Interacting protein	0.00193
YKL116C	PRR1	Pheromone Response Regulator	0.00193
YMR013C	SEC59	SECretory	0.00193
YBL019W	APN2	APurinic/aprimidinic eNdonuclease	0.00192
YDR501W	PLM2	PLasmid Maintenance	0.00192
YER073W	ALD5	ALdehyde Dehydrogenase	0.00192
YER114C	BOI2	Bem1 (One) Interacting protein	0.00192
YMR247C	RKR1	RING domain mutant Killed by Rtf1 deletion	0.00192
YBL054W	TOD6	Twin Of Dot6p	0.00191
YDL197C	ASF2	Anti-Silencing Function	0.00191
YGR227W	DIE2	Derepression of ITR1 Expression	0.00191
YJR132W	NMD5	Nonsense-Mediated mRNA Decay	0.00191
YKL039W	PTM1		0.00191
YLR004C	THI73	THlamine regulon	0.00191
YMR029C	FAR8	Factor ARrest	0.00191
YNL295W	MRX6	Mitochondrial oRganization of gene eXpression (MIOREX)	0.00191
YOR377W	ATF1	AcetylTransFerase	0.00191
YPL247C			0.00191
YDL088C	ASM4	Anti-Suppressor in Multicopy	0.0019

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YDL143W	CCT4	Chaperonin Containing TCP-1	0.0019
YGL056C	SDS23	homolog of S. pombe SDS23	0.0019
YKL045W	PRI2	DNA PRImase	0.0019
YNL077W	APJ1	Anti-Prion DnaJ	0.0019
YNR031C	SSK2	Suppressor of Sensor Kinase	0.0019
YBR239C	ERT1	Ethanol Regulated Transcription factor	0.00189
YDL020C	RPN4	Regulatory Particle Non-ATPase	0.00189
YDR127W	ARO1	AROmatic amino acid requiring	0.00189
YIL146C	ATG32	AuTophagy related	0.00189
YLL055W	YCT1	Yeast Cysteine Transporter	0.00189
YPR162C	ORC4	Origin Recognition Complex	0.00189
YDR488C	PAC11	Perish in the Absence of CIN8	0.00188
YMR110C	HFD1	Homolog of Fatty aldehyde Dehydrogenase	0.00188
YMR297W	PRC1	PRoteinase C	0.00188
YOL105C	WSC3	cell Wall integrity and Stress response Component	0.00188
YPR055W	SEC8	SECretory	0.00188
YFR006W			0.00187
YGR260W	TNA1	Transporter of Nicotinic Acid	0.00187
YBR286W	APE3	AminoPEptidase	0.00186
YDL207W	GLE1	GLFG (glycine-leucine-phenylalanine-glycine) LEthal	0.00186
YDR061W			0.00186
YDR291W	HRQ1	Homologous to RecQ protein	0.00186
YIR039C	YPS6	YaPSin	0.00186
YOL145C	CTR9	CIn Three (CLN3) Requiring	0.00186
YDR057W	YOS9	Yeast OS-9 homolog	0.00185
YER155C	BEM2	Bud EMergence	0.00185
YFL040W			0.00185
YGL045W	RIM8	Regulator of IME2	0.00185
YGL156W	AMS1	Alpha-MannoSidase	0.00185
YGR218W	CRM1	Chromosome Region Maintenance	0.00185
YIL112W	HOS4	Hda One Similar	0.00185
YKL020C	SPT23	SuPpressor of Ty	0.00185
YML116W	ATR1	AminoTriazole Resistance	0.00185
YMR279C			0.00185
YNL189W	SRP1	Suppressor of Rna Polymerase I	0.00185
YOL100W	PKH2	Pkb-activating Kinase Homolog	0.00185
YDL085W	NDE2	NADH Dehydrogenase, External	0.00184
YPL212C	PUS1	PseudoUridine Synthase	0.00184
YPR198W	SGE1	Suppression of Gal11 Expression	0.00184
YER168C	CCA1	tRNA CCA-pyrophosphorylase	0.00183
YFR051C	RET2	RETrieval from ER	0.00183
YNL154C	YCK2	Yeast Casein Kinase	0.00183
YNL291C	MID1	Mating pheromone-Induced Death	0.00183
YPR033C	HTS1	Histidine-Trna Synthetase	0.00183
YIL121W	QDR2	QuiniDine Resistance	0.00182
YJR131W	MNS1		0.00182
YMR171C	EAR1	Endosomal Adaptor of Rsp5p	0.00182
YNR030W	ALG12	Asparagine-Linked Glycosylation	0.00182
YOL055C	THI20	THlamine metabolism	0.00182
YOR132W	VPS17	Vacuolar Protein Sorting	0.00182
YPL258C	THI21	THlamine metabolism	0.00182

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YBR248C	HIS7	HIStidine requiring	0.00181
YDR283C	GCN2	General Control Nonderepressible	0.00181
YER082C	UTP7	U Three Protein	0.00181
YGL176C			0.00181
YGR276C	RNH70	RNase H	0.00181
YLR433C	CNA1	CalciNeurin A	0.00181
YMR036C	MIH1	Mitotic Inducer Homolog	0.00181
YNL117W	MLS1	MaLate Synthase	0.00181
YBR030W	RKM3	Ribosomal lysine (K) Methyltransferase	0.0018
YER065C	ICL1	IsoCitrate Lyase	0.0018
YJL163C			0.0018
YDL106C	PHO2	PHOsphate metabolism	0.00179
YGL084C	GUP1	Glycerol UPtake	0.00179
YJR039W	MLO127	Mitochondrially LOkalized protein of 127 kDa	0.00179
YKR072C	SIS2	Slt4 Suppressor	0.00179
YDR062W	LCB2	Long-Chain Base	0.00178
YDR261C	EXG2	EXo-1,3-beta-Glucanase	0.00178
YGR088W	CTT1	CaTalase T	0.00178
YLR134W	PDC5	Pyruvate DeCarboxylase	0.00178
YML104C	MDM1	Mitochondrial Distribution and Morphology	0.00178
YBR245C	ISW1	Imitation SWitch subfamily	0.00177
YCL036W	GFD2	Great for Full DEAD box protein activity	0.00177
YDR345C	HXT3	HeXose Transporter	0.00177
YGL003C	CDH1	CDC20 Homolog	0.00177
YGL151W	NUT1	Negative regulation of URS Two	0.00177
YGL171W	ROK1	Rescuer Of Kem1	0.00177
YLR417W	VPS36	Vacuolar Protein Sorting	0.00177
YNR023W	SNF12	Sucrose NonFermenting	0.00177
YPR070W	MED1	MEDIator complex	0.00177
YDR026C	NSI1	NTS1 SIlencing protein 1	0.00176
YDR120C	TRM1	tRNA Methyltransferase	0.00176
YHR094C	HXT1	HeXose Transporter	0.00176
YKR002W	PAP1	Poly(A) Polymerase	0.00176
YBR180W	DTR1	DiTyRosine	0.00175
YER124C	DSE1	Daughter Specific Expression	0.00175
YER158C			0.00175
YHR184W	SSP1		0.00175
YLR259C	HSP60	Heat Shock Protein	0.00175
YOL027C	MDM38	Mitochondrial Distribution and Morphology	0.00175
YHR037W	PUT2	Proline UTilization	0.00174
YHR196W	UTP9	U Three Protein	0.00174
YIR010W	DSN1	Dosage Suppressor of NNF1	0.00174
YNL073W	MSK1	Mitochondrial aminoacyl-tRNA Synthetase, lysine (K)	0.00174
YNL251C	NRD1	Nuclear pre-mRNA Down-regulation	0.00174
YPR171W	BSP1	Binding protein of Synaptojanin Polyphosphoinositide phosphata	0.00174
YBL039C	URA7	URAcil requiring	0.00173
YEL013W	VAC8	VACuole related	0.00173
YJR103W	URA8	URAcil requiring	0.00173
YLR361C	DCR2	Dose-dependent Cell cycle Regulator	0.00173
YMR282C	AEP2	ATPase ExPression	0.00173
YNR059W	MNT4	MaNnosylTransferase	0.00173

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YLR077W	FMP25	Found in Mitochondrial Proteome	0.00172
YLR133W	CKI1	Choline Kinase	0.00172
YML071C	COG8	Conserved Oligomeric Golgi complex	0.00172
YML127W	RSC9	Remodel the Structure of Chromatin	0.00172
YNL225C	CNM67	Chaotic Nuclear Migration	0.00172
YDR497C	ITR1	myo-Inositol TRansporter	0.00171
YHR109W	CTM1	Cytochrome c Methyltransferase	0.00171
YKR078W			0.00171
YLR032W	RAD5	RADiation sensitive	0.00171
YML013W	UBX2	UBiquitin regulatory X	0.00171
YMR250W	GAD1	Glutamate Decarboxylase	0.00171
YMR291W	TDA1	Topoisomerase I Damage Affected	0.00171
YNR055C	HOL1	Histidinol	0.00171
YOL015W	IRC10	Increased Recombination Centers	0.00171
YOL115W	PAP2	Poly(A) Polymerase	0.00171
YGL252C	RTG2	Retrograde regulation	0.0017
YKL014C	URB1	Unhealthy Ribosome Biogenesis	0.0017
YNL087W	TCB2	Three Calcium and lipid Binding domains (TriCalBins)	0.0017
YNL227C	JJJ1	J-protein (Type III)	0.0017
YPL007C	TFC8	Transcription Factor C	0.0017
YAL067C	SEO1	Suppressor of sulfoxide Ethionine resistance	0.00169
YCR088W	ABP1	Actin Binding Protein	0.00169
YGL251C	HFM1	Helicase Family Member	0.00169
YGR065C	VHT1	Vitamin H Transporter	0.00169
YGR278W	CWC22	Complexed With Cef1p	0.00169
YOL020W	TAT2	Tryptophan Amino acid Transporter	0.00169
YAR042W	SWH1		0.00168
YDR144C	MKC7	Multicopy suppressor of Kex2 Cold sensitivity	0.00168
YDR349C	YPS7	YaPSin	0.00168
YGR246C	BRF1	B-Related Factor	0.00168
YLR060W	FRS1	phenylalanyl (F)-tRNA Synthetase	0.00168
YMR198W	CIK1	Chromosome Instability and Karyogamy	0.00168
YGL192W	IME4	Inducer of MEiosis	0.00167
YKR093W	PTR2	Peptide TRansport	0.00167
YOR308C	SNU66	Small NUClear ribonucleoprotein associated	0.00167
YPL169C	MEX67	Messenger RNA EXport factor of 67 kDa	0.00167
YDR046C	BAP3	Branched-chain Amino acid Permease	0.00166
YDR200C	VPS64	Vacuolar Protein Sorting	0.00166
YLR353W	BUD8	BUD site selection	0.00166
YML057W	CMP2	CalModulin binding Protein	0.00166
YOR324C	FRT1	Functionally Related to TCP1	0.00166
YDR341C			0.00165
YHL028W	WSC4	cell Wall integrity and Stress response Component	0.00165
YLR173W			0.00165
YMR168C	CEP3	Centromere Protein	0.00165
YNR039C	ZRG17	Zinc Regulated Gene	0.00165
YPL005W	AEP3	ATPase Expression	0.00165
YPR026W	ATH1	Acid TreHalase	0.00165
YGR216C	GPI1	GlycosylPhosphatidylinositol anchoring biosynthesis	0.00164
YNL268W	LYP1	LYsine-specific Permease	0.00164
YKR019C	IRS4	Increased rDNA Silencing	0.00163

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YMR304W	UBP15	UBiquitin-specific Protease	0.00163
YNL257C	SIP3	SNF1-Interacting Protein	0.00163
YBR069C	TAT1	Tyrosine and tryptophan Amino acid Transporter	0.00162
YDL013W	SLX5	Synthetic Lethal of unknown [X] function	0.00162
YHR032W	ERC1	Ethionine Resistance Conferring	0.00162
YJL103C	GSM1	Glucose Starvation Modulator	0.00162
YJR066W	TOR1	Target Of Rapamycin	0.00162
YKR058W	GLG1	Glycogenin-Like Gene	0.00162
YNL121C	TOM70	Translocase of the Outer Mitochondrial membrane	0.00162
YFL041W	FET5	FErrous Transport	0.00161
YFL049W	SWP82	SWi/snf-associated Protein	0.00161
YHR206W	SKN7	Suppressor of Kre Null	0.00161
YAL011W	SWC3	SWr Complex	0.0016
YDR425W	SNX41	Sorting NeXin	0.0016
YIL055C			0.0016
YLR177W			0.0016
YOR348C	PUT4	Proline UTilization	0.0016
YCR061W			0.00159
YHR035W	NEL1	Non-ERES Localized Sec23 homolog 1	0.00159
YHR171W	ATG7	AuTophagy related	0.00159
YIL014W	MNT3	MaNnosylTransferase	0.00159
YKL155C	RSM22	Ribosomal Small subunit of Mitochondria	0.00159
YML046W	PRP39	Pre-mRNA Processing	0.00159
YBR021W	FUR4	5-FIUoRouridine sensitivity	0.00158
YCL025C	AGP1	high-Affinity Glutamine Permease	0.00158
YDR049W	VMS1	VCP/Cdc48-associated Mitochondrial Stress-responsive	0.00158
YDR419W	RAD30	RADiation sensitive	0.00158
YHR114W	BZZ1		0.00158
YJL045W			0.00158
YKL204W	EAP1	EIF4E-Associated Protein	0.00158
YBR280C	SAF1	SCF Associated Factor	0.00157
YDL070W	BDF2	BromoDomain Factor	0.00157
YDR266C	HEL2	Histone E3 Ligase	0.00157
YLR436C	ECM30	ExtraCellular Mutant	0.00157
YMR058W	FET3	FErrous Transport	0.00157
YOR070C	GYP1	Gtpase-activating protein for YPt1p	0.00157
YDR398W	UTP5	U Three Protein	0.00156
YDR484W	VPS52	Vacuolar Protein Sorting	0.00156
YGL060W	YBP2	Yap1-Binding Protein	0.00156
YHR023W	MYO1	MYOsin	0.00156
YKL048C	ELM1	ELongated Morphology	0.00156
YLR330W	CHS5	CHitin Synthase-related	0.00156
YPL210C	SRP72	Signal Recognition Particle	0.00156
YFL054C	AQY3	AQuaporin from Yeast	0.00155
YIL101C	XBP1	XhoI site-Binding Protein	0.00155
YKR036C	CAF4	CCR4 Associated Factor	0.00155
YNL115C			0.00155
YPL253C	VIK1	Vegetative Interaction with Kar3p	0.00155
YDL224C	WHI4	WHIskey	0.00154
YNL167C	SKO1	Suppressor of Kinase Overexpression	0.00154
YGL066W	SGF73	SaGa associated Factor, 73 kDa	0.00153

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YLR425W	TUS1	TOR Unique function Suppressor	0.00153
YOL113W	SKM1	STE20/PAK homologous Kinase related to Morphogenesis	0.00153
YLR299W	ECM38	ExtraCellular Mutant	0.00152
YLR454W	FMP27	Found in Mitochondrial Proteome	0.00152
YPL023C	MET12	METHionine requiring	0.00152
YDR137W	RGP1	Reduced Growth Phenotype	0.00151
YOR254C	SEC63	SECretory	0.00151
YDR189W	SLY1	Suppressor of Loss of Ypt1	0.0015
YDR320C	SWA2	Synthetic lethal With Arf1	0.0015
YEL007W	MIT1	Muc1 expressed Independent of TEC1	0.0015
YGL195W	GCN1	General Control Nonderepressible	0.0015
YJL057C	IKS1		0.0015
YKL029C	MAE1	MAlic Enzyme	0.0015
YLL043W	FPS1	fdp1 Suppressor	0.0015
YDR107C	TMN2	TransMembrane Nine	0.00149
YDR170C	SEC7	SECretory	0.00149
YDR362C	TFC6	Transcription Factor C	0.00149
YNL045W	LAP2	Leucine AminoPeptidases	0.00149
YNL103W	MET4	METHionine requiring	0.00149
YNL125C	ESBP6		0.00149
YDR452W	PPN1		0.00148
YFL036W	RPO41	RNA POlymerase	0.00148
YFR029W	PTR3	Peptide TRansport	0.00148
YLR384C	IKI3	Insensitive to Killer toxin	0.00148
YLR413W	INA1	INDicator of Abscission	0.00148
YMR104C	YPK2	Yeast Protein Kinase	0.00148
YBL024W	NCL1	NuCLear protein	0.00147
YEL023C			0.00147
YLR153C	ACS2	Acetyl CoA Synthetase	0.00147
YLR403W	SFP1	Split Finger Protein	0.00147
YOR336W	KRE5	Killer toxin RESistant	0.00147
YPL089C	RLM1	Resistance to Lethality of MKK1P386 overexpression	0.00147
YPR007C	REC8	RECombination	0.00147
YDL199C			0.00146
YDR172W	SUP35	SUPpressor	0.00146
YLR047C	FRE8		0.00146
YLR117C	CLF1	Crooked neck-Like Factor	0.00146
YLR143W	DPH6	DiPHthamide biosynthesis	0.00146
YLR399C	BDF1	BromoDomain Factor	0.00146
YOL011W	PLB3	PhosphoLipase B	0.00146
YDL141W	BPL1	Biotin:apoProtein Ligase	0.00145
YDR314C	RAD34	Homologous to RAD4	0.00145
YER077C	MRX1	Mitochondrial oRganization of gene eXpression (MIOREX)	0.00145
YGR099W	TEL2	TELomere maintenance	0.00145
YGR270W	YTA7	Yeast Tat-binding Analog	0.00145
YHR020W			0.00145
YMR301C	ATM1	ABC Transporter, Mitochondrial	0.00145
YOR354C	MSC6	Meiotic Sister-Chromatid recombination	0.00145
YPL222W	FMP40	Found in Mitochondrial Proteome	0.00145
YBR115C	LYS2	LYSine requiring	0.00144
YBR169C	SSE2	Stress Seventy subfamily E	0.00144

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YBR255W	MTC4	Maintenance of Telomere Capping	0.00144
YDR234W	LYS4	LYSine requiring	0.00144
YDR338C			0.00144
YER105C	NUP157	NUclear Pore	0.00144
YMR246W	FAA4	Fatty Acid Activation	0.00144
YOR384W	FRE5	Ferric REDuctase	0.00144
YDL214C	PRR2	Pheromone Response Regulator	0.00143
YDR221W	GTB1	Glucosidase Two Beta-subunit	0.00143
YGL131C	SNT2		0.00143
YLR233C	EST1	Ever Shorter Telomeres	0.00143
YGL249W	ZIP2	ZIPping up meiotic chromosomes	0.00142
YJR134C	SGM1	Slow growth on Galactose and Mannose	0.00142
YKL222C			0.00142
YMR176W	ECM5	ExtraCellular Mutant	0.00142
YDR146C	SWI5	SWItching deficient	0.00141
YFR015C	GSY1	Glycogen SYNthase	0.00141
YLR006C	SSK1	Suppressor of Sensor Kinase	0.00141
YLR440C	SEC39	SECretory	0.00141
YMR259C	TRM732	Transfer RNA Methyltransferase	0.00141
YOL057W			0.00141
YAL054C	ACS1	Acetyl CoA Synthetase	0.0014
YFL047W	RGD2	RhoGAP domain	0.0014
YHR074W	QNS1	glutamine (Q) dependent Nad+ Synthetase	0.0014
YJL061W	NUP82	NUclear Pore	0.0014
YKL104C	GFA1	Glutamine:Fructose-6-phosphate Amidotransferase	0.0014
YLR362W	STE11	STERile	0.0014
YNL101W	AVT4	Amino acid Vacuolar Transport	0.0014
YPL164C	MLH3	MutL Homolog	0.0014
YDL167C	NRP1	N (asparagine)-Rich Protein	0.00139
YLR335W	NUP2	NUclear Pore	0.00139
YNR060W	FRE4	Ferric REDuctase	0.00139
YPR159W	KRE6	Killer toxin RESistant	0.00139
YDR205W	MSC2	Meiotic Sister-Chromatid recombination	0.00138
YDR333C	RQC1	Ribosome Quality Control	0.00138
YEL053C	MAK10	MAintenance of Killer	0.00137
YER040W	GLN3	GLutamiNe metabolism	0.00137
YHR149C	SKG6	Suppressor of lethality of Kex2 Gas1 double null mutant	0.00137
YJL168C	SET2	SET domain-containing	0.00137
YLR149C			0.00137
YMR277W	FCP1	tfiiF-associating component of Ctd Phosphatase	0.00137
YOR019W			0.00137
YPL029W	SUV3	SUppressor of Var1	0.00136
YHR178W	STB5	Sin Three Binding protein	0.00135
YKR024C	DBP7	Dead Box Protein	0.00135
YKR067W	GPT2	Glycerol-3-Phosphate acylTransferase	0.00135
YLR054C	OSW2	Outer Spore Wall	0.00135
YFL023W	BUD27	BUD site selection	0.00134
YGL150C	INO80	INOsitol requiring	0.00134
YGR003W	CUL3	CULLin	0.00134
YJR042W	NUP85	NUclear Pore	0.00134
YBL084C	CDC27	Cell Division Cycle	0.00133

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YDR138W	HPR1	HyPerRecombination	0.00133
YER162C	RAD4	RADiation sensitive	0.00133
YKL187C	FAT3	FATty acid transporter 3	0.00133
YKR029C	SET3	SET domain-containing	0.00133
YLL008W	DRS1	Deficiency of Ribosomal Subunits	0.00133
YNL059C	ARP5	Actin-Related Protein	0.00133
YOR321W	PMT3	Protein O-MannosylTransferase	0.00133
YPL074W	YTA6	Yeast Tat-binding Analog	0.00133
YMR179W	SPT21	SuPpressor of Ty	0.00132
YDL138W	RGT2	Restores Glucose Transport	0.00131
YDR406W	PDR15	Pleiotropic Drug Resistance	0.00131
YER017C	AFG3	ATPase Family Gene	0.00131
YIR007W	EGH1	Cryptococcus neoformans EGCrP2 Homolog	0.00131
YKR027W	BCH2	Bud7 and Chs6 Homolog	0.00131
YNL311C	SKP2	homology with human SKP2	0.00131
YGR245C	SDA1	Severe Depolymerization of Actin	0.0013
YLR176C	RFX1	Regulatory Factor X	0.0013
YNL247W			0.0013
YBR001C	NTH2	Neutral TreHalase	0.00128
YBR058C	UBP14	UBiquitin-specific Protease	0.00128
YDR208W	MSS4	Multicopy Suppressor of Stt4 mutation	0.00128
YLR397C	AFG2	ATPase Family Gene	0.00128
YBR114W	RAD16	RADiation sensitive	0.00127
YDL239C	ADY3	Accumulation of DYads	0.00127
YDR239C			0.00127
YGR200C	ELP2	ELongator Protein	0.00127
YNR033W	ABZ1	para-AminoBenZoic acid (PABA) biosynthesis	0.00127
YBR284W			0.00126
YER184C	TOG1	Transcriptional regulator of Oleate utilization Genes	0.00126
YHL035C	VMR1	Vacuolar Multidrug Resistance	0.00126
YHR204W	MNL1	MaNnosidase-Like protein	0.00126
YCL030C	HIS4	HIStidine requiring	0.00125
YJL212C	OPT1	OligoPeptide Transporter	0.00125
YNL139C	THO2	suppressor of the Transcriptional defect of Hpr1 by Overexpress	0.00125
YOR233W	KIN4	KINase	0.00125
YGL216W	KIP3	Klnesin related Protein	0.00124
YIL068C	SEC6	SECretory	0.00124
YIL095W	PRK1	p53 Regulatory Kinase	0.00124
YDL132W	CDC53	Cell Division Cycle	0.00123
YDR258C	HSP78	Heat Shock Protein	0.00123
YNL238W	KEX2	Killer EXpression defective	0.00123
YGR198W	YPP1	alpha-sYnuclein Protective Protein	0.00122
YJL102W	MEF2	Mitochondrial Elongation Factor	0.00122
YJL187C	SWE1	Saccharomyces WEe1	0.00122
YNL297C	MON2	MONensin sensitivity	0.00122
YPL153C	RAD53	RADiation sensitive	0.00122
YJL176C	SWI3	SWItching deficient	0.00121
YJR140C	HIR3	Hlstone Regulation	0.00121
YKL176C	LST4	Lethal with Sec Thirteen	0.00121
YML103C	NUP188	NUclear Pore	0.00121
YMR089C	YTA12	Yeast Tat-binding Analog	0.00121

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YNL085W	MKT1	Maintenance of K2 Killer Toxin	0.00121
YNL256W	FOL1	FOLic acid synthesis	0.00121
YAL021C	CCR4	Carbon Catabolite Repression	0.0012
YBL004W	UTP20	U Three Protein	0.0012
YBL052C	SAS3	Something About Silencing	0.0012
YCR106W	RDS1	Regulator of Drug Sensitivity	0.0012
YDL140C	RPO21	RNA POLymerase	0.0012
YGL073W	HSF1	Heat Shock transcription Factor	0.0012
YML034W	SRC1	Spliced mRNA and Cell cycle regulated gene	0.0012
YOR018W	ROD1	Resistance to O-Dinitrobenzene	0.0012
YBL008W	HIR1	Hlstone Regulation	0.00119
YFL024C	EPL1	Enhancer of Polycomb Like	0.00119
YIL149C	MLP2	Myosin-Like Protein	0.00119
YKL022C	CDC16	Cell Division Cycle	0.00119
YML029W	USA1	U1-Snp1 Associating	0.00119
YNL041C	COG6	Conserved Oligomeric Golgi complex	0.00119
YNL298W	CLA4	CLn Activity dependant	0.00119
YBR237W	PRP5	Pre-mRNA Processing	0.00118
YER167W	BCK2	Bypass of C Kinase	0.00118
YLR057W	MNL2	MaNnosidase-Like protein	0.00118
YPL105C	SYH1	SmY2 Homolog	0.00118
YDR369C	XRS2	X-Ray Sensitive	0.00117
YDR505C	PSP1	Polymerase SuPpressor	0.00117
YJL165C	HAL5	HALotolerance	0.00117
YKL121W	DGR2	2-Deoxy-Glucose Resistant 2	0.00117
YDR351W	SBE2	Suppressor of BEm4	0.00116
YDR416W	SYF1	SYnthetic lethal with cdcForty	0.00116
YLR001C			0.00116
YLR115W	CFT2	Cleavage Factor Two	0.00116
YMR165C	PAH1	Phosphatidic Acid phosphoHydrolase	0.00116
YPL008W	CHL1	CHromosome Loss	0.00116
YPL141C	FRK1	Fatty acyl-CoA synthetase and RNA processing-associated Kina	0.00116
YBL023C	MCM2	MiniChromosome Maintenance	0.00115
YCR030C	SYP1	Suppressor of Yeast Profilin deletion	0.00115
YLR166C	SEC10	SECretory	0.00115
YNL172W	APC1	Anaphase Promoting Complex subunit	0.00115
YDR475C	JIP4	Jumonji domain Interacting Protein	0.00114
YLR386W	VAC14	VACuole morphology and inheritance mutant	0.00114
YNL325C	FIG4	Factor-Induced Gene	0.00114
YJL070C			0.00113
YBL014C	RRN6	Regulation of RNA polymerase I	0.00112
YLR092W	SUL2	SULfate	0.00112
YOR129C	AFI1	ArF3-Interacting protein	0.00112
YOR371C	GPB1		0.00112
YPL126W	NAN1	Net1 Associated Nuclear protein	0.00112
YPL249C	GYP5	Gtpase-activating protein for Ypt Proteins	0.00112
YDR409W	SIZ1	SAP and mIZ-finger domain	0.00111
YIL047C	SYG1	Suppressor of Yeast Gpa1	0.00111
YLR336C	SGD1	Suppressor of Glycerol Defect	0.00111
YPL150W			0.00111
YDR213W	UPC2	UPtake Control	0.0011

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YGL233W	SEC15	SECretory	0.0011
YLR309C	IMH1	shares with Integrins and Myosins significant Homology	0.0011
YNL321W	VNX1	Vacuolar Na ⁺ /H ⁺ eXchanger	0.0011
YIL017C	VID28	Vacuolar Import and Degradation	0.00109
YKL165C	MCD4	Morphogenesis Checkpoint Dependent	0.00109
YCR037C	PHO87	PHOsphate metabolism	0.00108
YCR057C	PWP2	Periodic tryptophan (W) Protein	0.00108
YER024W	YAT2		0.00108
YKR095W	MLP1	Myosin-Like Protein	0.00107
YLR024C	UBR2		0.00107
YPL195W	APL5	clathrin Adaptor Protein complex Large chain	0.00107
YDR395W	SXM1	Suppressor of mRNA eXport Mutant	0.00106
YIL137C	TMA108	Translation Machinery Associated	0.00106
YLR129W	DIP2	DOM34 Interacting Protein	0.00106
YMR124W	EPO1	Endoplasmic reticulum POLarization	0.00106
YEL043W			0.00105
YGR100W	MDR1	Mac1-Dependent Regulator	0.00105
YDL035C	GPR1	G-Protein coupled Receptor	0.00104
YNL023C	FAP1	FKBP12-Associated Protein	0.00104
YOL090W	MSH2	MutS Homolog	0.00104
YBL005W	PDR3	Pleiotropic Drug Resistance	0.00103
YDR238C	SEC26	SECretory	0.00103
YEL032W	MCM3	MiniChromosome Maintenance	0.00103
YMR275C	BUL1	Binds Ubiquitin Ligase	0.00103
YKL015W	PUT3	Proline UTilization	0.00102
YDR430C	CYM1	CYtosolic Metalloprotease	0.00101
YIR002C	MPH1	Mutator PHenotype	0.00101
YAL035W	FUN12	Function Unknown Now	0.001
YDR270W	CCC2	Cross-Complements Ca(2+) phenotype of csg1	0.001
YNL327W	EGT2	Early G1 Transcript	0.001
YOL021C	DIS3	homolog of S. pombe dis3 (chromosome DISjunction)	0.001
YOR363C	PIP2	Peroxisome Induction Pathway	0.001
YDR379W	RGA2	Rho GTPase Activating Protein	0.00099
YIL125W	KGD1	alpha-KetoGlutarate Dehydrogenase	0.00099
YJL207C	LAA1	Large AP-1 Accessory	0.00099
YOR127W	RGA1	Rho GTPase Activating Protein	0.00099
YOR349W	CIN1	Chromosome INstability	0.00099
YBL037W	APL3	clathrin Adaptor Protein complex Large chain	0.00098
YCR092C	MSH3	MutS Homolog	0.00098
YGR047C	TFC4	Transcription Factor class C	0.00098
YDR325W	YCG1	Yeast Cap G	0.00097
YFR030W	MET10	METHionine requiring	0.00097
YGL207W	SPT16	SuPpressor of Ty	0.00097
YGR258C	RAD2	RADiation sensitivity	0.00097
YIL031W	ULP2	UbL-specific Protease	0.00097
YLR389C	STE23	STERile	0.00097
YAL051W	OAF1	Oleate-Activated transcription Factor	0.00096
YBL104C	SEA4	SEh1-Associated	0.00096
YKL197C	PEX1	PEroXin	0.00096
YCR093W	CDC39	Cell Division Cycle	0.00095
YJL098W	SAP185	Sit4 Associated Protein	0.00095

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YML075C	HMG1	3-Hydroxy-3-MethylGlutaryl-coenzyme a reductase	0.00095
YMR261C	TPS3	Trehalose Phosphate Synthase	0.00095
YCR067C	SED4	Suppressor of Erd2 Deletion	0.00094
YDR310C	SUM1	SUPpressor of Mar1-1	0.00094
YGR274C	TAF1	TATA binding protein-Associated Factor	0.00094
YNL267W	PIK1	Phosphatidyl Inositol Kinase	0.00094
YNL278W	CAF120	CCR4 Associated Factor	0.00094
YBR150C	TBS1	ThiaBendazole Sensitive	0.00093
YFL034W	MIL1	Medium adaptin-Interacting Ligand	0.00093
YKR086W	PRP16	Pre-mRNA Processing	0.00093
YOR098C	NUP1	NUclear Pore	0.00093
YPR042C	PUF2	PUmilio-homology domain Family	0.00093
YHR077C	NMD2	Nonsense-mediated MRNA Decay	0.00092
YJR035W	RAD26	RADiation sensitive	0.00092
YMR308C	PSE1	Protein Secretion Enhancer	0.00092
YGR094W	VAS1	VAlyl-tRNA Synthetase	0.00091
YKL092C	BUD2	BUD site selection	0.00091
YML100W	TSL1	Trehalose Synthase Long chain	0.00091
YPL216W			0.00091
YBL063W	KIP1	Klnesin related Protein	0.0009
YBL101C	ECM21	ExtraCellular Mutant	0.0009
YGL094C	PAN2	Poly(A)-binding protein-dependent poly(A) riboNuclease	0.0009
YHR079C	IRE1	Inositol REquiring	0.0009
YMR047C	NUP116	NUclear Pore	0.0009
YNL163C	RIA1	RIbosome Assembly	0.0009
YER176W	ECM32	ExtraCellular Mutant	0.00089
YKL105C	SEG2	Stability of Eisosomes Guaranteed	0.00089
YOR304W	ISW2	Imitation SWitch subfamily	0.00089
YGR170W	PSD2	PhosphatidylSerine Decarboxylase	0.00088
YML117W	NAB6	Nucleic Acid Binding protein	0.00088
YPR022C	SDD4	Suppressor of Degenerative Death	0.00088
YDR128W	MTC5	Maintenance of Telomere Capping	0.00087
YDR507C	GIN4	Growth Inhibitory	0.00087
YIL026C	IRR1	IRRegular cell behavior	0.00087
YLR410W	VIP1		0.00087
YAL001C	TFC3	Transcription Factor class C	0.00086
YBR023C	CHS3	CHitin Synthase-related	0.00086
YFR031C	SMC2	Structural Maintenance of Chromosomes	0.00086
YJR041C	URB2	Unhealthy Ribosome Biogenesis	0.00085
YLR272C	YCS4	Yeast Condensin Subunit	0.00085
YOL078W	AVO1	Adheres VOraciously (to TOR2)	0.00085
YBR295W	PCA1	P-type Cation-transporting ATPase	0.00082
YDR335W	MSN5	Multicopy suppressor of SNf1 mutation	0.00082
YEL031W	SPF1	Sensitivity to Pichia Farinosa killer toxin	0.00082
YLR084C	RAX2		0.00082
YMR109W	MYO5	MYOsin	0.00082
YPR095C	SYT1	Suppressor of ypt3	0.00082
YHR155W	LAM1	Lipid transfer protein Anchored at Membrane contact sites	0.00081
YKL203C	TOR2	Target Of Rapamycin	0.00081
YNL273W	TOF1	TOpoisomerase I-interacting Factor	0.00081
YBL007C	SLA1	Synthetic Lethal with ABP1	0.0008

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YJL197W	UBP12	UBiquitin-specific Protease	0.0008
YML081W	TDA9	Topoisomerase I Damage Affected	0.0008
YDL019C	OSH2	OxySterol binding protein Homolog	0.00078
YDR407C	TRS120	TRapp Subunit	0.00078
YPL137C	GIP3	Glc7 Interacting Protein	0.00078
YDR159W	SAC3	Suppressor of ACTin	0.00077
YOL075C			0.00077
YDR216W	ADR1	Alcohol Dehydrogenase II synthesis Regulator	0.00076
YDR217C	RAD9	RADiation sensitive	0.00076
YIL030C	SSM4	Suppressor of mrna Stability Mutant	0.00076
YAL017W	PSK1	Pas domain-containing Serine/threonine protein Kinase	0.00074
YGR061C	ADE6	ADEnine requiring	0.00074
YIL126W	STH1	SNF Two Homolog	0.00074
YOL138C	RTC1	Restriction of Telomere Capping	0.00074
YIL159W	BNR1	BNi1 Related	0.00073
YKR054C	DYN1	DYNein	0.00073
YBL088C	TEL1	TELomere maintenance	0.00072
YJL042W	MHP1	MAP-Homologous Protein	0.00072
YJR127C	RSF2	ReSpiration Factor	0.00072
YCR042C	TAF2	TATA binding protein-Associated Factor	0.00071
YJR031C	GEA1	Guanine nucleotide Exchange on ARF	0.00071
YAL024C	LTE1	Low Temperature Essential	0.0007
YDR443C	SSN2	Suppressor of SNf1	0.0007
YDR464W	SPP41	Suppressor of PrP4	0.0007
YIL115C	NUP159	NUclear Pore	0.0007
YEL022W	GEA2	Guanine nucleotide Exchange on ARF	0.00069
YGR116W	SPT6	SuPpressor of Ty's	0.00069
YAL029C	MYO4	MYOsin	0.00068
YIR006C	PAN1	Poly(A)-binding protein-dependent poly(A) riboNuclease	0.00068
YLR087C	CSF1	Cold Sensitive for Fermentation	0.00068
YNL102W	POL1	POLymerase	0.00068
YOR291W	YPK9	Yeast PARK9	0.00068
YBL079W	NUP170	NUclear Pore	0.00067
YDR011W	SNQ2	Sensitivity to 4-NitroQuinoline-N-oxide	0.00067
YKL010C	UFD4	Ubiquitin Fusion Degradation protein	0.00067
YHR164C	DNA2	DNA synthesis defective	0.00066
YGL173C	XRN1	eXoRiboNuclease	0.00065
YHR186C	KOG1	Kontroller Of Growth	0.00064
YLL040C	VPS13	Vacuolar Protein Sorting	0.00064
YLR247C	IRC20	Increased Recombination Centers	0.00064
YOR326W	MYO2	MYOsin	0.00064
YLR310C	CDC25	Cell Division Cycle	0.00063
YGR098C	ESP1	Extra Spindle Pole bodies	0.00061
YLL048C	YBT1	Yeast Bile Transporter	0.0006
YML059C	NTE1	Neuropathy Target Esterase	0.0006
YMR229C	RRP5	Ribosomal RNA Processing	0.00058
YMR306W	FKS3	FK506 Sensitivity	0.00056
YGR032W	GSC2	Glucan Synthase of Cerevisiae	0.00053
YHR099W	TRA1	similar to human TRRAP	0.00053
YLR342W	FKS1	FK506 Sensitivity	0.00053
YPL231W	FAS2	Fatty Acid Synthetase	0.00053

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YGR271W	SLH1	SKI2-Like Helicase	0.00051
YDL171C	GLT1	GLuTamate synthase	0.00047
YNL262W	POL2	POLymerase	0.00045
YBR140C	IRA1	Inhibitory Regulator of the RAS-cAMP pathway	0.00032
YAL003W	EFB1	Elongation Factor Beta	0
YAL008W	FUN14	Function Unknown Now	0
YAL009W	SPO7	SPOrulation	0
YAL012W	CYS3	CYSThionine gamma-lyase	0
YAL013W	DEP1	Disability in regulation of Expression of genes involved in Phospl	0
YAL014C	SYN8	SYNtaxin	0
YAL015C	NTG1	eNdonuclease Three-like Glycosylase	0
YAL016C-A			0
YAL016W	TPD3	tRNA Processing Deficient	0
YAL019W	FUN30	Function Unknown Now	0
YAL019W-A			0
YAL020C	ATS1	Alpha Tubulin Suppressor	0
YAL022C	FUN26	Function Unknown Now	0
YAL025C	MAK16	MAintenance of Killer	0
YAL026C	DRS2	Deficiency of Ribosomal Subunits	0
YAL026C-A			0
YAL028W	FRT2	Functionally Related to TCP1	0
YAL030W	SNC1	Suppressor of the Null allele of CAP	0
YAL032C	PRP45	Pre-mRNA Processing	0
YAL033W	POP5	Processing Of Precursor RNAs	0
YAL034C	FUN19	Function Unknown Now	0
YAL036C	RBG1	RiBosome interacting Gtpase	0
YAL037C-A			0
YAL037C-B			0
YAL038W	CDC19	Cell Division Cycle	0
YAL039C	CYC3	CYtochrome C	0
YAL040C	CLN3	CycliN	0
YAL041W	CDC24	Cell Division Cycle	0
YAL042C-A			0
YAL042W	ERV46	ER Vesicle	0
YAL043C	PTA1	Pre-Trna Accumulation	0
YAL044C	GCV3	GlyCine cleaVage	0
YAL044W-A	BOL1	BolA-like protein	0
YAL045C			0
YAL046C	BOL3	BolA-like protein	0
YAL047W-A			0
YAL048C	GEM1	GTPase EF-hand protein of Mitochondria	0
YAL053W	FLC2	FLavin Carrier	0
YAL055W	PEX22	PEroXisome related	0
YAL056C-A			0
YAL056W	GPB2		0
YAL059C-A			0
YAL059W	ECM1	ExtraCellular Mutant	0
YAL060W	BDH1	Butanediol DeHydrogenase	0
YAL061W	BDH2		0
YAL062W	GDH3	Glutamate DeHydrogenase	0
YAR002C-A	ERP1	Emp24p/Erv25p Related Protein	0

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YAR003W	SWD1	Set1c, WD40 repeat protein	0
YAR007C	RFA1	Replication Factor A	0
YAR014C	BUD14	BUD site selection	0
YAR015W	ADE1	ADEnine requiring	0
YAR019C	CDC15	Cell Division Cycle	0
YAR019W-A			0
YAR020C	PAU7	seriPAUperin family	0
YAR023C			0
YAR027W	UIP3	Ulp1 Interacting Protein	0
YAR028W			0
YAR029W			0
YAR033W	MST28	Multicopy suppressor of Sec Twenty one	0
YAR035C-A			0
YAR035W	YAT1		0
YAR064W			0
YAR066W			0
YAR068W			0
YBL001C	ECM15	ExtraCellular Mutant	0
YBL002W	HTB2	Histone h Two B	0
YBL003C	HTA2	Histone h Two A	0
YBL006C	LDB7	Low Dye Binding	0
YBL006W-A			0
YBL008W-A			0
YBL010C			0
YBL011W	SCT1	Suppressor of Choline-Transport mutants	0
YBL013W	FMT1	Formyl-Methionyl-tRNA Transformylase	0
YBL015W	ACH1	Acetyl CoA Hydrolase	0
YBL016W	FUS3	cell FUSion	0
YBL018C	POP8	Processing Of Precursor RNAs	0
YBL020W	RFT1	Requiring Fifty-Three	0
YBL021C	HAP3	Heme Activator Protein	0
YBL022C	PIM1	Proteolysis In Mitochondria	0
YBL025W	RRN10	Regulation of RNA polymerase I	0
YBL026W	LSM2	Like SM	0
YBL027W	RPL19B	Ribosomal Protein of the Large subunit	0
YBL029C-A			0
YBL029W			0
YBL032W	HEK2	HEterogeneous nuclear rnp K-like gene	0
YBL033C	RIB1	RIBoflavin biosynthesis	0
YBL036C			0
YBL038W	MRPL16	Mitochondrial Ribosomal Protein, Large subunit	0
YBL039C-A			0
YBL039W-B	MIN6	mitochondrial MINi protein of ~6 kDa	0
YBL040C	ERD2	Endoplasmic reticulum Retention Defective	0
YBL041W	PRE7	PRoteinase yscE	0
YBL042C	FUI1	5-FIUorourldine resistance	0
YBL043W	ECM13	ExtraCellular Mutant	0
YBL045C	COR1	CORE protein of QH2 cytochrome c reductase	0
YBL046W	PSY4	Platinum Sensitivity	0
YBL047C	EDE1	EH Domains and Endocytosis	0
YBL048W	RRT1	Regulator of rDNA Transcription	0

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YBL049W	MOH1		0
YBL050W	SEC17	SECretory	0
YBL051C	PIN4	Psi+ INDucibility	0
YBL053W			0
YBL055C			0
YBL056W	PTC3	Phosphatase Two C	0
YBL059C-A	CMC2	Cx9C Motif-Containing protein	0
YBL059W	IAI11	Interactor of Alm11	0
YBL062W			0
YBL064C	PRX1	PeroxiRedoXin	0
YBL065W			0
YBL066C	SEF1	Suppressor of Essential Function	0
YBL068W	PRS4	PhosphoRibosylpyrophosphate Synthetase	0
YBL068W-A			0
YBL069W	AST1	ATPase STabilizing	0
YBL070C			0
YBL071C			0
YBL071C-B			0
YBL071W-A	KTI11	Kluveromyces lactis Toxin Insensitive	0
YBL074C	AAR2	A1-Alpha2 Repression	0
YBL075C	SSA3	Stress-Seventy subfamily A	0
YBL076C	ILS1	IsoLeucine-tRNA Synthetase	0
YBL077W			0
YBL078C	ATG8	AuTophagy related	0
YBL080C	PET112	PETite colonies	0
YBL083C			0
YBL085W	BOI1	Bem1 (One) Interacting protein	0
YBL086C			0
YBL087C	RPL23A	Ribosomal Protein of the Large subunit	0
YBL090W	MRP21	Mitochondrial Ribosomal Protein	0
YBL091C	MAP2	Methionine AminoPeptidase	0
YBL091C-A	SCS22	Suppressor of Choline Sensitivity	0
YBL092W	RPL32	Ribosomal Protein of the Large subunit	0
YBL093C	ROX3	Regulation by OXYgen	0
YBL094C			0
YBL095W	MRX3	Mitochondrial oRganization of gene eXpression (MIOREX)	0
YBL096C			0
YBL097W	BRN1	homolog of BaRreN	0
YBL098W	BNA4	Biosynthesis of Nicotinic Acid	0
YBL099W	ATP1	ATP synthase	0
YBL100W-C			0
YBL102W	SFT2	Suppressor of sed Five Ts	0
YBL103C	RTG3	ReTroGrade regulation	0
YBL107C	MIX23	Mitochondrial Intermembrane space CX(n)C motif protein	0
YBR003W	COQ1	COenzyme Q	0
YBR004C	GPI18	GlycosylPhosphatidylinositol	0
YBR006W	UGA2	Utilization of GAba	0
YBR008C	FLR1	FLuconazole Resistance	0
YBR014C	GRX7	GlutaRedoXin	0
YBR015C	MNN2	MaNNosyltransferase	0
YBR019C	GAL10	GALactose metabolism	0

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YBR020W	GAL1	GALactose metabolism	0
YBR022W	POA1	Phosphatase Of ADP-ribose 1"-phosphate	0
YBR024W	SCO2	Suppressor of Cytochrome Oxidase deficiency	0
YBR025C	OLA1	Obg-Like ATPase	0
YBR026C	ETR1	2-Enoyl Thioester Reductase	0
YBR028C	YPK3		0
YBR029C	CDS1	CDP-Diacylglycerol Synthase	0
YBR031W	RPL4A	Ribosomal Protein of the Large subunit	0
YBR032W			0
YBR033W	EDS1	Expression Dependent on Slt2	0
YBR034C	HMT1	HnRNP MethylTransferase	0
YBR035C	PDX3	PyriDoXine auxotrophy	0
YBR038W	CHS2	CHitin Synthase	0
YBR039W	ATP3	ATP synthase	0
YBR041W	FAT1	FATty acid transporter	0
YBR043C	QDR3	QuiniDine Resistance	0
YBR044C	TCM62	TriCarboxylic acid cycle Mutant	0
YBR046C	ZTA1	ZeTA-crystallin	0
YBR047W	FMP23	Found in Mitochondrial Proteome	0
YBR048W	RPS11B	Ribosomal Protein of the Small subunit	0
YBR052C	RFS1	Rad55 (Fifty-five) Suppressor	0
YBR054W	YRO2		0
YBR056C-B			0
YBR056W			0
YBR056W-A	MNC1	MaNganese Chelating protein 1	0
YBR057C	MUM2	MUddled Meiosis	0
YBR058C-A	TSC3	Temperature-sensitive Suppressors of Csg2 mutants	0
YBR059C	AKL1	Ark family Kinase-Like protein	0
YBR060C	ORC2	Origin Recognition Complex	0
YBR061C	TRM7	Transfer RNA Methyltransferase	0
YBR063C			0
YBR064W			0
YBR067C	TIP1	Temperature shock-Inducible Protein	0
YBR068C	BAP2	Branched-chain Amino acid Permease	0
YBR071W			0
YBR072C-A			0
YBR072W	HSP26	Heat Shock Protein	0
YBR076C-A			0
YBR076W	ECM8	ExtraCellular Mutant	0
YBR077C	SLM4	Synthetic Lethal with Mss4	0
YBR078W	ECM33	ExtraCellular Mutant	0
YBR079C	RPG1		0
YBR080C	SEC18	SECreatory	0
YBR082C	UBC4	UBiquitin-Conjugating	0
YBR084C-A	RPL19A	Ribosomal Protein of the Large subunit	0
YBR084W	MIS1	MItochondrial C1-tetrahydrofolate Synthase	0
YBR085C-A			0
YBR085W	AAC3	ADP/ATP Carrier	0
YBR087W	RFC5	Replication Factor C	0
YBR088C	POL30	POLymerase	0
YBR089C-A	NHP6B	Non-Histone Protein	0

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YBR091C	TIM12	Translocase of the Inner Membrane	0
YBR096W			0
YBR098W	MMS4	Methyl MethaneSulfonate sensitivity	0
YBR101C	FES1	Factor Exchange for Ssa1p	0
YBR102C	EXO84	EXOcyst	0
YBR103C-A			0
YBR104W	YMC2	Yeast Mitochondrial Carrier	0
YBR106W	SND3	SRP-iNDependent targeting	0
YBR107C	IML3	Increased Minichromosome Loss	0
YBR109C	CMD1	CalMoDulin	0
YBR109W-A			0
YBR110W	ALG1	Asparagine-Linked Glycosylation	0
YBR111C	YSA1		0
YBR111W-A	SUS1	Sl gene Upstream of ySa1	0
YBR116C			0
YBR121C-A			0
YBR124W			0
YBR126C	TPS1	Trehalose-6-Phosphate Synthase	0
YBR126W-A	MEO1	Mini ER ORF	0
YBR126W-B			0
YBR127C	VMA2	Vacuolar Membrane Atpase	0
YBR128C	ATG14	AuTophagy related	0
YBR129C	OPY1	Overproduction-induced Pheromone-resistant Yeast	0
YBR131C-A			0
YBR131W	CCZ1	Calcium Caffeine Zinc sensitivity	0
YBR132C	AGP2	high-Affinity Glutamine Permease	0
YBR133C	HSL7	Histone Synthetic Lethal	0
YBR135W	CKS1	Cdc28 Kinase Subunit	0
YBR136W	MEC1	Mitosis Entry Checkpoint	0
YBR137W			0
YBR138C			0
YBR139W	ATG42	AuTophagy	0
YBR141C	BMT2	Base MethylTransferase of 25S RNA	0
YBR141W-A			0
YBR142W	MAK5	MAintenance of Killer	0
YBR143C	SUP45	SUPpressor	0
YBR144C			0
YBR145W	ADH5	Alcohol DeHydrogenase	0
YBR146W	MRPS9	Mitochondrial Ribosomal Protein, Small subunit	0
YBR149W	ARA1	D-ARAbinose dehydrogenase	0
YBR151W	APD1	Actin Patches Distal	0
YBR152W	SPP381	Suppressor of PrP38-1	0
YBR154C	RPB5	RNA Polymerase B	0
YBR158W	AMN1	Antagonist of Mitotic exit Network	0
YBR159W	IFA38		0
YBR160W	CDC28	Cell Division Cycle	0
YBR161W	CSH1	CSG1/SUR1 Homolog	0
YBR162C	TOS1	Target Of Sbf	0
YBR162W-A	YSY6		0
YBR164C	ARL1	ADP-Ribosylation factor-Like	0
YBR165W	UBS1	UBiquitin-conjugating enzyme Suppressor	0

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YBR168W	PEX32	PEroXisome related	0
YBR170C	NPL4	Nuclear Protein Localization	0
YBR171W	SEC66	SECretory	0
YBR172C	SMY2	Suppressor of MYo2-66	0
YBR173C	UMP1	Ubiquitin-Mediated Proteolysis	0
YBR174C			0
YBR175W	SWD3	Set1c, WD40 repeat protein	0
YBR176W	ECM31	ExtraCellular Mutant	0
YBR177C	EHT1	Ethanol Hexanoyl Transferase	0
YBR178W			0
YBR179C	FZO1	FuZzy Onions homolog	0
YBR183W	YPC1	Yeast Phyto-Ceramidase	0
YBR184W			0
YBR185C	MBA1	Multi-copy Bypass of AFG3	0
YBR186W	PCH2	Pachytene CHeckpoint	0
YBR187W	GDT1	Gcr1 Dependent Translation factor	0
YBR188C	NTC20	Prp19p (NineTeen)-associated Complex	0
YBR189W	RPS9B	Ribosomal Protein of the Small subunit	0
YBR190W			0
YBR191W	RPL21A	Ribosomal Protein of the Large subunit	0
YBR191W-A			0
YBR192W	RIM2	Replication In Mitochondria	0
YBR193C	MED8	MEDIator complex	0
YBR194W	AIM4	Altered Inheritance rate of Mitochondria	0
YBR195C	MSI1	Multicopy Suppressor of IRA1	0
YBR196C	PGI1	PhosphoGlucolsomerase	0
YBR196C-A			0
YBR196C-B			0
YBR197C			0
YBR198C	TAF5	TATA binding protein-Associated Factor	0
YBR200W	BEM1	Bud EMergence	0
YBR200W-A			0
YBR201C-A	MIN7	mitochondrial MINi protein of ~7 kDa	0
YBR201W	DER1	Degradation in the Endoplasmic Reticulum	0
YBR203W	COS111	Ciclopirox Olamine Sensitive	0
YBR205W	KTR3	Kre Two Related	0
YBR206W			0
YBR207W	FTH1	FTR1 Homolog	0
YBR208C	DUR1,2	Degradation of URea	0
YBR209W			0
YBR210W	ERV15	ER Vesicle Protein	0
YBR211C	AME1	Associated with Microtubules and Essential	0
YBR212W	NGR1	Negative Growth Regulatory protein	0
YBR214W	SDS24	homolog of S. pombe SDS23	0
YBR215W	HPC2	Histone Periodic Control	0
YBR216C	YBP1	Yap1-Binding Protein	0
YBR217W	ATG12	AuTophagy related	0
YBR218C	PYC2	PYruvate Carboxylase	0
YBR219C			0
YBR220C			0
YBR221C	PDB1	Pyruvate Dehydrogenase Beta subunit	0

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YBR221W-A			0
YBR222C	PCS60	Peroxisomal CoA-dependent Synthetase	0
YBR223C	TDP1	Tyrosyl-DNA Phosphodiesterase	0
YBR223W-A			0
YBR224W			0
YBR225W			0
YBR226C			0
YBR227C	MCX1	Mitochondrial ClpX	0
YBR228W	SLX1	Synthetic Lethal of unknown (X) function	0
YBR229C	ROT2	Reversal Of Tor2 lethality	0
YBR230C	OM14	Outer Membrane Protein of 14 kDa	0
YBR230W-A	COQ21	COQ interacting protein	0
YBR232C			0
YBR233W	PBP2	Pbp1p Binding Protein	0
YBR233W-A	DAD3	Duo1 And Dam1 interacting	0
YBR234C	ARC40	ARp2/3 Complex subunit	0
YBR236C	ABD1		0
YBR238C			0
YBR240C	THI2	THIamine metabolism	0
YBR241C			0
YBR242W			0
YBR243C	ALG7	Asparagine-Linked Glycosylation	0
YBR244W	GPX2	Glutathione PeroXidase	0
YBR249C	ARO4	AROMATIC amino acid requiring	0
YBR251W	MRPS5	Mitochondrial Ribosomal Protein, Small subunit	0
YBR252W	DUT1	DUTp pyrophosphatase	0
YBR253W	SRB6	Suppressor of RNA polymerase B	0
YBR254C	TRS20	TRapp Subunit	0
YBR255C-A	RCF3	Respiratory superComplex Factor	0
YBR256C	RIB5	RIBoflavin biosynthesis	0
YBR257W	POP4	Processing Of Precursor RNAs	0
YBR258C	SHG1	Set1c, Hypothetical G	0
YBR261C	TAE1	Translation Associated Element	0
YBR262C	MIC12	Mitochondrial contact site and Cristae organizing system	0
YBR263W	SHM1	Serine HydroxyMethyltransferase	0
YBR266C	SLM6	Synthetic Lethal with Mss4	0
YBR267W	REI1	REquired for Isotropic bud growth	0
YBR269C	SDH8	Succinate DeHydrogenase	0
YBR271W	EFM2	Elongation Factor Methyltransferase	0
YBR273C	UBX7	UBiquitin regulatory X	0
YBR274W	CHK1	CHECKpoint Kinase	0
YBR275C	RIF1	RAP1-Interacting Factor	0
YBR277C			0
YBR278W	DPB3	DNA Polymerase B (II) subunit	0
YBR279W	PAF1	RNA Polymerase II Associated Factor	0
YBR282W	MRPL27	Mitochondrial Ribosomal Protein, Large subunit	0
YBR285W			0
YBR290W	BSD2	Bypass Sod1p Defects	0
YBR291C	CTP1	Citrate Transport Protein	0
YBR296C	PHO89	PHOSphate metabolism	0
YBR296C-A	TYC1	Tiny Yeast Comet 1	0

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YCL001W	RER1	Retention in the Endoplasmic Reticulum	0
YCL001W-A			0
YCL001W-B			0
YCL004W	PGS1	PhosphatidylGlycerolphosphate Synthase	0
YCL005W	LDB16	Low Dye Binding	0
YCL007C			0
YCL008C	STP22	STerile Pseudoreversion	0
YCL011C	GBP2	G-strand Binding Protein	0
YCL012C			0
YCL017C	NFS1	NiFS-like	0
YCL018W	LEU2	LEUcine biosynthesis	0
YCL021W-A			0
YCL023C			0
YCL026C-B	HBN1	Homologous to Bacterial Nitroreductases	0
YCL028W	RNQ1	Rich in asparagine (N) and glutamine (Q)	0
YCL029C	BIK1	BIlateral Karyogamy defect	0
YCL031C	RRP7	Ribosomal RNA Processing	0
YCL033C	MXR2	peptide Methionine sulfoXide Reductase	0
YCL035C	GRX1	GlutaRedoXin	0
YCL037C	SRO9	Suppressor of rho3	0
YCL038C	ATG22	AuTophagy related	0
YCL039W	GID7	Glucose Induced Degradation deficient	0
YCL040W	GLK1	GLucoKinase	0
YCL043C	PDI1	Protein Disulfide Isomerase	0
YCL044C	MGR1	Mitochondrial Genome Required	0
YCL045C	EMC1	ER Membrane protein Complex	0
YCL046W			0
YCL047C	POF1	Promoter Of Filamentation	0
YCL048W-A			0
YCL050C	APA1	AP4A phosphorylase	0
YCL054W	SPB1	Suppressor of PaB1 mutant	0
YCL055W	KAR4	KARyogamy	0
YCL056C	PEX34	PEroXin	0
YCL057C-A	MIC10	MItochondrial contact site and Cristae organizing system	0
YCL057W	PRD1	PRoteinase yscD	0
YCL058C	FYV5	Function required for Yeast Viability	0
YCL058W-A	ADF1	Antisense of Depressing Factor	0
YCL059C	KRR1	contains KRR-R motif	0
YCL063W	VAC17	VACuole related	0
YCL064C	CHA1	Catabolism of Hydroxy Amino acids	0
YCR001W			0
YCR002C	CDC10	Cell Division Cycle	0
YCR003W	MRPL32	Mitochondrial Ribosomal Protein, Large subunit	0
YCR004C	YCP4		0
YCR005C	CIT2	CITrate synthase	0
YCR008W	SAT4		0
YCR009C	RVS161	Reduced Viability on Starvation	0
YCR010C	ADY2	Accumulation of DYads	0
YCR011C	ADP1	ATP-Dependent Permease	0
YCR012W	PGK1	3-PhosphoGlycerate Kinase	0
YCR013C			0

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YCR014C	POL4	POLymerase	0
YCR015C	CTO1	Cold TOLerance	0
YCR020C-A	MAK31	MAintenance of Killer	0
YCR021C	HSP30	Heat Shock Protein	0
YCR022C			0
YCR023C			0
YCR024C	SLM5	Synthetic Lethal with Mss4	0
YCR024C-A	PMP1	Plasma Membrane Proteolipid	0
YCR024C-B			0
YCR025C			0
YCR027C	RHB1	RHeB homolog	0
YCR028C	FEN2	FENpropimorph resistance	0
YCR028C-A	RIM1	Replication In Mitochondria	0
YCR031C	RPS14A	Ribosomal Protein of the Small subunit	0
YCR034W	ELO2	fatty acid ELONGation	0
YCR035C	RRP43	Ribosomal RNA Processing	0
YCR036W	RBK1	RiBoKinase	0
YCR038W-A			0
YCR043C			0
YCR045W-A			0
YCR046C	IMG1	Integrity of Mitochondrial Genome	0
YCR047C	BUD23	BUD site selection	0
YCR047W-A			0
YCR048W	ARE1	Acyl-coenzyme A: cholesterol acyl transferase-Related Enzyme	0
YCR049C			0
YCR050C			0
YCR053W	THR4	THReonine requiring	0
YCR054C	CTR86	Copper TRansport protein	0
YCR059C	YIH1	Yeast Impact Homolog	0
YCR060W	TAH1	Tpr-containing protein Associated with Hsp90	0
YCR063W	BUD31	BUD site selection	0
YCR064C			0
YCR065W	HCM1	High-Copy suppressor of Calmodulin	0
YCR066W	RAD18	RADiation sensitive	0
YCR068W	ATG15	AuTophagy related	0
YCR069W	CPR4	Cyclosporin-sensitive Proline Rotamase	0
YCR071C	IMG2	Integrity of Mitochondrial Genome	0
YCR075C	ERS1	ERd Suppressor	0
YCR075W-A	EGO2	Exit from rapamycin-induced GrOWth arrest	0
YCR076C	FUB1	FUnction of Boundary	0
YCR077C	PAT1	Protein Associated with Topoisomerase II	0
YCR081C-A			0
YCR082W	AHC2	Ada Histone acetyltransferase complex Component	0
YCR083W	TRX3	ThioRedoXin	0
YCR084C	TUP1	dTMP-UPtake	0
YCR087C-A			0
YCR090C			0
YCR094W	CDC50	Cell Division Cycle	0
YCR095C	OCA4	Oxidant-induced Cell-cycle Arrest	0
YCR095W-A			0
YCR098C	GIT1	GlycerophosphoInosiTol	0

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YCR105W	ADH7	Alcohol DeHydrogenase	0
YDL002C	NHP10	Non-Histone Protein	0
YDL003W	MCD1	Mitotic Chromosome Determinant	0
YDL004W	ATP16	ATP synthase	0
YDL005C	MED2	MEDiator complex	0
YDL006W	PTC1	Phosphatase type Two C	0
YDL007W	RPT2	Regulatory Particle Triple-A protein, or Regulatory Particle Triphosphatase	0
YDL008W	APC11	Anaphase Promoting Complex	0
YDL009C			0
YDL012C			0
YDL014W	NOP1	Nucleolar Protein	0
YDL015C	TSC13	Temperature-sensitive Suppressors of Csg2 mutants	0
YDL017W	CDC7	Cell Division Cycle	0
YDL021W	GPM2	Glycerate Phosphomutase	0
YDL022C-A			0
YDL022W	GPD1	Glycerol-3-Phosphate Dehydrogenase	0
YDL025W-A			0
YDL028C	MPS1	MonoPolar Spindle	0
YDL029W	ARP2	Actin-Related Protein	0
YDL030W	PRP9	Pre-mRNA Processing	0
YDL031W	DBP10	Dead Box Protein	0
YDL032W			0
YDL033C	SLM3	Synthetic Lethal with Mss4	0
YDL040C	NAT1	N-terminal Acetyltransferase	0
YDL041W			0
YDL042C	SIR2	Silent Information Regulator	0
YDL043C	PRP11	Pre-mRNA Processing	0
YDL044C	MTF2	Mitochondrial Transcription Factor	0
YDL046W	NPC2	Niemann Pick type C homolog	0
YDL047W	SIT4	Suppressor of Initiation of Transcription	0
YDL049C	KNH1	Kre9(Nine) Homolog	0
YDL050C			0
YDL051W	LHP1	La-Homologous Protein	0
YDL053C	PBP4	Pbp1p Binding Protein	0
YDL054C	MCH1	MonoCarboxylate transporter Homolog	0
YDL055C	PSA1		0
YDL056W	MBP1	MluI-box Binding Protein	0
YDL057W			0
YDL058W	USO1	yUSOu - transport in Japanese	0
YDL059C	RAD59	RADiation sensitive	0
YDL060W	TSR1	Twenty S rRNA accumulation	0
YDL061C	RPS29B	Ribosomal Protein of the Small subunit	0
YDL062W			0
YDL063C	SYO1	SYnchronized impOrt or SYmpOrtin	0
YDL064W	UBC9	UBiquitin-Conjugating	0
YDL066W	IDP1	Isocitrate Dehydrogenase, NADP-specific	0
YDL067C	COX9	Cytochrome c OXidase	0
YDL068W			0
YDL069C	CBS1	Cytochrome B Synthesis	0
YDL071C			0
YDL072C	YET3	Yeast Endoplasmic reticulum Transmembrane protein	0

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YDL073W	AHK1	Associated with HKr1	0
YDL074C	BRE1	BREfeldin A sensitivity	0
YDL075W	RPL31A	Ribosomal Protein of the Large subunit	0
YDL078C	MDH3	Malate DeHydrogenase	0
YDL081C	RPP1A	Ribosomal Protein P1 Alpha	0
YDL082W	RPL13A	Ribosomal Protein of the Large subunit	0
YDL083C	RPS16B	Ribosomal Protein of the Small subunit	0
YDL084W	SUB2	SUPpressor of Brr1-1	0
YDL085C-A			0
YDL086C-A			0
YDL087C	LUC7	Lethal Unless Cap-binding complex is produced	0
YDL089W	NUR1	NUclear Rim1	0
YDL091C	UBX3	UBiquitin regulatory X	0
YDL094C			0
YDL095W	PMT1	Protein O-MannosylTransferase	0
YDL096C	OPI6	OverProducer of Inositol	0
YDL097C	RPN6	Regulatory Particle Non-ATPase	0
YDL098C	SNU23	Small NUclear ribonucleoprotein associated	0
YDL105W	NSE4	Non-SMC Element	0
YDL108W	KIN28	protein KINase	0
YDL110C	TMA17	Translation Machinery Associated	0
YDL114W-A			0
YDL115C	IWR1	Interacts With RNA polymerase II	0
YDL117W	CYK3	CYtoKinesis	0
YDL118W			0
YDL120W	YFH1	Yeast Frataxin Homolog	0
YDL121C	EXP1	ER eXport of Pma1	0
YDL126C	CDC48	Cell Division Cycle	0
YDL128W	VCX1	VaCuolar H+/Ca2+ eXchanger	0
YDL129W			0
YDL130W	RPP1B	Ribosomal Protein P1 Beta	0
YDL130W-A	STF1	STabilizing Factor	0
YDL133C-A	RPL41B	Ribosomal Protein of the Large subunit	0
YDL133W	SRF1	Spo14 Regulatory Factor	0
YDL134C	PPH21	Protein PHosphatase	0
YDL135C	RDI1	Rho GDP Dissociation Inhibitor	0
YDL136W	RPL35B	Ribosomal Protein of the Large subunit	0
YDL137W	ARF2	ADP-Ribosylation Factor	0
YDL144C			0
YDL146W	LDB17	Low Dye Binding	0
YDL147W	RPN5	Regulatory Particle Non-ATPase	0
YDL148C	NOP14	NucleOlar Protein	0
YDL149W	ATG9	AuTophagy related	0
YDL150W	RPC53	RNA Polymerase C	0
YDL151C	BUD30	BUD site selection	0
YDL152W			0
YDL153C	SAS10	Something About Silencing	0
YDL155W	CLB3	CycLin B	0
YDL156W	CMR1	Changed Mutation Rate	0
YDL157C			0
YDL159C-B			0

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YDL159W	STE7	STERile	0
YDL159W-A			0
YDL160C	DHH1	DEAD box Helicase Homolog	0
YDL160C-A	MHF2	Mph1-associated Histone-Fold protein	0
YDL161W	ENT1	Epsin N-Terminal homology	0
YDL163W			0
YDL164C	CDC9	Cell Division Cycle	0
YDL165W	CDC36	Cell Division Cycle	0
YDL166C	FAP7	Factor Activating Pos9	0
YDL169C	UGX2	Unidentified Gene X	0
YDL170W	UGA3	Utilization of GAba	0
YDL172C			0
YDL173W	PAR32	Phosphorylated After Rapamycin	0
YDL174C	DLD1	D-Lactate Dehydrogenase	0
YDL175C	AIR2	Arginine methyltransferase-Interacting RING finger protein	0
YDL176W			0
YDL177C			0
YDL178W	DLD2	D-Lactate Dehydrogenase	0
YDL179W	PCL9	Pho85 CycLin	0
YDL180W			0
YDL181W	INH1	INHibitor (of F1F0-ATPase)	0
YDL184C	RPL41A	Ribosomal Protein of the Large subunit	0
YDL185C-A			0
YDL185W	VMA1	Vacuolar Membrane Atpase	0
YDL187C			0
YDL188C	PPH22	Protein PHosphatase	0
YDL189W	RBS1	RNA-Binding Suppressor of PAS kinase	0
YDL190C	UFD2	Ubiquitin Fusion Degradation	0
YDL191W	RPL35A	Ribosomal Protein of the Large subunit	0
YDL192W	ARF1	ADP-Ribosylation Factor	0
YDL194W	SNF3	Sucrose NonFermenting	0
YDL200C	MGT1	O-6-MethylGuanine-DNA methylTTransferase	0
YDL202W	MRPL11	Mitochondrial Ribosomal Protein, Large subunit	0
YDL203C	ACK1	Activator of C Kinase 1	0
YDL205C	HEM3	HEME biosynthesis	0
YDL206W			0
YDL208W	NHP2	Non-Histone Protein	0
YDL210W	UGA4	Utilization of GAba	0
YDL211C			0
YDL212W	SHR3	Super high Histidine Resistant	0
YDL213C	NOP6	NucleOlar Protein	0
YDL217C	TIM22	Translocase of the Inner Mitochondrial membrane	0
YDL219W	DTD1	D-Tyr-tRNA(Tyr) Deacylase	0
YDL221W			0
YDL222C	FMP45	Found in Mitochondrial Proteome	0
YDL225W	SHS1	Seventh Homolog of Septin	0
YDL226C	GCS1	Growth Cold Sensitive	0
YDL227C	HO	HOmothallic switching endonuclease	0
YDL231C	BRE4	BREfeldin A sensitivity	0
YDL232W	OST4	OligoSaccharylTransferase	0
YDL234C	GYP7	Gtpase-activating protein for Ypt7 Protein	0

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YDL235C	YPD1	tYrosine Phosphatase Dependent	0
YDL236W	PHO13	PHOsphate metabolism	0
YDL237W	AIM6	Altered Inheritance rate of Mitochondria	0
YDL240C-A			0
YDL240W	LRG1	Lim-RhoGap homolog	0
YDL241W			0
YDL242W			0
YDR001C	NTH1	Neutral TreHalase	0
YDR002W	YRB1	Yeast Ran Binder	0
YDR003W	RCR2	Resistance to Congo Red	0
YDR003W-A			0
YDR004W	RAD57	RADiation sensitive	0
YDR005C	MAF1		0
YDR006C	SOK1	Suppressor Of Kinase	0
YDR007W	TRP1	TRyPtophan	0
YDR008C			0
YDR012W	RPL4B	Ribosomal Protein of the Large subunit	0
YDR013W	PSF1	Partner of Sld Five	0
YDR016C	DAD1	Duo1 And Dam1 interacting	0
YDR019C	GCV1	GlyCine cleaVage	0
YDR020C	DAS2	Dst1-delta 6-Azaauracil Sensitivity	0
YDR023W	SES1	SEryl-tRNA Synthetase	0
YDR024W	FYV1	Function required for Yeast Viability	0
YDR025W	RPS11A	Ribosomal Protein of the Small subunit	0
YDR028C	REG1	REsistance to Glucose repression	0
YDR029W			0
YDR030C	RAD28	RADiation sensitive	0
YDR032C	PST2	Protoplasts-SecreTed	0
YDR033W	MRH1	Membrane protein Related to Hsp30p	0
YDR034C	LYS14	LYSine requiring	0
YDR034C-A			0
YDR034W-B			0
YDR035W	ARO3	AROmatic amino acid requiring	0
YDR041W	RSM10	Ribosomal Small subunit of Mitochondria	0
YDR043C	NRG1	Negative Regulator of Glucose-repressed genes	0
YDR044W	HEM13	HEMe biosynthesis	0
YDR045C	RPC11	RNA Polymerase C	0
YDR047W	HEM12	HEMe biosynthesis	0
YDR048C			0
YDR050C	TPI1	Triose-Phosphate Isomerase	0
YDR051C	DET1	Decreased Ergosterol Transport	0
YDR052C	DBF4	DumbBell Former	0
YDR053W			0
YDR054C	CDC34	Cell Division Cycle	0
YDR056C	EMC10	ER Membrane protein Complex	0
YDR058C	TGL2	TriacylGlycerol Lipase	0
YDR059C	UBC5	UBiquitin-Conjugating	0
YDR064W	RPS13	Ribosomal Protein of the Small subunit	0
YDR067C	OCA6	Oxidant-induced Cell-cycle Arrest	0
YDR070C	FMP16	Found in Mitochondrial Proteome	0
YDR071C	PAA1	PolyAmine Acetyltransferase	0

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YDR075W	PPH3	Protein PHosphatase	0
YDR077W	SED1	Suppression of Exponential Defect	0
YDR079W	PET100	PETite colonies	0
YDR083W	RRP8	Ribosomal RNA Processing	0
YDR084C	TVP23	Tlg2-Vesicle Protein	0
YDR086C	SSS1	Sec Sixty-one Suppressor	0
YDR088C	SLU7	Synergistic Lethal with U5 snRNA	0
YDR089W	VTC5	Vacuole Transporter Chaperone	0
YDR090C	ILT1	Ionic Liquid Tolerance	0
YDR091C	RLI1	RNase L Inhibitor	0
YDR092W	UBC13	UBiquitin-Conjugating	0
YDR098C	GRX3	GlutaRedoXin	0
YDR099W	BMH2	Brain Modulosignalin Homolog	0
YDR101C	ARX1	Associated with Ribosomal eXport complex	0
YDR102C			0
YDR105C	TMS1		0
YDR108W	TRS85	TRapp Subunit	0
YDR109C			0
YDR110W	FOB1	FOrk Blocking less	0
YDR111C	ALT2	ALanine Transaminase	0
YDR112W	IRC2	Increased Recombination Centers	0
YDR113C	PDS1	Precocious Dissociation of Sisters	0
YDR116C	MRPL1	Mitochondrial Ribosomal Protein, Large subunit	0
YDR117C	TMA64	Translation Machinery Associated	0
YDR118W-A			0
YDR119W	VBA4	Vacuolar Basic Amino acid transporter	0
YDR119W-A	COX26		0
YDR121W	DPB4	DNA Polymerase B (II) subunit	0
YDR122W	KIN1	KINase	0
YDR124W			0
YDR125C	ECM18	ExtraCellular Mutant	0
YDR126W	SWF1	Spore Wall Formation	0
YDR129C	SAC6	Suppressor of ACTin	0
YDR130C	FIN1	Filaments In between Nuclei	0
YDR131C			0
YDR133C			0
YDR135C	YCF1	Yeast Cadmium Factor	0
YDR139C	RUB1	Related to UBiquitin	0
YDR141C	DOP1	homolog of A. nidulans DOPey	0
YDR142C	PEX7	PEroXin	0
YDR143C	SAN1	Sir Antagonist	0
YDR145W	TAF12	TATA binding protein-Associated Factor	0
YDR148C	KGD2	alpha-KetoGlutarate Dehydrogenase	0
YDR149C			0
YDR151C	CTH1	Cysteine-Three-Histidine	0
YDR152W	GIR2	Genetically Interacts with Ribosomal genes	0
YDR153C	ENT5	Epsin N-Terminal homology	0
YDR154C			0
YDR155C	CPR1	Cyclosporin A-sensitive Proline Rotamase	0
YDR156W	RPA14	RNA Polymerase A	0
YDR158W	HOM2	HOMoserine requiring	0

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YDR162C	NBP2	Nap1 Binding Protein	0
YDR163W	CWC15	Complexed With Cef1p	0
YDR164C	SEC1	SECretory	0
YDR165W	TRM82	Transfer RNA Methyltransferase	0
YDR166C	SEC5	SECretory	0
YDR167W	TAF10	TATA binding protein-Associated Factor	0
YDR168W	CDC37	Cell Division Cycle	0
YDR169C-A			0
YDR171W	HSP42	Heat Shock Protein	0
YDR173C	ARG82	ARGinine requiring	0
YDR174W	HMO1	High MObility group (HMG) family	0
YDR175C	RSM24	Ribosomal Small subunit of Mitochondria	0
YDR176W	NGG1		0
YDR178W	SDH4	Succinate DeHydrogenase	0
YDR179C	CSN9	Cop9 SigNalosome subunit	0
YDR179W-A	NVJ3	Nucleus-Vacuole Junction	0
YDR180W	SCC2	Sister Chromatid Cohesion	0
YDR182W	CDC1	Cell Division Cycle	0
YDR182W-A			0
YDR183C-A			0
YDR184C	ATC1	Aip Three Complex	0
YDR186C	SND1	Srp-iNDependent targeting	0
YDR187C			0
YDR188W	CCT6	Chaperonin Containing TCP-1	0
YDR190C	RVB1	RuVB-like	0
YDR192C	NUP42	NUclear Pore	0
YDR193W			0
YDR194W-A			0
YDR195W	REF2	RNA End Formation	0
YDR199W			0
YDR202C	RAV2	Regulator of (H+)-ATPase in Vacuolar membrane	0
YDR203W			0
YDR210W			0
YDR211W	GCD6	General Control Derepressed	0
YDR212W	TCP1	Tailless Complex Polypeptide	0
YDR218C	SPR28	SPorulation Regulated	0
YDR219C	MFB1	Mitochondria-associated F-Box protein	0
YDR224C	HTB1	Histone h Two B	0
YDR225W	HTA1	Histone h Two A	0
YDR228C	PCF11	Protein 1 of Cleavage and polyadenylation Factor I	0
YDR229W	IVY1	Interacting with Vps33p and Ypt7p	0
YDR230W			0
YDR231C	COX20	Cytochrome c OXidase	0
YDR232W	HEM1	HEMe biosynthesis	0
YDR237W	MRPL7	Mitochondrial Ribosomal Protein, Large subunit	0
YDR240C	SNU56	Small NUclear ribonucleoprotein associated	0
YDR241W	BUD26	BUD site selection	0
YDR242W	AMD2	AMiDase	0
YDR243C	PRP28	Pre-mRNA Processing	0
YDR244W	PEX5	PEroXin	0
YDR246W-A			0

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YDR248C			0
YDR249C			0
YDR250C			0
YDR251W	PAM1	Pp2A Multicopy suppressor	0
YDR252W	BTT1	BTf Three	0
YDR253C	MET32	METHionine requiring	0
YDR254W	CHL4	CHromosome Loss	0
YDR257C	RKM4	Ribosomal lysine (K) Methyltransferase	0
YDR260C	SWM1	Spore Wall Maturation	0
YDR265W	PEX10	PEroXin	0
YDR267C	CIA1	Cytosolic Iron-sulfur protein Assembly	0
YDR268W	MSW1	Mitochondrial aminoacyl-tRNA Synthetase, tryptophan (W)	0
YDR269C			0
YDR271C			0
YDR272W	GLO2	GLyOxalase	0
YDR275W	BSC2	Bypass of Stop Codon	0
YDR281C	PHM6	PHosphate Metabolism	0
YDR286C	MGP12	Mitochondrial Glutaredoxin-like Protein of 12 kDa	0
YDR290W			0
YDR292C	SRP101	Signal Recognition Particle	0
YDR297W	SUR2	SUPpressor of Rvs161 and rvs167 mutations	0
YDR299W	BFR2	BreFeldin A Resistance	0
YDR300C	PRO1	PROline requiring	0
YDR301W	CFT1	Cleavage Factor Two	0
YDR302W	GPI11	GlycosylPhosphatidylinositol anchor biosynthesis	0
YDR304C	CPR5	Cyclosporin-sensitive Proline Rotamase	0
YDR305C	HNT2	Histidine triad NucleoTide-binding	0
YDR306C			0
YDR308C	SRB7	Suppressor of RNA polymerase B	0
YDR309C	GIC2	GTPase Interactive Component	0
YDR311W	TFB1	Transcription Factor B	0
YDR313C	PIB1	Phosphatidylinositol(3)-phosphate Binding	0
YDR315C	IPK1	Inositol Polyphosphate Kinase	0
YDR316W	OMS1	OXA1 Multicopy Suppressor	0
YDR319C	YFT2		0
YDR320C-A	DAD4	Duo1 And Dam1 interacting	0
YDR321W	ASP1	ASParaginase	0
YDR322C-A	TIM11	Translocase of the Inner Mitochondrial membrane	0
YDR322W	MRPL35	Mitochondrial Ribosomal Protein, Large subunit	0
YDR324C	UTP4	U Three Protein	0
YDR327W			0
YDR328C	SKP1	Suppressor of Kinetochore Protein mutant	0
YDR330W	UBX5	UBiquitin regulatory X	0
YDR331W	GPI8	GlycosylPhosphatidylinositol anchor biosynthesis	0
YDR332W	IRC3	Increased Recombination Centers	0
YDR334W	SWR1	SWi2/snf2-Related	0
YDR336W	MRX8	Mitochondrial oRganization of gene eXpression (MIOREX)	0
YDR337W	MRPS28	Mitochondrial Ribosomal Protein, Small subunit	0
YDR339C	FCF1	Faf1p Copurifying Factor	0
YDR344C			0
YDR346C	SVF1	SurVival Factor	0

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YDR347W	MRP1	Mitochondrial Ribosomal Protein	0
YDR350C	ATP22	ATPase synthase	0
YDR352W	YPQ2	Yeast PQ-loop protein	0
YDR353W	TRR1	ThioRedoxin Reductase	0
YDR354C-A			0
YDR354W	TRP4	TRyPtophan	0
YDR355C			0
YDR357C	CNL1	CNo-Like	0
YDR358W	GGA1	Golgi-localized, Gamma-adaptin ear homology, Arf-binding prote	0
YDR359C	EAF1	Esa1p-Associated Factor	0
YDR360W	OPI7	OverProducer of Inositol	0
YDR361C	BCP1		0
YDR363W	ESC2	Establishment of Silent Chromatin	0
YDR363W-A	SEM1	Suppressor of Exocyst Mutations	0
YDR364C	CDC40	Cell Division Cycle	0
YDR365C	ESF1	Eighteen S rRNA Factor	0
YDR368W	YPR1	Yeast Putative Reductase	0
YDR370C	DXO1	Decapping eXOnuclease	0
YDR371C-A			0
YDR372C	VPS74	Vacuolar Protein Sorting	0
YDR373W	FRQ1	FReQuenin homolog	0
YDR374W-A	WIP1	W-Ilke Protein	0
YDR376W	ARH1	Adrenodoxin Reductase Homolog	0
YDR377W	ATP17	ATP synthase	0
YDR378C	LSM6	Like SM	0
YDR379C-A	SDH6		0
YDR380W	ARO10	AROmatic amino acid requiring	0
YDR381C-A	COI1	COx Interacting	0
YDR381W	YRA1	Yeast RNA Annealing protein	0
YDR382W	RPP2B	Ribosomal Protein P2 Beta	0
YDR383C	NKP1	Non-essential Kinetochore Protein	0
YDR386W	MUS81	MMS and UV Sensitive	0
YDR388W	RVS167	Reduced Viability on Starvation	0
YDR389W	SAC7	Suppressor of ACtin	0
YDR390C	UBA2	UBiquitin Activating	0
YDR391C			0
YDR392W	SPT3	SuPpressor of Ty's	0
YDR394W	RPT3	Regulatory Particle Triple-A protein, or Regulatory Particle Triph	0
YDR396W			0
YDR397C	NCB2	Negative Cofactor B	0
YDR399W	HPT1	Hypoxanthine guanine PhosphoribosylTransferase	0
YDR400W	URH1	URidine Hydrolase	0
YDR401W			0
YDR402C	DIT2	DITyrosine	0
YDR403W	DIT1	DITyrosine	0
YDR404C	RPB7	RNA Polymerase B	0
YDR406W-A			0
YDR408C	ADE8	ADEnine requiring	0
YDR410C	STE14	STERile	0
YDR411C	DFM1	Der1-like Family Member	0
YDR412W	RRP17	Ribosomal RNA Processing	0

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YDR413C			0
YDR415C			0
YDR417C			0
YDR418W	RPL12B	Ribosomal Protein of the Large subunit	0
YDR421W	ARO80	AROMatic amino acid requiring	0
YDR422C	SIP1	SNF1-Interacting Protein	0
YDR423C	CAD1	CADmium resistance	0
YDR424C	DYN2	DYNein	0
YDR427W	RPN9	Regulatory Particle Non-ATPase	0
YDR429C	TIF35	Translation Initiation Factor	0
YDR431W			0
YDR434W	GPI17	GlycosylPhosphatidylinositol anchor biosynthesis	0
YDR436W	PPZ2	Protein Phosphatase Z	0
YDR437W	GPI19	Glycosyl Phosphatidylinositol anchor biosynthesis	0
YDR438W	THI74	THlamine regulon	0
YDR439W	LRS4	Loss of RDNA Silencing	0
YDR440W	DOT1	Disruptor Of Telomeric silencing	0
YDR441C	APT2	Adenine PhosphoribosylTransferase	0
YDR444W			0
YDR447C	RPS17B	Ribosomal Protein of the Small subunit	0
YDR449C	UTP6	U Three Protein	0
YDR450W	RPS18A	Ribosomal Protein of the Small subunit	0
YDR451C	YHP1	Yeast Homeo-Protein	0
YDR453C	TSA2	Thiol-Specific Antioxidant	0
YDR454C	GUK1	GUanylate Kinase	0
YDR455C			0
YDR456W	NHX1	Na ⁺ /H ⁺ eXchanger	0
YDR457W	TOM1	Temperature dependent Organization in Mitotic nucleus or Trigg	0
YDR458C	HEH2	Helix-Extension-Helix domain	0
YDR459C	PFA5	Protein Fatty Acyltransferase	0
YDR460W	TFB3	Transcription Factor B subunit 3	0
YDR461C-A	CMI8	Cytosolic Mlni protein of ~8 kDa	0
YDR461W	MFA1	Mating Factor A	0
YDR463W	STP1	Species-specific tRNA Processing	0
YDR464C-A			0
YDR465C	RMT2	aRginine MeThyltransferase	0
YDR466W	PKH3	Pkb-activating Kinase Homolog	0
YDR467C			0
YDR468C	TLG1	T-snare affecting a Late Golgi compartment	0
YDR469W	SDC1	Set1c, homolog of Dpy30 from C.elegans	0
YDR470C	UGO1	UGO (Japanese for fusion)	0
YDR471W	RPL27B	Ribosomal Protein of the Large subunit	0
YDR472W	TRS31	TRapp Subunit	0
YDR476C			0
YDR477W	SNF1	Sucrose NonFermenting	0
YDR478W	SNM1	Suppressor of Nuclear Mitochondrial endoribonuclease	0
YDR479C	PEX29	PEroXisome related	0
YDR480W	DIG2	Down-regulator of Invasive Growth	0
YDR481C	PHO8	PHOspate metabolism	0
YDR482C	CWC21	Complexed With Cef1p	0
YDR483W	KRE2	Killer toxin RESistant	0

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YDR486C	VPS60	Vacuolar Protein Sorting	0
YDR487C	RIB3	RIBoflavin biosynthesis	0
YDR490C	PKH1	Pkb-activating Kinase Homolog	0
YDR491C			0
YDR493W	MZM1	Mitochondrial Zinc Maintenance	0
YDR494W	RSM28	Ribosomal Small subunit of Mitochondria	0
YDR498C	SEC20	SECretory	0
YDR499W	LCD1	Lethal, Checkpoint-defective, DNA damage sensitive	0
YDR500C	RPL37B	Ribosomal Protein of the Large subunit	0
YDR503C	LPP1	Lipid Phosphate Phosphatase	0
YDR510C-A			0
YDR510W	SMT3	Suppressor of Mif Two	0
YDR513W	GRX2	GlutaRedoXin	0
YDR516C	EMI2	Early Meiotic Induction	0
YDR517W	GRH1	GRasp65 (Golgi reassembly stacking protein of 65kD) Homolog	0
YDR518W	EUG1	ER protein Unnecessary for Growth	0
YDR519W	FPR2	FKBP Proline Rotamase	0
YDR520C	URC2	URacil Catabolism	0
YDR521W			0
YDR522C	SPS2	SPorulation Specific	0
YDR523C	SPS1	SPorulation Specific	0
YDR524C	AGE1	Arf Gap with Effector function(s)	0
YDR524C-A			0
YDR524C-B			0
YDR524W-C			0
YDR525W	API2	APIcal	0
YDR525W-A	SNA2	Sensitivity to NA+	0
YDR526C			0
YDR527W	RBA50	RNA polymerase II (B) Associated protein	0
YDR528W	HLR1	Homolog of LRe1	0
YDR529C	QCR7	ubiQuinol-cytochrome C oxidoReductase	0
YDR530C	APA2	AP4A phosphorylase	0
YDR533C	HSP31	Heat-Shock Protein	0
YDR535C			0
YDR537C			0
YDR538W	PAD1	Phenylacrylic Acid Decarboxylase	0
YDR539W	FDC1	Ferulic acid DeCarboxylase	0
YDR540C	IRC4	Increased Recombination Centers	0
YDR541C			0
YEL003W	GIM4	Gene Involved in Microtubule biogenesis	0
YEL008C-A			0
YEL008W			0
YEL014C			0
YEL017C-A	PMP2	Plasma Membrane Proteolipid	0
YEL017W	GTT3	GlutaThione Transferase	0
YEL018C-A			0
YEL018W	EAF5	Esa1p-Associated Factor	0
YEL019C	MMS21	Methyl MethaneSulfonate sensitivity	0
YEL020C	PXP1	PeroXisomal Protein	0
YEL020C-B			0
YEL020W-A	TIM9	Translocase of the Inner Mitochondrial membrane	0

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YEL024W	RIP1	Rieske Iron-sulfur Protein	0
YEL026W	SNU13	Small NUClear ribonucleoprotein associated	0
YEL027W	VMA3	Vacuolar Membrane Atpase	0
YEL028W			0
YEL030C-A			0
YEL032C-A			0
YEL034W	HYP2	HYPusine-containing protein	0
YEL038W	UTR4	Unidentified TRanscript	0
YEL039C	CYC7	CYtochrome C	0
YEL044W	IES6	Ino Eighty Subunit	0
YEL045C			0
YEL047C	FRD1	Fumarate ReDuctase	0
YEL048C	TCA17	TRAPP Complex Associated protein	0
YEL050C	RML2	Ribosomal Mitochondrial Large	0
YEL050W-A			0
YEL051W	VMA8	Vacuolar Membrane Atpase	0
YEL053W-A			0
YEL054C	RPL12A	Ribosomal Protein of the Large subunit	0
YEL056W	HAT2	Histone AcetylTransferase	0
YEL057C	SDD1	Suppressor of Degenerative Death	0
YEL059C-A	SOM1	SOrting Mitochondrial	0
YEL060C	PRB1	PRoteinase B	0
YEL061C	CIN8	Chromosome INstability	0
YEL062W	NPR2	Nitrogen Permease Regulator	0
YEL063C	CAN1	CANavanine resistance	0
YEL064C	AVT2	Amino acid Vacuolar Transport	0
YEL065W	SIT1	Siderophore Iron Transport	0
YEL066W	HPA3	Histone and other Protein Acetyltransferase	0
YEL067C			0
YEL071W	DLD3	D-Lactate Dehydrogenase	0
YEL072W	RMD6	Required for Meiotic nuclear Division	0
YEL073C			0
YER006W	NUG1	NUclear GTPase	0
YER009W	NTF2	Nuclear Transport Factor	0
YER012W	PRE1	PRoteinase yscE	0
YER014C-A	BUD25	BUD site selection	0
YER014W	HEM14	HEMe biosynthesis	0
YER015W	FAA2	Fatty Acid Activation	0
YER016W	BIM1	Blinding to Microtubules	0
YER019C-A	SBH2	Sec61 beta homolog 2	0
YER019W	ISC1	Inositol phosphoSphingolipid phospholipase C	0
YER020W	GPA2	G Protein Alpha subunit	0
YER022W	SRB4	Suppressor of RNA polymerase B	0
YER023C-A			0
YER023W	PRO3	PROline requiring	0
YER025W	GCD11	General Control Derepressed	0
YER027C	GAL83	GALactose metabolism	0
YER028C	MIG3	Multicopy Inhibitor of Growth	0
YER029C	SMB1	SmB/B' homolog	0
YER030W	CHZ1	Chaperone for Htz1/H2A-H2B dimer	0
YER031C	YPT31	Yeast Protein Two	0

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YER032W	FIR1	Factor Interacting with REF2	0
YER036C	ARB1	ATP-binding cassette protein involved in Ribosome Biogenesis	0
YER038W-A	FMP49	Found in Mitochondrial Proteome	0
YER039C-A			0
YER041W	YEN1		0
YER043C	SAH1	S-Adenosyl-I-Homocysteine hydrolase	0
YER044C	ERG28	ERGosterol biosynthesis	0
YER046W	SPO73	SPOrulation	0
YER048C	CAJ1		0
YER048W-A	ISD11	Iron-Sulfur protein biogenesis, Desulfurase-interacting protein	0
YER049W	TPA1	Termination and PolyAdenylation	0
YER053C	PIC2	PI Carrier	0
YER053C-A			0
YER054C	GIP2	Glc7-Interacting Protein	0
YER055C	HIS1	HISidine	0
YER056C-A	RPL34A	Ribosomal Protein of the Large subunit	0
YER057C	HMF1	Homologous Mmf1p Factor	0
YER059W	PCL6	Pho85 CycLin	0
YER060W	FCY21	FluoroCYtosine resistance	0
YER060W-A	FCY22	FluoroCYtosine resistance	0
YER062C	GPP2	Glycerol-3-Phosphate Phosphatase	0
YER063W	THO1	suppressor of the Transcriptional defect of Hpr1 by Overexpress	0
YER066C-A			0
YER066W	RRT13	Regulator of rDNA Transcription	0
YER067C-A			0
YER067W	RGI1	Respiratory Growth Induced	0
YER068C-A			0
YER068W	MOT2	Modulator Of Transcription	0
YER069W	ARG5,6	ARGinine requiring	0
YER070W	RNR1	RiboNucleotide Reductase	0
YER071C	TDA2	Topoisomerase I Damage Affected	0
YER072W	VTC1	Vacuolar Transporter Chaperone	0
YER074W	RPS24A	Ribosomal Protein of the Small subunit	0
YER074W-A	YOS1	Yip One Suppressor	0
YER078C	ICP55	Intermediate Cleaving Peptidase	0
YER078W-A			0
YER079C-A			0
YER079W			0
YER080W	AIM9	Altered Inheritance rate of Mitochondria	0
YER081W	SER3	SERine requiring	0
YER083C	GET2	Guided Entry of Tail-anchored proteins	0
YER084W			0
YER084W-A			0
YER085C			0
YER086W	ILV1	IsoLeucine-plus-Valine requiring	0
YER087C-A			0
YER087C-B	SBH1	Sec61 beta homolog 1	0
YER087W	AIM10	Altered Inheritance rate of Mitochondria	0
YER088C	DOT6	Disruptor Of Telomeric silencing	0
YER088C-A			0
YER088W-B			0

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YER089C	PTC2	Phosphatase Two C	0
YER090C-A			0
YER090W	TRP2	TRyPtophan	0
YER091C	MET6	METHionine requiring	0
YER091C-A			0
YER092W	IES5	Ino Eighty Subunit	0
YER093C-A	AIM11	Altered Inheritance rate of Mitochondria	0
YER094C	PUP3	PUtative Proteasome subunit	0
YER095W	RAD51	RADiation sensitive	0
YER096W	SHC1	Sporulation-specific Homolog of CSD4	0
YER098W	UBP9	UBiquitin-specific Protease	0
YER099C	PRS2	PhosphoRibosylpyrophosphate Synthetase	0
YER100W	UBC6	UBiquitin-Conjugating	0
YER101C	AST2	ATPase STabilizing	0
YER103W	SSA4	Stress-Seventy subfamily A	0
YER104W	RTT105	Regulator of Ty1 Transposition	0
YER110C	KAP123	KAryoPherin	0
YER112W	LSM4	Like SM	0
YER113C	TMN3	TransMembrane Nine	0
YER115C	SPR6	SPorulation Regulated	0
YER116C	SLX8	Synthetic Lethal of unknown (X) function	0
YER117W	RPL23B	Ribosomal Protein of the Large subunit	0
YER119C-A			0
YER120W	SCS2	Suppressor of Choline Sensitivity	0
YER121W			0
YER123W	YCK3	Yeast Casein Kinase	0
YER125W	RSP5	Reverses Spt- Phenotype	0
YER126C	NSA2	Nop Seven Associated	0
YER127W	LCP5	Lethal with Conditional Pap1	0
YER128W	VFA1	Vps Four-Associated	0
YER130C	COM2	Cousin of Msn2	0
YER131W	RPS26B	Ribosomal Protein of the Small subunit	0
YER133W	GLC7	GLyCogen	0
YER133W-A			0
YER134C			0
YER135C			0
YER136W	GDI1	GDP Dissociation Inhibitor	0
YER137C			0
YER137W-A			0
YER140W	EMP65	ER Membrane Protein of 65 kDa	0
YER141W	COX15	Cytochrome c OXidase	0
YER142C	MAG1	3-MethylAdenine DNA Glycosylase	0
YER143W	DDI1	DNA Damage Inducible	0
YER145C	FTR1	Fe TRansporter	0
YER146W	LSM5	Like SM	0
YER147C	SCC4	Sister Chromatid Cohesion	0
YER147C-A			0
YER148W	SPT15	SuPpressor of Ty insertions	0
YER150W	SPI1	Stationary Phase Induced	0
YER151C	UBP3	UBiquitin-specific Protease	0
YER152C			0

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YER153C	PET122	PETite colonies	0
YER154W	OXA1	cytochrome OXidase Activity	0
YER156C			0
YER158W-A			0
YER163C	GCG1	Gamma-glutamyl Cyclotransferase acting on Glutathione	0
YER164W	CHD1	Chromatin organization modifier, Helicase, and DNA-binding dor	0
YER165C-A			0
YER165W	PAB1	Poly(A) Binding protein	0
YER166W	DNF1	Drs2 Neo1 Family	0
YER170W	ADK2	ADenylate Kinase	0
YER171W	RAD3	RA DIation sensitive	0
YER172C-A			0
YER173W	RAD24	RA DIation sensitive	0
YER174C	GRX4	GlutaRedoXin	0
YER178W	PDA1	Pyruvate Dehydrogenase Alpha	0
YER179W	DMC1	Disrupted Meiotic cDNA	0
YER180C	ISC10	message Induced in Sporogenesis in S. Cervisiae	0
YER180C-A	SLO1	Scoco-Like Orf	0
YER182W	FMP10	Found in Mitochondrial Proteome	0
YER185W	PUG1	Protoporphyrin Uptake Gene	0
YER187W			0
YFL003C	MSH4	MutS Homolog	0
YFL005W	SEC4	SECretery	0
YFL007W	BLM10	BLeoMycin resistance	0
YFL008W	SMC1	Stability of MiniChromosomes	0
YFL010C	WWM1	WW domain containing protein interacting with Metacaspase	0
YFL012W-A			0
YFL013C	IES1	Ino Eighty Subunit	0
YFL013W-A			0
YFL017C	GNA1	GlucosamiNe-6-phosphate Acetyltransferase	0
YFL019C			0
YFL022C	FRS2	phenylalanyl (F)-tRNA Synthetase	0
YFL025C	BST1	Bypass of Sec Thirteen	0
YFL026W	STE2	STERile	0
YFL029C	CAK1	Cdk-Activating Kinase	0
YFL030W	AGX1	Alanine:Glyoxylate aminotrans(X)ferase	0
YFL031C-A			0
YFL031W	HAC1	Homologous to Atf/Creb1	0
YFL034C-A	RPL22B	Ribosomal Protein of the Large subunit	0
YFL037W	TUB2	TUBulin	0
YFL038C	YPT1	Yeast Protein Two	0
YFL039C	ACT1	ACTin	0
YFL042C	LAM5	Lipid transfer protein Anchored at Membrane contact site	0
YFL044C	OTU1	Ovarian TUmor	0
YFL045C	SEC53	SECretery	0
YFL050C	ALR2	ALuminum Resistance	0
YFL052W	ZNF1	ZiNc Finger protein	0
YFL053W	DAK2	DihydroxyAcetone Kinase	0
YFL057C	AAD16	Aryl Alcohol Dehydrogenase	0
YFR001W	LOC1	LOCalization of mRNA	0
YFR004W	RPN11	Regulatory Particle Non-ATPase	0

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YFR007W	YFH7		0
YFR008W	FAR7	Factor ARrest	0
YFR009W	GCN20	General Control Nonderepressible	0
YFR009W-A			0
YFR010W	UBP6	UBiquitin-specific Protease	0
YFR010W-A			0
YFR011C	MIC19	Mitochondrial contact site and Cristae organizing system	0
YFR012W	DCV1	Demands Cdc28 kinase activity for Viability	0
YFR012W-A			0
YFR013W	IOC3	Iswi One Complex	0
YFR014C	CMK1	CalModulin dependent protein Kinase	0
YFR017C	IGD1	Inhibitor of Glycogen Debranching	0
YFR020W	CSS2	Condition Specific Secretion	0
YFR021W	ATG18	AuTophagy related	0
YFR022W	ROG3	Revertant Of Glycogen synthase kinase mutation	0
YFR023W	PES4	Polymerase Epsilon Suppressor	0
YFR031C-A	RPL2A	Ribosomal Protein of the Large subunit	0
YFR032C	RRT5	Regulator of rDNA Transcription	0
YFR032C-A	RPL29	Ribosomal Protein of the Large subunit	0
YFR032C-B	MIN10	mitochondrial MINi protein of 10 kDa	0
YFR033C	QCR6	ubiQuinol-cytochrome C oxidoReductase	0
YFR036W	CDC26	Cell Division Cycle	0
YFR036W-A			0
YFR037C	RSC8	Remodel the Structure of Chromatin	0
YFR039C	OSW7	Outer Spore Wall	0
YFR041C	ERJ5	Endoplasmic Reticulum located J-protein	0
YFR042W	KEG1	Kre6-binding ER protein responsible for Glucan synthesis	0
YFR044C	DUG1	Deficient in Utilization of Glutathione	0
YFR045W			0
YFR046C	CNN1	Co-purified with NNf1p	0
YFR047C	BNA6	Biosynthesis of Nicotinic Acid	0
YFR048W	RMD8	Required for Meiotic nuclear Division	0
YFR049W	YMR31	Yeast Mitochondrial Ribosomal protein	0
YFR050C	PRE4	PRoteinase yscE	0
YFR052C-A			0
YFR052W	RPN12	Regulatory Particle Non-ATPase	0
YFR054C			0
YFR055W	IRC7	Increased Recombination Centers	0
YFR057W			0
YGL001C	ERG26	ERGosterol biosynthesis	0
YGL002W	ERP6	Emp24p/Erv25p Related Protein	0
YGL004C	RPN14	Regulatory Particle Non-ATPase	0
YGL005C	COG7	Conserved Oligomeric Golgi complex	0
YGL006W	PMC1	Plasma Membrane Calcium	0
YGL007C-A			0
YGL008C	PMA1	Plasma Membrane ATPase	0
YGL010W	MPO1	Metabolism of PHS to Odd-numbered fatty acids	0
YGL011C	SCL1	Suppressor of Crl3 ts Lethality	0
YGL014C-A			0
YGL014W	PUF4	PUmilio-homology domain Family	0
YGL015C			0

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YGL016W	KAP122	KAryoPherin	0
YGL018C	JAC1	J-type Accessory Chaperone	0
YGL020C	GET1	Guided Entry of Tail-anchored proteins	0
YGL024W			0
YGL025C	PGD1	PolyGlutamine Domain	0
YGL026C	TRP5	TRyPtophan	0
YGL028C	SCW11	Soluble Cell Wall protein	0
YGL029W	CGR1	Coiled-coil Growth-Regulated	0
YGL030W	RPL30	Ribosomal Protein of the Large subunit	0
YGL031C	RPL24A	Ribosomal Protein of the Large subunit	0
YGL032C	AGA2	a-AGglutinin	0
YGL034C			0
YGL035C	MIG1	Multicopy Inhibitor of GAL gene expression	0
YGL036W			0
YGL037C	PNC1	Pyrazinamidase and NiCotinamidase	0
YGL038C	OCH1	Outer CHain elongation	0
YGL039W			0
YGL040C	HEM2	HEMe biosynthesis	0
YGL041C			0
YGL041C-B			0
YGL041W-A	DPC13	Delta-Psi dependent mitochondrial import and Cleavage protein	0
YGL042C			0
YGL043W	DST1	DNA Strand Transfer	0
YGL044C	RNA15	poly(A) mRNA metabolism	0
YGL047W	ALG13	Asparagine-Linked Glycosylation	0
YGL048C	RPT6	Regulatory Particle Triple-A protein, or Regulatory Particle Triph	0
YGL049C	TIF4632	Translation Initiation Factor	0
YGL050W	TYW3	Trna-YW synthesizing protein	0
YGL054C	ERV14	ER Vesicle	0
YGL055W	OLE1	OLEic acid requiring	0
YGL057C	GEP7	GENetic interactors of Prohibitins	0
YGL058W	RAD6	RADiation sensitive	0
YGL059W	PKP2	Protein Kinase of PDH	0
YGL061C	DUO1	Death Upon Overproduction	0
YGL062W	PYC1	PYruvate Carboxylase	0
YGL063C-A			0
YGL063W	PUS2	PseudoUridine Synthase	0
YGL064C	MRH4	Mitochondrial RNA Helicase	0
YGL065C	ALG2	Asparagine-Linked Glycosylation	0
YGL068W	MNP1	Mitochondrial-Nucleoid Protein	0
YGL069C			0
YGL070C	RPB9	RNA Polymerase B	0
YGL071W	AFT1	Activator of Ferrous Transport	0
YGL072C			0
YGL074C			0
YGL075C	MPS2	MonoPolar Spindle	0
YGL076C	RPL7A	Ribosomal Protein of the Large subunit	0
YGL077C	HNM1	Hyper-resistance to Nitrogen Mustard	0
YGL078C	DBP3	Dead Box Protein	0
YGL080W	MPC1	Mitochondrial Pyruvate Carrier	0
YGL085W	LCL3	Long Chronological Lifespan 3	0

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YGL088W			0
YGL089C	MF(ALPHA)2	Mating Factor ALPHA	0
YGL091C	NBP35	Nucleotide Binding Protein	0
YGL093W	SPC105	Spindle Pole Component	0
YGL095C	VPS45	Vacuolar Protein Sorting	0
YGL101W	YGK1		0
YGL102C			0
YGL103W	RPL28	Ribosomal Protein of the Large subunit	0
YGL105W	ARC1	Aminoacyl-tRNA synthetase Cofactor	0
YGL106W	MLC1	Myosin Light Chain	0
YGL107C	RMD9	Required for Meiotic nuclear Division	0
YGL108C			0
YGL110C	CUE3	Coupling of Ubiquitin conjugation to ER degradation	0
YGL111W	NSA1	Nop Seven Associated	0
YGL112C	TAF6	TATA binding protein-Associated Factor	0
YGL113W	SLD3	Synthetically Lethal with Dpb11-1	0
YGL114W			0
YGL115W	SNF4	Sucrose NonFermenting	0
YGL116W	CDC20	Cell Division Cycle	0
YGL117W			0
YGL118C			0
YGL119W	COQ8	COenzyme Q	0
YGL120C	PRP43	Pre-mRNA Processing	0
YGL121C	GPG1	G Protein Gamma	0
YGL123C-A			0
YGL123W	RPS2	Ribosomal Protein of the Small subunit	0
YGL124C	MON1	MONensin sensitivity	0
YGL125W	MET13	METHionine requiring	0
YGL128C	CWC23	Complexed With Cef1p	0
YGL129C	RSM23	Ribosomal Small subunit of Mitochondria	0
YGL130W	CEG1	Capping Enzyme Guanylyltransferase	0
YGL132W			0
YGL133W	ITC1	Imitation switch Two Complex	0
YGL134W	PCL10	Pho85 CycLin	0
YGL136C	MRM2	Mitochondrial rRNA Methyl transferase	0
YGL137W	SEC27	SECretory	0
YGL138C			0
YGL139W	FLC3	FLavin Carrier	0
YGL140C			0
YGL141W	HUL5	Hect Ubiquitin Ligase	0
YGL142C	GPI10	GlycosylPhosphatidylinositol anchor biosynthesis	0
YGL143C	MRF1	Mitochondrial peptide chain Release Factor	0
YGL144C	ROG1	Revertant Of Glycogen synthase kinase mutation	0
YGL147C	RPL9A	Ribosomal Protein of the Large subunit	0
YGL148W	ARO2	AROMATIC amino acid requiring	0
YGL149W			0
YGL152C			0
YGL153W	PEX14	PEroXisome related	0
YGL154C	LYS5	LYSine requiring	0
YGL155W	CDC43	Cell Division Cycle	0
YGL159W			0

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YGL161C	YIP5	Ypt-Interacting Protein	0
YGL163C	RAD54	RADiation sensitive	0
YGL165C			0
YGL166W	CUP2		0
YGL167C	PMR1	Plasma Membrane ATPase Related	0
YGL168W	HUR1	HydroxyUrea Resistance	0
YGL169W	SUA5	Suppressor of Upstream AUG	0
YGL170C	SPO74	SPOrulation	0
YGL172W	NUP49	NUclear Pore	0
YGL174W	BUD13	BUD site selection	0
YGL175C	SAE2	Sporulation in the Absence of spo Eleven	0
YGL178W	MPT5	Multicopy suppressor of Pop Two	0
YGL180W	ATG1	AuTophagy related	0
YGL182C			0
YGL183C	MND1	Meiotic Nuclear Divisions	0
YGL184C	STR3	Sulfur TRansfer	0
YGL185C			0
YGL186C	TPN1	Transport of PyridoxiNe	0
YGL187C	COX4	Cytochrome c OXidase	0
YGL188C			0
YGL188C-A			0
YGL189C	RPS26A	Ribosomal Protein of the Small subunit	0
YGL190C	CDC55	Cell Division Cycle	0
YGL191W	COX13	Cytochrome c OXidase	0
YGL193C			0
YGL197W	MDS3	Mck1 Dosage Suppressor	0
YGL199C			0
YGL200C	EMP24	EndoMembrane Protein	0
YGL201C	MCM6	MiniChromosome Maintenance	0
YGL202W	ARO8	AROMATIC amino acid requiring	0
YGL203C	KEX1	Killer EXpression defective	0
YGL204C			0
YGL205W	POX1		0
YGL210W	YPT32	Yeast Protein Two	0
YGL211W	NCS6	Needs Cla4 to Survive	0
YGL213C	SKI8	SuperKiller	0
YGL214W			0
YGL215W	CLG1	Cyclin-Like Gene	0
YGL217C			0
YGL220W	BOL2	BolA-like protein	0
YGL221C	NIF3	Ngg1p-Interacting Factor	0
YGL222C	EDC1	Enhancer of mRNA DeCapping	0
YGL223C	COG1	Conserved Oligomeric Golgi complex	0
YGL224C	SDT1	Suppressor of Disruption of TFIIS	0
YGL226C-A	OST5	OligoSaccharylTransferase	0
YGL226W	MTC3	Maintenance of Telomere Capping	0
YGL230C			0
YGL231C	EMC4	ER Membrane protein Complex	0
YGL237C	HAP2	Heme Activator Protein	0
YGL238W	CSE1	Chromosome SEgregation	0
YGL239C			0

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YGL242C			0
YGL243W	TAD1	tRNA-specific Adenosine Deaminase	0
YGL244W	RTF1	Restores TBP Function	0
YGL245W	GUS1	GIUtamyl-tRNA Synthetase	0
YGL246C	RAI1	Rat1p Interacting Protein	0
YGL247W	BRR6	Bad Response to Refrigeration	0
YGL253W	HXK2	HeXoKinase	0
YGL254W	FZF1	Five Zinc Fingers	0
YGL255W	ZRT1	Zinc-Regulated Transporter	0
YGL256W	ADH4	Alcohol DeHydrogenase	0
YGL257C	MNT2	MaNnosylTransferase	0
YGL258W	VEL1	VELum formation	0
YGL258W-A			0
YGR002C	SWC4	SWr Complex	0
YGR004W	PEX31	PEroXisome related	0
YGR005C	TFG2	Transcription Factor G	0
YGR006W	PRP18	Pre-mRNA Processing	0
YGR007W	ECT1	Ethanolamine-phosphate CytidylylTransferase	0
YGR008C	STF2	STabilizing Factor	0
YGR010W	NMA2	Nicotinamide Mononucleotide Adenylyltransferase	0
YGR011W			0
YGR012W	MCY1	putative Mitochondrial CYsteine synthase	0
YGR013W	SNU71	Small NUClear ribonucleoprotein associated	0
YGR014W	MSB2	Multicopy Suppression of a Budding defect	0
YGR015C	EAT1	Ethanol AcetylTransferase	0
YGR016W			0
YGR017W			0
YGR018C			0
YGR020C	VMA7	Vacuolar Membrane Atpase	0
YGR021W	DPC29	Delta-Psi dependent mitochondrial import and Cleavage protein	0
YGR022C			0
YGR024C	THG1	tRNAHis Guanylyltransferase	0
YGR025W			0
YGR027C	RPS25A	Ribosomal Protein of the Small subunit	0
YGR028W	MSP1	Mitochondrial Sorting of Proteins	0
YGR029W	ERV1	Essential for Respiration and Viability	0
YGR030C	POP6	Processing Of Precursor RNAs	0
YGR031C-A	NAG1	Nested Antisense Gene	0
YGR031W	IMO32	Intermediate cleaved by Mitochondrial Octapeptidyl aminopeptid	0
YGR033C	TIM21	Translocase of the Inner Mitochondrial membrane	0
YGR034W	RPL26B	Ribosomal Protein of the Large subunit	0
YGR035C			0
YGR036C	CAX4	CAmodulin-dependent in cmd one two twenty-siX	0
YGR037C	ACB1	Acyl-CoA-Binding	0
YGR038W	ORM1		0
YGR040W	KSS1	Kinase Suppressor of Sst2 mutations	0
YGR043C	NQM1	Non-Quiescent Mutant	0
YGR045C			0
YGR048W	UFD1	Ubiquitin Fusion Degradation protein	0
YGR049W	SCM4	Suppressor of Cdc4 Mutation	0
YGR053C	MCO32	Mitochondrial Class One protein of 32 kDa	0

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YGR054W			0
YGR056W	RSC1	Remodel the Structure of Chromatin	0
YGR057C	LST7	Lethal with Sec Thirteen	0
YGR058W	PEF1	Penta-EF-Hand protein	0
YGR059W	SPR3	SPorulation Regulated	0
YGR060W	ERG25	ERGosterol biosynthesis	0
YGR062C	COX18	Cytochrome c OXidase	0
YGR063C	SPT4	SuPpressor of Ty's	0
YGR064W			0
YGR066C			0
YGR067C			0
YGR068C	ART5	Arrestin-Related Trafficking adaptors	0
YGR068W-A			0
YGR072W	UPF3	UP Frameshift	0
YGR073C			0
YGR074W	SMD1	snRNA Sm binding site protein D1	0
YGR075C	PRP38	Pre-mRNA Processing	0
YGR076C	MRPL25	Mitochondrial Ribosomal Protein, Large subunit	0
YGR078C	PAC10	Perish in the Absence of Cin8p	0
YGR079W			0
YGR080W	TWF1	TWinFilin	0
YGR081C	SLX9		0
YGR082W	TOM20	Translocase of the Outer Mitochondrial membrane	0
YGR083C	GCD2	General Control Derepressed	0
YGR086C	PIL1	Phosphorylation Inhibited by Long chain bases	0
YGR090W	UTP22	U Three Protein	0
YGR092W	DBF2	DumbBell Former	0
YGR095C	RRP46	Ribosomal RNA Processing	0
YGR103W	NOP7	NucleOlar Protein	0
YGR104C	SRB5	Suppressor of RNA polymerase B	0
YGR105W	VMA21	Vacuolar Membrane Atpase	0
YGR106C	VOA1	V0 Assembly protein	0
YGR109C	CLB6	CycLin B	0
YGR110W	CLD1	CardioLipin-specific Deacylase	0
YGR111W			0
YGR112W	SHY1	SURF Homolog of Yeast	0
YGR113W	DAM1	Duo1 And Mps1 interacting	0
YGR114C			0
YGR115C			0
YGR118W	RPS23A	Ribosomal Protein of the Small subunit	0
YGR120C	COG2	Conserved Oligomeric Golgi complex	0
YGR121C	MEP1		0
YGR121W-A			0
YGR122W			0
YGR123C	PPT1	Protein Phosphatase T	0
YGR124W	ASN2	ASparagiNe requiring	0
YGR125W			0
YGR126W			0
YGR127W			0
YGR128C	UTP8	U Three Protein	0
YGR129W	SYF2	SYnthetic lethal with cdc40 (Forty)	0

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YGR130C			0
YGR131W	FHN1	Functional Homolog of Nce102	0
YGR132C	PHB1	ProHiBitin	0
YGR133W	PEX4	PEroXin	0
YGR134W	CAF130	CCR4 Associated Factor	0
YGR135W	PRE9	PRoteinase yscE	0
YGR136W	LSB1	Las Seventeen Binding protein	0
YGR137W			0
YGR140W	CBF2	Centromere-Binding Factor	0
YGR141W	VPS62	Vacuolar Protein Sorting	0
YGR142W	BTN2	BaTteN disease	0
YGR143W	SKN1	Suppressor of Kre Null	0
YGR144W	THI4	THlamine metabolism	0
YGR145W	ENP2	Essential Nuclear Protein	0
YGR146C	ECL1	Extends Chronological Lifespan	0
YGR146C-A			0
YGR147C	NAT2	N-terminal AcetylTransferase	0
YGR148C	RPL24B	Ribosomal Protein of the Large subunit	0
YGR149W	GPC1	GlyceroPhosphoCholine acyltransferase	0
YGR151C			0
YGR152C	RSR1	RaS-Related	0
YGR153W			0
YGR154C	GTO1	Glutathione Transferase Omega-like	0
YGR155W	CYS4	CYStathionine beta-synthase	0
YGR156W	PTI1	PTa1p Interacting protein	0
YGR157W	CHO2	CHoline requiring	0
YGR158C	MTR3	MRNA TRansport	0
YGR159C	NSR1		0
YGR160W			0
YGR161C	RTS3		0
YGR161W-C			0
YGR162W	TIF4631	Translation Initiation Factor	0
YGR164W			0
YGR165W	MRPS35	Mitochondrial Ribosomal Protein, Small subunit	0
YGR166W	TRS65	TRapp Subunit	0
YGR167W	CLC1	Clathrin Light Chain	0
YGR168C	PEX35	PEroXin	0
YGR169C	PUS6	PseudoUridine Synthase	0
YGR169C-A	LSO2	Late-annotated Small Open reading frame	0
YGR173W	RBG2	RiBosome interacting Gtpase	0
YGR174C	CBP4	Cytochrome B mRNA Processing	0
YGR174W-A			0
YGR175C	ERG1	ERGosterol biosynthesis	0
YGR177C	ATF2	AcetylTransFerase	0
YGR178C	PBP1	Pab1p-Binding Protein	0
YGR179C	OKP1	Outer Kinetochore Protein	0
YGR180C	RNR4	RiboNucleotide Reductase	0
YGR181W	TIM13	Translocase of the Inner Mitochondrial membrane	0
YGR182C			0
YGR183C	QCR9	ubiQuinol-cytochrome C oxidoReductase	0
YGR184C	UBR1		0

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YGR185C	TYS1	TYrosyl-tRNA Synthetase	0
YGR186W	TFG1	Transcription Factor G	0
YGR187C	HGH1	HmG1/2 Homolog	0
YGR188C	BUB1	Budding Uninhibited by Benzimidazole	0
YGR189C	CRH1	Congo Red Hypersensitive	0
YGR190C			0
YGR191W	HIP1	HlIstidine Permease	0
YGR192C	TDH3	Triose-phosphate DeHydrogenase	0
YGR193C	PDX1	Pyruvate Dehydrogenase complex protein X	0
YGR194C	XKS1	XyluloKinaSe	0
YGR195W	SKI6	SuperKiller	0
YGR196C	FYV8	Function required for Yeast Viability	0
YGR197C	SNG1		0
YGR201C			0
YGR203W	YCH1	Yeast Cdc25 Homolog	0
YGR204C-A			0
YGR204W	ADE3	ADEnine requiring	0
YGR205W	TDA10	Topoisomerase I Damage Affected	0
YGR206W	MVB12	MultiVesicular Body sorting factor of 12 kilodaltons	0
YGR207C	CIR1	Changed Intracellular Redox state	0
YGR208W	SER2	SERine requiring	0
YGR209C	TRX2	ThioRedoXin	0
YGR210C			0
YGR211W	ZPR1	Zinc finger PRotein	0
YGR212W	SLI1	Sphingosine-Like Immunosuppressant resistant gene	0
YGR213C	RTA1	Resistance To 7-Aminocholesterol	0
YGR214W	RPS0A	Ribosomal Protein of the Small subunit	0
YGR215W	RSM27	Ribosomal Small subunit of Mitochondria	0
YGR219W			0
YGR221C	TOS2	Target Of Sbf	0
YGR223C	HSV2	Homologous with SVP1	0
YGR225W	AMA1	Activator of Meiotic APC/C	0
YGR226C			0
YGR230W	BNS1	Bypasses Need for Spo12p	0
YGR231C	PHB2	ProHiBitin	0
YGR237C			0
YGR238C	KEL2	KELch repeat	0
YGR239C	PEX21	PEroXin	0
YGR240C	PFK1	PhosphoFructoKinase	0
YGR243W	MPC3	Mitochondrial Pyruvate Carrier	0
YGR247W	CPD1	Cyclic nucleotide PhosphoDiesterase	0
YGR248W	SOL4	Suppressor Of Los1-1	0
YGR249W	MGA1		0
YGR252W	GCN5	General Control Nonderepressible	0
YGR253C	PUP2	PUtative Proteasome subunit	0
YGR257C	MTM1	Manganese Trafficking factor for Mitochondrial SOD2	0
YGR262C	BUD32	BUD site selection	0
YGR263C	SAY1	Steryl Acetyl hYdrolase	0
YGR267C	FOL2	FOLic acid synthesis	0
YGR268C	HUA1		0
YGR270C-A			0

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YGR271C-A	EFG1	Exit From G1	0
YGR273C		Ilm1p Binding	0
YGR275W	RTT102	Regulator of Ty1 Transposition	0
YGR277C	CAB4	Coenzyme A Biosynthesis	0
YGR279C	SCW4	Soluble Cell Wall protein	0
YGR281W	YOR1	Yeast Oligomycin Resistance	0
YGR282C	BGL2	Beta-GLucanase	0
YGR283C			0
YGR284C	ERV29	ER Vesicle	0
YGR285C	ZUO1	ZUOtin	0
YGR286C	BIO2	BIOtin	0
YHL001W	RPL14B	Ribosomal Protein of the Large subunit	0
YHL002C-A			0
YHL002W	HSE1	Has Symptoms of class E mutants; resembles Hbp, Stam and E	0
YHL003C	LAG1	Longevity Assurance Gene	0
YHL005C			0
YHL006C	SHU1	Suppressor of HU sensitivity	0
YHL006W-A			0
YHL007C	STE20	STERile	0
YHL010C	ETP1	Ethanol Tolerance Protein	0
YHL011C	PRS3	PhosphoRibosylpyrophosphate Synthetase	0
YHL012W			0
YHL013C	OTU2	member of the Ovarian Tumor family	0
YHL014C	YLF2		0
YHL015W	RPS20	Ribosomal Protein of the Small subunit	0
YHL015W-A			0
YHL016C	DUR3	Degradation of URea	0
YHL017W			0
YHL018W	MCO14	Mitochondrial Class One protein of 14 kDa	0
YHL019W-A			0
YHL020C	OPI1	OverProducer of Inositol	0
YHL023C	NPR3	Nitrogen Permease Regulator	0
YHL024W	RIM4	Regulator of IME2	0
YHL025W	SNF6	Sucrose NonFermenting	0
YHL026C			0
YHL027W	RIM101	Regulator of IME2	0
YHL029C	OCA5	Oxidant-induced Cell-cycle Arrest	0
YHL030W-A			0
YHL031C	GOS1	GOlgi Snare	0
YHL032C	GUT1	Glycerol UTilization	0
YHL034C	SBP1		0
YHL034W-A			0
YHL036W	MUP3	Methionine UPtake	0
YHL038C	CBP2	Cytochrome B mRNA Processing	0
YHL039W	EFM1	Elongation Factor Methyltransferase	0
YHL040C	ARN1	AFT1 ReguloN	0
YHL044W			0
YHL046W-A			0
YHL047C	ARN2	AFT1 ReguloN	0
YHR001W-A	QCR10	ubiQuinol-cytochrome C oxidoReductase	0
YHR002W	LEU5	LEUcine biosynthesis	0

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YHR003C	TCD1	tRNA ThreonylCarbamoylAdenosine Dehydratase	0
YHR005C	GPA1	G Protein Alpha subunit	0
YHR005C-A	TIM10	Translocase of the Inner Membrane	0
YHR008C	SOD2	SuperOxide Dismutase	0
YHR009C	TDA3	Topoisomerase I Damage Affected	0
YHR010W	RPL27A	Ribosomal Protein of the Large subunit	0
YHR011W	DIA4	Digs Into Agar	0
YHR012W	VPS29	Vacuolar Protein Sorting	0
YHR013C	ARD1	ARrest Defective	0
YHR015W	MIP6	Mex67-Interacting Protein	0
YHR016C	YSC84		0
YHR017W	YSC83		0
YHR018C	ARG4	ARGinine requiring	0
YHR019C	DED81	Defines Essential Domain	0
YHR021C	RPS27B	Ribosomal Protein of the Small subunit	0
YHR021W-A	ECM12	ExtraCellular Mutant	0
YHR022C-A			0
YHR024C	MAS2	Mitochondrial ASsembly	0
YHR026W	VMA16	Vacuolar Membrane Atpase	0
YHR030C	SLT2	Suppressor of the LyTic phenotype	0
YHR031C	RRM3	rDNA Recombination Mutation	0
YHR032C-A			0
YHR032W-A			0
YHR033W			0
YHR036W	BRL1	BRr6 Like protein	0
YHR038W	RRF1	Ribosome Recycling Factor	0
YHR039C	MSC7	Meiotic Sister-Chromatid recombination	0
YHR039C-A	VMA10		0
YHR040W	BCD1	Box C/D snoRNA accumulation	0
YHR041C	SRB2	Suppressor of RNA polymerase B	0
YHR042W	NCP1	NADP-Cytochrome P450 reductase	0
YHR044C	DOG1	DeOxyGlucose	0
YHR046C	INM1	INositol Monophosphatase	0
YHR047C	AAP1	Arginine/alanine AminoPeptidase	0
YHR049W	FSH1	Family of Serine Hydrolases	0
YHR051W	COX6	Cytochrome c OXidase	0
YHR052W-A			0
YHR053C	CUP1-1	Cu, copper, CUPrum	0
YHR057C	CPR2	Cyclosporin A-sensitive Proline Rotamase	0
YHR059W	FYV4	Function required for Yeast Viability	0
YHR060W	VMA22	Vacuolar Membrane Atpase	0
YHR063C	PAN5	PANtothenate biosynthesis	0
YHR063W-A			0
YHR064C	SSZ1		0
YHR065C	RRP3	Ribosomal RNA Processing	0
YHR068W	DYS1	DeoxyhYpusine Synthase	0
YHR069C-A			0
YHR071C-A			0
YHR071W	PCL5	Pho85 CycLin	0
YHR072W	ERG7	ERGosterol biosynthesis	0
YHR072W-A	NOP10	NucleOlar Protein	0

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YHR073C-B			0
YHR073W	OSH3	OxySterol binding protein Homolog	0
YHR073W-A			0
YHR075C	PPE1	Phosphoprotein Phosphatase methylEsterase	0
YHR078W			0
YHR079C-A	SAE3	Sporulation in the Absence of spo Eleven	0
YHR081W	LRP1	Like RrP6	0
YHR082C	KSP1	Kinase Suppressing Prp20-10	0
YHR083W	SAM35	Sorting and Assembly Machinery	0
YHR084W	STE12	STERile	0
YHR085W	IPI1	Involved in Processing ITS2	0
YHR086W	NAM8	Nuclear Accommodation of Mitochondria	0
YHR086W-A			0
YHR087W	RTC3	Restriction of Telomere Capping	0
YHR088W	RPF1	Ribosome Production Factor	0
YHR090C	YNG2	Yeast iNG1 homolog	0
YHR091C	MSR1	Mitochondrial tRNA Synthetase aRginine	0
YHR092C	HXT4	HeXose Transporter	0
YHR096C	HXT5	HeXose Transporter	0
YHR097C	PAL2	Pears And Lemons	0
YHR098C	SFB3	Sed Five Binding	0
YHR100C	GEP4	GEnetic interactors of Prohibitins	0
YHR103W	SBE22	similar to SBE2	0
YHR104W	GRE3	Genes de Respuesta a Estres (stress responsive genes)	0
YHR105W	YPT35		0
YHR106W	TRR2	ThioRedoxin Reductase	0
YHR107C	CDC12	Cell Division Cycle	0
YHR110W	ERP5	Emp24p/Erv25p Related Protein	0
YHR113W	APE4		0
YHR115C	DMA1	Defective in Mitotic Arrest	0
YHR116W	COX23	Cytochrome OXidase	0
YHR117W	TOM71	Translocase of the Outer Mitochondrial membrane	0
YHR118C	ORC6	Origin Recognition Complex	0
YHR119W	SET1	SET domain-containing	0
YHR120W	MSH1	MutS Homolog	0
YHR122W	CIA2	Cytosolic Iron-sulfur protein Assembly	0
YHR123W	EPT1	EthanolaminePhosphoTransferase	0
YHR124W	NDT80	Non-DiTyrosine	0
YHR126C	ANS1		0
YHR128W	FUR1	5-FluoroURidine resistant	0
YHR129C	ARP1	Actin-Related Protein	0
YHR130C			0
YHR131C			0
YHR131W-A			0
YHR132C	ECM14	ExtraCellular Mutant	0
YHR132W-A	IGO2	Initiation of G zerO	0
YHR133C	NSG1		0
YHR136C	SPL2	Suppressor of PLC1 deletion	0
YHR138C			0
YHR139C	SPS100	SPorulation Specific	0
YHR139C-A			0

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YHR140W			0
YHR141C	RPL42B	Ribosomal Protein of the Large subunit	0
YHR142W	CHS7	CHitin Synthase-related	0
YHR143W-A	RPC10	RNA Polymerase C	0
YHR144C	DCD1	dCMP Deaminase	0
YHR147C	MRPL6	Mitochondrial Ribosomal Protein, Large subunit	0
YHR148W	IMP3	Interacting with Mpp10p	0
YHR150W	PEX28	PEroXisome related	0
YHR151C	MTC6	Maintenance of Telomere Capping	0
YHR152W	SPO12	SPOrulation	0
YHR153C	SPO16	SPOrulation	0
YHR154W	RTT107	Regulator of Ty1 Transposition	0
YHR156C	LIN1	LiNk	0
YHR157W	REC104	RECombination	0
YHR159W	TDA11	Topoisomerase I Damage Affected	0
YHR160C	PEX18	PEroXin	0
YHR161C	YAP1801	Yeast Assembly Polypeptide	0
YHR162W	MPC2	Mitochondrial Pyruvate Carrier	0
YHR166C	CDC23	Cell Division Cycle	0
YHR170W	NMD3	Nonsense-Mediated mRNA Decay	0
YHR172W	SPC97	Spindle Pole Component	0
YHR175W	CTR2	Copper TRansport	0
YHR175W-A			0
YHR176W	FMO1	Flavin containing MonoOxygenase	0
YHR179W	OYE2	Old Yellow Enzyme	0
YHR180C-B			0
YHR180W-A			0
YHR181W	SVP26	Sed5 Vesicle Protein	0
YHR182C-A			0
YHR183W	GND1	6-phosphoGlucoNateDehydrogenase	0
YHR185C	PFS1	Prospore Formation at Spindles	0
YHR188C	GPI16	GlycosylPhosphatidylinositol anchor biosynthesis	0
YHR191C	CTF8	Chromosome Transmission Fidelity	0
YHR193C	EGD2	Enhancer of Gal4 DNA binding	0
YHR193C-A			0
YHR194W	MDM31	Mitochondrial Distribution and Morphology	0
YHR195W	NVJ1	Nucleus-Vacuole Junction	0
YHR198C	AIM18	Altered Inheritance rate of Mitochondria	0
YHR199C-A	NBL1	N-terminal-Borealin Like protein	0
YHR200W	RPN10	Regulatory Particle Non-ATPase	0
YHR201C	PPX1		0
YHR202W			0
YHR207C	SET5	SET domain-containing	0
YHR208W	BAT1	Branched-chain Amino acid Transaminase	0
YHR209W	CRG1	Cantharidin Resistance Gene	0
YHR210C			0
YHR212C			0
YHR215W	PHO12	PHOsphate metabolism	0
YIL002W-A	CMI7	Cytosolic Mlni protein of ~7 kDa	0
YIL003W	CFD1	Cytosolic Fe-S cluster Deficient	0
YIL004C	BET1	Blocked Early in Transport	0

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YIL005W	EPS1	ER-retained Pma1 Suppressing	0
YIL008W	URM1	Ubiquitin Related Modifier	0
YIL009W	FAA3	Fatty Acid Activation	0
YIL013C	PDR11	Pleiotropic Drug Resistance	0
YIL015W	BAR1	BARrier to the alpha factor response	0
YIL019W	FAF1	Forty (40) S Assembly Factor	0
YIL020C	HIS6	HIStidine requiring	0
YIL021W	RPB3	RNA Polymerase B	0
YIL022W	TIM44	Translocase of the Inner Mitochondrial membrane	0
YIL023C	YKE4	Yeast ortholog of mouse KE4	0
YIL024C			0
YIL029W-A			0
YIL030W-A			0
YIL032C			0
YIL033C	BCY1	Bypass of CYclic-AMP requirement	0
YIL034C	CAP2	CAPping	0
YIL036W	CST6	Chromosome STability	0
YIL037C	PRM2	Pheromone-Regulated Membrane protein	0
YIL039W	TED1	Trafficking of Emp24p/Erv25p-dependent cargo Disrupted	0
YIL041W	GVP36	Golgi Vesicle Protein	0
YIL042C	PKP1	Protein Kinase of PDH	0
YIL043C	CBR1	Cytochrome b Reductase	0
YIL044C	AGE2	ArfGAP Effector	0
YIL045W	PIG2	Protein Interacting with Gsy2p	0
YIL046W	MET30	METHionine requiring	0
YIL047C-A			0
YIL048W	NEO1	NEOmycin-resistance	0
YIL049W	DFG10	Defective for Filamentous Growth	0
YIL050W	PCL7	Pho85 CycLin	0
YIL051C	MMF1	Mitochondrial Matrix Factor	0
YIL052C	RPL34B	Ribosomal Protein of the Large subunit	0
YIL053W	GPP1	Glycerol-3-Phosphate Phosphatase	0
YIL057C	RGI2	Respiratory growth induced	0
YIL061C	SNP1		0
YIL064W	EFM4	Elongation Factor Methyltransferase	0
YIL065C	FIS1	mitochondrial FISsion	0
YIL066W-A			0
YIL067C			0
YIL068W-A			0
YIL069C	RPS24B	Ribosomal Protein of the Small subunit	0
YIL070C	MAM33	Mitochondrial Acidic Matrix protein	0
YIL071W-A			0
YIL072W	HOP1	HOmolog Pairing	0
YIL073C	SPO22	SPOrulation	0
YIL074C	SER33	SERine requiring	0
YIL076W	SEC28	SECretory	0
YIL077C	RCI37	Respiratory Chain Interacting protein of ~37 kDa	0
YIL078W	THS1	THreonyl tRNA Synthetase	0
YIL079C	AIR1	Arginine methyltransferase-Interacting RING finger protein	0
YIL084C	SDS3	Suppressor of Defective Silencing	0
YIL085C	KTR7	Kre Two Related	0

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YIL087C	AIM19	Altered Inheritance rate of Mitochondria	0
YIL089W			0
YIL091C	UTP25	U Three Protein	0
YIL094C	LYS12	LYSine requiring	0
YIL096C	BMT5	Base Methyltransferase of Twenty five S rRNA 5	0
YIL097W	FYV10	Function required for Yeast Viability	0
YIL098C	FMC1	Formation of Mitochondrial Complexes	0
YIL099W	SGA1	Sporulation-specific GlycoAmylase	0
YIL100C-A			0
YIL102C			0
YIL102C-A			0
YIL103W	DPH1	DiPHthamide biosynthesis	0
YIL105C	SLM1	Synthetic Lethal with Mss4	0
YIL105W-A			0
YIL106W	MOB1	Mps One Binder	0
YIL107C	PFK26	6-PhosphoFructo-2-Kinase	0
YIL108W			0
YIL109C	SEC24	SECretory	0
YIL110W	HPM1	Histidine Protein Methyltransferase	0
YIL111W	COX5B	Cytochrome c OXidase	0
YIL113W	SDP1	Stress-inducible Dual specificity Phosphatase	0
YIL114C	POR2	PORin	0
YIL116W	HIS5	HISTidine requiring	0
YIL117C	PRM5	Pheromone-Regulated Membrane protein	0
YIL122W	POG1	Promoter Of Growth	0
YIL127C	RRT14	Regulator of rDNA Transcription	0
YIL129C	TAO3	Transcriptional Activator of OCH1	0
YIL131C	FKH1	ForK head Homolog	0
YIL134C-A			0
YIL134W	FLX1	FLavin eXchange	0
YIL135C	VHS2	Viable in a Hal3 Sit4 background	0
YIL136W	OM45	Outer Membrane	0
YIL138C	TPM2	TroPoMyosin	0
YIL139C	REV7	REVersionless	0
YIL142C-A			0
YIL142W	CCT2	Chaperonin Containing TCP-1	0
YIL143C	SSL2	Suppressor of Stem-Loop mutation	0
YIL144W	NDC80	Nuclear Division Cycle	0
YIL147C	SLN1	Synthetic Lethal of N-end rule	0
YIL148W	RPL40A	Ribosomal Protein of the Large subunit	0
YIL150C	MCM10	MiniChromosome Maintenance	0
YIL151C	ESL1	EST/SMG-like	0
YIL152W			0
YIL153W	RRD1	Resistant to Rapamycin Deletion	0
YIL156W	UBP7	UBiquitin-specific Protease	0
YIL156W-B	MCO8	Mitochondrial Class One protein of 8 kDa	0
YIL160C	POT1	Peroxisomal Oxoacyl Thiolase	0
YIL161W			0
YIL162W	SUC2	SUCrose	0
YIL165C			0
YIL166C	SOA1	SulfOnAte transport	0

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YIR003W	AIM21	Altered Inheritance rate of Mitochondria	0
YIR005W	IST3	Increased Sodium Tolerance	0
YIR009W	MSL1	MUD Synthetic Lethal	0
YIR011C	STS1	Sec Twenty-three Suppressor 1	0
YIR013C	GAT4		0
YIR014W	VLD1	Vacuole Localized Dsc protein	0
YIR015W	RPR2	RNase P Ribonucleoprotein	0
YIR016W			0
YIR017C	MET28	METHionine	0
YIR017W-A			0
YIR018W	YAP5	Yeast AP-1	0
YIR020W-A			0
YIR021W-A			0
YIR022W	SEC11	SECretory	0
YIR026C	YVH1	Yeast vaccinia virus VH1 Homolog	0
YIR027C	DAL1	Degradation of Allantoin	0
YIR028W	DAL4	Degradation of Allantoin	0
YIR029W	DAL2	Degradation of Allantoin	0
YIR030C	DCG1	Dal80p-Controlled Gene	0
YIR030W-A			0
YIR032C	DAL3	Degradation of Allantoin	0
YIR033W	MGA2	Multicopy suppressor of GAm1 (snf2)	0
YIR034C	LYS1	LYSine requiring	0
YIR035C	NRE1	Novel REDuctase	0
YIR036C	IRC24	Increased Recombination Centers	0
YIR037W	HYR1	HYdroperoxide Resistance	0
YJL001W	PRE3	PRoteinase yscE	0
YJL003W	COX16	Cytochrome c OXidase	0
YJL004C	SYS1	Suppressor of Ypt Six	0
YJL005W	CYR1	CYclic AMP Requirement	0
YJL006C	CTK2	Carboxy-Terminal domain Kinase	0
YJL007C			0
YJL008C	CCT8	Chaperonin Containing TCP-1	0
YJL011C	RPC17	RNA Polymerase C	0
YJL012C	VTC4	Vacuolar Transporter Chaperone	0
YJL014W	CCT3	Chaperonin Containing TCP-1	0
YJL015C			0
YJL016W	TPH3	Twin PH domain-3	0
YJL019W	MPS3	MonoPolar Spindle	0
YJL020W-A			0
YJL022W			0
YJL023C	PET130	PETite colonies	0
YJL024C	APS3	clathrin Associated Protein complex Small subunit	0
YJL025W	RRN7	Regulation of RNA polymerase I	0
YJL026C-A			0
YJL026W	RNR2	RiboNucleotide Reductase	0
YJL027C			0
YJL029C	VPS53	Vacuolar Protein Sorting	0
YJL030W	MAD2	Mitotic Arrest-Deficient	0
YJL031C	BET4	Blocked Early in Transport	0
YJL032W			0

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YJL034W	KAR2	KARyogamy	0
YJL035C	TAD2	tRNA-specific Adenosine Deaminase	0
YJL036W	SNX4	Sorting NeXin	0
YJL037W	IRC18	Increased Recombination Centers	0
YJL038C	LOH1	Loss Of Heterozygosity	0
YJL039C	NUP192	NUclear Pore	0
YJL043W			0
YJL046W	AIM22	Altered Inheritance rate of Mitochondria	0
YJL047C	RTT101	Regulator of Ty1 Transposition	0
YJL047C-A			0
YJL048C	UBX6	UBiquitin regulatory X	0
YJL049W	CHM7	CHarged Multivesicular body protein	0
YJL050W	MTR4	Mrna TRansport	0
YJL051W	IRC8	Increased Recombination Centers	0
YJL052C-A			0
YJL052W	TDH1	Triose-phosphate DeHydrogenase	0
YJL058C	BIT61	Binding partner of Tor2p	0
YJL059W	YHC3	Yeast Homolog of human Cln3	0
YJL060W	BNA3	Biosynthesis of Nicotinic Acid	0
YJL062W	LAS21	Local Anestheticum Sensitive	0
YJL062W-A	COA3	Cytochrome Oxidase Assembly	0
YJL064W			0
YJL065C	DLS1	Dpb3-Like Subunit of ISW2/yCHRAC complex	0
YJL066C	MPM1	Mitochondrial Peculiar Membrane protein	0
YJL067W			0
YJL068C			0
YJL072C	PSF2	Partner of Sld Five	0
YJL077W-A			0
YJL081C	ARP4	Actin-Related Protein	0
YJL082W	IML2	Increased Minichromosome Loss	0
YJL083W	TAX4		0
YJL085W	EXO70	EXOcyst	0
YJL086C			0
YJL087C	TRL1	tRNA Ligase	0
YJL088W	ARG3	ARGinine requiring	0
YJL091C	GWT1	GPI-anchored Wall protein Transfer	0
YJL092W	SRS2	Suppressor of Rad Six	0
YJL094C	KHA1	K/H ion Antiporter	0
YJL095W	BCK1	Bypass of C Kinase	0
YJL096W	MRPL49	Mitochondrial Ribosomal Protein, Large subunit	0
YJL097W	PHS1	PTPLA Homolog involved in Sphingolipid biosynthesis 1	0
YJL099W	CHS6	CHitin Synthase-related	0
YJL100W	LSB6	Las Seventeen Binding protein	0
YJL101C	GSH1	glutathione (GSH)	0
YJL104W	PAM16	Presequence translocase-Associated Motor	0
YJL105W	SET4	SET domain-containing	0
YJL106W	IME2	Inducer of MEiosis	0
YJL107C			0
YJL108C	PRM10	Pheromone-Regulated Membrane protein	0
YJL110C	GZF3	Gata Zinc Finger protein	0
YJL111W	CCT7	Chaperonin Containing TCP-1	0

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YJL115W	ASF1	Anti-Silencing Function	0
YJL116C	NCA3	Nuclear Control of ATPase	0
YJL117W	PHO86	PHOspate metabolism	0
YJL118W			0
YJL120W			0
YJL121C	RPE1	Ribulose 5-Phosphate Epimerase	0
YJL125C	GCD14	General Control Nonderepressible	0
YJL127C	SPT10	SuPpressor of Ty	0
YJL127C-B	MCO6	Mitochondrial Class One protein of 6 kDa	0
YJL127W-A			0
YJL128C	PBS2	Polymyxin B Sensitivity	0
YJL130C	URA2	URAcil requiring	0
YJL131C	AIM23	Altered Inheritance rate of Mitochondria	0
YJL132W			0
YJL133C-A	DPI8	Delta-Psi dependent mitochondrial Import protein of 8 kDa	0
YJL133W	MRS3	Mitochondrial RNA Splicing	0
YJL136C	RPS21B	Ribosomal Protein of the Small subunit	0
YJL136W-A			0
YJL137C	GLG2	Glycogenin-Like Gene	0
YJL139C	YUR1	Yeast Unknown Reading frame	0
YJL140W	RPB4	RNA Polymerase B	0
YJL141C	YAK1	Yet Another Kinase	0
YJL142C	IRC9	Increased Recombination Centers	0
YJL143W	TIM17	Translocase of the Inner Mitochondrial membrane	0
YJL144W	ROQ1	Regulator Of Quality control	0
YJL145W	SFH5	Sec Fourteen Homolog	0
YJL146W	IDS2	IME2-Dependent Signaling	0
YJL147C	SMT1	Suppression of Mitochondrial Translation	0
YJL148W	RPA34	RNA Polymerase A	0
YJL149W	DAS1	Dst1-delta 6-Azauracil Sensitivity	0
YJL150W			0
YJL151C	SNA3	Sensitivity to NA+	0
YJL152W			0
YJL153C	INO1	INOsitol requiring	0
YJL154C	VPS35	Vacuolar Protein Sorting	0
YJL155C	FBP26	Fructose BisPhosphatase	0
YJL156C	SSY5	Sulfonylurea Sensitive on YPD	0
YJL156W-A			0
YJL157C	FAR1	Factor ARrest	0
YJL158C	CIS3	Clk1 Suppressing	0
YJL162C	JJJ2	J-protein (Type III)	0
YJL164C	TPK1	Takashi's Protein Kinase	0
YJL166W	QCR8	ubiQuinol-cytochrome C oxidoReductase	0
YJL167W	ERG20	ERGosterol biosynthesis	0
YJL169W			0
YJL170C	ASG7	a-Specific Gene	0
YJL171C	TOH1	TOS One Homolog	0
YJL172W	CPS1	CarboxyPeptidase yscS	0
YJL173C	RFA3	Replication Factor A	0
YJL174W	KRE9	Killer toxin REsistant	0
YJL175W			0

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YJL177W	RPL17B	Ribosomal Protein of the Large subunit	0
YJL178C	ATG27	AuTophagy related	0
YJL179W	PFD1	PreFoldin	0
YJL180C	ATP12	ATP synthase	0
YJL181W	RBH1	Ran Binding domain Homolog	0
YJL185C	ATG36	AuTophagy related	0
YJL186W	MNN5	MaNNosyltransferase	0
YJL188C	BUD19	BUD site selection	0
YJL189W	RPL39	Ribosomal Protein of the Large subunit	0
YJL190C	RPS22A	Ribosomal Protein of the Small subunit	0
YJL191W	RPS14B	Ribosomal Protein of the Small subunit	0
YJL196C	ELO1	ELongation defective	0
YJL197C-A			0
YJL198W	PHO90	PHOsphate metabolism	0
YJL199C	MBB1		0
YJL200C	ACO2	ACOnitase	0
YJL201W	ECM25	ExtraCellular Mutant	0
YJL202C			0
YJL203W	PRP21	Pre-mRNA Processing	0
YJL205C	NCE101	NonClassical Export	0
YJL206C			0
YJL208C	NUC1	NUClease	0
YJL209W	CBP1	Cytochrome B mRNA Processing	0
YJL210W	PEX2	PEroXin	0
YJL211C			0
YJL213W			0
YJR001W	AVT1	Amino acid Vacuolar Transport	0
YJR002W	MPP10	M Phase Phosphoproteins	0
YJR003C	MRX12	Mitochondrial oRganization of gene eXpression (MIOREX)	0
YJR004C	SAG1	Sexual AGglutination	0
YJR005C-A	LSO1	Late-annotated Small Open reading frame	0
YJR005W	APL1	clathrin Adaptor Protein complex Large chain	0
YJR006W	POL31	POLymerase	0
YJR007W	SUI2	SUPpressor of Initiator codon	0
YJR008W	MHO1	Memo HOMolog	0
YJR010C-A	SPC1	Signal Peptidase Complex	0
YJR010W	MET3	METHionine requiring	0
YJR011C			0
YJR012C			0
YJR014W	TMA22	Translation Machinery Associated	0
YJR016C	ILV3	IsoLeucine-plus-Valine requiring	0
YJR019C	TES1	ThioESTerase	0
YJR020W			0
YJR021C	REC107	RECombination	0
YJR022W	LSM8	Like SM	0
YJR023C			0
YJR024C	MDE1	Methylthioribulose-1-phosphate DEhydratase	0
YJR025C	BNA1	Biosynthesis of Nicotinic Acid	0
YJR030C	RBH2	Ran Binding domain Homolog	0
YJR032W	CPR7	Cyclosporin-sensitive Proline Rotamase	0
YJR034W	PET191	PETite colonies	0

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YJR038C			0
YJR040W	GEF1	Glycerol Ethanol, Ferric requiring	0
YJR043C	POL32	POLymerase	0
YJR044C	VPS55	Vacuolar Protein Sorting	0
YJR045C	SSC1	Stress-Seventy subfamily C	0
YJR046W	TAH11	Topo-A Hypersensitive	0
YJR047C	ANB1	ANaeroBically induced	0
YJR048W	CYC1	CYtochrome C	0
YJR049C	UTR1	Unidentified TRanscript	0
YJR050W	ISY1	Interactor of SYf1p	0
YJR052W	RAD7	RADiation sensitive	0
YJR053W	BFA1	Byr-Four-Alike	0
YJR055W	HIT1	Hlgh Temperature growth	0
YJR057W	CDC8	Cell Division Cycle	0
YJR058C	APS2	clathrin Associated Protein complex Small subunit	0
YJR059W	PTK2	Putative serine/Threonine protein Kinase	0
YJR060W	CBF1	Centromere Binding Factor	0
YJR061W	MNN14	MaNNosyltransferase regulator	0
YJR063W	RPA12	RNA Polymerase A	0
YJR064W	CCT5	Chaperonin Containing TCP-1	0
YJR068W	RFC2	Replication Factor C	0
YJR069C	HAM1	6-n-HydroxylAMinopurine sensitive	0
YJR070C	LIA1	Ligand of eIF5A	0
YJR072C	NPA3	Nucleolar Preribosomal Associated	0
YJR073C	OPI3	OverProducer of Inositol	0
YJR075W	HOC1	Homologous to OCh1	0
YJR076C	CDC11	Cell Division Cycle	0
YJR078W	BNA2	Biosynthesis of Nicotinic Acid	0
YJR080C	AIM24	Altered Inheritance rate of Mitochondria	0
YJR082C	EAF6	Esa1p-Associated Factor	0
YJR084W			0
YJR085C	TMH11	TMem14 Homolog of 11 kDa	0
YJR086W	STE18	STERile	0
YJR091C	JSN1	Just Say No	0
YJR094C	IME1	Inducer of MEiosis	0
YJR094W-A	RPL43B	Ribosomal Protein of the Large subunit	0
YJR095W	SFC1	Succinate-Fumarate Carrier	0
YJR096W			0
YJR097W	JJJ3	J-protein (Type III)	0
YJR100C	AIM25	Altered Inheritance of Mitochondria	0
YJR102C	VPS25	Vacuolar Protein Sorting	0
YJR104C	SOD1	SuperOxide Dismutase	0
YJR105W	ADO1	ADenOsine kinase	0
YJR109C	CPA2	Carbamyl Phosphate synthetase A	0
YJR110W	YMR1	Yeast Myotubularin Related	0
YJR111C	PXP2	PeroXisomal Protein	0
YJR112W	NNF1	Necessary for Nuclear Function	0
YJR112W-A			0
YJR113C	RSM7	Ribosomal Small subunit of Mitochondria	0
YJR114W			0
YJR116W	TDA4	Topoisomerase I Damage Affected	0

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YJR117W	STE24	STERile	0
YJR118C	ILM1	Increased Loss of Mitochondrial DNA	0
YJR120W			0
YJR121W	ATP2	ATP synthase	0
YJR123W	RPS5	Ribosomal Protein of the Small subunit	0
YJR124C			0
YJR125C	ENT3	Epsin N-Terminal homology	0
YJR130C	STR2	Sulfur TRansfer	0
YJR133W	XPT1	Xanthine Phosphoribosyl Transferase	0
YJR135C	MCM22	MiniChromosome Maintenance	0
YJR135W-A	TIM8	Translocase of the Inner Mitochondrial membrane	0
YJR137C	MET5	METHionine requiring	0
YJR138W	IML1	Increased Minichromosome Loss	0
YJR139C	HOM6	HOMoserine requiring	0
YJR140W-A			0
YJR143C	PMT4	Protein O-MannosylTransferase	0
YJR148W	BAT2	Branched-chain Amino acid Transaminase	0
YJR151W-A			0
YJR152W	DAL5	Degradation of Allantoin	0
YJR153W	PGU1	PolyGalactUronase	0
YKL001C	MET14	METHionine requiring	0
YKL003C	MRP17	Mitochondrial Ribosomal Protein	0
YKL004W	AUR1	AUreobasidin A Resistance	0
YKL005C	BYE1	BYpass of ESS1	0
YKL006C-A	SFT1	Suppressor of sed Five Ts	0
YKL007W	CAP1	CAPping	0
YKL008C	LAC1	Longevity-Assurance gene Cognate (LAG1 Cognate)	0
YKL009W	MRT4	mRNA Turnover 4	0
YKL011C	CCE1	Cruciform Cutting Endonuclease	0
YKL012W	PRP40	Pre-mRNA Processing	0
YKL013C	ARC19	ARp2/3 Complex subunit	0
YKL016C	ATP7	ATP synthase	0
YKL017C	HCS1	dna HeliCaSe	0
YKL018C-A	MCO12	Mitochondrial Class One protein of 12 kDa	0
YKL018W	SWD2	Set1c, WD40 repeat protein	0
YKL019W	RAM2	RAS protein and A-factor Maturation	0
YKL021C	MAK11	MAintenance of Killer	0
YKL023W			0
YKL025C	PAN3	Poly(A) Nuclease	0
YKL032C	IXR1	Intrastrand cross (X)-link Recognition	0
YKL034W	TUL1	Transmembrane Ubiquitin Ligase	0
YKL042W	SPC42	Spindle Pole Component	0
YKL043W	PHD1	PseudoHyphal Determinant	0
YKL046C	DCW1	Defective Cell Wall	0
YKL049C	CSE4	Chromosome SEgregation	0
YKL050C			0
YKL053C-A	MDM35	Mitochondrial Distribution and Morphology	0
YKL053W			0
YKL055C	OAR1	3-Oxoacyl-[Acyl-carrier-protein] Reductase	0
YKL056C	TMA19	Translation Machinery Associated	0
YKL058W	TOA2		0

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YKL059C	MPE1	Mutant PCF11 Extragenic suppressor	0
YKL060C	FBA1	Fructose-1,6-Bisphosphate Aldolase	0
YKL061W	BLI1	BLoc-1 Interactor	0
YKL063C			0
YKL064W	MNR2	MaNganese Resistance	0
YKL065C	YET1	Yeast Endoplasmic reticulum Transmembrane protein	0
YKL065W-A	DPC7	Delta-Psi dependent mitochondrial import and Cleavage protein	0
YKL067W	YNK1	Yeast Nucleoside diphosphate Kinase	0
YKL068W-A			0
YKL070W			0
YKL071W			0
YKL072W	STB6	Sin Three Binding protein	0
YKL073W	LHS1	Lumenal Hsp Seventy	0
YKL074C	MUD2	Mutant U1 Die	0
YKL075C			0
YKL076C	PSY1	Platinum Sensitivity	0
YKL077W	PSG1	Pma1 Stabilization in the Golgi	0
YKL078W	DHR2	DEAH-box RNA helicase	0
YKL079W	SMY1	Suppressor of MYo2-66	0
YKL080W	VMA5	Vacuolar Membrane Atpase	0
YKL081W	TEF4	Translation Elongation Factor	0
YKL083W			0
YKL085W	MDH1	Malate DeHydrogenase	0
YKL086W	SRX1	SulfiRedoXin	0
YKL087C	CYT2	CYTochrome-c1-heme-lyase	0
YKL091C			0
YKL093W	MBR1	Mitochondrial Biogenesis Regulation	0
YKL094W	YJU3		0
YKL096C-B			0
YKL096W	CWP1	Cell Wall Protein	0
YKL096W-A	CWP2	Cell Wall Protein	0
YKL097C			0
YKL098W	MTC2	Maintenance of Telomere Capping	0
YKL100C	YPF1	Yeast Presenilin-like Family 1	0
YKL100W-A			0
YKL101W	HSL1	Histone Synthetic Lethal	0
YKL102C			0
YKL103C	APE1	AminoPeptidase	0
YKL106C-A			0
YKL108W	SLD2	Synthetically Lethal with Dpb11-1	0
YKL109W	HAP4	Heme Activator Protein	0
YKL110C	KTI12	Kluveromyces lactis Toxin Insensitive	0
YKL111C			0
YKL113C	RAD27	RADiation sensitive	0
YKL114C	APN1	APurinic/aprimidinic eNdonuclease	0
YKL117W	SBA1	increased Sensitivity to Benzoquinone Ansamycins	0
YKL118W			0
YKL119C	VPH2	Vacuolar pH	0
YKL120W	OAC1	OxaloAcetate Carrier	0
YKL123W			0
YKL125W	RRN3	Regulation of RNA polymerase I	0

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YKL126W	YPK1	Yeast Protein Kinase	0
YKL128C	PMU1	PhosphoMUTase	0
YKL130C	SHE2	Swi5p-dependent HO Expression	0
YKL131W			0
YKL132C	RMA1	Reduced Mating A	0
YKL133C	RCI50	Respiratory Chain Interacting protein of ~50 kDa	0
YKL137W	CMC1	Cx9C Mitochondrial protein necessary for full assembly of Cytoc	0
YKL138C	MRPL31	Mitochondrial Ribosomal Protein, Large subunit	0
YKL138C-A	HSK3	Helper of ASK1	0
YKL139W	CTK1	Carboxy-Terminal domain Kinase	0
YKL140W	TGL1	TriGlyceride Lipase	0
YKL141W	SDH3	Succinate DeHydrogenase	0
YKL142W	MRP8	Mitochondrial Ribosomal Protein	0
YKL144C	RPC25	RNA Polymerase C	0
YKL145W	RPT1	Regulatory Particle Triple-A protein, or Regulatory Particle Triph	0
YKL145W-A			0
YKL146W	AVT3	Amino acid Vacuolar Transport	0
YKL148C	SDH1	Succinate DeHydrogenase	0
YKL149C	DBR1	DeBRanching	0
YKL150W	MCR1	Mitochondrial NADH-Cytochrome b5 Reductase	0
YKL151C	NNR2	Nicotinamide Nucleotide Repair	0
YKL152C	GPM1	Glycerate PhosphoMutase	0
YKL154W	SRP102	Signal Recognition Particle	0
YKL156C-A			0
YKL156W	RPS27A	Ribosomal Protein of the Small subunit	0
YKL159C	RCN1	Regulator of CalciNeurin	0
YKL160W	ELF1	ELongation Factor	0
YKL162C			0
YKL162C-A			0
YKL165C-A			0
YKL166C	TPK3	Takashi's Protein Kinase	0
YKL167C	MRP49	Mitochondrial Ribosomal Protein	0
YKL168C	KKQ8		0
YKL169C			0
YKL170W	MRPL38	Mitochondrial Ribosomal Protein, Large subunit	0
YKL171W	NNK1	Nitrogen Network Kinase	0
YKL172W	EBP2	EBNA1-binding protein (homolog)	0
YKL173W	SNU114	Small NUClear ribonucleoprotein associated	0
YKL174C	TPO5	Transporter of POLyamines	0
YKL175W	ZRT3	Zinc-Regulated Transporter	0
YKL177W			0
YKL178C	STE3	STERile	0
YKL180W	RPL17A	Ribosomal Protein of the Large subunit	0
YKL181W	PRS1	PhosphoRibosylpyrophosphate Synthetase	0
YKL182W	FAS1	Fatty Acid Synthetase	0
YKL183W	LOT5	LOW Temperature-responsive	0
YKL184W	SPE1	SPErmidine auxotroph	0
YKL185W	ASH1	Asymmetric Synthesis of HO	0
YKL186C	MTR2	Mrna TRansport	0
YKL188C	PXA2	PeroXisomal ABC-transporter	0
YKL189W	HYM1		0

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YKL190W	CNB1	CalciNeurin subunit B	0
YKL192C	ACP1	Acyl Carrier Protein	0
YKL194C	MST1	Mitochondrial aminoacyl-tRNA Synthetase, Threonine	0
YKL196C	YKT6		0
YKL205W	LOS1	Loss Of Suppression	0
YKL206C	ADD66	Alpha1-proteinase inhibitor-Degradation Deficient	0
YKL207W	EMC3	ER Membrane protein Complex	0
YKL208W	CBT1	Cytochrome B Termination	0
YKL212W	SAC1	Suppressor of Actin	0
YKL213C	DOA1	Degradation Of Alpha	0
YKL214C	YRA2	Yeast RNA Annealing protein	0
YKL215C	OXP1	OXoProlinase	0
YKL216W	URA1	URAcil requiring	0
YKL217W	JEN1		0
YKL218C	SRY1	Serine Racemase of Yeast	0
YKL220C	FRE2	Ferric REductase	0
YKR003W	OSH6	OxySterol binding protein Homolog	0
YKR005C			0
YKR006C	MRPL13	Mitochondrial Ribosomal Protein, Large subunit	0
YKR007W	MEH1	Multicopy suppressor of Ers1 Hygromycin B sensitivity	0
YKR009C	FOX2	Fatty acid OXidation	0
YKR011C			0
YKR013W	PRY2	Pathogen Related in Yeast	0
YKR014C	YPT52	Yeast Protein Two	0
YKR016W	MIC60	Mitochondrial contact site and Cristae organizing system	0
YKR017C	HEL1	Histone E3 Ligase	0
YKR018C			0
YKR020W	VPS51	Vacuolar Protein Sorting	0
YKR021W	ALY1	Arrestin-Like Yeast protein	0
YKR022C	NTR2	NineTeen complex Related protein	0
YKR025W	RPC37	RNA Polymerase C	0
YKR026C	GCN3	General Control Nonderepressible	0
YKR028W	SAP190	Sit4 Associated Protein	0
YKR030W	GMH1	Gea1-6 Membrane-associated High-copy suppressor	0
YKR031C	SPO14	SPOrulation	0
YKR033C			0
YKR034W	DAL80	Degradation of Allantoin	0
YKR035C	OPI8	OverProducer of Inositol	0
YKR035W-A	DID2	Doa4-Independent Degradation	0
YKR037C	SPC34	Spindle Pole Component	0
YKR038C	KAE1	Kinase-Associated Endopeptidase	0
YKR041W			0
YKR042W	UTH1	yoUTH	0
YKR045C			0
YKR046C	PLN1	PeriLipIN	0
YKR047W			0
YKR049C	FMP46	Found in Mitochondrial Proteome	0
YKR050W	TRK2	TRansport of potassium (K)	0
YKR051W	HFL1	Has Fused Lysosomes	0
YKR052C	MRS4	Mitochondrial RNA Splicing	0
YKR056W	TRM2	tRNA Methyltransferase	0

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YKR057W	RPS21A	Ribosomal Protein of the Small subunit	0
YKR061W	KTR2	Kre Two Related	0
YKR063C	LAS1	Lethal in the Absence of SSD1-v	0
YKR064W	OAF3	Oleate Activated transcription Factor	0
YKR065C	PAM17	Presequence translocase-Associated Motor	0
YKR068C	BET3	Blocked Early in Transport	0
YKR069W	MET1	METHionine requiring	0
YKR071C	DRE2	Derepressed for Ribosomal protein S14 Expression	0
YKR074W	AIM29	Altered Inheritance rate of Mitochondria	0
YKR077W	MSA2	Mbf and Sbf Associated	0
YKR079C	TRZ1	tRNase Z	0
YKR080W	MTD1	Methylene Tetrahydrofolate Dehydrogenase	0
YKR081C	RPF2	Ribosome Production Factor	0
YKR082W	NUP133	NUclear Pore	0
YKR084C	HBS1	Hsp70 subfamily B Suppressor	0
YKR085C	MRPL20	Mitochondrial Ribosomal Protein, Large subunit	0
YKR087C	OMA1	Overlapping activity with M-AAA protease	0
YKR089C	TGL4	TriacylGlycerol Lipase	0
YKR090W	PXL1	PaXillin-Like protein	0
YKR091W	SRL3	Suppressor of rad53 Lethality	0
YKR094C	RPL40B	Ribosomal Protein of the Large subunit	0
YKR095W-A	PCC1	Polarized growth Chromatin-associated Controller	0
YKR097W	PCK1	Phosphoenolpyruvate CarboxyKinase	0
YKR098C	UBP11	UBiquitin-specific Protease	0
YKR099W	BAS1	BASal	0
YKR100C	SKG1	Suppressor of lethality of Kex2 Gas1 double null mutant	0
YKR101W	SIR1	Silent Information Regulator	0
YKR103W	NFT1	New Full-length MRP-type Transporter	0
YKR104W			0
YLL001W	DNM1	DyNaMin-related	0
YLL002W	RTT109	Regulator of Ty1 Transposition	0
YLL005C	SPO75	SPOrulation	0
YLL006W-A			0
YLL009C	COX17	Cytochrome c OXidase	0
YLL010C	PSR1	Plasma membrane Sodium Response	0
YLL011W	SOF1	Suppressor Of Fibrillarin	0
YLL012W	YEH1	Yeast sterol Ester Hydrolase	0
YLL014W	EMC6	ER Membrane protein Complex	0
YLL015W	BPT1	Bile Pigment Transporter	0
YLL016W	SDC25	Suppressor of cdc25	0
YLL018C	DPS1		0
YLL018C-A	COX19	Cytochrome c OXidase	0
YLL019W-A			0
YLL025W	PAU17	seriPAUperin	0
YLL026W	HSP104	Heat Shock Protein	0
YLL029W	FRA1	Fe Repressor of Activation	0
YLL030C	RRT7	Regulator of rDNA Transcription	0
YLL031C	GPI13	GlycosylPhosphatidylinositol anchor biosynthesis	0
YLL034C	RIX7	Rlbosome eXport	0
YLL035W	GRC3		0
YLL038C	ENT4	Epsin N-Terminal homology	0

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YLL042C	ATG10	AuTophagy related	0
YLL049W	LDB18	Low Dye Binding	0
YLL050C	COF1	COFilin	0
YLL051C	FRE6	Ferric REductase	0
YLL052C	AQY2	AQuaporin from Yeast	0
YLL053C			0
YLL058W			0
YLL059C			0
YLL060C	GTT2	GlutaThione Transferase	0
YLL061W	MMP1	S-MethylMethionine Permease	0
YLL063C	AYT1	AcetYITransferase	0
YLR002C	NOC3	NucleOlar Complex associated	0
YLR003C	CMS1	Complementation of Mcm-10 Suppressor	0
YLR005W	SSL1	Suppressor of Stem-Loop mutation	0
YLR008C	PAM18	Presequence translocase-Associated Motor	0
YLR009W	RLP24	Ribosomal-Like Protein	0
YLR010C	TEN1	TElomeric pathways with STn1	0
YLR011W	LOT6	LOw Temperature-responsive	0
YLR012C			0
YLR013W	GAT3		0
YLR015W	BRE2	BREfeldin A sensitivity	0
YLR017W	MEU1	Multicopy Enhancer of UAS2	0
YLR018C	POM34	POre Membrane	0
YLR020C	YEH2	Yeast steryl Ester Hydrolase	0
YLR021W	IRC25	Increased Recombination Centers	0
YLR022C	SDO1		0
YLR025W	SNF7	Sucrose NonFermenting	0
YLR026C	SED5	Suppressor of Erd2 Deletion	0
YLR028C	ADE16	ADEnine	0
YLR029C	RPL15A	Ribosomal Protein of the Large subunit	0
YLR031W			0
YLR033W	RSC58	Remodel the Structure of Chromatin	0
YLR034C	SMF3		0
YLR037C	PAU23	seriPAUperin family	0
YLR038C	COX12	Cytochrome c OXidase	0
YLR040C	AFB1	A-Factor Barrier	0
YLR041W			0
YLR042C			0
YLR043C	TRX1	ThioRedoXin	0
YLR044C	PDC1	Pyruvate DeCarboxylase	0
YLR048W	RPS0B	Ribosomal Protein of the Small subunit	0
YLR049C	MLO50	Mitochondrially LOcalized protein of 50 kDa	0
YLR050C	EMA19	Efficient Mitochondria targeting-Associated protein	0
YLR051C	FCF2	Faf1p Copurifying Factor	0
YLR052W	IES3	Ino Eighty Subunit	0
YLR053C			0
YLR056W	ERG3	ERGosterol biosynthesis	0
YLR061W	RPL22A	Ribosomal Protein of the Large subunit	0
YLR062C	BUD28	BUD site selection	0
YLR064W	PER33	Pore and ER protein, 33 kDa	0
YLR066W	SPC3	Signal Peptidase Complex	0

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YLR067C	PET309	PETite colonies	0
YLR068W	FYV7	Function required for Yeast Viability	0
YLR070C	XYL2		0
YLR071C	RGR1	Resistant to Glucose Repression	0
YLR072W	LAM6	Lipid transfer protein Anchored at Membrane contact site	0
YLR073C	RFU1	Regulator of Free Ubiquitin chains	0
YLR074C	BUD20	BUD site selection	0
YLR075W	RPL10	Ribosomal Protein of the Large subunit	0
YLR076C			0
YLR078C	BOS1	Bet One Suppressor	0
YLR079W	SIC1	Substrate/Subunit Inhibitor of Cyclin-dependent protein kinase	0
YLR081W	GAL2	GALactose metabolism	0
YLR083C	EMP70		0
YLR086W	SMC4	Structural Maintenance of Chromosomes	0
YLR088W	GAA1	GPI Anchor Attachment	0
YLR089C	ALT1	ALanine Transaminase	0
YLR090W	XDJ1		0
YLR091W	GEP5	GENetic interactors of Prohibitins	0
YLR093C	NYV1	New Yeast V-SNARE	0
YLR094C	GIS3	Glg1-2 Suppressor	0
YLR096W	KIN2	KINase	0
YLR097C	HRT3	High level expression Reduces Ty3 transposition	0
YLR099C	ICT1	Increased Copper Tolerance	0
YLR099W-A	MIM2		0
YLR100W	ERG27	ERGosterol biosynthesis	0
YLR103C	CDC45	Cell Division Cycle	0
YLR105C	SEN2	Splicing ENdonuclease	0
YLR109W	AHP1	Alkyl HydroPeroxide reductase	0
YLR119W	SRN2	Suppressor of Rna mutations, Number 2	0
YLR120C	YPS1	YaPSin	0
YLR120W-A			0
YLR121C	YPS3	YaPSin	0
YLR124W			0
YLR125W			0
YLR126C			0
YLR127C	APC2	Anaphase Promoting Complex	0
YLR132C	USB1	U Six Biogenesis	0
YLR135W	SLX4	Synthetic Lethal of unknown (X) function	0
YLR136C	TIS11	similar to the mammalian TPA Induced Sequence gene family	0
YLR138W	NHA1	Na ⁺ /H ⁺ Antiporter	0
YLR142W	PUT1	Proline UTilization	0
YLR145W	RMP1	RNase MRP Protein	0
YLR146W-A			0
YLR147C	SMD3		0
YLR148W	PEP3	carboxyPEPtidase Y-deficient	0
YLR149C-A			0
YLR150W	STM1	Suppressor of ToM1	0
YLR154C	RNH203	RNase H	0
YLR163C	MAS1	Mitochondrial ASsembly	0
YLR163W-A			0
YLR164W	SHH4	SDH4 Homolog	0

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YLR165C	PUS5	PseudoUridine Synthase	0
YLR167W	RPS31	Ribosomal Protein of the Small subunit	0
YLR168C	UPS2	UnProceSsed	0
YLR169W			0
YLR170C	APS1	clathrin Associated Protein complex Small subunit	0
YLR172C	DPH5	DiPHthamide	0
YLR174W	IDP2	Isocitrate Dehydrogenase, NADP-specific	0
YLR175W	CBF5	Centromere Binding Factor	0
YLR178C	TFS1	cdc Twenty-Five Suppressor	0
YLR180W	SAM1	S-AdenosylMethionine requiring	0
YLR181C	VTA1	VpsTwenty Associated	0
YLR183C	TOS4	Target Of Sbf	0
YLR185W	RPL37A	Ribosomal Protein of the Large subunit	0
YLR186W	EMG1	Essential for Mitotic Growth	0
YLR187W	SKG3	Suppressor of lethality of Kex2 Gas1 double null mutant	0
YLR188W	MDL1	MultiDrug resistance-Like	0
YLR189C	ATG26	AuTophagy related	0
YLR190W	MMR1	Mitochondrial Myo2p Receptor-related	0
YLR191W	PEX13	PEroXin	0
YLR192C	HCR1	High-Copy suppressor of Rpg1	0
YLR193C	UPS1	UnProceSsed	0
YLR194C	NCW2	Novel Cell Wall protein	0
YLR195C	NMT1	N-Myristoyl Transferase	0
YLR196W	PWP1	Periodic tryptophan (W) Protein	0
YLR197W	NOP56	Nucleolar Protein of 56.8 kDa	0
YLR198C			0
YLR201C	COQ9	COenzyme Q	0
YLR203C	MSS51	Mitochondrial Splicing Suppressor	0
YLR204W	QRI5	Quasi-Renownless Information	0
YLR205C	HMX1	HeMe oXygenase	0
YLR206W	ENT2	Epsin N-Terminal homology	0
YLR207W	HRD3	HMG-coA Reductase Degradation	0
YLR208W	SEC13	SECretery	0
YLR209C	PNP1	purine nucleoside phosphorylase	0
YLR210W	CLB4	CycLin B	0
YLR211C	ATG38	AuTophagy related	0
YLR212C	TUB4	TUBulin	0
YLR213C	CRR1	CRH-Related	0
YLR214W	FRE1	Ferric REductase	0
YLR215C	CDC123	Cell Division Cycle	0
YLR216C	CPR6	Cyclosporin-sensitive Proline Rotamase	0
YLR217W			0
YLR218C	COA4	Cytochrome Oxidase Assembly factor	0
YLR219W	MSC3	Meiotic Sister-Chromatid recombination	0
YLR220W	CCC1	Cross-Complements Ca(2+) phenotype of csg1	0
YLR221C	RSA3	RiboSome Assembly	0
YLR222C	UTP13	U Three Protein	0
YLR222C-A			0
YLR223C	IFH1	Interacts with Fork Head	0
YLR224W	UCC1	Ubiquitination of Citrate synthase in the glyoxylate Cycle	0
YLR225C			0

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YLR226W	BUR2	Bypass UAS Requirement	0
YLR228C	ECM22	ExtraCellular Mutant	0
YLR229C	CDC42	Cell Division Cycle	0
YLR231C	BNA5	Biosynthesis of Nicotinic Acid	0
YLR232W			0
YLR234W	TOP3	TOPOisomerase	0
YLR236C			0
YLR237W	THI7	THIamine metabolism	0
YLR238W	FAR10	Factor ARrest	0
YLR239C	LIP2	LIPoyl ligase	0
YLR240W	VPS34	Vacuolar Protein Sorting	0
YLR241W	CSC1	Calcium permeable Stress-gated cation Channel	0
YLR242C	ARV1	ARE2 Required for Viability	0
YLR243W	GPN3	Gly-Pro-Asn (N) motif	0
YLR245C	CDD1	CytiDine Deaminase	0
YLR246W	ERF2	Effect on Ras Function	0
YLR249W	YEF3	Yeast Elongation Factor	0
YLR250W	SSP120	Saccharomyces Secretory Protein	0
YLR252W			0
YLR253W	MCP2	Mdm10 Complementing Protein	0
YLR258W	GSY2	Glycogen SYNthase	0
YLR260W	LCB5	Long-Chain Base	0
YLR261C	VPS63	Vacuolar Protein Sorting	0
YLR262C	YPT6	Yeast Protein Two	0
YLR262C-A	TMA7	Translation Machinery Associated	0
YLR264C-A			0
YLR264W	RPS28B	Ribosomal Protein of the Small subunit	0
YLR265C	NEJ1	Nonhomologous End-Joining defective	0
YLR267W	BOP2	Bypass Of Pam1	0
YLR268W	SEC22	SECretory	0
YLR270W	DCS1	DeCapping Scavenger	0
YLR273C	PIG1	Protein Interacting with Gsy2p	0
YLR274W	MCM5	MiniChromosome Maintenance	0
YLR275W	SMD2		0
YLR276C	DBP9	Dead Box Protein	0
YLR281C	RSO55	mitochondrial protein Related to Spastic paraplegia with Optic at	0
YLR282C			0
YLR284C	ECI1	Enoyl-CoA Isomerase	0
YLR285W	NNT1	Nicotinamide N-methylTTransferase	0
YLR286W-A			0
YLR287C			0
YLR287C-A	RPS30A	Ribosomal Protein of the Small subunit	0
YLR288C	MEC3	Mitosis Entry Checkpoint	0
YLR289W	GUF1	Gtpase of Unknown Function	0
YLR290C	COQ11	COenzyme Q	0
YLR291C	GCD7	General Control Derepressed	0
YLR292C	SEC72	SECretory	0
YLR293C	GSP1	Genetic Suppressor of Prp20-1	0
YLR294C			0
YLR295C	ATP14	ATP synthase	0
YLR299C-A			0

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YLR300W	EXG1	EXo-1,3-beta-Glucanase	0
YLR301W	HRI1	HRr25 Interacting	0
YLR303W	MET17	METHionine requiring	0
YLR304C	ACO1	ACOnitase	0
YLR307C-A	DPA10	Delta-Psi dependent mitochondrial Assembly protein of 10 kDa	0
YLR307W	CDA1	Chitin DeAcetylase	0
YLR308W	CDA2	Chitin DeAcetylase	0
YLR312C	ATG39	AuTophagy related	0
YLR312W-A	MRPL15	Mitochondrial Ribosomal Protein, Large subunit	0
YLR313C	SPH1	SPa2 Homolog	0
YLR314C	CDC3	Cell Division Cycle	0
YLR315W	NKP2	Non-essential Kinetochore Protein	0
YLR317W			0
YLR318W	EST2	Ever Shorter Telomeres	0
YLR319C	BUD6	BUD site selection	0
YLR320W	MMS22	Methyl MethaneSulfonate sensitivity	0
YLR321C	SFH1	Snf Five Homolog	0
YLR322W	VPS65	Vacuolar Protein Sorting	0
YLR323C	CWC24	Complexed With Cef1p	0
YLR324W	PEX30	PEroXisome related	0
YLR325C	RPL38	Ribosomal Protein of the Large subunit	0
YLR327C	TMA10	Translation Machinery Associated	0
YLR328W	NMA1	Nicotinamide Mononucleotide Adenylyltransferase	0
YLR329W	REC102	RECombination	0
YLR333C	RPS25B	Ribosomal Protein of the Small subunit	0
YLR338W	OPI9	OverProducer of Inositol	0
YLR340W	RPP0	Ribosomal Protein P0	0
YLR342W-A			0
YLR343W	GAS2	Glycophospholipid-Anchored Surface protein	0
YLR344W	RPL26A	Ribosomal Protein of the Large subunit	0
YLR347C	KAP95	KAryoPherin	0
YLR347W-A			0
YLR350W	ORM2		0
YLR351C	NIT3	NITrilase superfamily	0
YLR352W	LUG1	Lets [URE3]/ure2 Grow	0
YLR354C	TAL1	TransALdolase	0
YLR355C	ILV5	IsoLeucine-plus-Valine requiring	0
YLR356W	ATG33	AuTophagy related	0
YLR357W	RSC2	Remodel the Structure of Chromatin	0
YLR358C			0
YLR359W	ADE13	ADENine requiring	0
YLR360W	VPS38	Vacuolar Protein Sorting	0
YLR361C-A			0
YLR363C	NMD4	Nonsense-Mediated mRNA Decay	0
YLR364C-A			0
YLR364W	GRX8	GlutaRedoXin	0
YLR365W			0
YLR367W	RPS22B	Ribosomal Protein of the Small subunit	0
YLR368W	MDM30	Mitochondrial Distribution and Morphology	0
YLR369W	SSQ1	Stress-Seventy subfamily Q	0
YLR370C	ARC18	ARp2/3 Complex subunit	0

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YLR371W	ROM2	RhO1 Multicopy suppressor	0
YLR374C			0
YLR376C	PSY3	Platinum Sensitivity	0
YLR379W			0
YLR380W	CSR1	Chs5 Spa2 Rescue	0
YLR381W	CTF3	Chromosome Transmission Fidelity	0
YLR385C	SWC7	SWr Complex	0
YLR387C	REH1	REI1 Homolog	0
YLR388W	RPS29A	Ribosomal Protein of the Small subunit	0
YLR390W	ECM19	ExtraCellular Mutant	0
YLR390W-A	CCW14	Covalently linked Cell Wall protein	0
YLR392C	ART10	Arrestin-Related Trafficking adaptors	0
YLR393W	ATP10	ATP synthase	0
YLR395C	COX8	Cytochrome c OXidase	0
YLR399W-A			0
YLR400W			0
YLR401C	DUS3	DihydroUridine Synthase	0
YLR404W	SEI1	SElpin	0
YLR405W	DUS4	DihydroUridine Synthase	0
YLR406C	RPL31B	Ribosomal Protein of the Large subunit	0
YLR406C-A			0
YLR407W			0
YLR408C	BLS1	BLoS1-homolog	0
YLR412C-A			0
YLR412W	BER1	Benomyl REsistant 1	0
YLR414C	PUN1	Plasma membrane protein Upregulated during Nitrogen stress	0
YLR415C			0
YLR416C			0
YLR418C	CDC73	Cell Division Cycle	0
YLR419W			0
YLR420W	URA4	URAcil requiring	0
YLR421C	RPN13	Regulatory Particle Non-ATPase	0
YLR423C	ATG17	AuTophagy related	0
YLR426W	TDA5	Topoisomerase I Damage Affected	0
YLR427W	MAG2		0
YLR428C			0
YLR434C			0
YLR437C	DIF1	Damage-regulated Import Facilitator	0
YLR437C-A			0
YLR438C-A	LSM3	Like SM	0
YLR438W	CAR2	Catabolism of ARginine	0
YLR441C	RPS1A	Ribosomal Protein of the Small subunit	0
YLR443W	ECM7	ExtraCellular Mutant	0
YLR444C			0
YLR445W	GMC2	Grand Meiotic recombination Cluster	0
YLR446W			0
YLR447C	VMA6	Vacuolar Membrane Atpase	0
YLR448W	RPL6B	Ribosomal Protein of the Large subunit	0
YLR450W	HMG2	3-Hydroxy-3-MethylGlutaryl-coenzyme a reductase	0
YLR451W	LEU3	LEUcine biosynthesis	0
YLR452C	SST2	SuperSensiTive	0

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YLR456W			0
YLR457C	NBP1	Nap1 Binding Protein	0
YLR458W			0
YLR459W	GAB1	GPI and Actin Bar	0
YML001W	YPT7	Yeast Protein Two	0
YML007C-A	MIN4	mitochondrial MINi protein of 4 kDa	0
YML008C	ERG6	ERGosterol biosynthesis	0
YML009C	MRPL39	Mitochondrial Ribosomal Protein, Large subunit	0
YML009C-A			0
YML009W-B			0
YML011C	RAD33	RADiation sensitive	0
YML012C-A			0
YML012W	ERV25	ER Vesicle	0
YML014W	TRM9	TRna Methyltransferase	0
YML017W	PSP2	Polymerase SuPpressor	0
YML019W	OST6	OligoSaccharylTransferase	0
YML020W			0
YML021C	UNG1	Uracil DNA N-Glycosylase	0
YML022W	APT1	Adenine PhosphoribosylTransferase	0
YML023C	NSE5	Non-SMC Element 5	0
YML024W	RPS17A	Ribosomal Protein of the Small subunit	0
YML025C	YML6		0
YML026C	RPS18B	Ribosomal Protein of the Small subunit	0
YML027W	YOX1	Yeast homeobOX	0
YML030W	RCF1	Respiratory superComplex Factor	0
YML031C-A			0
YML031W	NDC1	Nuclear Division Cycle	0
YML034C-A			0
YML035C	AMD1	AMP Deaminase	0
YML036W	CGI121	homolog of human CGI-121	0
YML037C			0
YML041C	VPS71	Vacuolar Protein Sorting	0
YML043C	RRN11	Regulation of RNA polymerase I	0
YML047C	PRM6	Pheromone-Regulated Membrane protein	0
YML047W-A			0
YML048W	GSF2	Glucose Signaling Factor	0
YML051W	GAL80	GALactose metabolism	0
YML052W	SUR7	SUPpressor of Rvs167 mutation	0
YML053C			0
YML054C	CYB2	CYtochrome B	0
YML054C-A			0
YML055W	SPC2	Signal Peptidase Complex	0
YML056C	IMD4	IMP Dehydrogenase	0
YML058W	SML1	Suppressor of Mec1 Lethality	0
YML058W-A	HUG1		0
YML060W	OGG1	8-OxoGuanine Glycosylase/lyase	0
YML061C	PIF1	Petite Integration Frequency	0
YML062C	MFT1	Mitochondrial Fusion Targeting	0
YML063W	RPS1B	Ribosomal Protein of the Small subunit	0
YML065W	ORC1	Origin Recognition Complex	0
YML067C	ERV41	ER Vesicle	0

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YML068W	ITT1	Inhibitor of Translation Termination	0
YML069W	POB3	POI1 Binding	0
YML070W	DAK1	DihydroxyAcetone Kinase	0
YML072C	TCB3	Three Calcium and lipid Binding domains (TriCalBins)	0
YML073C	RPL6A	Ribosomal Protein of the Large subunit	0
YML074C	FPR3	Fk 506-sensitive Proline Rotamase	0
YML076C	WAR1	Weak Acid Resistance	0
YML077W	BET5	Blocked Early in Transport	0
YML078W	CPR3	Cyclosporin A-sensitive Proline Rotamase	0
YML079W			0
YML080W	DUS1	DihydroUridine Synthase	0
YML081C-A	ATP18	ATP synthase	0
YML084W			0
YML085C	TUB1	TUBulin	0
YML086C	ALO1	D-Arabinono-1,4-Lactone Oxidase	0
YML088W	UFO1	UV-F-box-HO	0
YML089C			0
YML091C	RPM2	RNase P Mitochondrial	0
YML092C	PRE8	PRoteinase yscE	0
YML093W	UTP14	U Three Protein	0
YML094C-A			0
YML094W	GIM5	Gene Involved in Microtubule biogenesis	0
YML095C	RAD10	RADiation sensitive	0
YML096W			0
YML098W	TAF13	TATA binding protein-Associated Factor	0
YML099W-A			0
YML101C	CUE4	Coupling of Ubiquitin conjugation to ER degradation	0
YML101C-A			0
YML102W	CAC2	Chromatin Assembly Complex	0
YML105C	SEC65	SECretory	0
YML106W	URA5	URAcil requiring	0
YML107C	PML39	Pre-mRNA Leakage	0
YML108W			0
YML109W	ZDS2	Zillion Different Screens	0
YML110C	COQ5	COenzyme Q	0
YML112W	CTK3	Carboxy-Terminal domain Kinase	0
YML113W	DAT1	DATin	0
YML114C	TAF8	TATA binding protein-Associated Factor	0
YML115C	VAN1	VANadate resistance protein	0
YML116W-A			0
YML120C	NDI1	NADH Dehydrogenase Internal	0
YML121W	GTR1	GTP binding protein Resemblance	0
YML123C	PHO84	PHOsphate metabolism	0
YML124C	TUB3	TUBulin	0
YML125C	PGA3	Processing of Gas1p and ALP	0
YML129C	COX14	Cytochrome c OXidase	0
YML130C	ERO1	ER Oxidation or Endoplasmic Reticulum Oxidoreductin	0
YMR001C	CDC5	Cell Division Cycle	0
YMR001C-A			0
YMR002W	MIX17	Mitochondrial Intermembrane space CX(n)C motif protein	0
YMR003W	AIM34	Altered Inheritance rate of Mitochondria	0

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YMR007W			0
YMR009W	ADI1	Acireductone Dloxygenase	0
YMR010W	ANY1	Antagonizes Neo1 Yeast phospholipid flippase	0
YMR011W	HXT2	HeXose Transporter	0
YMR013C-A			0
YMR013W-A			0
YMR015C	ERG5	ERGosterol biosynthesis	0
YMR016C	SOK2	Suppressor Of Kinase	0
YMR018W	PEX9	PEroXin	0
YMR019W	STB4	Sin Three Binding protein	0
YMR021C	MAC1	Metal binding ACticator	0
YMR022W	UBC7	UBiquitin-Conjugating enzyme	0
YMR023C	MSS1	Mitochondrial Splicing System	0
YMR025W	CSI1	Cop9 Signalosome Interactor	0
YMR028W	TAP42	Two A phosphatase Associated Protein	0
YMR030W	RSF1	ReSpiration Factor	0
YMR030W-A			0
YMR031C	EIS1	EISosome	0
YMR031W-A			0
YMR032W	HOF1	Homolog Of cdc Fifteen	0
YMR033W	ARP9	Actin-Related Protein	0
YMR034C	RCH1	Regulator of Calcium Homeostasis	0
YMR035W	IMP2	Inner Membrane Protease	0
YMR037C	MSN2	Multicopy suppressor of SNF1 mutation	0
YMR038C	CCS1	Copper Chaperone for SOD1	0
YMR039C	SUB1	SUppressor of TFIIb mutations	0
YMR040W	YET2	Yeast Endoplasmic reticulum Transmembrane protein	0
YMR041C	ARA2	ARAbinose	0
YMR043W	MCM1	MiniChromosome Maintenance	0
YMR054W	STV1	Similar To VPH1	0
YMR056C	AAC1	ADP/ATP Carrier	0
YMR059W	SEN15	Splicing ENdonuclease	0
YMR061W	RNA14	poly(A) mRNA metabolism	0
YMR062C	ARG7	ARGinine requiring	0
YMR063W	RIM9	Regulator of IME2	0
YMR064W	AEP1	ATPase ExPression	0
YMR065W	KAR5	KARyogamy	0
YMR066W	SOV1	Synthesis Of Var	0
YMR067C	UBX4	UBiquitin regulatory X	0
YMR068W	AVO2	Adheres VOraciously (to TOR2)	0
YMR071C	TVP18	Tlg2-Vesicle Protein	0
YMR072W	ABF2	ARS-Binding Factor	0
YMR073C	IRC21	Increased Recombination Centers	0
YMR075C-A			0
YMR075W	RCO1		0
YMR077C	VPS20	Vacuolar Protein Sorting	0
YMR078C	CTF18	Chromosome Transmission Fidelity	0
YMR079W	SEC14	SECretory	0
YMR082C			0
YMR083W	ADH3	Alcohol DeHydrogenase	0
YMR090W			0

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YMR096W	SNZ1	SNooZe	0
YMR097C	MTG1	MiTochondrial GTPase	0
YMR099C			0
YMR100W	MUB1	MUlti Budding	0
YMR101C	SRT1	Suppressor of Rer-Two	0
YMR103C			0
YMR105C	PGM2	PhosphoGlucoMutase	0
YMR105W-A			0
YMR106C	YKU80	Yeast KU protein	0
YMR107W	SPG4	Stationary Phase Gene	0
YMR108W	ILV2	IsoLeucine-plus-Valine requiring	0
YMR111C			0
YMR112C	MED11	MEDiator complex	0
YMR113W	FOL3	FOLic acid synthesis	0
YMR114C			0
YMR115W	MGR3	Mitochondrial Genome Required	0
YMR116C	ASC1	Absence of growth Suppressor of Cyp1	0
YMR117C	SPC24	Spindle Pole Component	0
YMR118C	SHH3	SDH3 Homolog	0
YMR119W-A			0
YMR120C	ADE17	ADEnine	0
YMR121C	RPL15B	Ribosomal Protein of the Large subunit	0
YMR122C			0
YMR122W-A	NCW1	Novel Cell Wall protein	0
YMR123W	PKR1	Pichia farinosa Killer toxin Resistance	0
YMR125W	STO1	Suppressor of TOp1	0
YMR126C	DLT1	Defect at Low Temperature	0
YMR127C	SAS2	Something About Silencing	0
YMR128W	ECM16	ExtraCellular Mutant	0
YMR129W	POM152	POre Membrane	0
YMR130W	DPI35	Delta-Psi dependent mitochondrial Import protein of 35 kDa	0
YMR131C	RRB1	Regulator of Ribosome Biogenesis	0
YMR135W-A			0
YMR136W	GAT2		0
YMR137C	PSO2	PSOralen derivative sensitive	0
YMR138W	CIN4	Chromosome INstability	0
YMR139W	RIM11	Regulator of IME2	0
YMR140W	SIP5	Snf1 Interacting Protein	0
YMR141C			0
YMR141W-A			0
YMR142C	RPL13B	Ribosomal Protein of the Large subunit	0
YMR143W	RPS16A	Ribosomal Protein of the Small subunit	0
YMR145C	NDE1	NADH Dehydrogenase, External	0
YMR146C	TIF34	Translation Initiation Factor	0
YMR147W	LDO45	Lipid Droplet Organization protein of 45 Kda	0
YMR150C	IMP1	Inner Membrane Protease	0
YMR151W	YIM2		0
YMR152W	YIM1		0
YMR153C-A			0
YMR153W	NUP53	NUclear Pore	0
YMR155W			0

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YMR156C	TPP1	Three Prime Phosphatase	0
YMR157C	AIM36	Altered Inheritance rate of Mitochondria	0
YMR158C-A			0
YMR158W	MRPS8	Mitochondrial Ribosomal Protein, Small subunit	0
YMR158W-B			0
YMR159C	ATG16	AuTophagy related	0
YMR160W			0
YMR161W	HLJ1	HomoLogous to E. coli dnaJ protein	0
YMR162C	DNF3	Drs2 Neo1 Family	0
YMR172C-A			0
YMR172W	HOT1	High-Osmolarity-induced Transcription	0
YMR174C	PAI3	Proteinase A Inhibitor	0
YMR181C			0
YMR182C	RGM1		0
YMR182W-A	MIN3	mitochondrial MINi protein of 3 kDa	0
YMR183C	SSO2	Supressor of Sec One	0
YMR184W	ADD37	Alpha1-proteinase inhibitor-Degradation Deficient	0
YMR185W	RTP1	Required for the nuclear Transport of RNA Pol II	0
YMR186W	HSC82		0
YMR187C			0
YMR189W	GCV2	GlyCine cleavage	0
YMR190C	SGS1	Slow Growth Suppressor	0
YMR191W	SPG5	Stationary Phase Gene	0
YMR192W	GYL1	GYp Like	0
YMR193W	MRPL24	Mitochondrial Ribosomal Protein, Large subunit	0
YMR194C-B	CMC4	Cx9C Motif-Containing protein	0
YMR194W	RPL36A	Ribosomal Protein of the Large subunit	0
YMR195W	ICY1	Interacting with the CYtoskeleton	0
YMR196W			0
YMR197C	VTI1	Vps10 (Ten) Interacting	0
YMR200W	ROT1	Reversal Of Tor2 lethality	0
YMR201C	RAD14	RADiation sensitive	0
YMR204C	INP1	INheritance of Peroxisomes	0
YMR208W	ERG12	ERGosterol biosynthesis	0
YMR209C			0
YMR212C	EFR3	PHO Eighty Five Requiring	0
YMR213W	CEF1	CErevisiae homolog of cdc Five	0
YMR217W	GUA1	GUanine Auxotroph	0
YMR220W	ERG8	ERGosterol biosynthesis	0
YMR222C	FSH2	Family of Serine Hydrolases	0
YMR223W	UBP8	UBiquitin-specific processing Protease	0
YMR224C	MRE11	Meiotic REcombination	0
YMR225C	MRPL44	Mitochondrial Ribosomal Protein, Large subunit	0
YMR226C			0
YMR228W	MTF1	Mitochondrial Transcription Factor	0
YMR230W	RPS10B	Ribosomal Protein of the Small subunit	0
YMR232W	FUS2	cell FUSion	0
YMR233W	TRI1		0
YMR234W	RNH1	RNase H	0
YMR235C	RNA1	rapid cessation of net RNA accumulation	0
YMR236W	TAF9	TATA binding protein-Associated Factor	0

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YMR237W	BCH1	Bud7 and Chs6 Homolog	0
YMR239C	RNT1	RNase Three	0
YMR240C	CUS1	Cold sensitive U2 snRNA Suppressor	0
YMR241W	YHM2	Yeast suppressor of HM mutant	0
YMR242C	RPL20A	Ribosomal Protein of the Large subunit	0
YMR242W-A			0
YMR244C-A	COA6	Cytochrome Oxidase Assembly	0
YMR244W			0
YMR247W-A			0
YMR251W-A	HOR7	HyperOsmolarity-Responsive	0
YMR252C	MLO1	Mitochondrially Localized protein	0
YMR253C			0
YMR254C			0
YMR255W	GFD1	Good For Dbp5p	0
YMR256C	COX7	Cytochrome c OXidase	0
YMR258C	ROY1	Repressor Of Ypt52	0
YMR260C	TIF11	Translation Initiation Factor	0
YMR262W			0
YMR264W	CUE1	Coupling of Ubiquitin conjugation to ER degradation	0
YMR266W	RSN1	Rescue of Sro7 at high NaCl	0
YMR267W	PPA2	PyroPhosphatase	0
YMR269W	TMA23	Translation Machinery Associated	0
YMR270C	RRN9	Regulation of RNA polymerase I	0
YMR271C	URA10	URAcil requiring	0
YMR272C	SCS7	Suppressor of Ca2+ Sensitivity	0
YMR272W-A			0
YMR273C	ZDS1	Zillion Different Screens	0
YMR274C	RCE1	Ras and a-factor Converting Enzyme	0
YMR276W	DSK2		0
YMR278W	PRM15	Phospho Ribo Mutase	0
YMR281W	GPI12	GlycosylPhosphatidylinositol anchor biosynthesis	0
YMR284W	YKU70	Yeast KU protein	0
YMR286W	MRPL33	Mitochondrial Ribosomal Protein, Large subunit	0
YMR292W	GOT1	GOlgi Transport	0
YMR294W-A			0
YMR298W	LIP1	Lag1p/Lac1p Interacting Protein	0
YMR299C	DYN3	DYNein	0
YMR300C	ADE4	ADENine requiring	0
YMR305C	SCW10	Soluble Cell Wall protein	0
YMR306C-A			0
YMR307C-A			0
YMR307W	GAS1	Glycophospholipid-Anchored Surface protein	0
YMR309C	NIP1	Nuclear ImPort	0
YMR310C			0
YMR311C	GLC8	GLyCogen	0
YMR312W	ELP6	ELongator Protein	0
YMR313C	TGL3	TriacylGlycerol Lipase	0
YMR314W	PRE5	PRoteinase yscE	0
YMR315W-A			0
YMR316C-B			0
YMR316W	DIA1	Digs Into Agar	0

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YMR320W			0
YNL001W	DOM34	Duplication Of Multilocus region	0
YNL002C	RLP7	Ribosomal-Like Protein	0
YNL003C	PET8	PETite colonies	0
YNL004W	HRB1	Hypothetical RNA-Binding protein	0
YNL005C	MRP7	Mitochondrial Ribosomal Protein	0
YNL006W	LST8	Lethal with Sec Thirteen	0
YNL007C	SIS1	Slr4 Suppressor	0
YNL008C	ASI3	Amino acid Sensor-Independent	0
YNL009W	IDP3	Isocitrate Dehydrogenase, NADP-dependent	0
YNL011C			0
YNL012W	SPO1	SPOrulation	0
YNL013C			0
YNL014W	HEF3	Homolog of EF-3	0
YNL015W	PBI2	Proteinase B Inhibitor	0
YNL016W	PUB1	PolyUridylate Binding	0
YNL020C	ARK1	Actin Regulating Kinase	0
YNL021W	HDA1	Histone DeAcetylase	0
YNL022C	RCM1		0
YNL024C	EFM6	Elongation Factor Methyltransferase	0
YNL024C-A	KSH1	KSH (similar to the Hungarian word for "small")	0
YNL027W	CRZ1	Calcineurin-Responsive Zinc finger	0
YNL028W			0
YNL029C	KTR5	Kre Two Related	0
YNL030W	HHF2	Histone H Four	0
YNL031C	HHT2	Histone H Three	0
YNL032W	SIW14	Synthetic Interaction with Whi2	0
YNL035C			0
YNL036W	NCE103	NonClassical Export	0
YNL037C	IDH1	Isocitrate DeHydrogenase	0
YNL038W	GPI15	GlycosylPhosphatidylinositol anchor biosynthesis	0
YNL039W	BDP1	B Double Prime	0
YNL040W			0
YNL042W	BOP3	Bypass Of Pam1	0
YNL042W-B			0
YNL043C			0
YNL044W	YIP3	Ypt-Interacting Protein	0
YNL046W			0
YNL047C	SLM2	Synthetic Lethal with Mss4	0
YNL048W	ALG11	Asparagine-Linked Glycosylation	0
YNL050C			0
YNL052W	COX5A	Cytochrome c OXidase	0
YNL055C	POR1	PORin	0
YNL057W			0
YNL058C			0
YNL061W	NOP2	NucleOlar Protein	0
YNL062C	GCD10	General Control Derepressed	0
YNL065W	AQR1	Acids Quinidine Resistance	0
YNL067W	RPL9B	Ribosomal Protein of the Large subunit	0
YNL067W-A			0
YNL067W-B			0

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YNL068C	FKH2	ForK head Homolog	0
YNL069C	RPL16B	Ribosomal Protein of the Large subunit	0
YNL070W	TOM7	Translocase of the Outer Mitochondrial membrane	0
YNL072W	RNH201	RNase H	0
YNL075W	IMP4	Interacting with Mpp10p	0
YNL076W	MKS1	Multicopy Kinase Suppressor	0
YNL078W	NIS1	Neck protein Interacting with Septins	0
YNL079C	TPM1	TroPoMyosin	0
YNL081C	SWS2	Sick Without Securin	0
YNL083W	SAL1	Suppressor of Aac2 Lethality	0
YNL084C	END3	ENDocytosis defective	0
YNL088W	TOP2	TOPoisomerase	0
YNL089C			0
YNL090W	RHO2	Ras HOmolog	0
YNL091W	NST1	Negatively affects Salt Tolerance	0
YNL092W			0
YNL093W	YPT53	Yeast Protein Two	0
YNL094W	APP1	Actin Patch Protein	0
YNL096C	RPS7B	Ribosomal Protein of the Small subunit	0
YNL097C	PHO23	PHOspate metabolism	0
YNL097C-B			0
YNL097W-A			0
YNL098C	RAS2	homologous to RAS proto-oncogene	0
YNL099C	OCA1	Oxidant-induced Cell-cycle Arrest	0
YNL100W	MIC27	Mitochondrial contact site and Cristae organizing system	0
YNL103W-A			0
YNL104C	LEU4	LEUcine biosynthesis	0
YNL105W	RRT16	Regulator of rDNA Transcription	0
YNL106C	INP52	INositol polyphosphate 5-Phosphatase	0
YNL107W	YAF9	Yeast homolog of the human leukemogenic protein AF9	0
YNL108C			0
YNL109W			0
YNL110C	NOP15	NucleOlar Protein	0
YNL111C	CYB5	CYtochrome B	0
YNL112W	DBP2	Dead Box Protein	0
YNL113W	RPC19	RNA Polymerase C	0
YNL114C			0
YNL116W	DMA2	Defective in Mitotic Arrest	0
YNL118C	DCP2	mRNA DeCaPping	0
YNL120C			0
YNL122C			0
YNL126W	SPC98	Spindle Pole Component	0
YNL129W	NRK1	Nicotinamide Riboside Kinase	0
YNL131W	TOM22	Translocase of the Outer Mitochondrial membrane	0
YNL133C	FYV6	Function required for Yeast Viability	0
YNL135C	FPR1	Fk 506-sensitive Proline Rotamase	0
YNL138W-A	YSF3	Yeast Splicing Factor 3b subunit	0
YNL140C			0
YNL141W	AAH1	Adenine AminoHydrolase	0
YNL144W-A			0
YNL145W	MFA2	Mating Factor A	0

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YNL146W			0
YNL147W	LSM7	Like SM	0
YNL149C	PGA2	Processing of Gas1p and ALP	0
YNL150W			0
YNL151C	RPC31	RNA Polymerase C	0
YNL153C	GIM3	Gene Involved in Microtubule biogenesis	0
YNL155W	CUZ1	Cdc48-associated UBL/Zn-finger protein	0
YNL156C	NSG2		0
YNL157W	IGO1	Initiation of G zero	0
YNL158W	PGA1	Processing of Gas1p and ALP	0
YNL162W	RPL42A	Ribosomal Protein of the Large subunit	0
YNL162W-A			0
YNL164C	IBD2	Inhibition of Bud Division 2	0
YNL165W			0
YNL168C	FMP41	Found in Mitochondrial Proteome	0
YNL169C	PSD1	PhosphatidylSerine Decarboxylase	0
YNL170W			0
YNL171C			0
YNL173C	MDG1	Multicopy suppressor of Defective G-protein	0
YNL174W			0
YNL175C	NOP13	Nucleolar Protein	0
YNL176C	TDA7	Topoisomerase I Damage Affected	0
YNL178W	RPS3	Ribosomal Protein of the Small subunit	0
YNL180C	RHO5	Ras HOMolog	0
YNL181W	PBR1	Potentiates Bioactive compound Response	0
YNL182C	IPI3	Involved in Processing ITS2	0
YNL183C	NPR1	Nitrogen Permease Reactivator	0
YNL184C			0
YNL185C	MRPL19	Mitochondrial Ribosomal Protein, Large subunit	0
YNL186W	UBP10	UBiquitin-specific Protease	0
YNL188W	KAR1	KARyogamy	0
YNL190W			0
YNL191W	DUG3	Deficient in Utilization of Glutathione	0
YNL192W	CHS1	CHitin Synthase	0
YNL193W			0
YNL194C			0
YNL195C			0
YNL196C	SLZ1		0
YNL197C	WHI3	WHIskey	0
YNL198C			0
YNL199C	GCR2	GlyColysis Regulation	0
YNL200C	NNR1	Nicotinamide Nucleotide Repair	0
YNL201C	PSY2	Platinum Sensitivity	0
YNL202W	SPS19	SPorulation-Specific	0
YNL203C			0
YNL204C	SPS18	SPorulation-Specific	0
YNL206C	RTT106	Regulator of Ty1 Transposition	0
YNL207W	RIO2	RIght Open reading frame	0
YNL208W			0
YNL211C	MRX7	Mitochondrial oRganization of gene eXpression (MIOREX)	0
YNL212W	VID27	Vacuolar Import and Degradation	0

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YNL213C	RRG9	Required for Respiratory Growth	0
YNL214W	PEX17	PEroXisome related	0
YNL215W	IES2	Ino Eighty Subunit	0
YNL216W	RAP1	Repressor/Activator site binding Protein	0
YNL217W	PPN2		0
YNL218W	MGS1	Maintenance of Genome Stability	0
YNL219C	ALG9	Asparagine-Linked Glycosylation	0
YNL220W	ADE12	ADEnine requiring	0
YNL222W	SSU72	Suppressor of SUa7, gene 2	0
YNL226W			0
YNL228W			0
YNL229C	URE2	UREidosuccinate transport	0
YNL236W	SIN4	Switch INdependent	0
YNL239W	LAP3	Leucine AminoPeptidases	0
YNL240C	NAR1	Nuclear Architecture Related	0
YNL243W	SLA2	Synthetic Lethal with ABP1	0
YNL244C	SUI1	SUPpressor of Initiator codon	0
YNL245C	CWC25	Complexed With Cef1p	0
YNL246W	VPS75	Vacuolar Protein Sorting	0
YNL248C	RPA49	RNA Polymerase A	0
YNL249C	MPA43	Multicopy PDC1 Activator	0
YNL250W	RAD50	RADIation sensitive	0
YNL252C	MRPL17	Mitochondrial Ribosomal Protein, Large subunit	0
YNL253W	TEX1	TrEX component	0
YNL254C	RTC4	Restriction of Telomere Capping	0
YNL255C	GIS2	Glg Suppressor	0
YNL258C	DSL1	Dependence on SLy1-20	0
YNL259C	ATX1	AnTioXidant	0
YNL260C	LTO1	required for biogenesis of the Large ribosomal subunit and initiat	0
YNL263C	YIF1	YIP1-Interacting Factor	0
YNL264C	PDR17	Pleiotropic Drug Resistance	0
YNL265C	IST1	Increased Sodium Tolerance	0
YNL266W			0
YNL269W	BSC4	Bypass of Stop Codon	0
YNL272C	SEC2	SECretory	0
YNL274C	GOR1	GlyOxylate Reductase	0
YNL275W	BOR1	BORon transporter	0
YNL276C			0
YNL277W-A			0
YNL279W	PRM1	Pheromone-Regulated Membrane protein	0
YNL280C	ERG24	ERGosterol biosynthesis	0
YNL281W	HCH1	High-Copy Hsp90 suppressor	0
YNL282W	POP3	Processing Of Precursor RNAs	0
YNL284C	MRPL10	Mitochondrial Ribosomal Protein, Large subunit	0
YNL286W	CUS2	Cold sensitive U2 snRNA Suppressor	0
YNL287W	SEC21	SECretory	0
YNL289W	PCL1	Pho85 CycLin	0
YNL290W	RFC3	Replication Factor C	0
YNL293W	MSB3	Multicopy Suppressor of Bud Emergence	0
YNL300W	TOS6		0
YNL302C	RPS19B	Ribosomal Protein of the Small subunit	0

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YNL303W			0
YNL305C	BXI1	BaX Inhibitor	0
YNL306W	MRPS18	Mitochondrial Ribosomal Protein, Small subunit	0
YNL307C	MCK1	Meiosis and Centromere regulatory Kinase	0
YNL308C	KRI1	KRR1-Interacting protein	0
YNL310C	ZIM17	ZInc finger Motif protein of 17 kDa	0
YNL312W	RFA2	Replication Factor A	0
YNL313C	EMW1	Essential for Maintenance of the cell Wall	0
YNL315C	ATP11	ATP synthase	0
YNL317W	PFS2	Polyadenylation Factor Subunit	0
YNL320W			0
YNL323W	LEM3	Ligand-Effect Modulator	0
YNL324W			0
YNL326C	PFA3	Protein Fatty Acyltransferase	0
YNL334C	SNO2	SNZ proximal Open reading frame	0
YNR001C	CIT1	CITrate synthase	0
YNR001W-A			0
YNR002C	ATO2	Ammonia (Ammonium) Transport Outward	0
YNR003C	RPC34	RNA Polymerase C	0
YNR003W-A			0
YNR004W	SWM2	Synthetic With mud2-delta	0
YNR005C			0
YNR006W	VPS27	Vacuolar Protein Sorting	0
YNR007C	ATG3	AuTophagy related	0
YNR008W	LRO1	Lecithin cholesterol acyl transferase Related Open reading frame	0
YNR010W	CSE2	Chromosome SEgregation	0
YNR013C	PHO91	PHOsphate metabolism	0
YNR014W			0
YNR016C	ACC1	Acetyl-CoA Carboxylase	0
YNR017W	TIM23	Translocase of the Inner Mitochondrial membrane	0
YNR018W	RCF2	Respiratory superComplex Factor	0
YNR019W	ARE2	Acyl-coenzyme A: cholesterol acyl transferase-Related Enzyme	0
YNR020C	ATP23		0
YNR022C	MRPL50	Mitochondrial Ribosomal Protein, Large subunit	0
YNR024W	MPP6	M-Phase Phosphoprotein 6 homolog	0
YNR025C			0
YNR026C	SEC12	SECretory	0
YNR027W	BUD17	BUD site selection	0
YNR028W	CPR8	Cyclosporin-sensitive Proline Rotamase	0
YNR029C			0
YNR032C-A	HUB1	Homologous to UBiquitin	0
YNR032W	PPG1	Protein Phosphatase involved in Glycogen accumulation	0
YNR034W	SOL1	Suppressor Of Los1-1	0
YNR034W-A	EGO4	Exit from rapamycin-induced GrOwth arrest	0
YNR035C	ARC35	ARp2/3 Complex subunit	0
YNR036C	MRPS12	Mitochondrial Ribosomal Protein, Small subunit	0
YNR037C	RSM19	Ribosomal Small subunit of Mitochondria	0
YNR040W	DPI29	Delta-Psi dependent mitochondrial Import protein of 29 kDa	0
YNR041C	COQ2	COenzyme Q	0
YNR042W			0
YNR043W	MVD1	MeValonate pyrophosphate Decarboxylase	0

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YNR046W	TRM112	TRna Methyltransferase	0
YNR050C	LYS9	LYSine requiring	0
YNR052C	POP2	PGK promoter directed OverProduction	0
YNR053C	NOG2	NucleOlar G-protein	0
YNR054C	ESF2	Eighteen S rRNA Factor 2	0
YNR058W	BIO3	BIOtin	0
YNR062C	PUL3	PULcherrimin	0
YNR071C			0
YNR074C	AIF1	Apoptosis-Inducing Factor	0
YNR075C-A			0
YOL001W	PHO80	PHOsphate metabolism	0
YOL002C	IZH2	Implicated in Zinc Homeostasis	0
YOL003C	PFA4	Protein Fatty Acyltransferase	0
YOL005C	RPB11	RNA Polymerase B	0
YOL007C	CSI2	Chitin Synthesis Involved	0
YOL009C	MDM12	Mitochondrial Distribution and Morphology	0
YOL012C	HTZ1	Histone Two A Z1	0
YOL013C	HRD1	HMG-coA Reductase Degradation	0
YOL013W-A			0
YOL013W-B			0
YOL014W			0
YOL017W	ESC8	Establishes Silent Chromatin	0
YOL018C	TLG2	T-snare affecting a Late Golgi compartment	0
YOL019W-A			0
YOL022C	TSR4	Twenty S rRNA accumulation	0
YOL023W	IFM1	Initiation Factor of Mitochondria	0
YOL024W			0
YOL025W	LAG2	Longevity Assurance Gene	0
YOL026C	MIM1	Mitochondrial IMport	0
YOL029C			0
YOL032W	OPI10	OverProducer of Inositol	0
YOL034W	SMC5	Structural Maintenance of Chromosomes	0
YOL035C			0
YOL037C			0
YOL038C-A			0
YOL038W	PRE6	PRoteinase yscE	0
YOL039W	RPP2A	Ribosomal Protein P2 Alpha	0
YOL041C	NOP12	NucleOlar Protein	0
YOL045W	PSK2	Pas domain-containing Serine/threonine protein Kinase	0
YOL046C			0
YOL048C	RRT8	Regulator of rDNA Transcription	0
YOL049W	GSH2	Glutathione	0
YOL050C			0
YOL051W	GAL11	GALactose metabolism	0
YOL052C	SPE2	SPERmidine auxotroph	0
YOL054W	PSH1	Pob3/Spt16 Histone associated	0
YOL056W	GPM3	Glycerate PhosphoMutase	0
YOL058W	ARG1	ARGinine requiring	0
YOL061W	PRS5	PhosphoRibosylpyrophosphate Synthetase	0
YOL062C	APM4	clathrin Adaptor Protein complex Medium chain	0
YOL064C	MET22	METHionine requiring	0

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YOL065C	INP54	INositol polyphosphate 5-Phosphatase	0
YOL067C	RTG1	ReTroGrade regulation	0
YOL068C	HST1	Homolog of SIR Two (SIR2)	0
YOL069W	NUF2	NUclear Filament-containing protein	0
YOL070C	NBA1	Nap1p and Bud neck Associated	0
YOL072W	THP1	Tho2/Hpr1 Phenotype	0
YOL077W-A	ATP19	ATP synthase	0
YOL083C-A			0
YOL084W	PHM7	PHosphate Metabolism	0
YOL085C			0
YOL085W-A			0
YOL086W-A	MHF1	Mph1-associated Histone-Fold protein	0
YOL087C	DUF1	DUB-associated Factor 1	0
YOL092W	YPQ1	Yeast PQ-loop protein	0
YOL093W	TRM10	Transfer RNA Methyltransferase	0
YOL094C	RFC4	Replication Factor C	0
YOL095C	HMI1	Helicase in MItochondria	0
YOL096C	COQ3	COenzyme Q	0
YOL097C	WRS1	W (tryptophan) RS (tRNA synthetase)	0
YOL098C	SDD3	Suppressor of Degenerative Death	0
YOL101C	IZH4	Implicated in Zinc Homeostasis	0
YOL103W	ITR2	myo-Inositol TRansporter	0
YOL107W			0
YOL108C	INO4	INOsitol requiring	0
YOL109W	ZEO1	ZEOcin resistance	0
YOL110W	SHR5	Suppressor of Hyperactive Ras	0
YOL111C	MDY2	Mating-Deficient Yeast	0
YOL112W	MSB4	Multicopy Suppression of a Budding defect	0
YOL114C	PTH4	peptidyl tRNA hydrolase 4	0
YOL116W	MSN1	Multicopy suppressor of SNF1 mutation	0
YOL117W	RRI2		0
YOL118C			0
YOL119C	MCH4	MonoCarboxylate transporter Homolog	0
YOL120C	RPL18A	Ribosomal Protein of the Large subunit	0
YOL121C	RPS19A	Ribosomal Protein of the Small subunit	0
YOL122C	SMF1	Suppressor of Mitochondria import Function	0
YOL123W	HRP1	Heterogenous nuclear RibonucleoProtein	0
YOL124C	TRM11	TRna Methyltransferase	0
YOL125W	TRM13	TRna Methyltransferase	0
YOL127W	RPL25	Ribosomal Protein of the Large subunit	0
YOL129W	VPS68	Vacuolar Protein Sorting	0
YOL133W	HRT1	High level expression Reduces Ty3 transposition	0
YOL137W	BSC6	Bypass of Stop Codon	0
YOL139C	CDC33	Cell Division Cycle	0
YOL140W	ARG8	ARGinine requiring	0
YOL141W	PPM2	Protein Phosphatase Methyltransferase	0
YOL142W	RRP40	Ribosomal RNA Processing	0
YOL144W	NOP8	NucleOlar Protein	0
YOL147C	PEX11	PEroXin	0
YOL150C			0
YOL151W	GRE2	Genes de Respuesta a Estres (stress responsive genes)	0

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YOL155W-A			0
YOL159C	CSS3	Condition Specific Secretion	0
YOL159C-A			0
YOR001W	RRP6	Ribosomal RNA Processing	0
YOR002W	ALG6	Asparagine-Linked Glycosylation	0
YOR003W	YSP3	Yeast Subtilisin-like Protease III	0
YOR004W	UTP23	U Three-associated Protein	0
YOR005C	DNL4	DNA Ligase	0
YOR006C	TSR3	Twenty S rRNA accumulation	0
YOR007C	SGT2	Small Glutamine-rich Tetratricopeptide repeat-containing protein	0
YOR008C	SLG1	Synthetic Lethal with Gap	0
YOR008W-B			0
YOR011W-A			0
YOR015W			0
YOR020C	HSP10	Heat Shock Protein	0
YOR020W-A	MCO10	Mitochondrial Class One protein of 10 kDa	0
YOR021C	SFM1	Spout Family Methyltransferase 1	0
YOR022C	DDL1	DDHD Domain-containing Lipase	0
YOR023C	AHC1	Ada Histone acetyltransferase complex Component	0
YOR024W			0
YOR026W	BUB3	Budding Uninhibited by Benzimidazole	0
YOR027W	STI1	STress Inducible	0
YOR028C	CIN5	Chromosome INstability	0
YOR029W			0
YOR030W	DFG16	Defective for Filamentous Growth	0
YOR031W	CRS5	Copper-Resistant Suppressor	0
YOR032W-A			0
YOR033C	EXO1	EXOnuclease	0
YOR034C	AKR2	AnKyrin Repeat-containing protein	0
YOR034C-A			0
YOR035C	SHE4	Swi5p-dependent HO Expression	0
YOR036W	PEP12	carboxyPEPTidase Y-deficient	0
YOR037W	CYC2	CYtochrome C	0
YOR038C	HIR2	Hlstone Regulation	0
YOR039W	CKB2	Casein Kinase Beta' subunit	0
YOR040W	GLO4	GLyOxalase	0
YOR045W	TOM6	Translocase of the Outer Mitochondrial membrane	0
YOR046C	DBP5	Dead Box Protein	0
YOR047C	STD1	Suppressor of Tbp Deletion	0
YOR049C	RSB1	Resistance to Sphingoid long-chain Base	0
YOR051C	ETT1	Enhancer of Translation Termination 1	0
YOR052C	TMC1	Trivalent Metalloid sensitive, Cuz1-related protein	0
YOR054C	VHS3	Viable in a Hal3 Sit4 background	0
YOR055W			0
YOR056C	NOB1	Nin1 (One) Binding protein	0
YOR057W	SGT1	Suppressor of G2 (Two) allele of skp1	0
YOR058C	ASE1	Anaphase Spindle Elongation	0
YOR061W	CKA2	Casein Kinase Alpha' subunit	0
YOR063W	RPL3	Ribosomal Protein of the Large subunit	0
YOR064C	YNG1	Yeast iNG1 homolog	0
YOR072W-B			0

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YOR073W-A			0
YOR074C	CDC21	Cell Division Cycle	0
YOR075W	UFE1	Unknown Function Essential	0
YOR076C	SKI7	SuperKiller	0
YOR077W	RTS2		0
YOR078W	BUD21	BUD site selection	0
YOR079C	ATX2	AnTioXidant	0
YOR080W	DIA2	Digs Into Agar	0
YOR081C	TGL5	TriacylGlycerol Lipase	0
YOR083W	WHI5	WHIskey	0
YOR085W	OST3	OligoSaccharylTransferase	0
YOR086C	TCB1	Three Calcium and lipid Binding domains (TriCalBins)	0
YOR089C	VPS21	Vacuolar Protein Sorting	0
YOR090C	PTC5	Phosphatase Two C	0
YOR091W	TMA46	Translation Machinery Associated	0
YOR092W	ECM3	ExtraCellular Mutant	0
YOR093C	CMR2	Changed Mutation Rate	0
YOR094W	ARF3	ADP-Ribosylation Factor	0
YOR095C	RKI1	Ribose-5-phosphate Ketol-Isomerase	0
YOR096W	RPS7A	Ribosomal Protein of the Small subunit	0
YOR097C			0
YOR100C	CRC1	CaRnitine Carrier	0
YOR101W	RAS1	homologous to RAS proto-oncogene	0
YOR102W			0
YOR103C	OST2	OligoSaccharylTransferase	0
YOR104W	PIN2	Psi+ INducibility	0
YOR105W			0
YOR106W	VAM3	VACuolar Morphogenesis	0
YOR108C-A			0
YOR108W	LEU9	LEUcine biosynthesis	0
YOR109W	INP53	INositol polyphosphate 5-Phosphatase	0
YOR112W	CEX1	Cytoplasmic EXport protein	0
YOR113W	AZF1	Asparagine-rich Zinc-Finger	0
YOR114W	DPI34	Delta-Psi dependent mitochondrial Import protein of ~34 kDa	0
YOR115C	TRS33	TRapp Subunit	0
YOR116C	RPO31	RNA POLymerase	0
YOR117W	RPT5	Regulatory Particle Triple-A protein, or Regulatory Particle Triphosphatase	0
YOR118W	RTC5	Restriction of Telomere Capping	0
YOR119C	RIO1	RIght Open reading frame	0
YOR120W	GCY1	Galactose-inducible Crystallin-like Yeast protein	0
YOR121C			0
YOR122C	PFY1	ProFilin of Yeast	0
YOR124C	UBP2	UBiquitin-specific Protease	0
YOR125C	CAT5	CATABolite repression	0
YOR126C	IAH1	Isoamyl Acetate-Hydrolyzing esterase	0
YOR128C	ADE2	ADENine requiring	0
YOR130C	ORT1	ORNithine Transporter	0
YOR135C	IRC14		0
YOR136W	IDH2	Isocitrate DeHydrogenase	0
YOR137C	SIA1	Suppressor of eIF5A	0
YOR138C	RUP1	Rsp5-Ubp2 interacting Protein	0

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YOR141C	ARP8	Actin-Related Protein	0
YOR142W	LSC1	Ligase of Succinyl-CoA	0
YOR143C	THI80	THIamine metabolism	0
YOR144C	ELG1	Enhanced Level of Genomic instability	0
YOR146W			0
YOR147W	MDM32	Mitochondrial Distribution and Morphology	0
YOR150W	MRPL23	Mitochondrial Ribosomal Protein, Large subunit	0
YOR151C	RPB2	RNA Polymerase B	0
YOR152C	ATG40	AuTophagy related	0
YOR153W	PDR5	Pleiotropic Drug Resistance	0
YOR154W	SLP1	SUN-Like Protein	0
YOR155C	ISN1	IMP-Specific 5'-Nucleotidase	0
YOR156C	NFI1	Neck Filament Interacting	0
YOR157C	PUP1	PUtative Proteasome subunit	0
YOR158W	PET123	PETite colonies	0
YOR159C	SME1	Sm protein E	0
YOR160W	MTR10	Mrna TRansport defective	0
YOR161C	PNS1	pH Nine Sensitive	0
YOR161C-C			0
YOR161W-A			0
YOR161W-B			0
YOR162C	YRR1	Yeast Reveromycin-A Resistant	0
YOR163W	DDP1	Diadenosine and Diphosphoinositol Polyphosphate phosphohydrolase	0
YOR164C	GET4	Guided Entry Tail-anchored proteins	0
YOR165W	SEY1	Synthetic Enhancement of YOP1	0
YOR166C	SWT1	Synthetically lethal With Trex	0
YOR167C	RPS28A	Ribosomal Protein of the Small subunit	0
YOR168W	GLN4	GLutamiNe metabolism	0
YOR169C			0
YOR170W			0
YOR171C	LCB4	Long-Chain Base	0
YOR172W	YRM1	Yeast Reveromycin resistance Modulator	0
YOR173W	DCS2	DeCapping Scavenger	0
YOR174W	MED4	MEDIator complex	0
YOR175C	ALE1	Acyltransferase for Lyso-phosphatidylEthanolamine	0
YOR176W	HEM15	HEME biosynthesis	0
YOR177C	MPC54	Meiotic Plaque Component	0
YOR178C	GAC1	Glycogen ACcumulation	0
YOR179C	SYC1	Similar to Ysh1 C-terminal	0
YOR180C	DCI1	delta(3,5)-delta(2,4)-Dienoyl-CoA Isomerase	0
YOR181W	LAS17		0
YOR182C	RPS30B	Ribosomal Protein of the Small subunit	0
YOR184W	SER1	SERine requiring	0
YOR185C	GSP2	Genetic Suppressor of Prp20-1	0
YOR186C-A			0
YOR186W			0
YOR187W	TUF1		0
YOR188W	MSB1	Multicopy Suppression of a Budding defect	0
YOR189W	IES4	Ino Eighty Subunit	0
YOR190W	SPR1	SPorulation Regulated	0
YOR191W	ULS1	Ubiquitin Ligase for SUMO conjugates	0

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YOR192C	THI72	THI7 homolog 2	0
YOR193W	PEX27	PEroXisome related	0
YOR194C	TOA1		0
YOR195W	SLK19	Synthetic Lethal Kar3p	0
YOR196C	LIP5	LIPoic acid	0
YOR197W	MCA1	MetaCAspase	0
YOR198C	BFR1	BreFeldin A Resistance	0
YOR200W			0
YOR201C	MRM1	Mitochondrial rRNA Methyltransferase	0
YOR202W	HIS3	HIStidine	0
YOR203W			0
YOR204W	DED1	Defines Essential Domain	0
YOR205C	GEP3	GENetic interactors of Prohibitins	0
YOR206W	NOC2	NucleOlar Complex associated	0
YOR207C	RET1	Reduced Efficiency of Termination	0
YOR208W	PTP2	Protein Tyrosine Phosphatase	0
YOR209C	NPT1	Nicotinate PhosphoribosylTransferase	0
YOR210W	RPB10	RNA Polymerase B	0
YOR211C	MGM1	Mitochondrial Genome Maintenance	0
YOR212W	STE4	STERile	0
YOR213C	SAS5	Something About Silencing	0
YOR214C	SPR2	SPorulation-Regulated	0
YOR215C	AIM41	Altered Inheritance of Mitochondria	0
YOR216C	RUD3	Relieves Uso1-1 transport Defect	0
YOR217W	RFC1	Replication Factor C	0
YOR218C			0
YOR219C	STE13	STERile	0
YOR220W	RCN2	Regulator of CalciNeurin	0
YOR221C	MCT1	Malonyl-CoA:ACP Transferase	0
YOR222W	ODC2	OxoDicarboxylate Carrier	0
YOR223W	DSC3	Defective for SREBP Cleavage	0
YOR224C	RPB8	RNA Polymerase B	0
YOR225W			0
YOR226C	ISU2	IscU homolog	0
YOR228C	MCP1	Mdm10 Complementing Protein	0
YOR230W	WTM1	WD repeat containing Transcriptional Modulator	0
YOR231C-A			0
YOR234C	RPL33B	Ribosomal Protein of the Large subunit	0
YOR236W	DFR1	DihydroFolate Reductase	0
YOR244W	ESA1		0
YOR245C	DGA1	DiacylGlycerol Acyltransferase	0
YOR247W	SRL1	Suppressor of Rad53 null Lethality	0
YOR248W			0
YOR251C	TUM1	ThioUridine Modification	0
YOR253W	NAT5	N-terminal AcetylTransferase	0
YOR256C	TRE2	Transferrin REceptor like	0
YOR257W	CDC31	Cell Division Cycle	0
YOR258W	HNT3	Histidine triad NucleoTide-binding	0
YOR259C	RPT4	Regulatory Particle Triple-A protein, or Regulatory Particle Triph	0
YOR260W	GCD1	General Control Derepressed	0
YOR262W	GPN2	Gly-Pro-Asn (N) motif	0

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YOR263C			0
YOR264W	DSE3	Daughter Specific Expression	0
YOR265W	RBL2	Rescues Beta-tubulin Lethality	0
YOR269W	PAC1	Perish in the Absence of Cin8p	0
YOR270C	VPH1	Vacuolar pH	0
YOR271C	FSF1	Fungal SideroFlexin 1	0
YOR272W	YTM1		0
YOR273C	TPO4	Transporter of POLyamines	0
YOR274W	MOD5	tRNA MODification	0
YOR275C	RIM20	Regulator of IME2	0
YOR276W	CAF20	Cap Associated Factor	0
YOR277C			0
YOR278W	HEM4	HEMe biosynthesis	0
YOR279C	RFM1	Repression Factor of Middle sporulation element	0
YOR280C	FSH3	Family of Serine Hydrolases	0
YOR281C	PLP2	Phosducin-Like Protein	0
YOR282W			0
YOR284W	HUA2		0
YOR285W	RDL1	RhoDanese-Like protein	0
YOR286W	RDL2	RhoDanese-Like protein	0
YOR287C	RRP36	Ribosomal RNA Processing	0
YOR288C	MPD1	Multicopy suppressor of PDI1 deletion	0
YOR289W			0
YOR290C	SNF2	Sucrose NonFermenting	0
YOR292C			0
YOR293C-A			0
YOR293W	RPS10A	Ribosomal Protein of the Small subunit	0
YOR294W	RRS1	Regulator of Ribosome Synthesis	0
YOR296W			0
YOR297C	TIM18	Translocase of the Inner Mitochondrial membrane	0
YOR298C-A	MBF1	Multiprotein Bridging Factor	0
YOR300W			0
YOR302W			0
YOR304C-A	BIL1	Bud6-Interacting Ligand	0
YOR305W	RRG7	Required for Respiratory Growth	0
YOR306C	MCH5	MonoCarboxylate transporter Homolog	0
YOR307C	SLY41	Suppressor of Loss of Ypt1	0
YOR309C			0
YOR310C	NOP58	NucleOlar Protein of 58 kDa	0
YOR311C	DGK1	DiacylGlycerol Kinase	0
YOR312C	RPL20B	Ribosomal Protein of the Large subunit	0
YOR314W			0
YOR314W-A			0
YOR315W	SFG1	SuperFicial pseudohyphal Growth	0
YOR316C-A			0
YOR317W	FAA1	Fatty Acid Activation	0
YOR318C			0
YOR319W	HSH49	Human Sap Homolog	0
YOR320C	GNT1	GlcNAc Transferase	0
YOR322C	LDB19	Low Dye Binding	0
YOR323C	PRO2	PROline requiring	0

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YOR325W			0
YOR327C	SNC2	Suppressor of the Null allele of CAP	0
YOR329C	SCD5	Suppressor of Clathrin Deficiency	0
YOR329W-A			0
YOR330C	MIP1	Mitochondrial DNA Polymerase	0
YOR331C			0
YOR332W	VMA4	Vacuolar Membrane Atpase	0
YOR333C			0
YOR334W	MRS2	Mitochondrial RNA Splicing	0
YOR335C	ALA1	ALAnyI-tRNA synthetase	0
YOR335W-A			0
YOR337W	TEA1	Ty Enhancer Activator	0
YOR338W			0
YOR339C	UBC11	UBiquitin Carrier	0
YOR341W	RPA190	RNA Polymerase A	0
YOR343C			0
YOR344C	TYE7	Ty1-mediated Expression	0
YOR345C			0
YOR353C	SOG2		0
YOR355W	GDS1		0
YOR356W	CIR2	Changed Intracellular Redox state	0
YOR357C	SNX3	Sorting NeXin	0
YOR358W	HAP5	Heme Activator Protein	0
YOR359W	VTS1	VTi1-2 Suppressor	0
YOR360C	PDE2	PhosphoDiEsterase	0
YOR361C	PRT1	PRoTein synthesis	0
YOR362C	PRE10	PRoteinase yscE	0
YOR364W			0
YOR366W			0
YOR367W	SCP1	S. cerevisiae CalPonin	0
YOR368W	RAD17	RADiation sensitive	0
YOR369C	RPS12	Ribosomal Protein of the Small subunit	0
YOR370C	MRS6	Mitochondrial RNA Splicing	0
YOR372C	NDD1	Nuclear Division Defective	0
YOR373W	NUD1		0
YOR374W	ALD4	ALdehyde Dehydrogenase	0
YOR375C	GDH1	Glutamate DeHydrogenase	0
YOR376W			0
YOR376W-A			0
YOR378W	AMF1	AMmonium Facilitator	0
YOR379C			0
YOR381W-A			0
YOR382W	FIT2	Facilitator of Iron Transport	0
YOR383C	FIT3	Facilitator of Iron Transport	0
YOR386W	PHR1	PHotoreactivation Repair deficient	0
YOR393W	ERR1	Enolase-Related Repeat	0
YPL001W	HAT1	Histone AcetylTransferase	0
YPL002C	SNF8	Sucrose NonFermenting	0
YPL006W	NCR1	Niemann-pick type C Related	0
YPL011C	TAF3	TATA binding protein-Associated Factor	0
YPL012W	RRP12	Ribosomal RNA Processing	0

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YPL013C	MRPS16	Mitochondrial Ribosomal Protein, Small subunit	0
YPL014W	CIP1	Cdk1 Interacting Protein	0
YPL015C	HST2	Homolog of SIR Two (SIR2)	0
YPL016W	SWI1	SWItching deficient	0
YPL017C	IRC15	Increased Recombination Centers	0
YPL018W	CTF19	Chromosome Transmission Fidelity	0
YPL019C	VTC3	Vacuolar Transporter Chaperone	0
YPL020C	ULP1	UbL-specific Protease	0
YPL021W	ECM23	ExtraCellular Mutant	0
YPL022W	RAD1	RADiation sensitive	0
YPL024W	RMI1	RecQ Mediated genome Instability	0
YPL027W	SMA1	Spore Membrane Assembly	0
YPL028W	ERG10	ERGosterol biosynthesis	0
YPL031C	PHO85	PHOsphate metabolism	0
YPL032C	SVL3	Styryl dye Vacuolar Localization	0
YPL033C	SRL4	Suppressor of Rad53 null Lethality or Suppressor of Rad53 and	0
YPL034W			0
YPL035C			0
YPL036W	PMA2	Plasma Membrane ATPase	0
YPL037C	EGD1	Enhancer of Gal4 DNA binding	0
YPL038W	MET31	METHionine requiring	0
YPL039W			0
YPL041C	MRX11	Mitochondrial oRganization of gene eXpression (MIOREX)	0
YPL042C	SSN3	Suppressor of SNf1	0
YPL043W	NOP4	NucleOlar Protein	0
YPL044C			0
YPL045W	VPS16	Vacuolar Protein Sorting	0
YPL046C	ELC1	ELongin C	0
YPL047W	SGF11	SaGa associated Factor 11kDa	0
YPL048W	CAM1	Calcium And Membrane-binding protein	0
YPL050C	MNN9	MaNNosyltransferase	0
YPL051W	ARL3	ADP-Ribosylation factor-Like	0
YPL053C	KTR6	Kre Two Related	0
YPL056C	LCL1	Long Chronological Lifespan	0
YPL057C	SUR1	SUPpressor of Rvs161 and rvs167 mutations	0
YPL058C	PDR12	Pleiotropic Drug Resistance	0
YPL059W	GRX5	GlutaRedoXin	0
YPL060W	MFM1	Mrs2 Function Modulating factor	0
YPL063W	TIM50	Translocase of the Inner Mitochondrial membrane	0
YPL064C	CWC27	Complexed With Cef1p	0
YPL065W	VPS28	Vacuolar Protein Sorting	0
YPL067C	HTC1	Histidine Triad with Channel	0
YPL068C			0
YPL069C	BTS1	Bet Two Suppressor	0
YPL070W	MUK1	coMpUtationally-linked to Kap95	0
YPL071C			0
YPL072W	UBP16	UBiquitin-specific Protease	0
YPL073C			0
YPL075W	GCR1	GlyColysis Regulation	0
YPL076W	GPI2	GlycosylPhosphatidylInositol anchor biosynthesis	0
YPL077C			0

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YPL079W	RPL21B	Ribosomal Protein of the Large subunit	0
YPL080C			0
YPL081W	RPS9A	Ribosomal Protein of the Small subunit	0
YPL084W	BRO1	BCK1-like Resistance to Osmotic shock	0
YPL086C	ELP3	ELongator Protein	0
YPL087W	YDC1	Yeast DihydroCeramidase	0
YPL088W			0
YPL092W	SSU1	Sensitive to SULfite	0
YPL093W	NOG1	NucleOlar G-protein	0
YPL094C	SEC62	SECretory	0
YPL095C	EEB1	Ethyl Ester Biosynthesis	0
YPL096C-A	ERI1	ER-associated Ras Inhibitor	0
YPL096W	PNG1	Peptide N-Glycanase	0
YPL098C	MGR2	Mitochondrial Genome Required	0
YPL100W	ATG21	AuTophagy related	0
YPL103C	FMP30	Found in Mitochondrial Proteome	0
YPL106C	SSE1	Stress Seventy subfamily E	0
YPL107W	DPC25	Delta-Psi dependent mitochondrial import and Cleavage protein	0
YPL109C	MCO76	Mitochondrial Class One protein of 76 kDa	0
YPL110C	GDE1	GlycerophosphoDiEsterase	0
YPL111W	CAR1	Catabolism of ARGinine	0
YPL113C			0
YPL114W			0
YPL115C	BEM3	Bud EMergence	0
YPL116W	HOS3	Hda One Similar	0
YPL117C	IDI1	Isopentenyl Diphosphate Isomerase	0
YPL120W	VPS30	Vacuolar Protein Sorting	0
YPL121C	MEI5	MEIosis	0
YPL122C	TFB2	Transcription Factor B subunit 2	0
YPL123C	RNY1	RiboNuclease from Yeast	0
YPL125W	KAP120	KAryoPherin	0
YPL127C	HHO1	Histone H One	0
YPL128C	TBF1	TTAGGG repeat-Binding Factor	0
YPL129W	TAF14	TATA binding protein-Associated Factor	0
YPL130W	SPO19	SPOrulation	0
YPL131W	RPL5	Ribosomal Protein of the Large subunit	0
YPL132W	COX11	Cytochrome c OXidase	0
YPL135C-A			0
YPL135W	ISU1	IScU homolog	0
YPL136W			0
YPL143W	RPL33A	Ribosomal Protein of the Large subunit	0
YPL144W	POC4	PrOteasome Chaperone	0
YPL145C	KES1	KrE11-1 Suppressor	0
YPL146C	NOP53	NucleOlar Protein	0
YPL147W	PXA1	PeroXisomal ABC-transporter	0
YPL148C	PPT2	Phosphopantetheine:Protein Transferase	0
YPL152W-A			0
YPL154C	PEP4	carboxyPEPtidase Y-deficient	0
YPL155C	KIP2	Klnesin related Protein	0
YPL159C	PET20	PETite colonies	0
YPL160W	CDC60	Cell Division Cycle	0

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YPL161C	BEM4	Bud EMergence	0
YPL163C	SVS1	Suppressor of Vanadate Sensitivity	0
YPL170W	DAP1	DAmage resistance Protein	0
YPL172C	COX10	Cytochrome c OXidase	0
YPL175W	SPT14	SuPpressor of Ty	0
YPL179W	PPQ1	Protein Phosphatase Q	0
YPL180W	TCO89	Tor Complex One	0
YPL182C			0
YPL183W-A	RTC6	Restriction of Telomere Capping	0
YPL184C	MRN1	Multicopy supressor of rsc nhp6	0
YPL185W			0
YPL186C	UIP4	Ulp1 Interacting Protein	0
YPL187W	MF(ALPHA)1	Mating Factor ALPHA	0
YPL188W	POS5	PerOxide Sensitive	0
YPL189C-A	COA2	Cytochrome Oxidase Assembly	0
YPL189W	GUP2	Glycerol UPtake	0
YPL191C			0
YPL192C	PRM3	Pheromone-Regulated Membrane protein	0
YPL194W	DDC1	DNA Damage Checkpoint	0
YPL196W	OXR1	OXidation Resistance	0
YPL197C			0
YPL199C			0
YPL202C	AFT2	Activator of Fe (iron) Transcription	0
YPL203W	TPK2	Takashi's Protein Kinase	0
YPL204W	HRR25	HO and Radiation Repair	0
YPL207W	TYW1	Trna-YW synthesizing protein	0
YPL208W	RKM1	Ribosomal lysine (K) Methyltransferase	0
YPL209C	IPL1	Increase in PLoidy	0
YPL211W	NIP7	Nuclear ImPort	0
YPL214C	THI6	THlamine biosynthesis	0
YPL215W	CBP3	Cytochrome B mRNA Processing	0
YPL217C	BMS1	BMh Sensitive	0
YPL218W	SAR1	Secretion-Associated, Ras-related	0
YPL219W	PCL8	Pho85 CycLin	0
YPL221W	FLC1	FLavin Carrier	0
YPL222C-A			0
YPL224C	MMT2	Mitochondrial Metal Transporter	0
YPL225W			0
YPL226W	NEW1	Nu+	0
YPL227C	ALG5	Asparagine-Linked Glycosylation	0
YPL228W	CET1	Capping Enzyme Triphosphatase	0
YPL229W			0
YPL232W	SSO1	Supressor of Sec One	0
YPL233W	NSL1	Nnf1 Synthetic Lethal	0
YPL234C	VMA11	Vacuolar Membrane Atpase	0
YPL235W	RVB2	RuVB-like	0
YPL237W	SUI3	SUPpressor of Initiator codon	0
YPL238C			0
YPL239W	YAR1	Yeast Ankyrin Repeat	0
YPL240C	HSP82	Heat Shock Protein	0
YPL242C	IQG1	IQGAP-related protein	0

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YPL243W	SRP68	Signal Recognition Particle	0
YPL244C	HUT1	Homolog of UDP-galactose Transporter	0
YPL245W			0
YPL246C	RBD2		0
YPL249C-A	RPL36B	Ribosomal Protein of the Large subunit	0
YPL250C	ATG41	AuTophagy related	0
YPL251W			0
YPL252C	YAH1	Yeast Adrenodoxin Homolog	0
YPL259C	APM1	clathrin Adaptor Protein complex Medium chain	0
YPL260W	CUB1	Cu2+ suppressing and Bleomycin sensitive	0
YPL261C			0
YPL262W	FUM1	FUMarase	0
YPL263C	KEL3	KELch	0
YPL265W	DIP5	Dlcarboxylic amino acid Permease	0
YPL266W	DIM1	DIMethylase	0
YPL267W	ACM1	APC/C[Cdh1] Modulator	0
YPL268W	PLC1	PhosphoLipase C	0
YPL269W	KAR9	KARyogamy	0
YPL270W	MDL2	MultiDrug resistance-Like	0
YPL271W	ATP15	ATP synthase	0
YPL272C	PBI1	PSTB2 Interacting protein 1	0
YPL281C	ERR2	Enolase-Related Repeat	0
YPR005C	HAL1	HALotolerance	0
YPR006C	ICL2	IsoCitrate Lyase	0
YPR008W	HAA1	Homolog of Ace1 Activator	0
YPR009W	SUT2	Sterol UpTake	0
YPR010C	RPA135	RNA Polymerase A	0
YPR010C-A	MIN8	mitochondrial MINi protein of 8 kDa	0
YPR011C			0
YPR016C	TIF6	Translation Initiation Factor	0
YPR016W-A			0
YPR017C	DSS4	Dominant Suppressor of Sec4	0
YPR019W	MCM4	MiniChromosome Maintenance	0
YPR020W	ATP20	ATP synthase	0
YPR023C	EAF3	Esa1p-Associated Factor	0
YPR024W	YME1	Yeast Mitochondrial Escape	0
YPR025C	CCL1		0
YPR027C			0
YPR029C	APL4	clathrin Adaptor Protein complex Large chain	0
YPR035W	GLN1	GLutamiNe metabolism	0
YPR036W	VMA13	Vacuolar Membrane Atpase	0
YPR036W-A	SPO24	SPOrulation	0
YPR037C	ERV2	Essential for Respiration and Viability	0
YPR038W	IRC16	Increased Recombination Centers	0
YPR039W			0
YPR040W	TIP41	Tap42 Interacting Protein	0
YPR041W	TIF5	Translation Initiation Factor	0
YPR043W	RPL43A	Ribosomal Protein of the Large subunit	0
YPR044C	OPI1	OverProducer of Inositol	0
YPR045C	THP3	THO-related Protein	0
YPR046W	MCM16	MiniChromosome Maintenance	0

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YPR047W	MSF1	Mitochondrial aminoacyl-tRNA Synthetase, Phenylalanine (F)	0
YPR048W	TAH18	Top1T722A mutant Hypersensitive	0
YPR049C	ATG11	AuTophagy related	0
YPR050C			0
YPR051W	MAK3	MAintenance of Killer	0
YPR052C	NHP6A	Non-Histone Protein	0
YPR053C			0
YPR056W	TFB4	Transcription Factor B subunit 4	0
YPR057W	BRR1	Bad Response to Refrigeration	0
YPR058W	YMC1	Yeast Mitochondrial Carrier	0
YPR059C			0
YPR060C	ARO7	AROMATIC amino acid requiring	0
YPR061C	JID1	DnaJ protein Involved in ER-associated Degradation	0
YPR062W	FCY1	FluoroCYtosine resistance	0
YPR063C			0
YPR064W			0
YPR065W	ROX1	Regulation by OXYgen	0
YPR066W	UBA3	UBiquitin-like protein-Activating enzyme	0
YPR067W	ISA2	Iron Sulfur Assembly	0
YPR068C	HOS1	Hda One Similar	0
YPR069C	SPE3	SPERMidine auxotroph	0
YPR071W			0
YPR072W	NOT5	Negative On TATA	0
YPR073C	LTP1	Low molecular weight protein Tyrosine Phosphatase	0
YPR074C	TKL1	TransKetoLase	0
YPR074W-A			0
YPR075C	OPY2	Overproduction-induced Pheromone-resistant Yeast	0
YPR076W			0
YPR077C			0
YPR078C			0
YPR079W	MRL1	Mannose 6-phosphate Receptor Like	0
YPR080W	TEF1	Translation Elongation Factor	0
YPR081C	GRS2	Glycyl-tRNA Synthase	0
YPR083W	MDM36	Mitochondrial Distribution and Morphology	0
YPR085C	ASA1	AStra Associated protein	0
YPR086W	SUA7	Suppressor of Upstream AUG	0
YPR088C	SRP54	Signal Recognition Particle 54-kD subunit	0
YPR091C	NVJ2	Nucleus-Vacuole Junction	0
YPR092W			0
YPR093C	ASR1	Alcohol Sensitive Ring/PHD finger	0
YPR094W	RDS3	Regulator of Drug Sensitivity	0
YPR096C			0
YPR097W			0
YPR099C			0
YPR100W	MRPL51	Mitochondrial Ribosomal Protein, Large subunit	0
YPR102C	RPL11A	Ribosomal Protein of the Large subunit	0
YPR103W	PRE2	PRoteinase yscE	0
YPR104C	FHL1	Fork Head-Like	0
YPR106W	ISR1	Inhibition of Staurosporine Resistance	0
YPR107C	YTH1	Yeast THirty kDa Homolog	0
YPR108W	RPN7	Regulatory Particle Non-ATPase	0

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YPR108W-A			0
YPR110C	RPC40	RNA Polymerase C	0
YPR111W	DBF20	DumbBell Forming	0
YPR112C	MRD1	Multiple RNA-binding domain	0
YPR113W	PIS1	Phosphatidyl Inositol Synthase	0
YPR114W			0
YPR115W	RGC1	Regulator of the Glycerol Channel	0
YPR116W	RRG8	Required for Respiratory Growth	0
YPR117W			0
YPR118W	MRI1	MethylthioRibose-1-phosphate Isomerase	0
YPR119W	CLB2	CycLin B	0
YPR120C	CLB5	CycLin B	0
YPR121W	THI22	THIamine metabolism	0
YPR122W	AXL1	AXiaL budding	0
YPR123C			0
YPR124W	CTR1	Copper TRansport	0
YPR125W	YLH47	Yeast LETM1 Homolog of 47 kD	0
YPR126C			0
YPR127W			0
YPR128C	ANT1	Adenine Nucleotide Transporter	0
YPR129W	SCD6	Suppressor of Clathrin Deficiency	0
YPR130C			0
YPR131C	NAT3	N-terminal AcetylTransferase	0
YPR132W	RPS23B	Ribosomal Protein of the Small subunit	0
YPR133C	SPN1	Suppresses Postrecruitment functions gene Number 1	0
YPR133W-A	TOM5	Translocase of the Outer Mitochondrial membrane	0
YPR134W	MSS18	Mitochondrial Splicing System	0
YPR135W	CTF4	Chromosome Transmission Fidelity	0
YPR136C			0
YPR137W	RRP9	Ribosomal RNA Processing	0
YPR138C	MEP3		0
YPR139C	LOA1	Lysophosphatidic acid: Oleoyl-CoA Acyltransferase	0
YPR140W	TAZ1	TAfaZzin	0
YPR141C	KAR3	KARyogamy	0
YPR142C			0
YPR143W	RRP15	Ribosomal RNA Processing	0
YPR144C	NOC4	NucleOlar Complex associated	0
YPR145C-A			0
YPR145W	ASN1	ASparagiNe requiring	0
YPR146C			0
YPR147C			0
YPR148C			0
YPR149W	NCE102	NonClassical Export	0
YPR150W			0
YPR151C	SUE1		0
YPR152C	URN1	U2-U5-U6 snRNP, RES complex, and NTC interacting protein	0
YPR153W	MAY24	genetic interaction profile similarity to MTC Annotated Yeast gen	0
YPR154W	PIN3	Psi+ INducibility	0
YPR155C	NCA2	Nuclear Control of ATPase	0
YPR160C-A			0
YPR160W-A			0

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YPR161C	SGV1	Suppressor of Gpa1-Val50 mutation	0
YPR164W	MMS1	Methyl MethaneSulfonate sensitivity	0
YPR165W	RHO1	Ras HOMolog	0
YPR166C	MRP2	Mitochondrial Ribosomal Protein	0
YPR167C	MET16	METHionine requiring	0
YPR170C			0
YPR170W-A			0
YPR170W-B			0
YPR177C			0
YPR181C	SEC23	SECreatory	0
YPR182W	SMX3		0
YPR187W	RPO26	RNA POLymerase	0
YPR188C	MLC2	Myo1p Light Chain	0
YPR191W	QCR2	QH2:cytochrome-C oxidoReductase	0
YPR195C			0
YPR199C	ARR1	ARsenicals Resistance	0
YPR200C	ARR2	ARsenicals Resistance	0
YPR201W	ARR3	ARsenicals Resistance	0

Competing interests

The author declares that there are no competing interests regarding the publication of this paper.