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Supporting Online Material for

Genome-Wide Analysis in Vivo of Translation with Nucleotide Resolution Using Ribosome Profiling

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Published 12 February 2009 on *Science* Express
DOI: 10.1126/science.1168978

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January 25, 2009

1 Materials and Methods

1.1 Overview of Library Preparation

When converting small RNAs into a sequenceable DNA library, it was critical to capture different RNA sequences with similar efficiency. Sequence biases in the library generation protocol would distort the observed frequency of different small RNAs, thereby changing the measured abundance of different ribosomal footprints and mRNA fragments. Randomly primed complementary DNA (cDNA) synthesis, which is typically used for transcriptome deep sequencing (*S1, S2*), was not a viable option as ribosomal footprints were too short. Furthermore, differential priming can lead to biases (*S3*).

We tested various strategies for attaching linkers to the 3' and the 5' termini of RNA fragments, either as RNA or as first-strand cDNA. In miRNA studies, short RNA fragments are converted to sequenceable DNA using the single-stranded RNA ligase T4 Rnl1 (*S4*). However, this enzyme shows significant sequence specificity (*S5*). We found that we achieved the most even sequence coverage using polyadenylation of RNA fragments to generate a primer site for first-strand cDNA synthesis (*S6*) (fig. S3). We also found that intramolecular ligation of first-strand cDNA gave better results than using either intermolecular or intramolecular RNA ligation for 5' linker attachment (data not shown).

1.2 Experimental Procedures

Media and Growth Conditions

Yeast strain BY4741 (MATa *his3*Δ1 *leu2*Δ0 *met15*Δ0 *ura3*Δ0) was grown in YEPD at 30 C with vigorous shaking. Cultures were grown from an initial OD_{600} of roughly 0.03 to mid-log phase, with an OD_{600} of 0.6 to 0.7.

Amino acid starvation was performed by pelleting cells for 5 min at 5000×g at 30 °C in a Sorvall SLA-3000 rotor, removing all media, and resuspending cells in an equal volume of pre-warmed SD media without amino acids. Cells were returned to 30 °C with vigorous shaking for 20 min.

Extract and Total RNA Preparation

Cycloheximide was added to a final concentration of 100 μg / ml and growth was continued for 2 min at 30 °C with vigorous shaking. Cells were harvested by filtration onto 0.45 um pore size nitrocellulose filters (Whatman).

The majority of the sample was resuspended in ice-cold polysome lysis buffer (20 mM Tris pH 8.0, 140 mM KCl, 1.5 mM $MgCl_2$, 100 μg / ml cycloheximide, 1% Triton) and dripped into a conical 50 ml tube filled with, and immersed in, ℓN_2. Frozen cells were pulverized for six cycles, each of 3 min. at 15 Hz, on a Retsch MM301 mixer mill. Sample chambers were pre-chilled in ℓN_2 and re-chilled between each pulverization cycle.

Pulverized cells were thawed and cell debris was removed by centrifugation at 4 °C, 3000× g for 5 min. The supernatant was recovered and clarified by spinning at 4 °C, 20000× g for 10 min. The supernatant beneath the buoyant membrane layer was recovered from this second spin. Aliquots of this extract were flash-frozen in ℓN_2. Typical yields were 0.80 ml of extract with A_{260} of 400-500.

A small amount of each sample was resuspended in ice-cold total RNA lysis buffer (10 mM EDTA, 50 mM NaOAc pH 5.5) and total RNA was purified by the hot acid phenol method. Typical yields were 1 mg of total RNA.

Random RNA Fragmentation

Poly-(A)+ mRNA was purified from 50 μg total RNA using magnetic oligo-dT DynaBeads (Invitrogen) according to the manufacturer's instructions. Purified RNA was eluted in 20 μl 10 mM Tris pH 8.0. This was mixed with an equal volume of 2× alkaline fragmentation solution (2 mM EDTA, 10 mM Na_2CO_3, 90 mM $NaHCO_3$, pH $\approx$ 9.3) and incubated 20 min at 95 °C. Fragmentation reactions were mixed with 0.56 ml ice-cold stop / precipitation solution (final 300 mM NaOAc pH 5.5, plus GlycoBlue (Ambion) as a coprecipitant), followed by isopropanol precipitation by standard methods.

Ribosome Footprinting

An aliquot of 100 A_{260} units of extract was split in half. A footprinting sample was treated with 750 U of *E. coli* RNase I (Ambion), while an undigested control was treated with 40 U of SUPERase·In RNase inhibitor (Ambion). Both samples were incubated 1 hour at room temperature with gentle mixing.

Sucrose density gradients (10%-50% w/v) were prepared in Sw41 ultracentrifuge tubes (Fisher) using a BioComp Gradient Master (BioComp Instruments) according to the manufacturer's instructions. Sucrose solutions were prepared in polysome gradient buffer (20 mM Tris pH 8.0, 140 mM

KCl, 5 mM $MgCl_2$, 100 μg / ml cycloheximide, 0.5 mM DTT, 20 U / ml SUPERase·In). Digested and control samples were loaded onto gradients, which were spun for 3 hours at 35,000 rpm, 4 °C in an Sw40 rotor. Gradients were fractionated at 0.75 ml / min using an Isco gradient fractionation system which continually monitored A_{260} values, and fractions corresponding to 30 s intervals were collected.

Fractions representing the monosome peak were pooled to produce a monosome sample and RNA was purified by the hot acid phenol method. RNA was resuspended in 0.50 ml 10 mM Tris pH 8.0 with 50 U SUPERase·In and short RNA was purified by loading the sample on a Microcon YM-100 microconcentrator (Millipore) and centrifuging for 28 min at 510×g at room temperature in a tabletop centrifuge. Roughly 0.425 ml of flow-through was recovered and RNA was precipitated by standard methods.

RNA Size Selection

Both fragmented mRNA and monosome samples were size-selected by gel electrophoresis. Samples were first dephosphorylated in a 10 μl reaction with final 1× T4 polynucleotide kinase buffer without ATP, 10 U SUPERase·In, and 10 U T4 polynucleotide kinase (NEB). Dephosphorylation was carried out for 1 hour at 37 °C, and the enzyme was then heat-inactivated 10 min at 75 °C.

Dephosphorylation reactions, along with a synthetic 28 base RNA oligonucleotide (oNTI199, 5'-AUGUACACGGAGUCGACCCGCAACGCGA), were mixed with 2× Novex TBE-Urea sample prep buffer (Invitrogen) and briefly denatured, then loaded on a Novex denaturing 15% polyacrylamide TBE-urea gel (Invitrogen) and run according to the manufacturer's instructions. The gel was stained with SYBR Gold (Invitrogen), then the 28 nt region was excised. The gel was physically disrupted and RNA was recovered by soaking overnight in gel elution buffer (300 mM NaOAc pH 5.5, 1 mM EDTA, 0.1 U / μl SUPERase·In). The gel debris was removed from the eluate using a Spin-X column (Corning) and RNA was precipitated with GlycoBlue as a coprecipitant by standard methods.

cDNA Synthesis

Gel-purified RNA fragments were resuspended in 10 mM Tris pH 8 and quantified using the BioAnalyzer Small RNA assay (Agilent). A sample of 10-20 pmol of RNA was denatured briefly, then used to prepare a poly-(A) tailing reaction in 6.6 μl with 1× poly-(A) polymerase buffer, ATP in 40-50:1 molar ratio with RNA, 0.75 U / μl SUPERase·In, and 3 U *E. coli* poly-(A) polymerase (NEB). Tailing was carried out for 30 min at 37 °C.

Reverse transcription was carried out using oNTI223 (5'-pGATCGTCGGACTGTAGAACTCT∅CAAGCAGAAGACGGCATACGATTTTTTTTTTTTTTTTTTTTVN) where the initial p indicates 5' phosphorylation, ∅ indicates the abasic dSpacer furan and V, N indicate degenerate nucleotides. A 5.0 μl aliquot of tailed RNA was supplemented with 570 nmol Tris 8.0, 8.2 nmol each dNTP, 50 pmol oNTI223 primer, and water to 14.25 μl. This was heated 3 min at 75 C, then chilled on ice. Then, 10 U SUPERase·In, 82 nmol DTT, and 164 U SuperScript III (Invitrogen) was added, and reverse transcription was performed for 30 min at 48 °C. RNA was eliminated by adding 1.8 μl 1M NaOH and incubating 20 min at 98 °C. The reaction was then neutralized with 1.8 μl 1M HCl.

Reverse transcription products were separated on a 10% polyacrylamide TBE-urea gel as described above. The extended first-strand product band was excised and DNA was recovered as described above, using DNA gel elution buffer (300 mM NaCl, 1 mM EDTA).

First-strand cDNA was circularized by resuspending DNA in 4.5 μl circularization mix (final in 5.0 μl: 1× CircLigase Buffer, 50 μM ATP, and 2.5 mM $MnCl_2$) and adding 0.5 μl CircLigase (Epicentre). Circularization was performed for 1 hour at 60 °C, and the reaction was heat-inactivated 10 min at 80 °C.

Circular single-stranded DNA was relinearized by adding 6.25 μl relinearization supplement (50 mM KCl, 1 mM DTT) followed by 12.5 U APE 1 (NEB). The reaction was incubated 1 hour at 37 °C. Relinearized ssDNA was run on a Novex 10% polyacrylamide TBE-urea gel (Invitrogen) as described above. The relinearized product band was excised–the circularized form migrates more slowly–and the DNA was recovered as described above.

Sequencing

Single-stranded template was amplified by PCR using the Phusion High-Fidelity enzyme (NEB) according to the manufacturer's instructions. The oligonucleotide primers oNTI200 (5'-CAAGCAGAAGACGGCATA) and oNTI201 (5'-AATGATACGGCGACCACCGACAGGTTCAGAGTTCTACAGTCCGACG) were used to create sequenceable DNA, *i.e.,* DNA with Illumina cluster generation sequences on each end and a sequencing primer binding site. PCR was carried out with an initial 30 s denaturation at 98 °C, followed by 8 - 14 cycles of 10 s denaturation at 98 °C, 10 s annealing at 60 °C, and 5 s extension at 72 °C. Several reactions, with different numbers of amplification cycles, were performed.Reactions were separated on a non-denaturing 8% polyacrylamide TBE gel as described above. In order to avoid distortions of the relative abundance of different products, it was desirable to stop amplification while it was still in a linear range. This was accomplished by selecting between reactions performed with different numbers of cycles to maximize the recovery of 115 b.p. product, but requiring that oligonucleotides remain to indicate that the reaction had not reached saturation. Product DNA from this optimal cycle was recovered as described above and quantified using the Agilent BioAnalyzer DNA 1000 assay. DNA was then sequenced on the Illumina Genome Analyzer 2 according to the manufacturer's instructions, using 3 to 5 pM template for cluster generation and sequencing primer oNTI202 (5'-CGACAGGTTCAGAGTTCTACAGTCCGACGATC)

Nuclease Protection Assay

A DNA fragment consisting of the first 500 bp of *TDH3* was amplified from yeast genomic DNA using the Phusion High-Fidelity polymerase with oligonucleotide primers oNTI156 (5'-ATGGTTAGAGTTGCTATTAACGG) and oNTI158 (5'-*TAATACGACTCACTATAGGG*CGAAAGCATCGTTGATAACC). The product contained a T7 RNA polymerase promoter site on the reverse-compelment strand, show in italics. This product was used as a template for *in vitro* transcription using the

MAXIscript kit (Ambion) according to the manufacturer's instructions, using 5.0 μl [α^{32}P] UTP, 3000 mCi / mmol, 40 mCi / ml as the only source of UTP.

Nuclease protection was performed using the mirVana miRNA detection kit (Ambion) according to the manufacturer's instructions. Equal volumes of different monosome fractions were used, corresponding to 2.8 μg to 8.4 μg RNA per sample, and 7.7 μg total RNA was used for the control. The RNA concentration in each sample, including the no-RNA control, was equalized to 8.4 μg by the addition of *Drosophila* S2 mRNA. Hybridization was performed overnight at 42 °C, and digestion was performed with 1:100 RNase A/T1 for 40 minutes at 37 °C. Products were analyzed by electrophoresis on a 15% polyacrylamide TBE-Urea gel, along with denatured 10 bp ladder (Invitrogen) radiolabeled with T4 polynucleotide kinase (NEB) according to the manufacturer's instructions. Gels were visualized by exposing a PhosphorImager screen (Molecular Dynamics) for 16 hours.

1.3 Data Analysis

Data analysis was performed using a collection of custom programs written in Haskell.

Sequencing Analysis

Primary data from the Illumina Genome Analyzer 2 was analyzed using the GAPipeline v0.3.0 to obtain sequencing reads, with matrix and phasing parameters estimated from a ϕX control lane. Duplicate read sequences were then collapsed and counted (scripted by our ProcessRaw program) to generate a file of distinct sequences and occurence counts.

Alignment of Sequences

Read sequences were composed of a variable-length region of captured RNA fragment sequence followed by a homopolymer A tail. Preliminary experiments indicated that essentially all RNA fragments were at least 21 nucleotides long. Beyond 21 nucleotides, a base might be derived from the captured RNA fragment or from the homopolymer tail. Alignments were thus seeded based on the first 21 nucleotides and then extended to encompass subsequent fragment-derived nucleotides and determine the length of the fragment.

The first 21 nucleotides of each sequencing read were aligned with the target sequence library using SOAP v1.10 (*S7*), allowing up to 3 mismatches and recovering all hits when there were multiple equally good possibilities. SOAP alignments from the first 21 nucleotides were subsequently processed to find the full length of the captured RNA sequence (using our AlignFromSoap program). All possible fragment lengths l were tested by taking l library sequence bases followed by an A_{36-l} tail and finding the number of mismatches between this constructed sequence and the actual sequencing read, $s(l)$. When the genomic alignment region ended in A bases, it was not possible to determine whether these nucleotides were derived from the captured RNA fragment or from the added homopolymer linker. This resulted in multiple library sequence fragment lengths $\arg\max_l s(l) = \ell^* = \{l_1, \cdots, l_i\}$ with equally good alignment scores. We addressed this ambiguity by finding the shortest and longest fragment lengths that achieved the best alignment score,

($\min \ell^*, \max \ell^*$). When the genomic sequence alignment ended in a non-A base, followed by another non-A base that was absent from the captured RNA fragment, there was a unique best-scoring fragment length.

The best SOAP alignment of the first 21 nucleotides is not guaranteed to identify the optimal genomic alignment of a full-length read. Sequencing errors in the first 21 nucleotides might result in a better alignment to one site in the genome while the full 28 nucleotide read would align better to a different site. However, empirically, these misalignments would represent an extremely small fraction of all reads. Very few alignments were changed when all candidate genomic sites with 3 or fewer mismatches in the first 18 nucleotides were aligned by dynamic programming against the actual sequencing read. Furthermore, the first 21 nucleotides have low error rates relative to later nucleotides.

Sequencing reads were filtered and alignments were performed in the following order:

Degenerate Read Elimination Reads in which 18 or more of the first 22 nucleotides were 'A' bases were eliminated.

rRNA Aligment Reads that were not eliminated as degenerate were aligned against a library of yeast rRNA sequences. Reads with any alignment against rRNA were eliminated from further consideration.

Transcript Alignments Non-degenerate, non-rRNA reads were aligned against three different libraries: yeast genomic sequences, yeast processed protein-coding genes, and yeast processed non-coding RNAs. These alignments were performed independently on all reads.

Splice Alignments Non-degenerate reads with no alignment against any yeast genomic sequences were re-aligned against the library of processed protein-coding transcripts.

This process was automated with our SoapAlign script. All alignments were carried out against a recent version of the yeast genome, downloaded from the Saccharomyces Genome Database (SGD, http://www.yeastgenome.org/) on 22 June 2008. Statistics on sequence alignment are reported in table S1.

Alignments were further filtered to eliminate those with more than 2 total mismatches, reads whose shortest possible genomic length was less than 20 nucleotides ($\min \ell^* < 20$), and reads with more than 18 A bases in the first 24 bases. These reads made up a small fraction of all reads, but constituted a large fraction of reads that mapped to intergenic, low-complexity sites. For analyses besides the length distribution of sequencing reads, only fragments whose length could be 22 to 32 nucleotides inclusive ($\min \ell^* \leq 32, \max \ell^* \geq 22$) were used.

Assigning RNA Fragments to Genomic Features

As yeast have relatively little splicing, genomic alignments were used to assign sequencing reads to transcribed features. Protein-coding genes, introns, and non-coding RNA sequences were taken from SGD annotations. Flanking 5' and 3' UTRs of protein-coding genes were taken from the

Nagalakshmi *et al.* transcriptome sequencing data (*S1*). Genomic alignments of sequencing reads were assigned to these features based on the position of the 5' end of the alignment.

Feature	**Fragment 5' End**	
	Start	**End**
Protein-coding gene	16 nt before first base	14 nt before last base
5' UTR	start of annotated UTR	17 nt before first base of CDS
3' UTR	13 nt before last base of CDS	28 nt before end of annotated UTR
intron	first base of intron	8 nt before last base of intron
Non-coding RNA	12 nt before first base	12 nt after last base

Ambiguously aligned reads were handled by empirically identifying features that were subject to ambiguous alignments. Ambiguous features were those where > 20% of aligning mRNA fragments could be mapped to a second site in the genome as well. Overlapping features had > 20% of aligning mRNA fragments mapped to sites where other features overlapped. Only unambiguous and non-overlapping features were used in subsequent analyses. Dubious ORFs are excluded from this analysis as they often overlap verified ORFs.

Feature Type	**Ambiguous**	**Overlapping**	**Unambiguous, Not Overlapping**
Protein-coding gene	398	37	5287
Intron	18	9	224
5' UTR	56	54	3544
3' UTR	145	59	4560

Our QUANTIFYEXPRESSION program reads our alignment data files, determines which features are ambiguous or overlapping, and quantifies RNA fragments aligning to unambiguous, non-overlapping features.

Quantifying mRNA and Ribosome Density

Read density was computed by scaling read counts for each feature by feature length and by the total number of CDS-aligned reads. Feature length was the number of nucleotide positions where, if the 5' end of a sequencing read fell on that nucleotide, the read would be assigned to the feature. For spliced protein-coding genes, where reads spanning splice junctions would not align to genomic sequences, 27 nt was subtracted from the feature length to account for nucleotide positions where a read would span the junction and thus be unalignable. Alignments mapping to any non-coding RNA were discarded. Otherwise, ambiguous reads were assigned to all possible features. Note that these ambiguous reads account for no more than 20% of total reads for a given feature.

If the absolute number of sequencing reads for a features is small, then the relative sampling error would be large. This sampling error can be modeled with simple counting statistics, controlled by the number of reads, which adds to error from biological variability and sample preparation. In particular, when a transcript is present at equal frequency in both samples, if the total number of counts between the two samples is sufficiently large, then it is very unlikely that sampling error will result in a large skew between the two samples. However, if the total number of counts is small, then most may be derived from one sample by chance. To minimize the effect of this error, an empirical cutoff of 128 total counts was selected based on replicate measurements of mRNA density (figs. S5 and S7). This criterion is particularly effective at excluding the false appearance of regulation. When a transcript is dramatically more abundant in one condition than another, one sample may have few counts, resulting in a substantial error in the measured ratio. The existence and direction of regulation can still be inferred reliably, but the quantitative change is sensitive to sampling error from the low-abundnace sample.

When comparing replicates of mRNA or ribosome density in protein-coding genes, in fig. S5 and Fig. 2D, reliably quantified features were those genes with at least 128 total read counts between the two replicates. When computing translation as the ratio of ribosome density to mRNA density, in Fig. 2E and Fig. 3B, reliable features needed at least 128 total read counts between mRNA and ribosome samples. In both cases, the ratios were normalized to set the mean ratio across all reliable protein-coding genes to 1.

When quantifying read density on untranslated features, in Fig. 3A, reliable features were those pairs of untranslated region and corresponding protein-coding gene where there were at least 128 sequencing reads in total. The majority of 3'UTRs and introns had no ribosome footprint reads. In order to estimate an upper bound on their translation, an 0.5 read pseudocount was used to compute a ribosome footprint density.

When comparing transcriptional and translational changes in Fig. 4, four pair-wise comparisons–mRNA fragments between two conditions, ribosome footprints between two conditions, and ribosome footprints to mRNA fragments in each condition–had to be reliable in that the total number of reads between the two compared values was at least 128. Changes in transcription and translation were scaled uniformly to set the median ratio across all genes to 1.

Averaging Position-Specific mRNA and Ribosome Density

When averaging sequencing read density at different codon positions, in Fig. 2F, profiles of read counts at each codon were computed separately for each gene. Densities were then normalized for each gene based on the average density in the first 151 codons, and any gene with fewer than 64 total reads in this region was excluded. The average normalized density was computed at each position by taking the mean normalized density across all genes that were long enough to include that position in the coding sequence, with each gene given equal weight.

uORF Identification

Canonical uORFs that initiate translation at an AUG codon were identified by finding AUG codons in annotated 5' UTRs and determining the extent of the following open reading frame. Non-AUG uORFs were identified similarly, but potential start codons were identified by finding a codon with a single mismatch from AUG with an initiation context score of at least 0.01, which identified 1615 non-AUG uORFs. AUG uORFs were considered to have a good initiation context when the score was at least 0.001. Initiation context scores were computed using a weight matrix model devised by Miyasaka based on the start codon context of highly-expressed genes (*S8*). The weight matrix scores six nucleotides before the start codon as well as three nucleotides after.

uORF Quantitation

Footprints were assigned to uORFs when they started no more than 14 nucleotides before the start of the uORF, and ended no more than 15 nucleotides before the end of the uORF or 21 nucleotides before the start of the downstream protein-coding gene. Thus, when a uORF overlapped a protein-coding gene or created a 5' extension, reads were attributed to the main CDS rather than the uORF. In a few cases, the upstream end of the uORF was less than 14 nucleotides from the beginning of the annotated 5' UTR and some reads were assigned to the uORF but not to the 5' UTR. Many uORFs overlap each other, so ribosome footprints could often be assigned to multiple uORFs in a single 5' UTR. Ribosome footprints assigned to one or more canonical AUG uORFs in a given 5' UTR were counted first. Those that could not be assigned to any canonical AUG uORF were then assigned to a predicted non-AUG uORF if possible. This procedure assigns ribosome footprints to standard AUG uORFs rather than non-AUG uORFs whenever possible.

A 5' UTR was considered to be ribosome-occupied when at least 1 rpM ribosome footprints were assigned to it. When at least half of those footprints were assigned to canonical AUG uORFs, the translation of that 5' UTR was attributed to these AUG uORFs. Similarly, when at least half were assigned to predicted non-AUG uORFs, the translation was attributed to these non-canonical uORFs. When neither of these categories accounted for a majority of the ribosome footprints, the translation was classified as unknown.

A 5' UTR was classified as highly-transcribed when the mRNA fragment density was at least 100 rpkM and it was at least 50% of the mRNA density of the associated protein-coding gene. The highly-transcribed uORFs were simply the AUG uORFs in these 5' UTRs, noting that some UTRs had more than one uORF. A specific uORF was considered to be highly translated when it accounted for at least half of the total 5' UTR ribosome footprints and when the ratio of ribosome footprint density to mRNA fragment density specificaly in the uORF was at least 0.00914. This ribosome to mRNA ratio was more than 3 standard deviations below the translation ratio of the median protein-coding gene.

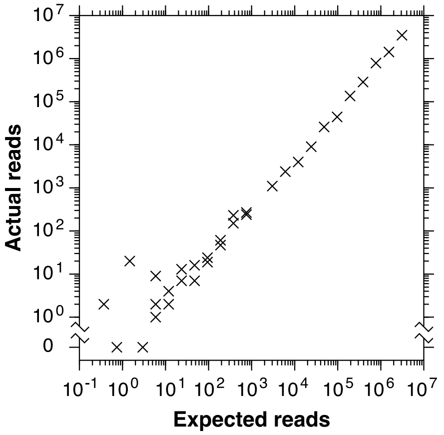

Figure S1. Quantifying sequences by deep sequencing. 32 synthetic DNA templates, each with a distinct sequence, were generated and quantified. Different templates were then mixed into a pool serially, so that oligos added early in the series would be at very low abundance in the final mixture. The dilution protocol was used to compute what fraction of the total pool each synthetic template represented, which then gave the expected fraction of total sequencing reads for that template sequence. The sample was then analyzed by deep sequencing and the number of reads derived from each synthetic template sequence was counted. The number of deep sequencing reads corresponds well to the concentration of the DNA template within the limits of statistical counting error for low-abundance templates.

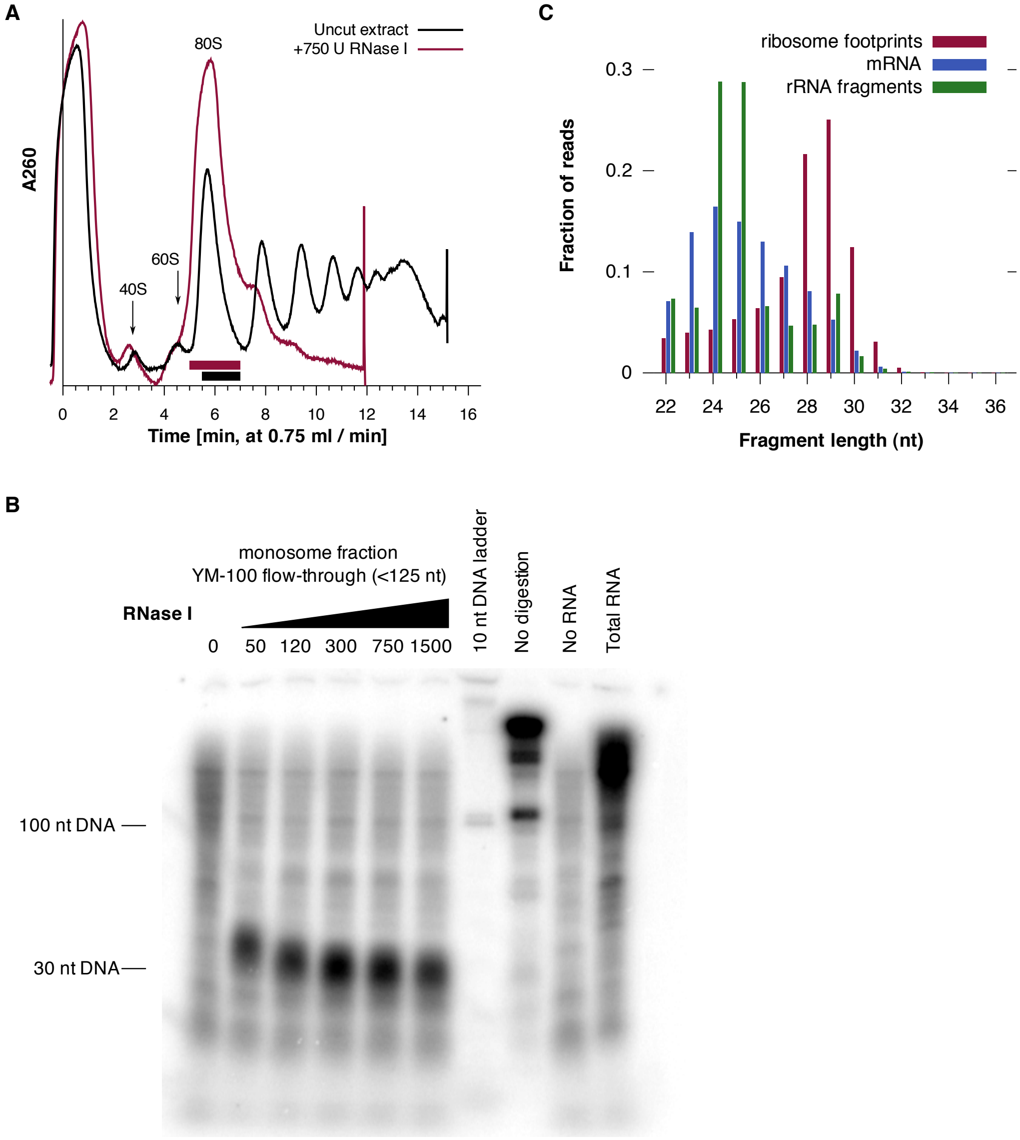

Figure S2. Footprinting translating ribosomes on mRNA. (**A**) Sucrose density gradient analysis of nuclease-digested extracts. The solid boxes indicate the fractions pooled for the monosome sample. (**B**) Nuclease protection assay showing ribosome-protected mRNA fragments. The probe is antisense to the 5'-most 500 nt of *TDH3*. The total RNA sample was not filtered, and thus contains long mRNAs. The no digestion sample shows the undigested probe. (**C**) Length distribution of ribosome footprint sequences. Ribosome footprints have a distinctive length which corresponds to the size of the fragments seen in (B). Only reads whose length was unambiguous were included. The rRNA fragments are the nuclease-generated rRNA contamination in the ribosome footprint sample. The mRNA fragments are from a randomly-fragmented sample that was size-selected and prepared in parallel to the footprint sample.

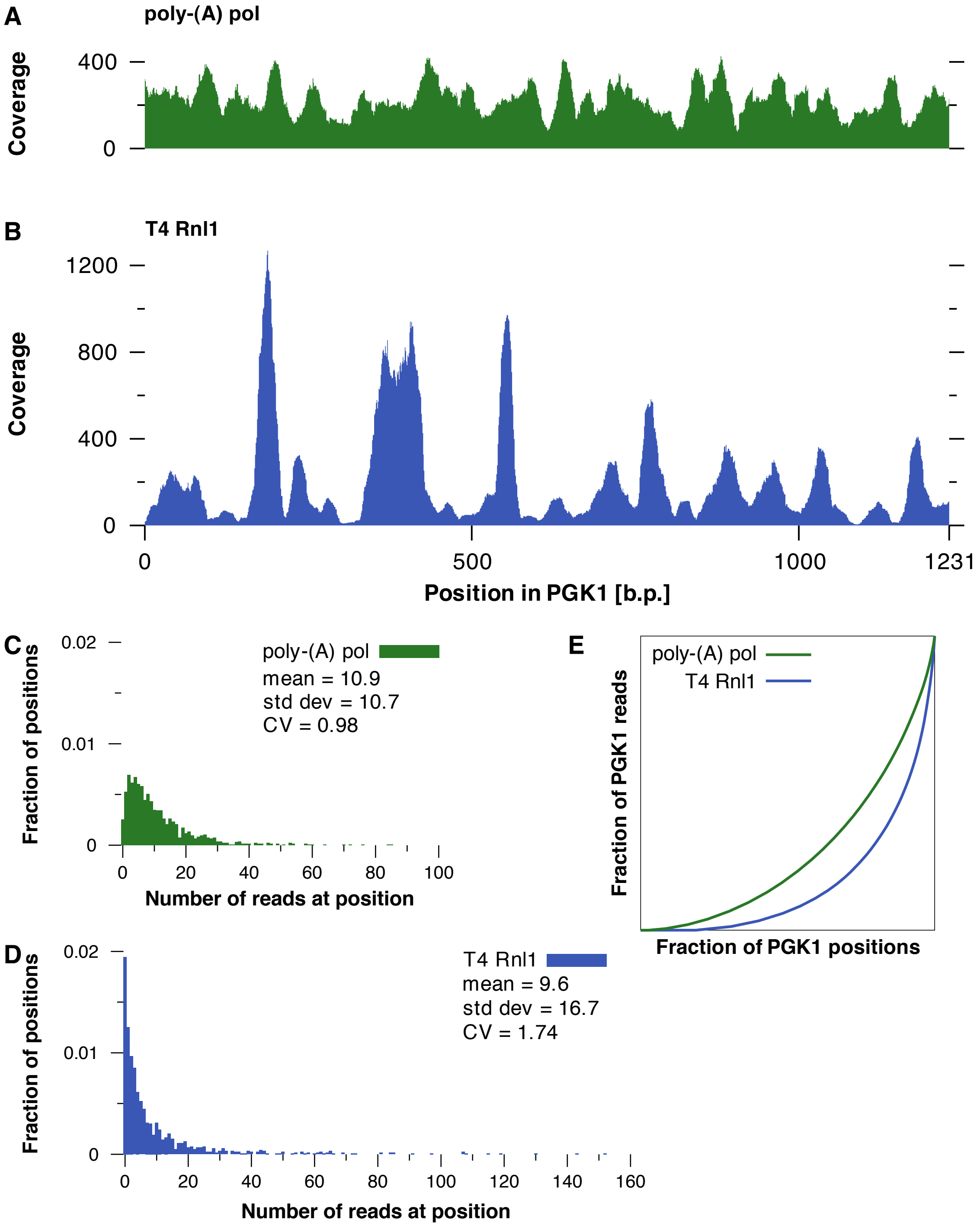
A
poly-(A) pol
Coverage
400
0
B
T4 Rnl1
Coverage
1200
800
400
0
0
500
1000
1231
Position in PGK1 [b.p.]
C
Fraction of positions
0.02
0.01
0
poly-(A) pol
mean = 10.9
std dev = 10.7
CV = 0.98
0
20
40
60
80
100
Number of reads at position
D
Fraction of positions
0.02
0.01
0
T4 Rnl1
mean = 9.6
std dev = 16.7
CV = 1.74
0
20
40
60
80
100
120
140
160
Number of reads at position
E
poly-(A) pol
T4 Rnl1
Fraction of PGK1 reads
Fraction of PGK1 positions

Figure S3

Figure S3. Quantifying and minimizing bias in converting RNA into sequenceable DNA. (**A** and **B**) Comparison of coverage from different 3' end capture strategies. The poly-(A) polymerase sample in (A) was generated as described in Fig. 1A, while the T4 Rnl1 sample used T4 Rnl1 to ligate an oligonucleotide linker and was otherwise the same. Coverage of sequencing reads on the *PGK1* CDS was approximated with a 21 nt moving average window, as this was the sequence length available for (B). (**C** and **D**) Histogram of sequence read density. The number of sequencing reads starting at each specific nucleotide position in the *PGK1* coding sequence was counted. The histogram value at n shows what fraction of nucleotide positions in the CDS have exactly n sequencing reads starting at that position. Uneven coverage results in a large number of nucleotide positions with few reads and a small number nucleotide positions with many reads. The mean, standard deviation, and CV of the number of sequencing reads starting at a given position is also quantified for each sample. (**E**) Lorenz curve of read starts. This curve represents the cumulative distribution of sequencing reads shown in (C) and (D). It shows the fraction of total reads accounted for by a given fraction of positions in the gene. For example, at $x = 0.1$, the y value of the curve shows the fraction of sequencing reads that occupy the 10% of the positions in the CDS with the lowest occupancy. Perfectly even coverage would give a diagonal line. Deviations below this diagonal line indicate biases in the capture, or the generation, of mRNA fragments during the construction of the sequencing library. They indicate that a small fraction of positions in the CDS account for a large fraction of total reads aligning to that CDS.

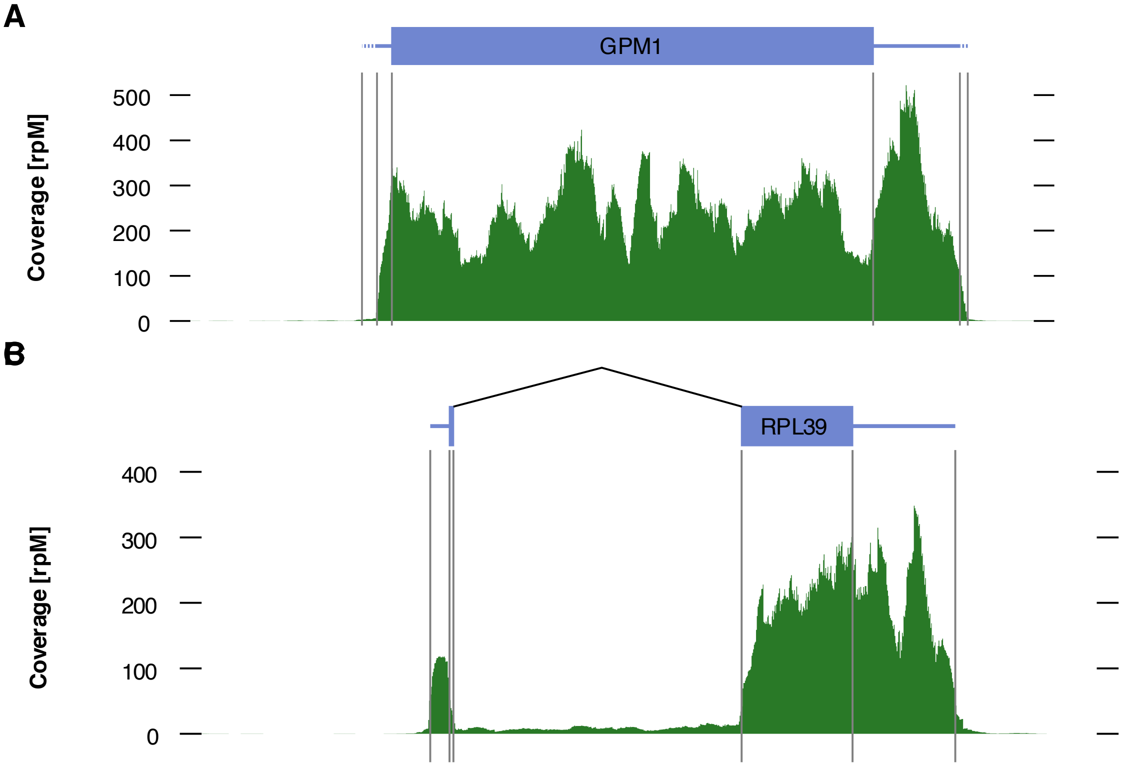

Figure S4. RNA-Seq using small mRNA fragments. (**A** and **B**) Read coverage of two well-expressed yeast genes. The UTR boundaries are taken from a large-scale full-length cDNA analysis (*S9*). Coverage varies only 3- to 4-fold within coding sequences, and is clearly much lower in the *RPL39* intron.

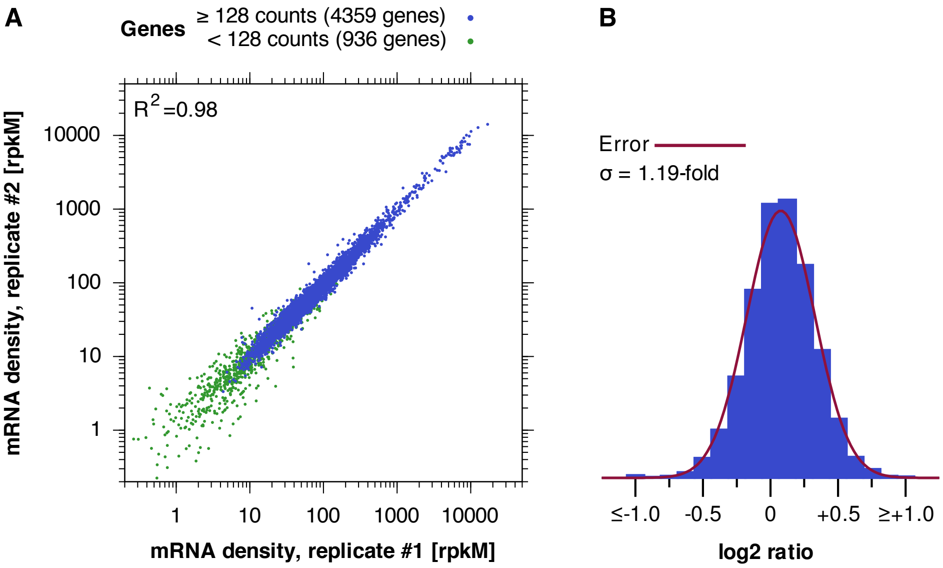

Figure S5. Reproducibility of mRNA abundance measurements between biological replicates. (**A**) mRNA fragment densities in two fully independent replicates. Density is expressed in terms of reads per kilobase per million (rpkM), which is corrected for total reads and CDS length. Genes with at least 128 total reads counted have low relative error from counting statistics (fig. S7) and thus represent the intrinsic error in the technique, which cannot be overcome by more sequencing. (**B**) Inter-replicate error distribution. Histogram of log2 ratios between the replicates for genes with low counting error (≥ 128 reads total), along with the normal error curve (mean = 0.076, std dev = 0.252 in log2 units).

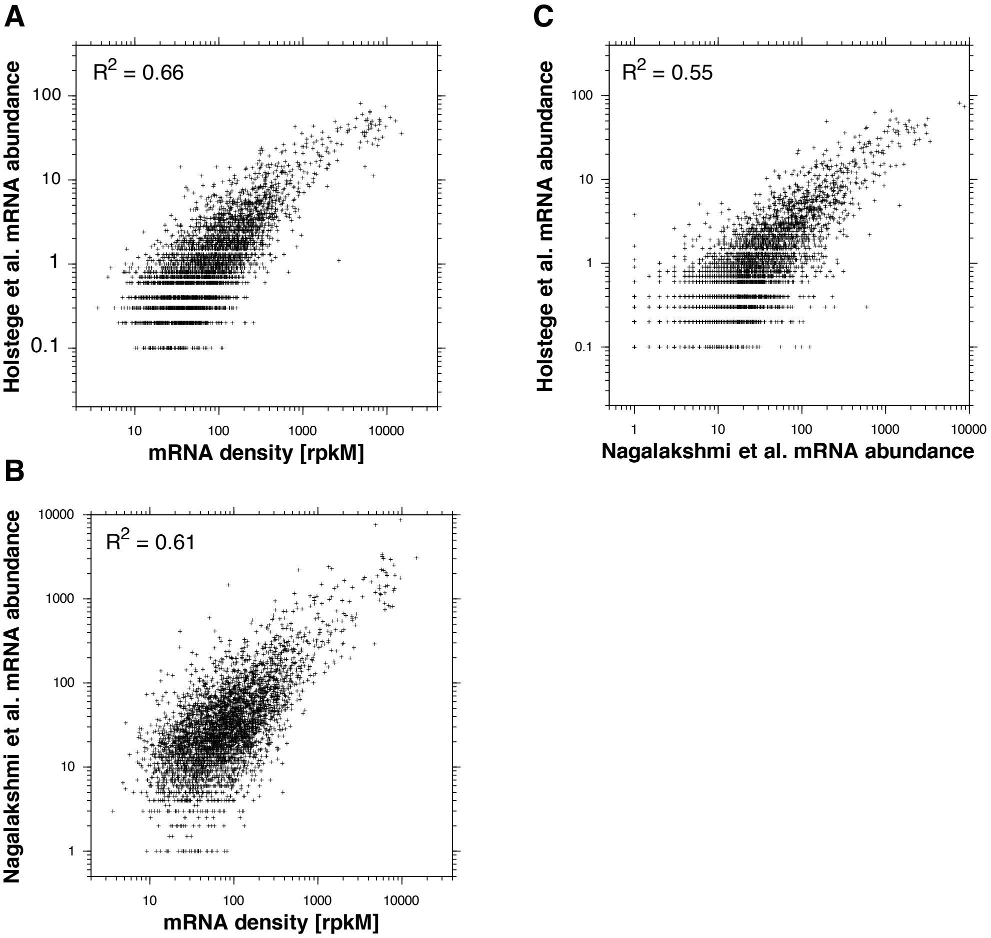

Figure S6. Correlation between various genome-wide mRNA abundance measurements. (**A**) Comparison between our mRNA abundance measurements and microarray data. Our measurement of mRNA abundance correlates well with the Holstege *et al.* data set (*S10*), which used single-channel microarrays normalized against genomic DNA to compare abundance between different mRNAs. (**B**) Comparison between our mRNA abundance measurement and an alternate transcriptome sequencing approach. The Nagalakshmi *et al.* data set (*S1*) used deep sequencing of unfragmented mRNAs and quantified only reads in a 30 bp window upstream of the stop codon. (**C**) Comparison between the two previous whole-genome measurements.

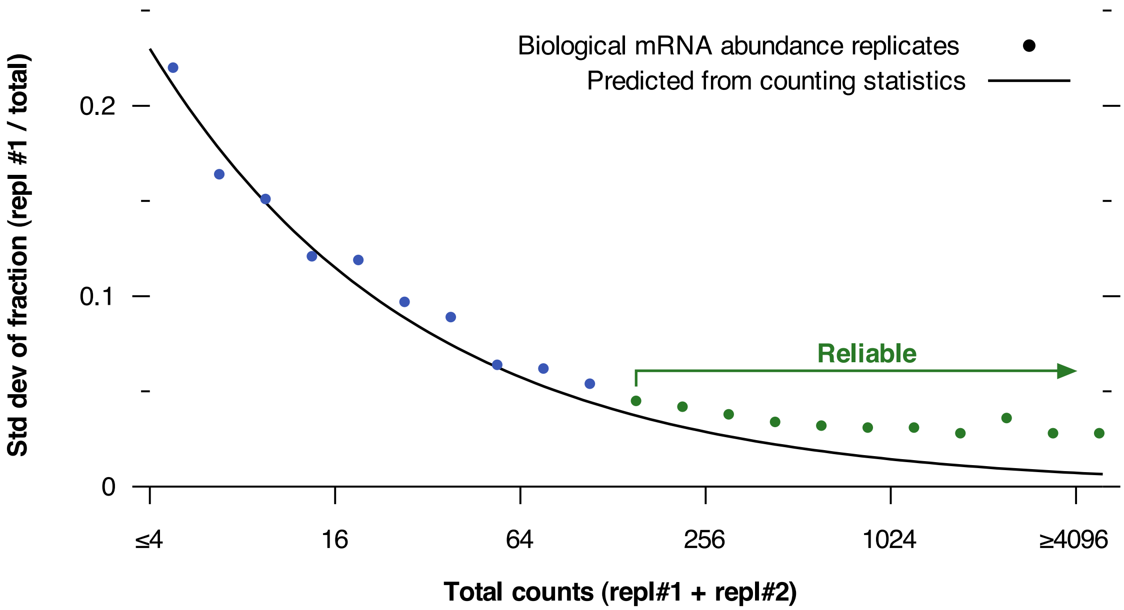

Figure S7. Effects of counting statistics on error in quantification. Fully independent biological replicates of mRNA abundance were used to measure reproducibility. For each gene, the fraction of the total number of sequencing reads that derived from replicate #1 was calculated. Genes were then binned based on the total number of reads and the standard deviation of fractions was computed across each bin. The standard deviation was predicted for counting statistics using simple binomial partitioning of the total number of reads between replicates #1 and #2. When few total counts are available, the effects of binomial partitioning dominate the inter-replicate variation, but when many counts are obtained, other sources of error predominate. A threshold of 128 total counts was chosen as a point where the inter-replicate variation approached its infinite-counts asymptote and counting statistics contributed little.

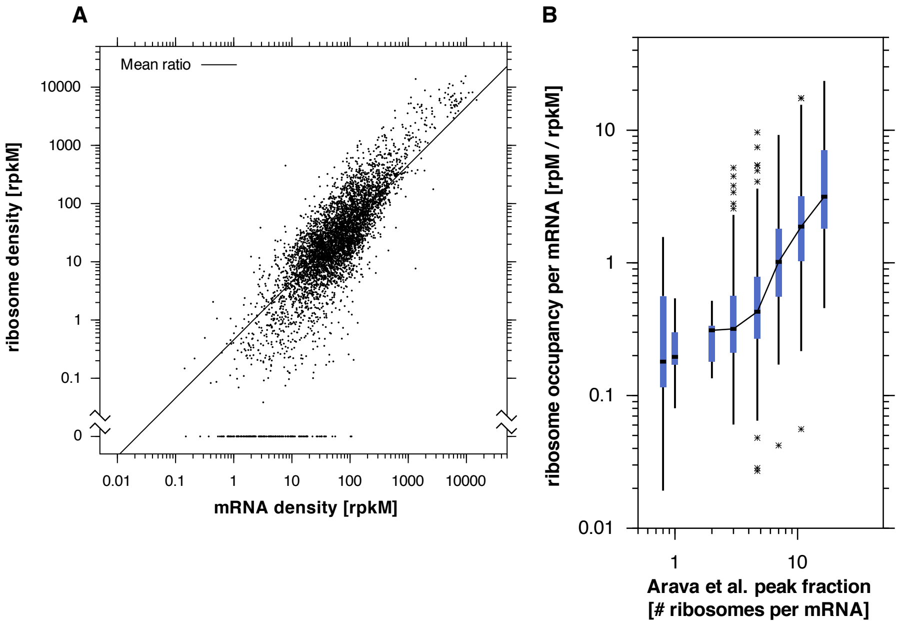

Figure S8. Ribosome density as a measure of protein synthesis. (**A**) Ribosome footprint abundance correlates well, but not perfectly, with mRNA abundance. Genes with more abundant mRNA are also translated more highly. The average ratio of footprint density to mRNA fragment density was computed from genes where the ratio could be reliably determined (Fig. S7) (**B**) Translational efficiency as a function of length. Genes were binned based on length and the median translational efficiency for each length class was normalized against the 1kb length class. (**C**) Ribosome occupancies of genes classified by whole-genome polysome profiling. A previous study quantified relative mRNA abundance in eight polysome fractions and found a distinct peak of mRNA abundance for each of 2128 genes (*S11*). Ribosome occupancy per transcript, which is the quantity directly measured by polysome profiling, was estimated for genes peaking in each of these fractions by scaling total ribosome counts by mRNA fragment density. Genes peaking in heavier polysome Vfractions tend to have higher ribosome occupancy. For the set of genes peaking in a polysome fraction, we show a five-number summary (minimum, lower quartile, median, upper quartile, and maximum) of ribosome occupancy values, along with the outliers.

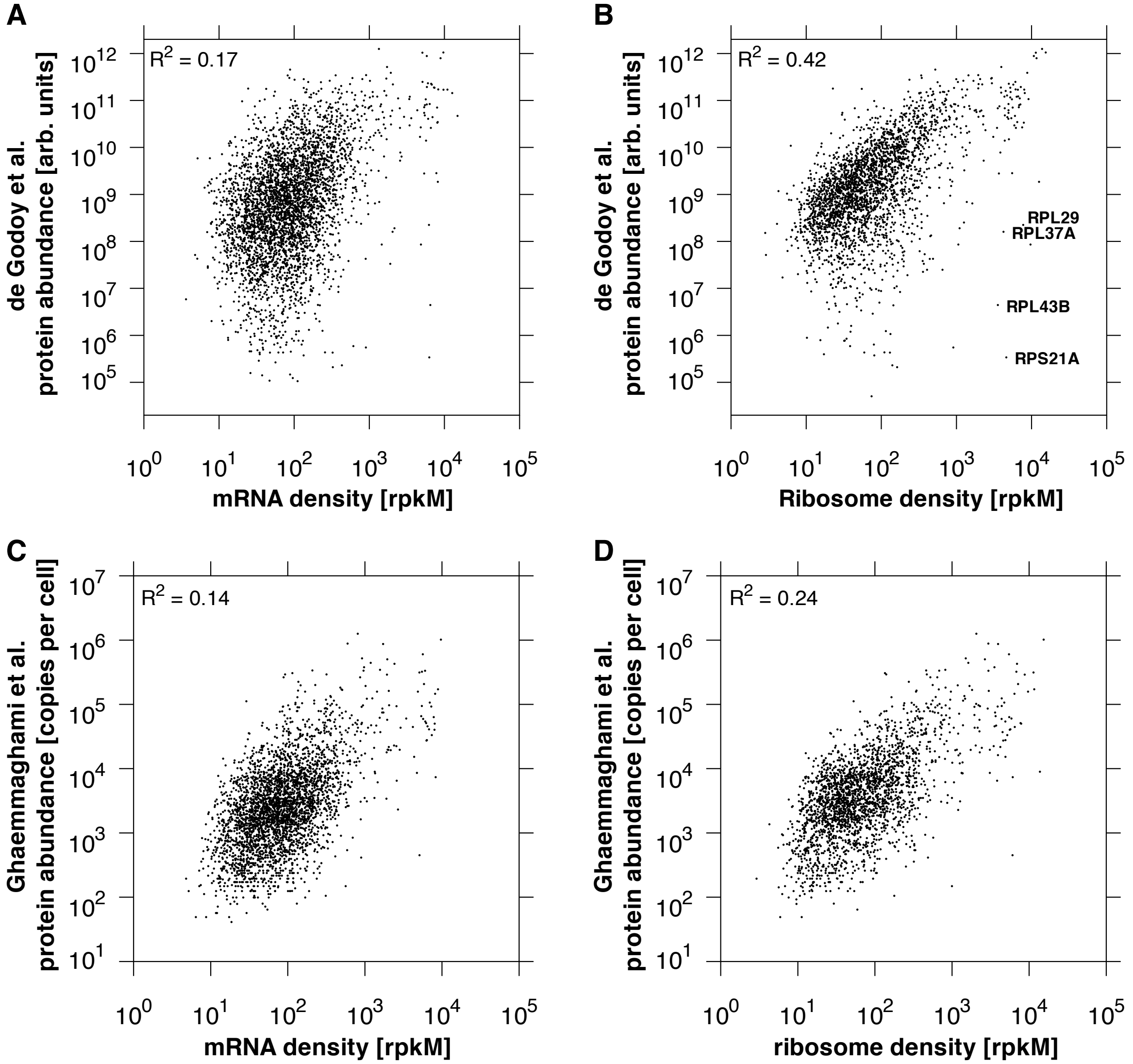

Figure S9. Correlation between protein abundance and gene expression measurements. (**A** and **B**) Protein abundance by mass spectrometry versus mRNA and ribosome density. Protein abundance (*S12*) correlates better with ribosome density than mRNA abundance. Furthermore, many outliers are ribosomal proteins, including the single-copy Rpl29p, that are likely to be high-abundance proteins and thus represent errors in the mass spectrometry data. Protein abundance was derived from summed ion intensity in haploid samples from de Godoy *et al.*. (**C** and **D**) As (A) and (B), using protein abundance from Western blotting against TAP-tagged proteins from Ghaemmaghami *et al.* (*S13*)

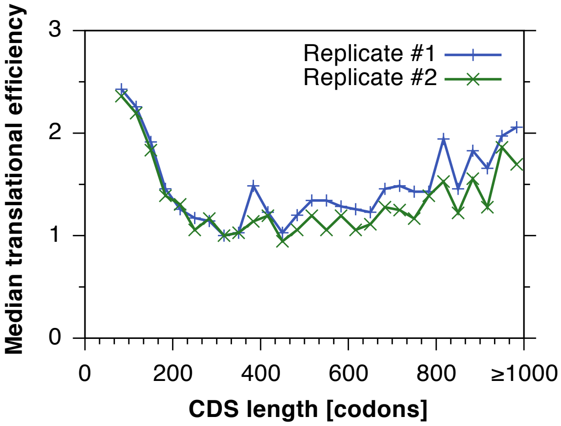

Figure S10. Translational efficiency as a function of length. Genes were binned based on the length of their coding sequence and the median translational efficiency was computed over the genes in each length class . Efficiencies were normalized against the 1kb length class.

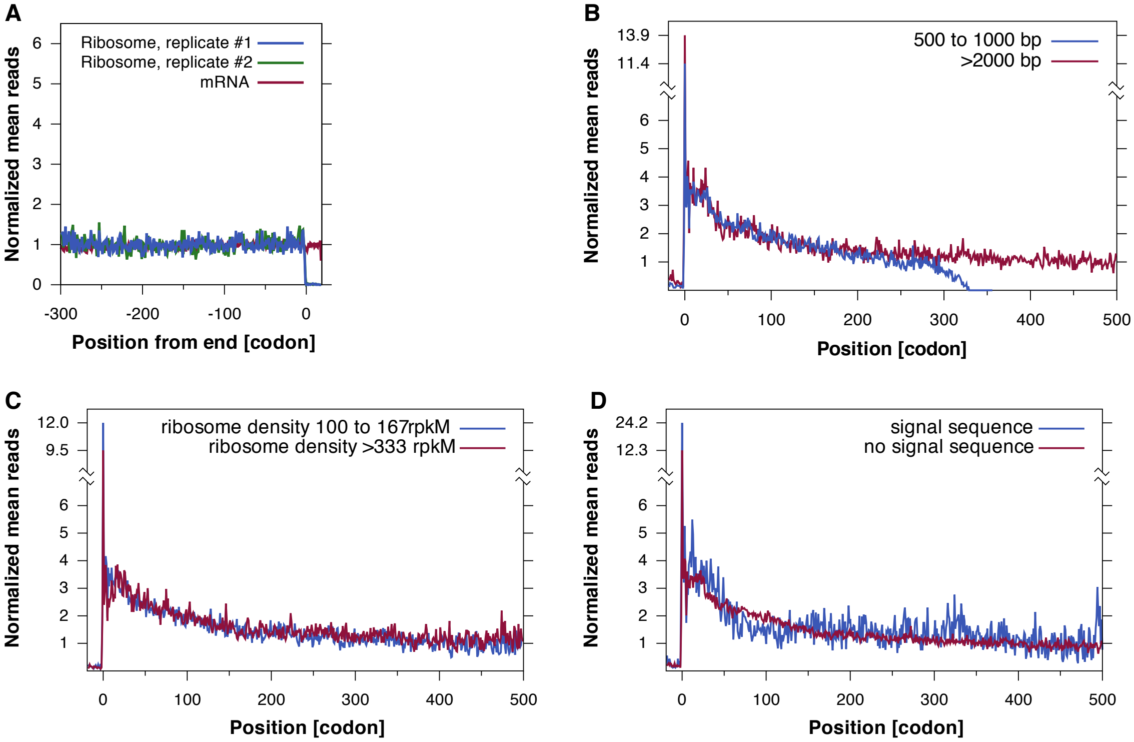

Figure S11. Read density as a function of position for subsets of genes. (**A**) Read density as a function of position relative to the end of the coding sequence. As in Fig. 2F, though only genes that are at least 500 codons long were included in the average to avoid any effect of the start of the gene on the window examined. Ribosome occupancy appears to be uniform at the end of the gene, then stops abruptly at the stop codon. (**B**) Comparison of short (500 - 1000 bp) and long (≥2000 bp) genes. (**C**) Comparison of moderately-expressed (100 to 167 rpkM ribosome footprint density) and highly-expressed (≥ 333 rpkM ribosome footprint density) genes. (**D**) Comparison of genes with and without predicted N-terminal signal sequences. The overall three-phase trend in ribosome density appears to be independent of length, expression level, and the presence of a signal sequence.

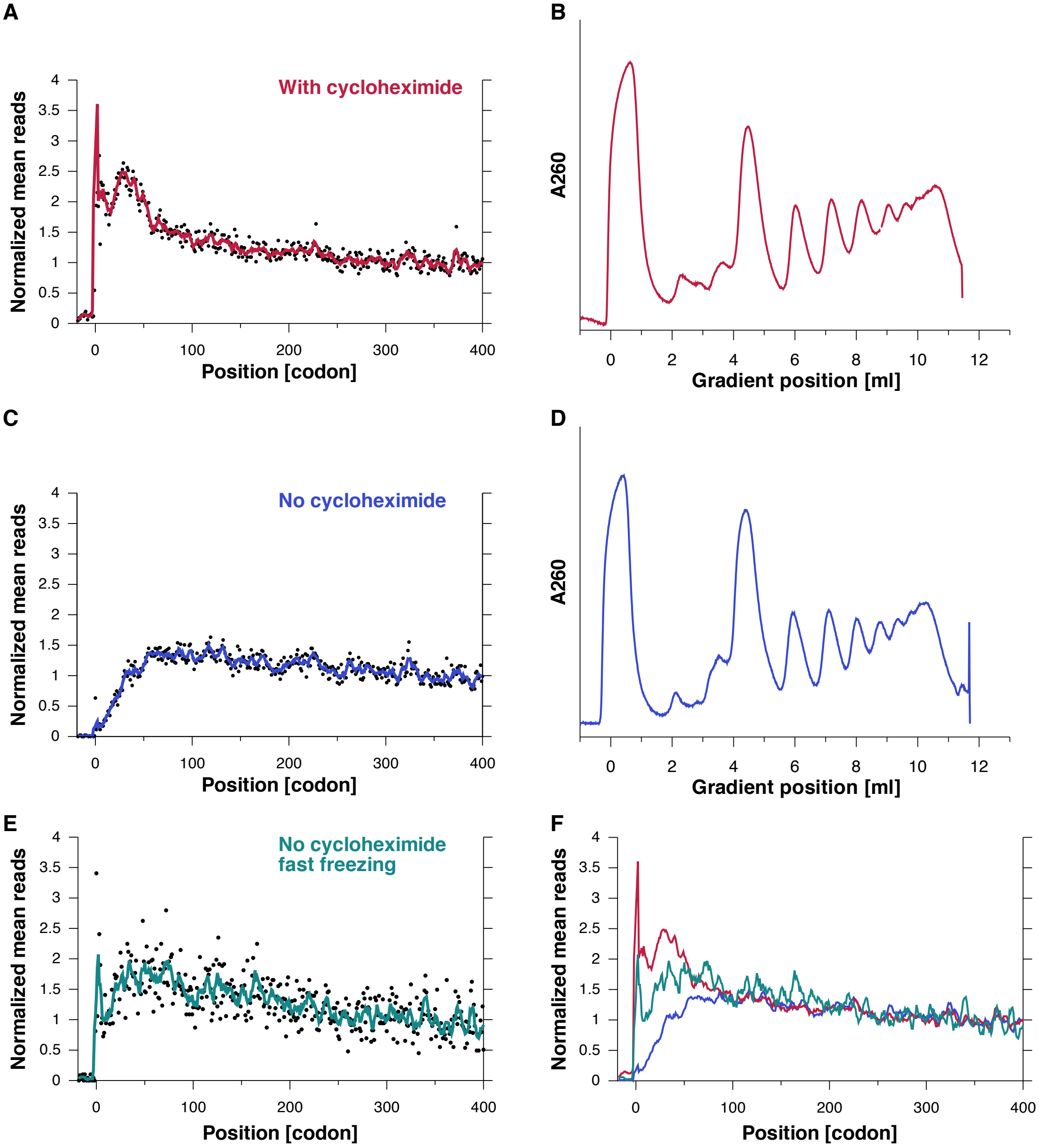
A
With cycloheximide
Normalized mean reads
Position [codon]
B
A260
Gradient position [ml]
C
No cycloheximide
Normalized mean reads
Position [codon]
D
A260
Gradient position [ml]
E
No cycloheximide
fast freezing
Normalized mean reads
Position [codon]
F
Normalized mean reads
Position [codon]
0
0.5
1
1.5
2
2.5
3
3.5
4
0
100
200
300
400
0
2
4
6
8
10
12

Figure S12.

Figure S12. Effects of cycloheximide and translational run-off on average ribosome density. (**A**) Density of ribosome footprints as a function of position. Density profiles for well-expressed genes were independently normalized and averaged with equal weight, as described above. Black dots show per-codon densities and solid lines show a 5-codon moving average centered on that position. Data were taken from a preliminary experiment using an earlier version of our library generation protocol. (**B**) Polysome analysis of cycloheximide-treated extract. An undigested portion of the extract sample used to prepare the library analyzed in (A) was analyzed by sucrose density gradient, as in fig. S2. (**C**) Density of ribosome footprints in extracts prepared without cycloheximide. As in (A), except that cycloheximide was excluded from all aspects of the experiment. Cells were harvested without cycloheximide treatment, resuspended in ice-cold cycloheximide-free lysis buffer, and dripped into ℓN_2. Extracts were analyzed on sucrose density gradients that contained no cycloheximide. Stress responses induced by harvesting cells out of rich media and resuspending them in cold, nutrient-free lysis buffer rapidly inhibit translation initiation. In the absence of cycloheximide treatment to immobilize ribosomes, elongation proceeds for a short time, thereby strongly depleting ribosomes from the first 50 - 100 codons. The nearly complete loss of ribosomes from the beginning of the gene argues that the excess ribosome density at the 5' end of CDSes represents elongating ribosomes and not, *e.g.*, terminally stalled translation events. However, the average ribosome density beyond codon 100 is indistinguishable from that of cycloheximide-treated cells. Furthermore, ribosome density is still several-fold higher at the initiation codon than at positions immediately downstream. (**D**) Cycloheximide-free polysome analysis. As in (B), using an undigested portion of the extract analyzed in (C). (**E**) Density of ribosome footprints in extracts prepared without cycloheximide and frozen very quickly. As in (C), except for modifications to the cell harvesting protocol designed to minimize run-off elongation. Specifically, cells were harvested by filtration and the cell paste was quickly scraped off of the filter and plunged directly into ℓN_2. Polysome lysis buffer was subsequently dripped into the ℓN_2 as well. Frozen cells and lysis buffer were kept frozen and pulverized together, and then processed as in (C). There is a much more modest loss of ribosomes from the beginning of genes, consistent with the model that a shorter delay between cell harvesting and freezing diminishes run-off elongation. There is a clear excess of ribosome density starting around codon 30 and by codon 50 the profile is indistinguishable from that of the cycloheximide-treated sample. Both the high ribosome density at the start codon and the elevated ribosome density over the first 100-200 codons can be reproduced in samples that are never treated with cycloheximide. (**F**) Comparison of average density profiles between the three samples.

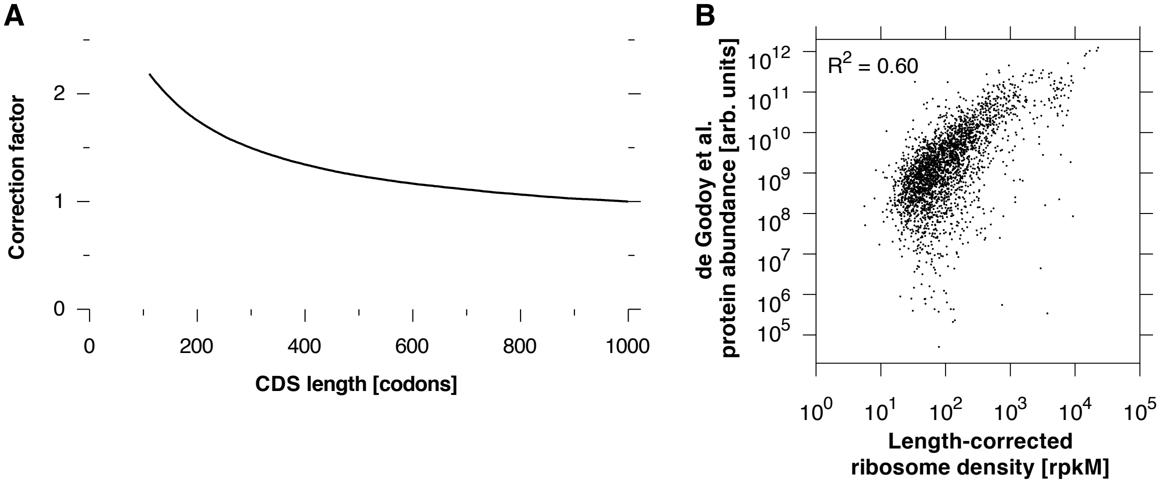

Figure S13. Protein synthesis estimates are improved by ribosome density correction. (**A**) Ribosome density correction factor as a function of length. The length correction factor at length L codons is the average ribosome density on the interval $[1, L]$ as shown in Fig. 2F, normalized to the average over $[1, 1000]$. (**B**) Protein abundance by mass spectrometry versus length-corrected ribosome density. Correcting the ribosome density on each gene by the factor shown in (A), based on its length, substantially improves the correlation with protein abundance.

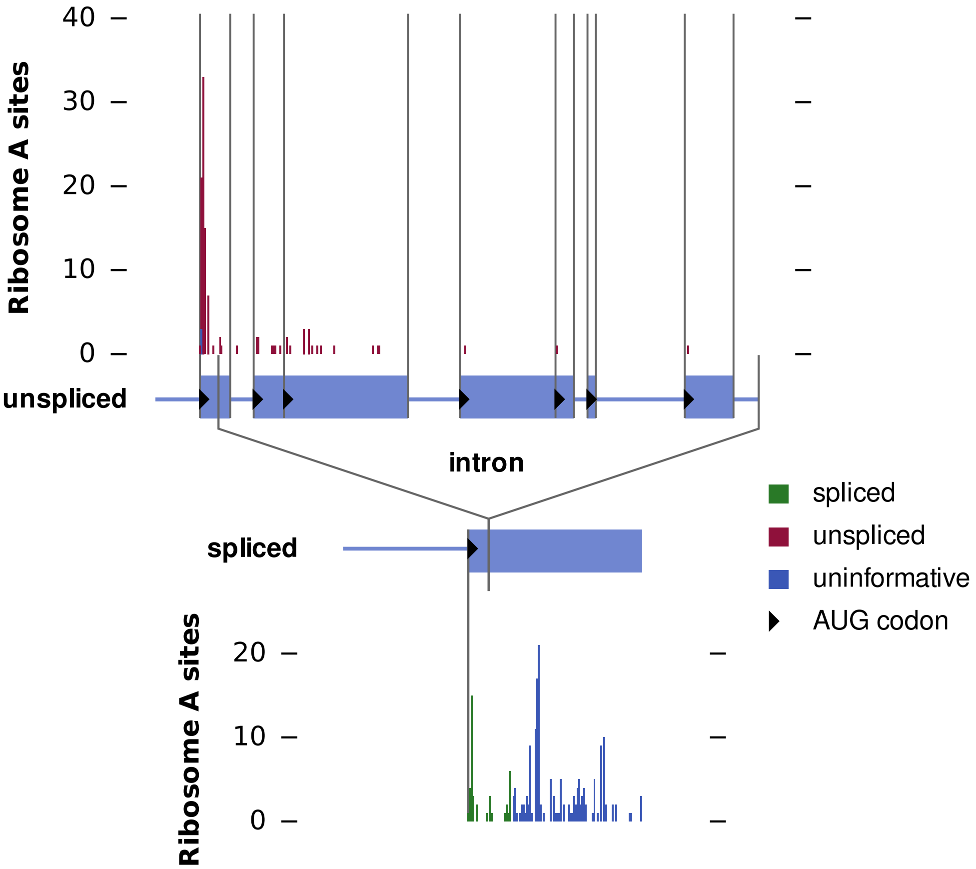

Figure S14. Reads aligning to spliced and unspliced *RPL22B*. Translation of the intron can be explained by reinitiation or leaky scanning following the normal AUG, which starts a 7 codon ORF in the unspliced form. Almost all intronic ribosome footprints are derived from the next downstream ORF in the intron, with three remaining reads distributed exactly at the sites of three other AUG codons. Only reads that were at least 27 nucleotides long, with no more than one mismatch, were used. These restrictions allow us to assign reads beginning on the start codon to either the spliced or the unspliced form because the 5' splice site is only 12 nucleotides downstream of the beginning of the gene. The downstream AUGs in the intron sequence are indicated, along with the next in-frame stop. Whenever a second AUG occurs in an open reading frame, it is in-frame, so there are no overlapping reading frames.

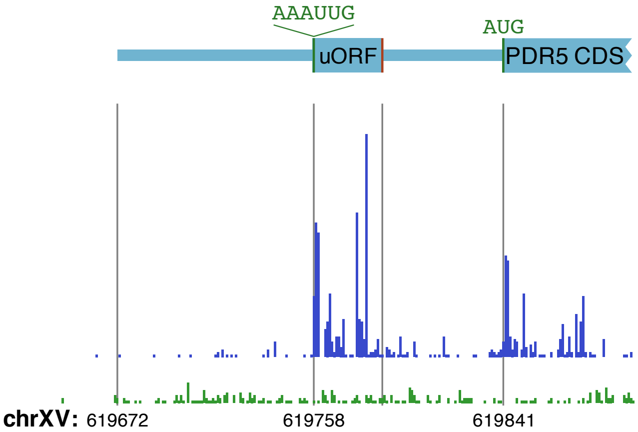

Figure S15. Ribosome and mRNA density showing non-AUG uORFs in *PDR5*. The proposed AAA*UUG* translational initiation site is shown, along with the subsequent open reading frame and stop codon (indicated by a vertical line).

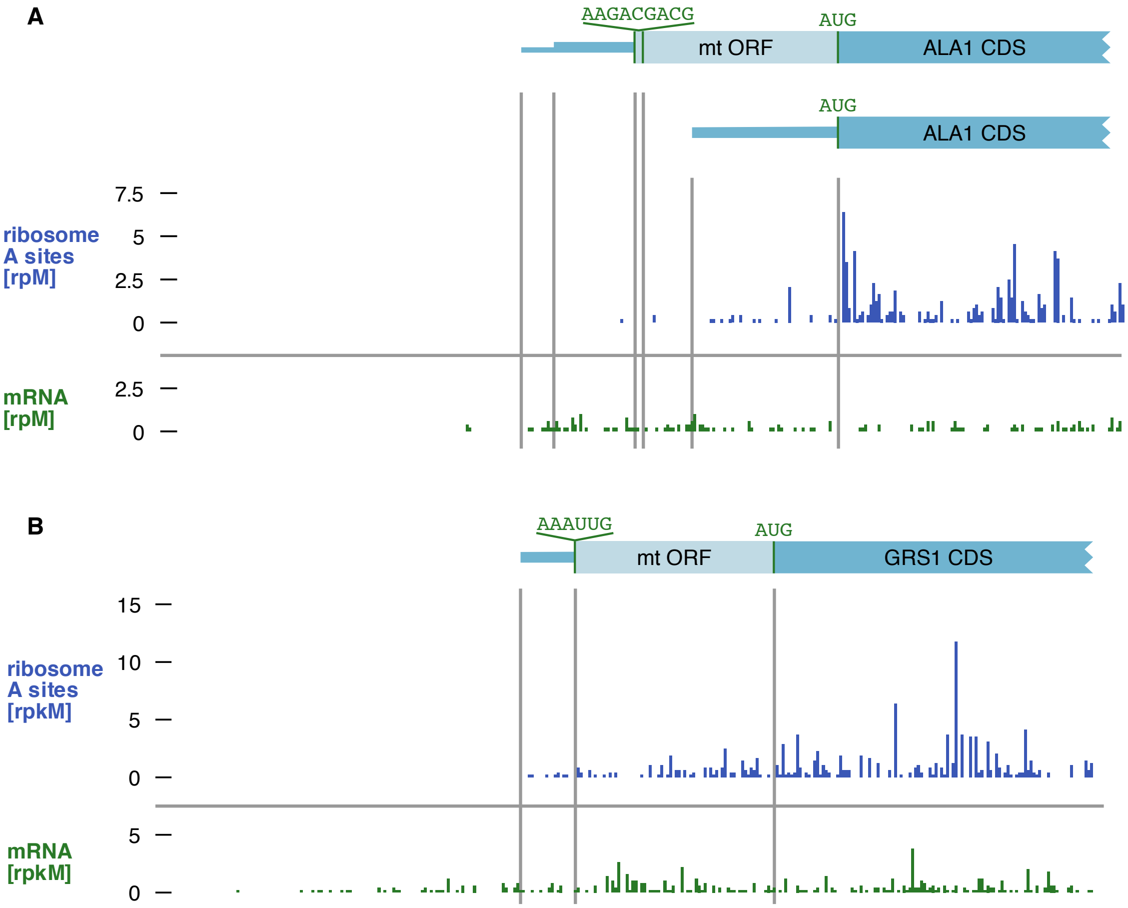

Figure S16. Known non-AUG initiation in yeast tRNA synthetases. (**A**) Ribosome footprint and mRNA fragment densities in *ALA1* transcripts. There are three characterized transcription start sites, resulting in two substantially different isoforms, depicted. In the longer isoforms, translation initiates at one of a pair of ACG codons and produces a protein with a mitochondrial signal sequence, “mt ORF.” In the shorter isoform, translation initiates at the canonical AUG to produce a cytosolic protein. (**B**) Ribosome footprint and mRNA fragment densities in *GRS1* transcripts. The mapped transcription start site is shown. Translation sometimes initiates at a UUG codon, resulting in a protein with a mitochondrial signal sequence, “mt ORF.”

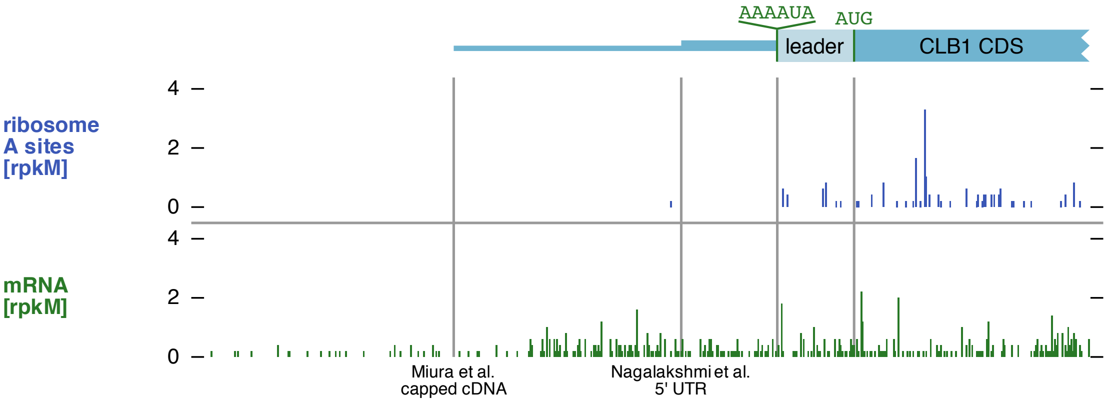

Figure S17. Novel non-AUG initiation in *CLB1* produces an N-terminal extension. Transcription start sites based on capped cDNA sequencing and transcriptome deep sequencing are indicated, but mRNA abundance suggests that most transcripts start between these two points. Translation initiation at a non-AUG site in-frame with the canonical AUG would explain essentially all ribosome footprints on the *CLB1* 5' UTR. Translation of this highly conserved region would add a 17 amino acid N-terminal extension to Clb1p.

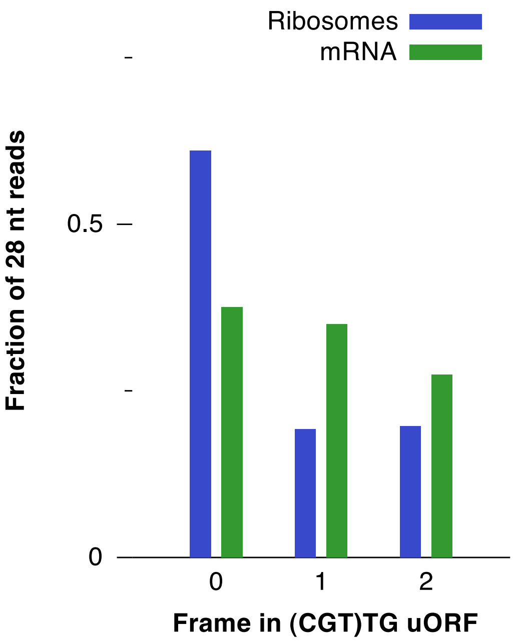

Figure S18. Position of ribosome footprints relative to proposed non-AUG start sites. The (C/G/U)UG candidate uORFs showed the highest translation efficiency in log-phase growth. The reading frame of unambiguous 28 nt sequencing reads relative to a proposed initiator codon was computed for all reads that mapped to the 12 codons downstream of the start site. Ribosome-protected fragments show a strong bias to start on the first nucleotide of a codon, in contrast to random mRNA fragments.

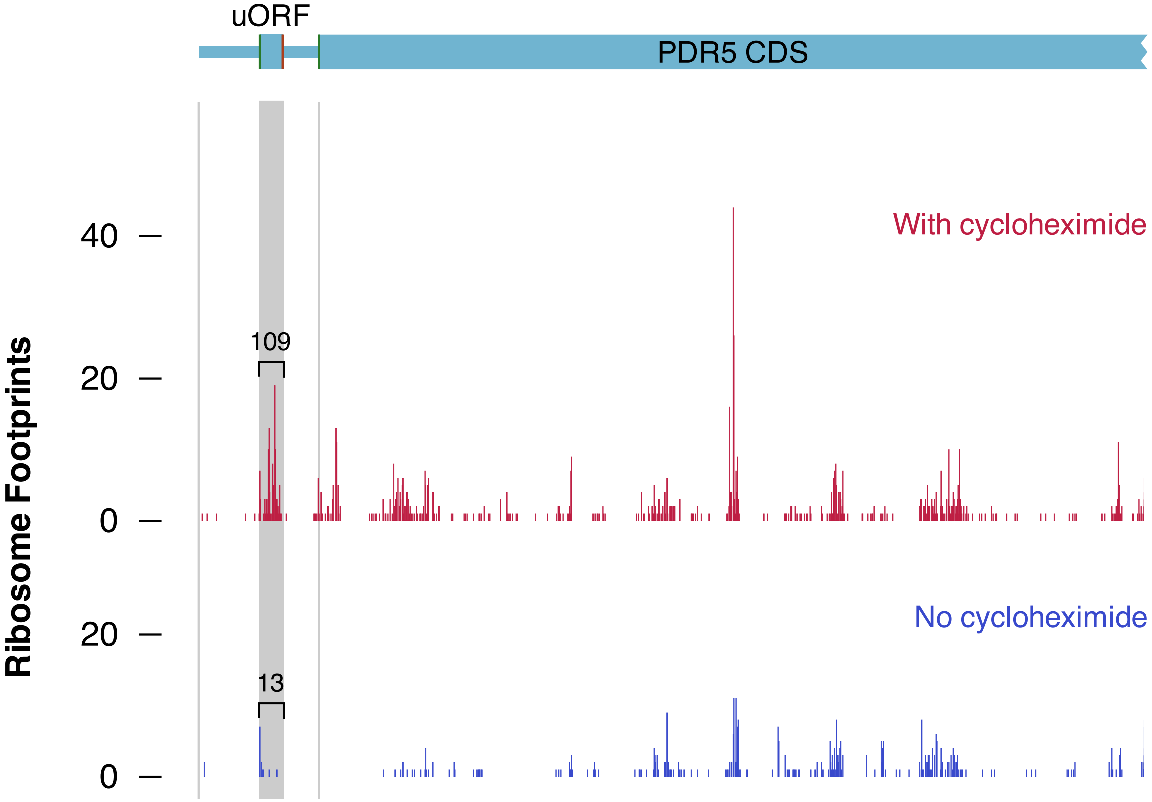

Figure S19. Translational run-off of non-AUG uORFs. Counts of ribosome-protected fragments from matched samples prepared with and without cycloheximide (fig. S12) are shown for the 5' end of the *PDR5* transcript. In a sample prepared without cycloheximide, ribosome-protected fragments are lost from the proposed non-AUG uORF in the 5' UTR, suggesting that these fragments are derived from actively elongating ribosomes. Ribosome footprints are also lost from the 5' end of the CDS, consistent with the average pattern of ribosome density seen in these samples.

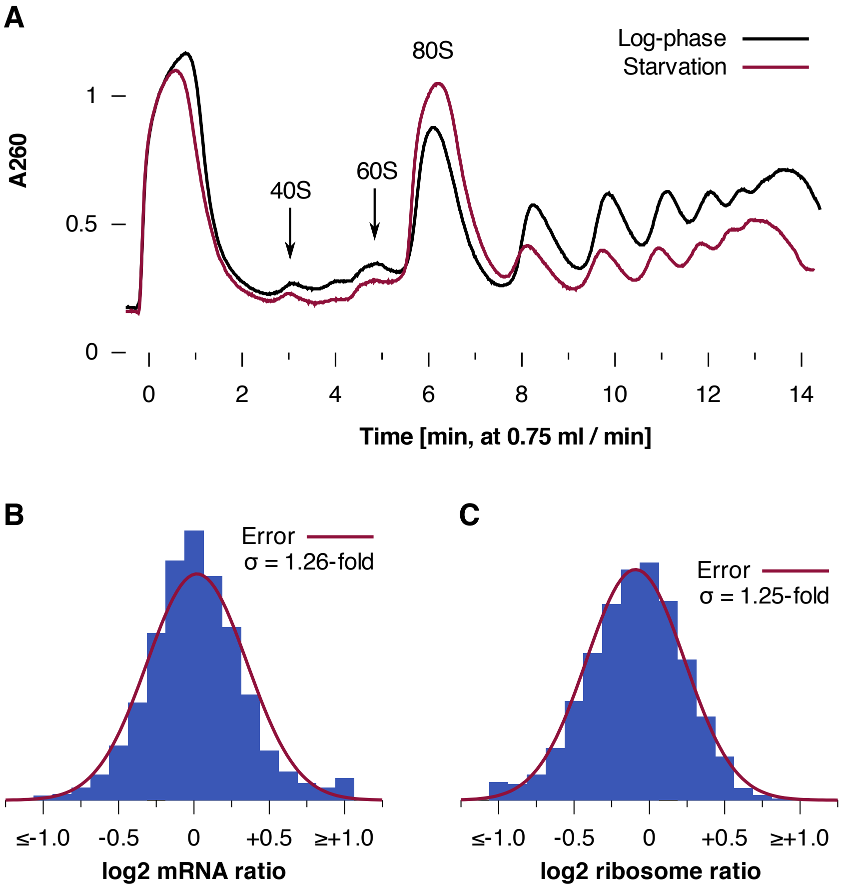

Figure S20. Ribosome footprinting of cells subjected to acute amino acid starvation. (**A**) Polysome profiles from a culture split in half, with one half transferred to minimal media without amino acids for 20 min. There is a substantial loss of polysomal ribosomes, with a corresponding increase in monosomal ribosomes, consistent with previous reports. (**B**) Reproducibility of mRNA abundance measurements following starvation. Histogram of $\log_2$ ratios between replicates for genes with at least 128 reads, along with the normal error curve (mean = 0.021, std dev = 0.332 in $\log_2$ units). (**C**) Reproducibility of ribosome footprint density following starvation. Histogram of $\log_2$ ratios between replicates for genes with at least 128 reads, along with the normal error curve (mean = -0.092, std dev = 0.326 in $\log_2$ units).

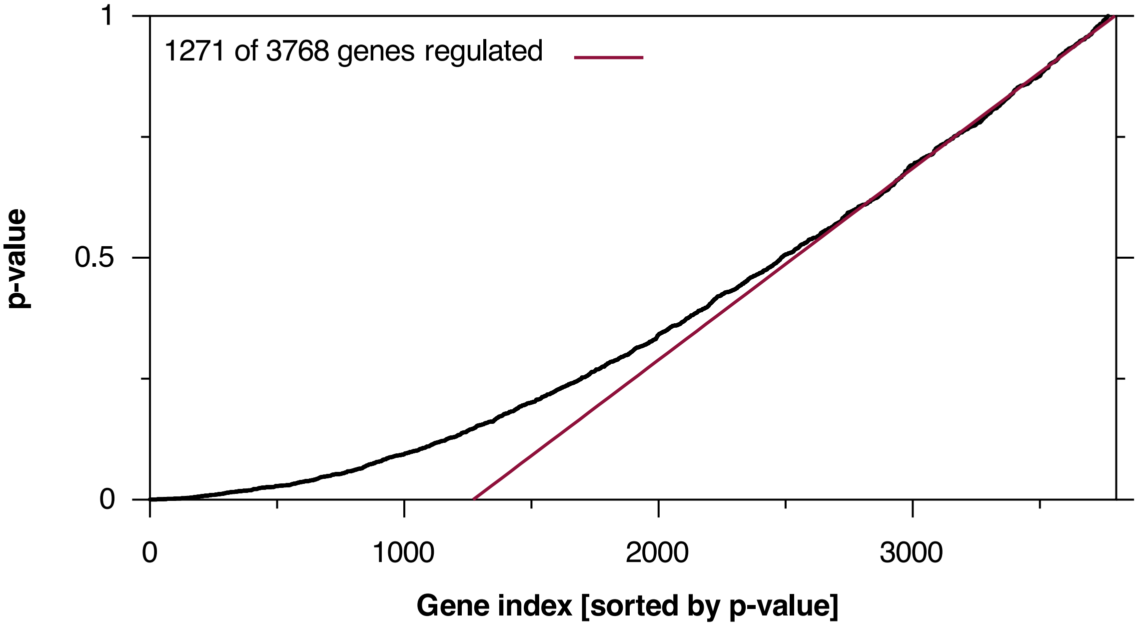

Figure S21. Estimation of the number of translationally regulated genes. The distribution of p-values is fit by a model in which roughly one-third of reliably measured genes (1271 of 3768) are translationally regulated. The no-change null hypothesis p-value for each gene was estimated from the distribution of inter-replicate ratios of translation in biological replicates of the log-phase and starvation samples. The unchanged genes should have a uniform distribution of p values, whereas the translationally regulated genes will have p values skewed strongly towards 0. Thus, most large p values will be derived from the unregulated subset, and the distribution of p values at the high-p limit can be extrapolated down to $p = 0$ to estimate the overall population of unregulated genes. The region of $p \geq 0.67$ was used to fit $p = 0.000396 \cdot index - 0.502$, giving $index(p = 0) = 1271.0$.

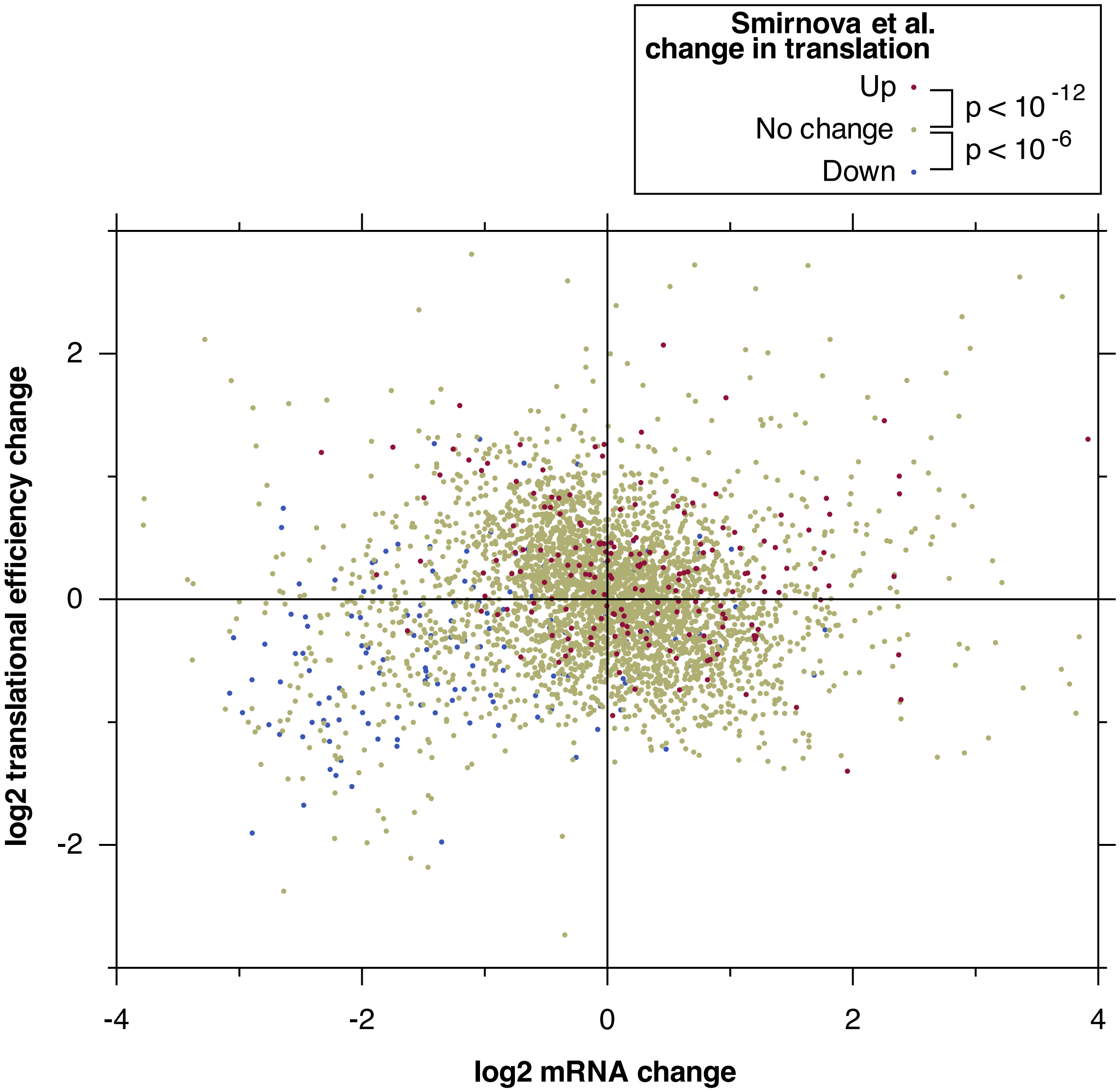

Figure S22. Comparison of ribosome footprinting results with polysome fraction measurements by Smirnova *et al.* following amino acid starvation. Genes were plotted as in Fig. 4A. Those genes whose messages showed a significant increase in polysome association in the Smirnova *et al.* data, indicating an increase in translation, were colored red. Similarly, genes whose messages showed decreased polysome association were colored blue. The change in translational efficiency, measured by ribosome profiling, was significantly higher for the genes with increased polysome association and lower for genes with decreased polysome association, relative to other genes, as shown; p values were calculated using a 1-sided Mann-Whitney U test .

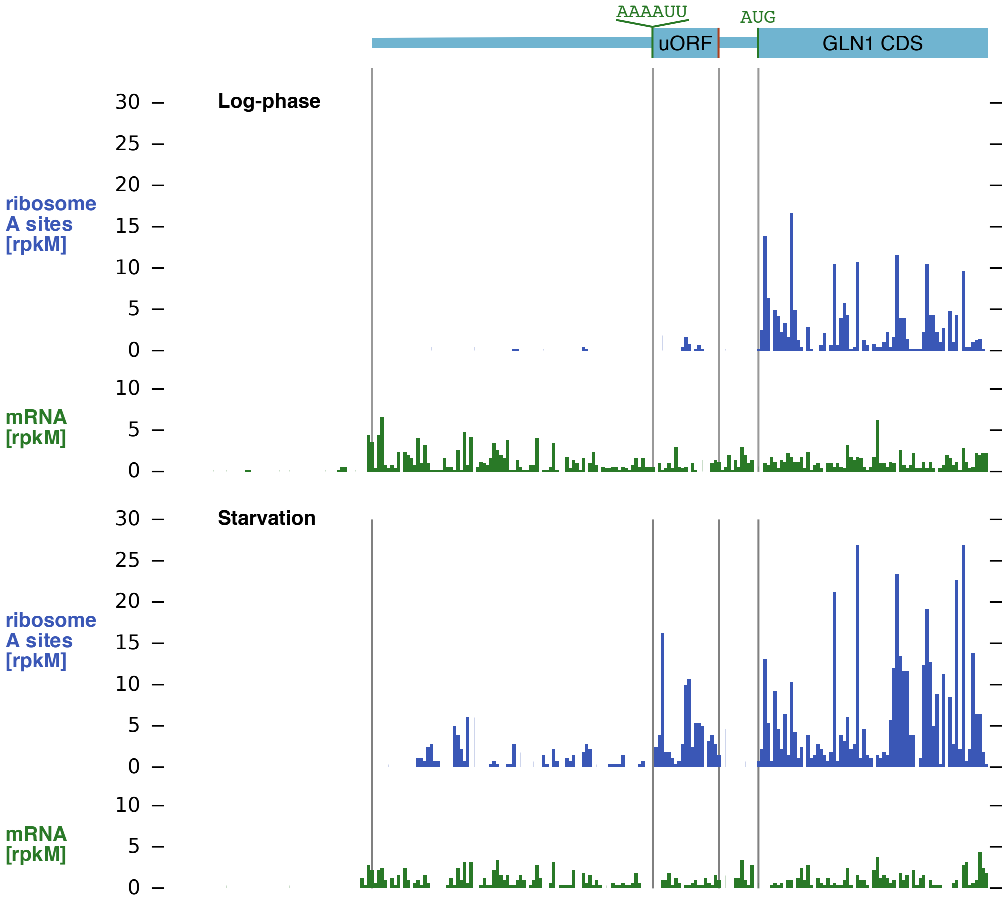

Figure S23. Translation in the *GLN1* 5' UTR induced by starvation. The translational efficiency of *GLN1* increases 3.3-fold in response to amino acid starvation. There is also a dramatic increase in ribosome density on the 5' UTR which is concentrated in the indicated non-AUG uORF, where some translation is detectable even in log-phase growth.

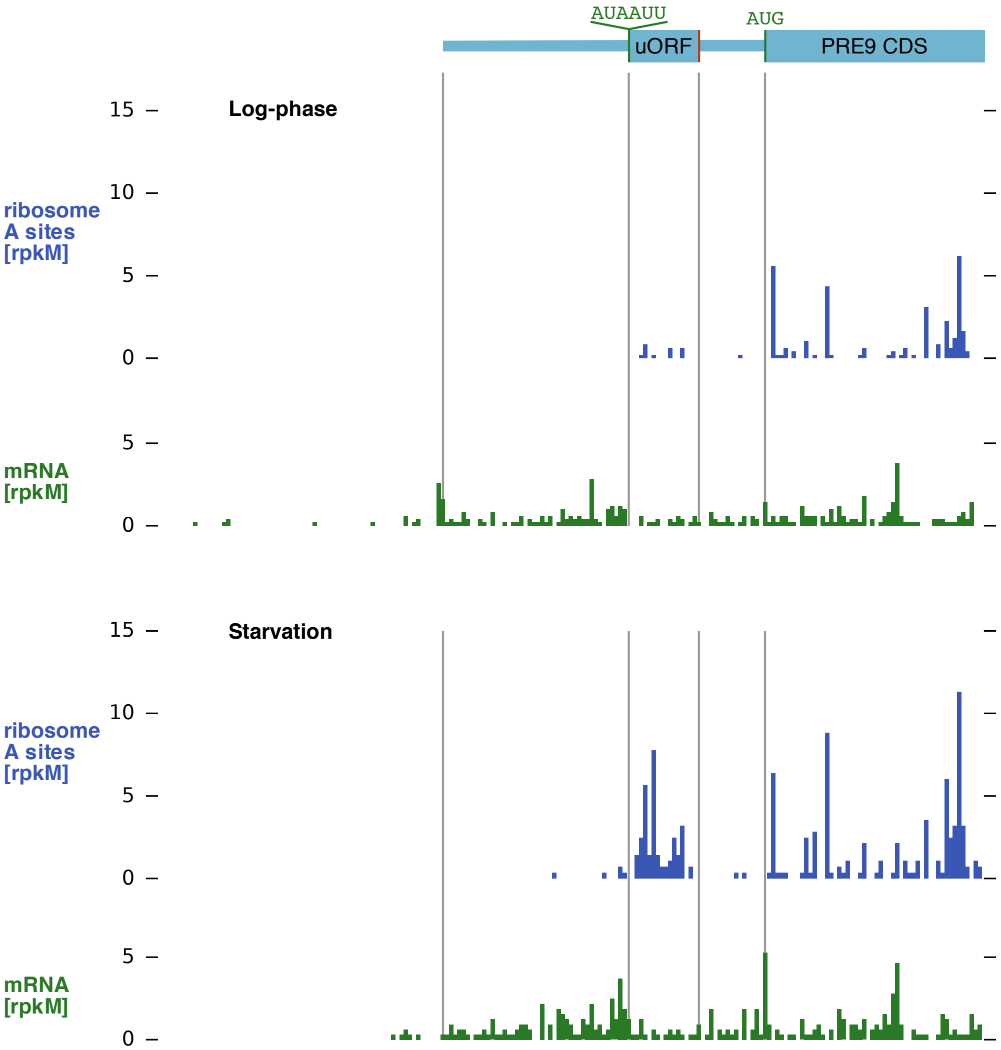

Figure S24. Translation in the *PRE9* 5' UTR induced by starvation. The mRNA abundance increases during starvation, but the translational efficiency is essentially unchanged. A non-AUG uORF which is weakly translated during log-phase growth is strongly induced upon starvation.

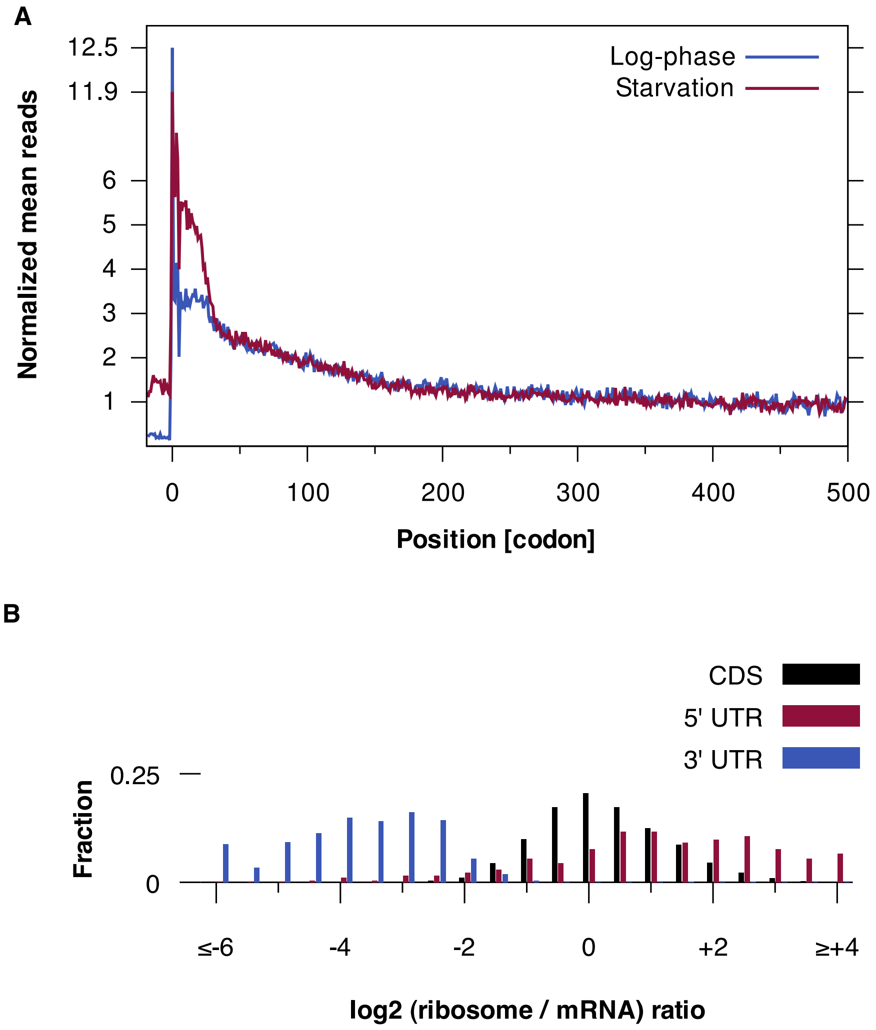

Figure S25. Global effects of starvation on translation. (**A**) Starvation further increases ribosome density on the first 30 codons. Ribosome density as a function of position was plotted during starvation versus log-phase growth, as in Fig. 2F. (**B**) Increased 5' UTR translation during starvation. As in Fig. 3B, for starvation samples.

Alignment	mrna rich1		mrna noaa1		mrna rich2		mrna noaa2	
Total	**4 700 324**		**4 135 727**		**13 018 070**		**10 659 366**	
Culled	239 822	5.1	314 000	7.6	133 668	1.0	51 956	0.5
Unculled	4 460 502	94.9	3 821 727	92.4	12 884 402	99.0	10 607 410	99.5
Unculled	**4 460 502**		**3 821 727**		**12 884 402**		**10 607 410**	
rRNA	1 925 728	43.2	2 172 947	56.9	4 978 873	38.6	5 387 823	50.8
No rRNA	2 534 774	56.8	1 648 780	43.1	7 905 529	61.4	5 219 587	49.2
Genomic	*2 454 964*	*55.0*	*1 572 289*	*41.1*	*5 721 013*	*44.4*	*3 502 836*	*33.0*
No rRNA	**2 534 774**		**1 648 780**		**7 905 529**		**5 219 587**	
Genomic	2 454 964	96.9	1 572 289	95.4	5 721 013	72.4	3 502 836	67.1
No genomic	79 810	3.1	76 491	4.6	2 184 516	27.6	1 716 751	32.9
CDSes +100 bp	2 266 754	89.4	1 462 372	88.7	5 210 137	65.9	3 229 889	61.9
Splices	*7 259*	*0.3*	*3 188*	*0.2*	*23 631*	*0.3*	*7 758*	*0.1*
Genomic	**2 454 964**		**1 572 289**		**5 721 013**		**3 502 836**	
CDSes +100 bp	*2 266 754*	*92.3*	*1 462 372*	*93.0*	*5 210 137*	*91.1*	*3 229 889*	*92.2*
Splices	*7 259*	*0.3*	*3 188*	*0.2*	*23 631*	*0.4*	*7 758*	*0.2*

Alignment	fp rich1		fp noaa1		fp rich2		fp noaa2	
Total	**13 561 039**		**9 073 940**		**28 616 240**		**18 841 676**	
Culled	467 489	3.4	467 281	5.1	256 924	0.9	70 898	0.4
Unculled	13 093 550	96.6	8 606 659	94.9	28 359 178	99.1	18 770 778	99.6
Unculled	**13 093 550**		**8 606 659**		**28 359 178**		**18 770 778**	
rRNA	10 952 914	83.7	7 531 522	87.5	17 828 899	62.9	14 023 989	74.7
No rRNA	2 140 636	16.3	1 075 137	12.5	10 530 279	37.1	4 746 789	25.3
Genomic	*2 000 107*	*15.3*	*986 611*	*11.5*	*5 138 796*	*18.1*	*2 671 653*	*14.2*
No rRNA	**2 140 636**		**1 075 137**		**10 530 279**		**4 746 789**	
Genomic	2 000 107	93.4	986 611	91.8	5 138 796	48.8	2 671 653	56.3
No genomic	140 529	6.6	88 526	8.2	5 391 483	51.2	2 075 136	43.7
CDSes +100 bp	1 926 044	90.0	930 091	86.5	5 031 093	47.8	2 568 616	54.1
Splices	*19 047*	*0.9*	*5 516*	*0.5*	*52 025*	*0.5*	*14 493*	*0.3*
Genomic	**2 000 107**		**986 611**		**5 138 796**		**2 671 653**	
CDSes +100 bp	*1 926 044*	*96.3*	*930 091*	*94.3*	*5 031 093*	*97.9*	*2 568 616*	*96.1*
Splices	*19 047*	*1.0*	*5 516*	*0.6*	*52 025*	*1.0*	*14 493*	*0.5*

Table S1. Alignment statistics for deep sequencing reads. The total number of sequencing reads at each stage of alignment is shown in bold, followed by the number of matching or non-matching reads at the next stage of the alignment, and the percentage of the total they represent. Informative comparisons that are not direct subsets of the total are shown in italics. Splice reads are reads with CDS alignments but no genome alignments.

Table S2A: GO Terms Over-represented in Highly Translated Genes

GO Term	GO ID	log$_{10}$ p value	Expected	Actual	Total
organic acid metabolic process	GO:0006082	-12.7	36.5	81	257
carboxylic acid metabolic process	GO:0019752	-12.7	36.5	81	257
amino acid metabolic process	GO:0006520	-11.6	23.2	58	163
amino acid and derivative metabolic process	GO:0006519	-11.5	25.1	61	177
biosynthetic process	GO:0009058	-9.9	108.0	167	760
cellular process	GO:0009987	-9.5	506.0	566	3562
amine metabolic process	GO:0009308	-9.4	27.8	61	196
nitrogen compound metabolic process	GO:0006807	-8.7	30.3	63	213
hexose catabolic process	GO:0019320	-7.6	3.3	15	23
glucose catabolic process	GO:0006007	-7.6	3.3	15	23
translation	GO:0006412	-7.3	39.1	72	275
amine biosynthetic process	GO:0009309	-7.1	14.1	35	99
amino acid biosynthetic process	GO:0008652	-7.0	12.9	33	91
nitrogen compound biosynthetic process	GO:0044271	-7.0	14.2	35	100
mRNA catabolic process, deadenylation-dependent decay	GO:0000288	-6.9	3.1	14	22
monosaccharide catabolic process	GO:0046365	-6.9	4.0	16	28
cellular biosynthetic process	GO:0044249	-6.8	42.3	75	298
oxidative phosphorylation	GO:0006119	-6.8	5.4	19	38
alcohol catabolic process	GO:0046164	-6.3	4.3	16	30
acetyl-CoA metabolic process	GO:0006084	-6.3	2.6	12	18
regulation of RNA stability	GO:0043487	-6.3	3.8	15	27
regulation of mRNA stability	GO:0043488	-6.3	3.8	15	27
catabolic process	GO:0009056	-6.0	50.4	83	355
cellular catabolic process	GO:0044248	-6.0	48.9	81	344
cellular metabolic process	GO:0044237	-5.9	363.4	419	2558
cellular carbohydrate catabolic process	GO:0044275	-5.8	5.5	18	39
carbohydrate catabolic process	GO:0016052	-5.8	5.5	18	39
metabolic process	GO:0008152	-5.8	377.2	432	2655
coenzyme metabolic process	GO:0006732	-5.6	16.6	36	117
regulation of RNA metabolic process	GO:0051252	-5.5	4.3	15	30
branched chain family amino acid metabolic process	GO:0009081	-5.3	2.1	10	15
regulation of cell redox homeostasis	GO:0030503	-5.3	1.4	8	10
cell redox homeostasis	GO:0045454	-5.3	1.4	8	10
cofactor metabolic process	GO:0051186	-5.2	20.6	41	145
age-dependent general metabolic decline	GO:0007571	-5.1	0.9	6	6

Continued on next page

Table S2A: GO Terms Over-represented in Highly Translated Genes, continued

GO Term	**GO ID**	**$\log_{10}$ *p* value**	**Expected**	**Actual**	**Total**
generation of precursor metabolites and energy	GO:0006091	-5.1	20.9	41	147
pyruvate metabolic process	GO:0006090	-5.1	3.6	13	25
glycolysis	GO:0006096	-5.0	2.3	10	16
glucose metabolic process	GO:0006006	-4.8	6.4	18	45
acetyl-CoA catabolic process	GO:0046356	-4.6	2.0	9	14
tricarboxylic acid cycle	GO:0006099	-4.6	2.0	9	14
primary metabolic process	GO:0044238	-4.6	348.6	397	2454
cellular macromolecule catabolic process	GO:0044265	-4.6	36.9	61	260
macromolecule biosynthetic process	GO:0009059	-4.5	63.2	93	445
endocytosis	GO:0006897	-4.4	11.6	26	82
branched chain family amino acid biosynthetic process	GO:0009082	-4.3	1.7	8	12
ATP metabolic process	GO:0046034	-4.3	2.6	10	18
purine nucleoside triphosphate metabolic process	GO:0009144	-4.3	2.6	10	18
purine ribonucleoside triphosphate metabolic process	GO:0009205	-4.3	2.6	10	18
membrane invagination	GO:0010324	-4.3	12.5	27	88
monovalent inorganic cation transport	GO:0015672	-4.3	3.6	12	25
age-dependent general metabolic decline during chronological cell aging	GO:0001323	-4.2	0.7	5	5
age-dependent response to oxidative stress during chronological cell aging	GO:0001324	-4.2	0.7	5	5
age-dependent response to oxidative stress	GO:0001306	-4.2	0.7	5	5
membrane organization and biogenesis	GO:0016044	-4.2	24.9	44	175
translational initiation	GO:0006413	-4.1	5.3	15	37
coenzyme catabolic process	GO:0009109	-4.1	2.7	10	19
cofactor catabolic process	GO:0051187	-4.1	2.7	10	19
response to oxidative stress	GO:0006979	-4.0	8.9	21	63
oxidoreductase activity	GO:0016491	-12.2	30.0	70	211
catalytic activity	GO:0003824	-6.9	237.9	298	1675
hydrogen ion transmembrane transporter activity	GO:0015078	-6.4	6.7	21	47
monovalent inorganic cation transmembrane transporter activity	GO:0015077	-6.0	7.0	21	49
translation factor activity, nucleic acid binding	GO:0008135	-5.0	5.1	16	36
translation regulator activity	GO:0045182	-4.8	6.4	18	45
metalloexopeptidase activity	GO:0008235	-4.3	1.0	6	7
cytoplasm	GO:0005737	-15.9	419.4	511	2952
cytosol	GO:0005829	-14.1	32.8	78	231
chitin- and beta-glucan-containing cell wall	GO:0009277	-12.1	8.1	31	57
external encapsulating structure	GO:0030312	-12.1	8.1	31	57
cell wall	GO:0005618	-12.1	8.1	31	57

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Table S2A: GO Terms Over-represented in Highly Translated Genes, continued

GO Term	**GO ID**	**$\log_{10}$ *p* value**	**Expected**	**Actual**	**Total**
cell part	GO:0044464	-10.8	610.0	647	4294
cell	GO:0005623	-10.8	610.1	647	4295
cytoplasmic part	GO:0044444	-10.6	294.5	373	2073
nucleoid	GO:0009295	-9.8	3.3	17	23
mitochondrial nucleoid	GO:0042645	-9.8	3.3	17	23
cytosolic ribosome (sensu Eukaryota)	GO:0005830	-8.6	11.9	34	84
cytosolic part	GO:0044445	-8.5	14.3	38	101
mitochondrial membrane part	GO:0044455	-6.3	13.1	32	92
mitochondrion	GO:0005739	-5.9	131.3	178	924
cytosolic large ribosomal subunit (sensu Eukaryota)	GO:0005842	-5.1	5.5	17	39
proton-transporting two-sector ATPase complex, catalytic domain	GO:0033178	-5.0	1.8	9	13
ribosome	GO:0005840	-4.9	34.5	59	243
cell cortex part	GO:0044448	-4.9	12.4	28	87
mitochondrial part	GO:0044429	-4.8	59.0	89	415
cell cortex	GO:0005938	-4.5	13.5	29	95
actin cytoskeleton	GO:0015629	-4.5	10.9	25	77
intracellular part	GO:0044424	-4.4	569.7	601	4010
cortical cytoskeleton	GO:0030863	-4.3	7.4	19	52
cortical actin cytoskeleton	GO:0030864	-4.3	7.4	19	52
mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)	GO:0000275	-4.2	0.7	5	5
proton-transporting ATP synthase complex, catalytic core F(1)	GO:0045261	-4.2	0.7	5	5
mitochondrial respiratory chain	GO:0005746	-4.2	3.1	11	22
actin cortical patch	GO:0030479	-4.1	5.8	16	41

Table S2B: GO Terms Under-represented in Highly Translated Genes

GO Term	GO ID	$\log_{10}$ *p* value	Expected	Actual	Total
nucleus	GO:0005634	-6.7	234.3	177	1649
nuclear part	GO:0044428	-6.0	124.0	81	873

Table S2C: GO Terms Under-represented in Poorly Translated Genes

GO Term	GO ID	$\log_{10}$ *p* value	Expected	Actual	Total
cellular process	GO:0009987	-13.0	510.6	433	3562
ribonucleoprotein complex biogenesis and assembly	GO:0022613	-8.0	51.7	19	361
cellular metabolic process	GO:0044237	-7.9	366.7	300	2558
ribosome biogenesis and assembly	GO:0042254	-7.7	43.1	14	301
metabolic process	GO:0008152	-7.3	380.6	317	2655
primary metabolic process	GO:0044238	-6.9	351.8	290	2454
cellular component organization and biogenesis	GO:0016043	-6.7	278.5	219	1943
vesicle-mediated transport	GO:0016192	-5.6	45.6	20	318
biosynthetic process	GO:0009058	-5.1	108.9	72	760
translation	GO:0006412	-4.6	39.4	18	275
secretion by cell	GO:0032940	-4.3	34.4	15	240
secretion	GO:0046903	-4.3	34.4	15	240
macromolecule metabolic process	GO:0043170	-4.3	300.3	254	2095
nuclear transport	GO:0051169	-4.2	17.2	4	120
nucleocytoplasmic transport	GO:0006913	-4.2	17.2	4	120
secretory pathway	GO:0045045	-4.1	33.5	15	234
structural molecule activity	GO:0005198	-6.9	34.7	10	242
structural constituent of ribosome	GO:0003735	-6.8	19.5	2	136
cell part	GO:0044464	-29.0	615.5	534	4294
cell	GO:0005623	-28.6	615.7	535	4295
intracellular	GO:0005622	-22.4	579.4	493	4042
intracellular part	GO:0044424	-20.5	574.8	491	4010
cytoplasm	GO:0005737	-11.4	423.2	343	2952
macromolecular complex	GO:0032991	-9.5	204.7	138	1428
organelle lumen	GO:0043233	-8.5	103.8	56	724
membrane-enclosed lumen	GO:0031974	-8.5	103.8	56	724
ribosomal subunit	GO:0033279	-7.4	20.9	2	146
cytosolic part	GO:0044445	-6.9	14.5	0	101
organelle	GO:0043226	-6.7	479.2	423	3343
intracellular organelle	GO:0043229	-6.7	479.1	423	3342
ribosome	GO:0005840	-6.4	34.8	11	243
protein complex	GO:0043234	-6.1	159.0	111	1109
cytosolic ribosome (sensu Eukaryota)	GO:0005830	-5.7	12.0	0	84
ribonucleoprotein complex	GO:0030529	-5.1	60.2	32	420
organelle part	GO:0044422	-4.7	272.4	224	1900

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Table S2C: GO Terms Under-represented in Poorly Translated Genes, continued

GO Term	**GO ID**	**$\log_{10} p$ value**	**Expected**	**Actual**	**Total**
intracellular organelle part	GO:0044446	-4.7	272.4	224	1900
large ribosomal subunit	GO:0015934	-4.4	11.9	1	83
nuclear lumen	GO:0031981	-4.3	74.3	46	518
membrane-bound organelle	GO:0043227	-4.3	445.5	401	3108
intracellular membrane-bound organelle	GO:0043231	-4.3	445.5	401	3108

Table S2. GO term analysis of translational efficiency. Gene ontology (GO) term analysis (*S14*) was performed with the GOstats package (*S15*). The 660 genes with translational efficiency at least 1 standard deviation above the median (A,B) and the 666 genes with translational efficiency with translational efficiency at least 1 standard deviation below the median (C) were compared to all 4648 genes with reliable translation measurements. All GO terms over-represented (A) or under-represented (B,C) with $\log_{10} p < -4$ are displayed, sorted by significance within each category. There were no significantly over-represented GO terms amongst the poorly translated genes.

Table S3: All uORFs

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrI@129038to128994	YAL014C	SYN8	aaatagATGcgt	45	-25	5	3	8	64.4	47.3	20.4
chrI@67835to67824	YAL040C	CLN3	agtcaaATGgat	12	304	0	0	3	13.9	16.5	6.4
chrI@62752to62763	YAL041W	CDC24	gtggctATGgta	12	77	0	0	0	19.5	46.5	19.2
chrI@33225to33248	YAL061W	BDH2	cggcagATGcga	24	200	0	1	8	8.5	15.6	6.4
chrI@33252to33275	YAL061W	BDH2	tagttaATGctt	24	173	0	0	8	8.5	15.6	6.4
chrI@33266to33352	YAL061W	BDH2	gataaaATGtat	87	96	0	0	8	8.5	15.6	6.4
chrI@33287to33352	YAL061W	BDH2	gtcgtaATGtgc	66	96	0	0	8	8.5	15.6	6.4
chrI@158892to158978	YAR008W	SEN34	tcgtatATGgct	87	-12	9	14	10	57.5	98.9	9.9
chrI@179999to179940	YAR023C		ttaaacATGcaa	60	123	5	6	7	31.9	29.9	1.5
chrI@179972to179940	YAR023C		acactcATGtca	33	123	1	3	7	31.9	29.9	1.5
chrI@179876to179817	YAR023C		cagaggATGagt	60	0	0	13	7	31.9	29.9	1.5
chrII@207174to207191	YBL009W	ALK2	acatacATGcgc	18	5	15	2	8	11.1	16.8	21.5
chrII@192273to192299	YBL016W	FUS3	ttttagATGatg	27	154	0	0	1	32.4	74.9	31.4
chrII@192276to192299	YBL016W	FUS3	tagatgATGcgg	24	154	0	0	1	32.4	74.9	31.4
chrII@186489to186457	YBL018C	POP8	tgataaATGgcc	33	-19	1	2	1	128.7	207.0	63.2
chrII@182258to182302	YBL020W	RFT1	cgtaatATGgta	45	101	0	2	4	32.4	74.5	14.9
chrII@182322to182360	YBL020W	RFT1	aagacaATGcgt	39	43	4	4	4	32.4	74.5	14.9
chrII@171359to171367	YBL025W	RRN10	aagcgaATGtca	9	116	0	0	3	47.8	133.4	29.5
chrII@171364to171390	YBL025W	RRN10	aatgtcATGaaa	27	93	0	0	3	47.8	133.4	29.5
chrII@171369to171398	YBL025W	RRN10	catgaaATGcag	30	85	0	0	3	47.8	133.4	29.5
chrII@171399to171464	YBL025W	RRN10	aagtaaATGttt	66	19	2	14	3	47.8	133.4	29.5
chrII@164851to164822	YBL029C-A		gaataaATGtca	30	48	16	10	17	55.8	89.3	35.9
chrII@153758to153744	YBL035C	POL12	aataatATGagc	15	132	0	0	1	19.9	15.6	21.8
chrII@143191to143238	YBL039W-B		agagcgATGaag	48	157	12	7	15	71.7	80.3	18.1
chrII@136557to136610	YBL043W	ECM13	ccctgtATGacc	54	80	0	3	0	11.9	4.1	0.8
chrII@92363to93394	YBL068W	PRS4	tacataATGcac	1032	-983	2	14	5	94.9	154.4	85.9
chrII@86577to86473	YBL075C	SSA3	taagggATGtat	105	28	0	21	0	41.1	37.0	5.3
chrII@86549to86529	YBL075C	SSA3	aaacgaATGgaa	21	84	0	1	0	41.1	37.0	5.3
chrII@86500to86468	YBL075C	SSA3	tcttgtATGtca	33	23	0	11	0	41.1	37.0	5.3
chrII@86494to86468	YBL075C	SSA3	atgtcaATGttt	27	23	0	8	0	41.1	37.0	5.3
chrII@254274to254251	YBR008C	FLR1	atccttATGccg	24	42	0	2	0	18.7	23.6	0.1
chrII@254257to254240	YBR008C	FLR1	gtcattATGgtg	18	31	0	1	0	18.7	23.6	0.1
chrII@324008to323898	YBR043C	QDR3	aggcatATGtat	111	-46	11	26	12	62.3	70.2	2.2
chrII@323975to323898	YBR043C	QDR3	acgtctATGcta	78	-46	5	6	12	62.3	70.2	2.2
chrII@326071to326063	YBR044C	TCM62	tctcttATGctt	9	6	8	4	9	57.8	63.2	8.9
chrII@340779to340771	YBR053C		gtttatATGcat	9	23	0	0	0	27.8	79.8	42.0
chrII@392368to392360	YBR077C	SLM4	actctaATGaat	9	74	0	0	2	64.2	162.3	94.1
chrII@409034to409060	YBR083W	TEC1	ttacatATGaca	27	102	0	3	2	24.5	16.2	31.1
chrII@409061to409159	YBR083W	TEC1	ttataaATGttt	99	3	2	12	2	24.5	16.2	31.1
chrII@409067to409159	YBR083W	TEC1	atgtttATGaaa	93	3	0	10	2	24.5	16.2	31.1
chrII@423096to423061	YBR086C	IST2	cgatttATGgct	36	27	28	7	36	23.4	46.0	57.3
chrII@451993to451952	YBR105C	VID24	ttgtgcATGaca	42	-10	0	2	0	53.4	17.3	8.5
chrII@454629to454612	YBR107C	IML3	aaaaaaATGccg	18	89	0	0	1	8.0	24.1	3.3
chrII@454615to454607	YBR107C	IML3	accgatATGaaa	9	84	0	0	1	8.0	24.1	3.3
chrII@454589to454560	YBR107C	IML3	agtgggATGatc	30	37	1	2	1	8.0	24.1	3.3

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrII@454572to454396	YBR107C	IML3	`gactgcATGgtt`	177	-127	1	4	1	8.0	24.1	3.3
chrII@454528to454499	YBR107C	IML3	`ctttggATGgaa`	30	-24	0	0	1	8.0	24.1	3.3
chrII@479279to479323	YBR119W	MUD1	`aaaaaaATGgaa`	45	8	1	5	1	17.9	40.3	17.6
chrII@494113to494072	YBR128C	ATG14	`cctagtATGaca`	42	-36	0	0	2	22.9	19.3	1.6
chrII@554434to554267	YBR157C	ICS2	`aaataaATGaga`	168	-36	6	48	6	69.2	128.7	30.8
chrII@554393to554388	YBR157C	ICS2	`acaaatATGtga`	6	85	1	0	6	69.2	128.7	30.8
chrII@556326to556334	YBR158W	AMN1	`aactatATGtgt`	9	208	13	14	41	441.6	247.2	41.1
chrII@565172to565183	YBR162W-A	YSY6	`cattacATGcag`	12	42	1	5	2	223.6	694.9	570.1
chrII@595918to595929	YBR183W	YPC1	`ttatatATGtct`	12	180	0	2	3	128.2	50.0	6.5
chrII@599958to599950	YBR185C	MBA1	`aagcttATGaga`	9	-3	0	0	0	66.8	54.4	25.6
chrII@602514to602531	YBR187W	GDT1	`acgtttATGaaa`	18	97	24	29	10	327.0	420.0	144.9
chrII@614474to614430	YBR196C-A		`tcggacATGcta`	45	263	0	3	0	11.7	14.5	0.0
chrII@614386to614312	YBR196C-A		`tgaactATGttg`	75	145	0	3	0	11.7	14.5	0.0
chrII@614321to614292	YBR196C-A		`aaaaatATGtca`	30	125	0	3	0	11.7	14.5	0.0
chrII@614315to614292	YBR196C-A		`atgtcaATGagg`	24	125	0	3	0	11.7	14.5	0.0
chrII@614298to614209	YBR196C-A		`accgggATGgta`	90	42	0	1	0	11.7	14.5	0.0
chrII@620815to620838	YBR200W	BEM1	`atatggATGcac`	24	28	6	3	1	21.7	47.4	24.4
chrII@642514to642452	YBR208C	DUR1,2	`acgcagATGttt`	63	248	9	48	14	98.3	13.7	6.2
chrII@642451to642431	YBR208C	DUR1,2	`aattgaATGttt`	21	227	0	8	14	98.3	13.7	6.2
chrII@642425to642390	YBR208C	DUR1,2	`gagcagATGagg`	36	186	0	17	14	98.3	13.7	6.2
chrII@653262to653306	YBR215W	HPC2	`cacacaATGcag`	45	44	0	1	0	10.1	24.8	22.9
chrII@653274to653306	YBR215W	HPC2	`aaactgATGcgg`	33	44	0	1	0	10.1	24.8	22.9
chrII@657818to657829	YBR217W	ATG12	`gaaccaATGaca`	12	-3	0	2	0	84.3	97.1	5.5
chrII@668444to668436	YBR222C	PCS60	`atagagATGgta`	9	91	0	0	0	14.4	42.0	64.4
chrII@668439to668419	YBR222C	PCS60	`gatggtATGatt`	21	74	0	1	0	14.4	42.0	64.4
chrII@668415to668371	YBR222C	PCS60	`taatagATGctc`	45	26	0	2	0	14.4	42.0	64.4
chrII@699950to699921	YBR239C		`acattgATGaat`	30	-16	0	2	1	14.2	8.1	4.1
chrII@704558to704596	YBR242W		`cactgaATGgtt`	39	68	6	12	15	72.6	93.0	50.5
chrII@723227to723286	YBR253W	SRB6	`attgtgATGata`	60	-22	8	35	8	239.0	152.4	47.1
chrII@749569to749676	YBR274W	CHK1	`ctgtatATGggc`	108	-88	1	1	1	20.7	55.4	7.5
chrII@784700to784674	YBR291C	CTP1	`agaacaATGaaa`	27	107	0	0	5	28.8	80.4	17.1
chrII@784658to784641	YBR291C	CTP1	`cgtaaaATGtcg`	18	74	0	0	5	28.8	80.4	17.1
chrII@784624to784613	YBR291C	CTP1	`attttgATGtca`	12	46	0	2	5	28.8	80.4	17.1
chrII@784616to784590	YBR291C	CTP1	`gtcacaATGaaa`	27	23	1	7	5	28.8	80.4	17.1
chrII@792794to792817	YBR295W	PCA1	`ttcgagATGctt`	24	25	5	1	7	4.0	7.5	1.3
chrII@792814to792906	YBR295W	PCA1	`tatacaATGaaa`	93	-64	3	0	7	4.0	7.5	1.3
chrIII@103401to103342	YCL011C	GBP2	`taagctATGggc`	60	-15	1	51	1	527.4	365.0	119.6
chrIII@83424to83486	YCL021W-A		`ccctccATGctc`	63	133	0	13	0	33.6	38.5	0.0
chrIII@83448to83486	YCL021W-A		`aaccctATGtgg`	39	133	0	9	0	33.6	38.5	0.0
chrIII@83463to83486	YCL021W-A		`tcgattATGcga`	24	133	0	4	0	33.6	38.5	0.0
chrIII@83532to83546	YCL021W-A		`agtgaaATGgaa`	15	73	0	1	0	33.6	38.5	0.0
chrIII@78006to77938	YCL025C	AGP1	`tctttgATGgtc`	69	20	0	8	2	27.6	36.3	12.7
chrIII@77989to77984	YCL025C	AGP1	`acaacaATGtag`	6	66	0	1	2	27.6	36.3	12.7
chrIII@77971to77966	YCL025C	AGP1	`tttattATGtaa`	6	48	0	1	2	27.6	36.3	12.7
chrIII@126903to126874	YCR007C		`ggggctATGctt`	30	147	0	1	0	11.2	27.2	6.9
chrIII@126837to126802	YCR007C		`gagtttATGaac`	36	75	0	1	0	11.2	27.2	6.9

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrIII@126807to126802	YCR007C		`ctgaaaATGtaa`	6	75	0	1	0	11.2	27.2	6.9
chrIII@155266to155295	YCR020W-B	HTL1	`aattttATGata`	30	22	4	13	3	117.6	326.8	162.2
chrIII@160424to160374	YCR023C		`aaaggaATGcta`	51	6	17	10	17	40.1	47.6	9.8
chrIII@160391to160374	YCR023C		`aagcatATGaac`	18	6	5	2	17	40.1	47.6	9.8
chrIII@179390to179395	YCR032W	BPH1	`tcgttgATGtga`	6	120	0	0	0	22.8	12.7	2.7
chrIII@186240to186245	YCR033W	SNT1	`tgaattATGtaa`	6	239	0	0	5	13.7	24.7	14.5
chrIII@223318to223304	YCR057C	PWP2	`ctaggtATGtac`	15	81	0	1	2	45.1	73.3	36.9
chrIII@238849to238920	YCR069W	CPR4	`taaataATGtat`	72	130	0	2	11	25.8	38.4	60.4
chrIII@267135to267146	YCR089W	FIG2	`accataATGctg`	12	284	1	0	7	7.1	4.1	1.3
chrIII@267175to267234	YCR089W	FIG2	`aagtgtATGgta`	60	196	1	2	7	7.1	4.1	1.3
chrIII@267182to267223	YCR089W	FIG2	`tggtacATGgtg`	42	207	0	2	7	7.1	4.1	1.3
chrIII@267196to267234	YCR089W	FIG2	`ttccttATGctc`	39	196	1	2	7	7.1	4.1	1.3
chrIII@267227to267256	YCR089W	FIG2	`tagtctATGtat`	30	174	1	1	7	7.1	4.1	1.3
chrIII@267263to267274	YCR089W	FIG2	`gctacaATGgaa`	12	156	3	0	7	7.1	4.1	1.3
chrIII@267284to267325	YCR089W	FIG2	`taagaaATGcat`	42	105	1	2	7	7.1	4.1	1.3
chrIII@267288to267314	YCR089W	FIG2	`aaatgcATGaag`	27	116	0	2	7	7.1	4.1	1.3
chrIII@267336to267485	YCR089W	FIG2	`agtacaATGgaa`	150	-55	2	3	7	7.1	4.1	1.3
chrIV@447616to447578	YDL002C	NHP10	`aattggATGaga`	39	4	2	28	5	189.1	224.4	53.7
chrIV@366054to366049	YDL049C	KNH1	`acgaacATGtaa`	6	176	0	1	3	50.7	13.6	2.3
chrIV@366033to366004	YDL049C	KNH1	`gacattATGtgc`	30	131	2	9	3	50.7	13.6	2.3
chrIV@366021to366004	YDL049C	KNH1	`tcgttcATGtat`	18	131	1	5	3	50.7	13.6	2.3
chrIV@366007to365999	YDL049C	KNH1	`tattacATGagg`	9	126	0	2	3	50.7	13.6	2.3
chrIV@365968to365948	YDL049C	KNH1	`gtatcgATGaaa`	21	75	1	2	3	50.7	13.6	2.3
chrIV@352706to352717	YDL056W	MBP1	`caacagATGaaa`	12	159	0	0	4	20.8	29.8	13.7
chrIV@352714to352797	YDL056W	MBP1	`gaaaaaATGaaa`	84	79	1	2	4	20.8	29.8	13.7
chrIV@345018to344965	YDL059C	RAD59	`tagcacATGctt`	54	13	5	11	5	38.9	44.3	8.9
chrIV@337300to336248	YDL065C	PEX19	`gaagaaATGcca`	1053	-1028	1	3	0	40.1	96.0	62.6
chrIV@326562to326609	YDL073W		`cttcgtATGcta`	48	3	3	7	4	58.7	71.6	8.8
chrIV@326180to326145	YDL074C	BRE1	`gtttttATGcta`	36	-3	1	16	2	108.9	134.1	38.5
chrIV@321654to321640	YDL076C	RXT3	`aattccATGaca`	15	89	6	2	11	100.1	159.2	27.9
chrIV@222371to222394	YDL133W		`aagtgaATGata`	24	32	17	10	18	95.5	130.3	13.8
chrIV@192698to192709	YDL146W	LDB17	`taacttATGtca`	12	41	5	3	6	45.2	22.8	5.3
chrIV@141749to141714	YDL177C		`gtattgATGttt`	36	-7	8	6	17	106.0	157.1	11.2
chrIV@135609to135725	YDL180W		`tgactaATGtca`	117	171	1	6	11	42.9	82.5	8.1
chrIV@135649to135672	YDL180W		`gtcccaATGcgg`	24	224	1	0	11	42.9	82.5	8.1
chrIV@135687to135725	YDL180W		`tggaacATGgaa`	39	171	0	3	11	42.9	82.5	8.1
chrIV@122080to122166	YDL189W	RBS1	`gacagtATGttg`	87	50	2	9	3	30.9	39.0	31.2
chrIV@122102to122128	YDL189W	RBS1	`cttataATGggc`	27	88	0	2	3	30.9	39.0	31.2
chrIV@104619to104605	YDL198C	GGC1	`cttttgATGgtt`	15	54	15	5	16	40.4	52.9	72.7
chrIV@101078to101064	YDL200C	MGT1	`atctaaATGgac`	15	-3	3	6	0	57.2	89.4	26.1
chrIV@94350to94370	YDL204W	RTN2	`tttgagATGctt`	21	235	0	2	0	30.3	13.2	0.7
chrIV@94499to94525	YDL204W	RTN2	`actttgATGaaa`	27	80	0	5	0	30.3	13.2	0.7
chrIV@94540to94545	YDL204W	RTN2	`tcaattATGtag`	6	60	0	1	0	30.3	13.2	0.7
chrIV@93874to93848	YDL205C	HEM3	`gtttgcATGgta`	27	103	4	12	8	118.0	149.1	40.4
chrIV@90141to90170	YDL206W		`ttgtaaATGcta`	30	6	5	3	2	30.8	17.8	1.6
chrIV@483903to483862	YDR018C		`aaagaaATGaac`	42	6	0	4	0	20.7	1.5	1.0

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrIV@521236to521262	YDR034W-B		atttaaATGttt	27	48	0	0	0	6.0	5.1	10.4
chrIV@521249to521257	YDR034W-B		tcagttATGttg	9	53	0	0	0	6.0	5.1	10.4
chrIV@548367to548356	YDR045C	RPC11	cgttatATGgct	12	49	32	18	34	333.2	352.7	117.6
chrIV@550626to550573	YDR046C	BAP3	ctattgATGgat	54	0	11	30	17	129.2	125.3	44.6
chrIV@551675to551710	YDR047W	HEM12	agcgaaATGttc	36	147	0	13	6	93.9	143.2	38.6
chrIV@551713to551736	YDR047W	HEM12	ttagtgATGttc	24	121	4	10	6	93.9	143.2	38.6
chrIV@583472to583410	YDR067C		agctatATGtat	63	-52	0	0	4	118.3	162.1	20.7
chrIV@587727to587689	YDR069C	DOA4	tgatacATGctt	39	-27	0	1	3	21.5	10.3	6.0
chrIV@592335to592400	YDR073W	SNF11	ccgtttATGata	66	35	7	5	7	30.5	32.1	22.6
chrIV@592389to592400	YDR073W	SNF11	aattcaATGtgc	12	35	1	1	7	30.5	32.1	22.6
chrIV@602984to602976	YDR078C	SHU2	agcaagATGcgc	9	111	1	0	1	20.2	75.8	8.0
chrIV@602909to602895	YDR078C	SHU2	ttggtgATGaag	15	30	0	0	1	20.2	75.8	8.0
chrIV@610359to610409	YDR082W	STN1	gaatatATGaaa	51	28	2	19	7	75.4	95.0	1.4
chrIV@610424to610444	YDR082W	STN1	ttaataATGggt	21	-7	4	4	7	75.4	95.0	1.4
chrIV@614007to613921	YDR084C	TVP23	ttacgaATGaaa	87	-79	0	0	0	51.4	97.8	54.8
chrIV@626107to626048	YDR090C		taaataATGctt	60	54	1	6	0	38.4	68.1	18.7
chrIV@658134to658139	YDR103W	STE5	ggcgatATGtag	6	207	0	0	0	11.1	37.1	15.5
chrIV@658158to658193	YDR103W	STE5	cacatcATGtac	36	153	0	3	0	11.1	37.1	15.5
chrIV@658180to658200	YDR103W	STE5	caaaatATGaaa	21	146	0	0	0	11.1	37.1	15.5
chrIV@699484to699425	YDR123C	INO2	aaatacATGgaa	60	-39	1	1	5	18.2	38.9	11.9
chrIV@704325to704360	YDR127W	ARO1	ccgcaaATGtcg	36	120	0	0	1	34.7	30.0	86.2
chrIV@751488to751658	YDR147W	EKI1	aagtgtATGcaa	171	-31	1	33	1	52.2	82.0	15.5
chrIV@751510to751527	YDR147W	EKI1	caatagATGtcg	18	100	0	8	1	52.2	82.0	15.5
chrIV@784231to784199	YDR164C	SEC1	gtgcacATGctt	33	-12	1	1	3	17.8	26.7	16.5
chrIV@819220to819113	YDR179C	CSN9	acagtgATGacc	108	-79	1	6	1	25.6	69.7	21.0
chrIV@819421to819465	YDR179W-A		ttctatATGtgt	45	-36	0	0	0	31.0	69.0	8.6
chrIV@827365to827330	YDR181C	SAS4	aagcatATGaga	36	-21	3	3	4	50.1	51.3	9.4
chrIV@829564to829596	YDR183W	PLP1	acgtatATGaag	33	-15	5	2	7	44.5	55.9	35.0
chrIV@867535to867512	YDR207C	UME6	atttgcATGgac	24	-6	1	0	2	16.4	12.8	13.0
chrIV@930875to931036	YDR234W	LYS4	taatcgATGagt	162	88	3	41	11	56.2	74.6	47.3
chrIV@930932to931036	YDR234W	LYS4	aatctcATGtcc	105	88	3	35	11	56.2	74.6	47.3
chrIV@946535to946552	YDR242W	AMD2	agtattATGtgt	18	250	0	3	6	13.4	27.5	1.1
chrIV@946589to946645	YDR242W	AMD2	tctcaaATGccg	57	157	1	3	6	13.4	27.5	1.1
chrIV@946611to946619	YDR242W	AMD2	ttgctcATGata	9	183	0	0	6	13.4	27.5	1.1
chrIV@946634to946645	YDR242W	AMD2	aataatATGata	12	157	1	1	6	13.4	27.5	1.1
chrIV@946642to946863	YDR242W	AMD2	gataatATGata	222	-61	5	11	6	13.4	27.5	1.1
chrIV@946732to946863	YDR242W	AMD2	ttttcaATGggg	132	-61	5	8	6	13.4	27.5	1.1
chrIV@952778to952843	YDR245W	MNN10	ttgtgcATGtac	66	-48	1	18	5	346.8	303.3	57.6
chrIV@958354to958334	YDR248C		aagcgtATGgat	21	0	3	8	3	95.6	91.9	27.9
chrIV@958350to958300	YDR248C		gtatggATGgac	51	-34	3	7	3	95.6	91.9	27.9
chrIV@964678to964652	YDR253C	MET32	ctatccATGgta	27	92	0	1	1	9.3	7.6	4.3
chrIV@964669to964652	YDR253C	MET32	gtatatATGtat	18	92	0	1	1	9.3	7.6	4.3
chrIV@964665to964648	YDR253C	MET32	atatgtATGcat	18	88	0	2	1	9.3	7.6	4.3
chrIV@964637to964605	YDR253C	MET32	ggtttcATGtca	33	45	0	2	1	9.3	7.6	4.3
chrIV@964630to964613	YDR253C	MET32	tgtcatATGcca	18	53	0	2	1	9.3	7.6	4.3
chrIV@1019240to1019266	YDR279W	RNH202	agcgcgATGaga	27	97	1	0	6	29.7	73.7	24.8

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5' UTR # Rib	5' UTR mRNA	CDS mRNA	CDS Rib
chrIV@1019266to1019328	YDR279W	RNH202	`tggttaATGatt`	63	35	5	9	6	29.7	73.7	24.8
chrIV@1030052to1030035	YDR283C	GCN2	`catactATGtat`	18	-9	0	1	25	18.3	19.8	11.2
chrIV@1037144to1037170	YDR288W	NSE3	`atcagtATGcta`	27	20	2	12	0	181.5	138.0	17.6
chrIV@1062912to1062898	YDR300C	PRO1	`gaactaATGctt`	15	112	0	0	2	39.4	152.1	66.7
chrIV@1062901to1062863	YDR300C	PRO1	`ttctcgATGaat`	39	77	0	0	2	39.4	152.1	66.7
chrIV@1062863to1062783	YDR300C	PRO1	`agattaATGtct`	81	-3	2	22	2	39.4	152.1	66.7
chrIV@1078457to1078434	YDR308C	SRB7	`cattatATGctc`	24	-10	2	9	4	228.9	154.1	67.9
chrIV@1116860to1116916	YDR325W	YCG1	`aaaatcATGggg`	57	204	1	3	1	15.5	40.5	7.0
chrIV@1116890to1116916	YDR325W	YCG1	`gagataATGcag`	27	204	0	1	1	15.5	40.5	7.0
chrIV@1117002to1117013	YDR325W	YCG1	`ccgcatATGaaa`	12	107	0	2	1	15.5	40.5	7.0
chrIV@1117073to1117225	YDR325W	YCG1	`tcagtaATGcct`	153	-105	0	3	1	15.5	40.5	7.0
chrIV@1130927to1130998	YDR332W	IRC3	`ttcataATGtca`	72	-3	0	7	2	45.1	30.1	2.5
chrIV@1130979to1131017	YDR332W	IRC3	`ggagccATGagt`	39	-22	0	0	2	45.1	30.1	2.5
chrIV@1135874to1135942	YDR334W	SWR1	`aaatttATGaat`	69	-16	19	6	21	25.8	20.9	6.5
chrIV@1149550to1149521	YDR338C		`tatttgATGctg`	30	62	0	3	0	25.3	36.9	11.0
chrIV@1178180to1178160	YDR350C	ATP22	`actttaATGttc`	21	-6	1	2	10	89.0	61.2	3.9
chrIV@1178259to1178264	YDR351W	SBE2	`atcttcATGtaa`	6	394	0	0	14	20.8	37.7	16.1
chrIV@1178281to1178475	YDR351W	SBE2	`cctttttATGcaa`	195	183	0	3	14	20.8	37.7	16.1
chrIV@1178293to1178475	YDR351W	SBE2	`tctataATGtta`	183	183	0	3	14	20.8	37.7	16.1
chrIV@1178364to1178369	YDR351W	SBE2	`aaagagATGtaa`	6	289	0	0	14	20.8	37.7	16.1
chrIV@1189625to1189596	YDR357C		`ttttacATGaaa`	30	37	10	23	9	156.1	146.3	38.3
chrIV@1198786to1198778	YDR362C	TFC6	`agtttcATGtcc`	9	90	1	0	2	37.6	41.0	11.2
chrIV@1204224to1204192	YDR364C	CDC40	`cacggcATGtac`	33	-9	0	3	3	37.1	87.0	12.6
chrIV@1204206to1204192	YDR364C	CDC40	`gagcagATGaaa`	15	-9	0	0	3	37.1	87.0	12.6
chrIV@1206467to1206441	YDR365C	ESF1	`agcataATGgta`	27	67	0	29	1	176.5	250.2	64.3
chrIV@1233555to1233550	YDR379C-A		`aagataATGtag`	6	42	2	0	6	65.4	100.1	20.4
chrIV@1230147to1230200	YDR379W	RGA2	`attttgATGaaa`	54	-42	3	0	4	10.1	22.1	8.3
chrIV@1249921to1249895	YDR387C		`ccttatATGtgc`	27	83	0	7	10	38.1	53.0	2.5
chrIV@1249891to1249820	YDR387C		`tagtccATGgtc`	72	8	10	12	10	38.1	53.0	2.5
chrIV@1258574to1258579	YDR392W	SPT3	`cgaaccATGtaa`	6	108	0	0	0	24.1	51.1	15.0
chrIV@1267332to1267340	YDR398W	UTP5	`gaagcgATGagg`	9	122	0	1	4	94.6	178.7	55.8
chrIV@1267369to1267401	YDR398W	UTP5	`ggatatATGtat`	33	61	2	11	4	94.6	178.7	55.8
chrIV@1267373to1267378	YDR398W	UTP5	`atatgtATGtaa`	6	84	0	2	4	94.6	178.7	55.8
chrIV@1267385to1267417	YDR398W	UTP5	`agatagATGcag`	33	45	3	12	4	94.6	178.7	55.8
chrIV@1270940to1272076	YDR400W	URH1	`cttttgATGgaa`	1137	-1022	0	2	1	11.6	39.3	27.2
chrIV@1296820to1296785	YDR414C	ERD1	`atattgATGgca`	36	108	1	9	6	77.3	54.3	14.2
chrIV@1317932to1317918	YDR422C	SIP1	`tctctgATGgaa`	15	154	0	0	0	7.4	25.7	15.4
chrIV@1317908to1315317	YDR422C	SIP1	`ttaacaATGgta`	2592	-2447	0	6	0	7.4	25.7	15.4
chrIV@1338020to1338136	YDR438W	THI74	`cataatATGggg`	117	129	0	16	0	24.8	36.8	0.0
chrIV@1338034to1338066	YDR438W	THI74	`actggaATGtat`	33	199	0	8	0	24.8	36.8	0.0
chrIV@1338038to1338136	YDR438W	THI74	`gaatgtATGcac`	99	129	0	12	0	24.8	36.8	0.0
chrIV@1338060to1338074	YDR438W	THI74	`tattatATGgtg`	15	191	0	1	0	24.8	36.8	0.0
chrIV@1338074to1338136	YDR438W	THI74	`gctgtaATGctt`	63	129	0	5	0	24.8	36.8	0.0
chrIV@1338150to1338224	YDR438W	THI74	`atatagATGaaa`	75	41	0	10	0	24.8	36.8	0.0
chrIV@1338162to1338224	YDR438W	THI74	`gttgaaATGaat`	63	41	0	10	0	24.8	36.8	0.0
chrIV@1338190to1338249	YDR438W	THI74	`ataataATGcag`	60	16	0	4	0	24.8	36.8	0.0

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrIV@1338217to1338249	YDR438W	THI74	`ttagatATGtat`	33	16	0	0	0	24.8	36.8	0.0
chrIV@1338230to1338256	YDR438W	THI74	`agagtgATGgta`	27	9	0	2	0	24.8	36.8	0.0
chrIV@1339425to1339478	YDR439W	LRS4	`aattatATGtct`	54	189	0	5	6	13.3	20.9	14.4
chrIV@1339456to1339527	YDR439W	LRS4	`aagttaATGtct`	72	140	0	4	6	13.3	20.9	14.4
chrIV@1339466to1339567	YDR439W	LRS4	`ctataaATGccc`	102	100	2	4	6	13.3	20.9	14.4
chrIV@1339500to1339517	YDR439W	LRS4	`ttttgcATGgta`	18	150	0	0	6	13.3	20.9	14.4
chrIV@1339505to1339567	YDR439W	LRS4	`catggtATGtat`	63	100	2	0	6	13.3	20.9	14.4
chrIV@1339564to1339572	YDR439W	LRS4	`aagaaaATGatg`	9	95	2	0	6	13.3	20.9	14.4
chrIV@1339567to1339572	YDR439W	LRS4	`aaaatgATGtga`	6	95	2	0	6	13.3	20.9	14.4
chrIV@1345232to1345020	YDR441C	APT2	`aatcttATGttg`	213	-33	2	42	2	44.1	38.0	42.1
chrIV@1345084to1345040	YDR441C	APT2	`gtgtatATGcct`	45	-13	0	7	2	44.1	38.0	42.1
chrIV@1362719to1362748	YDR452W	PPN1	`ggttttATGgta`	30	121	6	3	5	109.8	132.7	27.7
chrIV@1383438to1383388	YDR459C	PFA5	`ttgtatATGaat`	51	-46	0	0	0	46.7	87.6	5.1
chrIV@1385760to1385515	YDR461C-A		`cagattATGatg`	246	-242	0	0	0	150.2	114.4	51.3
chrIV@1395105to1395122	YDR466W	PKH3	`attggtATGaca`	18	-10	0	0	0	19.8	20.1	8.2
chrIV@1417130to1417141	YDR480W	DIG2	`aaagtgATGcac`	12	249	0	1	6	13.6	23.9	12.9
chrIV@1417138to1417185	YDR480W	DIG2	`gcacgtATGatg`	48	205	4	3	6	13.6	23.9	12.9
chrIV@1417141to1417185	YDR480W	DIG2	`cgtatgATGata`	45	205	4	3	6	13.6	23.9	12.9
chrIV@1417195to1417251	YDR480W	DIG2	`tgtgatATGtca`	57	139	0	1	6	13.6	23.9	12.9
chrIV@1417251to1417274	YDR480W	DIG2	`tacataATGtgc`	24	116	0	0	6	13.6	23.9	12.9
chrIV@1417304to1417351	YDR480W	DIG2	`ttattaATGtta`	48	39	2	4	6	13.6	23.9	12.9
chrIV@1417341to1417355	YDR480W	DIG2	`gtatttATGtgg`	15	35	0	1	6	13.6	23.9	12.9
chrIV@1420927to1420916	YDR482C	CWC21	`tcaagaATGgca`	12	87	0	1	0	35.8	78.2	22.6
chrIV@1421091to1421102	YDR483W	KRE2	`cattttATGaat`	12	46	7	3	4	70.7	226.6	150.9
chrIV@1468513to1468463	YDR508C	GNP1	`tgctttATGttt`	51	28	12	24	12	91.4	196.8	116.4
chrIV@1477114to1477158	YDR517W	GRH1	`aaagaaATGggc`	45	72	0	4	1	51.2	85.9	48.4
chrIV@1488995to1488981	YDR524C	AGE1	`ttctggATGttc`	15	0	13	2	13	34.2	21.3	10.4
chrIV@1489297to1489305	YDR524W-C		`tagataATGaat`	9	89	0	0	0	3.6	2.2	0.0
chrIV@1498206to1498298	YDR531W		`gagtgcATGcga`	93	-75	0	9	0	155.8	177.1	43.4
chrIV@1520864to1520856	YDR541C		`agggatATGata`	9	175	2	0	2	18.0	28.2	2.8
chrV@140123to140112	YEL009C	GCN4	`tgaaaaATGgct`	12	350	698	25	878	407.8	614.3	38.4
chrV@140055to140047	YEL009C	GCN4	`agaattATGtgt`	9	285	26	6	878	407.8	614.3	38.4
chrV@139938to139927	YEL009C	GCN4	`gctatcATGtac`	12	165	61	13	878	407.8	614.3	38.4
chrV@139913to139902	YEL009C	GCN4	`ttcaagATGttt`	12	140	14	19	878	407.8	614.3	38.4
chrV@126337to126281	YEL016C	NPP2	`gcgttgATGgaa`	57	64	4	11	5	67.2	69.0	5.0
chrV@126313to126281	YEL016C	NPP2	`ctttatATGact`	33	64	1	6	5	67.2	69.0	5.0
chrV@84571to84551	YEL036C	ANP1	`gctttcATGcaa`	21	0	1	4	4	73.7	115.8	38.1
chrV@69663to69674	YEL044W	IES6	`tgaggaATGgaa`	12	82	1	0	1	58.2	213.0	45.9
chrV@42706to42638	YEL059C-A	SOM1	`atagagATGgac`	69	15	0	6	0	16.4	17.6	10.0
chrV@31249to31238	YEL064C	AVT2	`atatacATGttc`	12	0	1	0	0	80.1	36.7	8.1
chrV@27538to27546	YEL065W	SIT1	`tttgtgATGcga`	9	110	2	2	2	31.1	90.2	31.1
chrV@27543to27617	YEL065W	SIT1	`gatgcgATGatt`	75	39	2	8	2	31.1	90.2	31.1
chrV@27568to27591	YEL065W	SIT1	`taagcaATGgac`	24	65	0	2	2	31.1	90.2	31.1
chrV@27588to27617	YEL065W	SIT1	`tcaccgATGagg`	30	39	0	2	2	31.1	90.2	31.1
chrV@13599to13634	YEL072W	RMD6	`aacagtATGgat`	36	85	10	6	8	38.2	53.1	2.7
chrV@13696to13719	YEL072W	RMD6	`tctatcATGccc`	24	0	0	6	8	38.2	53.1	2.7

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrV@164468to164482	YER007W	PAC2	tttattATGttt	15	43	0	3	0	54.8	44.1	6.2
chrV@164500to164523	YER007W	PAC2	tataaaATGcaa	24	2	0	4	0	54.8	44.1	6.2
chrV@211952to211932	YER028C	MIG3	cttgccATGagt	21	58	0	1	0	4.4	8.4	5.2
chrV@213414to213896	YER030W	CHZ1	caatacATGgaa	483	-461	5	1	5	58.4	171.8	179.5
chrV@254417to254400	YER050C	RSM18	agatgaATGcca	18	15	10	6	8	87.6	210.3	81.7
chrV@259734to259720	YER053C	PIC2	cagtcaATGaca	15	83	1	0	1	29.0	31.2	10.0
chrV@280864to280814	YER062C	HOR2	cttttgATGttg	51	135	1	0	3	20.9	67.6	80.3
chrV@280836to280804	YER062C	HOR2	atatatATGcgc	33	125	1	1	3	20.9	67.6	80.3
chrV@287152to287147	YER065C	ICL1	cccagtATGtga	6	236	1	1	1	7.2	14.5	0.5
chrV@303882to303887	YER073W	ALD5	agccccATGtaa	6	139	1	0	9	123.4	209.1	167.8
chrV@335619to335605	YER088C	DOT6	cgtcccATGagg	15	422	0	0	1	14.9	48.5	39.5
chrV@335590to335414	YER088C	DOT6	gcgcggATGttt	177	231	0	5	1	14.9	48.5	39.5
chrV@335581to335414	YER088C	DOT6	tttccgATGcaa	168	231	0	5	1	14.9	48.5	39.5
chrV@335565to335284	YER088C	DOT6	gaaaggATGgac	282	101	0	16	1	14.9	48.5	39.5
chrV@348468to348448	YER093C-A		attaggATGggg	21	53	0	1	0	11.8	22.2	18.7
chrV@349545to349540	YER094C	PUP3	gtagtcATGtga	6	199	0	0	8	202.3	571.4	190.2
chrV@349535to349446	YER094C	PUP3	gaccggATGgca	90	105	0	0	8	202.3	571.4	190.2
chrV@349506to349492	YER094C	PUP3	gtgcaaATGcag	15	151	0	0	8	202.3	571.4	190.2
chrV@349495to349430	YER094C	PUP3	ggggcgATGaaa	66	89	0	6	8	202.3	571.4	190.2
chrV@349470to349462	YER094C	PUP3	gagtttATGgca	9	121	0	0	8	202.3	571.4	190.2
chrV@402281to402292	YER121W		aaataaATGaat	12	78	0	0	0	5.9	16.7	3.6
chrV@416936to416950	YER129W	SAK1	tagcatATGgaa	15	326	1	2	7	34.6	32.9	8.7
chrV@417160to417168	YER129W	SAK1	taattgATGttt	9	108	1	2	7	34.6	32.9	8.7
chrV@492114to492106	YER159C	BUR6	agggcaATGcac	9	154	11	3	7	38.2	98.5	90.9
chrV@503784to503773	YER163C		agttgtATGgcc	12	-3	0	0	0	20.0	74.9	22.9
chrV@540433to540419	YER175C	TMT1	tttagtATGttt	15	62	0	5	0	50.1	47.7	9.1
chrV@540400to540383	YER175C	TMT1	gttgttATGaga	18	26	0	8	0	50.1	47.7	9.1
chrV@550622to550560	YER180C	ISC10	tcactcATGatc	63	39	0	35	0	83.1	94.4	0.3
chrV@562644to562603	YER186C		tagtatATGatc	42	-16	0	21	0	190.3	135.0	0.9
chrVI@81941to81933	YFL027C	GYP8	tagcaaATGaca	9	24	0	0	0	38.2	143.8	9.1
chrVI@79195to79145	YFL029C	CAK1	ggccagATGaag	51	-13	1	4	1	23.6	43.0	11.0
chrVI@155911to155867	YFR005C	SAD1	ctcttcATGgtt	45	0	0	6	0	38.8	118.5	19.0
chrVI@206318to206268	YFR026C		aggataATGatc	51	24	0	1	0	18.9	16.4	0.0
chrVI@246080to246142	YFR048W	RMD8	gttcgtATGcaa	63	-10	5	11	5	48.7	41.4	11.7
chrVI@246094to246135	YFR048W	RMD8	ttgcatATGgag	42	-3	5	9	5	48.7	41.4	11.7
chrVII@494409to494453	YGL002W	ERP6	caagatATGggg	45	67	1	11	1	81.4	139.2	22.4
chrVII@490627to490607	YGL005C	COG7	gtgataATGcat	21	57	0	4	1	34.7	116.1	20.1
chrVII@490610to490596	YGL005C	COG7	ttccatATGaaa	15	46	1	1	1	34.7	116.1	20.1
chrVII@490603to490544	YGL005C	COG7	tgaaatATGtct	60	-6	1	6	1	34.7	116.1	20.1
chrVII@436945to436904	YGL032C	AGA2	ggtgatATGtta	42	67	6	10	12	38.1	71.5	87.6
chrVII@436907to436839	YGL032C	AGA2	tctagaATGatt	69	2	7	9	12	38.1	71.5	87.6
chrVII@392205to392216	YGL059W	PKP2	tggtcaATGgat	12	11	0	0	0	28.6	29.8	3.6
chrVII@371932to371964	YGL071W	AFT1	cgattcATGcta	33	50	10	1	12	17.4	18.2	16.4
chrVII@359419to359436	YGL079W		aaaataATGgtt	18	10	2	2	2	34.3	31.3	11.9
chrVII@352365to352291	YGL084C	GUP1	atatagATGtta	75	-9	0	6	0	24.5	63.9	27.7
chrVII@346940to346875	YGL087C	MMS2	ctgtatATGcaa	66	-31	1	9	1	62.6	63.1	110.1

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrVII@343298to343333	YGL090W	LIF1	`cattggATGact`	36	-12	2	3	2	33.4	16.9	2.4
chrVII@343309to343314	YGL090W	LIF1	`ttatttATGtag`	6	7	0	0	2	33.4	16.9	2.4
chrVII@334481to334464	YGL094C	PAN2	`ttctgaATGgtg`	18	-3	10	2	16	26.9	14.7	8.0
chrVII@334474to334460	YGL094C	PAN2	`tggtgaATGtat`	15	-7	0	0	16	26.9	14.7	8.0
chrVII@325135to325236	YGL096W	TOS8	`aaataaATGctg`	102	97	1	5	1	12.8	18.3	2.5
chrVII@325180to325236	YGL096W	TOS8	`atatatATGgaa`	57	97	0	5	1	12.8	18.3	2.5
chrVII@325215to325292	YGL096W	TOS8	`acagtcATGcat`	78	41	0	12	1	12.8	18.3	2.5
chrVII@295847to295891	YGL113W	SLD3	`aaagtgATGggc`	45	43	0	2	0	16.5	37.7	3.1
chrVII@255643to255654	YGL134W	PCL10	`tattccATGcgc`	12	13	2	7	3	72.0	78.3	3.5
chrVII@253895to253860	YGL136C	MRM2	`gaagtaATGact`	36	-3	6	6	4	43.5	77.6	4.5
chrVII@186027to186113	YGL169W	SUA5	`tttttaATGgta`	87	-49	9	9	13	59.5	74.0	24.4
chrVII@174518to174664	YGL174W	BUD13	`actcgaATGgtg`	147	-114	1	0	0	7.4	24.7	23.9
chrVII@173205to173185	YGL176C		`tggcatATGgga`	21	101	0	1	0	17.7	22.1	2.8
chrVII@173175to173167	YGL176C		`aaggcaATGaga`	9	83	0	0	0	17.7	22.1	2.8
chrVII@173170to173132	YGL176C		`aatgagATGaac`	39	48	0	3	0	17.7	22.1	2.8
chrVII@173160to173089	YGL176C		`acaacaATGgaa`	72	5	0	9	0	17.7	22.1	2.8
chrVII@165181to165116	YGL179C	TOS3	`tatataATGctc`	66	20	0	6	1	10.6	18.7	5.8
chrVII@150532to150497	YGL187C	COX4	`tttgaaATGtat`	36	321	0	2	20	97.1	227.1	153.1
chrVII@150528to150520	YGL187C	COX4	`aaatgtATGtta`	9	344	0	0	20	97.1	227.1	153.1
chrVII@150500to150459	YGL187C	COX4	`aaatacATGaga`	42	283	0	3	20	97.1	227.1	153.1
chrVII@150495to150490	YGL187C	COX4	`catgagATGtag`	6	314	0	1	20	97.1	227.1	153.1
chrVII@150310to150206	YGL187C	COX4	`catataATGaag`	105	30	2	22	20	97.1	227.1	153.1
chrVII@150298to150206	YGL187C	COX4	`aattcgATGcga`	93	30	1	20	20	97.1	227.1	153.1
chrVII@150206to150189	YGL187C	COX4	`attttgATGttg`	18	13	0	2	20	97.1	227.1	153.1
chrVII@139987to139982	YGL194C-A		`cagttcATGtaa`	6	16	0	1	0	103.2	137.3	38.7
chrVII@124477to124488	YGL197W	MDS3	`tttctgATGaat`	12	214	0	0	0	11.4	10.2	8.1
chrVII@124594to124611	YGL197W	MDS3	`cattacATGgtg`	18	91	0	0	0	11.4	10.2	8.1
chrVII@92487to92549	YGL211W	NCS6	`gacgatATGgta`	63	-34	0	8	0	63.2	139.0	17.3
chrVII@78988to78953	YGL224C	SDT1	`atatatATGttt`	36	98	0	10	5	51.5	92.2	20.5
chrVII@78968to78909	YGL224C	SDT1	`gtatctATGtgg`	60	54	0	6	5	51.5	92.2	20.5
chrVII@78892to78845	YGL224C	SDT1	`gaatacATGagt`	48	-10	4	8	5	51.5	92.2	20.5
chrVII@38824to38810	YGL246C	RAI1	`tgtaatATGgtg`	15	31	2	2	2	115.2	201.1	35.2
chrVII@31834to31875	YGL250W	RMR1	`gtatatATGatt`	42	34	0	1	0	9.5	26.4	8.5
chrVII@31897to32634	YGL250W	RMR1	`gtatcaATGgaa`	738	-725	0	0	0	9.5	26.4	8.5
chrVII@14725to14790	YGL256W	ADH4	`ccttcaATGagc`	66	119	3	29	16	59.0	113.7	14.0
chrVII@14773to14790	YGL256W	ADH4	`agtgtgATGttg`	18	119	2	6	16	59.0	113.7	14.0
chrVII@14781to14840	YGL256W	ADH4	`gttgacATGgtt`	60	69	1	25	16	59.0	113.7	14.0
chrVII@14809to14934	YGL256W	ADH4	`tttgtgATGatg`	126	-25	12	23	16	59.0	113.7	14.0
chrVII@14812to14934	YGL256W	ADH4	`gtgatgATGgct`	123	-25	12	19	16	59.0	113.7	14.0
chrVII@14843to14866	YGL256W	ADH4	`ttagctATGaaa`	24	43	10	2	16	59.0	113.7	14.0
chrVII@14902to14934	YGL256W	ADH4	`tttaatATGtca`	33	-25	0	0	16	59.0	113.7	14.0
chrVII@14216to14178	YGL257C	MNT2	`attcgcATGagt`	39	22	4	19	4	90.5	129.7	8.4
chrVII@506934to506957	YGR007W	MUQ1	`agacaaATGctt`	24	15	0	2	0	100.1	134.3	55.5
chrVII@532610to532572	YGR024C	THG1	`ttcctaATGcga`	39	-27	0	2	1	125.2	306.0	31.4
chrVII@546318to546359	YGR031W		`cagtacATGtgt`	42	85	0	3	0	43.5	116.6	29.4
chrVII@577485to577493	YGR041W	BUD9	`catcctATGaaa`	9	-3	0	0	22	38.3	29.7	16.3

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrVII@579469to579498	YGR042W		gatcgcATGaca	30	-19	0	0	0	160.2	100.9	11.6
chrVII@584761to584781	YGR046W	TAM41	gagtagATGttt	21	117	0	1	9	52.4	79.4	13.3
chrVII@584781to584786	YGR046W	TAM41	taaataATGtga	6	112	0	0	9	52.4	79.4	13.3
chrVII@591195to591248	YGR049W	SCM4	atataaATGaga	54	69	11	3	12	12.3	18.0	41.2
chrVII@605584to605573	YGR057C	LST7	cgataaATGaag	12	69	1	1	8	28.2	87.9	7.3
chrVII@605529to605506	YGR057C	LST7	gtttaaATGgtt	24	2	8	2	8	28.2	87.9	7.3
chrVII@605522to605514	YGR057C	LST7	tggttgATGaaa	9	10	1	2	8	28.2	87.9	7.3
chrVII@605513to604776	YGR057C	LST7	aaatagATGcat	738	-728	0	0	8	28.2	87.9	7.3
chrVII@619971to619948	YGR065C	VHT1	atctgcATGact	24	87	1	2	2	20.2	78.8	14.6
chrVII@634092to634063	YGR071C		tagcatATGtac	30	-3	6	1	7	11.8	26.2	8.5
chrVII@656950to656982	YGR089W	NNF2	ggatccATGcac	33	-19	6	0	23	21.4	30.4	12.0
chrVII@670341to670352	YGR093W		gggcttATGgtt	12	39	4	2	0	95.1	93.6	23.6
chrVII@687897to687911	YGR099W	TEL2	ttcctcATGaaa	15	-9	0	0	5	80.1	53.8	8.8
chrVII@698542to698577	YGR105W	VMA21	gctaaaATGaac	36	25	3	25	3	241.2	284.3	228.9
chrVII@733063to733031	YGR121C	MEP1	tcgataATGcag	33	100	0	3	0	19.6	15.6	1.4
chrVII@732992to732972	YGR121C	MEP1	aggcttATGatc	21	41	0	0	0	19.6	15.6	1.4
chrVII@746712to746720	YGR127W		tagtatATGaag	9	82	0	0	0	8.3	18.3	7.4
chrVII@788884to788925	YGR149W		ccctaaATGggt	42	110	1	20	4	54.0	45.4	10.1
chrVII@796005to796067	YGR153W		tcgtaaATGgta	63	29	0	7	0	22.5	34.5	7.5
chrVII@797924to797895	YGR154C	GTO1	ggagagATGgcc	30	23	1	1	1	25.9	43.9	0.2
chrVII@830469to830498	YGR166W	KRE11	ctctatATGgac	30	21	5	1	7	11.8	25.9	8.3
chrVII@834511to834491	YGR168C		gagctaATGaga	21	5	14	6	15	60.7	84.5	3.8
chrVII@846535to846543	YGR174W-A		actactATGgtg	9	116	2	1	3	12.3	11.3	2.3
chrVII@846578to846613	YGR174W-A		actattATGtat	36	46	0	2	3	12.3	11.3	2.3
chrVII@903272to903267	YGR201C		gcctagATGtag	6	66	0	0	0	18.5	49.5	2.4
chrVII@904922to904981	YGR203W		caaacaATGgta	60	260	0	2	1	7.2	20.5	26.2
chrVII@905012to905023	YGR203W		aaaagaATGact	12	218	0	0	1	7.2	20.5	26.2
chrVII@905057to905146	YGR203W		tcctacATGcaa	90	95	1	6	1	7.2	20.5	26.2
chrVII@905079to905189	YGR203W		cgggtaATGcac	111	52	1	6	1	7.2	20.5	26.2
chrVII@910413to910439	YGR206W	MVB12	atagcaATGgga	27	-3	2	1	2	33.4	106.6	51.5
chrVII@970184to970146	YGR239C	PEX21	ttggcaATGttc	39	89	0	0	0	9.9	31.8	12.1
chrVII@995519to995650	YGR251W		ctagcgATGaga	132	-7	0	19	0	33.1	115.8	58.8
chrVII@995567to995650	YGR251W		tataagATGttg	84	-7	0	19	0	33.1	115.8	58.8
chrVII@1007366to1007340	YGR257C	MTM1	aatcgtATGagc	27	30	5	9	5	83.7	93.9	8.8
chrVII@1025951to1025907	YGR267C	FOL2	attttaATGctc	45	167	2	4	12	194.2	319.8	130.3
chrVII@1025932to1025825	YGR267C	FOL2	tcaaacATGtct	108	85	4	83	12	194.2	319.8	130.3
chrVII@1026920to1026967	YGR270W	YTA7	gaggaaATGgca	48	408	1	0	7	6.7	20.2	15.8
chrVII@1026974to1027012	YGR270W	YTA7	aagttaATGctg	39	363	0	0	7	6.7	20.2	15.8
chrVII@1026988to1026996	YGR270W	YTA7	tttgagATGttt	9	379	0	0	7	6.7	20.2	15.8
chrVII@1027159to1027242	YGR270W	YTA7	acggccATGtgt	84	133	0	1	7	6.7	20.2	15.8
chrVII@1065184to1065077	YGR286C	BIO2	gagacgATGcct	108	131	2	13	2	50.7	157.2	39.6
chrVII@1065134to1065129	YGR286C	BIO2	caggctATGtag	6	183	0	0	2	50.7	157.2	39.6
chrVII@1070255to1070302	YGR288W	MAL13	aagtaaATGaaa	48	-3	4	2	4	5.7	19.3	2.2
chrVIII@94551to94540	YHL008C		tatttcATGgaa	12	35	0	4	0	25.8	16.9	6.3
chrVIII@54243to54235	YHL026C		ttcaagATGtta	9	72	1	0	2	23.7	21.9	2.8
chrVIII@54202to54185	YHL026C		atatatATGcat	18	22	1	2	2	23.7	21.9	2.8

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5' UTR # Rib	5' UTR mRNA	CDS mRNA	CDS Rib
chrVIII@151536to151628	YHR023W	MYO1	ttgtttATGacc	93	30	0	6	0	7.7	19.5	18.3
chrVIII@195404to195448	YHR045W		cattgaATGgaa	45	95	1	13	2	103.3	122.5	16.8
chrVIII@195536to195631	YHR045W		aagttgATGagc	96	-88	0	0	2	103.3	122.5	16.8
chrVIII@198323to198267	YHR046C	INM1	ttttggATGaat	57	-10	2	9	2	132.4	113.2	39.2
chrVIII@239037to239057	YHR072W	ERG7	ccagtaATGtac	21	42	1	5	1	35.9	104.5	16.8
chrVIII@266990to266973	YHR080C		ggttgaATGatt	18	134	0	2	0	9.5	15.2	1.4
chrVIII@266865to266839	YHR080C		ctctccATGgat	27	0	0	0	0	9.5	15.2	1.4
chrVIII@325498to325518	YHR106W	TRR2	cactcgATGggg	21	82	0	3	0	21.9	60.2	9.2
chrVIII@325505to325513	YHR106W	TRR2	tggggaATGcct	9	87	0	2	0	21.9	60.2	9.2
chrVIII@325524to325592	YHR106W	TRR2	accgcaATGaaa	69	8	0	9	0	21.9	60.2	9.2
chrVIII@335716to335708	YHR112C		cttcaaATGttg	9	43	0	0	2	16.7	37.5	21.4
chrVIII@335704to335696	YHR112C		tagtacATGcta	9	31	2	2	2	16.7	37.5	21.4
chrVIII@364203to364171	YHR129C	ARP1	gagtacATGcta	33	16	21	5	22	12.3	35.5	8.4
chrVIII@364197to364171	YHR129C	ARP1	atgctaATGcta	27	16	18	1	22	12.3	35.5	8.4
chrVIII@374392to374378	YHR135C	YCK1	gttttcATGtgg	15	66	2	1	4	29.5	58.6	68.5
chrVIII@374386to374378	YHR135C	YCK1	atgtggATGcca	9	66	1	0	4	29.5	58.6	68.5
chrVIII@375549to375575	YHR137W	ARO9	ttgccgATGctt	27	136	0	4	0	64.9	259.4	50.1
chrVIII@388756to388745	YHR144C	DCD1	gtgtgaATGcta	12	17	0	0	0	94.9	108.8	31.1
chrVIII@422599to422543	YHR161C	YAP1801	aagaatATGatg	57	255	0	3	0	24.5	58.7	13.7
chrVIII@422596to422543	YHR161C	YAP1801	aatatgATGata	54	255	0	2	0	24.5	58.7	13.7
chrVIII@422478to422458	YHR161C	YAP1801	agcggtATGgta	21	170	0	4	0	24.5	58.7	13.7
chrVIII@422473to422399	YHR161C	YAP1801	tatggtATGcac	75	111	0	12	0	24.5	58.7	13.7
chrVIII@422467to422399	YHR161C	YAP1801	atgcacATGgtg	69	111	0	11	0	24.5	58.7	13.7
chrVIII@422458to422399	YHR161C	YAP1801	gtgttgATGctt	60	111	0	9	0	24.5	58.7	13.7
chrVIII@480747to480721	YHR186C	KOG1	tttcgaATGcat	27	50	4	0	6	11.1	12.8	8.5
chrVIII@480697to480671	YHR186C	KOG1	tattgcATGcag	27	0	2	2	6	11.1	12.8	8.5
chrVIII@506113to506142	YHR204W	MNL1	ctcaccATGgtt	30	176	0	0	8	17.9	64.5	5.3
chrVIII@506246to506254	YHR204W	MNL1	ttgaatATGtat	9	64	0	1	8	17.9	64.5	5.3
chrVIII@506254to506268	YHR204W	MNL1	gtattaATGggt	15	50	0	0	8	17.9	64.5	5.3
chrVIII@506271to506345	YHR204W	MNL1	gtaaccATGata	75	-27	8	9	8	17.9	64.5	5.3
chrVIII@506290to506316	YHR204W	MNL1	atttccATGgat	27	2	8	5	8	17.9	64.5	5.3
chrVIII@512435to512440	YHR206W	SKN7	catcgaATGtga	6	291	0	0	12	17.0	22.1	33.5
chrVIII@519421to520311	YHR209W		ctgtcaATGgaa	891	-875	0	1	0	23.7	27.8	8.7
chrIX@326039to326083	YIL014W	MNT3	catcacATGagt	45	17	6	11	6	50.8	98.7	13.3
chrIX@315068to315085	YIL019W	FAF1	gtacaaATGacc	18	5	3	6	3	83.4	148.2	58.3
chrIX@301347to301321	YIL029C		gcagttATGcaa	27	67	13	15	16	66.8	72.0	0.5
chrIX@301324to301301	YIL029C		gggcaaATGaac	24	47	2	13	16	66.8	72.0	0.5
chrIX@301298to301278	YIL029C		gtaaggATGctg	21	24	1	2	16	66.8	72.0	0.5
chrIX@282667to282587	YIL038C	NOT3	cattgtATGttt	81	-63	3	2	32	42.4	47.0	51.9
chrIX@258591to258623	YIL050W	PCL7	tataacATGgac	33	288	0	3	4	22.3	53.1	33.6
chrIX@258631to258639	YIL050W	PCL7	catactATGgct	9	272	0	1	4	22.3	53.1	33.6
chrIX@258709to258744	YIL050W	PCL7	cttgcgATGggt	36	167	1	2	4	22.3	53.1	33.6
chrIX@254107to254078	YIL055C		gtcgtaATGttg	30	156	0	1	0	3.9	9.6	3.1
chrIX@187689to187672	YIL094C	LYS12	gtatctATGcga	18	44	9	22	2	233.7	368.3	155.1
chrIX@173653to173642	YIL102C-A		ctctaaATGcaa	12	54	1	0	3	18.5	42.7	15.2
chrIX@173634to173629	YIL102C-A		tcaaaaATGtga	6	41	2	0	3	18.5	42.7	15.2

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrIX@137975to137943	YIL119C	RPI1	`cagttcATGgta`	33	70	10	7	10	56.1	34.1	37.8
chrIX@113447to113388	YIL129C	TAO3	`atcgttATGgtt`	60	152	0	0	0	4.7	13.1	8.3
chrIX@113363to113325	YIL129C	TAO3	`aggcaaATGaag`	39	89	0	1	0	4.7	13.1	8.3
chrIX@113346to113335	YIL129C	TAO3	`aagcaaATGtgg`	12	99	0	0	0	4.7	13.1	8.3
chrIX@96459to96307	YIL135C	VHS2	`ggtgatATGcaa`	153	-67	4	8	4	25.0	38.9	31.1
chrIX@37262to37375	YIL162W	SUC2	`atagatATGtat`	114	9	0	7	0	8.9	18.5	30.9
chrIX@37381to38982	YIL162W	SUC2	`acgtatATGatg`	1602	-1598	0	0	0	8.9	18.5	30.9
chrIX@380920to380891	YIR013C	GAT4	`actagaATGctc`	30	511	0	0	2	7.9	1.6	0.0
chrIX@380902to380891	YIR013C	GAT4	`gtacccATGatg`	12	511	0	0	2	7.9	1.6	0.0
chrIX@380899to380891	YIR013C	GAT4	`cccatgATGcat`	9	511	0	0	2	7.9	1.6	0.0
chrIX@380851to380813	YIR013C	GAT4	`cgaattATGgct`	39	433	0	0	2	7.9	1.6	0.0
chrIX@380830to380813	YIR013C	GAT4	`attgcgATGaca`	18	433	0	0	2	7.9	1.6	0.0
chrIX@380816to380790	YIR013C	GAT4	`gtcaatATGaaa`	27	410	0	0	2	7.9	1.6	0.0
chrIX@380776to380735	YIR013C	GAT4	`ccacctATGccc`	42	355	0	1	2	7.9	1.6	0.0
chrIX@380760to380728	YIR013C	GAT4	`ttgaaaATGgta`	33	348	0	1	2	7.9	1.6	0.0
chrIX@380558to380499	YIR013C	GAT4	`acatccATGtgt`	60	119	0	2	2	7.9	1.6	0.0
chrIX@380537to380499	YIR013C	GAT4	`tgtgccATGgaa`	39	119	0	2	2	7.9	1.6	0.0
chrIX@380512to380474	YIR013C	GAT4	`ttcatcATGaat`	39	94	0	1	2	7.9	1.6	0.0
chrIX@380479to380474	YIR013C	GAT4	`tttcacATGtaa`	6	94	0	0	2	7.9	1.6	0.0
chrIX@414708to414679	YIR031C	DAL7	`tagagtATGtgt`	30	4	0	14	2	91.7	107.2	1.2
chrX@405248to405283	YJL016W		`agctgaATGaaa`	36	299	0	1	0	18.8	27.1	6.0
chrX@359678to359667	YJL044C	GYP6	`tcgcttATGcaa`	12	-3	0	1	1	117.4	92.2	21.8
chrX@352369to352389	YJL046W		`tctttgATGttt`	21	-9	5	10	0	66.8	58.8	6.5
chrX@348775to348710	YJL048C	UBX6	`ttccacATGaat`	66	79	0	22	2	76.0	60.9	7.8
chrX@348725to348594	YJL048C	UBX6	`atatatATGcac`	132	-37	2	31	2	76.0	60.9	7.8
chrX@254489to254421	YJL094C	KHA1	`catcaaATGata`	69	-15	3	5	3	25.0	33.0	8.0
chrX@192418to192435	YJL117W	PHO86	`cttttcATGttt`	18	94	0	1	0	118.9	345.2	139.8
chrX@191141to191103	YJL121C	RPE1	`aatttcATGcaa`	39	15	0	4	0	23.8	75.5	198.4
chrX@184300to184265	YJL127C	SPT10	`cgggggATGagt`	36	48	0	1	6	20.8	23.3	8.1
chrX@181831to181781	YJL127C-B		`agttaaATGtac`	51	75	0	15	0	162.3	307.3	67.9
chrX@172746to172714	YJL130C	URA2	`ttgagtATGttt`	33	351	2	2	118	24.0	40.6	202.7
chrX@172737to172714	YJL130C	URA2	`ttttttATGatt`	24	351	1	2	118	24.0	40.6	202.7
chrX@172714to172634	YJL130C	URA2	`gccttaATGttg`	81	271	0	4	118	24.0	40.6	202.7
chrX@172693to172634	YJL130C	URA2	`cagaccATGcga`	60	271	0	3	118	24.0	40.6	202.7
chrX@172688to172623	YJL130C	URA2	`catgcgATGcca`	66	260	0	3	118	24.0	40.6	202.7
chrX@172615to172541	YJL130C	URA2	`tctgcgATGatg`	75	178	0	3	118	24.0	40.6	202.7
chrX@172612to172541	YJL130C	URA2	`gcgatgATGtcg`	72	178	0	3	118	24.0	40.6	202.7
chrX@172529to172497	YJL130C	URA2	`atcttcATGgca`	33	134	2	0	118	24.0	40.6	202.7
chrX@159899to159840	YJL133C-A		`gttttaATGatt`	60	-3	2	15	2	81.1	172.9	123.5
chrX@160592to160600	YJL133W	MRS3	`atatttATGtta`	9	15	8	3	15	49.1	110.8	20.5
chrX@153049to153023	YJL139C	YUR1	`aatctaATGctt`	27	28	16	3	0	36.9	44.9	8.0
chrX@150404to150393	YJL141C	YAK1	`tttcacATGcta`	12	7	1	1	4	13.7	24.2	10.2
chrX@128982to128962	YJL156C	SSY5	`ttttgcATGtac`	21	14	3	5	3	37.7	39.4	15.0
chrX@117194to117208	YJL161W		`aacttgATGcaa`	15	32	0	0	0	13.4	16.2	4.2
chrX@115650to115612	YJL162C	JJJ2	`cagtttATGcta`	39	-12	4	7	5	45.9	48.3	7.6
chrX@111194to111180	YJL164C	TPK1	`cagtgcATGaat`	15	28	3	0	14	22.0	27.1	17.4

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrX@50489to50415	YJL205C	NCE101	`atacaaATGttc`	75	-27	2	3	2	22.9	78.7	45.5
chrX@37999to38049	YJL209W	CBP1	`ctttccATGcaa`	51	-45	0	0	0	41.8	34.8	3.9
chrX@32049to32105	YJL213W		`ccgttgATGaag`	57	57	1	52	1	109.5	115.0	0.2
chrX@32088to32105	YJL213W		`gtaagtATGtca`	18	57	0	29	1	109.5	115.0	0.2
chrX@32115to32153	YJL213W		`acagtcATGtcc`	39	9	0	5	1	109.5	115.0	0.2
chrX@452283to452288	YJR008W		`ccactcATGtga`	6	134	0	2	8	22.3	32.4	1.6
chrX@452309to452359	YJR008W		`gataacATGcgg`	51	63	8	9	8	22.3	32.4	1.6
chrX@507701to507784	YJR040W	GEF1	`cggtgaATGttg`	84	-46	3	2	2	37.1	36.7	15.0
chrX@535876to535923	YJR054W		`aaagaaATGttg`	48	125	0	3	6	33.6	97.1	7.4
chrX@535898to535969	YJR054W		`gaatagATGttt`	72	79	3	9	6	33.6	97.1	7.4
chrX@535907to535969	YJR054W		`tttcaaATGaaa`	63	79	3	8	6	33.6	97.1	7.4
chrX@535920to536024	YJR054W		`tagaccATGagg`	105	24	6	18	6	33.6	97.1	7.4
chrX@535959to536024	YJR054W		`cccttgATGatt`	66	24	6	14	6	33.6	97.1	7.4
chrX@535981to536016	YJR054W		`atctttATGgtt`	36	32	2	9	6	33.6	97.1	7.4
chrX@536013to536024	YJR054W		`aatttcATGaat`	12	24	1	2	6	33.6	97.1	7.4
chrX@587702to587725	YJR089W	BIR1	`tacctcATGgga`	24	-15	0	0	0	20.8	25.0	7.9
chrX@617383to617354	YJR100C		`tacgaaATGaaa`	30	28	2	5	2	30.5	110.5	15.3
chrX@649693to649740	YJR122W	IBA57	`tattagATGcgc`	48	29	3	2	2	17.9	36.1	5.7
chrX@667194to667120	YJR130C	STR2	`agtagaATGacg`	75	-10	3	7	2	16.7	54.4	5.6
chrX@667185to667120	YJR130C	STR2	`acgctcATGtgc`	66	-10	2	7	2	16.7	54.4	5.6
chrX@695888to695899	YJR141W		`aaacaaATGcaa`	12	0	3	1	4	89.0	128.5	6.9
chrX@719524to719532	YJR152W	DAL5	`gattggATGaag`	9	127	0	0	1	14.7	18.5	0.0
chrX@719536to719580	YJR152W	DAL5	`taatatATGtat`	45	79	0	1	1	14.7	18.5	0.0
chrX@719546to719593	YJR152W	DAL5	`atataaATGgac`	48	66	1	2	1	14.7	18.5	0.0
chrX@719577to719630	YJR152W	DAL5	`gagatcATGagg`	54	29	1	6	1	14.7	18.5	0.0
chrX@727054to727089	YJR155W	AAD10	`cccaatATGatt`	36	309	1	5	1	37.6	36.9	0.5
chrX@727120to727179	YJR155W	AAD10	`cccaaaATGtgc`	60	219	0	15	1	37.6	36.9	0.5
chrX@727134to727364	YJR155W	AAD10	`ttcgaaATGtct`	231	34	0	47	1	37.6	36.9	0.5
chrX@727242to727364	YJR155W	AAD10	`ggaggtATGtct`	123	34	0	27	1	37.6	36.9	0.5
chrX@727272to727364	YJR155W	AAD10	`ggattcATGgga`	93	34	0	24	1	37.6	36.9	0.5
chrX@727281to727364	YJR155W	AAD10	`ggatcaATGgac`	84	34	0	19	1	37.6	36.9	0.5
chrX@727312to727431	YJR155W	AAD10	`tacttgATGctt`	120	-33	0	19	1	37.6	36.9	0.5
chrX@727366to727431	YJR155W	AAD10	`attagtATGagc`	66	-33	0	7	1	37.6	36.9	0.5
chrX@727394to727420	YJR155W	AAD10	`cggtgaATGgat`	27	-22	0	0	1	37.6	36.9	0.5
chrXI@434634to434605	YKL005C	BYE1	`cttgcaATGaaa`	30	86	3	6	1	102.0	50.2	15.6
chrXI@402164to402238	YKL019W	RAM2	`ttaattATGgta`	75	-28	5	9	10	71.8	79.2	24.7
chrXI@393318to393329	YKL023W		`tatacaATGcaa`	12	34	0	0	0	5.9	20.8	27.1
chrXI@389671to389651	YKL026C	GPX1	`ttgcttATGgtg`	21	126	0	0	5	7.6	22.6	5.3
chrXI@389635to389609	YKL026C	GPX1	`acagtaATGtac`	27	84	2	1	5	7.6	22.6	5.3
chrXI@389614to389609	YKL026C	GPX1	`ttagtcATGtag`	6	84	0	0	5	7.6	22.6	5.3
chrXI@359639to359668	YKL041W	VPS24	`aaaaatATGcta`	30	117	0	0	9	53.8	130.2	59.7
chrXI@359687to359740	YKL041W	VPS24	`atatatATGtat`	54	45	9	20	9	53.8	130.2	59.7
chrXI@334666to334631	YKL056C	TMA19	`tggttaATGttt`	36	73	5	18	6	1645.3	6368.8	4929.3
chrXI@334653to334582	YKL056C	TMA19	`cattcaATGgtt`	72	24	5	234	6	1645.3	6368.8	4929.3
chrXI@317183to317188	YKL064W	MNR2	`tttgatATGtga`	6	219	1	1	16	36.3	25.9	13.8
chrXI@317306to317335	YKL064W	MNR2	`catttgATGact`	30	72	14	6	16	36.3	25.9	13.8

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXI@305719to305739	YKL070W		tctattATGtcc	21	115	0	0	0	1.3	1.2	0.0
chrXI@305741to305761	YKL070W		attaggATGgta	21	93	0	1	0	1.3	1.2	0.0
chrXI@231621to231650	YKL109W	HAP4	tcgtatATGcta	30	220	4	0	12	2.6	9.9	12.5
chrXI@231809to231820	YKL109W	HAP4	attttaATGggt	12	50	8	1	12	2.6	9.9	12.5
chrXI@229645to229619	YKL110C	KTI12	atcgcgATGgaa	27	96	0	1	4	46.3	122.0	32.1
chrXI@229633to229619	YKL110C	KTI12	aaagaaATGaag	15	96	0	1	4	46.3	122.0	32.1
chrXI@229619to229608	YKL110C	KTI12	tacttgATGaac	12	85	0	2	4	46.3	122.0	32.1
chrXI@229584to229531	YKL110C	KTI12	atcagaATGagg	54	8	2	19	4	46.3	122.0	32.1
chrXI@193093to193070	YKL133C		attgtaATGaag	24	2	5	2	5	8.0	21.4	2.1
chrXI@193081to193070	YKL133C		aaatttATGctc	12	2	2	1	5	8.0	21.4	2.1
chrXI@166418to166450	YKL150W	MCR1	ataagaATGcag	33	98	0	0	2	31.1	101.3	53.2
chrXI@166434to166478	YKL150W	MCR1	ctcgcaATGccc	45	70	0	3	2	31.1	101.3	53.2
chrXI@166150to166091	YKL151C		ctagaaATGgac	60	157	4	6	4	26.0	70.4	23.9
chrXI@166140to166072	YKL151C		actcttATGatc	69	138	2	5	4	26.0	70.4	23.9
chrXI@166072to166067	YKL151C		ggagtgATGtga	6	133	0	1	4	26.0	70.4	23.9
chrXI@166067to166062	YKL151C		gatgtgATGtga	6	128	0	1	4	26.0	70.4	23.9
chrXI@166062to166030	YKL151C		gatgtgATGcga	33	96	0	5	4	26.0	70.4	23.9
chrXI@166057to166052	YKL151C		gatgcgATGtga	6	118	0	0	4	26.0	70.4	23.9
chrXI@166052to166035	YKL151C		gatgtgATGggt	18	101	0	3	4	26.0	70.4	23.9
chrXI@166020to166015	YKL151C		atatatATGtaa	6	81	0	0	4	26.0	70.4	23.9
chrXI@150909to150835	YKL161C		tcgacaATGacg	75	144	0	8	3	26.5	23.2	0.3
chrXI@150893to150846	YKL161C		tttcagATGgtt	48	155	0	6	3	26.5	23.2	0.3
chrXI@150849to150835	YKL161C		acttttATGatg	15	144	0	0	3	26.5	23.2	0.3
chrXI@150846to150835	YKL161C		tttatgATGtta	12	144	0	0	3	26.5	23.2	0.3
chrXI@150818to150813	YKL161C		tatttaATGtaa	6	122	1	0	3	26.5	23.2	0.3
chrXI@150788to150762	YKL161C		gactggATGaaa	27	71	2	2	3	26.5	23.2	0.3
chrXI@150773to150762	YKL161C		gacaaaATGgaa	12	71	0	0	3	26.5	23.2	0.3
chrXI@127371to127403	YKL171W		ggtcttATGttc	33	76	0	0	4	7.7	8.0	2.3
chrXI@118209to118201	YKL176C	LST4	tagtggATGgtt	9	211	0	0	8	47.8	53.7	6.0
chrXI@100534to100554	YKL182W	FAS1	tcttatATGctc	21	121	187	6	302	76.2	86.3	345.0
chrXI@70325to70314	YKL198C	PTK1	acctccATGtat	12	92	4	0	3	4.1	12.8	4.5
chrXI@11525to11469	YKL220C	FRE2	ggctcaATGatg	57	243	2	0	2	15.6	8.9	0.1
chrXI@11522to11469	YKL220C	FRE2	tcaatgATGcta	54	243	2	0	2	15.6	8.9	0.1
chrXI@11492to11469	YKL220C	FRE2	gaaaatATGggt	24	243	0	0	2	15.6	8.9	0.1
chrXI@11392to11354	YKL220C	FRE2	tttctgATGaac	39	128	0	6	2	15.6	8.9	0.1
chrXI@11298to11242	YKL220C	FRE2	caaaaaATGaac	57	16	0	5	2	15.6	8.9	0.1
chrXI@11292to11242	YKL220C	FRE2	atgaacATGatt	51	16	0	5	2	15.6	8.9	0.1
chrXI@11245to11141	YKL220C	FRE2	aagcttATGaaa	105	-85	0	0	2	15.6	8.9	0.1
chrXI@444961to445011	YKR003W	OSH6	agttacATGaag	51	12	4	11	4	45.1	49.6	31.9
chrXI@444976to445011	YKR003W	OSH6	gagttcATGcaa	36	12	3	4	4	45.1	49.6	31.9
chrXI@473140to473132	YKR017C		tgaagaATGctg	9	141	0	1	0	31.7	46.9	4.5
chrXI@478868to478909	YKR021W	ALY1	tcctctATGact	42	-33	0	0	1	6.9	14.2	6.3
chrXI@482804to482796	YKR022C	NTR2	ctagcaATGtta	9	15	1	2	1	100.1	91.2	12.7
chrXI@490902to490964	YKR027W	BCH2	aacaaaATGaca	63	42	3	5	3	16.8	39.7	6.9
chrXI@527368to527382	YKR050W	TRK2	agagaaATGata	15	74	0	0	0	6.1	7.3	0.2
chrXI@527394to527549	YKR050W	TRK2	tttcagATGatg	156	-93	0	2	0	6.1	7.3	0.2

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXI@527397to527549	YKR050W	TRK2	cagatgATGaga	153	-93	0	2	0	6.1	7.3	0.2
chrXI@552264to552287	YKR058W	GLG1	ctatatATGtcg	24	124	0	1	5	11.4	15.6	1.0
chrXI@552300to552335	YKR058W	GLG1	ctgaaaATGttt	36	76	4	3	5	11.4	15.6	1.0
chrXI@552320to552400	YKR058W	GLG1	taagctATGcct	81	11	3	4	5	11.4	15.6	1.0
chrXI@552405to554261	YKR058W	GLG1	agtgtgATGgga	1857	-1850	0	0	5	11.4	15.6	1.0
chrXI@561957to561898	YKR063C	LAS1	aaagcaATGaaa	60	-40	0	0	0	25.0	64.3	10.2
chrXI@608023to608018	YKR089C	TGL4	aggtatATGtaa	6	12	3	0	4	17.8	21.7	15.3
chrXII@125473to125553	YLL012W	YEH1	atatagATGgct	81	-21	1	5	1	12.5	18.6	12.4
chrXII@108353to108321	YLL019C	KNS1	aacgatATGgct	33	424	0	2	7	38.1	19.8	5.4
chrXII@108346to108296	YLL019C	KNS1	tggcttATGgcc	51	399	0	10	7	38.1	19.8	5.4
chrXII@108332to108321	YLL019C	KNS1	gttgcaATGctg	12	424	0	0	7	38.1	19.8	5.4
chrXII@108231to108214	YLL019C	KNS1	tatattATGaag	18	317	3	4	7	38.1	19.8	5.4
chrXII@80314to80228	YLL031C	GPI13	aaataaATGggt	87	25	0	8	0	13.6	27.6	20.8
chrXII@80283to80275	YLL031C	GPI13	aagcatATGttt	9	72	0	0	0	13.6	27.6	20.8
chrXII@49922to49930	YLL043W	FPS1	attctaATGcat	9	6	1	6	1	45.2	48.8	29.4
chrXII@39523to39509	YLL051C	FRE6	gcagcaATGatt	15	40	0	5	0	28.6	38.3	7.1
chrXII@39492to39472	YLL051C	FRE6	tgaagcATGacg	21	3	0	2	0	28.6	38.3	7.1
chrXII@35265to35257	YLL054C		acaaagATGatg	9	55	0	0	2	10.3	16.7	3.0
chrXII@35262to35257	YLL054C		aagatgATGtga	6	55	0	0	2	10.3	16.7	3.0
chrXII@35230to35219	YLL054C		aaatctATGaca	12	17	2	1	2	10.3	16.7	3.0
chrXII@29886to29891	YLL055W	YCT1	acggtgATGtaa	6	217	0	0	0	15.6	35.2	1.4
chrXII@29893to29898	YLL055W	YCT1	tgtaatATGtag	6	210	0	0	0	15.6	35.2	1.4
chrXII@29942to29959	YLL055W	YCT1	gtcaagATGaat	18	149	0	0	0	15.6	35.2	1.4
chrXII@29962to29976	YLL055W	YCT1	ttaaaaATGcgt	15	132	0	2	0	15.6	35.2	1.4
chrXII@28388to28347	YLL056C		tcaactATGctt	42	43	1	5	1	12.9	7.1	0.0
chrXII@21909to21877	YLL060C	GTT2	tctcaaATGatt	33	39	0	3	0	60.4	46.9	0.6
chrXII@21899to21801	YLL060C	GTT2	ttaataATGtgc	99	-37	0	7	0	60.4	46.9	0.6
chrXII@168999to169073	YLR011W	LOT6	tttgacATGcct	75	28	7	16	5	62.9	40.5	16.4
chrXII@174994to174977	YLR014C	PPR1	acgaagATGatg	18	-3	16	0	33	28.6	27.6	2.8
chrXII@174991to174977	YLR014C	PPR1	aagatgATGatt	15	-3	13	0	33	28.6	27.6	2.8
chrXII@183587to183634	YLR021W	IRC25	aaaagaATGggc	48	-13	7	11	3	64.1	87.2	35.8
chrXII@204181to204198	YLR031W		aaacagATGgtt	18	27	0	3	0	39.1	75.8	0.7
chrXII@239234to239217	YLR046C		ggccctATGtac	18	404	0	0	4	33.1	44.0	0.3
chrXII@239126to239100	YLR046C		cgaaaaATGaca	27	287	0	3	4	33.1	44.0	0.3
chrXII@239110to239048	YLR046C		atattaATGgat	63	235	0	9	4	33.1	44.0	0.3
chrXII@239065to239048	YLR046C		atttgtATGtct	18	235	0	2	4	33.1	44.0	0.3
chrXII@239046to239008	YLR046C		tataagATGaat	39	195	0	3	4	33.1	44.0	0.3
chrXII@239003to238980	YLR046C		gaatacATGaca	24	167	0	6	4	33.1	44.0	0.3
chrXII@238911to238840	YLR046C		ctgattATGaag	72	27	4	16	4	33.1	44.0	0.3
chrXII@238899to238840	YLR046C		gtttttATGcat	60	27	1	15	4	33.1	44.0	0.3
chrXII@247187to247198	YLR052W	IES3	tcttcaATGgaa	12	3	1	1	1	50.1	54.6	44.8
chrXII@270964to270996	YLR068W	FYV7	acaagaATGata	33	12	0	7	0	77.9	129.0	88.2
chrXII@278842to278853	YLR072W		gagagcATGgta	12	9	0	0	0	100.1	32.5	8.3
chrXII@320647to320694	YLR090W	XDJ1	agagatATGccg	48	7	0	9	0	50.1	92.6	18.1
chrXII@346050to346000	YLR103C	CDC45	gtagtaATGcca	51	59	1	2	1	20.9	32.5	6.5
chrXII@346545to346583	YLR104W		ataggcATGgtt	39	2	0	10	0	115.5	129.3	39.4

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Table S3: All uORFs, continued

uORF	**CDS**	**Gene**	**Initiator Site**	**Length**	**uORF end to CDS**	**# Rib**	**# mRNA**	**5' UTR # Rib**	**5' UTR mRNA**	**CDS mRNA**	**CDS Rib**
chrXII@371317to371514	YLR113W	HOG1	`ccctacATGgtc`	198	106	16	165	22	205.5	221.1	60.1
chrXII@390370to390329	YLR121C	YPS3	`atatatATGtac`	42	59	0	7	1	24.0	12.8	9.2
chrXII@390349to390329	YLR121C	YPS3	`ttatatATGaat`	21	59	0	2	1	24.0	12.8	9.2
chrXII@395578to395570	YLR126C		`aaaattATGcat`	9	50	3	5	3	75.1	67.9	29.4
chrXII@398346to398332	YLR127C	APC2	`atatttATGgct`	15	13	0	0	0	10.8	19.1	4.1
chrXII@399580to399585	YLR129W	DIP2	`atatagATGtag`	6	72	0	0	0	60.5	156.0	39.9
chrXII@404201to404145	YLR130C	ZRT2	`ctatatATGatg`	57	83	28	44	29	200.3	281.1	12.3
chrXII@404198to404145	YLR130C	ZRT2	`tatatgATGata`	54	83	28	44	29	200.3	281.1	12.3
chrXII@444866to444852	YLR152C		`gggtcaATGtct`	15	164	0	1	7	17.0	20.3	1.1
chrXII@444760to444710	YLR152C		`ttctacATGtgt`	51	22	7	4	7	17.0	20.3	1.1
chrXII@444730to444710	YLR152C		`ttttatATGgtg`	21	22	4	2	7	17.0	20.3	1.1
chrXII@444698to444636	YLR152C		`caataaATGaac`	63	-52	0	0	7	17.0	20.3	1.1
chrXII@493831to493881	YLR164W		`gttctaATGaat`	51	3	0	11	2	45.2	51.2	2.0
chrXII@528248to528277	YLR188W	MDL1	`acttacATGaga`	30	24	16	5	16	27.6	32.1	17.1
chrXII@534469to534452	YLR189C	ATG26	`aaagtcATGgct`	18	58	1	2	7	33.4	26.8	6.4
chrXII@534427to534416	YLR189C	ATG26	`cactttATGctt`	12	22	7	2	7	33.4	26.8	6.4
chrXII@541653to541648	YLR194C		`ataagtATGtaa`	6	74	0	2	2	121.7	82.8	52.4
chrXII@568446to568451	YLR214W	FRE1	`taaatcATGtaa`	6	117	0	0	4	78.4	203.1	97.5
chrXII@568485to568511	YLR214W	FRE1	`tcttccATGctt`	27	57	3	7	4	78.4	203.1	97.5
chrXII@586424to586468	YLR224W		`tgtactATGcct`	45	-3	4	7	13	62.2	79.4	8.7
chrXII@641350to641487	YLR251W	SYM1	`agtgatATGata`	138	-22	16	35	15	62.3	83.7	4.8
chrXII@641370to641390	YLR251W	SYM1	`atttgaATGcta`	21	75	5	2	15	62.3	83.7	4.8
chrXII@641375to641437	YLR251W	SYM1	`aatgctATGttg`	63	28	12	18	15	62.3	83.7	4.8
chrXII@642601to642621	YLR253W		`agttgaATGttt`	21	7	19	7	20	52.6	64.2	10.6
chrXII@707082to706969	YLR284C	ECI1	`gagtgtATGgca`	114	-72	1	3	0	37.1	46.5	7.6
chrXII@715060to715077	YLR289W	GUF1	`agagccATGaat`	18	13	1	4	1	23.6	25.4	4.0
chrXII@715066to715077	YLR289W	GUF1	`atgaatATGgga`	12	13	1	3	1	23.6	25.4	4.0
chrXII@725885to725911	YLR299W	ECM38	`atatatATGtgt`	27	159	1	2	3	9.7	10.0	9.6
chrXII@779147to779185	YLR324W	PEX30	`gtgggcATGcaa`	39	29	0	5	0	22.7	24.9	20.2
chrXII@784823to784831	YLR328W	NMA1	`atctgcATGgta`	9	81	11	1	18	31.7	51.1	48.1
chrXII@834343to834372	YLR353W	BUD8	`ttctacATGaag`	30	-22	0	0	4	22.3	25.8	6.9
chrXII@846060to846104	YLR360W	VPS38	`gaattgATGgtt`	45	-3	13	8	13	58.9	68.8	7.6
chrXII@873562to873530	YLR376C	PSY3	`tagcgaATGgaa`	33	-22	0	0	1	42.2	52.3	7.3
chrXII@873557to873540	YLR376C	PSY3	`aatggaATGgga`	18	-12	0	0	1	42.2	52.3	7.3
chrXII@879718to879741	YLR381W	CTF3	`ttttacATGaat`	24	-19	0	1	1	34.8	20.4	2.9
chrXII@885282to885290	YLR383W	SMC6	`tgctaaATGgta`	9	-3	0	0	0	15.0	15.9	5.4
chrXII@902745to902728	YLR389C	STE23	`tcctgaATGaat`	18	69	0	0	0	15.8	31.4	27.1
chrXII@903057to903077	YLR390W	ECM19	`aacgcgATGaag`	21	-12	0	0	3	10.8	25.8	42.9
chrXII@924491to924477	YLR401C	DUS3	`acattaATGaac`	15	30	0	0	0	35.8	67.1	39.0
chrXII@982707to982787	YLR425W	TUS1	`gagaggATGatc`	81	103	1	2	13	5.5	9.7	4.6
chrXII@982818to982829	YLR425W	TUS1	`actgttATGaac`	12	61	7	1	13	5.5	9.7	4.6
chrXII@988354to988374	YLR427W	MAG2	`cgttggATGtgg`	21	50	0	1	0	45.6	49.7	16.2
chrXII@993382to993429	YLR430W	SEN1	`ctctgtATGgca`	48	1	10	0	19	8.9	11.8	11.7
chrXII@1035949to1035984	YLR451W	LEU3	`aaagtaATGagc`	36	105	0	0	5	28.4	36.3	14.2
chrXII@1035974to1036048	YLR451W	LEU3	`agtatcATGata`	75	41	4	8	5	28.4	36.3	14.2
chrXII@1043989to1043994	YLR454W		`cggtatATGtag`	6	1	0	0	2	2.6	8.7	4.3

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5' UTR # Rib	5' UTR mRNA	CDS mRNA	CDS Rib
chrXIII@253762to253782	YML007W	YAP1	ttgtgcATGaac	21	65	2	12	12	110.3	83.4	39.0
chrXIII@251525to251496	YML009C	MRPL39	atatttATGtgc	30	-19	6	8	6	357.6	217.0	197.6
chrXIII@241727to241701	YML016C	PPZ1	caatacATGtta	27	166	19	35	29	154.1	62.2	19.1
chrXIII@228709to228683	YML023C	NSE5	agatatATGaag	27	20	2	5	1	45.2	54.0	2.7
chrXIII@228689to228666	YML023C	NSE5	cggcaaATGgtg	24	3	1	6	1	45.2	54.0	2.7
chrXIII@221305to221331	YML027W	YOX1	ttcagtATGatt	27	74	0	0	0	32.6	21.8	28.6
chrXIII@191780to191748	YML043C	RRN11	tctaatATGatg	33	-18	1	1	3	87.6	73.1	5.7
chrXIII@191777to191748	YML043C	RRN11	aatatgATGcat	30	-18	1	1	3	87.6	73.1	5.7
chrXIII@164477to164472	YML056C	IMD4	gccctaATGtga	6	297	0	0	66	201.6	583.5	304.6
chrXIII@164422to164375	YML056C	IMD4	ttcgagATGctg	48	200	12	0	66	201.6	583.5	304.6
chrXIII@164343to164233	YML056C	IMD4	caaatcATGctt	111	58	38	174	66	201.6	583.5	304.6
chrXIII@164274to164233	YML056C	IMD4	gaaaaaATGgtg	42	58	35	131	66	201.6	583.5	304.6
chrXIII@137489to137497	YML068W	ITT1	tatgtcATGgtg	9	52	2	2	13	77.4	63.7	3.8
chrXIII@137529to137558	YML068W	ITT1	taactgATGaaa	30	-9	10	7	13	77.4	63.7	3.8
chrXIII@97724to97623	YML086C	ALO1	tagttgATGggc	102	253	0	0	12	17.0	50.5	102.6
chrXIII@97670to97623	YML086C	ALO1	atttccATGatt	48	253	0	0	12	17.0	50.5	102.6
chrXIII@97583to97461	YML086C	ALO1	aaaaaaATGgaa	123	91	0	9	12	17.0	50.5	102.6
chrXIII@97577to97461	YML086C	ALO1	atggaaATGagg	117	91	0	9	12	17.0	50.5	102.6
chrXIII@77220to77237	YML098W	TAF13	tgcaacATGaaa	18	29	5	3	4	41.1	114.4	35.0
chrXIII@56727to56750	YML106W	URA5	cattgtATGaag	24	22	39	28	134	516.0	564.8	402.1
chrXIII@46769to46819	YML111W	BUL2	acagatATGcgt	51	122	4	2	5	32.3	33.9	16.8
chrXIII@38099to38155	YML116W	ATR1	tataaaATGaat	57	40	35	27	33	98.0	105.0	8.5
chrXIII@38108to38155	YML116W	ATR1	aataaaATGcat	48	40	29	23	33	98.0	105.0	8.5
chrXIII@30515to30547	YML119W		ttgtacATGaaa	33	63	0	0	0	26.6	90.3	19.9
chrXIII@26809to26889	YML121W	GTR1	agttcaATGtgg	81	40	7	27	7	78.4	184.4	27.8
chrXIII@26837to26857	YML121W	GTR1	gtgattATGgta	21	72	3	9	7	78.4	184.4	27.8
chrXIII@16778to16761	YML128C	MSC1	ccactcATGgag	18	85	1	1	6	42.6	42.2	6.8
chrXIII@16759to16673	YML128C	MSC1	cctagcATGatt	87	-3	6	18	6	42.6	42.2	6.8
chrXIII@282832to282797	YMR008C	PLB1	tagaagATGact	36	214	1	4	3	20.4	23.3	27.5
chrXIII@284870to284899	YMR010W		tcttccATGgag	30	199	4	5	18	37.3	57.8	25.5
chrXIII@296836to296795	YMR013C	SEC59	tattctATGaaa	42	59	0	1	0	33.0	79.0	7.9
chrXIII@325506to325477	YMR026C	PEX12	ttttgcATGaag	30	44	17	9	20	65.4	86.8	8.4
chrXIII@337775to337783	YMR033W	ARP9	tactatATGcat	9	3	0	4	4	215.7	154.8	42.5
chrXIII@340826to340770	YMR034C		ccgtctATGcta	57	50	2	2	0	8.0	17.5	2.4
chrXIII@350326to350376	YMR040W	YET2	tggagcATGaat	51	3	4	10	4	38.4	49.6	3.0
chrXIII@350333to350338	YMR040W	YET2	tgaattATGtga	6	41	1	0	4	38.4	49.6	3.0
chrXIII@352532to352585	YMR042W	ARG80	gtagctATGcga	54	16	1	8	2	27.3	44.5	10.4
chrXIII@406228to406251	YMR068W	AVO2	ttgaaaATGtat	24	51	0	1	0	12.5	31.5	4.0
chrXIII@408921to408926	YMR070W	MOT3	cttttgATGtaa	6	226	0	0	3	13.7	25.7	22.8
chrXIII@413691to413696	YMR075W	RCO1	ttcctcATGtag	6	284	0	2	0	24.1	35.7	13.7
chrXIII@431225to431202	YMR081C	ISF1	aagtgtATGagc	24	109	0	0	0	6.3	1.0	0.4
chrXIII@458226to458303	YMR096W	SNZ1	ttcttcATGact	78	103	0	12	0	19.6	22.1	0.9
chrXIII@458320to458367	YMR096W	SNZ1	agagctATGgac	48	39	0	2	0	19.6	22.1	0.9
chrXIII@458333to458386	YMR096W	SNZ1	aagtctATGgta	54	20	0	1	0	19.6	22.1	0.9
chrXIII@497476to497426	YMR114C		tacctgATGcta	51	-21	3	4	0	35.3	23.5	9.1
chrXIII@505320to505334	YMR119W	ASI1	gaaactATGcta	15	-3	1	0	25	50.1	66.5	10.4

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXIII@523439to523434	YMR127C	SAS2	`tagagtATGtag`	6	91	1	0	3	78.3	85.7	10.9
chrXIII@537721to537759	YMR134W		`gcctttATGaaa`	39	77	0	1	1	13.1	45.3	37.4
chrXIII@563028to563036	YMR152W	YIM1	`atttgaATGgag`	9	58	0	0	1	32.8	45.7	42.5
chrXIII@599231to599196	YMR168C	CEP3	`aagagaATGaaa`	36	40	0	0	2	9.7	24.9	3.9
chrXIII@599196to599149	YMR168C	CEP3	`caggtgATGaca`	48	-7	2	3	2	9.7	24.9	3.9
chrXIII@605681to605670	YMR171C	EAR1	`tgctgcATGgag`	12	152	2	2	15	39.8	46.2	12.5
chrXIII@611703to611732	YMR176W	ECM5	`tcgtgtATGttc`	30	6	2	1	3	14.7	15.9	2.3
chrXIII@625181to625107	YMR182C	RGM1	`attagcATGaca`	75	-58	1	1	1	6.6	6.0	1.0
chrXIII@647060to647077	YMR192W	GYL1	`tactgcATGtat`	18	39	3	2	5	8.7	19.5	21.0
chrXIII@647074to647103	YMR192W	GYL1	`actcttATGatt`	30	13	3	3	5	8.7	19.5	21.0
chrXIII@653981to654010	YMR195W	ICY1	`aaactaATGaca`	30	22	108	40	110	245.5	471.6	110.6
chrXIII@659206to659165	YMR197C	VTI1	`tgctgcATGgct`	42	-31	0	0	1	50.1	83.0	72.9
chrXIII@683585to683568	YMR207C	HFA1	`caaacaATGgta`	18	6	1	0	1	7.1	7.9	1.5
chrXIII@740183to740197	YMR234W	RNH1	`aatttcATGgca`	15	67	4	0	6	35.0	40.9	14.0
chrXIII@784306to784298	YMR258C		`gctcacATGata`	9	19	13	1	13	55.2	78.7	12.0
chrXIII@794863to794910	YMR263W	SAP30	`gtgataATGcaa`	48	7	2	14	2	64.5	179.2	45.8
chrXIII@801726to801752	YMR267W	PPA2	`gcttgtATGcgt`	27	18	3	11	4	87.5	101.7	32.6
chrXIII@806529to806482	YMR270C	RRN9	`atattgATGtgt`	48	61	0	15	0	101.0	145.5	11.1
chrXIII@835103to835083	YMR282C	AEP2	`aaatttATGatt`	21	-13	0	0	4	50.1	68.1	10.4
chrXIII@914710to914696	YMR319C	FET4	`gattcgATGctc`	15	161	1	8	5	206.3	331.3	29.8
chrXIII@914661to914653	YMR319C	FET4	`cacggcATGaat`	9	118	4	3	5	206.3	331.3	29.8
chrXIV@625861to625853	YNL003C	PET8	`acaccgATGaac`	9	23	2	2	8	158.5	103.1	16.4
chrXIV@613423to613397	YNL011C		`aagaatATGtcg`	27	227	1	4	4	40.8	91.2	10.2
chrXIV@613413to613387	YNL011C		`cgtacaATGtgt`	27	217	0	2	4	40.8	91.2	10.2
chrXIV@613366to613307	YNL011C		`cgtgtaATGctt`	60	137	1	13	4	40.8	91.2	10.2
chrXIV@613353to613297	YNL011C		`gatattATGtgg`	57	127	1	12	4	40.8	91.2	10.2
chrXIV@613297to613250	YNL011C		`acgctaATGtgt`	48	80	2	9	4	40.8	91.2	10.2
chrXIV@613290to613270	YNL011C		`tgtgtgATGttt`	21	100	1	4	4	40.8	91.2	10.2
chrXIV@613253to613197	YNL011C		`cggactATGaaa`	57	27	0	10	4	40.8	91.2	10.2
chrXIV@609543to609563	YNL012W	SPO1	`ttttttATGttt`	21	123	0	2	1	5.4	7.0	1.5
chrXIV@609625to609651	YNL012W	SPO1	`aagtaaATGcac`	27	35	0	0	1	5.4	7.0	1.5
chrXIV@602756to602794	YNL016W	PUB1	`taaagcATGcct`	39	113	3	1	4	65.8	96.5	401.0
chrXIV@585349to585317	YNL025C	SSN8	`caaaaaATGccc`	33	26	4	5	4	40.9	23.9	6.1
chrXIV@548062to548103	YNL042W	BOP3	`cattacATGgaa`	42	-3	13	4	13	23.6	21.3	8.0
chrXIV@537934to537911	YNL049C	SFB2	`ccattaATGatc`	24	0	0	0	0	16.7	32.2	23.3
chrXIV@529667to529723	YNL053W	MSG5	`acaggaATGtac`	57	219	0	10	3	20.5	34.1	11.5
chrXIV@529689to529694	YNL053W	MSG5	`aggaaaATGtag`	6	248	0	0	3	20.5	34.1	11.5
chrXIV@529706to529723	YNL053W	MSG5	`tttttgATGttt`	18	219	0	6	3	20.5	34.1	11.5
chrXIV@529757to529807	YNL053W	MSG5	`acaaaaATGtta`	51	135	0	1	3	20.5	34.1	11.5
chrXIV@529839to529853	YNL053W	MSG5	`agggttATGcaa`	15	89	3	2	3	20.5	34.1	11.5
chrXIV@517244to517252	YNL056W	OCA2	`ttcttgATGcta`	9	-3	0	0	8	130.2	167.7	39.1
chrXIV@507641to507670	YNL063W	MTQ1	`cggtcaATGtct`	30	88	3	5	8	26.9	44.4	5.7
chrXIV@507721to507837	YNL063W	MTQ1	`agttgaATGgta`	117	-79	5	3	8	26.9	44.4	5.7
chrXIV@503631to503675	YNL065W	AQR1	`aaaattATGgat`	45	49	2	15	2	104.1	100.5	9.5
chrXIV@483399to483407	YNL076W	MKS1	`atttgaATGatc`	9	149	6	3	11	44.1	44.5	13.3
chrXIV@447458to447469	YNL094W	APP1	`tgtcatATGttt`	12	143	5	3	15	34.2	32.9	4.0

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXIV@392816to392827	YNL124W	NAF1	aaaaagATGgta	12	66	0	1	0	18.5	43.7	23.1
chrXIV@392824to392871	YNL124W	NAF1	ggtaggATGata	48	22	0	1	0	18.5	43.7	23.1
chrXIV@392836to392871	YNL124W	NAF1	ggtaggATGaag	36	22	0	1	0	18.5	43.7	23.1
chrXIV@392846to392890	YNL124W	NAF1	agcggtATGaaa	45	3	0	1	0	18.5	43.7	23.1
chrXIV@357139to357144	YNL142W	MEP2	taagaaATGtaa	6	310	1	0	15	23.6	18.5	1.9
chrXIV@357228to357359	YNL142W	MEP2	ttatcaATGaag	132	95	12	13	15	23.6	18.5	1.9
chrXIV@357299to357307	YNL142W	MEP2	ttacacATGtgc	9	147	1	2	15	23.6	18.5	1.9
chrXIV@350725to350847	YNL147W	LSM7	tgctctATGttc	123	94	0	9	24	59.1	199.1	244.2
chrXIV@350856to350897	YNL147W	LSM7	atacgcATGtac	42	44	19	22	24	59.1	199.1	244.2
chrXIV@349795to349787	YNL149C	PGA2	gaaaagATGtta	9	30	1	2	8	383.1	621.3	239.9
chrXIV@349790to349767	YNL149C	PGA2	gatgttATGaag	24	10	8	23	8	383.1	621.3	239.9
chrXIV@342136to341912	YNL156C	NSG2	acattgATGata	225	-57	24	105	27	136.1	195.8	35.2
chrXIV@326340to326299	YNL164C	IBD2	attttcATGcca	42	-22	2	5	4	201.6	157.3	16.4
chrXIV@297686to297678	YNL182C	IPI3	gggcatATGcgt	9	50	1	2	0	158.4	184.9	38.6
chrXIV@289372to289386	YNL186W	UBP10	aggagcATGcat	15	113	4	3	9	81.0	87.0	38.9
chrXIV@287772to288038	YNL187W		acatagATGgta	267	-43	6	21	6	19.1	19.4	1.0
chrXIV@287788to287799	YNL187W		ggcattATGagt	12	196	0	0	6	19.1	19.4	1.0
chrXIV@287809to287823	YNL187W		gaaaaaATGatg	15	172	4	1	6	19.1	19.4	1.0
chrXIV@287812to287823	YNL187W		aaaatgATGaaa	12	172	2	1	6	19.1	19.4	1.0
chrXIV@287820to288038	YNL187W		gaaagaATGaat	219	-43	2	20	6	19.1	19.4	1.0
chrXIV@287824to287874	YNL187W		gaatgaATGcaa	51	121	1	7	6	19.1	19.4	1.0
chrXIV@287878to287910	YNL187W		tagcgaATGtat	33	85	0	5	6	19.1	19.4	1.0
chrXIV@287882to287899	YNL187W		gaatgtATGgaa	18	96	0	2	6	19.1	19.4	1.0
chrXIV@287903to287926	YNL187W		taaggaATGgtt	24	69	1	4	6	19.1	19.4	1.0
chrXIV@287976to288038	YNL187W		atcaatATGaca	63	-43	0	0	6	19.1	19.4	1.0
chrXIV@286304to286360	YNL188W	KAR1	gagttcATGaat	57	-52	0	0	2	292.7	80.5	8.9
chrXIV@280399to280419	YNL191W	DUG3	atttgaATGtat	21	13	6	3	6	34.5	43.2	18.6
chrXIV@250338to250318	YNL211C		aagaatATGttt	21	3	23	7	23	90.4	92.9	25.1
chrXIV@218738to218733	YNL230C	ELA1	atacatATGtaa	6	71	1	0	4	32.4	18.1	4.3
chrXIV@218727to218692	YNL230C	ELA1	acttacATGcaa	36	30	2	6	4	32.4	18.1	4.3
chrXIV@218708to218637	YNL230C	ELA1	ttgttcATGgaa	72	-25	2	2	4	32.4	18.1	4.3
chrXIV@218688to218659	YNL230C	ELA1	tagtgaATGtat	30	-3	1	2	4	32.4	18.1	4.3
chrXIV@218672to218637	YNL230C	ELA1	cgattgATGtcg	36	-25	1	1	4	32.4	18.1	4.3
chrXIV@202258to202299	YNL238W	KEX2	tttcatATGcat	42	129	7	10	14	32.0	41.8	23.5
chrXIV@200482to201933	YNL239W	LAP3	tgttacATGctt	1452	-1364	22	13	29	33.8	46.9	80.4
chrXIV@200097to200056	YNL240C	NAR1	catcgcATGaag	42	79	0	0	0	18.7	41.5	11.3
chrXIV@200085to200056	YNL240C	NAR1	aaaaaaATGata	30	79	0	0	0	18.7	41.5	11.3
chrXIV@200069to200004	YNL240C	NAR1	cgttttATGgtg	66	27	0	6	0	18.7	41.5	11.3
chrXIV@200063to200004	YNL240C	NAR1	atggtgATGact	60	27	0	6	0	18.7	41.5	11.3
chrXIV@181092to181051	YNL249C	MPA43	ttaaaaATGtat	42	29	5	5	5	17.1	53.8	2.9
chrXIV@181054to181031	YNL249C	MPA43	ctttaaATGaga	24	9	0	0	5	17.1	53.8	2.9
chrXIV@169322to169308	YNL254C		gtagcgATGaga	15	60	0	0	1	41.4	39.5	10.9
chrXIV@169296to169264	YNL254C		tactgtATGtgc	33	16	1	7	1	41.4	39.5	10.9
chrXIV@164558to164569	YNL256W	FOL1	tagtaaATGcaa	12	54	1	0	2	51.5	94.0	19.6
chrXIV@164376to164281	YNL257C	SIP3	agctgcATGagt	96	-39	10	4	10	11.6	24.6	6.4
chrXIV@117050to117166	YNL277W	MET2	ttgtggATGcac	117	182	0	0	0	6.3	23.1	8.9

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXIV@117078to117239	YNL277W	MET2	taagtcATGtta	162	109	0	0	0	6.3	23.1	8.9
chrXIV@117163to117291	YNL277W	MET2	caatagATGagc	129	57	0	3	0	6.3	23.1	8.9
chrXIV@80281to80240	YNL294C	RIM21	cactcgATGaat	42	-19	1	7	2	103.5	103.8	5.4
chrXIV@22679to22629	YNL329C	PEX6	gcatatATGtgt	51	-3	0	5	0	19.7	27.8	4.1
chrXIV@635912to635947	YNR004W		gactaaATGcat	36	-3	0	4	0	19.8	38.9	15.8
chrXIV@647373to647390	YNR012W	URK1	atttatATGcga	18	43	1	4	1	65.0	77.0	24.2
chrXIV@652348to652413	YNR014W		acacaaATGtat	66	53	3	1	5	8.5	5.3	4.8
chrXIV@652358to652381	YNR014W		atatatATGtgt	24	85	2	0	5	8.5	5.3	4.8
chrXIV@652364to652381	YNR014W		atgtgtATGtat	18	85	0	0	5	8.5	5.3	4.8
chrXIV@652372to652413	YNR014W		gtatatATGtat	42	53	1	1	5	8.5	5.3	4.8
chrXIV@652384to652413	YNR014W		ataggtATGtgt	30	53	0	1	5	8.5	5.3	4.8
chrXIV@652413to652451	YNR014W		aaactaATGatc	39	15	1	5	5	8.5	5.3	4.8
chrXIV@661716to661705	YNR016C	ACC1	cggtgcATGtgt	12	330	2	0	210	30.3	55.6	228.3
chrXIV@687601to687696	YNR033W	ABZ1	tacacgATGacc	96	-60	0	5	0	36.4	42.0	16.1
chrXIV@699677to699694	YNR040W		tatcttATGtgg	18	-3	1	2	1	36.4	63.0	14.1
chrXIV@711443to711469	YNR048W		catcagATGaag	27	162	1	1	2	19.2	44.1	8.7
chrXIV@711466to711480	YNR048W		ttttcaATGaac	15	151	0	1	2	19.2	44.1	8.7
chrXIV@711475to711480	YNR048W		aactctATGtag	6	151	0	0	2	19.2	44.1	8.7
chrXIV@711539to711559	YNR048W		agaaggATGgcg	21	72	1	0	2	19.2	44.1	8.7
chrXIV@715464to715441	YNR050C	LYS9	aattacATGgga	24	52	1	3	3	104.6	157.6	136.2
chrXIV@730401to730381	YNR055C	HOL1	tatttcATGcta	21	195	7	3	19	82.8	93.6	22.7
chrXIV@760937to760908	YNR068C		ctagtaATGctt	30	24	0	0	0	7.2	14.6	0.0
chrXIV@760895to760881	YNR068C		aacaaaATGtat	15	-3	0	0	0	7.2	14.6	0.0
chrXV@324901to324957	YOL001W	PHO80	catttgATGaat	57	292	12	12	29	59.4	38.1	4.0
chrXV@324962to325054	YOL001W	PHO80	aatctaATGccc	93	195	17	42	29	59.4	38.1	4.0
chrXV@324394to323411	YOL002C	IZH2	ttaattATGctg	984	-953	4	18	4	135.3	388.2	39.3
chrXV@324387to324349	YOL002C	IZH2	tgctgcATGttg	39	-15	4	16	4	135.3	388.2	39.3
chrXV@310206to310129	YOL009C	MDM12	tctaacATGaga	78	-10	0	8	0	16.7	35.0	10.1
chrXV@310194to310129	YOL009C	MDM12	aaaagcATGcca	66	-10	0	7	0	16.7	35.0	10.1
chrXV@310184to310179	YOL009C	MDM12	catcctATGtaa	6	40	0	0	0	16.7	35.0	10.1
chrXV@305209to305244	YOL011W	PLB3	actactATGtta	36	105	0	18	0	95.4	36.5	9.5
chrXV@299638to299721	YOL014W		gtgagaATGtct	84	-28	31	35	38	117.3	159.9	6.0
chrXV@292117to292067	YOL018C	TLG2	caattgATGtac	51	-7	6	11	6	56.1	94.3	24.0
chrXV@271377to271339	YOL028C	YAP7	ctttcaATGgat	39	-31	0	0	9	50.6	53.9	25.6
chrXV@256489to256527	YOL036W		gcctatATGccc	39	216	19	8	24	33.4	34.8	17.2
chrXV@255045to255019	YOL038C-A		caattgATGgga	27	0	5	10	14	81.7	22.5	18.9
chrXV@255027to255019	YOL038C-A		acttatATGatt	9	0	0	0	14	81.7	22.5	18.9
chrXV@249564to249532	YOL043C	NTG2	caaaaaATGtat	33	0	4	6	4	29.5	33.2	3.1
chrXV@212178to212252	YOL061W	PRS5	gatgagATGaga	75	-9	2	23	2	94.0	188.2	96.7
chrXV@168581to168592	YOL082W	ATG19	tagtatATGttt	12	134	0	2	0	97.8	111.7	15.8
chrXV@168626to168634	YOL082W	ATG19	atctccATGata	9	92	0	6	0	97.8	111.7	15.8
chrXV@168631to168678	YOL082W	ATG19	catgatATGagt	48	48	0	30	0	97.8	111.7	15.8
chrXV@159167to159175	YOL086W-A		tagtagATGcaa	9	-3	0	0	0	76.3	128.2	51.7
chrXV@153570to153562	YOL089C	HAL9	gaataaATGtct	9	73	1	0	0	14.9	18.8	6.9
chrXV@139056to138106	YOL096C	COQ3	agtcttATGgga	951	-938	2	3	2	66.8	43.2	19.5
chrXV@136005to136046	YOL097W-A		atttacATGaat	42	173	0	0	3	41.0	39.4	1.1

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXV@136029to136046	YOL097W-A		ggaaaaATGcag	18	173	0	0	3	41.0	39.4	1.1
chrXV@136184to136231	YOL097W-A		taaagtATGgta	48	-12	2	9	3	41.0	39.4	1.1
chrXV@129156to129179	YOL100W	PKH2	atcttgATGaac	24	57	13	2	14	12.5	13.6	6.1
chrXV@123991to125829	YOL103W	ITR2	tttttcATGgct	1839	-1829	5	1	29	83.3	121.0	18.7
chrXV@117662to117654	YOL104C	NDJ1	taatccATGtgg	9	201	0	1	3	34.7	51.5	0.2
chrXV@117594to117562	YOL104C	NDJ1	ttacaaATGgaa	33	109	1	6	3	34.7	51.5	0.2
chrXV@117505to117476	YOL104C	NDJ1	attgtcATGaac	30	23	0	6	3	34.7	51.5	0.2
chrXV@115857to115837	YOL105C	WSC3	cattatATGaaa	21	30	0	6	1	39.7	35.0	2.6
chrXV@115848to115837	YOL105C	WSC3	aaattcATGtcc	12	30	0	6	1	39.7	35.0	2.6
chrXV@108987to108970	YOL111C	MDY2	gaaaacATGcac	18	75	3	1	5	13.4	44.4	121.3
chrXV@106577to106588	YOL112W	MSB4	ttacggATGatt	12	121	11	4	13	47.0	75.6	4.9
chrXV@106701to106712	YOL112W	MSB4	cccggcATGaca	12	-3	0	1	13	47.0	75.6	4.9
chrXV@91476to91465	YOL122C	SMF1	tatttcATGaat	12	47	2	1	2	71.5	91.6	23.7
chrXV@83787to83846	YOL125W	TRM13	ggtgctATGaag	60	-13	2	12	2	61.9	62.8	15.7
chrXV@74297to74314	YOL130W	ALR1	ttctacATGgaa	18	85	32	3	38	83.6	89.9	22.6
chrXV@65456to65473	YOL137W	BSC6	atatcgATGttt	18	147	0	0	9	20.5	30.5	18.2
chrXV@65514to65525	YOL137W	BSC6	ccgatcATGcat	12	95	0	0	9	20.5	30.5	18.2
chrXV@65546to65554	YOL137W	BSC6	tctaaaATGcta	9	66	9	2	9	20.5	30.5	18.2
chrXV@65406to65377	YOL138C		atacatATGgtg	30	28	0	1	0	4.2	11.5	4.2
chrXV@40614to40643	YOL152W	FRE7	ttcattATGcac	30	103	0	5	1	28.3	35.2	10.6
chrXV@40647to40688	YOL152W	FRE7	taaaccATGcct	42	58	1	3	1	28.3	35.2	10.6
chrXV@34496to34552	YOL154W	ZPS1	ccgcacATGctt	57	104	0	4	0	23.2	34.1	0.8
chrXV@21323to21312	YOL158C	ENB1	tcgtgaATGtct	12	3	0	2	0	114.4	164.9	22.6
chrXV@15604to15584	YOL159C-A		tattaaATGaat	21	81	0	1	0	65.3	100.5	39.7
chrXV@9464to9478	YOL163W		tattgcATGatt	15	117	0	0	0	3.3	6.3	0.4
chrXV@9479to9520	YOL163W		gtttaaATGcta	42	75	0	0	0	3.3	6.3	0.4
chrXV@331288to331323	YOR003W	YSP3	cgagcaATGgcg	36	132	0	8	0	35.9	18.5	1.7
chrXV@337437to337396	YOR005C	DNL4	ctaactATGaaa	42	53	0	0	0	13.8	19.2	2.4
chrXV@337416to337396	YOR005C	DNL4	aaacatATGtta	21	53	0	0	0	13.8	19.2	2.4
chrXV@337408to337376	YOR005C	DNL4	gttaatATGtgg	33	33	0	0	0	13.8	19.2	2.4
chrXV@347226to347155	YOR010C	TIR2	tccgtaATGatc	72	206	1	5	1	16.6	26.4	9.0
chrXV@347176to347165	YOR010C	TIR2	tgtaagATGttc	12	216	1	0	1	16.6	26.4	9.0
chrXV@347142to347137	YOR010C	TIR2	agcatcATGtga	6	188	0	0	1	16.6	26.4	9.0
chrXV@347105to347076	YOR010C	TIR2	aaagtaATGttc	30	127	0	8	1	16.6	26.4	9.0
chrXV@347047to346922	YOR010C	TIR2	cgaacaATGaga	126	-27	0	9	1	16.6	26.4	9.0
chrXV@377725to377708	YOR023C	AHC1	gtgtatATGtcc	18	-3	0	0	1	8.3	19.4	12.8
chrXV@389189to389209	YOR031W	CRS5	actacaATGtca	21	3	0	2	0	20.0	32.1	0.0
chrXV@394610to394599	YOR033C	EXO1	atctatATGctc	12	76	7	1	7	38.0	56.8	5.5
chrXV@412873to412923	YOR044W	IRC23	ctgttgATGtat	51	83	4	20	6	106.6	177.1	25.1
chrXV@423817to423710	YOR049C	RSB1	ttcaaaATGtcc	108	-22	4	3	4	9.8	7.7	1.2
chrXV@423740to423699	YOR049C	RSB1	ccctttATGgtg	42	-33	0	0	4	9.8	7.7	1.2
chrXV@432120to432131	YOR057W	SGT1	agcactATGaca	12	56	6	0	4	53.9	73.5	35.5
chrXV@432131to432148	YOR057W	SGT1	aaagtaATGgca	18	39	4	5	4	53.9	73.5	35.5
chrXV@436354to436259	YOR058C	ASE1	cttttgATGttg	96	-87	1	0	6	15.0	23.6	12.9
chrXV@441433to441450	YOR061W	CKA2	gtttgtATGatt	18	85	19	5	32	110.3	164.0	86.8
chrXV@446794to446684	YOR064C	YNG1	actgaaATGtat	111	-55	0	14	0	50.1	85.0	6.9

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXV@446790to446779	YOR064C	YNG1	`aaatgtATGatg`	12	40	0	3	0	50.1	85.0	6.9
chrXV@446787to446779	YOR064C	YNG1	`tgtatgATGcgc`	9	40	0	3	0	50.1	85.0	6.9
chrXV@480511to480777	YOR084W	LPX1	`tgcgtaATGtgc`	267	-189	0	6	0	16.7	14.9	0.2
chrXV@487628to487666	YOR087W	YVC1	`tattcaATGcaa`	39	42	2	0	2	30.3	46.1	16.4
chrXV@494806to494913	YOR092W	ECM3	`gaatatATGttt`	108	214	0	16	3	18.2	25.4	11.1
chrXV@494864to494887	YOR092W	ECM3	`tattatATGctt`	24	240	0	3	3	18.2	25.4	11.1
chrXV@516850to516449	YOR103C	OST2	`gaatacATGact`	402	-392	1	7	23	317.7	336.2	145.1
chrXV@521346to521405	YOR107W	RGS2	`cagcacATGcca`	60	-52	0	0	1	13.4	10.5	0.2
chrXV@533988to534008	YOR113W	AZF1	`ctatagATGgtc`	21	67	2	0	5	15.2	9.3	12.3
chrXV@539516to539508	YOR115C	TRS33	`gacctcATGcca`	9	43	1	0	0	105.7	210.2	33.4
chrXV@602458to602441	YOR143C	THI80	`gcgtgaATGata`	18	99	1	0	0	109.8	156.8	27.6
chrXV@609225to609199	YOR148C	SPP2	`ggtaaaATGtct`	27	2	1	8	1	37.6	132.7	20.3
chrXV@609204to609199	YOR148C	SPP2	`tctaggATGtag`	6	2	0	0	1	37.6	132.7	20.3
chrXV@618487to618467	YOR152C		`gataatATGtgg`	21	179	0	5	2	39.9	17.6	5.6
chrXV@624682to624702	YOR154W	SLP1	`gacgcaATGgat`	21	27	1	2	2	34.1	93.9	8.6
chrXV@658551to658583	YOR174W	MED4	`aaagaaATGcga`	33	164	0	3	2	66.8	165.0	15.2
chrXV@658742to658774	YOR174W	MED4	`caacgaATGtta`	33	-27	0	0	2	66.8	165.0	15.2
chrXV@682449to682297	YOR185C	GSP2	`gtcaagATGctc`	153	191	0	5	20	7.7	23.2	30.4
chrXV@682370to682215	YOR185C	GSP2	`ccttacATGgcg`	156	109	0	3	20	7.7	23.2	30.4
chrXV@682333to682244	YOR185C	GSP2	`tatacaATGtca`	90	138	0	1	20	7.7	23.2	30.4
chrXV@682274to682215	YOR185C	GSP2	`agccgcATGtgg`	60	109	0	0	20	7.7	23.2	30.4
chrXV@682225to682190	YOR185C	GSP2	`gtgtaaATGgta`	36	84	0	0	20	7.7	23.2	30.4
chrXV@682183to682163	YOR185C	GSP2	`ttcttgATGgaa`	21	57	18	2	20	7.7	23.2	30.4
chrXV@710411to710449	YOR193W	PEX27	`tagactATGacc`	39	-3	2	4	0	26.1	29.3	5.8
chrXV@741632to738924	YOR211C	MGM1	`gaaagcATGagt`	2709	-2645	18	10	23	21.4	28.6	19.5
chrXV@755067to755029	YOR219C	STE13	`agcctcATGacc`	39	20	4	2	4	19.2	23.0	9.6
chrXV@757926to757931	YOR222W	ODC2	`tatcaaATGtaa`	6	399	5	11	63	424.1	215.4	9.8
chrXV@757937to757951	YOR222W	ODC2	`aggacaATGaga`	15	379	22	18	63	424.1	215.4	9.8
chrXV@757944to757973	YOR222W	ODC2	`tgagacATGgtt`	30	357	11	49	63	424.1	215.4	9.8
chrXV@758046to758054	YOR222W	ODC2	`tctaacATGaaa`	9	276	0	15	63	424.1	215.4	9.8
chrXV@758066to758170	YOR222W	ODC2	`ctacgaATGcta`	105	160	0	269	63	424.1	215.4	9.8
chrXV@758079to758288	YOR222W	ODC2	`tattctATGcca`	210	42	2	450	63	424.1	215.4	9.8
chrXV@758170to758232	YOR222W	ODC2	`ttgttgATGact`	63	98	0	94	63	424.1	215.4	9.8
chrXV@758206to758232	YOR222W	ODC2	`ctcgacATGcat`	27	98	0	40	63	424.1	215.4	9.8
chrXV@762789to762797	YOR227W		`ttgtatATGtat`	9	28	0	0	0	16.7	12.7	5.7
chrXV@772530to772559	YOR231W	MKK1	`tcatttATGgtt`	30	42	1	1	1	14.3	42.4	11.3
chrXV@796855to796787	YOR246C		`aagacaATGgtt`	69	-6	18	63	16	257.5	334.9	26.9
chrXV@803511to803494	YOR251C		`caaacaATGagg`	18	30	0	0	0	50.1	132.4	77.1
chrXV@841089to841069	YOR275C	RIM20	`ttatctATGgag`	21	2	2	0	0	20.0	28.1	8.7
chrXV@875359to875336	YOR297C	TIM18	`acggtgATGcga`	24	17	3	0	3	41.0	75.1	46.5
chrXV@889009to889056	YOR305W		`taaaacATGata`	48	-37	16	2	21	121.7	172.3	18.9
chrXV@891588to891532	YOR306C	MCH5	`tgcttgATGtac`	57	103	7	40	7	111.4	155.6	7.5
chrXV@894198to894160	YOR307C	SLY41	`tattatATGctt`	39	72	16	7	32	39.2	73.3	18.3
chrXV@894188to894135	YOR307C	SLY41	`ttatatATGcaa`	54	47	22	9	32	39.2	73.3	18.3
chrXV@904698to904709	YOR315W	SFG1	`gtaaatATGttt`	12	47	3	5	19	75.1	177.4	67.4
chrXV@912762to912782	YOR319W	HSH49	`gtaaaaATGaat`	21	36	0	1	0	42.6	109.5	14.4

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXV@912766to912843	YOR319W	HSH49	`aaatgaATGggc`	78	-25	0	7	0	42.6	109.5	14.4
chrXV@967755to967663	YOR342C		`ctcctaATGagt`	93	42	4	19	3	67.3	106.0	33.0
chrXV@967712to967677	YOR342C		`tcatctATGgta`	36	56	2	6	3	67.3	106.0	33.0
chrXV@1010109to1010114	YOR358W	HAP5	`gagataATGtaa`	6	44	2	0	3	37.6	38.9	12.7
chrXV@1023258to1023172	YOR363C	PIP2	`gagcggATGaaa`	87	-37	5	1	4	12.1	16.4	3.0
chrXV@1055479to1055499	YOR381W	FRE3	`aagagaATGatt`	21	43	0	2	1	15.4	29.5	0.5
chrXV@1055499to1055612	YOR381W	FRE3	`ttgctgATGaac`	114	-70	1	3	1	15.4	29.5	0.5
chrXVI@552008to552040	YPL003W	ULA1	`ccgtagATGaaa`	33	-24	0	0	0	54.6	70.1	5.9
chrXVI@543888to543865	YPL007C	TFC8	`agcagcATGact`	24	21	3	15	3	89.8	71.3	9.3
chrXVI@539236to539277	YPL008W	CHL1	`cagttgATGaca`	42	104	4	0	5	18.9	36.1	3.4
chrXVI@539285to539296	YPL008W	CHL1	`cagcacATGcta`	12	85	0	3	5	18.9	36.1	3.4
chrXVI@506647to506679	YPL022W	RAD1	`tgctaaATGtgt`	33	15	5	5	5	21.6	40.0	3.7
chrXVI@495461to495481	YPL029W	SUV3	`tcaactATGaaa`	21	22	0	0	0	17.2	47.3	6.5
chrXVI@467154to467189	YPL045W	VPS16	`tccctaATGatt`	36	67	8	3	5	16.7	38.0	7.7
chrXVI@466961to466944	YPL046C	ELC1	`aaatttATGaat`	18	5	3	5	3	66.8	122.0	36.9
chrXVI@453197to453180	YPL057C	SUR1	`cttcgcATGttt`	18	127	24	7	29	31.8	27.8	26.9
chrXVI@426163to426207	YPL066W		`tgtgggATGctt`	45	22	1	6	0	24.6	32.2	4.4
chrXVI@426189to426200	YPL066W		`ttttctATGggt`	12	29	0	0	0	24.6	32.2	4.4
chrXVI@420530to420489	YPL071C		`gtttaaATGact`	42	-25	4	6	4	53.9	72.8	22.7
chrXVI@410387to410494	YPL076W	GPI2	`tttcgtATGacc`	108	-55	9	8	9	22.9	22.5	10.0
chrXVI@381918to381923	YPL088W		`ccaactATGtaa`	6	38	0	0	0	89.5	106.8	3.2
chrXVI@375458to375484	YPL091W	GLR1	`cttcatATGtat`	27	14	6	14	7	89.0	179.1	130.2
chrXVI@359421to359320	YPL103C	FMP30	`gattgcATGcct`	102	-82	1	1	0	57.2	37.1	8.5
chrXVI@289168to289151	YPL140C	MKK2	`atttatATGttg`	18	119	0	7	1	37.7	44.3	8.9
chrXVI@289145to289119	YPL140C	MKK2	`atttgcATGaaa`	27	87	0	0	1	37.7	44.3	8.9
chrXVI@277546to277514	YPL146C	NOP53	`acgttaATGaat`	33	-13	0	4	3	100.1	174.0	136.7
chrXVI@272857to272813	YPL148C	PPT2	`tttctaATGaac`	45	0	5	24	5	84.5	63.8	3.9
chrXVI@272825to272292	YPL148C	PPT2	`ctttgaATGcct`	534	-521	0	1	5	84.5	63.8	3.9
chrXVI@271224to271232	YPL149W	ATG5	`taaataATGaag`	9	76	0	0	14	119.7	154.0	6.0
chrXVI@271234to271275	YPL149W	ATG5	`agtagcATGctc`	42	33	3	40	14	119.7	154.0	6.0
chrXVI@271250to271300	YPL149W	ATG5	`gtgcgaATGaat`	51	8	5	46	14	119.7	154.0	6.0
chrXVI@271297to271305	YPL149W	ATG5	`aaacctATGatg`	9	3	2	0	14	119.7	154.0	6.0
chrXVI@271300to271305	YPL149W	ATG5	`cctatgATGtaa`	6	3	1	0	14	119.7	154.0	6.0
chrXVI@267567to267520	YPL151C	PRP46	`ccgaggATGcag`	48	-13	6	4	6	22.9	64.3	9.4
chrXVI@267549to267520	YPL151C	PRP46	`tgttacATGgag`	30	-13	2	4	6	22.9	64.3	9.4
chrXVI@256844to256800	YPL156C	PRM4	`atatatATGttc`	45	35	2	28	3	54.9	29.0	15.4
chrXVI@254445to254431	YPL158C		`acaaatATGttg`	15	123	0	0	1	14.3	34.3	27.5
chrXVI@244116to244108	YPL162C		`acttgaATGtac`	9	83	0	1	0	15.0	39.4	13.5
chrXVI@222867to222811	YPL174C	NIP100	`actcatATGctg`	57	40	15	9	15	15.1	22.0	1.2
chrXVI@222852to222811	YPL174C	NIP100	`gactttATGttg`	42	40	14	7	15	15.1	22.0	1.2
chrXVI@214282to214265	YPL177C	CUP9	`ttattcATGtac`	18	305	0	1	29	41.6	125.6	79.5
chrXVI@214201to214184	YPL177C	CUP9	`atattaATGatt`	18	224	0	0	29	41.6	125.6	79.5
chrXVI@214187to214128	YPL177C	CUP9	`ttttctATGact`	60	168	0	0	29	41.6	125.6	79.5
chrXVI@214147to214121	YPL177C	CUP9	`ctcttaATGcct`	27	161	0	0	29	41.6	125.6	79.5
chrXVI@214116to214072	YPL177C	CUP9	`aagattATGtta`	45	112	11	10	29	41.6	125.6	79.5
chrXVI@213995to213957	YPL177C	CUP9	`acttttATGcta`	39	-3	10	19	29	41.6	125.6	79.5

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Table S3: All uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXVI@181333to181404	YPL193W	RSA1	`tcattgATGcta`	72	-3	2	16	3	31.9	56.0	23.0
chrXVI@181394to181411	YPL193W	RSA1	`tgcgacATGgac`	18	-10	0	0	3	31.9	56.0	23.0
chrXVI@163651to163535	YPL206C	PGC1	`ttgttgATGtta`	117	-60	5	19	4	100.1	125.0	76.3
chrXVI@150245to150219	YPL214C	THI6	`ctaaccATGgtt`	27	30	6	5	0	45.5	46.7	6.1
chrXVI@121256to121248	YPL227C	ALG5	`aattggATGctg`	9	82	2	10	3	147.3	230.7	51.2
chrXVI@117061to117069	YPL229W		`tattacATGaaa`	9	-3	0	0	0	18.6	28.6	13.6
chrXVI@85371to85357	YPL246C	RBD2	`agggggATGgga`	15	61	0	1	0	50.5	106.3	56.8
chrXVI@55379to55347	YPL258C	THI21	`tctttaATGata`	33	195	0	8	1	19.5	14.6	0.2
chrXVI@55368to55243	YPL258C	THI21	`acgtatATGtat`	126	91	1	18	1	19.5	14.6	0.2
chrXVI@55339to55325	YPL258C	THI21	`agatcgATGcat`	15	173	0	0	1	19.5	14.6	0.2
chrXVI@55284to55243	YPL258C	THI21	`agagaaATGctc`	42	91	1	7	1	19.5	14.6	0.2
chrXVI@28270to28163	YPL272C		`atttgtATGggg`	108	0	0	4	0	10.1	12.5	1.3
chrXVI@585700to585686	YPR013C		`tgttctATGgct`	15	105	0	0	0	17.9	15.9	2.6
chrXVI@594423to594431	YPR018W	RLF2	`aattatATGttt`	9	41	2	2	2	44.1	32.7	21.4
chrXVI@603543to603523	YPR021C	AGC1	`ttttatATGtta`	21	170	3	3	8	21.7	21.3	6.6
chrXVI@603394to603371	YPR021C	AGC1	`gaaagtATGcag`	24	18	4	3	8	21.7	21.3	6.6
chrXVI@634044to634106	YPR032W	SRO7	`tggaatATGtta`	63	13	0	3	0	9.5	11.0	17.8
chrXVI@682192to682197	YPR067W	ISA2	`ttgtacATGtga`	6	19	6	1	11	68.8	30.4	21.4
chrXVI@690080to690145	YPR072W	NOT5	`gattgcATGaaa`	66	-42	4	6	6	118.5	82.7	101.7
chrXVI@709869to709831	YPR085C		`ggtgtgATGtgc`	39	6	3	4	3	18.2	32.1	4.5
chrXVI@709840to708494	YPR085C		`attacaATGggc`	1347	-1331	1	0	3	18.2	32.1	4.5
chrXVI@729780to729797	YPR100W	MRPL51	`gaatatATGgag`	18	-9	0	2	4	333.8	196.5	116.4
chrXVI@744660to744683	YPR109W		`taatctATGttt`	24	3	4	9	12	67.3	106.6	9.3
chrXVI@754820to754861	YPR115W		`ctttttATGgct`	42	13	2	2	2	6.6	19.0	4.8
chrXVI@759722to759745	YPR117W		`ggctgtATGatt`	24	277	0	0	0	10.1	5.8	0.3
chrXVI@759812to759841	YPR117W		`atacacATGcat`	30	181	0	1	0	10.1	5.8	0.3
chrXVI@778463to778534	YPR121W	THI22	`attataATGttg`	72	44	0	12	0	43.2	36.0	0.4
chrXVI@778567to778596	YPR121W	THI22	`agcagtATGcct`	30	-18	0	0	0	43.2	36.0	0.4
chrXVI@790011to790049	YPR127W		`ttttctATGtta`	39	29	3	5	3	22.5	33.9	10.7
chrXVI@790016to790021	YPR127W		`tatgttATGtag`	6	57	2	1	3	22.5	33.9	10.7
chrXVI@812554to812540	YPR138C	MEP3	`caatcaATGcag`	15	92	1	5	10	68.1	46.4	8.5
chrXVI@825056to824994	YPR145C-A		`agcataATGgca`	63	73	0	2	1	32.0	15.1	12.9
chrXVI@833496to833428	YPR152C	URN1	`tctgatATGtat`	69	-25	0	5	0	33.4	54.1	14.4
chrXVI@841196to841276	YPR157W		`ccgtcaATGaca`	81	-15	0	2	0	7.9	8.7	0.4
chrXVI@887843to887829	YPR173C	VPS4	`tagtagATGggg`	15	-3	2	2	2	116.3	162.4	45.3
chrXVI@895804to895772	YPR179C	HDA3	`ataaaaATGata`	33	13	1	1	1	14.3	45.6	7.7
chrXVI@907206to907346	YPR185W	ATG13	`aatagcATGagt`	141	-133	0	0	2	19.4	16.6	8.2

Table S3. All uORFs. All upstream AUG codons in a 5’UTR, as annotated by Nagalakshmi *et al.* (*S1*), were used to predict candidate uORFs. The genomic coordinates of the uORF are listed, along with the downstream protein-coding gene and the initiation sequence context. The length of the uORF is shown, along with the distance from the last nucleotide in the uORF to the first nucleotide in the coding sequence. When the uORF ends downstream of the start codon, this distance will be negative. In a few cases, such as *LAP3* and *MGM1*, the uORF extends in-frame into the protein-coding gene and thus represents an alternate initiation site rather than a uORF. The raw number sequencing reads is shown for ribosome footprints in the uORF specifically, for mRNA fragments in the uORF specifically, and for ribosome footprints on the entire annotated 5’ UTR. The density of sequencing reads (in rpkM) is shown for mRNA fragments in the 5’ UTR and the associated CDS, and for ribosome footprints in the CDS.

Table S4: uORFs in Abundant mRNAs

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrV@140123to140112	YEL009C	GCN4	`tgaaaaATGgct`	12	350	698	25	878	407.8	614.3	38.4
chrXIII@653981to654010	YMR195W	ICY1	`aaactaATGaca`	30	22	108	40	110	245.5	471.6	110.6
chrV@139938to139927	YEL009C	GCN4	`gctatcATGtac`	12	165	61	13	878	407.8	614.3	38.4
chrXIII@56727to56750	YML106W	URA5	`cattgtATGaag`	24	22	39	28	134	516.0	564.8	402.1
chrIV@548367to548356	YDR045C	RPC11	`cgttatATGgct`	12	49	32	18	34	333.2	352.7	117.6
chrXV@299638to299721	YOL014W		`gtgagaATGtct`	84	-28	31	35	38	117.3	159.9	6.0
chrXII@404201to404145	YLR130C	ZRT2	`ctatatATGatg`	57	83	28	44	29	200.3	281.1	12.3
chrXII@404198to404145	YLR130C	ZRT2	`tatatgATGata`	54	83	28	44	29	200.3	281.1	12.3
chrV@140055to140047	YEL009C	GCN4	`agaattATGtgt`	9	285	26	6	878	407.8	614.3	38.4
chrII@602514to602531	YBR187W	GDT1	`acgtttATGaaa`	18	97	24	29	10	327.0	420.0	144.9
chrXIV@342136to341912	YNL156C	NSG2	`acattgATGata`	225	-57	24	105	27	136.1	195.8	35.2
chrXV@757937to757951	YOR222W	ODC2	`aggacaATGaga`	15	379	22	18	63	424.1	215.4	9.8
chrXIII@241727to241701	YML016C	PPZ1	`caatacATGtta`	27	166	19	35	29	154.1	62.2	19.1
chrXV@441433to441450	YOR061W	CKA2	`gtttgtATGatt`	18	85	19	5	32	110.3	164.0	86.8
chrXV@796855to796787	YOR246C		`aagacaATGgtt`	69	-6	18	63	16	257.5	334.9	26.9
chrXII@371317to371514	YLR113W	HOG1	`ccctacATGgtc`	198	106	16	165	22	205.5	221.1	60.1
chrXV@889009to889056	YOR305W		`taaaacATGata`	48	-37	16	2	21	121.7	172.3	18.9
chrV@139913to139902	YEL009C	GCN4	`ttcaagATGttt`	12	140	14	19	878	407.8	614.3	38.4
chrII@556326to556334	YBR158W	AMN1	`aactatATGtgt`	9	208	13	14	41	441.6	247.2	41.1
chrIV@550626to550573	YDR046C	BAP3	`ctattgATGgat`	54	0	11	30	17	129.2	125.3	44.6
chrXV@757944to757973	YOR222W	ODC2	`tgagacATGgtt`	30	357	11	49	63	424.1	215.4	9.8
chrIV@1189625to1189596	YDR357C		`ttttacATGaaa`	30	37	10	23	9	156.1	146.3	38.3
chrIX@187689to187672	YIL094C	LYS12	`gtatctATGcga`	18	44	9	22	2	233.7	368.3	155.1
chrII@723227to723286	YBR253W	SRB6	`attgtgATGata`	60	-22	8	35	8	239.0	152.4	47.1
chrIV@141749to141714	YDL177C		`gtattgATGttt`	36	-7	8	6	17	106.0	157.1	11.2
chrXIV@349790to349767	YNL149C	PGA2	`gatgttATGaag`	24	10	8	23	8	383.1	621.3	239.9
chrXV@891588to891532	YOR306C	MCH5	`tgcttgATGtac`	57	103	7	40	7	111.4	155.6	7.5
chrIV@321654to321640	YDL076C	RXT3	`aattccATGaca`	15	89	6	2	11	100.1	159.2	27.9
chrIV@1362719to1362748	YDR452W	PPN1	`ggttttATGgta`	30	121	6	3	5	109.8	132.7	27.7
chrXIII@251525to251496	YML009C	MRPL39	`atatttATGtgc`	30	-19	6	8	6	357.6	217.0	197.6
chrXV@757926to757931	YOR222W	ODC2	`tatcaaATGtaa`	6	399	5	11	63	424.1	215.4	9.8
chrXVI@271250to271300	YPL149W	ATG5	`gtgcgaATGaat`	51	8	5	46	14	119.7	154.0	6.0
chrXVI@163651to163535	YPL206C	PGC1	`ttgttgATGtta`	117	-60	5	19	4	100.1	125.0	76.3
chrIV@93874to93848	YDL205C	HEM3	`gtttgcATGgta`	27	103	4	12	8	118.0	149.1	40.4
chrVII@1025932to1025825	YGR267C	FOL2	`tcaaacATGtct`	108	85	4	83	12	194.2	319.8	130.3
chrXIII@914661to914653	YMR319C	FET4	`cacggcATGaat`	9	118	4	3	5	206.3	331.3	29.8
chrXV@412873to412923	YOR044W	IRC23	`ctgttgATGtat`	51	83	4	20	6	106.6	177.1	25.1
chrXVI@690080to690145	YPR072W	NOT5	`gattgcATGaaa`	66	-42	4	6	6	118.5	82.7	101.7
chrVII@698542to698577	YGR105W	VMA21	`gctaaaATGaac`	36	25	3	25	3	241.2	284.3	228.9
chrXI@434634to434605	YKL005C	BYE1	`cttgcaATGaaa`	30	86	3	6	1	102.0	50.2	15.6
chrXVI@271234to271275	YPL149W	ATG5	`agtagcATGctc`	42	33	3	40	14	119.7	154.0	6.0
chrIV@447616to447578	YDL002C	NHP10	`aattggATGaga`	39	4	2	28	5	189.1	224.4	53.7
chrIV@1037144to1037170	YDR288W	NSE3	`atcagtATGcta`	27	20	2	12	0	181.5	138.0	17.6
chrIV@1078457to1078434	YDR308C	SRB7	`cattatATGctc`	24	-10	2	9	4	228.9	154.1	67.9
chrVII@38824to38810	YGL246C	RAI1	`tgtaatATGgtg`	15	31	2	2	2	115.2	201.1	35.2

Continued on next page

Table S4: uORFs in Abundant mRNAs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrVII@1025951to1025907	YGR267C	FOL2	`atttaATGctc`	45	167	2	4	12	194.2	319.8	130.3
chrVIII@198323to198267	YHR046C	INM1	`ttttggATGaat`	57	-10	2	9	2	132.4	113.2	39.2
chrXIII@253762to253782	YML007W	YAP1	`ttgtgcATGaac`	21	65	2	12	12	110.3	83.4	39.0
chrXIV@625861to625853	YNL003C	PET8	`acaccgATGaac`	9	23	2	2	8	158.5	103.1	16.4
chrXIV@503631to503675	YNL065W	AQR1	`aaaattATGgat`	45	49	2	15	2	104.1	100.5	9.5
chrXIV@326340to326299	YNL164C	IBD2	`attttcATGcca`	42	-22	2	5	4	201.6	157.3	16.4
chrXV@758079to758288	YOR222W	ODC2	`tattctATGcca`	210	42	2	450	63	424.1	215.4	9.8
chrXVI@121256to121248	YPL227C	ALG5	`aattggATGctg`	9	82	2	10	3	147.3	230.7	51.2
chrXVI@887843to887829	YPR173C	VPS4	`tagtagATGggg`	15	-3	2	2	2	116.3	162.4	45.3
chrII@186489to186457	YBL018C	POP8	`tgataaATGgcc`	33	-19	1	2	1	128.7	207.0	63.2
chrIII@103401to103342	YCL011C	GBP2	`taagctATGggc`	60	-15	1	51	1	527.4	365.0	119.6
chrIV@326180to326145	YDL074C	BRE1	`gttttttATGcta`	36	-3	1	16	2	108.9	134.1	38.5
chrIV@952778to952843	YDR245W	MNN10	`ttgtgcATGtac`	66	-48	1	18	5	346.8	303.3	57.6
chrVIII@195404to195448	YHR045W		`cattgaATGgaa`	45	95	1	13	2	103.3	122.5	16.8
chrX@32049to32105	YJL213W		`ccgttgATGaag`	57	57	1	52	1	109.5	115.0	0.2
chrXI@482804to482796	YKR022C	NTR2	`ctagcaATGtta`	9	15	1	2	1	100.1	91.2	12.7
chrXIII@914710to914696	YMR319C	FET4	`gattcgATGctc`	15	161	1	8	5	206.3	331.3	29.8
chrXIV@349795to349787	YNL149C	PGA2	`gaaaagATGtta`	9	30	1	2	8	383.1	621.3	239.9
chrXIV@297686to297678	YNL182C	IPI3	`gggcatATGcgt`	9	50	1	2	0	158.4	184.9	38.6
chrXIV@80281to80240	YNL294C	RIM21	`cactcgATGaat`	42	-19	1	7	2	103.5	103.8	5.4
chrXIV@715464to715441	YNR050C	LYS9	`aattacATGgga`	24	52	1	3	3	104.6	157.6	136.2
chrXV@516850to516449	YOR103C	OST2	`gaatacATGact`	402	-392	1	7	23	317.7	336.2	145.1
chrII@595918to595929	YBR183W	YPC1	`ttatatATGtct`	12	180	0	2	3	128.2	50.0	6.5
chrIV@1206467to1206441	YDR365C	ESF1	`agcataATGgta`	27	67	0	29	1	176.5	250.2	64.3
chrIV@1498206to1498298	YDR531W		`gagtgcATGcga`	93	-75	0	9	0	155.8	177.1	43.4
chrV@562644to562603	YER186C		`tagtatATGatc`	42	-16	0	21	0	190.3	135.0	0.9
chrVII@506934to506957	YGR007W	MUQ1	`agacaaATGctt`	24	15	0	2	0	100.1	134.3	55.5
chrX@181831to181781	YJL127C-B		`agttaaATGtac`	51	75	0	15	0	162.3	307.3	67.9
chrX@32115to32153	YJL213W		`acagtcATGtcc`	39	9	0	5	1	109.5	115.0	0.2
chrX@32088to32105	YJL213W		`gtaagtATGtca`	18	57	0	29	1	109.5	115.0	0.2
chrXII@346545to346583	YLR104W		`ataggcATGgtt`	39	2	0	10	0	115.5	129.3	39.4
chrXII@541653to541648	YLR194C		`ataagtATGtaa`	6	74	0	2	2	121.7	82.8	52.4
chrXIII@337775to337783	YMR033W	ARP9	`tactatATGcat`	9	3	0	4	4	215.7	154.8	42.5
chrXIII@806529to806482	YMR270C	RRN9	`atattgATGtgt`	48	61	0	15	0	101.0	145.5	11.1
chrXV@21323to21312	YOL158C	ENB1	`tcgtgaATGtct`	12	3	0	2	0	114.4	164.9	22.6
chrXV@758206to758232	YOR222W	ODC2	`ctcgacATGcat`	27	98	0	40	63	424.1	215.4	9.8
chrXV@758170to758232	YOR222W	ODC2	`ttgttgATGact`	63	98	0	94	63	424.1	215.4	9.8
chrXV@758066to758170	YOR222W	ODC2	`ctacgaATGcta`	105	160	0	269	63	424.1	215.4	9.8
chrXV@758046to758054	YOR222W	ODC2	`tctaacATGaaa`	9	276	0	15	63	424.1	215.4	9.8
chrXVI@277546to277514	YPL146C	NOP53	`acgttaATGaat`	33	-13	0	4	3	100.1	174.0	136.7
chrXVI@729780to729797	YPR100W	MRPL51	`gaatatATGgag`	18	-9	0	2	4	333.8	196.5	116.4

Table S4. uORFs in abundant mRNAs. All uORFS in 5’ UTRs with abundant messages are listed, as in table S3, sorted by the number of ribosome footprints observed.

Table S5: All Translated uORFs

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5' UTR # Rib	5' UTR mRNA	CDS mRNA	CDS Rib
chrV@140123to140112	YEL009C	GCN4	`tgaaaaATGgct`	12	350	698	25	878	407.8	614.3	38.4
chrXI@100534to100554	YKL182W	FAS1	`tcttatATGctc`	21	121	187	6	302	76.2	86.3	345.0
chrXIII@653981to654010	YMR195W	ICY1	`aaactaATGaca`	30	22	108	40	110	245.5	471.6	110.6
chrXIII@164343to164233	YML056C	IMD4	`caaatcATGctt`	111	58	38	174	66	201.6	583.5	304.6
chrXIII@164274to164233	YML056C	IMD4	`gaaaaaATGgtg`	42	58	35	131	66	201.6	583.5	304.6
chrXIII@38099to38155	YML116W	ATR1	`tataaaATGaat`	57	40	35	27	33	98.0	105.0	8.5
chrIV@548367to548356	YDR045C	RPC11	`cgttatATGgct`	12	49	32	18	34	333.2	352.7	117.6
chrXV@74297to74314	YOL130W	ALR1	`ttctacATGgaa`	18	85	32	3	38	83.6	89.9	22.6
chrXV@299638to299721	YOL014W		`gtgagaATGtct`	84	-28	31	35	38	117.3	159.9	6.0
chrXIII@38108to38155	YML116W	ATR1	`aataaaATGcat`	48	40	29	23	33	98.0	105.0	8.5
chrII@423096to423061	YBR086C	IST2	`cgatttATGgct`	36	27	28	7	36	23.4	46.0	57.3
chrXII@404201to404145	YLR130C	ZRT2	`ctatatATGatg`	57	83	28	44	29	200.3	281.1	12.3
chrXII@404198to404145	YLR130C	ZRT2	`tatatgATGata`	54	83	28	44	29	200.3	281.1	12.3
chrII@602514to602531	YBR187W	GDT1	`acgtttATGaaa`	18	97	24	29	10	327.0	420.0	144.9
chrXIV@342136to341912	YNL156C	NSG2	`acattgATGata`	225	-57	24	105	27	136.1	195.8	35.2
chrXVI@453197to453180	YPL057C	SUR1	`cttcgcATGttt`	18	127	24	7	29	31.8	27.8	26.9
chrXIV@250338to250318	YNL211C		`aagaatATGttt`	21	3	23	7	23	90.4	92.9	25.1
chrXIV@200482to201933	YNL239W	LAP3	`tgttacATGctt`	1452	-1364	22	13	29	33.8	46.9	80.4
chrXV@894188to894135	YOR307C	SLY41	`ttatatATGcaa`	54	47	22	9	32	39.2	73.3	18.3
chrVIII@364203to364171	YHR129C	ARP1	`gagtacATGcta`	33	16	21	5	22	12.3	35.5	8.4
chrIV@1135874to1135942	YDR334W	SWR1	`aaatttATGaat`	69	-16	19	6	21	25.8	20.9	6.5
chrXII@642601to642621	YLR253W		`agttgaATGttt`	21	7	19	7	20	52.6	64.2	10.6
chrXIII@241727to241701	YML016C	PPZ1	`caatacATGtta`	27	166	19	35	29	154.1	62.2	19.1
chrXIV@350856to350897	YNL147W	LSM7	`atacgcATGtac`	42	44	19	22	24	59.1	199.1	244.2
chrXV@256489to256527	YOL036W		`gcctatATGccc`	39	216	19	8	24	33.4	34.8	17.2
chrXV@441433to441450	YOR061W	CKA2	`gtttgtATGatt`	18	85	19	5	32	110.3	164.0	86.8
chrVIII@364197to364171	YHR129C	ARP1	`atgctaATGcta`	27	16	18	1	22	12.3	35.5	8.4
chrXV@682183to682163	YOR185C	GSP2	`ttcttgATGgaa`	21	57	18	2	20	7.7	23.2	30.4
chrXV@741632to738924	YOR211C	MGM1	`gaaagcATGagt`	2709	-2645	18	10	23	21.4	28.6	19.5
chrXV@796855to796787	YOR246C		`aagacaATGgtt`	69	-6	18	63	16	257.5	334.9	26.9
chrIII@160424to160374	YCR023C		`aaaggaATGcta`	51	6	17	10	17	40.1	47.6	9.8
chrIV@222371to222394	YDL133W		`aagtgaATGata`	24	32	17	10	18	95.5	130.3	13.8
chrXIII@325506to325477	YMR026C	PEX12	`ttttgcATGaag`	30	44	17	9	20	65.4	86.8	8.4
chrXV@324962to325054	YOL001W	PHO80	`aatctaATGccc`	93	195	17	42	29	59.4	38.1	4.0
chrII@164851to164822	YBL029C-A		`gaataaATGtca`	30	48	16	10	17	55.8	89.3	35.9
chrX@153049to153023	YJL139C	YUR1	`aatctaATGctt`	27	28	16	3	0	36.9	44.9	8.0
chrXII@371317to371514	YLR113W	HOG1	`ccctacATGgtc`	198	106	16	165	22	205.5	221.1	60.1
chrXII@528248to528277	YLR188W	MDL1	`acttacATGaga`	30	24	16	5	16	27.6	32.1	17.1
chrXII@641350to641487	YLR251W	SYM1	`agtgatATGata`	138	-22	16	35	15	62.3	83.7	4.8
chrXV@889009to889056	YOR305W		`taaaacATGata`	48	-37	16	2	21	121.7	172.3	18.9
chrXV@894198to894160	YOR307C	SLY41	`tattatATGctt`	39	72	16	7	32	39.2	73.3	18.3
chrII@207174to207191	YBL009W	ALK2	`acatacATGcgc`	18	5	15	2	8	11.1	16.8	21.5
chrIV@104619to104605	YDL198C	GGC1	`cttttgATGgtt`	15	54	15	5	16	40.4	52.9	72.7
chrXVI@222867to222811	YPL174C	NIP100	`actcatATGctg`	57	40	15	9	15	15.1	22.0	1.2
chrVII@834511to834491	YGR168C		`gagctaATGaga`	21	5	14	6	15	60.7	84.5	3.8

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Table S5: All Translated uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXI@317306to317335	YKL064W	MNR2	catttgATGact	30	72	14	6	16	36.3	25.9	13.8
chrXVI@222852to222811	YPL174C	NIP100	gactttATGttg	42	40	14	7	15	15.1	22.0	1.2
chrIV@1488995to1488981	YDR524C	AGE1	ttctggATGttc	15	0	13	2	13	34.2	21.3	10.4
chrIX@301347to301321	YIL029C		gcagttATGcaa	27	67	13	15	16	66.8	72.0	0.5
chrXII@846060to846104	YLR360W	VPS38	gaattgATGgtt	45	-3	13	8	13	58.9	68.8	7.6
chrXIII@784306to784298	YMR258C		gctcacATGata	9	19	13	1	13	55.2	78.7	12.0
chrXIV@548062to548103	YNL042W	BOP3	cattacATGgaa	42	-3	13	4	13	23.6	21.3	8.0
chrXV@129156to129179	YOL100W	PKH2	atcttgATGaac	24	57	13	2	14	12.5	13.6	6.1
chrII@143191to143238	YBL039W-B		agagcgATGaag	48	157	12	7	15	71.7	80.3	18.1
chrIV@1468513to1468463	YDR508C	GNP1	tgctttATGttt	51	28	12	24	12	91.4	196.8	116.4
chrVII@14812to14934	YGL256W	ADH4	gtgatgATGgct	123	-25	12	19	16	59.0	113.7	14.0
chrVII@14809to14934	YGL256W	ADH4	tttgtgATGatg	126	-25	12	23	16	59.0	113.7	14.0
chrXII@641375to641437	YLR251W	SYM1	aatgctATGttg	63	28	12	18	15	62.3	83.7	4.8
chrXIV@357228to357359	YNL142W	MEP2	ttatcaATGaag	132	95	12	13	15	23.6	18.5	1.9
chrII@324008to323898	YBR043C	QDR3	aggcatATGtat	111	-46	11	26	12	62.3	70.2	2.2
chrIV@550626to550573	YDR046C	BAP3	ctattgATGgat	54	0	11	30	17	129.2	125.3	44.6
chrV@492114to492106	YER159C	BUR6	agggcaATGcac	9	154	11	3	7	38.2	98.5	90.9
chrVII@591195to591248	YGR049W	SCM4	atataaATGaga	54	69	11	3	12	12.3	18.0	41.2
chrXII@784823to784831	YLR328W	NMA1	atctgcATGgta	9	81	11	1	18	31.7	51.1	48.1
chrXV@106577to106588	YOL112W	MSB4	ttacggATGatt	12	121	11	4	13	47.0	75.6	4.9
chrIV@1189625to1189596	YDR357C		ttttacATGaaa	30	37	10	23	9	156.1	146.3	38.3
chrIV@1249891to1249820	YDR387C		tagtccATGgtc	72	8	10	12	10	38.1	53.0	2.5
chrV@13599to13634	YEL072W	RMD6	aacagtATGgat	36	85	10	6	8	38.2	53.1	2.7
chrV@254417to254400	YER050C	RSM18	agatgaATGcca	18	15	10	6	8	87.6	210.3	81.7
chrVII@371932to371964	YGL071W	AFT1	cgattcATGcta	33	50	10	1	12	17.4	18.2	16.4
chrVII@334481to334464	YGL094C	PAN2	ttctgaATGgtg	18	-3	10	2	16	26.9	14.7	8.0
chrVII@14843to14866	YGL256W	ADH4	ttagctATGaaa	24	43	10	2	16	59.0	113.7	14.0
chrIX@137975to137943	YIL119C	RPI1	cagttcATGgta	33	70	10	7	10	56.1	34.1	37.8
chrXII@993382to993429	YLR430W	SEN1	ctctgtATGgca	48	1	10	0	19	8.9	11.8	11.7
chrXIII@137529to137558	YML068W	ITT1	taactgATGaaa	30	-9	10	7	13	77.4	63.7	3.8
chrXIV@164376to164281	YNL257C	SIP3	agctgcATGagt	96	-39	10	4	10	11.6	24.6	6.4
chrI@158892to158978	YAR008W	SEN34	tcgtatATGgct	87	-12	9	14	10	57.5	98.9	9.9
chrII@642514to642452	YBR208C	DUR1,2	acgcagATGttt	63	248	9	48	14	98.3	13.7	6.2
chrVII@186027to186113	YGL169W	SUA5	tttttaATGgta	87	-49	9	9	13	59.5	74.0	24.4
chrIX@187689to187672	YIL094C	LYS12	gtatctATGcga	18	44	9	22	2	233.7	368.3	155.1
chrXI@359687to359740	YKL041W	VPS24	atatatATGtat	54	45	9	20	9	53.8	130.2	59.7
chrXV@65546to65554	YOL137W	BSC6	tctaaaATGcta	9	66	9	2	9	20.5	30.5	18.2
chrXVI@410387to410494	YPL076W	GPI2	tttcgtATGacc	108	-55	9	8	9	22.9	22.5	10.0
chrII@326071to326063	YBR044C	TCM62	tctcttATGctt	9	6	8	4	9	57.8	63.2	8.9
chrII@723227to723286	YBR253W	SRB6	attgtgATGata	60	-22	8	35	8	239.0	152.4	47.1
chrVII@605529to605506	YGR057C	LST7	gtttaaATGgtt	24	2	8	2	8	28.2	87.9	7.3
chrVIII@506290to506316	YHR204W	MNL1	atttccATGgat	27	2	8	5	8	17.9	64.5	5.3
chrVIII@506271to506345	YHR204W	MNL1	gtaaccATGata	75	-27	8	9	8	17.9	64.5	5.3
chrX@160592to160600	YJL133W	MRS3	atatttATGtta	9	15	8	3	15	49.1	110.8	20.5
chrX@452309to452359	YJR008W		gataacATGcgg	51	63	8	9	8	22.3	32.4	1.6
chrXI@231809to231820	YKL109W	HAP4	attttaATGggt	12	50	8	1	12	2.6	9.9	12.5

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Table S5: All Translated uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXIV@349790to349767	YNL149C	PGA2	gatgttATGaag	24	10	8	23	8	383.1	621.3	239.9
chrXVI@467154to467189	YPL045W	VPS16	tccctaATGatt	36	67	8	3	5	16.7	38.0	7.7
chrIV@592335to592400	YDR073W	SNF11	ccgtttATGata	66	35	7	5	7	30.5	32.1	22.6
chrIV@1421091to1421102	YDR483W	KRE2	cattttATGaat	12	46	7	3	4	70.7	226.6	150.9
chrVII@436907to436839	YGL032C	AGA2	tctagaATGatt	69	2	7	9	12	38.1	71.5	87.6
chrXII@168999to169073	YLR011W	LOT6	tttgacATGcct	75	28	7	16	5	62.9	40.5	16.4
chrXII@183587to183634	YLR021W	IRC25	aaaagaATGggc	48	-13	7	11	3	64.1	87.2	35.8
chrXII@444760to444710	YLR152C		ttctacATGtgt	51	22	7	4	7	17.0	20.3	1.1
chrXII@534427to534416	YLR189C	ATG26	cactttATGctt	12	22	7	2	7	33.4	26.8	6.4
chrXII@982818to982829	YLR425W	TUS1	actgttATGaac	12	61	7	1	13	5.5	9.7	4.6
chrXIII@26809to26889	YML121W	GTR1	agttcaATGtgg	81	40	7	27	7	78.4	184.4	27.8
chrXIV@202258to202299	YNL238W	KEX2	tttcatATGcat	42	129	7	10	14	32.0	41.8	23.5
chrXV@394610to394599	YOR033C	EXO1	atctatATGctc	12	76	7	1	7	38.0	56.8	5.5
chrXV@891588to891532	YOR306C	MCH5	tgcttgATGtac	57	103	7	40	7	111.4	155.6	7.5
chrII@554434to554267	YBR157C	ICS2	aaataaATGaga	168	-36	6	48	6	69.2	128.7	30.8
chrII@620815to620838	YBR200W	BEM1	atatggATGcac	24	28	6	3	1	21.7	47.4	24.4
chrIV@321654to321640	YDL076C	RXT3	aattccATGaca	15	89	6	2	11	100.1	159.2	27.9
chrIV@1362719to1362748	YDR452W	PPN1	ggttttATGgta	30	121	6	3	5	109.8	132.7	27.7
chrVII@436945to436904	YGL032C	AGA2	ggtgatATGtta	42	67	6	10	12	38.1	71.5	87.6
chrVII@253895to253860	YGL136C	MRM2	gaagtaATGact	36	-3	6	6	4	43.5	77.6	4.5
chrVII@634092to634063	YGR071C		tagcatATGtac	30	-3	6	1	7	11.8	26.2	8.5
chrIX@326039to326083	YIL014W	MNT3	catcacATGagt	45	17	6	11	6	50.8	98.7	13.3
chrX@535959to536024	YJR054W		cccttgATGatt	66	24	6	14	6	33.6	97.1	7.4
chrX@535920to536024	YJR054W		tagaccATGagg	105	24	6	18	6	33.6	97.1	7.4
chrXIII@251525to251496	YML009C	MRPL39	atatttATGtgc	30	-19	6	8	6	357.6	217.0	197.6
chrXIII@16759to16673	YML128C	MSC1	cctagcATGatt	87	-3	6	18	6	42.6	42.2	6.8
chrXIV@483399to483407	YNL076W	MKS1	atttgaATGatc	9	149	6	3	11	44.1	44.5	13.3
chrXIV@287772to288038	YNL187W		acatagATGgta	267	-43	6	21	6	19.1	19.4	1.0
chrXIV@280399to280419	YNL191W	DUG3	atttgaATGtat	21	13	6	3	6	34.5	43.2	18.6
chrXV@292117to292067	YOL018C	TLG2	caattgATGtac	51	-7	6	11	6	56.1	94.3	24.0
chrXV@432120to432131	YOR057W	SGT1	agcactATGaca	12	56	6	0	4	53.9	73.5	35.5
chrXVI@375458to375484	YPL091W	GLR1	cttcatATGtat	27	14	6	14	7	89.0	179.1	130.2
chrXVI@267567to267520	YPL151C	PRP46	ccgaggATGcag	48	-13	6	4	6	22.9	64.3	9.4
chrXVI@150245to150219	YPL214C	THI6	ctaaccATGgtt	27	30	6	5	0	45.5	46.7	6.1
chrXVI@682192to682197	YPR067W	ISA2	ttgtacATGtga	6	19	6	1	11	68.8	30.4	21.4
chrI@129038to128994	YAL014C	SYN8	aaatagATGcgt	45	-25	5	3	8	64.4	47.3	20.4
chrI@179999to179940	YAR023C		ttaaacATGcaa	60	123	5	6	7	31.9	29.9	1.5
chrII@792794to792817	YBR295W	PCA1	ttcgagATGctt	24	25	5	1	7	4.0	7.5	1.3
chrIV@345018to344965	YDL059C	RAD59	tagcacATGctt	54	13	5	11	5	38.9	44.3	8.9
chrIV@192698to192709	YDL146W	LDB17	taacttATGtca	12	41	5	3	6	45.2	22.8	5.3
chrIV@90141to90170	YDL206W		ttgtaaATGcta	30	6	5	3	2	30.8	17.8	1.6
chrIV@829564to829596	YDR183W	PLP1	acgtatATGaag	33	-15	5	2	7	44.5	55.9	35.0
chrIV@946732to946863	YDR242W	AMD2	ttttcaATGggg	132	-61	5	8	6	13.4	27.5	1.1
chrIV@946642to946863	YDR242W	AMD2	gataatATGata	222	-61	5	11	6	13.4	27.5	1.1
chrIV@1019266to1019328	YDR279W	RNH202	tggttaATGatt	63	35	5	9	6	29.7	73.7	24.8
chrV@213414to213896	YER030W	CHZ1	caatacATGgaa	483	-461	5	1	5	58.4	171.8	179.5

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Table S5: All Translated uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrVI@246094to246135	YFR048W	RMD8	`ttgcatATGgag`	42	-3	5	9	5	48.7	41.4	11.7
chrVI@246080to246142	YFR048W	RMD8	`gttcgtATGcaa`	63	-10	5	11	5	48.7	41.4	11.7
chrVII@830469to830498	YGR166W	KRE11	`ctctatATGgac`	30	21	5	1	7	11.8	25.9	8.3
chrVII@1007366to1007340	YGR257C	MTM1	`aatcgtATGagc`	27	30	5	9	5	83.7	93.9	8.8
chrX@352369to352389	YJL046W		`tctttgATGttt`	21	-9	5	10	0	66.8	58.8	6.5
chrXI@402164to402238	YKL019W	RAM2	`ttaattATGgta`	75	-28	5	9	10	71.8	79.2	24.7
chrXI@334666to334631	YKL056C	TMA19	`tggttaATGttt`	36	73	5	18	6	1645.3	6368.8	4929.3
chrXI@334653to334582	YKL056C	TMA19	`cattcaATGgtt`	72	24	5	234	6	1645.3	6368.8	4929.3
chrXI@193093to193070	YKL133C		`attgtaATGaag`	24	2	5	2	5	8.0	21.4	2.1
chrXIII@77220to77237	YML098W	TAF13	`tgcaacATGaaa`	18	29	5	3	4	41.1	114.4	35.0
chrXIV@507721to507837	YNL063W	MTQ1	`agttgaATGgta`	117	-79	5	3	8	26.9	44.4	5.7
chrXIV@181092to181051	YNL249C	MPA43	`ttaaaaATGtat`	42	29	5	5	5	17.1	53.8	2.9
chrXV@1023258to1023172	YOR363C	PIP2	`gagcggATGaaa`	87	-37	5	1	4	12.1	16.4	3.0
chrXVI@506647to506679	YPL022W	RAD1	`tgctaaATGtgt`	33	15	5	5	5	21.6	40.0	3.7
chrXVI@272857to272813	YPL148C	PPT2	`tttctaATGaac`	45	0	5	24	5	84.5	63.8	3.9
chrXVI@163651to163535	YPL206C	PGC1	`ttgttgATGtta`	117	-60	5	19	4	100.1	125.0	76.3

Table S5. Translated uORFs. All uORFs with at least 1 rpM ribosome footprint occupancy are listed, as in table S3, sorted by the number of ribosome footprints observed.

Table S6: Translated Non-AUG uORFs

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5’ UTR # Rib	5’ UTR mRNA	CDS mRNA	CDS Rib
chrXV@619757to619789	YOR153W	PDR5	`aataaaTTGgca`	33	51	420	36	497	256.5	300.7	321.0
chrVII@482724to482689	YGL008C	PMA1	`aagaaaATCatt`	36	19	247	73	324	811.1	807.6	2063.5
chrXI@100392to100544	YKL182W	FAS1	`ataaaaAAGtac`	153	131	196	82	302	76.2	86.3	345.0
chrIII@262605to262417	YCR084C	TUP1	`gaacaaCTGgct`	189	-31	171	29	172	36.6	34.4	85.2
chrII@483429to481357	YBR121C	GRS1	`gaaaaaTTGtcg`	2073	-2003	99	113	103	363.6	429.2	320.8
chrXIII@56653to56730	YML106W	URA5	`ttcaaaATTtcc`	78	42	90	204	134	516.0	564.8	402.1
chrXVI@279829to279716	YPL145C	KES1	`tatacaTTGgat`	114	19	75	132	83	231.1	221.9	142.6
chrXVI@857308to857493	YPR159W	KRE6	`taaaatATTttt`	186	85	75	71	84	84.4	99.4	93.1
chrXVI@279818to279723	YPL145C	KES1	`tagaaaCTGgct`	96	26	65	104	83	231.1	221.9	142.6
chrXVI@732296to732307	YPR103W	PRE2	`attaaaTTGaat`	12	39	59	21	61	243.4	355.9	160.2
chrXVI@829826to829894	YPR149W	NCE102	`ataaacATTtct`	69	19	58	65	83	230.0	286.7	652.8
chrVII@856374to855268	YGR180C	RNR4	`taaaaaATTgct`	1107	-1037	51	49	67	139.5	468.5	734.9
chrXVI@279766to279716	YPL145C	KES1	`acagaaATAtat`	51	19	49	51	83	231.1	221.9	142.6
chrXVI@261057to260971	YPL154C	PEP4	`aacaaaAAGtat`	87	42	46	37	54	81.0	121.1	242.9
chrXVI@875279to875338	YPR165W	RHO1	`aacaaaATTaat`	60	25	44	157	68	537.7	722.2	392.8
chrVII@180343to180176	YGL173C	KEM1	`taaaatCTGttt`	168	58	43	18	58	22.7	35.5	120.0
chrXIV@91928to92056	YNL287W	SEC21	`tacaaaATAact`	129	-63	43	13	53	50.6	84.7	132.4
chrXIV@718707to718462	YNR051C	BRE5	`taagatATTgct`	246	134	39	94	68	68.5	81.7	50.4
chrXIII@164391to164233	YML056C	IMD4	`aaaaaaCTGaaa`	159	58	38	176	66	201.6	583.5	304.6
chrXV@74287to74436	YOL130W	ALR1	`tataaaATAttt`	150	-37	37	49	38	83.6	89.9	22.6
chrXVI@875296to875325	YPR165W	RHO1	`aaaagaATCgct`	30	38	35	111	68	537.7	722.2	392.8
chrXV@74289to74318	YOL130W	ALR1	`taaaatATTtct`	30	81	34	9	38	83.6	89.9	22.6
chrIII@120361to120248	YCR004C	YCP4	`aaaaaaAAGaga`	114	-67	33	21	43	121.5	208.9	260.4
chrXII@809945to809962	YLR342W	FKS1	`aaaaaaATTaaa`	18	34	32	4	62	77.8	88.9	163.1
chrXVI@642172to642192	YPR035W	GLN1	`acaaaaATTaaa`	21	12	32	62	47	1172.2	1571.1	817.4
chrIV@1168681to1168652	YDR346C	SVF1	`aaagaaACGaat`	30	0	30	17	47	276.4	317.3	114.9
chrXV@894266to894135	YOR307C	SLY41	`agaaaaAAGaat`	132	47	30	27	32	39.2	73.3	18.3
chrXIV@91942to91974	YNL287W	SEC21	`acaaatACGgat`	33	19	28	6	53	50.6	84.7	132.4
chrXIII@556511to556500	YMR145C	NDE1	`ataataTTGact`	12	27	26	6	27	61.6	61.3	63.0
chrXII@180158to180226	YLR019W	PSR2	`taagatATAtct`	69	60	22	26	29	54.8	52.6	32.9
chrXI@338475to338419	YKL054C	DEF1	`aaaaaaATCacc`	57	23	21	20	22	78.4	89.0	307.1
chrXV@123898to123939	YOL103W	ITR2	`taaacaTTGtcg`	42	61	21	15	29	83.3	121.0	18.7
chrVII@650718to650599	YGR086C	PIL1	`aagaaaATTtgt`	120	-21	20	61	23	137.8	220.1	558.8
chrXII@699575to699546	YLR277C	YSH1	`gaaacaTTGtat`	30	50	20	5	24	37.6	45.4	12.7
chrXIII@701140to701090	YMR216C	SKY1	`tcaaaaTTGtta`	51	53	20	9	28	30.3	41.6	28.6
chrIV@465871to465918	YDR011W	SNQ2	`aaaaaaGTGgat`	48	-3	19	3	31	23.3	39.1	36.6
chrVIII@385295to385378	YHR143W	DSE2	`gaaacaAAGaat`	84	134	19	95	38	216.9	239.3	318.7
chrIV@1263292to1263339	YDR395W	SXM1	`acaacaAAGgag`	48	-24	18	5	26	55.6	90.0	72.1
chrVIII@121740to121708	YHR007C	ERG11	`gaaaaaATTttt`	33	31	18	87	31	346.1	365.5	262.8
chrXII@574000to574149	YLR219W	MSC3	`aataaaTTGctt`	150	3	18	13	18	17.8	13.5	15.1
chrXV@682193to682173	YOR185C	GSP2	`taaacaATAatt`	21	67	18	2	20	7.7	23.2	30.4
chrVII@257631to257675	YGL133W	ITC1	`tttacaATTact`	45	36	17	4	23	11.2	18.0	8.6
chrVIII@383500to383538	YHR142W	CHS7	`tcaaaaATTgtg`	39	2	17	23	19	96.6	167.9	38.5
chrVIII@383455to383538	YHR142W	CHS7	`tcaaagCTGtct`	84	2	17	51	19	96.6	167.9	38.5
chrVIII@383412to383600	YHR142W	CHS7	`taaaaaAAGtca`	189	-60	17	79	19	96.6	167.9	38.5

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Table S6: Translated Non-AUG uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5' UTR # Rib	5' UTR mRNA	CDS mRNA	CDS Rib
chrXV@894250to894167	YOR307C	SLY41	`aaaaaaAAGaaa`	84	79	17	17	32	39.2	73.3	18.3
chrVII@650716to650648	YGR086C	PIL1	`gaaaatTTGtct`	69	28	16	46	23	137.8	220.1	558.8
chrXIII@701141to701112	YMR216C	SKY1	`ttcaaaATTgtt`	30	75	16	9	28	30.3	41.6	28.6
chrXIV@662784to662897	YNR017W	TIM23	`aaaaaaAAGacc`	114	17	16	65	26	89.2	114.9	114.0
chrIII@136961to136884	YCR011C	ADP1	`ataaaaATTaag`	78	14	15	10	18	50.1	89.7	32.6
chrVIII@301992to301969	YHR098C	SFB3	`gaagaaATTagt`	24	33	15	4	15	13.6	37.4	46.3
chrXI@299069to299197	YKL072W	STB6	`aaaaaaAAGaag`	129	28	15	15	22	20.0	25.8	9.8
chrVII@703588to705054	YGR108W	CLB1	`gccaaaATAttt`	1467	-1415	14	47	14	184.3	256.2	28.4
chrVIII@490667to490816	YHR195W	NVJ1	`caaaaaTTGgaa`	150	-70	14	56	15	117.5	141.3	14.3
chrXI@321183to321115	YKL063C		`actaaaGTGatt`	69	-46	14	4	16	72.3	124.7	89.6
chrXI@278696to278785	YKL085W	MDH1	`tatacaATAtat`	90	-19	14	31	16	96.1	130.9	118.1
chrIV@906928to906848	YDR219C	MFB1	`tacaaaATAtca`	81	1	12	11	13	37.8	74.4	20.9
chrIV@1434815to1434874	YDR492W	IZH1	`acaaaaGTGatt`	60	41	12	37	18	70.1	85.5	37.4
chrVII@761363to761380	YGR135W	PRE9	`ttaataATTgat`	18	16	12	54	13	431.7	516.2	216.0
chrVII@888838to888867	YGR195W	SKI6	`tataaaAAGatt`	30	19	12	12	18	63.7	80.3	84.6
chrIX@148736to148707	YIL115C	NUP159	`ataaatATAtat`	30	2	12	3	13	11.0	34.7	46.9
chrXII@371380to371514	YLR113W	HOG1	`aaagaaAAGgcc`	135	106	12	131	22	205.5	221.1	60.1
chrXII@982736to982888	YLR425W	TUS1	`ttcaaaATCcat`	153	2	12	5	13	5.5	9.7	4.6
chrIII@136928to136884	YCR011C	ADP1	`aaaaaaATTaat`	45	14	11	6	18	50.1	89.7	32.6
chrIV@310134to310111	YDL081C	RPP1A	`tctaaaATAaca`	24	-10	11	194	17	5627.0	5380.7	4922.3
chrV@111365to111427	YEL022W	GEA2	`aataaaCTGatt`	63	-7	11	3	13	22.3	29.9	22.8
chrXIV@87849to87944	YNL289W	PCL1	`acaaaaACGata`	96	-48	11	15	17	81.1	105.8	76.6
chrII@23632to23546	YBL103C	RTG3	`acaaaaACGaca`	87	12	10	23	10	39.7	46.3	17.1
chrII@447373to447359	YBR102C	EXO84	`aacaaaAAGcct`	15	43	10	1	6	4.3	15.7	21.4
chrIII@94307to94263	YCL017C	NFS1	`attaaaATAtat`	45	-6	10	10	17	57.6	61.4	96.3
chrIV@906915to906871	YDR219C	MFB1	`aacaaaTTGgcc`	45	24	10	9	13	37.8	74.4	20.9
chrVIII@512629to514599	YHR206W	SKN7	`aacgaaATTgct`	1971	-1868	10	15	12	17.0	22.1	33.5
chrX@143234to144697	YJL146W	IDS2	`tcaaatATAttt`	1464	-1409	10	22	10	70.1	44.1	11.4
chrX@143200to143295	YJL146W	IDS2	`gcaaagATAtct`	96	-7	10	28	10	70.1	44.1	11.4
chrXI@205210to205257	YKL126W	YPK1	`ttagaaTTGgtt`	48	93	10	20	16	79.4	95.2	52.7
chrXI@577816to577742	YKR072C	SIS2	`aaagaaATAtta`	75	-22	10	10	17	35.6	46.0	36.2
chrXIII@560266to560301	YMR148W		`tcaagaATAtct`	36	63	10	6	14	24.9	27.2	19.7
chrXV@558692to558657	YOR124C	UBP2	`aataaaGTGgta`	36	15	10	4	11	15.2	26.2	29.4
chrXVI@164164to164253	YPL204W	HRR25	`agaaaaATAttt`	90	21	10	25	11	56.0	80.3	52.0
chrIV@135813to135893	YDL180W		`ttcaaaATTtct`	81	3	9	41	11	42.9	82.5	8.1
chrIV@1249882to1249820	YDR387C		`gtcaaaAAGtat`	63	8	9	12	10	38.1	53.0	2.5
chrV@404690to404863	YER123W	YCK3	`ttaaaaAAGaag`	174	-55	9	23	10	35.7	54.5	24.8
chrXV@925548to925685	YOR326W	MYO2	`acaaaaAAGtct`	138	32	9	41	13	53.5	59.1	55.7
chrXVI@164190to164267	YPL204W	HRR25	`taaaaaAAGtcg`	78	7	9	14	11	56.0	80.3	52.0
chrIV@444621to444731	YDL003W	MCD1	`caaaaaAGGact`	111	-52	8	18	11	80.1	87.6	36.2
chrIV@444620to444715	YDL003W	MCD1	`acaaaaAAGgac`	96	-36	8	18	11	80.1	87.6	36.2
chrIV@576408to576473	YDR062W	LCB2	`gaaaaaAAGcat`	66	-3	8	43	9	154.6	178.7	73.7
chrVII@584789to584848	YGR046W	TAM41	`gtgaaaAAGgtt`	60	50	8	13	9	52.4	79.4	13.3
chrVII@1050011to1049946	YGR279C	SCW4	`tctacaATCgtt`	66	-18	8	13	11	73.9	134.5	818.0
chrVIII@490666to490704	YHR195W	NVJ1	`acaaaaATTgga`	39	42	8	34	15	117.5	141.3	14.3
chrXI@231692to231820	YKL109W	HAP4	`ataaaaAAGggt`	129	50	8	2	12	2.6	9.9	12.5

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Table S6: Translated Non-AUG uORFs, continued

uORF	CDS	Gene	Initiator Site	Length	uORF end to CDS	# Rib	# mRNA	5' UTR # Rib	5' UTR mRNA	CDS mRNA	CDS Rib
chrXIV@349777to349763	YNL149C	PGA2	gaaaaaCTGccg	15	6	8	23	8	383.1	621.3	239.9
chrXVI@812519to812472	YPR138C	MEP3	ttgaaaTTGttt	48	24	8	14	10	68.1	46.4	8.5
chrIV@862004to862096	YDR206W	EBS1	aagaaaATAtct	93	-46	7	12	9	66.3	95.4	14.3
chrIV@861927to862037	YDR206W	EBS1	aaaaagAAGgct	111	13	7	35	9	66.3	95.4	14.3
chrIV@1013682to1013665	YDR276C	PMP3	aatacaATTgat	18	27	7	14	4	366.2	566.7	1074.6
chrIV@1468479to1468432	YDR508C	GNP1	aaaactATCgct	48	-3	7	43	12	91.4	196.8	116.4
chrV@73703to73786	YEL042W	GDA1	tcaacaATCttt	84	-16	7	12	11	26.9	53.4	103.4
chrV@451296to451261	YER139C	RTR1	tctaaaATAtct	36	24	7	9	7	51.4	72.1	19.3
chrVII@548169to548243	YGR032W	GSC2	tacaaaAGGatt	75	24	7	3	13	35.1	11.1	8.2
chrVII@775101to775169	YGR143W	SKN1	aaagaaACGgta	69	28	7	7	11	16.5	35.1	11.6
chrVII@909131to909184	YGR205W		aataaaATAacg	54	33	7	6	13	20.4	25.2	32.3
chrVII@993660to991180	YGR250C		caaaaaAAGtgt	2481	-2345	7	11	7	20.4	31.9	14.7
chrXII@116369to116419	YLL015W	BPT1	ttagcaGTGgtt	51	11	7	4	8	15.0	22.2	13.2
chrXII@932860to932955	YLR407W		ttcaatATAgct	96	10	7	142	8	300.0	383.2	58.7
chrXIII@253814to253843	YML007W	YAP1	cccaaaACGttt	30	4	7	13	12	110.3	83.4	39.0
chrXIII@662521to662577	YMR199W	CLN1	gaagaaATTagt	57	65	7	8	11	27.0	40.5	30.2
chrXV@304037to303999	YOL012C	HTZ1	gaaaaaATAtcg	39	16	7	7	9	85.1	99.9	198.1
chrXV@271472to270633	YOL028C	YAP7	ttgaaaATTgct	840	-737	7	20	9	50.6	53.9	25.6
chrXV@394643to394599	YOR033C	EXO1	caaaaaATAtca	45	76	7	6	7	38.0	56.8	5.5
chrXVI@812520to812509	YPR138C	MEP3	tttgaaATTgtt	12	61	7	7	10	68.1	46.4	8.5
chrII@613925to613884	YBR196C	PGI1	tgcaaaATCgat	42	-10	6	59	7	600.8	905.7	1948.4
chrIV@931086to931178	YDR234W	LYS4	aataaaATAgaa	93	-54	6	6	11	56.2	74.6	47.3
chrVII@634099to631484	YGR071C		tccgaaATAgca	2616	-2582	6	2	7	11.8	26.2	8.5
chrVII@1027253to1027390	YGR270W	YTA7	agcaaaACGtct	138	-15	6	10	7	6.7	20.2	15.8
chrX@184252to184223	YJL127C	SPT10	gccaaaGTGatt	30	6	6	1	6	20.8	23.3	8.1
chrXI@362177to362233	YKL039W	PTM1	ttaaaaATTgaa	57	31	6	14	8	54.9	49.0	66.7
chrXII@163920to163894	YLR006C	SSK1	tcaaaaACGaat	27	3	6	2	9	14.7	21.3	7.9
chrXV@877711to877676	YOR298C-A	MBF1	acaaaaAAGtta	36	-7	6	160	6	1284.1	1206.0	1385.7
chrXV@978117to978037	YOR344C	TYE7	gcaaaaATAaaa	81	-28	6	10	7	111.5	84.6	81.0
chrXV@978111to978037	YOR344C	TYE7	ataaaaATAaag	75	-28	6	10	7	111.5	84.6	81.0
chrI@33423to33473	YAL061W	BDH2	ataacaATAaat	51	-25	5	4	8	8.5	15.6	6.4
chrII@549040to548945	YBR154C	RPB5	tacaaaATTtgt	96	-57	5	53	9	409.0	656.9	314.4
chrIV@741694to741518	YDR142C	PEX7	gtcgaaATCgtt	177	-78	5	26	5	50.1	44.0	4.7
chrIV@946651to946863	YDR242W	AMD2	ataataATAgat	213	-61	5	11	6	13.4	27.5	1.1
chrIV@1171844to1171653	YDR348C		agaaaaATTgat	192	-165	5	5	10	98.2	107.6	44.8
chrIV@1171843to1171820	YDR348C		gaaaaaTTGata	24	2	5	4	10	98.2	107.6	44.8
chrIV@1296783to1296658	YDR414C	ERD1	tataaaTTGttt	126	-19	5	47	6	77.3	54.3	14.2
chrV@404715to404729	YER123W	YCK3	caagaaTTGtct	15	79	5	2	10	35.7	54.5	24.8
chrV@492069to491524	YER159C	BUR6	tacaaaAGGgga	546	-428	5	20	7	38.2	98.5	90.9
chrVI@246088to246135	YFR048W	RMD8	gcaaaaTTGcat	48	-3	5	9	5	48.7	41.4	11.7
chrVII@472323to469096	YGL013C	PDR1	acagaaAAGaat	3228	-3206	5	1	6	8.9	15.7	12.6
chrVII@962096to962061	YGR235C		acaaaaATAact	36	-3	5	41	5	287.9	176.7	63.6
chrVIII@274103to276241	YHR084W	STE12	tcaaacAAGact	2139	-2066	5	11	8	20.0	26.9	29.9
chrX@184289to184230	YJL127C	SPT10	taaaaaGTGtac	60	13	5	6	6	20.8	23.3	8.1
chrX@636729to635848	YJR111C		taaaaaATAcat	882	-851	5	5	5	27.2	64.5	22.9
chrXII@524797to524862	YLR187W	SKG3	accaaaATTgaa	66	4	5	1	10	2.9	5.1	16.0

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Table S6: Translated Non-AUG uORFs, continued

uORF	**CDS**	**Gene**	**Initiator Site**	**Length**	**uORF end to CDS**	**# Rib**	**# mRNA**	**5’ UTR # Rib**	**5’ UTR mRNA**	**CDS mRNA**	**CDS Rib**
chrXIII@647044to647103	YMR192W	GYL1	`acaacaATTgca`	60	13	5	3	5	8.7	19.5	21.0
chrXIV@352399to352461	YNL145W	MFA2	`acaacaATAact`	63	-46	5	51	6	1211.2	974.4	1486.6
chrXIV@135602to135495	YNL271C	BNI1	`ataaaaTTGgac`	108	112	5	4	7	7.4	10.4	11.5
chrXV@68792to67560	YOL136C	PFK27	`aagaaaAGGgat`	1233	-1193	5	4	8	37.9	54.8	18.6
chrXVI@373750to375165	YPL092W	SSU1	`ttaaaaACGttt`	1416	-1376	5	10	9	90.4	137.7	28.3
chrXVI@866470to866414	YPR161C	SGV1	`aagaaaTTGtat`	57	-3	5	10	5	34.1	52.6	22.0

Table S6. Translated Non-AUG uORFs. Non-AUG uORFs that we predicted based on initiation context and that were found to be translated experimentally are listed, as in Table S3, sorted by the number of ribosome footprints observed. Many of these uORFs partly or completely overlap each other.

Table S7: Translational Regulation in Response to Starvation

CDS	Gene	Trl Change	mRNA Change	Trl NoAA	Trl Rich	# mRNA NoAA	# Rib NoAA	# mRNA Rich	# Rib Rich
YPR169W	JIP5	0.150	0.786	0.083	0.548	724	32	1275	369
YGR159C	NSR1	0.193	0.161	0.354	1.827	408	77	3517	3395
YCL037C	SRO9	0.220	0.363	3.212	14.496	70	120	267	2045
YNL061W	NOP2	0.232	0.329	0.749	3.216	155	62	652	1108
YCL054W	SPB1	0.253	0.257	0.321	1.262	286	49	1540	1027
YNL308C	KRI1	0.254	0.392	0.532	2.084	264	75	932	1026
YDL148C	NOP14	0.259	0.214	0.355	1.361	206	39	1332	958
YER165W	PAB1	0.263	0.775	3.929	14.888	711	1491	1270	9990
YMR229C	RRP5	0.267	0.134	1.170	4.354	205	128	2111	4856
YBR247C	ENP1	0.270	0.287	0.464	1.709	113	28	546	493
YDR299W	BFR2	0.290	0.282	0.356	1.222	205	39	1005	649
YOR091W	TMA46	0.301	0.336	0.833	2.757	117	52	482	702
YPL043W	NOP4	0.303	0.274	0.524	1.719	218	61	1103	1002
YKR081C	RPF2	0.313	0.180	0.618	1.967	103	34	793	824
YEL026W	SNU13	0.325	0.370	2.221	6.809	140	166	524	1885
YDL031W	DBP10	0.331	0.363	0.537	1.617	265	76	1010	863
YMR128W	ECM16	0.335	0.215	0.639	1.897	129	44	832	834
YOR310C	NOP58	0.347	0.236	0.839	2.404	462	207	2710	3442
YDR060W	MAK21	0.363	0.164	0.588	1.611	169	53	1423	1211
YLR009W	RLP24	0.363	0.179	0.836	2.290	112	50	867	1049
YNL175C	NOP13	0.370	0.216	0.568	1.528	211	64	1355	1094
YML093W	UTP14	0.376	0.245	0.546	1.447	264	77	1489	1138
YCR088W	ABP1	0.379	3.877	6.858	17.995	728	2665	260	2472
YKR092C	SRP40	0.383	0.209	0.896	2.330	163	78	1081	1331
YKL210W	UBA1	0.385	2.707	1.482	3.830	3369	2665	1723	3487
YPL058C	PDR12	0.387	0.454	0.496	1.278	117	31	357	241
YPL217C	BMS1	0.392	0.279	0.402	1.020	270	58	1341	723
YBL039C	URA7	0.394	0.141	0.560	1.413	308	92	3017	2252
YGR142W	BTN2	0.394	0.464	0.636	1.605	106	36	316	268
YNL300W		0.399	1.042	3.265	8.140	70	122	93	400
YLL040C	VPS13	0.401	2.474	3.330	8.269	436	775	244	1066
YDL153C	SAS10	0.402	0.222	0.336	0.831	262	47	1633	717
YCL009C	ILV6	0.403	2.100	2.664	6.570	505	718	333	1156
YKL029C	MAE1	0.404	0.823	1.081	2.661	369	213	621	873
YKL014C	URB1	0.405	0.217	0.620	1.521	127	42	810	651

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Table S7: Translational Regulation in Response to Starvation, continued

CDS	**Gene**	**Trl Change**	**mRNA Change**	**Trl NoAA**	**Trl Rich**	**# mRNA NoAA**	**# Rib NoAA**	**# mRNA Rich**	**# Rib Rich**
YNL138W	SRV2	0.407	3.019	4.167	10.176	857	1906	393	2113
YGL120C	PRP43	0.409	0.222	0.699	1.701	185	69	1156	1039
YMR093W	UTP15	0.409	0.371	0.397	0.966	198	42	739	377
YHR099W	TRA1	0.410	0.838	1.326	3.222	250	177	413	703
YNL241C	ZWF1	0.410	6.445	2.437	5.911	1173	1526	252	787
YLR276C	DBP9	0.414	0.215	0.464	1.115	198	49	1276	752
YDL126C	CDC48	0.414	3.746	1.232	2.962	9118	5997	3370	5274
YER043C	SAH1	0.415	1.678	5.216	12.514	1259	3505	1039	6870
YGL009C	LEU1	0.420	7.509	1.410	3.338	22631	17035	4173	7360
YBL042C	FUI1	0.422	1.628	0.420	0.990	589	132	501	262
YOR377W	ATF1	0.424	0.347	0.278	0.652	128	19	511	176
YKL205W	LOS1	0.425	0.561	0.323	0.757	371	64	915	366
YFL022C	FRS2	0.427	1.283	1.923	4.485	797	818	860	2038
YIL091C		0.427	0.253	0.242	0.564	232	30	1268	378
YML010W	SPT5	0.429	1.392	1.764	4.091	908	855	903	1952
YAL038W	CDC19	0.430	1.557	3.608	8.348	16312	31417	14510	64000
YJL130C	URA2	0.433	2.355	3.989	9.170	2294	4885	1349	6536
YPL093W	NOG1	0.433	0.186	0.432	0.992	230	53	1713	898
YOR206W	NOC2	0.434	0.219	0.527	1.207	288	81	1823	1163
YCL014W	BUD3	0.434	1.278	1.572	3.601	180	151	195	371
YCR073W-A	SOL2	0.434	3.123	1.300	2.978	291	202	129	203
YLR401C	DUS3	0.436	0.304	0.468	1.069	148	37	673	380
YGL071W	AFT1	0.437	1.363	0.725	1.652	186	72	189	165
YBR011C	IPP1	0.443	2.426	4.512	10.128	2683	6462	1531	8193
YKR054C	DYN1	0.444	1.394	0.500	1.120	296	79	294	174
YNR046W	TRM112	0.445	0.827	1.076	2.406	141	81	236	300
YGL099W	LSG1	0.446	0.366	1.794	4.005	118	113	447	946
YJL122W	ALB1	0.448	0.208	0.549	1.218	99	29	659	424
YCL061C	MRC1	0.449	1.524	0.953	2.110	230	117	209	233
YJL172W	CPS1	0.450	3.114	2.671	5.906	578	824	257	802
YCL057W	PRD1	0.450	2.891	1.504	3.324	806	647	386	678
YDL014W	NOP1	0.450	0.202	1.493	3.298	281	224	1928	3360
YJL010C	NOP9	0.453	0.305	0.557	1.223	175	52	794	513
YEL046C	GLY1	0.453	0.363	1.991	4.371	192	204	733	1693
YGR116W	SPT6	0.454	1.271	1.580	3.463	971	819	1058	1936
YAL025C	MAK16	0.454	0.273	0.453	0.993	219	53	1109	582

Continued on next page

Table S7: Translational Regulation in Response to Starvation, continued

CDS	Gene	Trl Change	mRNA Change	Trl NoAA	Trl Rich	# mRNA NoAA	# Rib NoAA	# mRNA Rich	# Rib Rich
YAL012W	CYS3	0.457	8.604	5.764	12.537	3225	9923	519	3438
YNL248C	RPA49	0.460	0.179	0.741	1.602	187	74	1448	1226
YBR079C	RPG1	0.462	0.528	1.689	3.635	600	541	1572	3019
YOR074C	CDC21	0.463	2.105	3.055	6.559	111	181	73	253
YDL112W	TRM3	0.463	0.420	0.725	1.557	217	84	716	589
YLR438W	CAR2	0.465	3.125	6.016	12.884	246	790	109	742
YJR070C	LIA1	0.466	0.157	1.371	2.924	138	101	1218	1882
YHL030W	ECM29	0.470	3.019	1.472	3.118	835	656	383	631
YCR072C	RSA4	0.470	0.228	0.382	0.808	108	22	656	280
YCL043C	PDI1	0.470	2.392	2.732	5.781	3028	4416	1753	5354
YPR086W	SUA7	0.473	1.223	0.583	1.226	537	167	608	394
YJL050W	MTR4	0.473	0.137	0.792	1.666	168	71	1701	1497
YMR079W	SEC14	0.474	1.493	3.017	6.337	511	823	474	1587
YLR044C	PDC1	0.474	1.227	8.992	18.874	10057	48270	11349	113172
YER178W	PDA1	0.475	2.109	3.758	7.865	1205	2417	791	3287
YOR272W	YTM1	0.476	0.160	0.365	0.764	159	31	1380	557
YLR002C	NOC3	0.477	0.198	0.516	1.077	156	43	1093	622
YLR259C	HSP60	0.479	1.542	6.140	12.750	1282	4202	1151	7754
YCL024W	KCC4	0.480	0.947	0.390	0.808	173	36	253	108
YHR094C	HXT1	0.481	1.115	1.107	2.290	430	254	534	646
YKL101W	HSL1	0.483	1.042	0.773	1.593	395	163	525	442
YJR002W	MPP10	0.483	0.317	0.316	0.652	367	62	1605	553
YJR131W	MNS1	0.483	1.945	1.175	2.418	177	111	126	161
YPR112C	MRD1	0.484	0.139	0.441	0.905	204	48	2028	970
YLR056W	ERG3	0.486	0.611	1.009	2.067	609	328	1380	1507
YKL216W	URA1	0.489	1.682	0.672	1.366	4980	1787	4100	2960
YOR007C	SGT2	0.490	1.736	1.050	2.133	2873	1611	2292	2583
YDR243C	PRP28	0.490	1.232	0.506	1.028	259	70	291	158
YHR039C-A	VMA10	0.491	1.439	2.927	5.936	633	989	609	1910
YOR204W	DED1	0.491	0.540	6.357	12.875	267	906	684	4653
YOR274W	MOD5	2.037	0.376	0.633	0.309	148	50	545	89
YPL064C	CWC27	2.038	0.876	0.473	0.231	436	110	689	84
YFR015C	GSY1	2.039	6.128	1.651	0.806	447	394	101	43
YJR101W	RSM26	2.040	0.473	0.640	0.312	325	111	952	157
YKR051W		2.040	1.144	0.474	0.231	352	89	426	52
YHR198C		2.041	0.882	1.194	0.582	149	95	234	72

Continued on next page

Table S7: Translational Regulation in Response to Starvation, continued

CDS	Gene	Trl Change	mRNA Change	Trl NoAA	Trl Rich	# mRNA NoAA	# Rib NoAA	# mRNA Rich	# Rib Rich
YIL007C	NAS2	2.042	0.984	0.889	0.433	177	84	249	57
YER069W	ARG5,6	2.045	3.011	1.775	0.864	572	542	263	120
YIL116W	HIS5	2.059	2.087	0.902	0.436	2881	1387	1911	440
YER130C		2.069	0.491	0.600	0.288	228	73	643	98
YDR305C	HNT2	2.076	0.694	0.825	0.395	168	74	335	70
YDR533C	HSP31	2.086	1.358	1.246	0.594	203	135	207	65
YHR090C	YNG2	2.098	0.724	0.641	0.304	228	78	436	70
YJL179W	PFD1	2.108	0.381	1.561	0.737	174	145	632	246
YBL015W	ACH1	2.114	1.083	3.710	1.746	151	299	193	178
YBR157C	ICS2	2.119	0.341	0.937	0.440	122	61	495	115
YHR009C		2.126	0.645	1.024	0.479	366	200	786	199
YGL098W	USE1	2.127	0.859	0.849	0.397	278	126	448	94
YPR101W	SNT309	2.132	0.596	0.747	0.348	271	108	630	116
YPL051W	ARL3	2.145	0.844	0.953	0.442	175	89	287	67
YGR108W	CLB1	2.148	0.381	0.439	0.203	499	117	1814	195
YBR067C	TIP1	2.154	0.508	5.114	2.362	418	1141	1140	1423
YBR175W	SWD3	2.156	0.624	0.330	0.152	437	77	969	78
YLR058C	SHM2	2.165	2.316	4.972	2.285	7940	21074	4747	5730
YNL274C	GOR1	2.171	5.643	1.908	0.875	538	548	132	61
YBR165W	UBS1	2.171	0.709	0.774	0.355	276	114	539	101
YMR233W	TRI1	2.174	0.578	1.003	0.459	155	83	371	90
YLR258W	GSY2	2.174	4.130	1.119	0.512	1566	935	525	142
YIL031W	ULP2	2.175	0.716	1.684	0.770	89	80	172	70
YBR290W	BSD2	2.178	0.828	0.727	0.332	528	205	883	155
YML107C	PML39	2.193	0.699	0.548	0.249	246	72	487	64
YER101C	AST2	2.196	0.457	1.768	0.801	71	67	215	91
YNL311C		2.197	0.698	0.632	0.286	240	81	476	72
YJL180C	ATP12	2.206	0.660	0.825	0.372	286	126	600	118
YBL029C-A		2.210	1.579	1.642	0.739	146	128	128	50
YGR033C	TIM21	2.214	0.497	0.635	0.285	431	146	1201	181
YDR262W		2.231	0.536	1.394	0.622	211	157	545	179
YAL040C	CLN3	2.238	0.846	1.597	0.710	88	75	144	54
YGR046W	TAM41	2.244	0.972	0.696	0.309	323	120	460	75
YNL065W	AQR1	2.257	0.895	0.393	0.173	572	120	885	81
YGL166W	CUP2	2.264	0.669	0.639	0.281	267	91	553	82
YPL202C	AFT2	2.271	0.431	1.029	0.451	255	140	819	195

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Table S7: Translational Regulation in Response to Starvation, continued

CDS	**Gene**	**Trl Change**	**mRNA Change**	**Trl NoAA**	**Trl Rich**	**# mRNA NoAA**	**# Rib NoAA**	**# mRNA Rich**	**# Rib Rich**
YDL044C	MTF2	2.274	0.510	0.745	0.326	186	74	505	87
YBL093C	ROX3	2.278	0.502	0.775	0.339	389	161	1073	192
YDR022C	CIS1	2.287	1.771	1.372	0.597	142	104	111	35
YGL055W	OLE1	2.292	0.199	2.584	1.122	361	498	2515	1491
YML038C	YMD8	2.298	0.574	0.652	0.282	342	119	825	123
YNL291C	MID1	2.301	0.545	0.778	0.336	195	81	495	88
YJL127C-B		2.305	1.306	0.941	0.406	233	117	247	53
YHR079C	IRE1	2.319	0.477	1.471	0.631	93	73	270	90
YHR106W	TRR2	2.326	1.300	0.657	0.281	291	102	310	46
YMR020W	FMS1	2.328	1.464	0.352	0.151	532	100	503	40
YJL133W	MRS3	2.333	0.423	0.796	0.340	160	68	524	94
YLR120C	YPS1	2.335	0.418	3.340	1.424	106	189	351	264
YDR174W	HMO1	2.336	0.514	2.580	1.099	713	982	1922	1116
YGR161C	RTS3	2.359	0.298	1.959	0.826	66	69	307	134
YFL027C	GYP8	2.362	0.569	0.276	0.116	441	65	1074	66
YPR009W	SUT2	2.366	0.933	1.036	0.436	161	89	239	55
YDL027C		2.366	1.262	1.102	0.463	216	127	237	58
YGR183C	QCR9	2.372	1.188	1.440	0.604	242	186	282	90
YDR371W	CTS2	2.372	0.946	0.591	0.248	339	107	496	65
YHR136C	SPL2	2.374	0.137	1.425	0.597	96	73	967	305
YDL133W		2.377	0.665	0.465	0.195	411	102	856	88
YPR167C	MET16	2.385	16.343	0.745	0.311	3305	1315	280	46
YOR385W		2.389	0.528	0.830	0.346	167	74	438	80
YBR161W	CSH1	2.394	0.611	0.900	0.374	154	74	349	69
YDR055W	PST1	2.396	0.982	2.301	0.956	653	802	921	465
YKL006C-A	SFT1	2.406	0.376	0.859	0.355	133	61	490	92
YBR262C		2.430	0.710	0.880	0.361	183	86	357	68
YGL028C	SCW11	2.440	0.264	3.090	1.260	211	348	1107	737
YDR067C		2.446	0.869	0.577	0.235	344	106	548	68
YGR065C	VHT1	2.449	1.083	0.836	0.340	549	245	702	126
YMR136W	GAT2	2.464	1.076	2.818	1.138	115	173	148	89
YPL168W		2.465	0.617	0.763	0.308	167	68	375	61
YOL016C	CMK2	2.466	0.761	0.725	0.293	700	271	1274	197
YER103W	SSA4	2.467	15.092	2.140	0.863	7412	8466	680	310
YCR018C	SRD1	2.469	0.486	0.999	0.403	165	88	470	100
YMR274C	RCE1	2.471	0.644	1.796	0.723	73	70	157	60

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Table S7: Translational Regulation in Response to Starvation, continued

CDS	Gene	Trl Change	mRNA Change	Trl NoAA	Trl Rich	# mRNA NoAA	# Rib NoAA	# mRNA Rich	# Rib Rich
YHR195W	NVJ1	2.471	0.922	0.461	0.186	455	112	683	67
YBR192W	RIM2	2.484	0.364	0.960	0.384	203	104	773	157
YDL130W-A	STF1	2.486	6.223	4.054	1.622	409	885	91	78
YOR166C	SWT1	2.492	0.383	0.525	0.209	200	56	723	80
YDR043C	NRG1	2.498	0.479	2.036	0.811	92	100	266	114
YOR092W	ECM3	2.519	0.432	2.027	0.801	73	79	234	99
YLR130C	ZRT2	2.552	0.598	0.207	0.081	770	85	1784	76
YML116W	ATR1	2.556	0.860	0.381	0.148	531	108	855	67
YGR149W		2.569	1.211	1.060	0.411	258	146	295	64
YJL134W	LCB3	2.589	0.345	0.803	0.309	252	108	1012	165
YPL213W	LEA1	2.609	0.824	0.810	0.309	259	112	435	71
YIL117C	PRM5	2.617	0.713	0.961	0.365	493	253	958	185
YIL077C		2.655	1.004	0.833	0.312	198	88	273	45
YKL068W-A		2.656	0.830	3.009	1.127	160	257	267	159
YBR145W	ADH5	2.659	2.648	1.412	0.528	459	346	240	67
YOL048C		2.664	2.400	0.567	0.212	449	136	259	29
YMR120C	ADE17	2.686	2.409	2.579	0.955	9901	13630	5690	2872
YDR019C	GCV1	2.702	3.057	0.967	0.356	6464	3338	2928	551
YDL110C	TMA17	2.739	4.775	3.214	1.167	369	633	107	66
YGR019W	UGA1	2.742	1.803	2.079	0.754	565	627	434	173
YLR271W		2.756	2.378	0.821	0.296	395	173	230	36
YMR291W		2.764	1.328	6.009	2.163	188	603	196	224
YER175C	TMT1	2.775	2.518	0.982	0.352	391	205	215	40
YDL021W	GPM2	2.782	4.535	0.706	0.252	393	148	120	16
YNL142W	MEP2	2.809	7.282	0.538	0.191	731	210	139	14
YNL183C	NPR1	2.811	0.779	2.890	1.023	153	236	272	147
YBR085C-A		2.835	2.896	1.809	0.635	1284	1240	614	206
YGR150C		2.887	0.677	0.610	0.210	264	86	540	60
YDL215C	GDH2	2.900	0.881	0.668	0.229	1041	371	1636	198
YCR037C	PHO87	2.902	0.648	0.507	0.174	525	142	1122	103
YMR319C	FET4	2.945	0.135	0.489	0.165	268	70	2748	240
YPL265W	DIP5	2.985	0.434	1.331	0.444	1181	839	3767	883
YLR407W		3.016	0.165	0.854	0.282	158	72	1324	197
YOL002C	IZH2	3.040	0.372	0.568	0.186	498	151	1853	182
YDR074W	TPS2	3.057	1.643	3.824	1.244	731	1492	616	405
YKR093W	PTR2	3.077	0.205	12.575	4.065	66	443	446	958

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Table S7: Translational Regulation in Response to Starvation, continued

CDS	Gene	Trl Change	mRNA Change	Trl NoAA	Trl Rich	# mRNA NoAA	# Rib NoAA	# mRNA Rich	# Rib Rich
YPR026W	ATH1	3.118	1.953	1.379	0.440	182	134	129	30
YML100W	TSL1	3.126	4.346	6.854	2.181	700	2561	223	257
YDR391C		3.162	1.581	1.899	0.598	217	220	190	60
YJL193W		3.247	0.295	0.825	0.253	134	59	629	84
YOL011W	PLB3	3.273	0.390	1.573	0.478	106	89	376	95
YPR035W	GLN1	3.323	0.751	3.194	0.956	4745	8090	8747	4420
YNL036W	NCE103	3.346	1.222	3.168	0.942	764	1292	866	431
YOR273C	TPO4	3.425	0.922	1.095	0.318	301	176	452	76
YPL245W		3.435	0.119	0.671	0.194	120	43	1392	143
YGL125W	MET13	3.437	5.425	9.046	2.619	286	1381	73	101
YLR177W		3.490	2.237	0.987	0.281	315	166	195	29
YIL136W	OM45	3.531	3.369	1.372	0.387	691	506	284	58
YMR250W	GAD1	3.586	6.772	1.250	0.347	1521	1015	311	57
YGL215W	CLG1	3.704	0.885	2.797	0.751	211	315	330	131
YKR080W	MTD1	3.784	1.120	1.017	0.267	3521	1911	4354	615
YBL075C	SSA3	3.998	1.016	1.053	0.262	265	149	361	50
YOR161C	PNS1	4.019	2.475	1.937	0.480	529	547	296	75
YJL133C-A		4.088	2.183	5.396	1.313	309	890	196	136
YOR028C	CIN5	4.107	0.887	2.313	0.560	132	163	206	61
YLR178C	TFS1	4.120	7.759	3.649	0.881	650	1266	116	54
YLL019C	KNS1	4.198	1.372	2.115	0.501	217	245	219	58
YLR092W	SUL2	4.229	18.068	2.176	0.512	1592	1849	122	33
YNL160W	YGP1	4.332	3.517	5.068	1.164	475	1285	187	115
YBR296C	PHO89	4.332	0.103	1.295	0.298	94	65	1266	199
YMR196W		4.930	7.411	1.653	0.334	1488	1313	278	49
YCR005C	CIT2	5.123	0.345	0.622	0.121	4623	1536	18569	1186
YOL082W	ATG19	5.244	1.051	1.374	0.261	529	388	697	96
YML128C	MSC1	5.520	13.058	1.648	0.297	3065	2696	325	51
YMR090W		5.773	2.309	0.746	0.129	442	176	265	18
YHL021C		5.841	1.424	7.465	1.272	329	1311	320	215
YEL009C	GCN4	6.031	0.799	0.697	0.115	1500	558	2601	158
YHR137W	ARO9	6.128	0.054	2.186	0.355	78	91	2000	375
YMR105C	PGM2	6.162	10.266	5.526	0.892	1038	3062	140	66
YPR184W	GDB1	6.577	3.103	3.244	0.491	242	419	108	28
YDR379C-A		6.597	1.636	2.489	0.375	143	190	121	24
YOR222W	ODC2	7.008	0.464	0.589	0.084	334	105	996	44

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Table S7: Translational Regulation in Response to Starvation, continued

CDS	**Gene**	**Trl Change**	**mRNA Change**	**Trl NoAA**	**Trl Rich**	**# mRNA NoAA**	**# Rib NoAA**	**# mRNA Rich**	**# Rib Rich**
YER081W	SER3	10.225	9.462	2.546	0.248	10701	14545	1566	205
YLL055W	YCT1	12.579	1.518	0.937	0.074	308	154	281	11
YGR088W	CTT1	12.586	3.359	2.265	0.179	359	434	148	14
YKR058W	GLG1	13.050	1.567	1.552	0.118	163	135	144	9
YOR120W	GCY1	13.562	3.061	1.255	0.092	409	274	185	9

Table S7. Translational Regulation in Response to Starvation. Genes whose translational efficiency changed at least 2-fold in either direction upon starvation, relative to the median gene, are listed in order of fold-change. The ratios of translational efficiency and of mRNA abundance are listed, along with the translational efficiency in starvation and in log-phase growth. The total number of ribosome footprint and mRNA fragment sequencing reads are listed as well.

Table S8A: GO Terms Over-represented in Genes that are Translationally Upregulated upon Starvation

GO Term	**GO ID**	**$\log_{10}$ *p* value**	**Expected**	**Actual**	**Total**
ion transport	GO:0006811	-5.4	12.5	29	85
metal ion transport	GO:0030001	-4.1	6.4	17	44
energy derivation by oxidation of organic compounds	GO:0015980	-4.0	14.4	29	98

Table S8B: GO Terms Under-represented in Genes that are Translationally Upregulated upon Starvation

GO Term	**GO ID**	**$\log_{10}$ *p* value**	**Expected**	**Actual**	**Total**
cellular component organization and biogenesis	GO:0016043	-14.0	240.5	159	1642
organelle organization and biogenesis	GO:0006996	-11.1	143.7	82	981
cellular process	GO:0009987	-10.1	439.8	381	3002
ribonucleoprotein complex biogenesis and assembly	GO:0022613	-10.0	44.1	11	301
ribosome biogenesis and assembly	GO:0042254	-9.0	36.3	8	248
macromolecule metabolic process	GO:0043170	-5.3	255.8	208	1746
cellular component assembly	GO:0022607	-5.2	48.3	23	330
primary metabolic process	GO:0044238	-4.5	303.5	260	2072
DNA metabolic process	GO:0006259	-4.3	52.9	29	361
biopolymer metabolic process	GO:0043283	-4.3	196.3	156	1340
protein-RNA complex assembly	GO:0022618	-4.1	15.1	3	103
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	GO:0006139	-4.1	152.5	116	1041
cellular metabolic process	GO:0044237	-4.1	317.3	276	2166
binding	GO:0005488	-4.5	121.3	86	828
ATPase activity	GO:0016887	-4.4	22.6	7	154
ATPase activity, coupled	GO:0042623	-4.0	14.8	3	101
macromolecular complex	GO:0032991	-9.6	183.1	121	1250
non-membrane-bound organelle	GO:0043228	-9.1	96.0	49	655
intracellular non-membrane-bound organelle	GO:0043232	-9.1	96.0	49	655
intracellular part	GO:0044424	-7.8	491.4	451	3354
intracellular	GO:0005622	-7.7	495.9	457	3385
protein complex	GO:0043234	-6.9	143.0	95	976
organelle part	GO:0044422	-6.5	234.5	181	1601
intracellular organelle part	GO:0044446	-6.5	234.5	181	1601
nucleolus	GO:0005730	-6.5	24.6	5	168
nuclear part	GO:0044428	-6.0	103.9	65	709
cytosolic ribosome (sensu Eukaryota)	GO:0005830	-5.8	12.2	0	83
cytosolic part	GO:0044445	-5.7	14.6	1	100
nuclear lumen	GO:0031981	-5.3	64.5	35	440
cell part	GO:0044464	-5.0	524.3	502	3579
cell	GO:0005623	-5.0	524.3	502	3579
cell cortex part	GO:0044448	-4.5	12.0	1	82
nucleus	GO:0005634	-4.1	196.3	157	1340
organelle	GO:0043226	-4.1	407.3	370	2780
intracellular organelle	GO:0043229	-4.1	407.1	370	2779

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Table S8B: GO Terms Under-represented in Genes that are Translationally Upregulated upon Starvation, continued

GO Term	**GO ID**	**$\log_{10}$ *p* value**	**Expected**	**Actual**	**Total**
cell cortex	GO:0005938	-4.1	13.0	2	89

Table S8C: GO Terms Over-represented in Genes that are Translationally Downregulated upon Starvation

GO Term	GO ID	$\log_{10}$ *p* value	Expected	Actual	Total
ribonucleoprotein complex biogenesis and assembly	GO:0022613	-46.6	39.0	135	301
ribosome biogenesis and assembly	GO:0042254	-40.9	32.1	115	248
rRNA metabolic process	GO:0016072	-25.3	18.0	68	139
rRNA processing	GO:0006364	-24.7	17.4	66	134
organelle organization and biogenesis	GO:0006996	-17.9	127.1	210	981
RNA processing	GO:0006396	-16.1	39.5	92	305
cellular component organization and biogenesis	GO:0016043	-14.8	212.7	294	1642
ribosomal large subunit biogenesis and assembly	GO:0042273	-13.8	7.1	31	55
cellular process	GO:0009987	-13.7	388.8	447	3002
protein-RNA complex assembly	GO:0022618	-12.1	13.3	42	103
RNA metabolic process	GO:0016070	-10.4	94.0	150	726
macromolecule metabolic process	GO:0043170	-8.2	226.1	285	1746
metabolic process	GO:0008152	-8.1	290.4	347	2242
primary metabolic process	GO:0044238	-8.1	268.3	326	2072
ribosome assembly	GO:0042255	-7.5	5.8	21	45
cellular metabolic process	GO:0044237	-7.4	280.5	335	2166
maturation of 5.8S rRNA	GO:0000460	-7.1	3.4	15	26
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0000466	-7.1	3.4	15	26
maturation of SSU-rRNA	GO:0030490	-6.9	3.9	16	30
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0000462	-6.9	3.9	16	30
ribosomal large subunit assembly and maintenance	GO:0000027	-6.4	4.1	16	32
ribosomal subunit assembly	GO:0042257	-6.1	4.8	17	37
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	GO:0006139	-6.0	134.8	180	1041
cellular component assembly	GO:0022607	-5.7	42.7	72	330
biopolymer metabolic process	GO:0043283	-5.5	173.5	219	1340
macromolecular complex assembly	GO:0065003	-5.0	32.1	56	248
hexose catabolic process	GO:0019320	-4.3	3.0	11	23
glucose catabolic process	GO:0006007	-4.3	3.0	11	23
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0000463	-4.3	1.7	8	13
maturation of LSU-rRNA	GO:0000470	-4.3	1.7	8	13
organic acid metabolic process	GO:0006082	-4.1	28.8	49	222
carboxylic acid metabolic process	GO:0019752	-4.1	28.8	49	222
RNA modification	GO:0009451	-4.1	6.3	17	49
RNA helicase activity	GO:0003724	-9.9	4.3	20	33
RNA-dependent ATPase activity	GO:0008186	-9.3	3.0	16	23

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Table S8C: GO Terms Over-represented in Genes that are Translationally Downregulated upon Starvation, continued

GO Term	**GO ID**	**log$_{10}$ p value**	**Expected**	**Actual**	**Total**
ATP-dependent RNA helicase activity	GO:0004004	-8.5	2.8	15	22
nucleic acid binding	GO:0003676	-7.5	47.8	84	369
helicase activity	GO:0004386	-7.1	6.6	22	51
RNA binding	GO:0003723	-6.8	24.2	50	187
snoRNA binding	GO:0030515	-6.5	3.6	15	28
binding	GO:0005488	-5.9	107.2	149	828
ATP-dependent helicase activity	GO:0008026	-5.7	4.5	16	35
translation factor activity, nucleic acid binding	GO:0008135	-5.4	4.3	15	33
translation regulator activity	GO:0045182	-5.2	4.9	16	38
ATPase activity	GO:0016887	-4.4	19.9	38	154
nucleolus	GO:0005730	-37.0	21.8	89	168
non-membrane-bound organelle	GO:0043228	-26.3	84.8	176	655
intracellular non-membrane-bound organelle	GO:0043232	-26.3	84.8	176	655
nuclear lumen	GO:0031981	-14.6	57.0	114	440
nucleolar part	GO:0044452	-12.6	10.0	36	77
nuclear part	GO:0044428	-11.3	91.8	150	709
small subunit processome	GO:0032040	-8.8	3.9	18	30
organelle lumen	GO:0043233	-8.7	81.9	130	632
membrane-enclosed lumen	GO:0031974	-8.7	81.9	130	632
ribonucleoprotein complex	GO:0030529	-8.1	48.2	86	372
nucleus	GO:0005634	-7.0	173.5	226	1340
intracellular part	GO:0044424	-5.6	434.4	462	3354
nucleolar preribosome	GO:0030685	-5.4	1.7	9	13
preribosome	GO:0030684	-4.6	1.9	9	15
cytosol	GO:0005829	-4.5	27.8	49	215
cell part	GO:0044464	-4.5	463.5	480	3579
cell	GO:0005623	-4.5	463.5	480	3579
intracellular	GO:0005622	-4.4	438.4	462	3385

Table S8D: GO Terms Under-represented in Genes that are Translationally Downregulated upon Starvation

GO Term	**GO ID**	**$\log_{10}$ *p* value**	**Expected**	**Actual**	**Total**
membrane	GO:0016020	-5.2	101.5	66	784
organellar ribosome	GO:0000313	-4.8	10.1	0	78
mitochondrial ribosome	GO:0005761	-4.8	10.1	0	78
mitochondrial part	GO:0044429	-4.6	46.1	23	356
organelle membrane	GO:0031090	-4.0	65.4	40	505

Table S8. GO term analysis of translational regulation in response to starvation. As in Table S2, except using the genes whose translational efficiency increase (552 genes; A,B) or decrease (488 genes; C,D) upon starvation is at least 1 standard deviation away from the median gene.

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