Accurate design of translational output by a neural network model of ribosome distribution

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Abstract

Synonymous codon choice can have dramatic effects on ribosome speed and protein expression. Ribosome profiling experiments have underscored that ribosomes do not move uniformly along mRNAs. We modeled this variation in translation elongation using a feedforward neural network to predict the ribosome density at each codon as a function of its sequence neighborhood. Our approach revealed sequence features affecting translation elongation and characterized large technical biases in ribosome profiling. We applied our model to design synonymous variants of a fluorescent protein spanning the range of translation speeds predicted with our model. Levels of the fluorescent protein in budding yeast closely tracked the predicted translation speeds across their full range. We therefore demonstrate that our model captures information determining translation dynamics *in vivo*, that we can harness this information to design coding sequences, and that control of translation elongation alone is sufficient to produce large, quantitative differences in protein output.

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Introduction

As the ribosome moves along a transcript, it encounters diverse codons, tRNAs, and amino acids. This diversity affects translation elongation and, ultimately, gene expression. For instance, exogenous gene expression can be seriously hampered by a mismatch between the choice of synonymous codons and the availability of tRNAs. The consequences of endogenous variation in codon use have been more elusive, but new methods have revealed that synonymous coding mutations, upregulation of tRNAs, and mutations within tRNAs can have dramatic effects on protein expression, folding, and stability[1–3]. Codon usage can directly affect the speed of translation elongation[4]. However, translation initiation has been considered the rate-limiting step in translation, implying that changes in elongation speed should have limited effects[5]. Recent work has suggested a relationship between codon use and RNA stability; slower translation may destabilize mRNAs and thus decrease protein expression[6,7]. These opposing viewpoints have yet to be fully reconciled, leaving us with an incomplete understanding of what defines a favorable sequence for translation.

With the advent of high-throughput methods to measure translation elongation *in vivo*, we can understand the functional implications of codon usage. Ribosome profiling measures translation transcriptome-wide by capturing and sequencing the regions of mRNA protected within ribosomes, called ribosome footprints[8]. Each footprint reflects the position of an individual ribosome on a transcript, and we can reliably infer the A site codon – the site of tRNA decoding – in each footprint (Fig. 1a). This codon-level resolution yields the distribution of ribosomes along mRNAs from each gene. We can use the counts of footprints on each codon to infer translation elongation rates: slowly translated codons yield more footprints, and quickly translated codons yield fewer (Fig. 1b). Analyses of ribosome profiling data have shown a relationship between translation elongation rate and biochemical features like tRNA abundance, wobble base pairing, amino acid polarity, and mRNA structure[9–18]. Expanded probabilistic and machine learning models have shown that the sequence context of a ribosome contributes to its elongation rate, both directly and through higher order features such as nascent protein sequence[15–17,19]. Computational modeling has also indicated that technical artifacts and biases contribute to the distribution of ribosome footprints[18–21]. However, it remains a challenge to distinguish experimental artifacts from the biological determinants of elongation rate. Here, we have used neural networks to model ribosome distribution along transcripts. The model captured both biological variation in translation elongation speed and technical biases affecting footprint count, which we confirmed experimentally. We have implemented a tool, Iχnos, that applies our model to design coding sequences, and used this to design sequences spanning a range of predicted translation elongation speeds. We found that the predicted elongation speeds accurately tracked protein expression, supporting a role for the elongation phase of translation in modulating gene expression.

Results

Design and performance of a neural network model of translation elongation

First, we developed a regression framework to model the distribution of ribosomes along transcripts as a function of local sequence features. As our measure of ribosome density on individual codon positions, we calculated scaled footprint counts by dividing the raw footprint count at each codon position by the average footprint count on its transcript (Fig. 1b). This normalization controls for variable mRNA abundances and translation initiation rates across transcripts. The scaled count thus reflects the relative speed of translation elongation at each position. We used a sequence neighborhood around the A site as the predictive region for scaled counts, and encoded this neighborhood as input to a regression model via one-hot encoding of the codons and nucleotides in this region (Supplementary Fig. 1). Then we learned a regression function with a feedforward neural network, trained on a large, high quality ribosome profiling data set from *Saccharomyces cerevisiae*[22]. We chose the top 500 genes by footprint density and coverage criteria, and sorted these into training and test sets of 333 and 167 genes, respectively.

We determined the sequence neighborhood that best predicted ribosome density by comparing a series of models ranging from an A-site-only model to a model spanning codon positions −7 to +5 (Fig. 1c). The identity of the A site codon was an important, but limited, predictor of the distribution of ribosome footprints (Pearson's $r = 0.28$). Expanding the sequence context around the A site steadily improved the predictive performance, up to the full span of a ribosome footprint (codons −5 to +4). Additional sequence context beyond the boundaries of the ribosome did not improve performance. We also observed a large boost in predictive performance by including redundant nucleotide features in addition to codon features over the same sequence neighborhood, especially near the ends of the ribosome footprint (Fig. 1c, $r = 0.53$ for −5 to +4 model including nucleotide features, $r = 0.08$ relative to no-nucleotide model). Linear regression models that only included codon features performed similarly to the neural networks we tested, but they did not improve with the inclusion of nucleotide features. This suggests that the neural network models learn a meaningful and nonlinear predictive relationship in nucleotide features, particularly toward the flanking ends of footprints, that makes them more successful than linear models.

Next we assessed the contribution of local mRNA structure to footprint distributions. We computed mRNA folding energies in sliding 30 nt windows over all transcripts, and trained a series of models that each included one window from nucleotide positions −45 to +72 relative to the A site. Performance improved upon including structure scores at nucleotide positions −17, −16, and −15, i.e., the windows that span the actual ribosome footprint ($r = 0.03$; Fig. 1c and Supplementary Fig. 2). No individual windows downstream of the footprint improved our predictions, and the maximum structure score over 30 sliding windows downstream of the ribosome had only a slight effect ($r < 0.01$) (Fig. 1c). Thus, our approach does not capture a conclusive effect of downstream mRNA structure on elongation rate. We were surprised to see an effect of structure within the ribosome, so we tested the direction of the effect and found that more structure in these windows led to lower predicted footprint counts. This suggests that stable mRNA structure in the footprint

fragments themselves is inhibiting their *in vitro* recovery in ribosome profiling experiments, and our model is capturing the bias that this introduces to the data.

Our best model incorporated a sequence window from codons −5 to +4 represented as both codons and nucleotides, as well as structure features of the three windows spanning the footprint. It captured sufficient information to accurately predict footprint distributions on individual genes (Fig. 1e), and yielded a correlation of 0.57 (Pearson's *r*) between predicted and true scaled counts over all positions in the test set (Fig. 1d). Although our model performed well across a range of scaled counts, it had difficulty predicting very high scaled footprint counts at a small number of sites. These sites may represent ribosome stalling that is determined by biological factors encoded outside of this local sequence neighborhood[16].

Our model was trained on highly expressed genes because abundant ribosome footprints enable more accurate sampling of ribosome positions. However, highly expressed genes can have biased codon usage[23]. To ensure that our model was accurately predicting translation on genes across the full range of expression and codon usage, we computed the correlation between the observed and predicted scaled counts for all yeast genes. Performance decreased with lower expression (Fig. 2a), but we hypothesized that the decreased performance reflected noisier observed footprint counts arising from less-abundant mRNAs, rather than differences in their codon composition. To test this, we downsampled the footprints for each of the 1000 highest-expression genes to match the average counts per codon of the 1000th gene, and repeated this procedure for the top 2000, 3000, and 4000 genes. We then compared the predictions of our model, which had been trained on the full data from highly expressed genes, against the downsampled data. At each coverage level, our method performed equally well on high-expression genes and low-expression genes. Thus, our model had no decrease in performance on genes that tend to have less favored codon content, after controlling for data density.

We also compared the performance of our model against two earlier approaches that incorporate information from the sequence neighborhood of each codon to predict ribosome distributions: RUST, which computes the expected ribosome density at each codon based on its sequence window[19], and riboshape, which uses wavelet decomposition to denoise the observed counts by projecting them into different subspaces at different levels of resolution (smoothness), and then predicts ribosome density after transformation into these subspaces[15]. To compare riboshape to our own method and to RUST, we evaluated how well its predictions in the highest resolution subspace (*i.e.*, closest to the raw data) correlated with the observed footprint counts. Our model out-performed both models, with an average Pearson correlation per gene of 0.56 versus 0.48 (RUST) and 0.41 (riboshape) across all genes that were included in all three analyses (Fig. 2b). We also found that our predictions of the raw data were better than riboshape's predictions of the transformed data at each resolution (Supplementary Table 1).

Sequences near the A site and at the ends of footprints contribute to footprint density

To quantify the influence of distinct positions in the sequence neighborhood on elongation rate, we trained a series of leave-one-out models that excluded individual codon positions from the input sequence neighborhood, and compared their performance to a reference

model that included all positions. We found that the A site codon contributed the most to predictive performance ($r = 0.13$), but we also saw contributions from the surrounding sequence context, including the P and E sites ($r = 0.03$ and 0.03) (Fig. 3a). Each codon position from −5 to +4, the span of a typical 28 nt ribosome footprint, improved performance of the full model, whereas positions outside the span of a footprint decreased performance. Contributions from the E and P sites suggest that the continued presence of tRNAs at these positions modulates elongation rate. In contrast, the large contribution of the +3 codon ($r = 0.06$), at the 3′ end of the footprint, likely reflects artifactual biases arising from the ribosome profiling process, corroborating previous reports of fragment end biases[19,20].

We were also interested in understanding the relative influence of the A site codon and its immediate environment. Overall, the A site codon and its immediate environment predict ribosome density similarly well (Pearson's $r = 0.28$ for the A site only, $r = 0.26$ for the codons from −3 to +2 excluding the A site). To identify A-site codons that tend to dominate the prediction, contributing relatively more than their context, we compared the performance of a −3:+2 model and a model with codons −3 to +2 but excluding the A site (Supplementary Fig. 4). We found that the presence of lysine codons AAA and AAG in the A site led to the strongest predictions, in agreement with a major effect of charged lysine residues on translation[11]. Conversely, we also identified a number of sequence contexts that tended to dominate the prediction, by looking at the sequence contexts of the positions with higher squared error arising from the A-site-only prediction at that position than the no-A-site context (Supplementary Fig. 4).

Next, we examined what our model had learned about the relationship between sequence and ribosome density. The raw parameters of a neural network can be difficult to interpret, so we determined a score for each codon at each position by computing the mean increase in predicted scaled counts due to that codon (Fig. 3b and Supplementary Table 2). Time spent finding the correct tRNA is considered to be a main driver of elongation speed, and consequently footprint counts[24]. Indeed, the A site codon scores exhibited the widest range of codon scores, and scores at this position but not other positions correlated with tRNA Adaptation Index (tAI), a measure of tRNA availability[25], as has been widely observed (Pearson's $r = 0.50$; $p = 0.0005$ after Bonferroni correction). Our results highlighted the well-characterized slow translation of CCG (Pro), CGA (Arg), and CGG (Arg) codons at the A site[26]. Our data also underscore that sequences in the P site contribute to elongation speed. The CGA codon showed a particularly strong inhibitory effect in the P site, in keeping with recent results[26,27]. We noted that this codon forms a disfavored I:A wobble pair with its cognate tRNA, distorting the anticodon loop[28], while the four fastest P site codons all form I:C wobble pairs (Fig. 3c). Overall, I:C base pairs in the P site contributed to faster translation (Mann-Whitney $p = 0.014$ after Bonferroni correction, Fig. 3c). From this, we concluded that the conformation of the tRNA:mRNA duplex can influence its passage through the ribosome, not just initial recognition in the A site.

We also observed strong sequence preferences at the 3′ end of ribosome footprints. Sequence bias has previously been noted in the 5′ and 3′ ends of ribosome footprints, and this bias has been suggested to arise from ligase preferences during library preparation[19,20].

To compare features of ribosome profiling data generated in different experiments, we applied our model to a large ribosome profiling dataset that we generated from yeast using a standard ribosome profiling protocol[29]. Models trained on these data learned disconcertingly high weights for both the −5 and +3 codon positions (Fig. 3d). The -5 codon, i.e., the 5′ end of a footprint, was the single strongest predictor of footprint counts, exceeding even the A site. We found similarly large 5′ end contributions in published yeast and human datasets generated using similar protocols[30,31] (Supplementary Fig. 5). These experiments, like our own, made use of CircLigase enzymes to circularize ribosome footprints after reverse transcription. In contrast, the experiment we first modeled used T4 RNA ligase to attach 5′ linkers directly onto ribosome footprint fragments[22]. To compare end sequence preferences between experiments, we trained models on only 28-nt footprints so that the ends of the footprints corresponded to the -5 codon position. Comparing the T4 ligase yeast data with CircLigase yeast data[31], we observed no relationship between the scores learned at 5′ footprint ends ($r = 0.05$), but a high correlation between scores at the A site, where we would expect biological similarity ($r = 0.86$). In contrast, we observed a high correlation at the -5 position between our CircLigase yeast data and the CircLigase-generated human data set[30] ($r = 0.83$, Fig. 3e), but no significant relationship at the A site, where we would expect species-specific codon bias ($r = −0.21$, $p = 0.11$, Fig. 3f). This suggested that the fragment end scores reflected experimental artifacts rather than *in vivo* biology.

To directly test the impact of enzyme biases on recovery of ribosome-protected fragments, we experimentally measured the ligation of synthetic oligonucleotides with end sequences shown to be favored or disfavored in our model. The relative ligation efficiency of each substrate closely mirrored the end sequence scores learned by our model for both CircLigase I and CircLigase II (Fig. 3g and Supplementary Fig. 6). The least-favored sequences were ligated by CircLigase II with only 20% the efficiency of the most-favored sequences, meaning that some ribosome footprints would be represented at five times the frequency of other footprints for purely technical reasons. This biased recovery of fragments could skew the results of ribosome profiling experiments, affecting estimates of elongation and overall per-gene translation.

Expression of synonymous reporters closely tracks predicted translation speeds

Our model captured the quantitative preferences of ligases for footprint end sequences and established that a substantial portion of the predictive information of these end regions is due to technical artifacts. However, the biologically sensible weights learned for codons in the A site showed that the model captured substantial biology as well. We reasoned that, if our model were capturing biological aspects of translation elongation, we could use the parameters learned by the model to design sequences that would be translated at different rates. We relied on the information found in the codons closer to the A site, to focus on the biological contributions and reduce the influence of biases from the ends of footprints (discussed further in Supplementary Note 1).

To test our model's ability to predict translation, we expressed synonymous variants of the yellow fluorescent protein eCitrine in yeast (Fig. 4a). First, using the yeast ribosome profiling data from Weinberg *et al.*, we trained a neural network model with a sequence

neighborhood extending from codon positions −3 to +2. Next, we designed a dynamic programming algorithm to compute the maximum- and minimum-translation-time synonymous versions of eCitrine based on our model. We defined the overall translation time (in arbitrary units) of a gene as the sum of predicted scaled counts over all codons in the gene. We also generated and scored a set of 100,000 random synonymous eCitrine CDSs and selected the sequences at the 0th, 33rd, 67th, and 99th percentiles of predicted translation time within that set (Fig. 4b). We used flow cytometry to measure the fluorescence of diploid yeast, each containing an eCitrine variant along with the red fluorescent protein mCherry as a control, and calculated relative fluorescence of each variant (Fig. 4c, Supplementary Fig. 7).

The expression of eCitrine in each yeast strain closely tracked its predicted elongation rate, with the predicted fastest sequence producing six-fold higher fluorescence than the predicted slowest sequence (Fig. 4c). However, the existing yeast-optimized yECitrine sequence[32] produced three-fold higher fluorescence than our predicted fastest sequence (Supplementary Fig. 8). To understand the source of this discrepancy, we measured eCitrine mRNA from all strains and found that sequences designed by our method had approximately equivalent mRNA levels, while yECitrine had five-fold more mRNA (Supplementary Fig. 8). Calculating translation efficiencies, or protein produced per mRNA, reconciled this disagreement. We observed a clear linear relationship between predicted elongation rate and translation efficiency (Fig. 4d).

Discussion

These experiments demonstrate that our model is able to predict large, quantitative differences in protein production, based only on information about translation elongation. The sequences we designed and tested have predicted translation speeds that span the range of natural yeast genes (Fig. 4b). This supports an effect of elongation rate on the translation efficiency and protein output of endogenous genes. Initiation rather than elongation is usually thought to be rate limiting for protein production of most endogenous genes[5,24]. Models have suggested that highly expressed trans-genes might deplete the effective supply of ribosomes, lowering initiation and thus causing elongation to be rate-limiting, but our reporter is expressed at the level of many endogenous genes and should represent well under 1% of mRNA. It remains to determine how translation speed can control translation efficiency. One contribution could come from pileups behind stalled or slow-moving ribosomes, diminishing the maximum throughput of protein production[17]. In particular, codon choice near the beginning of a gene, affecting elongation speed, can interfere with translation initiation and therefore control protein output[33]. Although codon choice can also affect mRNA stability and thus total protein output[6,7], our fast and slow predicted sequences have equivalent steady-state mRNA. Further, an effect arising purely from mRNA stability would affect protein output but not translation efficiency, counter to our observations. Instead, our results indicate that optimized elongation rates do result in more protein per mRNA, and this does not depend entirely on mRNA stability. The landscape of factors affecting codon optimality is complex[34], and codon preferences vary across species, tissues, and conditions. Our approach can capture empirical information about codon preferences in

any system where translation can be measured by ribosome profiling, and apply it to design sequences for quantitative expression in that system.

Online Methods

Ribosome profiling

Yeast ribosome profiling was performed exactly according to McGlincy & Ingolia[29] with the following modifications:

250 mL of YEPD media was inoculated from an overnight culture of BY474 to an OD600 of 0.1. Yeast were grown to mid-log phase and harvested at an OD600 of 0.565. Lysis proceeded according to McGlincy & Ingolia[29] except with no cycloheximide in the lysis buffer (20 mM Tris pH 7.4, 150 mM NaCl, 5 mM MgCl2, 1 mM DTT, 1% v/v Triton X-1000, 25 U/ml Turbo DNase I). To quantify RNA content of the lysate, total RNA was purified from 200 μL of lysate using the Direct-zol RNA MiniPrep kit (Zymo Research) and the concentration of RNA was measured with a NanoDrop 2000 spectrophotometer (ThermoFisher).

Lysate containing 30 μg of total RNA was thawed on ice and diluted to 200 μL with polysome buffer with no cycloheximide (20 mM Tris pH 7.4, 150 mM NaCl, 5 mM MgCl2, 1 mM DTT). 0.1 μl (1 U) of RNase I (Epicentre) was added to the diluted cell lysate and then incubated at room temperature for 45 minutes. Digestion and monosome isolation proceeded according to McGlincy & Ingolia[29], except with no cycloheximide in the sucrose cushion.

Purified RNA was separated on a 15% TBE/Urea gel, and fragments of 18–34 nt were gel extracted. Size was determined relative to RNA size markers NI-NI-800 and NI-NI-801[29] and NEB microRNA size marker (New England Biolabs). Library preparation proceeded according to McGlincy & Ingolia[29]. The library was made with downstream linker NI-NI-811 (/5Phos/NNNNNAGCTAAGATCGGAAGAGCACACGTCTGAA/3ddC/) and a modified RT primer with a preferred CircLigase II substrate (AG) at the 5′ end (oLFL075, 5′-/5Phos/AGATCGGAAGAGCGTCGTGTAGGGAAAGAG/iSp18/ GTGACTGGAGTTCAGACGTGTGCTC). Library amplification PCR used primers NI-NI-798 and NI-NI-825 (Illumina index ACAGTG). The resulting library was sequenced as single-end 51 nt reads on an Illumina HiSeq4000 according to the manufacturer's protocol by the Vincent J. Coates Genomics Sequencing Laboratory at the University of California, Berkeley.

Sequencing data processing and mapping

A custom yeast transcriptome file was generated based on all chromosomal ORF coding sequences in orf_coding.fasta from the Saccharomyces Genome Database genome annotation R64-2-1 for reference genome version R64-1-1 (UCSC sacCer3) for *Saccharomyces cerevisiae* strain S288C. A human transcriptome file was generated from GRCh38.p2, Gencode v. 22, to include one transcript per gene based on the ENSEMBL 'canonical transcript' tag. For both human and yeast, the transcriptome file included 13 nt of 5′ UTR sequence and 10 nt of 3′ UTR sequence to accommodate footprint reads from

ribosomes at the first and last codons. For yeast transcripts with no annotated UTR, the flanking genomic sequence was included. For human transcripts with no annotated UTR, or UTRs shorter than 13 or 10 nt, the sequence was padded with N.

Yeast ribosome profiling reads from Weinberg et al.[22] (SRR1049521) were trimmed to remove the ligated 3′ linker (TCGTATGCCGTCTTCTGCTTG) off of any read that ended with any prefix of that string, and to remove 8 random nucleotides at the 5′ end (added as part of the 5′ linker). Yeast ribosome profiling reads generated in our own experiments (GEO accession GSE106572) were trimmed to remove the ligated 3′ linker, which included 5 random nucleotides and a 5-nt index of AGCTA (NNNNNIIIIIAGATCGGAAGAGCACACGTCTGAAC). Human ribosome profiling reads from Iwasaki et al.[30] (SRR2075925, SRR2075926) were trimmed to remove the ligated 3′ linker (CTGTAGGCACCATCAAT). Yeast ribosome profiling reads from Schuller et al.[31] (SRR5008134, SRR5008135) were trimmed to remove the ligated 3′ linker (CTGTAGGCACCATCAAT).

Trimmed fastq sequences of longer than 10 nt were aligned to yeast or human ribosomal and noncoding RNA sequences using bowtie v. 1.2.1.1[35], with options "bowtie -v 2 -S". Reads that did not match rRNA or ncRNA were mapped to the transcriptome with options "bowtie -a --norc -v 2 -S". Mapping weights for multimapping reads were computed using RSEM v. 1.2.31[36].

Assignment of A sites

A site codons were identified in each footprint using simple rules for the offset of the A site from the 5′ end of the footprint. These rules were based on the length of the footprint and the frame of the 5′ terminal nucleotide. For each data set, the set of lengths that included appreciable footprint counts was determined (e.g. Weinberg 27–31 nt.). For each length, the counts of footprints mapping to each frame were computed. The canonical 28 nucleotide footprint starts coherently in frame 0, with the 5′ end 15 nt upstream of the A site (citation). For all other lengths, rules were defined if footprints mapped primarily to 1 or 2 frames, and offsets were chosen to be consistent with over digestion or under digestion relative to a 28 nucleotide footprint. Footprints mapping to other frames were discarded.

Scaled counts

For each codon, the raw footprint counts were computed by summing the RSEM mapping weights of each footprint with its A site at that codon. Scaled footprint counts were computed by dividing the raw counts at each codon by the average raw counts over all codons in its transcript. This controlled for variable initiation rates and copy numbers across transcripts. The resulting scaled counts are mean centered at 1, with scaled counts higher than 1 indicating slower than average translation. The first 20 and last 20 codons in each gene were excluded from all computations and data sets, to avoid the atypical footprint counts observed at the beginning and end of genes.

Genes were excluded from analysis if they had fewer than 200 raw footprint counts in the truncated CDS, or fewer than 100 codons with mapped footprints in this region. Then the top 500 genes were selected by footprint density (average footprint counts/codon). 2/3 of

these genes were selected at random as the training set, and the remaining 1/3 of genes were used as the test set.

Input features

The model accepts user defined sets of codon and nucleotide positions around the A site to encode as input features for predicting ribosome density. The A site is indexed as the 0th codon, and its first nucleotide is indexed as the 0th nucleotide, with negative indices in the 5′ direction, and positive indices in the 3′ direction. Each codon and nucleotide feature is converted to a binary vector via one-hot encoding, and these vectors are concatenated as input into the regression models. The model also accepts RNA folding energies from the RNAfold package, and allows the user to define window sizes and positions to score RNA structure and include as inputs into the regression models.

In our best-performing model, codons −5 to +4 and nucleotides −15 to +14 were chosen, as well as folding energies from three 30-nt windows starting at nucleotides −17, −16, and −15.

Model construction

All models were constructed as feedforward artificial neural networks, using the Python packages Lasagne v. 0.2.dev1[37] and Theano v. 0.9.0[38]. Each network contained one fully connected hidden layer of 200 units with a tanh activation function, and an output layer of one unit with a ReLU activation function. Models were trained using mini-batch stochastic gradient descent with Nesterov momentum (batch size 500).

Comparisons to other models

RUST[19] was run via https://ribogalaxy.ucc.ie/ according to the authors' instructions. First, we computed a codon metafootprint on the Weinberg dataset, aligned to the transcriptome as described above. We used an A-site offset of 15 and limited the analysis to 28-nt footprints (the most abundant), in keeping with the authors' analysis. Then, we ran the "similarity of observed and expected profiles" analysis using that codon metafootprint and retrieved the correlation of the observed and expected footprint distribution for each individual gene.

Riboshape[15] was downloaded from https://sourceforge.net/projects/riboshape/ on 2/1/2018. We generated the riboshape data structure according to the README file, with custom scripts (process_data.py and make_data_structure.m, available on GitHub), on our processed footprint counts data from the Weinberg dataset. We restricted the analysis to the 2170 genes present in both our transcriptome and the chxdata.mat data structure that is shipped with riboshape. We binned our genes by truncated lengths 100–210, 211–460, 461–710, 711–960, and 961–4871, which matched the bins in Liu and Song after accounting for our 20 codon truncation regions at either end of genes. Then we trained riboshape models on these bins, using σ parameters of 1, 3, 5, 12.5, 25, 37.5, 50, and 75. We report the per gene correlations between the true footprint data and their regression fits (waveforms) in their wavelet decomposition subspace with the least amount of denoising. The values in this subspace are closest to the observed footprint data, and their model trained for this subspace performs the best at predicting observed footprint density. We also report for each subspace the

correlation between their denoised footprint data and the regression fits in that subspace. The prior is more directly comparable to our work.

Feature importance measurements

A series of leave-one-out models was trained, excluding one codon position at a time from the sequence neighborhood. The importance of each codon position to predictive performance was computed as the difference in MSE between the reduced and full models.

The contribution of codon c at position i to predicted scaled counts was calculated as the average increase in predicted scaled counts due to having that codon at that position, over all instances where codon c was observed at position i in the test set. This increase was computed relative to the expected predicted scaled counts when the codon at position i was varied according to its empirical frequency in the test set (Supplementary Note 2).

Sequence optimization

The overall translation time of a coding sequence was computed as the sum of the predicted scaled counts over all codons in that coding sequence. This quantity corresponds to total translation time in arbitrary units. A dynamic programming algorithm was developed to find the fastest and slowest translated coding sequences in the set of synonymous coding sequences for a given protein, under a predictive model of scaled counts (Supplementary Note 3). This algorithm runs in $O(CM^L)$ time, where C is the length of the coding sequence in codons, M is the maximum multiplicity of synonymous codons (i.e. 6), and L is the length in codons of the predictive model's sequence neighborhood. This achieves considerable efficiency over the naive $O(C^L)$ model, by assuming that only codons within the sequence neighborhood influence scaled counts.

This algorithm was used to determine the fastest and slowest translating coding sequences for eCitrine, under a predictive model using a sequence window from codons −3 to +2, and using no structure features. Then 100,000 synonymous coding sequences for eCitrine were generated by selecting a synonymous codon uniformly at random for each amino acid. These coding sequences were scored, and the sequences at the 0th, 33rd, 67th, and 100th percentiles were selected for expression experiments.

Measuring circularization efficiency

We designed oligonucleotides that mimic the structure of the single-stranded cDNA molecule that is circularized by CircLigase during the McGlincy & Ingolia (2017) ribosome profiling protocol. These oligonucleotides have the structure:

/5Phos/AGATCGGAAGAGCGTCGTGTAGGGAAAGAG/iSp18/
GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCACAGTCATCGTTCGCATTA
CCCTGTTATCCCTAAJJJ,

where /5Phos/ indicates a 5′ phosphorylation; /iSP18/ indicates an 18-atom hexa-ethyleneglycol spacer; and JJJ indicates the reverse complement of the nucleotides at the 5′ of the footprint favored or disfavored under the model (oligos defined in Supplementary Table 3). Circularization reactions were performed using CircLigase I or II (Epicentre) as

described in the manufacturer's instructions, using 1 pmol oligonucleotide in each reaction. Circularization reactions were diluted 1/20 before being subjected to qPCR using DyNAmo HS SYBR Green qPCR Kit (Thermo Scientific) on a CFX96 Touch Real Time PCR Detection System (Biorad). For each circularization reaction, two qPCR reactions were performed: one where the formation of a product was dependent upon oligo circularization, and one where it was not (oligos defined in Supplementary Table 3). qPCR data was analyzed using custom R scripts whose core functionality is based on the packages qpcR[39] & dpcR[40] (qpcr_functions.R, available on github). The signal from the circularization dependent amplicon was normalized to that from the circularization independent amplicon, and then expressed as a fold-change compared to the mean of the oligonucleotide with the most favored sequence under the model.

Plasmid and yeast strain construction

Yeast integrating plasmids expressing either mCherry or a differentially optimized version of eCitrine were constructed. The differentially optimized versions of eCitrine were synthesized as gBlocks by Integrated DNA Technologies inserted into the plasmid backbone by Gibson assembly[41]. Transcription of both mCherry and eCitrine is directed by a PGK1 promoter and an ADH1 terminator. To enable yeast transformants to grow in the absence of leucine, the plasmids contain the LEU2 expression cassette from *Kluyveromyces lactis* taken from pUG73[42], which was obtained from EUROSCARF. To enable integration into the yeast genome, the plasmids contain two 300 bp sequences from the his3 1 locus of BY4742. Genbank files describing the plasmids are provided in Supplementary Data Set 1. To construct yeast strains expressing these plasmids, the plasmids were linearized at the *SbfI* site and ~1 μg linearized plasmid was used to transform yeast by the high efficiency lithium acetate/single-stranded carrier DNA/PEG method, as described[43]. Transformants were selected by growth on SCD -LEU plates, and plasmid integration into the genome was confirmed by yeast colony PCR with primers flanking both the upstream and downstream junctions between the plasmid sequence and the genome (oligos defined in Supplementary Table 3). PCR was performed using GoTaq DNA polymerase (Promega M8295). Haploid BY4742 and BY4741 strains expressing the eCitrine variants and mCherry, respectively, were then mated. For each eCitrine variant, eight transformants were mated to a single mCherry transformant. Diploids were isolated by their ability to grow on SCD -MET-LYS plates. Strains with sequence-confirmed mutations or copy number variation were excluded from further analysis.

Assessing fluorescent protein expression by flow cytometry

Overnight cultures of diploid yeast in YEPD were diluted in YEPD so that their optical density at 600 nm (OD_{600}) was equal to 0.1 in a 1 mL culture, and then grown for six hours in a 2 mL deep-well plate supplemented with a sterile glass bead, at 30 °C with shaking at 250 rpm. This culture was pelleted by five minutes centrifugation at $3000 \times g$ and fixed by resuspension in 16% paraformaldehyde followed by 30 minutes incubation in the dark at room temperature. Cells were washed twice in DPBS (Gibco 14190-44) and stored in DPBS at 4 °C until analysis. Upon analysis, cells were diluted ca. 1:4 in DPBS and subject to flow cytometry measurements on a BD Biosciences (San Jose, CA) LSR Fortessa X20 analyzer. Forward Light Scatter measurements (FSC) for relative size, and Side-Scatter measurements

(SSC) for intracellular refractive index were made using the 488nm laser. eCitrine fluorescence was measured using the 488 nm (Blue) laser excitation and detected using a 505 nm Long Pass optical filter, followed by 530/30 nm optical filter with a bandwidth of 30nm (530/30, or 515 nm-545 nm). mCherry fluorescence was measured using a 561 nm (yellow-green) laser, for excitation and a 595 nm long-pass optical filter, followed by 610/20 nm band-pass optical filter with a bandwidth of 20 nm (or 600 nm – 620 nm). PMT values for each color channel were adjusted such that the mean of a sample of BY4743 yeast was 100. 50000 events were collected for each sample. Flow cytometry data was analyzed using a custom R script (gateFlowData.R, available on github) whose core functionality is based on the Bioconductor packages flowCore[44], flowStats, and flowViz[45]. In summary, for each sample, events that had values for red or yellow fluorescence that were less that one had those values set to one. Then, in order to select events that represented normal cells, we used the curv2filter method to extract events that had FSC and side-scatter SSC values within the values of the region of highest local density of all events as considered by their FSC and SSC values. For these events the red fluorescence intensity was considered a measure of mCherry protein expression and yellow fluorescence intensity a measure of eCitrine protein expression.

Measuring eCitrine and mCherry mRNA expression by qRT-PCR

Overnight cultures of diploid yeast in YEPD were diluted in YEPD so that their OD_{600} was equal to 0.1 in a 20 mL culture, and then grown at 30 °C with shaking at 250 rpm until their OD_{600} reached 0.4 – 0.6. 10 mL of culture was then pelleted by centrifugation for 5 minutes at $3000 \times g$ and snap frozen in liquid nitrogen. Total RNA was extracted from pelleted yeast cultures according to the method of Ares[46]. Thereafter, 10 μg of this RNA was treated with Turbo DNase I (ambion) according to the manufacturer's instructions, then 1 μg DNase treated RNA was reverse transcribed using anchored oligo dT and Protoscript II (NEB) according to the manufacturer's instructions. $1/20^{th}$ of this reaction was then subjected to qPCR using the DyNAmo HS SYBR Green qPCR Kit (Thermo Scientific) on a CFX96 Touch Real Time PCR Detection System (Biorad). For each reverse transcription reaction, two qPCR reactions were performed: one with primers specific to the mCherry ORF, and one with primers specific to the eCitrine variant ORF in question (oligos defined in Supplementary Table 3). qPCR data was analyzed using custom R scripts whose core functionality is based on the packages qpcR[39,46] & dpcR[40] (qpcr_functions.R, available on github). The signal from each eCitrine variant ORF was normalized to that from the mCherry ORF in the same sample, and then expressed as a fold-change compared to the median of these values for the MIN (fastest predicted sequence) eCitrine variant.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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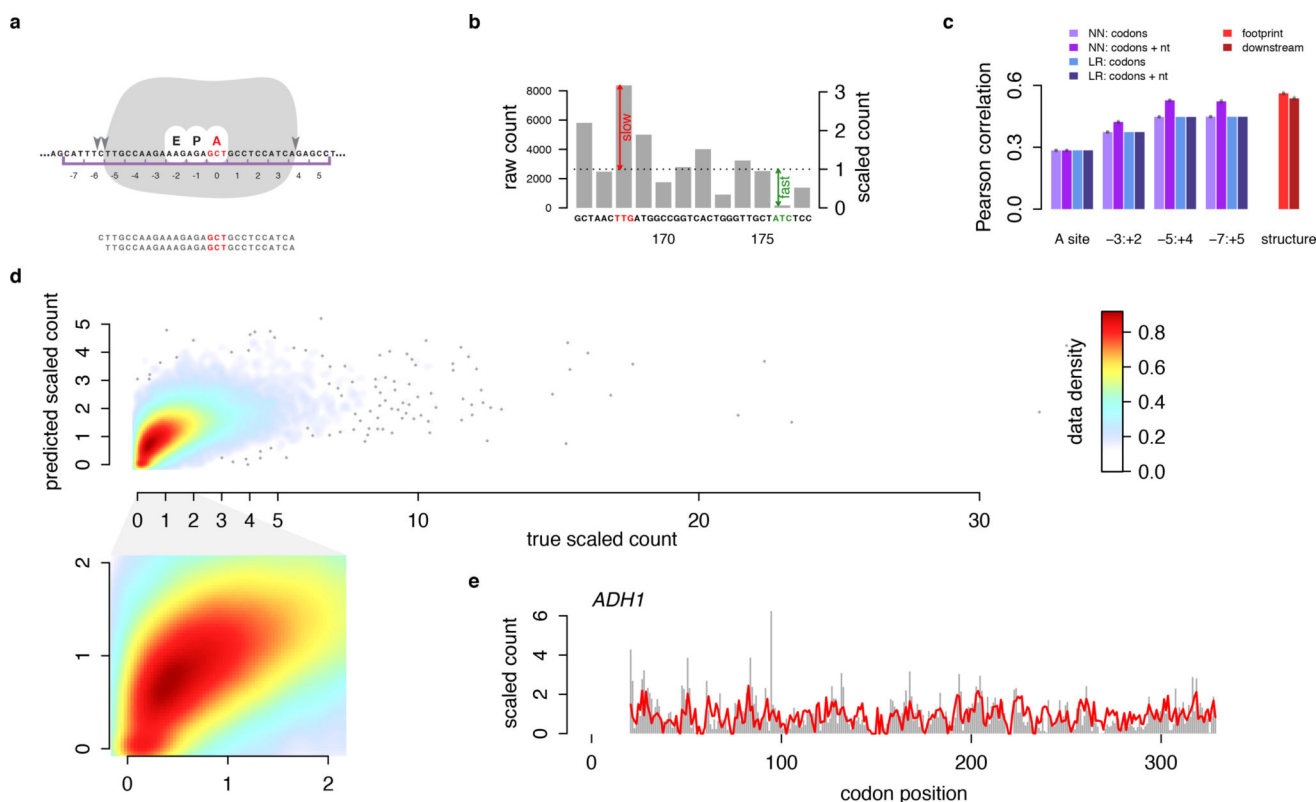
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Figure 1. Design and performance of a neural network model of translation elongation
a, Each ribosome protects an mRNA footprint of approximately 28–29 nt. Sequence coordinates in a neighborhood around a ribosome are indexed relative to the codon in the A site of the ribosome. **b,** Read count rescaling. For each gene, the counts of footprints assigned to each A site codon are divided by the average counts per codon over that gene. The resulting scaled footprint counts are used for model training and prediction. **c,** Model performances (Pearson correlations between predicted and true scaled counts over the test set) for neural network and linear regression models over a range of sequence neighborhoods, with and without nucleotide features, as well as correlations for models that also incorporate structure scores of the three 30-nt windows overlapping the footprint region, or the maximum structure score within 59 nt downstream of the ribosome. Bars show the mean of 10 runs of each model; the 10 individual runs for each model are overlaid as gray points. **d,** True vs. predicted scaled counts for the test set, under a model with codon and nucleotide features spanning codon positions −5 to +4. Color scale shows density of data points. **e,** True scaled counts (gray bars) and predicted scaled counts (red line) for a highly translated gene.
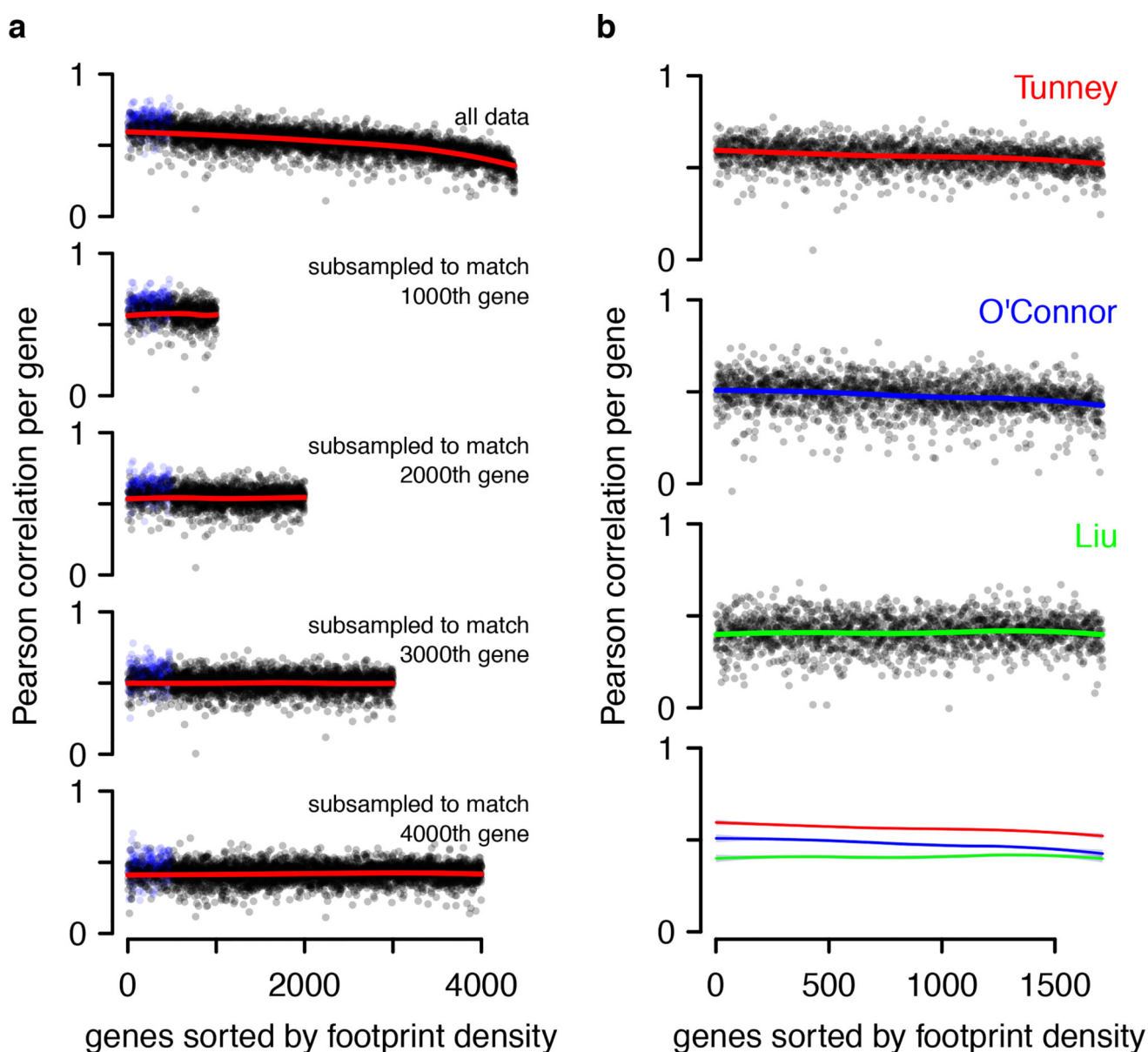
Figure 2. Performance comparisons on low coverage genes and with competing models
a, Top, per-gene correlations between true and predicted scaled counts, for all 4375 genes in our transcriptome that passed filtering criteria. Training set genes in blue (333/top 500 genes by footprint density). Loess curve on test set genes shown in red. Below, as above, with footprint counts on the top 1000, 2000, 3000, and 4000 genes subsampled to the density of footprint counts on the 1000th, 2000th, 3000th, and 4000th gene, respectively, and 'true' scaled counts recomputed. **b,** Comparison of Iχnos with similar models, RUST[19] and riboshape[15]. Shown are per-gene correlations between true and predicted scaled counts, on 1711 genes passing the filtering criteria from all three methods. Training set genes from Iχnos are excluded. Colored lines are loess curves, which are also compared in the bottom panel.
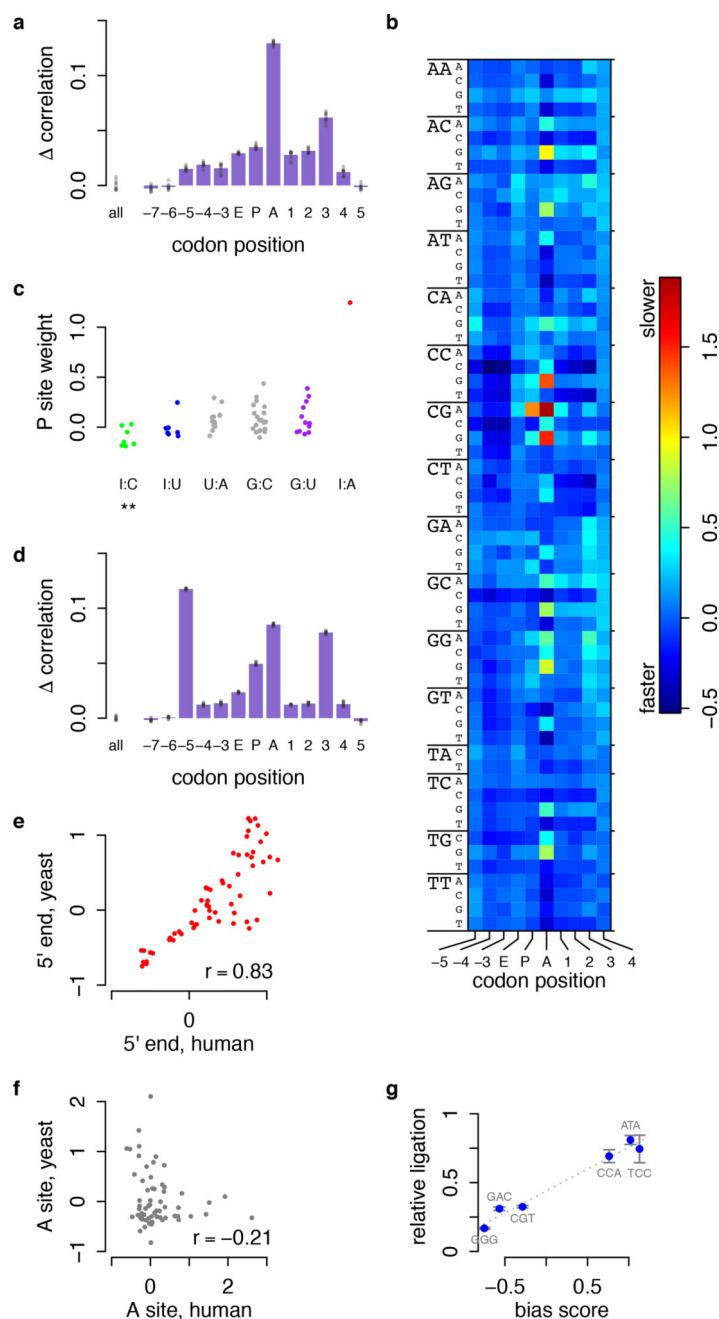
Figure 3. Interpretation of models of translation elongation rates

a, Predictive value of codon positions in a yeast ribosome profiling dataset[22]. We computed Pearson correlations between true and predicted scaled counts on the test set, for a reference model including codon and nucleotide features from codon positions −7 to +5, and for a series of leave-one-out models, each excluding one codon position. Gray points show differences between Pearson's *r* for 10 runs of each leave-one-out model and the mean *r* of 10 runs of the reference model. Bars represent the mean of these values. **b,** Mean contributions to scaled counts by codon identity and position. **c,** P site codon contributions grouped by the codon:anticodon base pair formed by the third nucleotide of each codon.

Asterisks indicate $p < 0.05$ after Bonferroni correction, unpaired two-sided Mann-Whitney U test between each group and all other codons. I:C, $p = 0.014$. **d,** Predictive value of codon positions as in A, from a yeast ribosome profiling library we constructed using CircLigase II as described by McGlincy and Ingolia[29]. **e, f,** Contributions from **(e)** codon position -5, at the 5′ ends of footprints, and **(f)** the A site, in human ribosome profiling data[30] versus our yeast ribosome profiling data, both using CircLigaseII. Analysis was limited to 28-nt footprints to avoid frame biases. **g,** Ligation efficiency of CircLigase II. Oligonucleotide substrates resembling ribosome footprints at the circularization step of the protocol, with different three-nucleotide end sequences, were ligated by both enzymes. Circularization was assayed by qPCR using primers spanning the ligation as compared to primers in a contiguous region of the oligo. Ligation was calculated relative to CircLigase I ligation of the best-ligated substrate. Each point represents the ratio of the means of three qPCR replicates; error bars represent the standard error of that ratio.
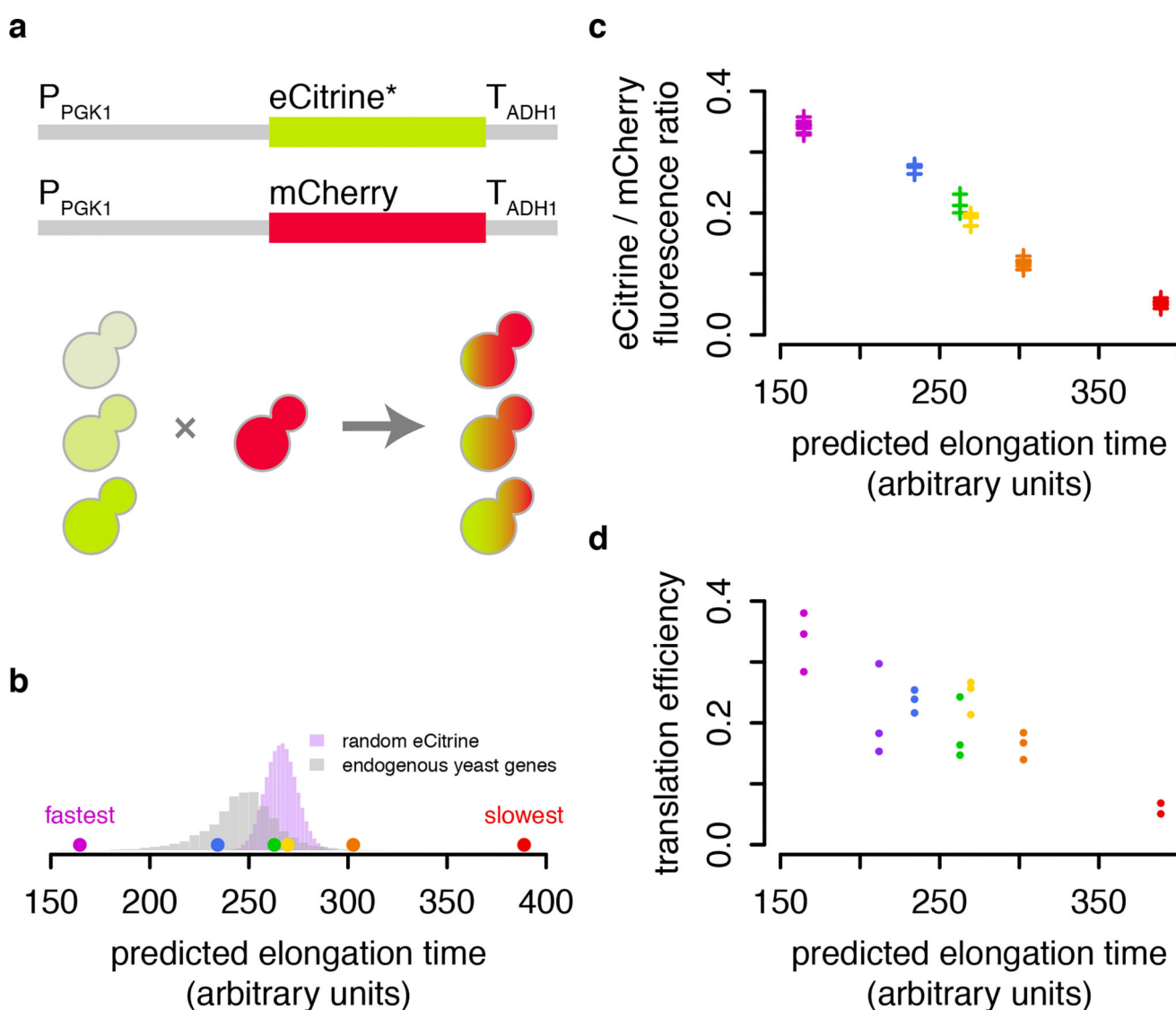
Figure 4. Design of synonymous sequences shows elongation rate affects translation output
a, Six reporter constructs with distinct synonymous eCitrine coding sequences were inserted into the *his3 1* locus of BY4742 yeast, and an equivalent construct with a constant mCherry coding sequence was inserted into the *his3 1* locus of BY4741 yeast. The haploids were mated to produce diploid yeast with both reporters, whose fluorescence was then measured with flow cytometry. **b,** The synonymous eCitrine sequences included the fastest and slowest predicted sequences under our model (magenta and red), plus sequences with predicted translation elongation times at the 0th, 33rd, 67th, and 100th percentiles of a randomly generated set of 100,000 synonymous eCitrine sequences (blue, green, yellow, and orange, respectively). The score distribution of 100,000 random eCitrine sequences is shown in lavender. The scores of endogenous yeast genes, rescaled by length to compare with eCitrine, are shown in gray. **c,** eCitrine:mCherry fluorescence ratio, as measured by flow cytometry of 11,000–18,000 yeast, versus the predicted elongation time of each sequence. Each + symbol represents the median ratio of yellow and red fluorescence from one biological replicate of the given eCitrine strain. Eight biological replicates, each an

independent integration of the reporter construct, are included for each strain, except for the strains shown in blue and orange, which have seven, and the strain shown in green, which has three. Colors as in (**b**). **d,** Translation efficiency, or median eCitrine:mCherry fluorescence ratio divided by relative eCitrine:mCherry mRNA ratio (ratio of medians of three qPCR replicates), for each eCitrine variant, versus the predicted elongation time of each sequence. Purple, yECitrine sequence; other colors as in (**b**). Each point represents one biological replicate of the given eCitrine strain; three biological replicates were measured for each strain except two for the strain shown in red.