

2 **Decomposing mutation and selection to identify**
3 **mismatched codon usage**

4 CEDRIC LANDERER^{1,2,*}, RUSSELL ZARETZKI³, AND MICHAEL
5 A. GILCHRIST^{1,2}

6 ¹Department of Ecology & Evolutionary Biology, University of Tennessee, Knoxville, TN 37996-
7 1610

8 ²National Institute for Mathematical and Biological Synthesis, Knoxville, TN 37996-3410

9 ³Department of Business Analytics & Statistics, Knoxville, TN 37996-0532

10 *Corresponding author. E-mail: cedric.landerer@gmail.com

Version dated: October 12, 2018

Abstract

Codon usage has been used as a measure for adaptation of genes to their cellular environment for decades. The introgression of genes from one cellular environment to another may cause well adapted genes to suddenly be less adapted due to them having evolved in a different environment. As a result, we expect that transferred genes result in a large fitness burden for the new host organism. Here we examine the yeast *Lachancea kluyveri* which has experienced a large introgression, replacing the left arm of chromosome C ($\sim 10\%$ of its genome). The *L. kluyveri* genome provides an opportunity to study the evolution of introgressed genes to a novel cellular environment and estimate the fitness cost such a transfer imposes. We quantified the effects of mutation bias and selection against translation inefficiency on the codon usage pattern of the endogenous and introgressed exogenous genes using a Bayesian mixture framework. We found substantial differences in codon usage between the endogenous and exogenous genes, and show that these differences can be largely attributed to a shift in mutation bias from A/T ending codons in the endogenous genes to C/G ending codons in the exogenous genes. Recognizing the two different signatures of mutation and selection bias improved our ability to predict protein synthesis rate by 17% and allowed us to accurately assess codon preferences. In addition we utilize the estimates of mutation bias and selection against translation inefficiency to determine *Eremothecium gossypii* as potential source lineage, estimate the time since introgression to be on the order of 6×10^8 and assess the fitness burden across introgressed loci, showing the advantage of mechanistic models when analyzing codon data.

Introduction

Mutation, selection and genetic drift can be used to quantify the environment a genome has evolved in. Mutation bias is purely determined by the cellular environment, while the strength and efficacy of selection relative to drift is determined by the cellular environment, e.g. tRNA abundance, and the natural environment e.g. gene expression. A lineages effective population size determines the efficacy of selection relative to drift. Synonymous codon usage, the non-uniform usage of codons encoding the same amino acid, is a reflection of both, the cellular and the natural environment. Decomposing codon usage, therefore, provides us the necessary information to describe the environment a genome has evolved in in terms of its codon usage.

In general, the strength of selection on codon usage increases with gene expression (??). Conversely, the impact of mutation bias on codon usage declines with gene expression. Thus, we can easily imagine that with increasing gene expression, codon usage shifts from a process dominated mutation to a process dominated by selection. Together, the mutation process favoring specific synonymous codons - or mutation bias - and the selection for translation efficiency scaled by gene expression and effective population size - or selection bias - shape codon usage in a genome. This mutation-selection-drift balance model allows us to explicitly describe the environment in which genes evolve with respect to mutation and selection bias. Here we show that estimating the influence of mutation bias and selection bias on a gene's codon usage allows us to not only predict protein synthesis rate ϕ , but also, to infer its history and make predictions about its future with respect to these forces.

Most studies implicitly assume that synonymous codon usage of a genome is shaped by a single cellular environment. However, it is easy to think about the influence of multiple cellular environments within a cell, as genes are horizontally transferred, introgress, or as species hybridize. Genes introduced via horizontal gene transfer, introgression, or hybridization may carry the signature of a different, foreign cellular environment. These transferred genes may be less adapted to their new cellular environment, potentially imposing large fitness burdens

to the organism. We expect a greater fitness burden of transferred genes if donor and recipient environment differ greatly in their selection bias, making such transfers less likely. More practically, if transferred genes are unaccounted for, they may distort parameters by biasing estimates. This can lead to the conclusion of the wrong codon preference for an amino acid when analyzing a genome that has experienced such transfer events.

In this study, we analyze the synonymous codon usage of the genome of *Lachancea kluyveri*, the earliest diverging lineage of the Lachancea clade. The Lachancea clade diverged from the Saccharomyces clade prior to the whole genome duplication, about 100 Mya ago. Since its divergence from the other Lachancea, *L. kluyveri* has experienced a large introgression of exogenous genes. The introgression replaced the left arm of the C chromosome and displays a 13% higher GC content than the endogenous *L. kluyveri* genome (??). These characteristics make *L. kluyveri* an ideal model to study the effects of an introgressed cellular environment and the resulting mismatch codon usage.

Using ROC SEMPPR, a population genetics Bayesian model, allows us to quantify the cellular environment in which genes have evolved by separating and estimating effects of mutation bias and selection bias, and predicting protein production rate (?). We use ROC SEMPPR to describe two cellular environments reflected in the *L. kluyveri* genome, a native endogenous and an introgressed exogenous environment. Our results indicate that the difference in GC content between endogenous and exogenous genes mostly to differences in mutation bias. Recognizing the differences in codon usage between the endogenous and exogenous gene sets also improves our ability to predict protein synthesis rate from the sequence data alone.

With our improved model fits, we obtained more reliable estimates of mutation bias, selection bias and protein synthesis rate, allowing us to address more refined questions of biological importance. First we determine a potential source lineage of the exogenous genes using a combination of information in codon usage and gene synteny. We compared estimates of mutation bias (ΔM) and selection bias ($\Delta \eta$) for the exogenous genes to 38 yeast lineages

and further investigated candidate lineages using synteny. Second, we estimate the time since introgression and the persistence of the signal of the exogenous cellular environment from our estimates of ΔM using an exponential model of decay. Third, we estimate the selective cost of the mismatched codon usage for the introgression, using our estimates of $\Delta\eta$ and protein synthesis rate ϕ . Thus, in addition to being able to estimate codon preference and gene expression to describe codon usage patterns, we also gain insights into the evolution of genes that have been transferred between lineages.

Results

Model selection and validation confirmed that the *L. kluyveri* genome contains signatures of at least two cellular environments. We compared model fits of ROC SEMPPR to the homogeneous *L. kluyveri* genome and the separated sets of endogenous and exogenous genes of 4864 and 497 genes respectively, using AnaCoDa (?). We compared estimates of the cellular environment to describe differences in endogenous and exogenous codon usage. Furthermore, we utilize the differences in model fit and parameters estimated from the endogenous and exogenous genes to explore the evolution of the exogenous gene set.

AIC indicates that parameter estimates for mutation bias (ΔM) and selection bias ($\Delta\eta$) differ greatly between exogenous and endogenous gene sets. As a result, the partitioning of the *L. kluyveri* genome into an endogenous and exogenous gene set is clearly favored by model selection. The inclusion of 81 additional parameters (40 for ΔM , 40 for $\Delta\eta$, and one for s_ϕ) necessary to describe both gene sets separately improves our model fit by $\sim 75,000$ AIC units (5,311,060 for the combined gene set vs 5,235,598 for the separated gene sets).

In addition to model selection, we utilized independent information on gene expression to evaluate model fit. Recognizing differences in ΔM and $\Delta\eta$ for the endogenous and exogenous gene sets substantially improves our ability to predict protein synthesis rate ϕ ($\rho = 0.69$ vs. $\rho = 0.59$ for the full genome; Figure ??).

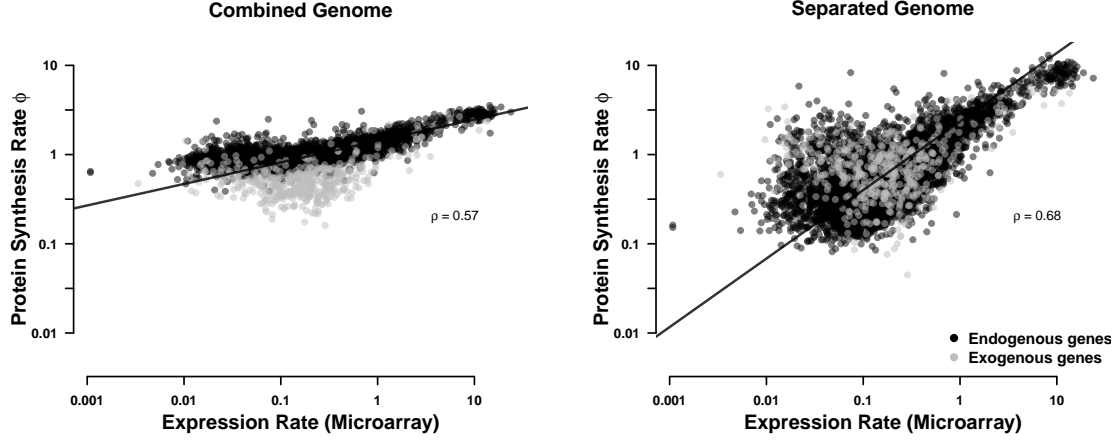


Figure 1: Comparison of predicted protein synthesis rate ϕ to Microarray data from XX for (a) the combined genome and (b) the separated endogenous and exogenous genes. Endogenous genes are displayed in black and exogenous genes in red. Black line indicates type II regression line.

Differences in the Endogenous and Exogenous Codon Usage

As our estimates of parameters for a codon family coding for an amino acid are relative to a reference codon, changes in the reference codon will change the order between sets. To better compare our estimates of mutation bias (ΔM) and selection bias ($\Delta \eta$) obtained from fitting ROC SEMPPR between the endogenous and exogenous gene sets, we express our estimates relative to the mean for each codon family. As we find larger differences between ΔM than $\Delta \eta$ (Figure ??). Estimates of ΔM in the endogenous genes negatively correlate with the ΔM estimates for the exogenous genes ($\rho = -0.49$) indicating strong discordance in the mutation environment between *L. kluyveri* and the donor lineage of the exogenous genes. For example, $\sim 95\%$ of codon families show mutation preference for A/T ending codons, in contrast, the exogenous genes display an equally strong mutation bias towards C/G ending codons. Only the two codon amino acid Phenylalanine (Phe, F) shows complete concordance between endogenous and exogenous genes in their ΔM values.

Estimates of $\Delta \eta$ show higher agreement between endogenous and exogenous genes ($\rho = 0.69$) than our estimates of ΔM . However, only nine codon families favor the same codon

Determining Source of Exogenous Genes

We combined our estimates of mutation bias (ΔM) and selection bias ($\Delta\eta$) with synteny information and searched for potential source lineages of the introgressed region. We examined 38 yeast lineages of which two (*Eremothecium gossypii* and *Candida dubliniensis*) showed a strong positive correlation in codon usage (Figure ??a). The endogenous *L. kluyveri* genome

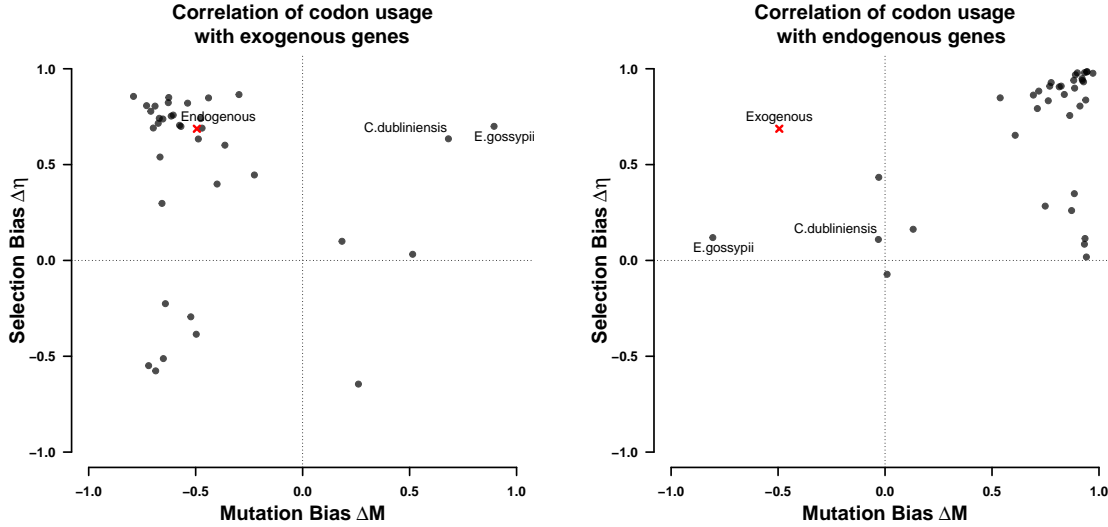


Figure 3: Correlation of ΔM and $\Delta\eta$ of the (a) exogenous and (b) endogenous genes with 38 examined yeast lineages. Dots indicate the correlation of ΔM and $\Delta\eta$ of the lineages with the endogenous and exogenous parameter estimates. All regressions were performed using a type II regression.

exhibits codon usage very similar to most yeast lineages examined, indicating little variation in codon usage among the examined yeasts (Figure ??b). Four lineages show a positive correlation for ΔM and $\Delta\eta$ with the exogenous genes and have a weak to moderate positive correlation in selection bias with the endogenous genes; but, like the exogenous genes, tend to have a negative correlation in ΔM with the endogenous genes.

Comparing synteny between the exogenous left arm of chromosome C, and *E. gossypii* and *C. dubliniensis* as well as closely related yeast species we find that *E. gossypii* displays the highest synteny coverage (Figure ??a,b). *C. dubliniensis*, even though it displays similar codon usage does not show synteny with the exogenous region. Furthermore, the synteny

relationship between the exogenous region and other yeasts appears to be limited to the Saccharomycetaceae group (Figure ??b). Given these results, we conclude that the *E. gossypii* lineage is the most likely source of the introgressed exogenous genes.

Estimating Introgression Age

We estimated the introgression age using an exponential model of decay for mutation bias, by assuming that *E. gossypii* is still representative of the mutation bias of its ancestral source lineage at the time of the introgression. We utilize the ΔM estimates for all two codon amino acids and infer the age of the introgression to be on the order of $6.2 \pm 1.2 \times 10^8$ generations. We assume a mutation rate of 3.8×10^{-10} per nucleotide per generation, a value in line with other estimates (??). *L. kluyveri* experiences between one and eight generations per day, we therefore expect the introgression to have occurred about 205,000 to 1,600,000 years ago which is longer than previous estimates of ?. However, our estimates are likely overestimates as they assume a purely neutral decay.

Furthermore, we estimated the persistence of the signal of the foreign cellular environment. Assuming that differences in mutation bias will decay more slowly than differences in selection bias, we predict that the ΔM signal of the source cellular environment will have decayed to be within one percent of the *L. kluyveri* environment within about $5.4 \pm 0.2 \times 10^9$ generations.

Fitness Burden of the Exogenous Genes

Estimates of selection bias for the exogenous genes show that, while well correlated with the endogenous genes, only nine amino acids share the optimal codon. We therefore expect that the introgressed genes represent a significant reduction in fitness, or genetic load for *L. kluyveri*, and even more so at the time of introgression. As the introgression occurred before the diversification of *L. kluyveri* and has fixed since then throughout the various populations, we are left without the original chromosome arm (?). However, using our estimates of ΔM

and $\Delta\eta$ from the endogenous genes, we can estimate the genetic load of the exogenous genes relative to an expected gene set. We define genetic load as the difference between the fitness of an expected, replaced endogenous gene and the inferred introgressed gene relative to drift $sN_e \propto \phi\Delta\eta$ (See Methods for details).

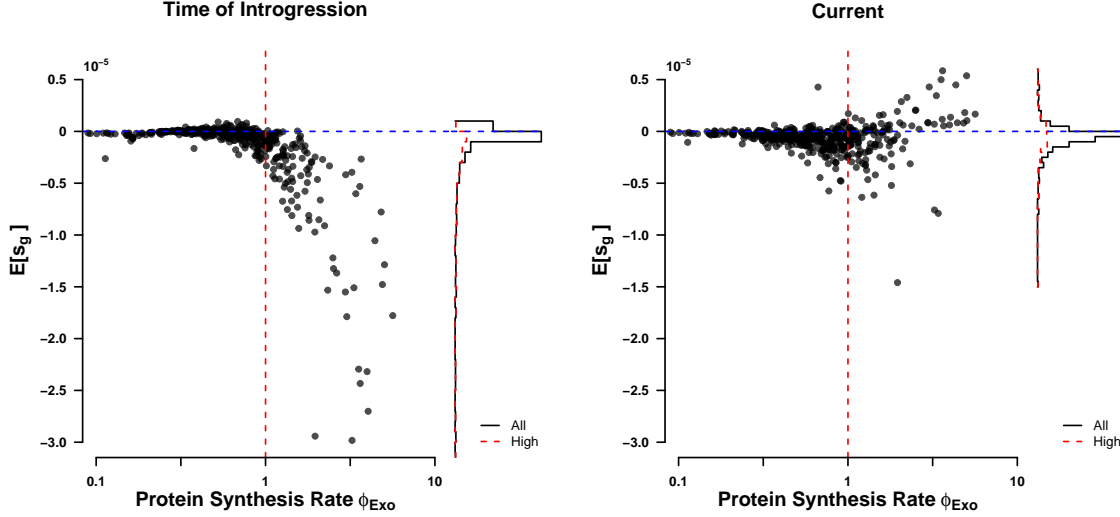


Figure 4: Fitness burden ΔsN_e (a) at the time of introgression ($\kappa = 5$), and (b) currently ($\kappa = 1$).

We estimate the genetic load of the exogenous genes at the time of introgression (Figure ??a) and currently (Figure ??b). These estimates are dependent on three key assumptions. First, we assume again that the current cellular environment of *E. gossypii* is reflective of the ancestral environment. Second, we assume that the current amino acid composition of the exogenous genes is the same as in the replaced endogenous genes. Third, we assume that the difference in the efficacy of selection between *E. gossypii* and *L. kluyveri* can be described with a simple scaling term we call κ (Figure ??b). As $\Delta\eta$ is defined as $\Delta\eta = 2N_e q(\eta_i - \eta_j)$, we can not distinguish if κ is a scaling on protein synthesis rate ϕ , effective population size N_e the value of an ATP $q(?)$.

At the time of the introgression, we predict that only a few genes were weakly exapted (Figure ??a) with all high expression genes ($\phi > 1$) being maladapted to the novel cellular environment. However, these highly expressed genes show the greatest rate of adaptation to

the *L. kluyveri* cellular environment (Figures ??a, ??).

Discussion

Using ROC SEMPPR we show that the *L. kluyveri* genome contains two distinct signatures of cellular environments, its own endogenous and a foreign exogenous one obtained by an introgression event ($\Delta AIC = 78,000$). Following ?, who defined the boundary of the anomalous chromosome region based on its elevated GC content, we partitioned the *L. kluyveri* genome into an endogenous and an exogenous gene set using gene location. We estimated the codon usage of the entire *L. kluyveri* genome and the separated endogenous and exogenous gene sets (Figure ??). Both, Mutation bias and selection bias differ between endogenous and exogenous genes. The endogenous genes show a strong mutation bias towards A/T ending codons, while the exogenous genes show mutation is bias towards G/C ending codons. We observed the reversed to be true in selection bias, leading to a strong mismatch in codon usage between the gene sets, supporting our notion of two distinct signatures of codon usage.

Only half of the codon families share the same optimal codon in the endogenous and exogenous gene sets. However, we find that the strength of selection within a codon family differs between gene sets, causing a change in rank order. Nevertheless, we find a high correlation for our estimates of selection bias $\Delta\eta$ between the two gene sets. Our estimates of the optimal codon differ in nine cases between endogenous and exogenous genes. Interestingly, when the difference in codon usage is ignored, we find that in seven out of these nine cases the exogenous codon preference is inferred as optimal (Table ??). We find even greater discordance in our estimates of ΔM between endogenous and exogenous gene sets (Table ??). Without recognizing this difference in codon preference our estimates would not have been reflective of the actual codon usage of the *L. kluyveri* genome but of a relatively small introgressed gene set. This shows that a small number of exogenous genes ($\sim 9\%$ of genes) can have a disproportional impact on our estimates of ΔM and $\Delta\eta$ when fitting ROC SEMPPR

221 to the entire *L. kluyveri* genome. While this is surprising, it highlights the importance to
 222 recognize differences in codon usage within a genome. Our results also indicate that we can
 223 attribute the higher GC content in the exogenous genes mostly to differences in mutation
 224 bias favoring G/C ending codons rather than a novel selective force.

225 Separating the endogenous and exogenous genes improves our estimates of protein syn-
 226 thesis rate ϕ by 17% relative to the full genome estimate ($\rho = 0.59$ vs. $\rho = 0.69$, respectively).
 227 Furthermore, we find that the variation in our estimates of ϕ is more consistent with the
 228 current understanding of gene expression (compare Figure ??a and b). Small variation in ϕ
 229 estimates may serve as an indicator for the presents of the signature of multiple cellular en-
 230 vironments in future work. In the case of the *L. kluyveri* genome, finding a severe mismatch
 231 in ΔM causes ϕ values for low expression genes ($\phi < 1$) to increase towards the inflection
 232 point where the dominance of mutation gives way to selection. In the case of the two codon
 233 amino acids, the inflection point represents the point at which mutation and selection are
 234 contributing equally to the probability of a codons occurrence. We find this inflection point
 235 around $\phi = 1$ for most amino acids (Figure ??). However, ROC SEMPPR assumes that
 236 estimates of ϕ follow a log-normal distribution with an expected value $E[\phi] = 1$. This as-
 237 sumption allows us to interpret $\Delta\eta$ as the strength of selection relative to drift (sN_e) for a
 238 codon in a gene with the average protein synthesis rate $\phi = 1$. However, tying the mean
 239 and standard deviation of the prior distribution together. Therefore, an increase in ϕ for low
 240 expression genes has to be meet with a decrease of ϕ for high expression genes, reducing the
 241 overall variance in ϕ (see ? for details).

242 Having shown that the introgressed exogenous genes reflect a foreign cellular environ-
 243 ment, we used the quantitative estimates of mutation bias ΔM and selection bias $\Delta\eta$ from
 244 ROC SEMPPR to identify potential source lineages. The comparison of the endogenous
 245 and exogenous ΔM and $\Delta\eta$ estimates to 38 other yeast lineages revealed that most yeasts
 246 examined share similarity in mutation bias (Figure ??). Similar, we find strong similari-
 247 ties in selection bias between examined yeasts, potentially indicating stabilizing selection on

codon usage. However, the exogenous genes do not share this commonality (Figure ??a), as their mutation bias strongly deviates from the endogenous genes and most other yeast species examined. This large difference in mutation bias between endogenous and exogenous genes allowed us to limit our candidate list to only two likely lineages, *C. dubliniensis* and *E. gossypii*. Interestingly, we did not find *Lachancea thermotolerance*, a thermophilic lineage closely related to *L. kluyveri*, as a potential candidate. While *L. thermotolerance* does have a strong synteny relationship with *L. kluyveri*, it does not show similarity in codon usage with the exogenous genes and does not share their high GC content.

Inference of synteny relationships between the exogenous region and *C. dubliniensis* and *E. gossypii* as well as closely related species showed that synteny relationship is limited to the Saccharomycetaceae clade (Figure ??b). *E. gossypii* showed the highest synteny coverage and is the only species with similar codon usage. Furthermore, *E. gossypii* is the only species examined with a GC content $> 50\%$ like it is observed in the exogenous region. The synteny coverage extends along the whole exogenous regions with the exception to the very 3' and 5' end of the region. The lack of synteny at the ends of the region also coincides with a drop in GC content, potentially indicating remains of the original replaced region or increased adaptation. The ancestral introgressed region may have also broken up in *E. gossypii* as we find non overlapping synteny with chromosomes VI and V as well as have indication that the C chromosome of *L. kluyveri* very robust to recombination events (??).

With *E. gossypii* identified as potential source lineage of the introgressed region, we inferred the time past since the introgression occurred using our estimates of mutation bias ΔM . The ΔM estimates are well suited for this task as they are free of the influence of selection and unbiased by N_e and other scaling terms, which is in contrast to our estimates of $\Delta \eta$ (?). We estimated the time since introgression to be on the order of 6×10^8 generations, which is ~ 10 times longer time than a previous estimate by ? of a minimum of 5.6×10^7 generations. However, our estimate implicitly assumes all mutations are neutral, it is therefore a conservative estimate, potentially overestimating the time since introgression. Our

estimate also depend on the assumption that the *E. gossypii* cellular environment reflects the ancestral environment at the time of the introgression. If the the ancestral mutation environment was more similar to the *L. kluyveri* environment at the time of the introgression than the *E. gossypii* environment is today, we would overestimate this time. On the other hand, we would underestimate the time since introgression if the two cellular environments were more dissimilar. We could have attempted to reconstruct the ancestral state of *E. gossypii*, however, as methods for ancestral state reconstruction are phenomenological, assumptions would be unclear.

The estimates of mutation bias ΔM also allow us to infer the time until the signature of the exogenous cellular environment will have decayed to be indistinguishable at about one percent difference. Our estimate of decay is an order of magnitude greater than our estimate of the time since introgression (5×10^9 and 6×10^8 generations). Estimates of decay based on ΔM are more conservative as we expect differences in $\Delta \eta$ to decay before due to selection favoring the decay.

As we have determined that the introgression event has a long persisting exogenous signature, it is important to understand the fitness consequences of such an event. We estimated the genetic load that the exogenous genes represent assuming that the replaced endogenous genes and the new exogenous genes had the same amino acid composition. This assumption, along with the assumption that the current *L. kluyveri* cellular environment is reflective of the cellular environment at the time of the introgression is necessary to estimate the expected endogenous sequence that was replaced. Our results show that individual low expression genes contribute little to the genetic load, and show less adaptation to the novel cellular environment (Figure ??, ??). A small number of low expression genes even appear adapted, likely due to the mutation bias in the endogenous genes matching the selection bias in the exogenous genes for G/C ending codons. Highly expressed genes on the other hand have greatly adapted to the *L. kluyveri* cellular environment. This, however, does not mean that these genes show a higher rate of evolution, but that small changes in their

sequence have large impacts on the fitness burden these sequences represent. To this day, the exogenous genes represent a significant fitness burden on *L. kluyveri*. However, our estimates are conservative as we do not account for potential changes in the codon usage of *E. gossypii*. While divergent evolution in codon usage between *E. gossypii* and *L. kluyveri* would cause us to overestimate the genetic load, convergent evolution, on the other hand, would cause us to underestimate the genetic load. However, as the introgression appears to have reached fixation (?), the genetic load relative to the replaced chromosome arm is only of theoretical interest.

The large genetic load the exogenous genes represented at the time of the introgression indicates that the fixation of the introgression was a very unlikely event in a population with a large N_e as it is typical for yeasts. It is hard to contextualize the probability of this introgression being fixed as we are not aware of any estimates of the frequency at which such large scale introgressions of genes with very different signatures of codon usage occur. One example is *Saccharomyces bayanus*, a hybrid of *Saccharomyces uvarum*, *Saccharomyces cerevisiae*, and *Saccharomyces eubayanus*. However, unlike with *L. kluyveri* and *E. gossypii* it appears that the donor lineages show similar codon usage. *Saccharomyces cerevisiae* and *Saccharomyces eubayanus* show a very strong correlation between selection bias $\Delta\eta$ of $\rho = 0.98$ and a strong correlation between mutation bias ΔM of $\rho = 0.83$. We were unable to identify codon usage for *Saccharomyces uvarum*. However, *L. kluyveri* diverged about 85 Mya ago from the rest of the Lachancea clade. This represents between 10^{10} to 10^{11} generations. Assuming for yeasts typical effective population size on the order of 10^8 , we are left with 10^{18} to 10^{19} opportunities for such an event to occur. In addition, the strong mutation bias towards G/C ending codons in the exogenous genes may have contributed to the fixation of this introgression (include figure of ΔM v $\Delta\eta$). It is, on the other hand, also possible that despite their mismatch in codon usage, the exogenous genes have represented a fitness increase due to external environmental factors resulting in the fixation of the introgression.

In conclusion, our results show the usefulness of the separation of mutation bias and se-

lection bias and the importance of recognizing the presence of multiple cellular environments in the study of codon usage. We also illustrate how a mechanistic model like ROC SEMPPR and the quantitative estimates it provides can be used for more sophisticated hypothesis testing in the future. In contrast to other approaches used to study codon usage like CAI (?) or tAI (?), ROC SEMPPR is sensitive to differences in mutation bias. We highlight potential pitfalls when estimating codon preferences, as estimates can be biased by the signature of a second, historical cellular environment. In addition, we show how quantitative estimates of mutation bias and selection relative to drift can be obtained from codon data and used to infer the fitness cost of an introgression as well as its history and potential future.

Materials and Methods

Separating endogenous and exogenous genes

A GC-rich region was identified by ? in the *L. kluyveri* genome extending from position 1 to 989,693 of chromosome C. This region was later identified as an introgression by ?. We obtained the *L. kluyveri* genome from SGD Project <http://www.yeastgenome.org/download-data/> (last accessed: 09-27-2014) and the annotation for *L. kluyveri* NRRL Y-12651 (assembly ASM14922v1) from NCBI (last accessed: 12-09-2014). We assigned 457 genes located on chromosome C with a location within the $\sim 1Mb$ window to the exogenous gene set. All other 4864 genes of the *L. kluyveri* genome were assigned to the exogenous genes. All genes could be uniquely assigned to one or the other gene set.

Model Fitting with ROC SEMPPR

ROC SEMPPR was fitted to each genome using AnaCoDa (0.1.1) (?) and R (3.4.1). ROC SEMPPR was run from multiple starting values for at least 250,000 iterations, every 50th sample was collected to reduce autocorrelation. After manual inspection to verify that the MCMC had converged, parameter posterior means were estimated from the last 500 samples.

Comparing codon specific parameter estimates

Choice of reference codon does reorganize codon families coding for an amino acid relative to each other, therefore all parameter estimates are relative to the mean for each codon family.

$$\Delta M_{i,a}^c = \Delta M_{i,a} - \Delta \bar{M}_a \quad (1)$$

$$\Delta \eta_{i,a}^c = \Delta \eta_{i,a} - \Delta \bar{\eta}_a \quad (2)$$

Comparison of codon specific parameters (ΔM and $\Delta \eta$) was performed using the function `lmodel2` in the R package `lmodel2` (1.7.3) and R version 3.4.1. Type II regression was performed with re-centered parameter estimates, accounting for noise in dependent and independent variable.

Synteny

We obtained complete genome sequences from NCBI (last accessed: 02-05-2017). Genomes were aligned and checked for synteny using SyMAP (4.2) with default settings (??). We assessed Synteny as percentage non-overlapping coverage of the exogenous gene region (Figure ??b).

Determining introgression timeline

We modeled the change in codon frequency over time using an exponential model for all two codon amino acids, and describing the change in codon c_1 as

$$\frac{dc_1}{dt} = -\mu_{1,2}c_1 - \mu_{2,1}(1 - c_1) \quad (3)$$

where $\mu_{i,j}$ is the rate at which codon i mutates to codon j and c_1 is the frequency of the reference codon. Our estimates of ΔM_{endo} can be directly related to the steady state of

equation ??.

$$\frac{\mu_{2,1}}{\mu_{1,2} + \mu_{2,1}} = \frac{1}{1 + \exp(\Delta M_{endo})} \quad (4)$$

Solving for $\mu_{1,2}$ gives us $\mu_{1,2} = \Delta M_{endo} \exp(\mu_{2,1})$ which allows us to rewrite and solve equation ?? as

$$c_1(t) = \frac{\exp(-t(1 + \Delta M_{endo})\mu_{2,1}) \exp(t(1 + \Delta M_{endo})\mu_{2,1}) + (1 + \Delta M_{endo})K}{1 + \Delta M_{endo}} \quad (5)$$

where K is

$$K = \frac{-1 + c_1(0) + c_1(0)\Delta M_{endo}}{1 + \Delta M_{endo}} \quad (6)$$

Equation ?? was solved over time with a mutation rate $m_{2,1}$ of 3.8×10^{-10} per nucleotide per generation (?). Initial codon frequencies $c_1(0)$ for each codon family were taken from our estimates of ΔM_{gos} from *E. gossypii*. Current codon frequencies for each codon family were taken from our estimates of ΔM from the exogenous genes. Mathematica (9.0.1.0) (?) was used to calculate the time t_{exo} it takes for the initial codon frequencies $c_1(0)$ for each codon family to change to the current exogenous codon frequencies. The same equation was used to determine the time t_{endo} at which the signal of the exogenous cellular environment has decayed to within 1% of the endogenous environment.

Estimating fitness burden

To estimate the fitness burden, we made three key assumptions. First, we assumed that the current exogenous amino acid composition of genes is representative of the replaced endogenous genes. Second, we assume that the currently observed cellular environment of *E. gossypii* reflects the cellular environment that the exogenous genes experienced before transfer to *L. kluyveri*. Lastly, we assume that the difference in the efficacy of selection between the cellular environments of the source lineage and *L. kluyveri* can be expressed as a scaling constant and that protein synthesis rate ϕ has not changed between the replaced

380 endogenous and the introgressed exogenous genes.

We calculated the fitness burden each gene represents assuming additive fitness effects as

$$(sN_e)_g = \sum_i^C -\kappa\phi_g\Delta\eta_i n_{g,i} \quad (7)$$

where $(sN_e)_g$ is the selection against translation inefficiency relative to drift. ϕ_g is the estimated protein synthesis rate for gene g in the exogenous gene set. $n_{g,i}$ is the codon count of each codon i in the codon set C for each gene g . κ is a constant, scaling the efficacy of selection between cellular environments. Like stated previously, our $\Delta\eta$ are relative to the mean of the codon family. We find that the fitness burden of the introgressed genes is minimized at $\kappa \sim 5$ (Figure ??b). Thus, we set $\kappa = 1$ if we calculate the $(sN_e)_g$ for the endogenous and the current exogenous genes, and $\kappa = 5$ for $(sN_e)_g$ for the fitness burden at the time of introgression. Since we are unable to observe codon counts for the replaced endogenous genes and for the exogenous genes at the time of introgression, we calculate expected codon counts

$$E[n_{g,i}] = \frac{\exp(-\Delta M_i - \Delta\eta_i\phi_g)}{\sum_j^C \exp(-\Delta M_j - \Delta\eta_j\phi_g)} \times m_{a_i} \quad (8)$$

381 m_{a_i} is the number of occurrences of amino acid a that codon i codes for.

382 We report the fitness burden of the introgression as $\Delta sN_e = (sN_e)_{Intro} - (sN_e)_{Endo}$ where
 383 $(sN_e)_{Intro}$ is either the fitness burden at the time of the introgression or presently.

384 Acknowledgments

385 This work was supported in part by NSF Awards MCB-1120370 (MAG and RZ) and DEB-
 386 1355033 (BCO, MAG, and RZ) with additional support from The University of Tennessee
 387 Knoxville. CL received support as a Graduate Student Fellow at the National Institute
 388 for Mathematical and Biological Synthesis, an Institute sponsored by the National Science

389 Foundation through NSF Award DBI-1300426, with additional support from UTK. The
390 authors would like to thank Brian C. O'Meara and Alexander Cope for their helpful criticisms
391 and suggestions for this work.

Amino Acid	<i>E. gossypii</i>	Endogenous	Exogenous	<i>L. kluyveri</i>
Ala A	GCG	GCA	GCG	GCG
Cys C	TGC	TGT	TGC	TGC
Asp D	GAC	GAT	GAC	GAC
Glu E	GAG	GAA	GAG	GAG
Phe F	TTC	TTT	TTT	TTT
Gly G	GGC	GGT	GGC	GGC
His H	CAC	CAT	CAC	CAC
Ile I	ATC	ATT	ATC	ATA
Lys K	AAG	AAA	AAG	AAA
Leu L	CTG	TTG	CTG	CTG
Asn N	AAC	AAT	AAC	AAT
Pro P	CCG	CCA	CCG	CCG
Gln Q	CAG	CAA	CAG	CAG
Arg R	CGC	AGA	AGG	CGG
Ser ₄ S	TCG	TCT	TCG	TCG
Thr T	ACG	ACA	ACG	ACG
Val V	GTG	GTT	GTG	GTG
Tyr Y	TAC	TAT	TAC	TAC
Ser ₂ Z	AGC	AGT	AGC	AGC

Table S1: Synonymous codon preference in the various data sets based on our estimates of ΔM

Supplementary Material

Supporting Materials for *Fitness consequences of mismatched codon usage* by Landerer *et al.*

Amino Acid	<i>E. gossypii</i>	Endogenous	Exogenous	<i>L. kluyveri</i>
Ala A	GCT	GCT	GCT	GCT
Cys C	TGT	TGT	TGT	TGT
Asp D	GAT	GAC	GAT	GAT
Glu E	GAA	GAA	GAA	GAA
Phe F	TTT	TTC	TTC	TTC
Gly G	GGA	GGT	GGT	GGT
His H	CAT	CAC	CAT	CAT
Ile I	ATA	ATC	ATT	ATT
Lys K	AAA	AAG	AAA	AAG
Leu L	TTA	TTG	TTG	TTG
Asn N	AAT	AAC	AAT	AAC
Pro P	CCA	CCA	CCT	CCA
Gln Q	CAA	CAA	CAA	CAA
Arg R	AGA	AGA	AGA	AGA
Ser ₄ S	TCA	TCC	TCT	TCT
Thr T	ACT	ACC	ACT	ACT
Val V	GTT	GTC	GTT	GTT
Tyr Y	TAT	TAC	TAT	TAC
Ser ₂ Z	AGT	AGT	AGT	AGT

Table S2: Synonymous codon preference in the various data sets based on our estimates of $\Delta\eta$

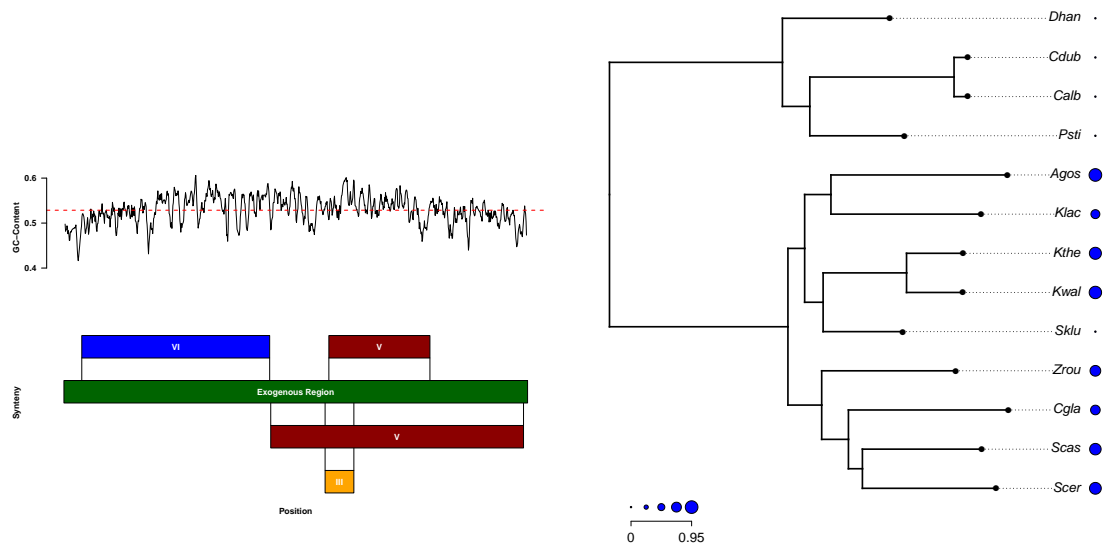


Figure S1: Suppl Fig: Synteny relationship of *E. gossypii* and the exogenous genes (left), Amount of synteny for each species (Units of std dev) checked for synteny.

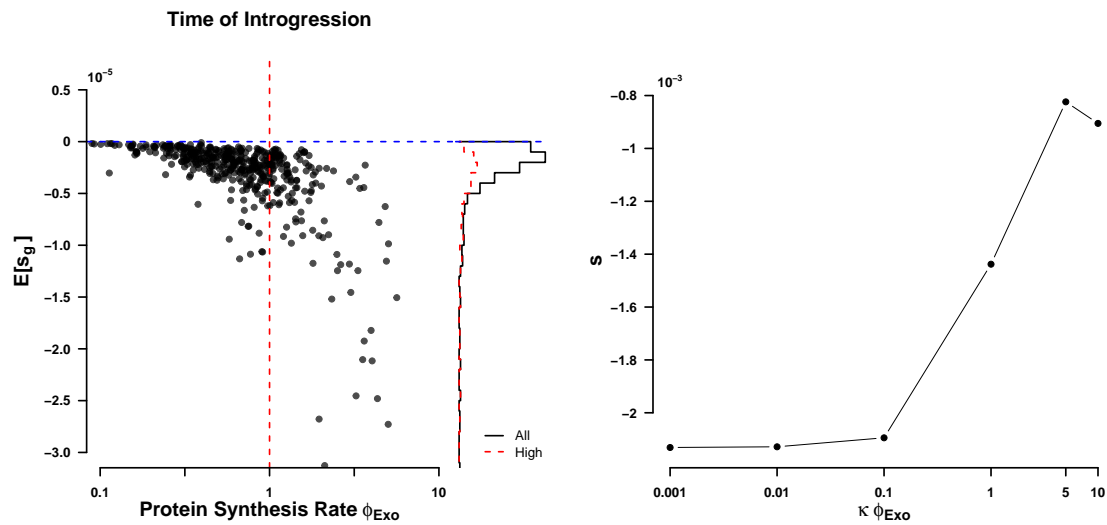
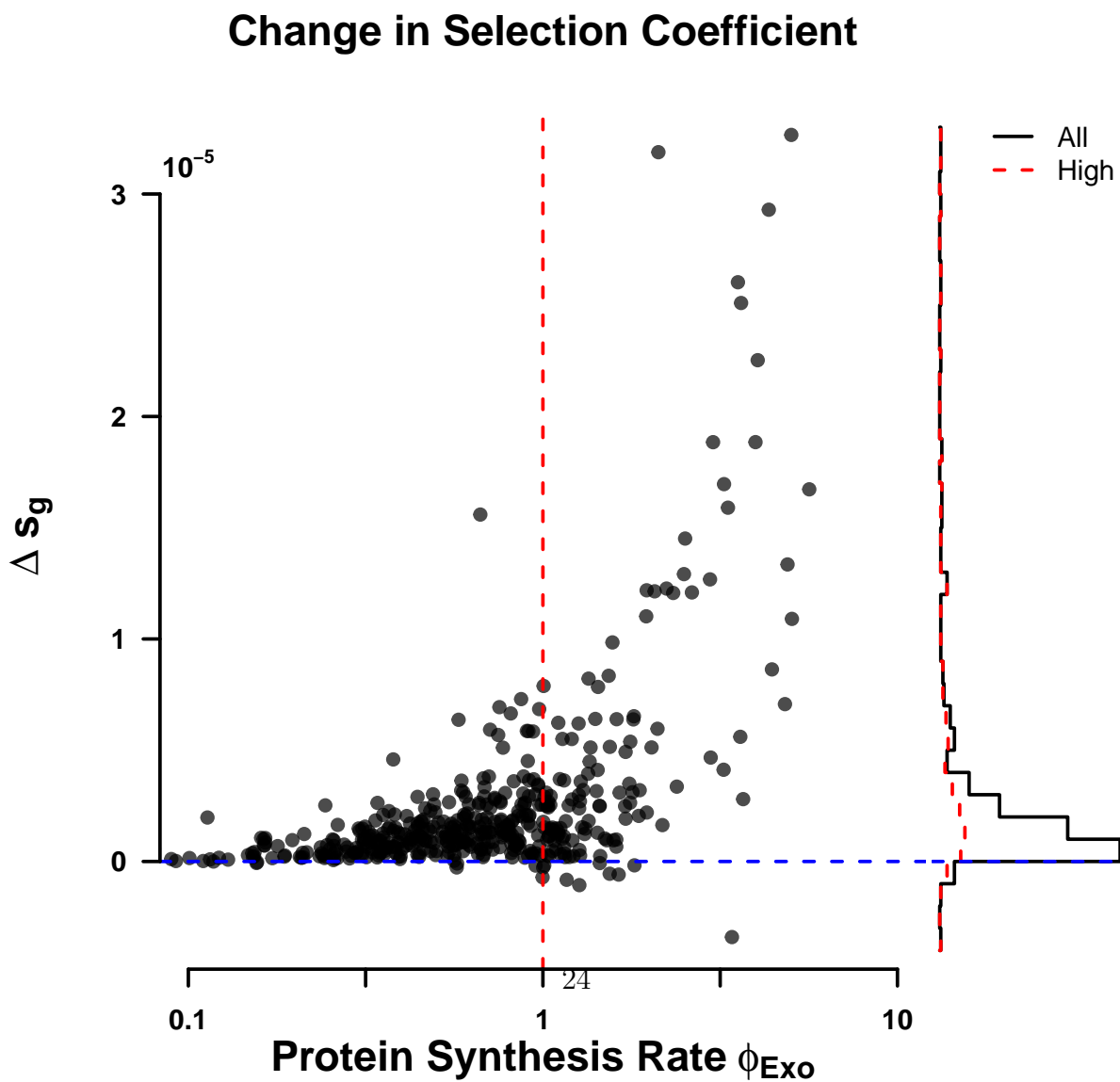


Figure S2: Suppl Fig: Fitness burden (left) without scaling of ϕ , and change of total fitness burden with scaling κ



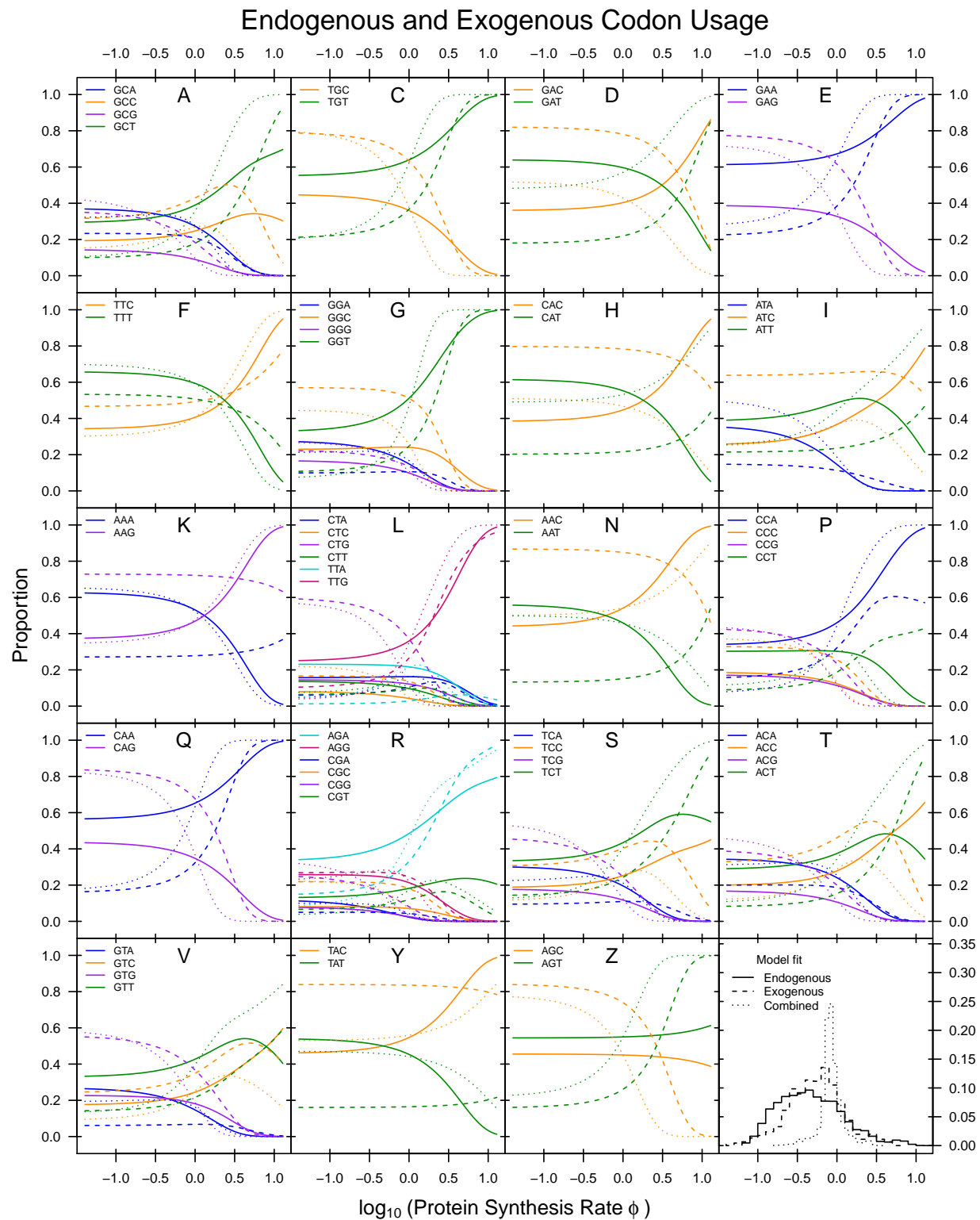


Figure S4: Suppl Fig