

SUPPLEMENTARY TABLES

Table S1: Correlations between all explanatory variables used in this study (excluding “essential genes”, as this is a binary variable). Significant correlations are indicated in bold (significance threshold of 0.05).

	<i>dN/dS</i>	<i>length</i>	<i>multifunc.</i>	<i>PPI.degree</i>	<i>num.domains</i>	<i>CAI</i>	<i>expression</i>	<i>gc</i>	<i>r</i>
<i>dS</i>	-0.0436	0.1205	0.0244	0.0028	0.0613	0.0047	-0.0174	-0.0117	0.0060
<i>dN/dS</i>		0.0797	-0.2201	-0.2181	-0.1127	-0.3691	-0.2498	-0.1733	-0.0649
<i>length</i>			0.2343	0.0377	0.3845	-0.0789	-0.1315	-0.2930	-0.1132
<i>multifunc.</i>				0.1705	0.2085	0.1022	0.0666	-0.0120	-0.0253
<i>PPI.degree</i>					0.0954	0.2142	0.1524	0.0263	0.0176
<i>num.domains</i>						0.0734	0.0160	-0.0183	-0.0342
<i>CAI</i>							0.7819	0.1911	0.0726
<i>expression</i>								0.2262	0.0780
<i>gc</i>									0.3241

Table S2: P-values and change in pseudo-R² for synonymous mutation models including each of the genomic variables. The tested regression models are all of the form $\text{Pois}(\lambda_S = \text{constant} * L_i * \text{variable}_i^a)$ and compared using a likelihood-ratio test against a null model of $\text{Pois}(\lambda_S = \text{constant} * L_i)$.

Variable	P-value	ΔR^2
<i>dS</i>	0.090	0.0005
<i>dN/dS</i>	0.034	0.0024
<i>multifunc</i>	0.565	0.0004
<i>PPI</i>	0.791	0.0005
<i>num.dom</i>	0.590	<0.0001
<i>CAI</i>	0.043	0.0011
<i>expr</i>	0.089	0.0017
<i>gc</i>	0.125	<0.0001
<i>r</i>	0.572	0.0007