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Supporting Texts

Text S1. Assessing the statistical significance in different types of amino acid changes by rate ratio tests

In this section, we explain how to apply rate ratio test (Fay, 2010) to quantify the statistical significance (p-value) of the difference between pathogenic versus benign mutations for the same type of amino acid change. As an example, we will consider the mutation from amino acid type L to P. $n_{path}(L \rightarrow P) = 1171$ and $n_{ben}(L \rightarrow P) = 466$ mutations are for amino acid change from L to P among $N_{path} = 31132$ pathogenic mutations and $N_{ben} = 39465$ benign mutations, respectively. Therefore, the observed rates of L to P mutations among pathogenic and benign mutations are 0.0376 and 0.0118, respectively:

$$\begin{cases} P_{path}(L \rightarrow P) = n_{path}(L \rightarrow P)/N_{path} = 0.0376 \\ P_{ben}(L \rightarrow P) = n_{ben}(L \rightarrow P)/N_{ben} = 0.0118 \end{cases} \quad (S1)$$

Without loss of generality, we suppose $P_{path}(L \rightarrow P) \geq P_{ben}(L \rightarrow P)$. Note that $P_{path}(L \rightarrow P)$ and $P_{ben}(L \rightarrow P)$ are observed rates, while the (unknown) real rates of $L \rightarrow P$ among pathogenic and benign mutations are $\lambda_{path}(L \rightarrow P)$ and $\lambda_{ben}(L \rightarrow P)$, respective. The null and alternative of rate ratio test for $L \rightarrow P$ are:

$$\begin{cases} H_0: RR(L \rightarrow P) = \frac{\lambda_{path}(L \rightarrow P)}{\lambda_{ben}(L \rightarrow P)} = 1 \\ H_1: RR(L \rightarrow P) = \frac{\lambda_{path}(L \rightarrow P)}{\lambda_{ben}(L \rightarrow P)} > 1 \end{cases} \quad (S2)$$

For ease of discussion, we denote:

$$N(L \rightarrow P) = n_{path}(L \rightarrow P) + n_{ben}(L \rightarrow P) \quad (S3)$$

$$p(L \rightarrow P) = \frac{N_{path} \cdot \lambda_{path}(L \rightarrow P)}{N_{path} \cdot \lambda_{path}(L \rightarrow P) + N_{ben} \cdot \lambda_{ben}(L \rightarrow P)} \quad (S4)$$

Since any $L \rightarrow P$ mutations we discuss here are either pathogenic or benign, with probability $p(L \rightarrow P)$ and $1 - p(L \rightarrow P)$, respectively, the number of $L \rightarrow P$ mutations that are pathogenic should follow a binomial distribution:

$$n_{path}(L \rightarrow P) \sim \text{binom}(N(L \rightarrow P), p(L \rightarrow P)) \quad (S5)$$

The p-value can thus be calculated as:

$$\begin{aligned} p\text{-value}(RR(L \rightarrow P) > 1) &= P\left(n_{path}(L \rightarrow P) \leq \text{binom}(N(L \rightarrow P), p(L \rightarrow P))\right) \\ &= 1 - P\left(n_{path}(L \rightarrow P) > \text{binom}(N(L \rightarrow P), p(L \rightarrow P))\right) \end{aligned} \quad (S6)$$

Since $n_{path}(L \rightarrow P)$ is a discrete variable (i.e. an integer), equation (S6) can be rewritten into:

$$\begin{aligned} p\text{-value}(RR(L \rightarrow P) > 1) &= 1 - P\left(n_{path}(L \rightarrow P) + 1 \geq \text{binom}(N(L \rightarrow P), p(L \rightarrow P))\right) \\ &= 1 - p\text{binom}\left(n_{path}(L \rightarrow P) + 1, N(L \rightarrow P), p(L \rightarrow P)\right) \end{aligned} \quad (S7)$$

The term $p\text{binom}\left(n_{path}(L \rightarrow P) + 1, N(L \rightarrow P), p(L \rightarrow P)\right)$ is the value of Cumulative Distribution Function (CDF) for binomial distribution $\text{binom}(N(L \rightarrow P), p(L \rightarrow P))$ at quantile $n_{path}(L \rightarrow P) + 1$. Under any null hypothesis regarding the rate ratio parameter, equation (S4) can be re-written as:

$$p(L \rightarrow P) = \frac{N_{path} \cdot \lambda_{path}(L \rightarrow P)}{N_{path} \cdot \lambda_{path}(L \rightarrow P) + N_{ben} \cdot \lambda_{ben}(L \rightarrow P)} = \frac{N_{path}}{N_{path} + N_{ben}} \quad (S8)$$

Therefore, equation (S7) can be rewritten into:

$$p - value(RR(L \rightarrow P) > 1) = 1 - pbinom\left(n_{path}(L \rightarrow P) + 1, N(L \rightarrow P), \frac{N_{path}}{N_{path} + N_{ben}}\right) \quad (S9)$$

Our program for rate ratio test is available at <https://zhanglab.ccmb.med.umich.edu/RAR>, as part of our previous study (Wei, et al., 2020). Similar to the above procedure, we can also calculate the rate ratio test p -value to assess the statistical significance in difference between forward and reverse L to P mutations (i.e. mutation $L \rightarrow P$ versus mutation $P \rightarrow L$) among all pathogenic mutations (Table S2) or among all benign mutations (Table S3).

Reference

- Fay, M.P. Two-sided Exact Tests and Matching Confidence Intervals for Discrete Data. *R J* 2010;2(1):53-58.
Wei, X., et al. Detecting Gene Ontology misannotations using taxon-specific rate ratio comparisons. *Bioinformatics* 2020;36(16):4383-4388.

Supporting Tables

Table S1. Statistics for different types of amino acid changes for pathogenic versus benign mutations. This table is ranked in descending order of rate differences, and only includes the 251 pairs of amino acid type change that occurs among any mutations.

Mutation	Rate among pathogenic mutation	Rate among benign mutation	P-value of rate ratio test
L→P	3.761e-02	1.181e-02	2.220e-16
G→R	3.864e-02	1.490e-02	2.220e-16
R→C	3.649e-02	1.974e-02	2.220e-16
R→W	3.296e-02	1.629e-02	2.220e-16
C→Y	1.747e-02	4.561e-03	2.220e-16
Y→C	1.902e-02	7.196e-03	2.220e-16
G→D	1.975e-02	8.235e-03	2.220e-16
C→R	1.667e-02	5.245e-03	2.220e-16
G→V	1.551e-02	5.245e-03	2.220e-16
R→P	1.307e-02	4.029e-03	2.220e-16
G→E	1.481e-02	6.689e-03	2.220e-16
L→R	1.086e-02	3.345e-03	2.220e-16
C→F	6.874e-03	1.216e-03	2.220e-16
E→K	2.592e-02	2.030e-02	1.086e-06
W→R	8.673e-03	3.953e-03	1.998e-15
G→C	6.489e-03	1.900e-03	2.220e-16
R→L	9.026e-03	4.840e-03	2.389e-11
D→Y	6.938e-03	2.838e-03	3.553e-15
W→C	5.268e-03	1.318e-03	2.220e-16
F→S	7.709e-03	3.953e-03	6.138e-11
C→G	4.658e-03	1.140e-03	2.220e-16
C→W	4.433e-03	1.090e-03	2.220e-16
A→P	9.669e-03	6.411e-03	1.687e-06
C→S	6.456e-03	3.243e-03	8.749e-10
I→N	4.882e-03	1.774e-03	4.148e-13
D→V	5.685e-03	2.661e-03	4.525e-10
A→D	6.521e-03	3.674e-03	1.353e-07
G→S	1.844e-02	1.568e-02	5.812e-03
M→R	3.533e-03	8.362e-04	2.665e-15
D→G	9.412e-03	6.943e-03	3.459e-04
Y→D	3.180e-03	8.869e-04	5.151e-12
V→D	3.405e-03	1.115e-03	8.643e-11
V→F	4.401e-03	2.331e-03	2.503e-06
M→K	2.859e-03	8.108e-04	9.611e-11
V→G	5.461e-03	3.471e-03	9.428e-05
I→S	2.955e-03	1.014e-03	5.048e-09
V→E	3.501e-03	1.571e-03	3.704e-07
P→R	7.741e-03	5.828e-03	2.420e-03
F→C	3.276e-03	1.419e-03	3.615e-07
R→G	1.131e-02	9.451e-03	1.768e-02
S→F	8.673e-03	6.867e-03	7.579e-03
W→S	2.377e-03	5.828e-04	2.228e-10
Q→P	4.722e-03	2.965e-03	2.051e-04
D→H	5.782e-03	4.029e-03	1.078e-03
H→P	3.598e-03	1.850e-03	1.018e-05
W→G	2.345e-03	6.335e-04	1.970e-09
N→I	3.052e-03	1.343e-03	1.376e-06
T→R	3.501e-03	1.951e-03	9.867e-05
L→Q	3.148e-03	1.672e-03	8.005e-05
F→V	2.923e-03	1.470e-03	4.581e-05
R→H	2.865e-02	2.724e-02	2.741e-01
G→W	2.313e-03	9.629e-04	1.045e-05

Y→N	2.120e-03	7.855e-04	3.361e-06
I→F	3.373e-03	2.052e-03	9.485e-04
N→K	7.067e-03	5.803e-03	4.147e-02
A→E	3.822e-03	2.711e-03	1.191e-02
Y→S	2.538e-03	1.470e-03	1.940e-03
R→S	6.489e-03	5.499e-03	1.003e-01
W→L	1.510e-03	6.588e-04	7.656e-04
L→H	2.088e-03	1.292e-03	1.292e-02
S→L	9.508e-03	8.919e-03	4.404e-01
S→W	1.221e-03	6.335e-04	1.400e-02
I→K	8.673e-04	3.041e-04	2.692e-03
N→Y	1.735e-03	1.216e-03	9.020e-02
F→I	1.702e-03	1.216e-03	1.115e-01
I→R	8.673e-04	4.054e-04	2.098e-02
H→L	1.670e-03	1.267e-03	1.942e-01
T→P	5.075e-03	4.713e-03	5.279e-01
Y→H	5.750e-03	5.397e-03	5.656e-01
S→P	9.026e-03	8.691e-03	6.666e-01
R→T	2.248e-03	1.976e-03	4.823e-01
H→D	1.735e-03	1.470e-03	4.334e-01
K→I	7.067e-04	4.561e-04	2.196e-01
L→W	1.028e-03	8.362e-04	4.774e-01
L→S	4.015e-03	3.902e-03	8.579e-01
L→G	9.636e-05	0	0
A→F	9.636e-05	0	0
G→L	9.636e-05	2.534e-05	4.591e-01
V→Q	6.424e-05	0	0
G→K	6.424e-05	0	0
A→C	6.424e-05	0	0
T→K	2.313e-03	2.255e-03	9.341e-01
E→V	2.281e-03	2.230e-03	9.486e-01
S→I	2.505e-03	2.458e-03	9.578e-01
R→E	9.636e-05	5.068e-05	7.807e-01
S→H	6.424e-05	2.534e-05	8.238e-01
F→T	6.424e-05	2.534e-05	8.238e-01
D→F	6.424e-05	2.534e-05	8.238e-01
A→I	6.424e-05	2.534e-05	8.238e-01
W→F	3.212e-05	0	0
V→P	3.212e-05	0	0
T→H	3.212e-05	0	0
R→N	3.212e-05	0	0
P→F	3.212e-05	0	0
N→V	3.212e-05	0	0
N→G	3.212e-05	0	0
M→N	3.212e-05	0	0
I→Y	3.212e-05	0	0
I→P	3.212e-05	0	0
H→T	3.212e-05	0	0
H→A	3.212e-05	0	0
G→T	3.212e-05	0	0
F→A	3.212e-05	0	0
D→I	3.212e-05	0	0
D→C	3.212e-05	0	0
C→V	3.212e-05	0	0
A→Y	3.212e-05	0	0
A→N	3.212e-05	0	0
A→K	6.424e-05	5.068e-05	1
S→R	6.039e-03	6.031e-03	1
W→K	3.212e-05	2.534e-05	1
S→V	3.212e-05	2.534e-05	1

R→D	3.212e-05	2.534e-05	1
R→A	3.212e-05	2.534e-05	1
Q→W	3.212e-05	2.534e-05	1
Q→G	3.212e-05	2.534e-05	1
P→V	3.212e-05	2.534e-05	1
I→A	3.212e-05	2.534e-05	1
F→N	3.212e-05	2.534e-05	1
F→H	3.212e-05	2.534e-05	1
F→G	3.212e-05	2.534e-05	1
E→M	3.212e-05	2.534e-05	1
D→Q	3.212e-05	2.534e-05	1
C→H	3.212e-05	2.534e-05	1
A→L	6.424e-05	7.602e-05	1
L→Y	3.212e-05	5.068e-05	1
R→Q	3.145e-02	3.147e-02	1
Y→T	0	2.534e-05	0
Y→R	0	2.534e-05	0
Y→M	0	2.534e-05	0
Y→I	0	2.534e-05	0
W→P	0	2.534e-05	0
W→E	0	2.534e-05	0
V→T	0	2.534e-05	0
V→S	0	2.534e-05	0
T→L	0	2.534e-05	0
T→G	0	2.534e-05	0
T→D	0	2.534e-05	0
R→Y	0	2.534e-05	0
R→F	0	2.534e-05	0
Q→S	0	2.534e-05	0
Q→N	0	2.534e-05	0
Q→D	0	2.534e-05	0
P→I	0	2.534e-05	0
P→G	0	2.534e-05	0
P→D	0	2.534e-05	0
M→S	0	2.534e-05	0
M→Q	0	2.534e-05	0
L→T	0	2.534e-05	0
L→D	0	2.534e-05	0
K→V	0	2.534e-05	0
K→L	0	2.534e-05	0
K→D	0	2.534e-05	0
K→A	0	2.534e-05	0
G→Q	0	2.534e-05	0
G→N	0	2.534e-05	0
F→D	0	2.534e-05	0
E→W	0	2.534e-05	0
E→S	0	2.534e-05	0
E→R	0	2.534e-05	0
D→R	0	2.534e-05	0
C→Q	0	2.534e-05	0
C→K	0	2.534e-05	0
A→Q	0	2.534e-05	0
Y→V	0	5.068e-05	0
Y→G	0	5.068e-05	0
W→Q	0	5.068e-05	0
T→E	0	5.068e-05	0
S→D	0	5.068e-05	0
Q→Y	0	5.068e-05	0
N→E	0	5.068e-05	0
L→C	0	5.068e-05	0

H→C	0	5.068e-05	0
E→T	0	5.068e-05	0
E→N	0	5.068e-05	0
E→L	0	5.068e-05	0
A→M	0	5.068e-05	0
L→A	3.212e-05	1.014e-04	5.398e-01
A→R	0	7.602e-05	0
D→N	1.490e-02	1.500e-02	9.428e-01
D→S	0	1.014e-04	0
Y→L	0	1.267e-04	0
R→M	5.461e-04	7.348e-04	4.096e-01
S→Y	2.441e-03	2.661e-03	6.211e-01
D→A	1.959e-03	2.204e-03	5.345e-01
T→N	2.602e-03	2.939e-03	4.414e-01
K→M	7.709e-04	1.115e-03	1.785e-01
R→I	4.818e-04	9.375e-04	3.516e-02
F→L	9.444e-03	1.001e-02	4.742e-01
I→T	1.253e-02	1.310e-02	5.270e-01
P→H	2.281e-03	2.863e-03	1.512e-01
H→N	1.221e-03	1.824e-03	5.281e-02
H→Y	5.589e-03	6.233e-03	2.923e-01
N→H	1.799e-03	2.509e-03	5.374e-02
P→Q	1.895e-03	2.711e-03	3.097e-02
Q→L	1.124e-03	1.951e-03	7.376e-03
N→T	1.702e-03	2.534e-03	2.180e-02
K→T	1.927e-03	2.813e-03	2.065e-02
F→Y	5.782e-04	1.520e-03	1.852e-04
Y→F	8.994e-04	1.976e-03	2.584e-04
G→A	5.172e-03	6.259e-03	6.542e-02
Q→K	2.248e-03	3.446e-03	3.932e-03
E→A	2.184e-03	3.522e-03	1.247e-03
P→L	2.358e-02	2.516e-02	1.892e-01
P→T	4.240e-03	5.904e-03	2.505e-03
I→L	1.221e-03	3.041e-03	2.622e-07
H→Q	3.341e-03	5.245e-03	1.620e-04
M→T	6.071e-03	8.083e-03	1.907e-03
S→C	3.405e-03	5.448e-03	6.617e-05
N→D	4.208e-03	6.385e-03	1.005e-04
K→Q	1.510e-03	3.725e-03	1.421e-08
M→L	1.124e-03	3.345e-03	6.352e-10
I→M	3.533e-03	5.777e-03	1.873e-05
K→E	7.452e-03	9.730e-03	1.397e-03
K→N	4.625e-03	6.918e-03	8.690e-05
M→I	3.822e-03	6.132e-03	2.036e-05
L→I	8.994e-04	3.573e-03	5.281e-14
L→M	1.253e-03	4.029e-03	8.915e-13
L→F	8.448e-03	1.130e-02	1.815e-04
E→G	5.461e-03	8.337e-03	6.272e-06
T→I	1.038e-02	1.335e-02	3.619e-04
Q→E	1.927e-03	4.916e-03	1.790e-11
E→Q	3.244e-03	6.994e-03	5.778e-12
H→R	7.452e-03	1.135e-02	1.429e-07
P→A	2.634e-03	6.664e-03	6.310e-15
S→A	6.103e-04	4.916e-03	2.496e-29
A→G	2.345e-03	6.740e-03	5.752e-18
V→L	5.172e-03	9.958e-03	4.841e-13
Q→H	3.694e-03	8.615e-03	1.316e-16
T→M	1.086e-02	1.586e-02	1.399e-08
M→V	6.424e-03	1.163e-02	6.213e-13
D→E	3.662e-03	9.046e-03	4.506e-19

S→T	1.702e-03	7.374e-03	1.096e-29
A→S	2.602e-03	8.286e-03	1.170e-24
R→K	2.184e-03	8.159e-03	1.065e-28
L→V	5.172e-03	1.117e-02	2.087e-18
V→M	1.230e-02	1.845e-02	7.989e-11
T→S	1.510e-03	8.083e-03	6.867e-38
S→G	2.505e-03	9.122e-03	3.869e-31
E→D	3.790e-03	1.052e-02	5.117e-26
S→N	4.208e-03	1.178e-02	2.386e-29
N→S	9.508e-03	1.713e-02	3.686e-18
K→R	3.501e-03	1.133e-02	8.420e-34
Q→R	6.328e-03	1.432e-02	2.814e-25
P→S	1.018e-02	1.832e-02	2.959e-19
V→A	5.075e-03	1.460e-02	2.539e-37
A→V	1.683e-02	2.742e-02	7.812e-21
T→A	5.139e-03	1.926e-02	5.415e-66
A→T	1.738e-02	3.264e-02	4.106e-37
I→V	3.084e-03	2.374e-02	8.747e-134
V→I	4.658e-03	2.792e-02	4.945e-137

Table S2. Statistics for forward versus reverse amino acid changes among pathogenic mutations. This table is ranked in descending order of rate differences, and only includes the 117 pairs of amino acid type change that occurs among pathogenic mutations. The first column lists the forward mutation. For example, the first row means that the rates of pathogenic mutations R→Q and Q→R are 3.145e-2 and 6.328e-3, respectively.

Mutation	Probability of forward mutation	Probability of reverse mutation	P-value of rate ratio test
R→Q	3.145e-02	6.328e-03	2.220e-16
R→W	3.296e-02	8.673e-03	2.220e-16
R→H	2.865e-02	7.452e-03	2.220e-16
R→C	3.649e-02	1.667e-02	2.220e-16
A→V	1.683e-02	5.075e-03	2.220e-16
D→N	1.490e-02	4.208e-03	2.220e-16
G→V	1.551e-02	5.461e-03	2.220e-16
V→M	1.230e-02	6.424e-03	2.953e-14
S→L	9.508e-03	4.015e-03	2.220e-16
R→P	1.307e-02	7.741e-03	7.181e-11
T→M	1.086e-02	6.071e-03	8.609e-11
D→Y	6.938e-03	3.180e-03	3.797e-11
C→F	6.874e-03	3.276e-03	2.794e-10
G→A	5.172e-03	2.345e-03	8.702e-09
Q→P	4.722e-03	1.895e-03	7.487e-10
D→V	5.685e-03	3.405e-03	2.896e-05
I→F	3.373e-03	1.702e-03	4.281e-05
V→I	4.658e-03	3.084e-03	1.927e-03
V→F	4.401e-03	2.923e-03	2.800e-03
H→P	3.598e-03	2.281e-03	3.002e-03
E→Q	3.244e-03	1.927e-03	1.538e-03
S→F	8.673e-03	7.709e-03	1.990e-01
T→N	2.602e-03	1.702e-03	1.934e-02
T→P	5.075e-03	4.240e-03	1.420e-01
R→S	6.489e-03	6.039e-03	5.104e-01
I→L	1.221e-03	8.994e-04	2.678e-01
S→T	1.702e-03	1.510e-03	6.173e-01
L→M	1.253e-03	1.124e-03	7.275e-01
R→E	9.636e-05	0	0
D→F	6.424e-05	0	0
A→F	9.636e-05	3.212e-05	6.250e-01
A→L	6.424e-05	3.212e-05	1
A→I	6.424e-05	3.212e-05	1
S→V	3.212e-05	0	0
R→N	3.212e-05	0	0
R→D	3.212e-05	0	0
R→A	3.212e-05	0	0
Q→W	3.212e-05	0	0
Q→G	3.212e-05	0	0
P→F	3.212e-05	0	0
N→V	3.212e-05	0	0
N→G	3.212e-05	0	0
L→Y	3.212e-05	0	0
I→Y	3.212e-05	0	0
H→A	3.212e-05	0	0
E→M	3.212e-05	0	0
D→Q	3.212e-05	0	0
D→I	3.212e-05	0	0
D→C	3.212e-05	0	0
C→V	3.212e-05	0	0
A→Y	3.212e-05	0	0
V→L	5.172e-03	5.172e-03	1
G→L	9.636e-05	9.636e-05	1

P→V	3.212e-05	3.212e-05	1
H→T	3.212e-05	3.212e-05	1
G→W	2.313e-03	2.345e-03	1
T→G	0	3.212e-05	0
P→I	0	3.212e-05	0
N→M	0	3.212e-05	0
N→F	0	3.212e-05	0
N→A	0	3.212e-05	0
K→W	0	3.212e-05	0
H→F	0	3.212e-05	0
H→C	0	3.212e-05	0
G→F	0	3.212e-05	0
F→W	0	3.212e-05	0
T→F	0	6.424e-05	0
Q→V	0	6.424e-05	0
K→G	0	6.424e-05	0
K→A	0	6.424e-05	0
H→S	0	6.424e-05	0
C→A	0	6.424e-05	0
S→Y	2.441e-03	2.538e-03	8.724e-01
D→E	3.662e-03	3.790e-03	8.439e-01
K→I	7.067e-04	8.673e-04	5.682e-01
H→Y	5.589e-03	5.750e-03	8.314e-01
I→M	3.533e-03	3.822e-03	5.971e-01
F→Y	5.782e-04	8.994e-04	1.839e-01
H→Q	3.341e-03	3.694e-03	4.993e-01
K→T	1.927e-03	2.313e-03	3.384e-01
R→I	4.818e-04	8.673e-04	8.843e-02
N→Y	1.735e-03	2.120e-03	3.153e-01
H→L	1.670e-03	2.088e-03	2.672e-01
S→I	2.505e-03	2.955e-03	3.187e-01
L→W	1.028e-03	1.510e-03	1.147e-01
H→N	1.221e-03	1.799e-03	7.898e-02
K→Q	1.510e-03	2.248e-03	4.150e-02
C→W	4.433e-03	5.268e-03	1.501e-01
L→F	8.448e-03	9.444e-03	2.036e-01
S→W	1.221e-03	2.377e-03	8.606e-04
S→P	9.026e-03	1.018e-02	1.523e-01
E→V	2.281e-03	3.501e-03	5.668e-03
R→T	2.248e-03	3.501e-03	4.375e-03
R→K	2.184e-03	3.501e-03	2.543e-03
C→Y	1.747e-02	1.902e-02	1.631e-01
E→A	2.184e-03	3.822e-03	2.359e-04
C→G	4.658e-03	6.489e-03	2.595e-03
R→L	9.026e-03	1.086e-02	2.432e-02
N→I	3.052e-03	4.882e-03	3.469e-04
S→A	6.103e-04	2.602e-03	2.703e-10
Q→L	1.124e-03	3.148e-03	4.292e-08
K→M	7.709e-04	2.859e-03	5.684e-10
T→I	1.038e-02	1.253e-02	1.339e-02
K→N	4.625e-03	7.067e-03	8.004e-05
R→M	5.461e-04	3.533e-03	7.387e-18
S→C	3.405e-03	6.456e-03	6.417e-08
H→D	1.735e-03	5.782e-03	5.026e-17
D→A	1.959e-03	6.521e-03	5.285e-19
S→N	4.208e-03	9.508e-03	9.128e-16
P→A	2.634e-03	9.669e-03	1.671e-30
E→G	5.461e-03	1.481e-02	6.010e-32
D→G	9.412e-03	1.975e-02	4.874e-27
T→A	5.139e-03	1.738e-02	3.270e-49

P→L	2.358e-02	3.761e-02	1.087e-23
S→G	2.505e-03	1.844e-02	2.920e-94
K→E	7.452e-03	2.592e-02	5.939e-75
R→G	1.131e-02	3.864e-02	8.526e-109

Table S3. Statistics for forward versus reverse amino acid changes among benign mutations. This table is ranked in descending order of rate differences, and only includes the 133 pairs of amino acid type change that occurs among benign mutations. The first column lists the forward mutation. For example, the first row means that the rates of pathogenic mutations R→Q and Q→R are 3.147e-2 and 1.432e-2, respectively.

Mutation	Probability of forward mutation	Probability of reverse mutation	P-value of rate ratio test
R→Q	3.147e-02	1.432e-02	2.220e-16
R→H	2.724e-02	1.135e-02	2.220e-16
R→C	1.974e-02	5.245e-03	2.220e-16
P→L	2.516e-02	1.181e-02	2.220e-16
A→V	2.742e-02	1.460e-02	2.220e-16
R→W	1.629e-02	3.953e-03	2.220e-16
D→N	1.500e-02	6.385e-03	2.220e-16
T→M	1.586e-02	8.083e-03	2.220e-16
V→M	1.845e-02	1.163e-02	5.551e-15
S→L	8.919e-03	3.902e-03	2.220e-16
V→I	2.792e-02	2.374e-02	2.794e-04
S→F	6.867e-03	3.953e-03	2.867e-08
S→C	5.448e-03	3.243e-03	3.052e-06
E→Q	6.994e-03	4.916e-03	1.804e-04
D→Y	2.838e-03	8.869e-04	1.365e-10
G→V	5.245e-03	3.471e-03	1.900e-04
E→G	8.337e-03	6.689e-03	8.530e-03
D→V	2.661e-03	1.115e-03	6.256e-07
R→L	4.840e-03	3.345e-03	1.216e-03
S→I	2.458e-03	1.014e-03	1.220e-06
L→F	1.130e-02	1.001e-02	8.462e-02
S→Y	2.661e-03	1.470e-03	2.881e-04
K→N	6.918e-03	5.803e-03	5.485e-02
V→F	2.331e-03	1.470e-03	6.852e-03
I→F	2.052e-03	1.216e-03	4.650e-03
H→Y	6.233e-03	5.397e-03	1.352e-01
E→A	3.522e-03	2.711e-03	4.788e-02
L→M	4.029e-03	3.345e-03	1.273e-01
E→V	2.230e-03	1.571e-03	4.087e-02
K→T	2.813e-03	2.255e-03	1.374e-01
R→I	9.375e-04	4.054e-04	5.486e-03
N→Y	1.216e-03	7.855e-04	7.116e-02
T→N	2.939e-03	2.534e-03	3.074e-01
G→W	9.629e-04	6.335e-04	1.299e-01
K→M	1.115e-03	8.108e-04	2.067e-01
K→Q	3.725e-03	3.446e-03	5.523e-01
Q→L	1.951e-03	1.672e-03	4.031e-01
Q→P	2.965e-03	2.711e-03	5.477e-01
P→A	6.664e-03	6.411e-03	6.920e-01
T→I	1.335e-02	1.310e-02	7.806e-01
L→W	8.362e-04	6.588e-04	4.350e-01
K→I	4.561e-04	3.041e-04	3.616e-01
S→W	6.335e-04	5.828e-04	8.854e-01
D→S	1.014e-04	5.068e-05	6.875e-01
Q→Y	5.068e-05	0	0
E→L	5.068e-05	0	0
A→M	5.068e-05	0	0
R→E	5.068e-05	2.534e-05	1
H→C	5.068e-05	2.534e-05	1
T→G	2.534e-05	0	0
R→F	2.534e-05	0	0
P→V	2.534e-05	0	0
P→I	2.534e-05	0	0

K→V	2.534e-05	0	0
K→L	2.534e-05	0	0
K→D	2.534e-05	0	0
G→L	2.534e-05	0	0
E→S	2.534e-05	0	0
E→M	2.534e-05	0	0
R→T	1.976e-03	1.951e-03	1
E→T	5.068e-05	5.068e-05	1
E→N	5.068e-05	5.068e-05	1
T→L	2.534e-05	2.534e-05	1
S→V	2.534e-05	2.534e-05	1
R→Y	2.534e-05	2.534e-05	1
R→D	2.534e-05	2.534e-05	1
Q→G	2.534e-05	2.534e-05	1
E→W	2.534e-05	2.534e-05	1
D→Q	2.534e-05	2.534e-05	1
D→F	2.534e-05	2.534e-05	1
A→I	2.534e-05	2.534e-05	1
H→L	1.267e-03	1.292e-03	1
Q→W	2.534e-05	5.068e-05	1
K→A	2.534e-05	5.068e-05	1
T→Y	0	2.534e-05	0
T→V	0	2.534e-05	0
T→F	0	2.534e-05	0
S→Q	0	2.534e-05	0
S→M	0	2.534e-05	0
Q→M	0	2.534e-05	0
Q→C	0	2.534e-05	0
Q→A	0	2.534e-05	0
P→W	0	2.534e-05	0
N→Q	0	2.534e-05	0
N→G	0	2.534e-05	0
N→F	0	2.534e-05	0
M→Y	0	2.534e-05	0
K→W	0	2.534e-05	0
K→C	0	2.534e-05	0
I→Y	0	2.534e-05	0
H→S	0	2.534e-05	0
H→F	0	2.534e-05	0
G→P	0	2.534e-05	0
G→F	0	2.534e-05	0
D→T	0	2.534e-05	0
D→P	0	2.534e-05	0
D→L	0	2.534e-05	0
A→L	7.602e-05	1.014e-04	1
R→A	2.534e-05	7.602e-05	6.250e-01
V→Y	0	5.068e-05	0
G→Y	0	5.068e-05	0
C→L	0	5.068e-05	0
L→Y	5.068e-05	1.267e-04	4.531e-01
R→M	7.348e-04	8.362e-04	7.035e-01
C→F	1.216e-03	1.419e-03	4.926e-01
C→W	1.090e-03	1.318e-03	4.119e-01
I→M	5.777e-03	6.132e-03	5.488e-01
N→I	1.343e-03	1.774e-03	1.488e-01
F→Y	1.520e-03	1.976e-03	1.476e-01
G→A	6.259e-03	6.740e-03	4.268e-01
R→S	5.499e-03	6.031e-03	3.485e-01
I→L	3.041e-03	3.573e-03	2.157e-01
H→N	1.824e-03	2.509e-03	4.646e-02

S→T	7.374e-03	8.083e-03	2.743e-01
C→G	1.140e-03	1.900e-03	7.847e-03
H→P	1.850e-03	2.863e-03	4.118e-03
T→P	4.713e-03	5.904e-03	2.451e-02
V→L	9.958e-03	1.117e-02	1.036e-01
D→G	6.943e-03	8.235e-03	4.097e-02
D→A	2.204e-03	3.674e-03	1.698e-04
D→E	9.046e-03	1.052e-02	4.015e-02
R→P	4.029e-03	5.828e-03	3.736e-04
H→D	1.470e-03	4.029e-03	4.643e-12
C→Y	4.561e-03	7.196e-03	1.581e-06
R→K	8.159e-03	1.133e-02	7.435e-06
H→Q	5.245e-03	8.615e-03	1.420e-08
S→A	4.916e-03	8.286e-03	6.109e-09
S→N	1.178e-02	1.713e-02	4.540e-10
R→G	9.451e-03	1.490e-02	4.159e-12
S→G	9.122e-03	1.568e-02	1.095e-16
S→P	8.691e-03	1.832e-02	8.397e-32
K→E	9.730e-03	2.030e-02	2.625e-34
T→A	1.926e-02	3.264e-02	1.126e-31

Supporting Figures

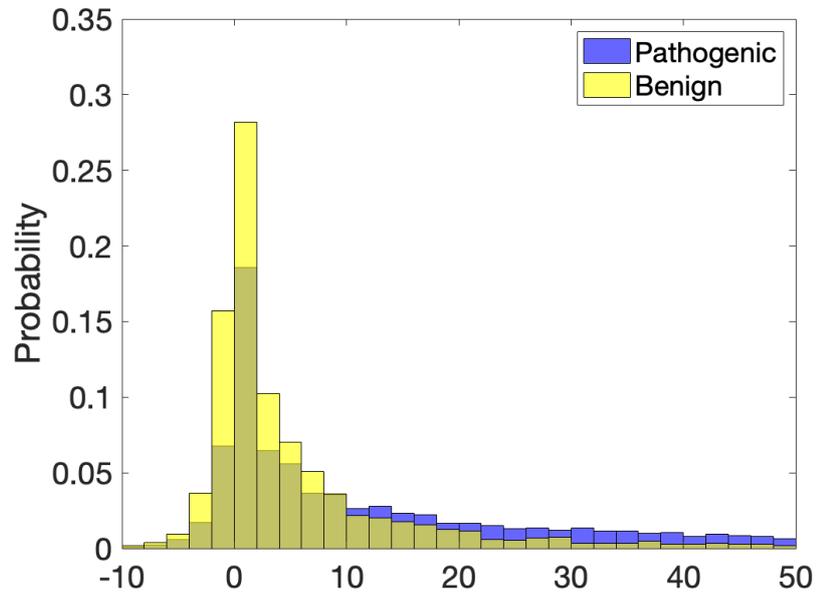


Figure S1. Histograms of FoldX free energy change predictions for pathogenic and benign mutations. T-test p -value = 4.7×10^{-186} . Overall correlation of 0.96 with EvoEF values.