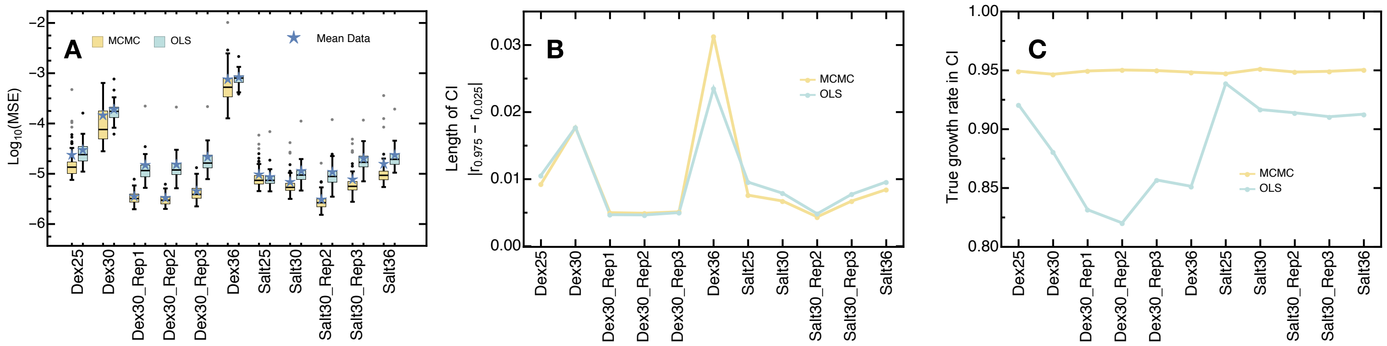


Figure S1: Comparison between the performance of empiricIST and OLS regression with varying number of time points sampled with respect to A) the mean square error (MSE), B) the length of the 95% credibility interval (CI) and C) the fraction of the true growth rate that is contained in the CI. The data was obtained by drawing growth rates from a mixture distribution based on estimates from the experimental data (which we will refer to as mix-data). Similar to what was observed for the simulated data, empiricISTs MSE is lower than that of the OLS regression when applied to mix-data. Furthermore, 95% CIs are generally smaller for empiricIST while remaining well-calibrated as compared to the OLS counterpart. In summary, the *empiricIST* outperforms the OLS regression, with respect to the length of CI and in particular by capturing the true growth rate within the credibility interval.

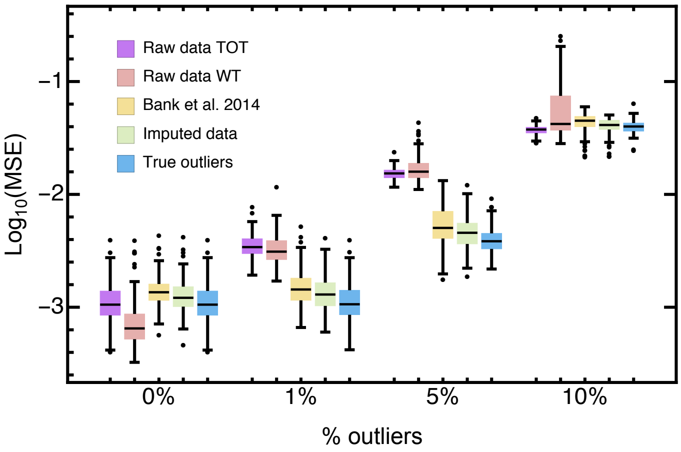


Figure S2: Comparison between the mean square errors (MSE) of the growth rate estimates for several estimation methods, in the presence of 0%, 1%, 5%, and 10% outliers. These estimation methods represent different strategies for calculating growth rates (WT and TOT) or outlier detection and removal (Bank *et. al.* (2014), imputed data and True outliers). In general, we found that if the data set contains outliers, imputing data points improves growth rate estimation.
In the **TOT** approach log-ratios are calculated with respect to the total number of sequencing reads in the data per time point; in the **WT** method log-ratios are calculated with respect to the wild type's number of sequencing reads per time point; in the **Bank *et. al.* (2014)** method outliers are identified as data points with DFBETA> 2 and removed from the data set; in the **imputed data** method outliers are identified as data points DFBETA> 2 and SR> 3 and replaced by average data points; finally, in the **True outliers** approach only the true (and known) outliers are imputed.

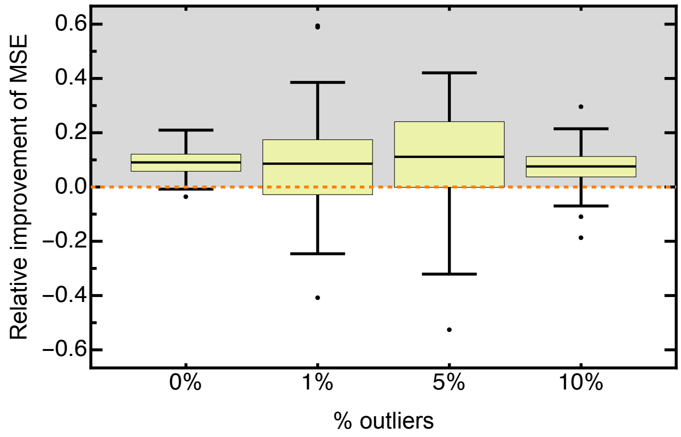


Figure S3: Comparison between the outlier detection method used in Bank *et. al.* (2014) and the imputation method used in *empiricIST* in the presence of 0%, 1%, 5%, and 10% outliers in the data set. In general, imputing outliers improves growth rate estimation by roughly 10%.

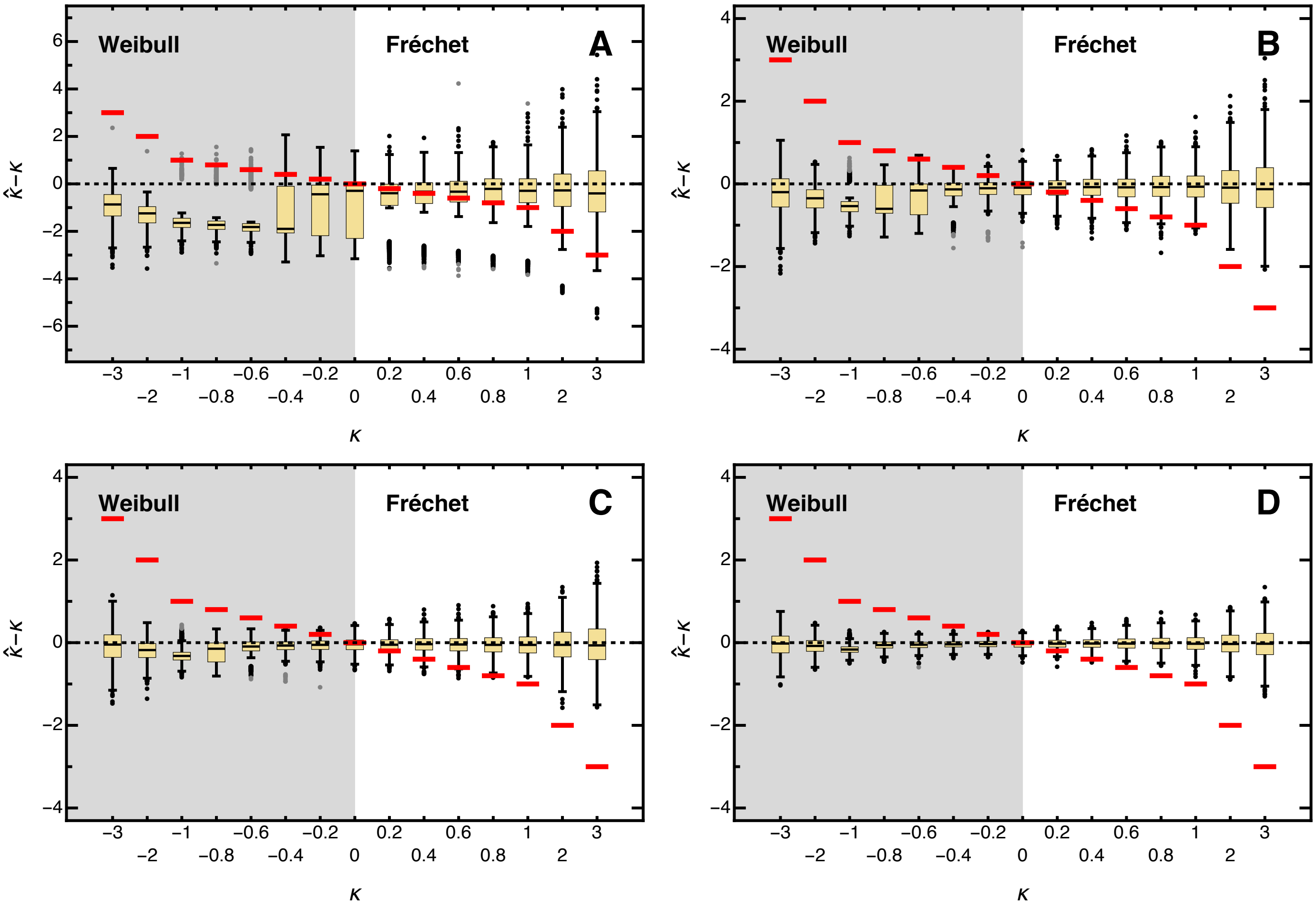


Figure S4: Difference between the estimated and the true shape parameter of the beneficial tail (y axis) for distributions of fitness effects with varying true shape parameters (κ) (x axis). The different subfigures correspond to different sample sizes (i.e., beneficial mutations): A) 10, B) 30, C) 50 and D)100. When sample sizes are low (A and B) there is a large variance and a slight negative bias when estimating κ. However, as sample size increases the variance of the maximum-likelihood estimate decreases and the bias vanishes (C and D). Furthermore, while κ typically falls into the correct domain (even for low sample sizes), the statistical power for detecting deviations from the null hypothesis is low due to the large associated variances (unless sample sizes are large).

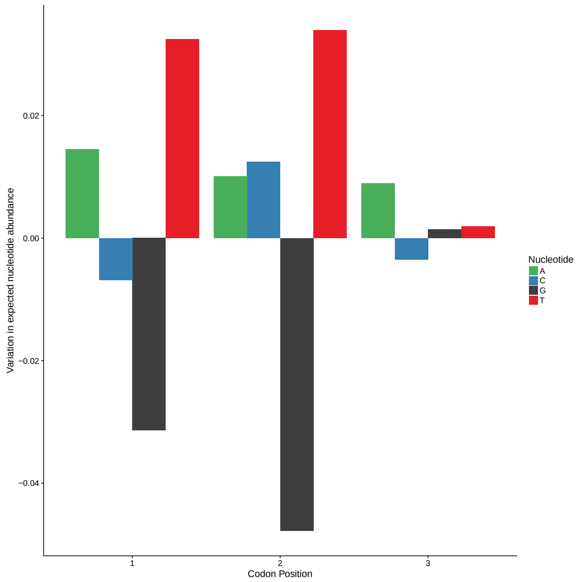
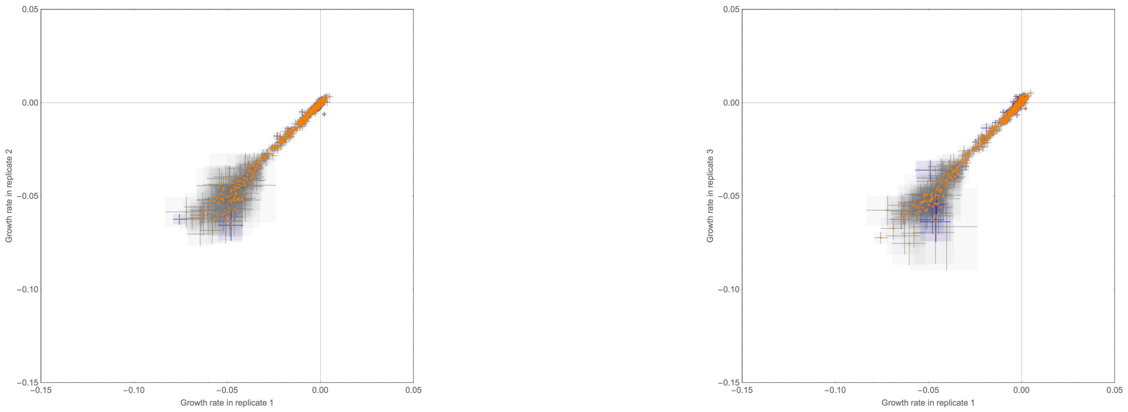
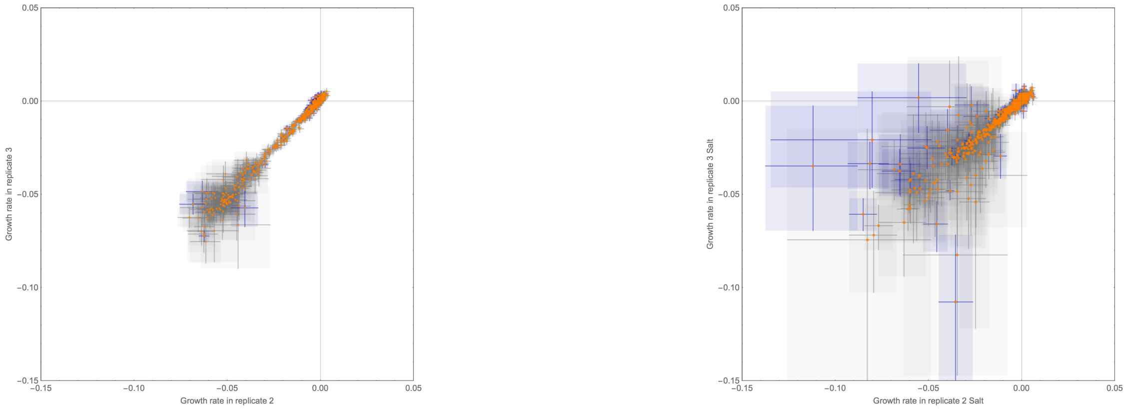


Figure S5: Nucleotide abundance during library construction using the EMPIRIC method. The deviation from expected 25% abundance of each nucleotide (y axis) was obtained by calculating the abundance of each nucleotide after library construction for each codon position (x axis). There is a clear positive bias towards the presence of A or T nucleotides in the data. The data were extracted from figure 7C of Hietpas et al. 2011.



(a) Replicates 1 and 2 normal environment

(b) Replicates 1 and 3 normal environment



(c) Replicates 2 and 3 normal environment

(d) Replicates 2 and 3 salt environment

Figure S6: Overlap of the credibility intervals between pairs of replicates for each mutant. In general, there is a consistent pattern between replicates within the same environment, as evidenced by the large overlap between the normalised mean growth rate of replicate pairs and their 95% credibility intervals of the posterior distribution. Non-overlapping intervals are indicated in blue, and overlapping intervals in gray. a) Overlap between replicates 1 and 2 in 30N - 98%; b) Correlation between replicates 1 and 3 in 30N - 91%; c) Correlation between replicates 2 and 3 in 30N - 90%; d) Correlation between replicates 2 and 3 in 30S - 90%.

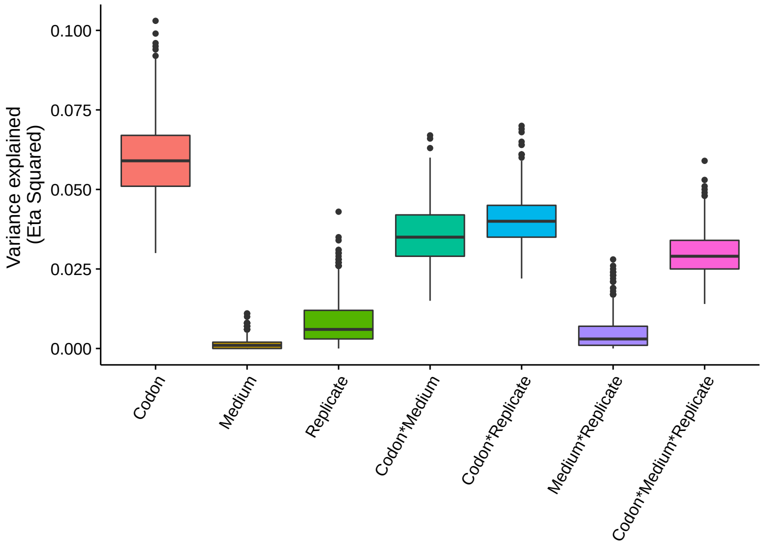


Figure S7: Contribution of Codon, Medium, Replicate and their interactions to the variance in fitness effects of mutations across 1000 posterior samples. Synonymous mutations have a higher mean effect on fitness than replicates, indicating that these effects can be detected despite the presence of experimental error. Interestingly, the effect of synonymous mutations changes in high salinity and also between replicates. The changes observed are mostly due to a reduction in effect size of synonymous mutations in the high salinity environment, possibly due to the reduction in absolute growth rate of the wild type.

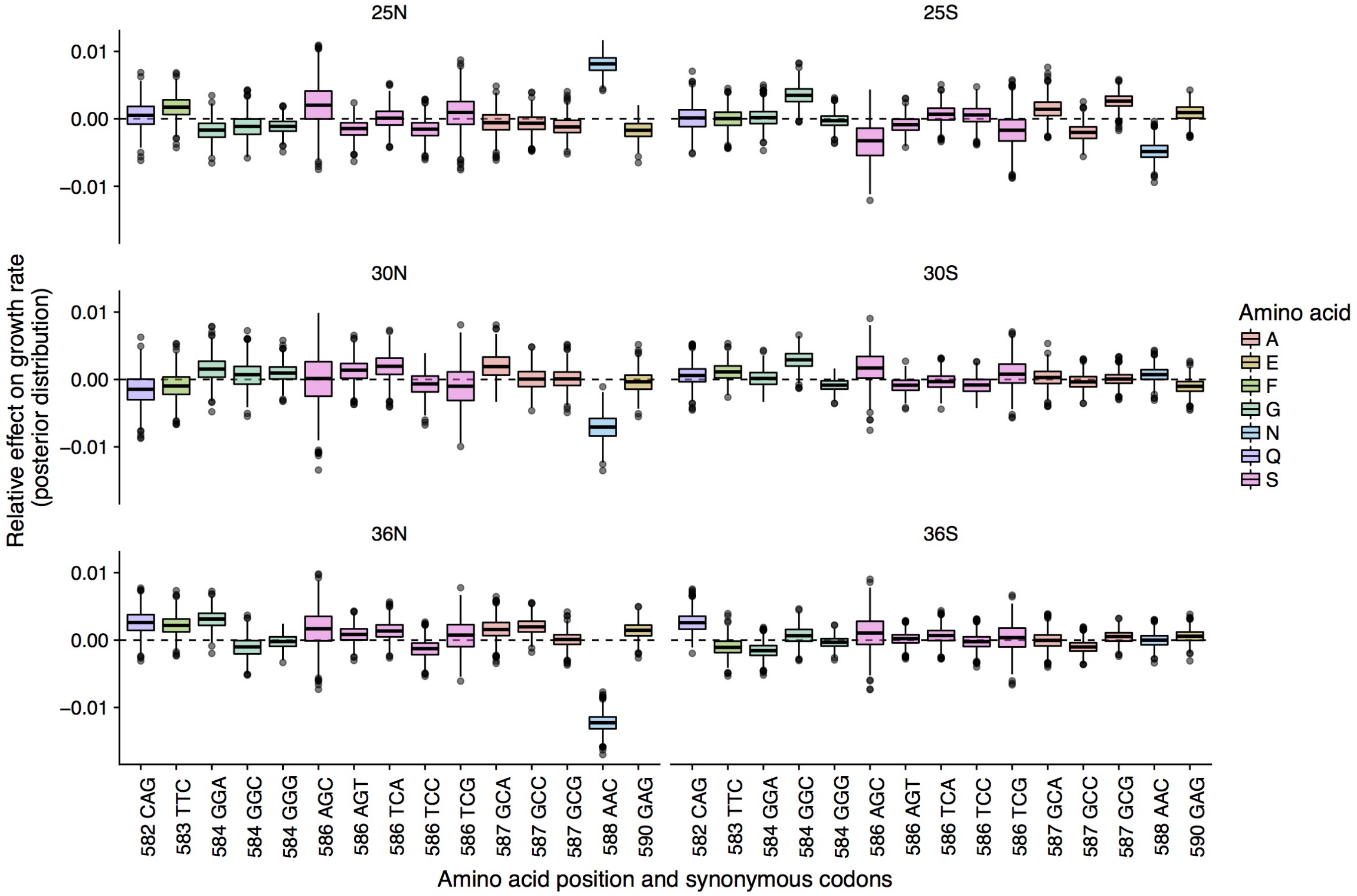


Figure S8: Estimated selection coefficients of the mutations that are synonymous to the wild-type reference sequence across environments. On the x axis are the different synonymous codons across 7 positions, on the y axis is the relative effect of synonymous mutations on the growth rate. Boxplots correspond to 1000 posterior samples. Since the wild-type synonyms are used to normalize all selection coefficients, the distribution of synonymous effects is necessarily centered around 0. The AAC codon in position 588 is an outlier in all standard mediums and in the 25S environment. This is a reproduction of Figure 9 and Figure S7 from Bank *et al* 2014 after re-estimation of selection coefficients with empiricIST

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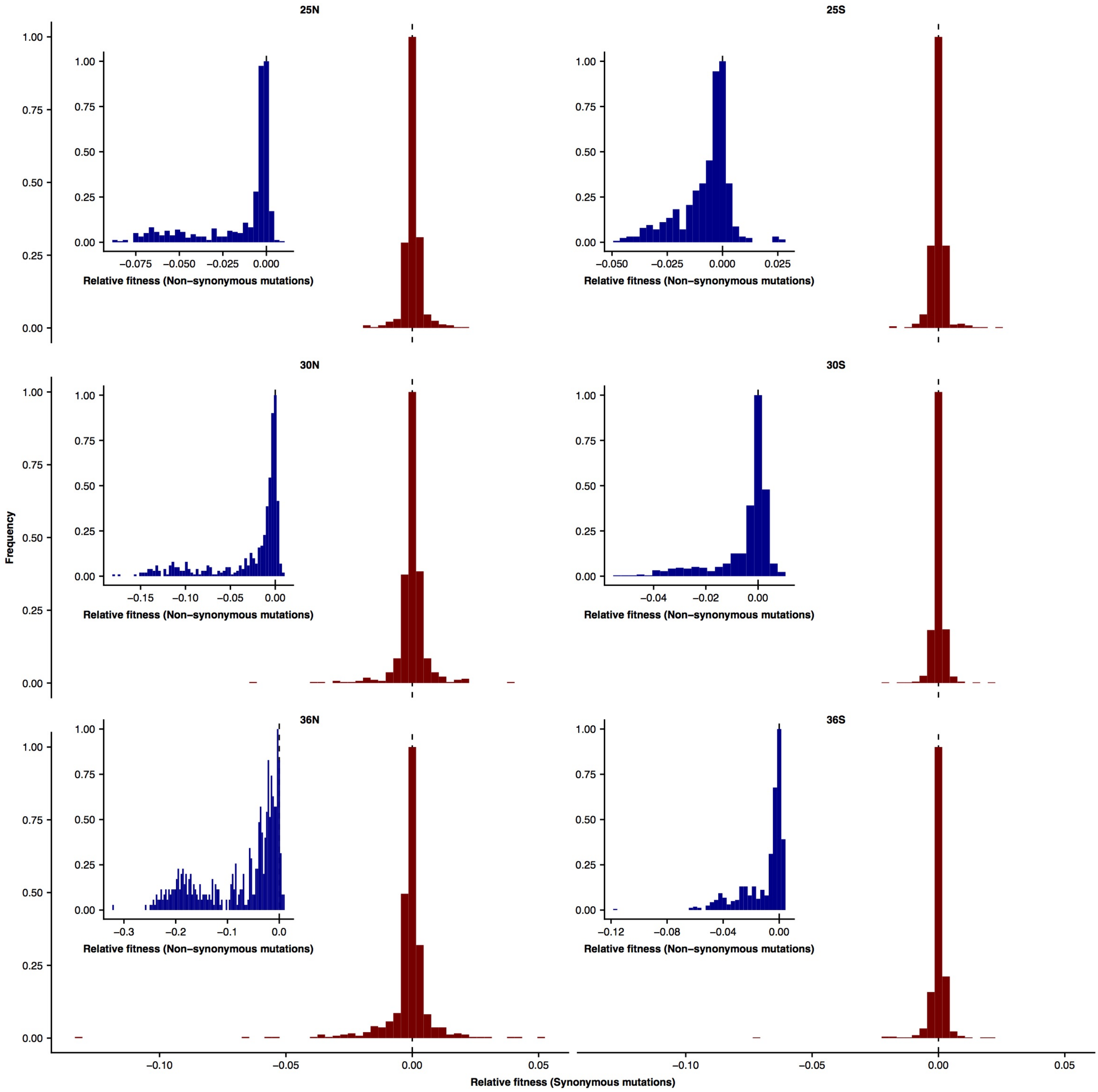


Figure S9: Distribution of fitness effects for synonymous (red) and non-synonymous (dark blue - inset) mutations across 6 environments. On the x axis is the relative fitness effect, and on the y axis its observation frequency. Since we obtain the synonymous effect as differences from the amino-acid average, the synonymous effect distribution is necessarily concentrated around 0.

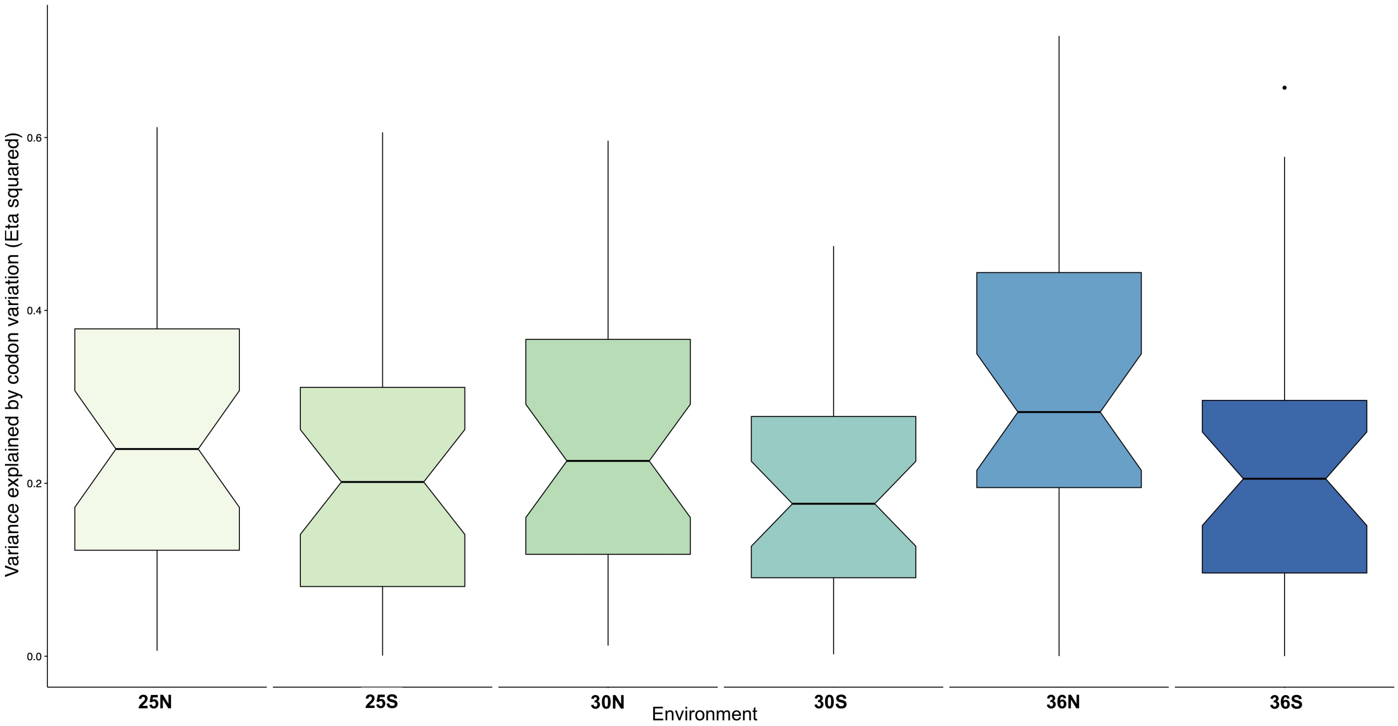


Figure S10: Variance explained by codon variation within each amino-acid for the 6 environments obtained for 1000 posterior samples. On average 20% of the variance within amino-acid can be explained by changes in codon. This value increases to around 30% in the 36N environment, suggesting that the impact of synonymous mutations is strongly dependent on the environmental conditions.

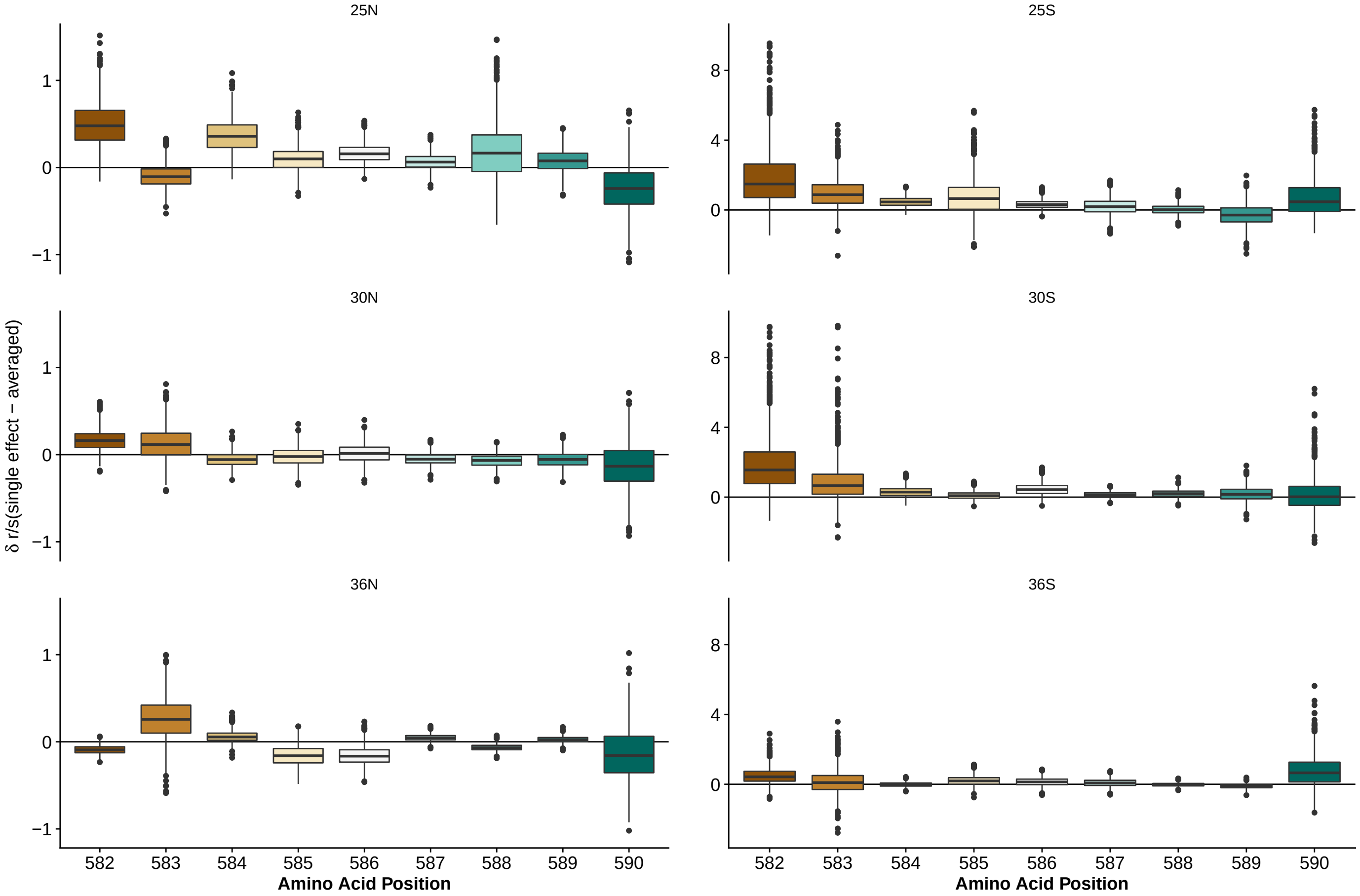


Figure S11: Difference in roughness-to-slope ratio between single-effect and averaged landscapes across amino-acid positions and environments obtained from 1000 posterior samples. On the x axis is the amino-acid position and on the y axis the difference between single-effect and average landscapes. The 0 line indicates no differences between the two landscapes. Overall, single-effect landscapes are more epistatic, albeit these differences are in general small. In fact only positions 582 and 584 in 25N show significantly higher roughness-to-slope ratio in single-effect landscapes than in averaged landscapes (i.e. the 95% interval of the posterior distribution does not overlap with 0). Interestingly, at high salinity differences between landscapes are larger; note the different y axis ranges between standard (left column) and high-salinity (right column) environments.

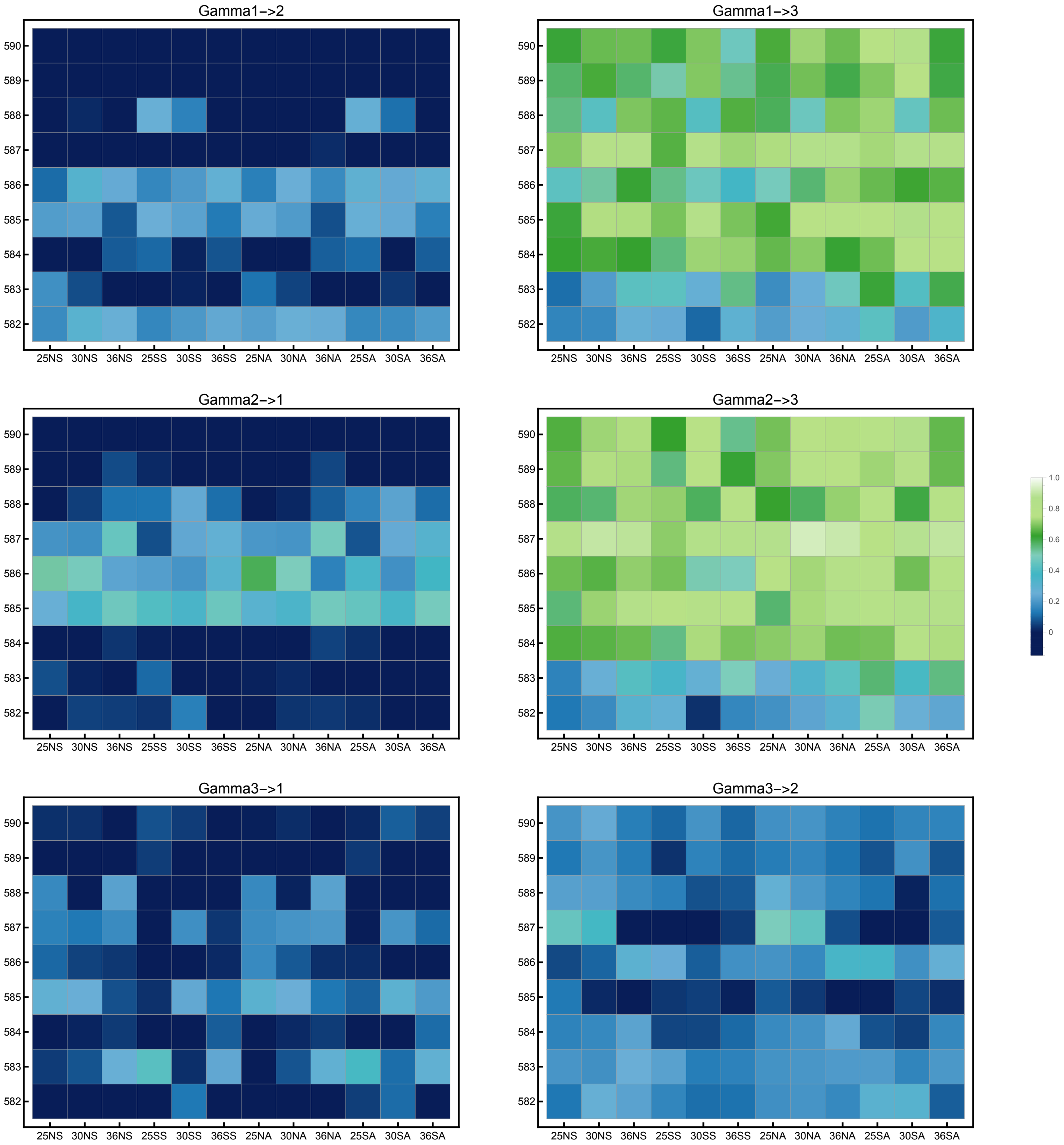
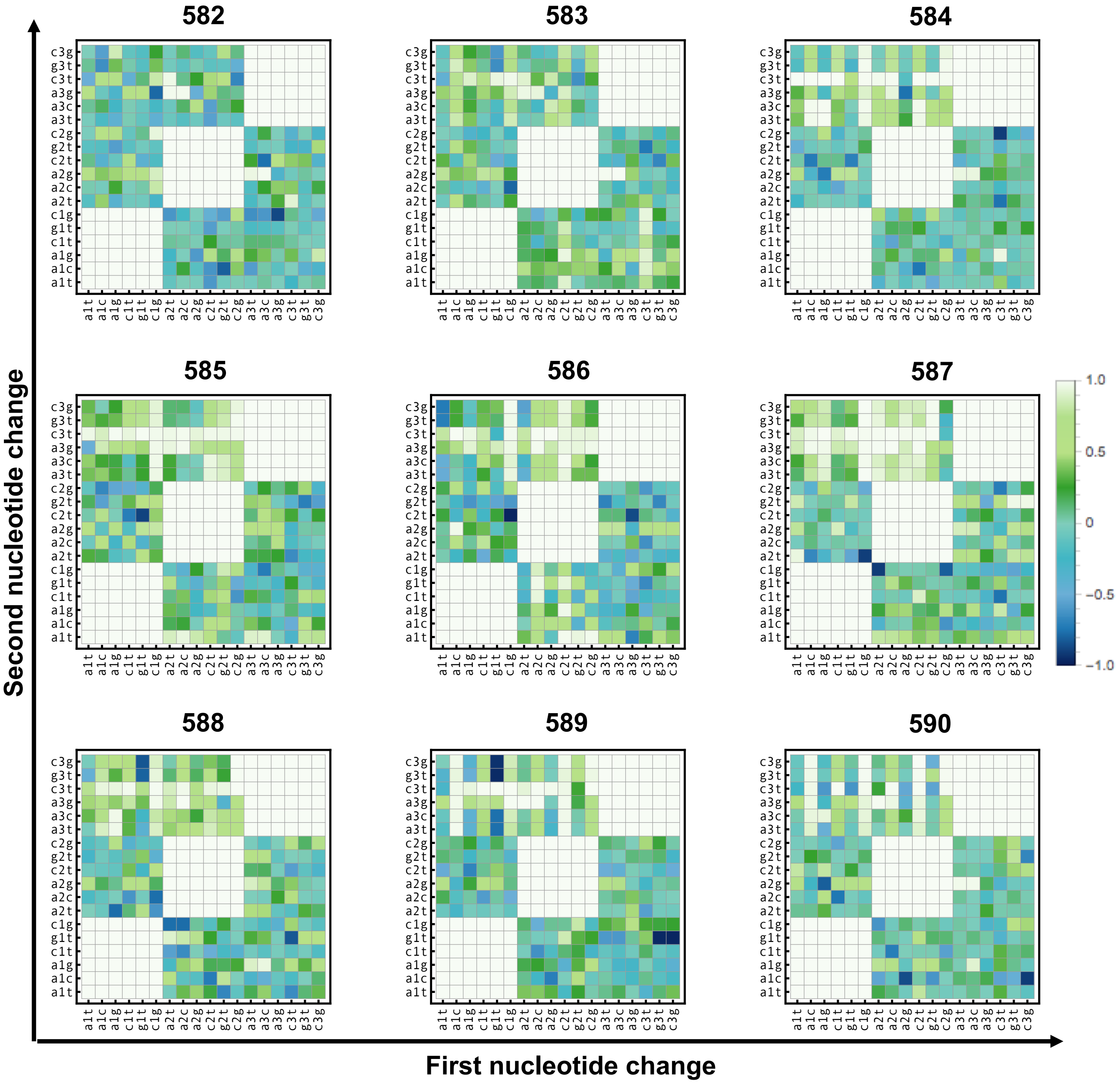
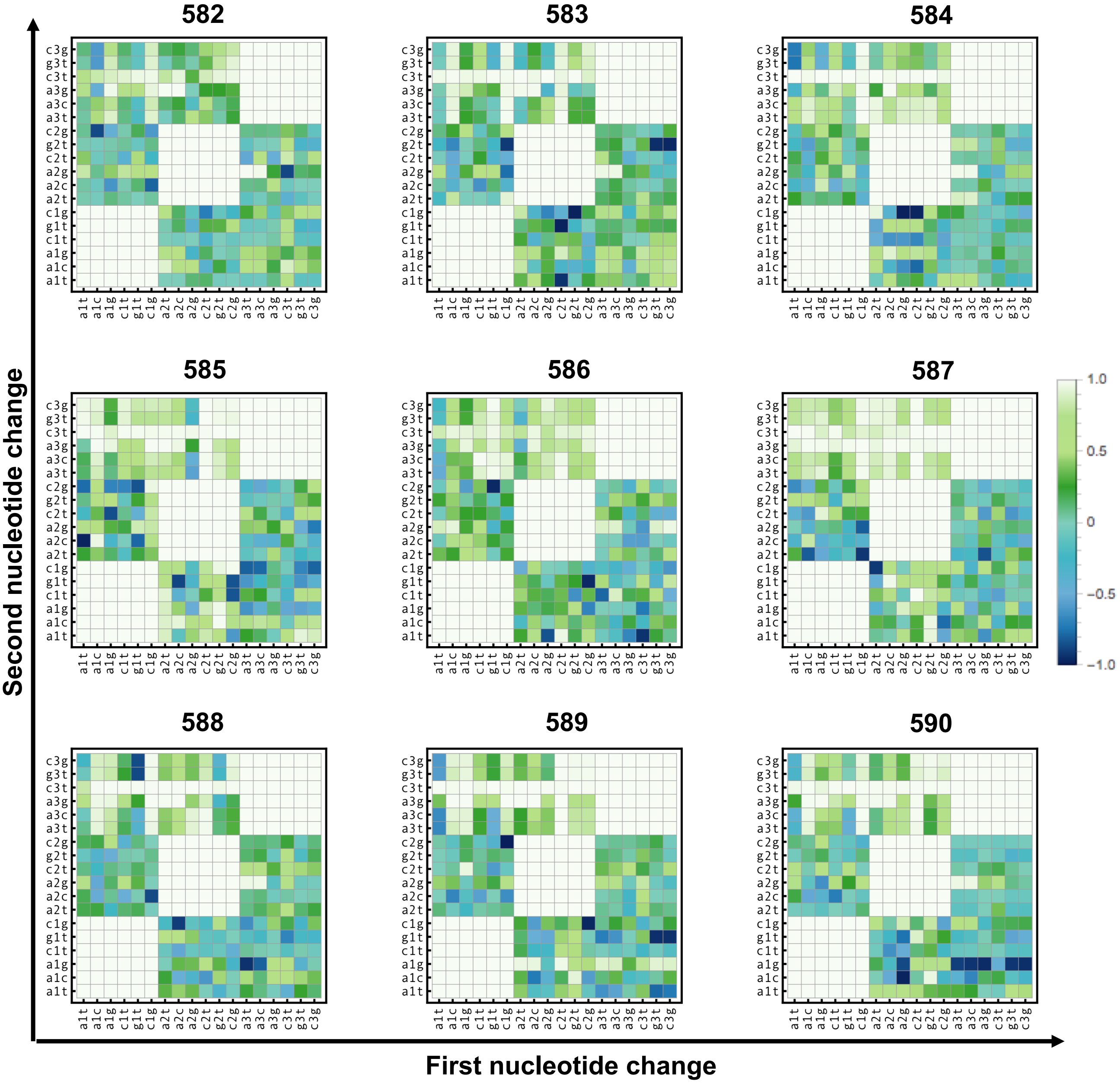


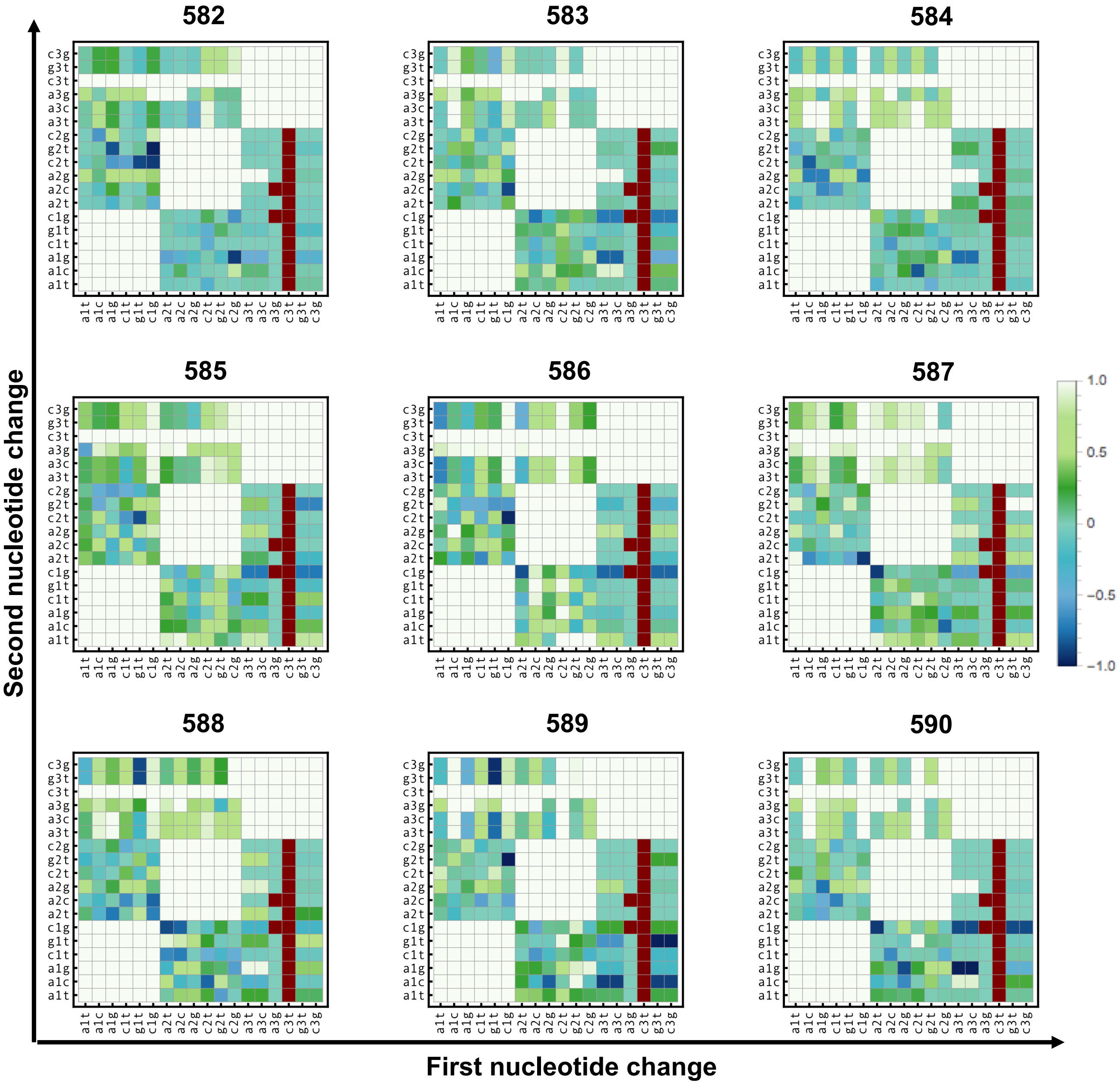
Figure S12: $\gamma_{i\to j}$ statistic estimated for pairs of mutations in different codon positions across 9 amino acid positions (y axis) for single-effect (S) and averaged (A) landscapes in 6 different environments (x axis). In general, there are no differences between single-effect and averaged landscapes. Variation between positions has a stronger impact on the γ than variation across environments, although there is not a clear pattern across any of these factors.



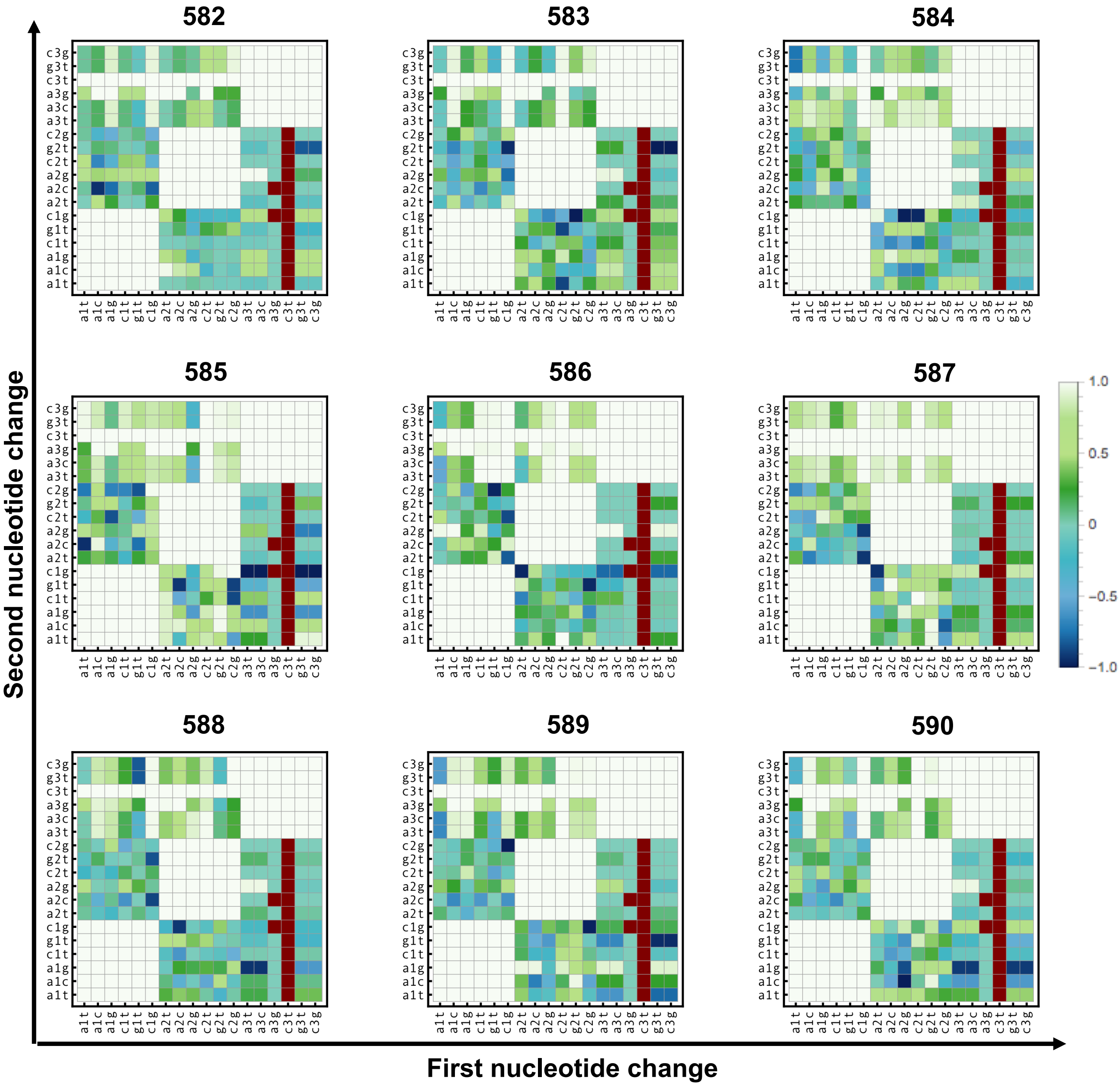
(a) Single-effect 25N



(b) Single-effect 36N



(c) Averagedt 25N



(d) Averaged 36N

Figure S13: $\gamma_{i \to j}$ statistic estimated for pairs of mutations at the nucleotide level in different codon positions across 9 amino acid positions for single-effect (S) and averaged (A) landscapes in 2 different environments. A) single-effect landscape 25N, B) single-effect landscape 36N, C) averaged landscape 25N, D) averaged landscape 36N. The x-axis refers to the first mutation from the initial genotype, the y-axis refers to the second mutation. In general, single-effect and averaged landscapes show a similar epistastic profile. In contrast changes between temperatures (25N to 36N) lead to a slight increase in the prevalence of epistasis. Due to the lack of variation in synonymous mutations in the averaged landscape, gamma could not be estimated for some combinations, indicated by red squares.

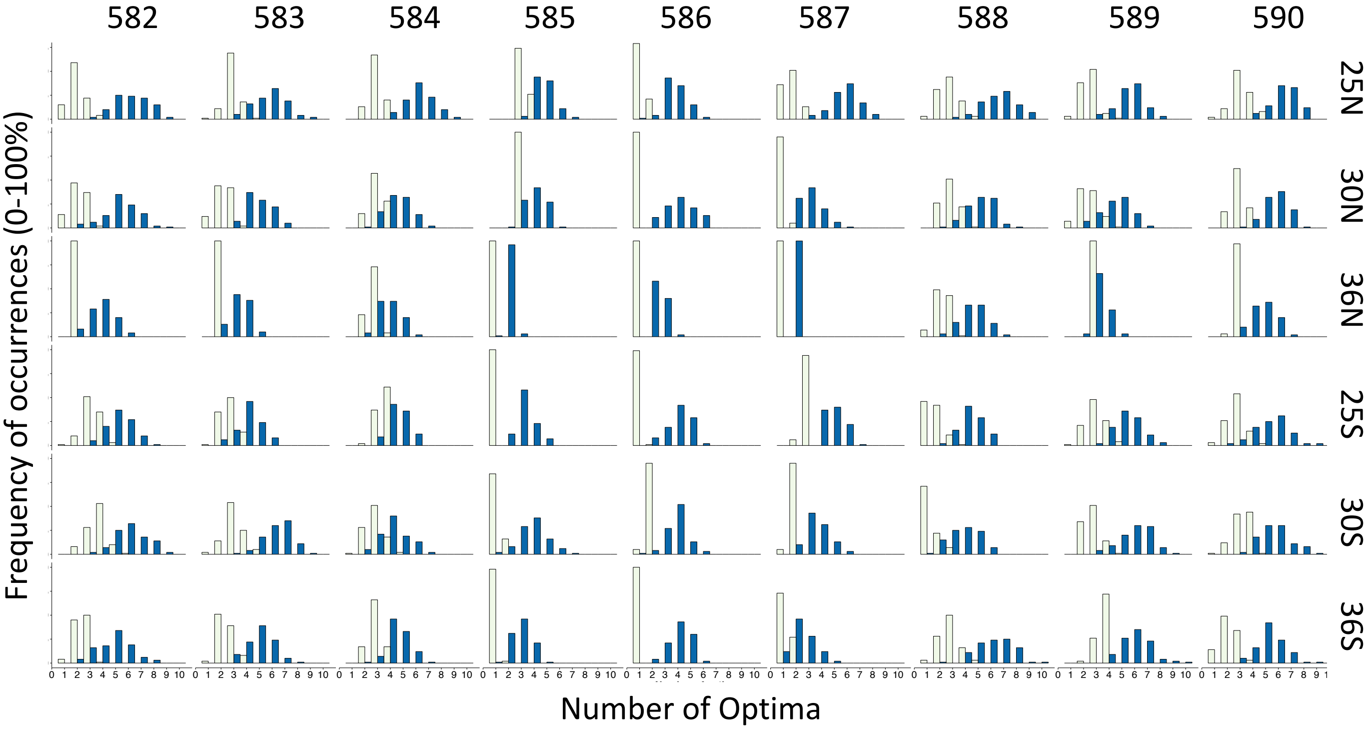


Figure S14: Number of fitness peaks for single-effect (dark blue) and averaged (light blue) landscapes across residue positions and environments (top to bottom) computed from 100 random samples of the posterior. The number of optima is consistently higher in the single-effect than in averaged landscapes across the different environments, as indicated by the distribution of number of optima being shifted to the right. In general the number of optima is reduced at high temperatures, indicating a constraint on the number of mutations that confer high fitness in this environment. This is consistent with the small number of beneficial mutations observed by Bank *et. al.* 2014 in this environment. The observed differences between the number of peaks in averaged and single-effect landscapes suggests that synonymous mutations can impact adaptation to a new environment by possibly trapping the population in a local optima and preventing accessibility of the global optimum. Variation in the differences between single-effect and averaged landscapes is not consistent within buried and exposed positions (see Material and Methods), suggesting that the observed effect of synonymous mutations may not be due to changes in the structural level of the protein. The mean and median of the distributions are significantly different according to Welch Two Sample t-test and Wilcoxon test, $p < 0.00001$ after Bonferroni correction for 54 comparisons

S 1 Tables

Table S1: Sequencing coverage for the 6 environments studied. Several statistics (mean, median, maximum and minimum) are provided for all time points for each environment. Time points correspond to the number of hours after start of the experiment. The total number of hours sampled for high-salinity environments was larger due to the slow growth of populations.

Environment	Time points (hours)	Mean	Median	Min	Max	total
25N	20	1017.2	778.5	96.0	32205.0	577779.0
	24	769.6	578.5	29.0	23956.0	437159.0
	32	823.6	633.5	22.0	25387.0	467810.0
	40	974.0	772.5	9.0	25359.0	553222.0
	48	748.9	603.0	5.0	18542.0	425402.0
	60	743.6	569.0	8.0	24128.0	422361.0
25S	48	461.7	353.5	14.0	10210.0	262233.0
	60	600.5	468.5	15.0	14901.0	341087.0
	72	461.5	361.5	4.0	10142.0	262145.0
	85	521.3	406.0	3.0	13783.0	296116.0
	96	350.0	271.0	5.0	9177.0	198820.0
	108	746.0	551.0	6.0	20942.0	423737.0
30N	16	811.5	638.0	61.0	15876.0	460930.0
	20	870.4	692.5	15.0	18674.0	494385.0
	24	759.2	600.0	30.0	17451.0	431253.0
	32	1259.2	995.5	6.0	30371.0	715253.0
	40	804.4	631.0	2.0	22183.0	456902.0
	48	692.5	537.0	1.0	18332.0	393337.0
30S	24	705.2	560.0	39.0	13503.0	400549.0
	32	839.1	663.0	26.0	19543.0	476633.0
	40	539.2	423.5	3.0	12453.0	306282.0
	48	371.1	295.0	2.0	9244.0	210782.0
	60	620.8	495.0	3.0	15569.0	352631.0
	72	817.1	664.0	2.0	16755.0	464085.0
36N	16	713.7	559.5	49.0	14151.0	405391.0
	20	859.4	673.0	21.0	20331.0	488160.0
	24	714.1	535.5	17.0	17924.0	405635.0
	32	794.0	533.0	3.0	29246.0	451000.0
	40	748.5	435.5	0.0	32838.0	425171.0
	48	1112.2	571.0	0.0	47880.0	631726.0
36S	20	542.2	426.5	43.0	9346.0	307980.0
	32	460.7	360.0	16.0	9518.0	261678.0
	40	501.5	402.5	5.0	11197.0	284846.0
	48	362.9	285.0	5.0	8290.0	206113.0
	60	420.4	332.5	0.0	10030.0	238796.0
	72	353.4	276.5	0.0	8461.0	200738.0

Table S2: Analyses of Variance (ANOVA) to compare the impact of experimental error (replicates) and medium (standard vs. high salinity). *Medium* clearly affects the fitness effects of mutations, with most mutations being neutral when in high-salinity medium. Mutants do not change their effect across the different replicates as indicated by the non-significant term in *replicates* and reinforced by the marginally signifcant interaction between *replicates* and *salt*. Due to the non-orthogonality of the design we used a type II ANOVA.

	Sum Sq	Df	F value	Pr(>F)
Medium	0.02	1	43.65	0.0000 ***
Replicate	0.00	2	0.45	0.6370
Medium*Replicate	0.00	1	3.59	0.0582 m.s.
Residuals	0.97	2795		

Table S3: Effect sizes of synonymous mutations. a) Effect of wild-type synonymous mutations on the growth rate. In general, synonymous mutations increase the growth rate. However, this effect is significant (i.e., the CI does not include 0) only for 25N. b) Statistics of synonymous effect sizes, computed as absolute differences to the average effect of the respective amino acid (see Material and Methods).

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Statistic	25N	25S	30N	30S	36N	36S
Maximum	0.008	0.003	0.002	0.003	0.003	0.003
Minimum	-0.002	-0.005	-0.007	-0.001	-0.012	-0.002
Standard Deviation	0.001	0.001	0.001	0.000	0.001	0.000

(a)

Statistic	25N	25S	30N	30S	36N	36S
Median	0.001	0.001	0.002	0.001	0.002	0.001
Mean	0.002	0.002	0.003	0.001	0.004	0.002
Max	0.019	0.010	0.022	0.014	0.045	0.023
Upper 95%	0.006	0.005	0.012	0.004	0.020	0.004

(b)

Table S4: Descriptive statistics for 1000 pairwise differences between random amino-acid pairs, codon pairs (coding for the same amino acid), and posterior samples (coding for the same codon). The analysis was performed for each environmental condition independently. As expected, amino-acid effects are much larger than synonymous effects. Synonymous effects are larger than the experimental uncertainty.

Level	Statstic	25N	25S	30N	30S	36N	36S
Amino Acid	Mean	0.0175	0.0091	0.0289	0.0080	0.0597	0.0115
	Median	0.0044	0.0056	0.0109	0.0033	0.0326	0.0055
	Maximum	0.0734	0.0493	0.1529	0.0420	0.2178	0.0505
	Upper 95%	0.0627	0.0304	0.1092	0.0299	0.1769	0.0364
Codon	Mean	0.0034	0.0031	0.0054	0.0024	0.0071	0.0031
	Median	0.0023	0.0018	0.0032	0.0016	0.0030	0.0016
	Maximum	0.0375	0.0301	0.0817	0.0312	0.1331	0.0901
	Upper 95%	0.0111	0.0106	0.0189	0.0068	0.0290	0.0091
Posterior	Mean	0.0030	0.0029	0.0040	0.0023	0.0049	0.0025
	Median	0.0020	0.0018	0.0024	0.0016	0.0025	0.0016
	Maximum	0.0320	0.0653	0.0548	0.0398	0.1394	0.0532
	Upper 95%	0.0100	0.0088	0.0123	0.0068	0.0180	0.0073

Table S5: Effect of synonymous mutations. Initial model selection used three criteria: minimum BIC (Model 1), maximum R^2 (Model 2), minimum Mallows Cp (Model 3). The best model (Model 2) includes Temperature, Medium, Codon Preference, GC Content and Melting Temperature as factors and several interactions. For each model the median and 95% credibility intervals (in brackets) based on 1000 samples from the posterior were calculated for several statistics (BIC, AIC, R^2, and adjusted R^2). The three models overlap in BIC or AIC scores. However, Model 2 shows a higher R^2 and adjusted R^2, especially in comparison with Model 1. Due to similarities between all criteria, the best model was identified by performing an ANOVA to compare the three models indicates significant differences between models 1 and 2 (F= 1.7035, P =0.0145).

Model	Selection Criteria	BIC	AIC	R^2	Adjusted R^2
Model 1	BIC	-23909 (-24580: -22736)	-23927 (-24599: -22755	0.00238 (0.00035 : 0.00574)	0.002 (0.00006 : 0.005)
Model 2	Adj $R\hat{2}$	-23738 (-24412: -22557)	-23916 (-24590: -22735)	0.014 (0.008 : 0.024)	0.006 (0.0001 : 0.016)
Model3	Cp	-23903 (-24572: -22729)	-23933 (-24602 : -22759)	0.005 (0.001 : 0.011)	0.004 (0.0005 : 0.011)

$$\text{Model 1:}\quad Y = \text{Intercept} + \text{Temperature*Melting Temperature} + \epsilon$$

$$\begin{aligned}
\text{Model 2 :}\quad Y = {} & \text{Intercept} + \text{Temperature} + \text{Medium} + \text{Temperature*Medium} + \text{Temperature*Codon Preference} \\
& + \text{Medium*Codon Preference} + \text{Temperature*GC content} + \text{Medium*GC content} \\
& + \text{Temperature*Melting Temperature} + \text{Medium*Melting Temperature} \\
& + \text{Temperature*Medium*Codon Preference} + \text{Temperature*Medium*GC content} \\
& + \text{Temperature*Codon Preference*GC content} + \text{Medium*Codon Preference*GC content} \\
& + \text{Temperature*Medium*Melting Temperature} + \text{Temperature*Codon Preference*Melting Temperature} \\
& + \text{Temperature*Codon Preference*Melting Temperature} + \text{Temperature*Residue depth*Melting Temperature} \\
& + \text{Medium*Codon Preference*Melting Temperature} + \text{Temperature*GC content*Melting Temperature} \\
& + \text{Medium*GC content*Melting Temperature} + \text{Temperature*Medium*Codon Preference*GC content} \\
& + \text{Temperature*Medium*Codon Preference*Melting Temperature} \\
& + \text{Temperature*Codon Preference*Residue depth*Melting Temperature} \\
& + \text{Temperature*Medium*GC content*Melting Temperature} \\
& + \text{Temperature*Codon Preference*GC content*Melting Temperature} \\
& + \text{Medium*Codon Preference*GC content*Melting Temperature} + \\
& \text{Temperature*Medium*Codon Preference*GC content*Melting Temperature} + \epsilon
\end{aligned}$$

$$\begin{aligned}
Model3 :\quad Y = {} & \text{Intercept} + \text{Temperature*Melting Temperature} + \text{Medium*Melting Temperature} + \\
& \text{Temperature*Medium:Melting Temperature} + \epsilon
\end{aligned}$$

Table S6: Mean number of steps of adaptive walks for Single (S) and Averaged(A) landscapes. Several statistics are provided according to column labels. Statistical significant comparisons (non-overlapping 95% credibility intervals) between single and averaged landscapes are indicated by $*$.

Env	Position	Mean$_S$	Median$_S$	Lower$_S$	Upper$_S$	Mean$_A$	Median$_A$	Lower$_A$	Upper$_A$
25N	582	2.057	2.012	1.685	2.668	2.247	2.206	1.605	3.118
	583	2.184	2.144	1.768	2.753	2.367	2.357	1.979	3.033
	584	2.073	2.050	1.727	2.619	1.957	1.823	1.610	3.145
	585	2.520	2.477	2.128	3.117	2.477	2.537	2.074	2.740
	586	2.482	2.452	2.066	3.159	2.664	2.644	1.865	3.276
	587	2.181	2.156	1.876	2.720	2.265	2.167	1.812	3.338
	588	2.104	2.039	1.719	2.713	2.521	2.576	1.679	3.349
	589	2.151	2.092	1.791	2.730	2.150	2.060	1.707	2.977
	590	1.980	1.941	1.751	2.459	2.190	2.142	1.612	2.949
25S	582	2.069	2.043	1.746	2.454	1.901	1.840	1.491	2.686
	583	2.347	2.299	2.006	2.838	2.058	2.045	1.708	2.534
	584	2.401	2.377	1.942	3.029	1.900	1.797	1.708	2.327
	585	2.626	2.613	2.215	3.421	2.824	2.867	2.571	2.974
	586	2.363	2.305	1.950	3.045	2.282	2.373	1.960	2.509
	587	2.188	2.189	1.914	2.506	1.692	1.640	1.597	2.398
	588	2.339	2.325	2.040	2.732	2.058	2.072	1.617	2.519
	589	2.182	2.200	1.886	2.494	2.335	2.348	1.830	3.020
	590	2.213	2.156	1.802	2.833	2.197	2.051	1.631	3.142
30N	582	2.250	2.189	1.789	2.959	2.020	1.986	1.628	2.943
	583	2.243	2.198	1.892	2.807	2.492	2.471	1.861	3.423
	584	2.549	2.547	2.061	3.098	2.065	2.039	1.737	2.793
	585	2.643	2.629	2.196	3.305	2.607	2.660	2.388	2.720
	586	2.517	2.490	2.074	3.344	2.346	2.423	2.015	2.526
	587	2.684	2.657	2.218	3.170	2.343	2.339	2.046	2.487
	588	2.204	2.136	1.895	2.863	2.484	2.529	1.769	3.439
	589	2.372	2.299	2.012	3.014	2.402	2.352	1.668	3.333
	590	2.076	2.042	1.784	2.492	2.042	1.998	1.578	2.787
30S	582	1.996	1.925	1.687	2.699	2.036	2.053	1.480	2.870
	583	1.989	1.927	1.656	2.462	2.108	2.000	1.506	2.963
	584	2.513	2.484	1.942	3.214	2.501	2.586	1.736	3.102
	585	2.539	2.488	2.055	3.340	2.724	2.741	2.086	3.094
	586	2.468	2.428	2.038	3.151	2.828	2.837	2.444	3.411
	587	2.496	2.492	2.043	2.969	1.795	1.757	1.688	2.670
	588	2.582	2.468	2.121	3.491	2.279	2.302	1.774	2.611
	589	2.077	2.003	1.747	2.854	2.399	2.348	1.627	3.539
	590	2.235	2.175	1.802	2.792	2.244	2.127	1.846	2.915
36N	582*	2.553	2.497	2.137	3.407	1.735	1.731	1.650	1.836
	583	2.708	2.693	2.330	3.166	2.549	2.548	2.532	2.572
	584	3.046	3.029	2.395	3.911	2.366	2.294	1.912	2.872
	585*	3.033	3.012	2.807	3.199	3.539	3.538	3.525	3.554
	586*	2.604	2.608	2.386	2.857	1.924	1.920	1.879	1.991
	587*	2.883	2.885	2.771	2.985	2.303	2.304	2.283	2.322
	588	2.644	2.492	2.121	4.129	2.853	2.817	2.504	3.331
	589	2.586	2.623	2.323	2.810	2.278	2.274	2.245	2.326
	590	2.330	2.264	1.992	3.155	2.077	2.074	1.791	2.513
36S	582	2.330	2.299	1.887	2.981	2.358	2.345	1.862	3.212
	583	2.127	2.095	1.822	2.692	2.098	2.044	1.696	2.622
	584	2.583	2.537	2.053	3.664	2.144	2.162	1.729	2.799
	585	2.683	2.638	2.256	3.285	2.713	2.722	2.508	2.832
	586	2.423	2.387	2.062	2.993	2.219	2.074	1.965	2.654
	587	2.818	2.847	2.225	3.518	2.261	2.297	1.841	2.686
	588	2.085	2.049	1.723	2.527	2.171	2.058	1.693	3.093
	589	2.126	2.102	1.810	2.523	2.170	2.129	1.704	2.764
	590	2.135	2.100	1.770	2.521	2.317	2.318	1.569	3.281

Table S7: Variance in the number of steps of adaptive walks for Single (S) and Averaged(A) landscapes. Several statistics are provided. Statistical significant comparisons (non overlapping 95% credibility intervals) between single and averaged landscapes are indicated by $*$.

Env	Position	Mean$_S$	Median$_S$	Lower$_S$	Upper$_S$	Mean$_A$	Median$_A$	Lower$_A$	Upper$_A$
25N	582	0.672	0.592	0.393	1.239	0.637	0.548	0.285	1.301
	583	0.781	0.717	0.446	1.306	0.656	0.591	0.381	1.352
	584	0.672	0.628	0.395	1.180	0.500	0.421	0.282	1.186
	585	1.097	1.029	0.689	1.720	0.769	0.742	0.505	1.033
	586	0.870	0.836	0.588	1.426	0.687	0.664	0.426	1.163
	587	0.746	0.709	0.468	1.123	0.641	0.588	0.389	1.195
	588	0.779	0.693	0.480	1.599	0.928	0.920	0.348	1.662
	589	0.703	0.647	0.435	1.279	0.671	0.555	0.317	1.542
	590	0.612	0.553	0.378	1.049	0.580	0.532	0.307	1.166
25S	582	0.629	0.572	0.349	1.033	0.550	0.473	0.281	1.168
	583	0.841	0.819	0.553	1.365	0.602	0.571	0.356	1.154
	584	1.056	1.039	0.570	1.735	0.601	0.555	0.437	0.956
	585	0.940	0.851	0.620	1.827	1.194	1.307	0.595	1.528
	586	0.854	0.805	0.531	1.602	0.531	0.533	0.372	0.696
	587	0.758	0.732	0.507	1.108	0.504	0.450	0.396	1.065
	588	0.771	0.751	0.553	1.152	0.522	0.471	0.277	1.002
	589	0.720	0.715	0.471	1.081	0.752	0.695	0.397	1.450
	590	0.787	0.738	0.482	1.407	0.711	0.604	0.364	1.440
30N	582	0.841	0.731	0.425	1.860	0.463	0.436	0.292	0.802
	583	0.762	0.691	0.454	1.364	0.829	0.800	0.476	1.342
	584	1.112	1.083	0.641	1.710	0.625	0.604	0.374	1.074
	585	1.080	1.040	0.668	1.925	0.815	0.896	0.547	0.936
	586	0.935	0.884	0.574	1.818	0.566	0.588	0.422	0.746
	587	1.006	0.971	0.694	1.553	0.565	0.552	0.413	0.716
	588	0.700	0.633	0.449	1.267	0.846	0.794	0.387	1.711
	589	0.790	0.737	0.510	1.191	0.829	0.684	0.440	2.070
	590	0.654	0.609	0.413	1.197	0.638	0.592	0.296	1.178
30S	582	0.628	0.569	0.395	1.500	0.613	0.582	0.253	1.316
	583	0.620	0.551	0.358	1.213	0.622	0.572	0.267	1.321
	584	1.012	0.958	0.547	1.618	0.911	0.922	0.466	1.378
	585	0.896	0.809	0.527	1.829	0.772	0.741	0.546	1.104
	586	0.902	0.825	0.571	1.671	1.494	1.558	0.901	1.810
	587	0.832	0.793	0.545	1.275	0.322	0.281	0.245	1.065
	588	0.947	0.843	0.613	1.725	0.603	0.572	0.329	0.909
	589	0.700	0.637	0.393	1.458	0.845	0.763	0.291	1.597
	590	0.854	0.754	0.464	1.627	0.692	0.623	0.410	1.319
36N	582	1.069	0.918	0.527	2.594	0.469	0.454	0.343	0.627
	583*	0.958	0.923	0.712	1.307	0.548	0.545	0.530	0.568
	584	1.922	1.836	1.098	2.925	1.034	0.942	0.710	1.678
	585*	0.998	0.961	0.821	1.240	0.732	0.732	0.723	0.742
	586*	0.735	0.705	0.535	1.014	0.344	0.336	0.273	0.426
	587*	1.048	1.043	0.876	1.242	0.530	0.530	0.510	0.549
	588	1.284	0.926	0.612	3.479	1.084	1.095	0.665	1.415
	589*	0.759	0.748	0.571	1.058	0.466	0.460	0.433	0.534
	590	0.898	0.802	0.584	2.008	0.505	0.470	0.324	0.938
36S	582	0.811	0.759	0.486	1.501	0.740	0.676	0.377	1.604
	583	0.660	0.600	0.412	1.161	0.687	0.648	0.337	1.382
	584	1.225	1.154	0.729	2.317	0.766	0.743	0.389	1.432
	585	0.957	0.913	0.603	1.506	0.738	0.749	0.609	0.832
	586	0.871	0.823	0.559	1.463	0.488	0.445	0.354	0.710
	587	0.836	0.786	0.524	1.291	0.516	0.439	0.347	0.874
	588	0.694	0.651	0.438	1.104	0.578	0.549	0.367	0.878
	589	0.712	0.644	0.450	1.230	0.655	0.579	0.359	1.222
	590	0.668	0.641	0.432	1.084	0.788	0.680	0.305	1.909