

	positive selection		Distribution of fitness effects			
Site type	α	ω	0-1	1-10	10-100	100-Inf
0fold	0.417391	0.083841	0.136569	0.152498	0.303932	0.407
3utr	0.276083	0.150881	0.453332	0.33022	0.213531	0.002917
5utr	0.393226	0.251128	0.45836	0.417524	0.124102	0.000014
intergenic	NA	NA	0.999702	0.000298	0	0
intronic	NA	NA	0.698462	0.30153	0.000008	0
2/3 fold	0.173876	0.122638	0.611852	0.120999	0.139095	0.128055
CNS	0.545225	0.279022	0.275543	0.342483	0.363507	0.018467
3UTR _{cns} 0.517609	0.255635	0.281223	0.332566	0.363655	0.022556	
DownstreamCNS	0.526032	0.225976	0.248254	0.434956	0.31525	0.001541
5UTR _{cns}	0.424353	0.157474	0.253091	0.319996	0.39247	0.034442
UpstreamCNS	0.530125	0.224175	0.239224	0.366778	0.381506	0.012493
intronicCNS	0.50238	0.372934	0.41499	0.256174	0.28281	0.046026
IntergenicCNS	0.579499	0.255211	0.225545	0.401574	0.367618	0.005262
sncCNS	0.705816	0.174081	0.089996	0.38704	0.517114	0.00585
AmbiguousCNS	0.399807	0.158877	0.284093	0.368947	0.338238	0.008722
High expression	0.641085	0.107721	0.069669	0.066187	0.128722	0.735421
Mid-high expression	0.60684	0.122296	0.092334	0.099879	0.204814	0.602973
Mid-low expression	0.5052	0.11113	0.125454	0.11427	0.214865	0.545411
Low expression	0.504903	0.124287	0.14065	0.1352	0.256773	0.467376

Table 1: Allele frequency spectra, summary of diversity statistics, and DFE-alpha model parameters for each site category.