

Table S1: Strand bias of EvoFold predictions

Genic region	count	ass. statistic	P-value ^b
coding	10551	0.496	0.47
5'UTR	207	0.553	0.164
3'UTR	2725	0.646	$< 2.2e - 16$
intron	9603	0.558	$< 2.2e - 16$
combined	23086	0.549	$< 2.2e - 16$

^bThe association statistic was assumed to be binomial distributed with parameter $p=0.5$. The alternative hypothesis is that p deviates from 0.5.