

exons vs. decoy regions

selection for single-strandedness in exons:

773 of 2268 neutral motifs	34.08%		
450 of 867 ESE motifs	51.90%	differential fraction	17.82%
149 of 457 ESS motifs	32.60%	differential fraction	-1.48%
<u>Fisher's exact test:</u>			
	ESE vs. ESS	P-value: <0.0001	(odds ratio 2.23)
	ESE vs. neutral	P-value: <0.0001	(odds ratio 2.09)
	ESS vs. neutral	P-value: 0.5517	(odds ratio 1.07)

selection for single-strandedness in decoy regions:

211 of 353 neutral motifs	59.77%		
58 of 112 ESE motifs	51.79%	differential fraction	-7.99%
36 of 39 ESS motifs	92.31%	differential fraction	32.53%
<u>Fisher's exact test:</u>			
	ESE vs. ESS	P-value: <0.0001	(odds ratio 11.17)
	ESE vs. neutral	P-value: 0.1536	(odds ratio 1.38)
	ESS vs. neutral	P-value: <0.0001	(odds ratio 8.08)

exons vs. pseudo exons

selection for single-strandedness in exons:

684 of 2618 neutral motifs	26.13%		
426 of 979 ESE motifs	43.51%	differential fraction	17.39%
133 of 496 ESS motifs	26.81%	differential fraction	0.69%
<u>Fisher's exact test:</u>			
	ESE vs. ESS	P-value: <0.0001	(odds ratio 2.10)
	ESE vs. neutral	P-value: <0.0001	(odds ratio 2.18)
	ESS vs. neutral	P-value: 0.7388	(odds ratio 0.97)

selection for single-strandedness in pseudo exons:

2 of 3 neutral motifs	66.67%		
0 of 0 ESE motifs	0.00%	differential fraction	-
0 of 0 ESS motifs	0.00%	differential fraction	-

exons vs. intron flanks

selection for single-strandedness in exons:

515 of 1820 neutral motifs	28.30%		
343 of 675 ESE motifs	50.81%	differential fraction	22.52%
145 of 439 ESS motifs	33.03%	differential fraction	4.73%
<u>Fisher's exact test:</u>			
	ESE vs. ESS	P-value: <0.0001	(odds ratio 2.09)
	ESE vs. neutral	P-value: <0.0001	(odds ratio 2.62)
	ESS vs. neutral	P-value: 0.0537	(odds ratio 0.80)

selection for single-strandedness in intron flanks:

583 of 801 neutral motifs	72.78%		
173 of 304 ESE motifs	56.91%	differential fraction	-15.88%
52 of 57 ESS motifs	91.23%	differential fraction	18.44%
<u>Fisher's exact test:</u>			
	ESE vs. ESS	P-value: <0.0001	(odds ratio 7.88)
	ESE vs. neutral	P-value: <0.0001	(odds ratio 2.03)

Table S4: Number of ESEs, ESSs and neutral motifs that are selected for single-strandedness comparing exons with decoy regions, pseudo exons and intron flanks.