Table S2: Summary of promoter positions with significant mutation rates following both selection screens[a]

Position	Site	WT Base	# Mutations (Selected library)		Expected # Mutations[b] (Unselected library)		Log_{10}(p-value) (pairwise)[c]		Log_{10}(Min p-value^2)[d]
			Activate	Deactivate	Activate	Deactivate	Activate	Deactivate	Combined
380	Sp1 III, p4	G	15	10	0.225	0.235	<-25	-12.7	-25.5
426	TATA, p2	A	9	6	0.917	0.958	-6.29	-3.28	-6.56
412	Core (n.i.[e])	C	3	19	0.173	0.179	-3.10	<-25	-6.20
382	Sp1 III, p6	G	10	3	0.218	0.235	-13.1	-2.72	-5.43
391	Sp1 II, p4	G	3	3	0.225	0.235	-2.77	-2.72	-5.43
192	U3 (n.i.)	A	5	17	0.917	0.958	-2.54	-15.5	-5.07
431	TATA, p7	A	5	5	0.917	0.958	-2.54	-2.45	-4.90

a. Mutated positions were considered significant if both pairwise p-values < -2 (p < 0.01) and the $\log_{10}$*(min p-value*^{2}*) < -4.*

b. Expected mutation rate is base-type specific but not position-specific in the initial library.

c. Pairwise comparison of mutation rates between an individual screen and the unselected library

d. Log_{10} *of the square of the minimum of the pairwise p-values, which is a measure of the probability of the weaker screen giving that p-value or better, under the null hypothesis that the all 3 rates are the same.*

e. n.i. = Not identified