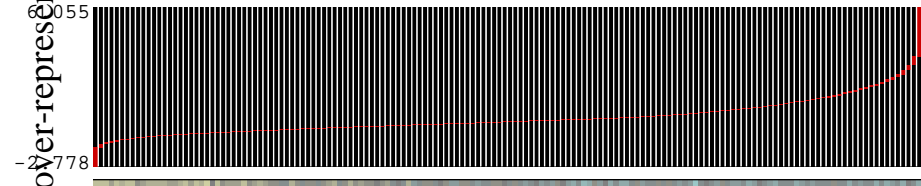


over-representation



under-representation

-20



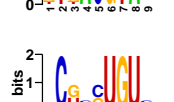
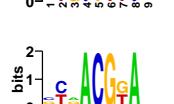
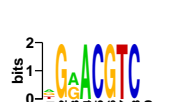
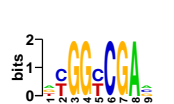
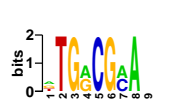
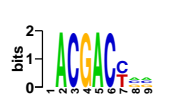
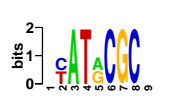
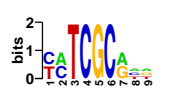
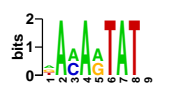
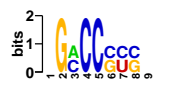
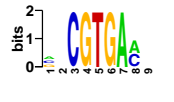
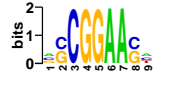
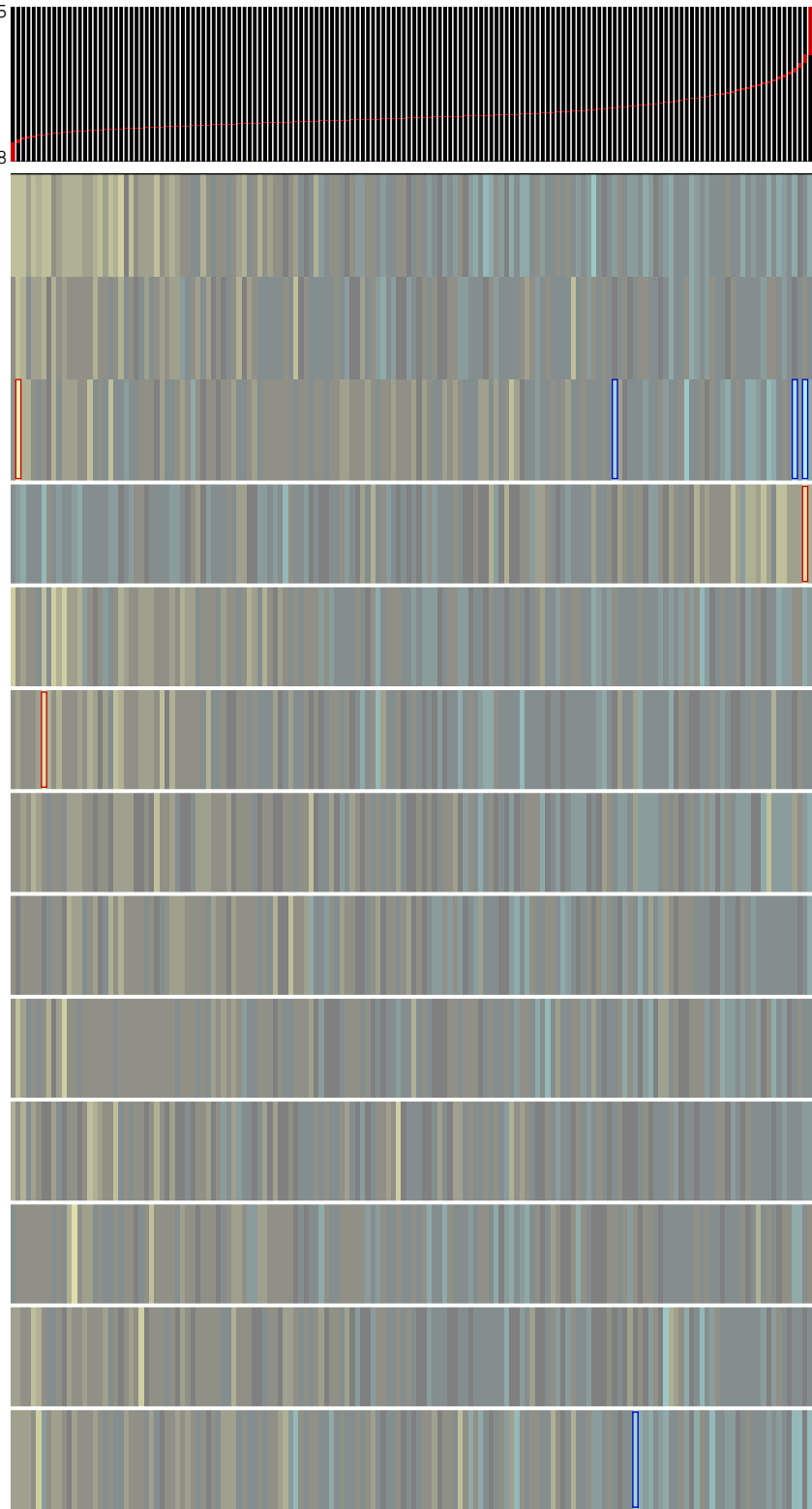
oxidoreductase activity, acting on NADH or NADPH, protein transport, p<0.001

ribonucleoprotein complex, p<0.01
protein biosynthesis, p<1e-04

contractile fiber part, p<0.01
extracellular space, p<0.01

GTPase regulator activity, p<0.001

olfactory receptor activity, p<0.01



Optimized motif	location	MI (bits)	z-score	Robustness	Position bias	orientation bias	conservation index	seed	motif name
	5'	0.028	25.7	10/10	-	-	1.00	CCGGAAG	Elk-1
	5'	0.014	8.9	10/10	Y	←	0.96	ACGTGAC	Pax2
	3'UTR	0.014	8.0	10/10	-	→	1.00	GACCCUC	-
	5'	0.016	11.0	10/10	Y	-	1.00	AAAATAT	-
	5'	0.015	9.9	8/10	-	-	0.96	CTCGCGA	-
	5'	0.015	9.6	9/10	-	-	1.00	CATGCCG	-
	5'	0.015	9.3	10/10	-	→	0.49	ACGACCG	-
	5'	0.014	8.1	8/10	-	←	0.30	TGACGCA	CREB
	5'	0.013	7.4	6/10	-	-	0.92	CGGCCGA	-
	5'	0.013	6.9	9/10	-	→	0.03	GAACGTC	bZIP910
	5'	0.013	7.1	7/10	-	-	0.36	AGCGTTC	-
	5'	0.013	6.8	7/10	-	→	0.93	CGACGGA	-
	3'UTR	0.013	6.9	7/10	-	→	0.85	CUGCUGU	-