

over-representation

under-representation

20

-20

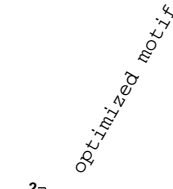
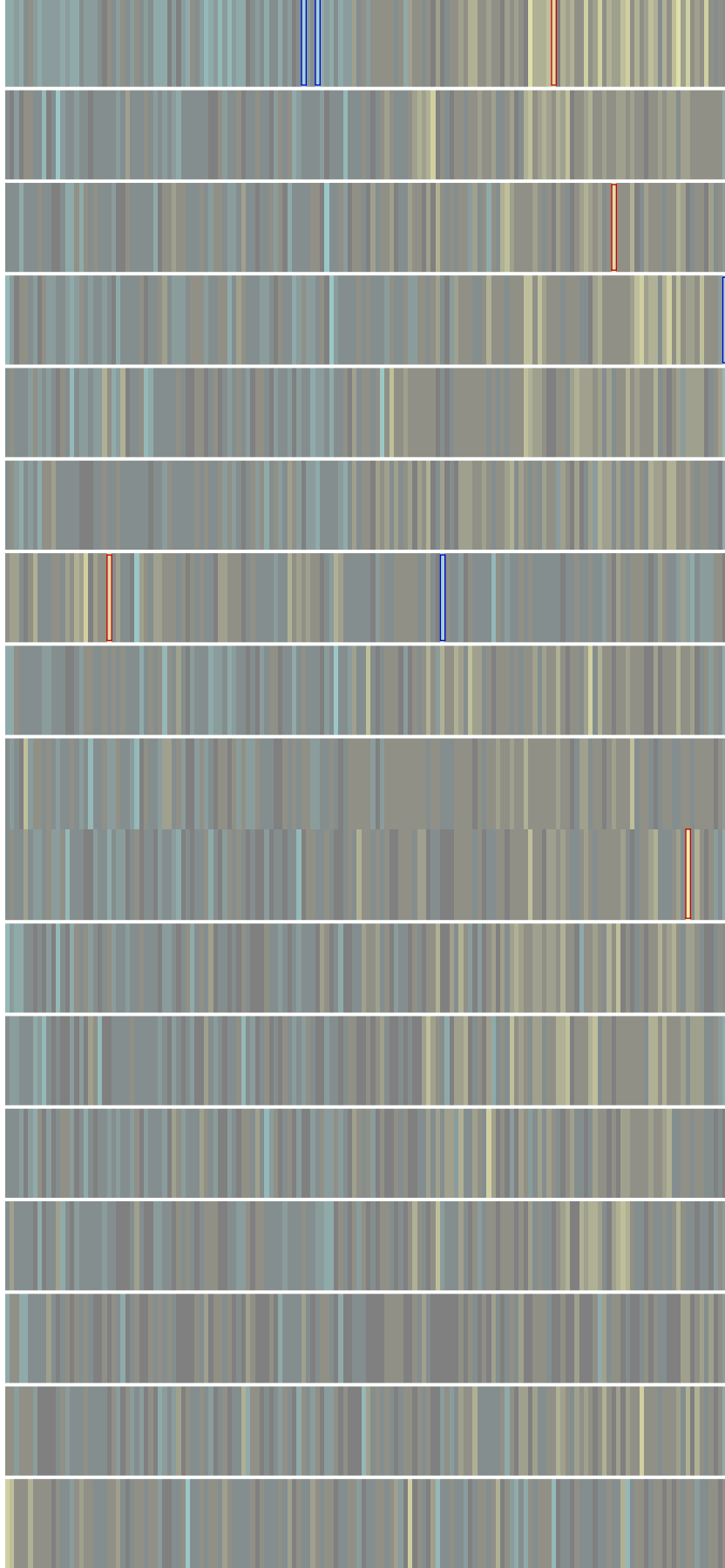
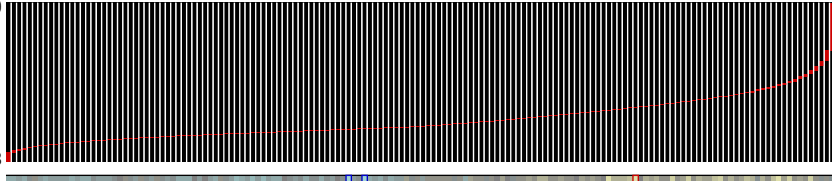
rhodopsin-like receptor activity, p<0.001
olfactory receptor activity, p<0.01

striatal long-term potentiation of muscle, p<0.01
extracellular space, p<0.01

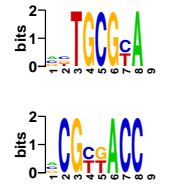
DNA-dependent DNA replication, p<0.01

ribosome, p<0.01

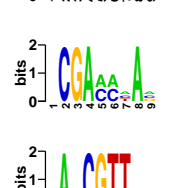
RNA binding, p<0.001



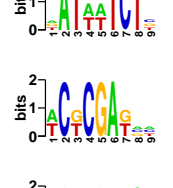
bits
0 1 2
1 2 3 4 5 6 7 8 9



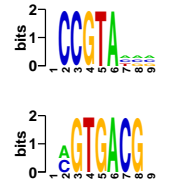
bits
0 1 2
1 2 3 4 5 6 7 8 9



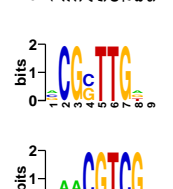
bits
0 1 2
1 2 3 4 5 6 7 8 9



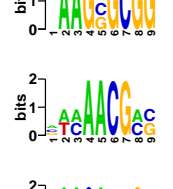
bits
0 1 2
1 2 3 4 5 6 7 8 9



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0 1 2
1 2 3 4 5 6 7 8 9



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0 1 2
1 2 3 4 5 6 7 8 9



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1 2 3 4 5 6 7 8 9



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1 2 3 4 5 6 7 8 9

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0 1 2
1 2 3 4 5 6 7 8 9

bits
0 1 2
1 2 3 4 5 6 7 8 9

location

MI (bits)

z-score

robustness

position bias

orientation bias

conservation index

seed

motif name

motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
CCGGAAG	5'	0.033	32.4	10/10	Y	-	1.00	CCGGAAG	ELK4
CTGCGCA	5'	0.016	10.9	10/10	-	-	0.98	CTGCGCA	-
CGCGACC	5'	0.016	10.8	10/10	-	-	0.99	CGCGACC	-
CUUUUUU	3'UTR	0.015	9.7	9/10	-	→	0.99	CUUUUUU	-
CGACCCA	5'	0.015	9.5	9/10	-	→	0.86	CGACCCA	-
ACCGTTC	5'	0.015	9.2	9/10	-	-	0.58	ACCGTTC	-
ATTTTCT	5'	0.014	8.8	10/10	-	←	0.98	ATTTTCT	-
CGCGAGA	5'	0.014	8.7	10/10	-	←	0.95	CGCGAGA	StuAp
CGCCCTA	5'	0.014	8.4	8/10	-	←	0.78	CGCCCTA	-
CCGTACC	5'	0.013	7.9	9/10	-	→	0.89	CCGTACC	-
AGTGACG	5'	0.014	7.9	9/10	-	→	0.94	AGTGACG	CREB
CGACACG	5'	0.014	8.1	9/10	-	→	0.83	CGACACG	-
CGCTTGA	5'	0.013	7.9	7/10	-	←	0.93	CGCTTGA	Myb
CACGTCG	5'	0.013	7.5	7/10	-	-	0.64	CACGTCG	-
AAGGGCG	5'	0.013	7.4	7/10	-	←	0.92	AAGGGCG	-
ACAACGA	5'	0.013	7.0	7/10	-	-	0.95	ACAACGA	-
AACACTG	5'	0.013	6.7	6/10	-	→	0.82	AACACTG	-