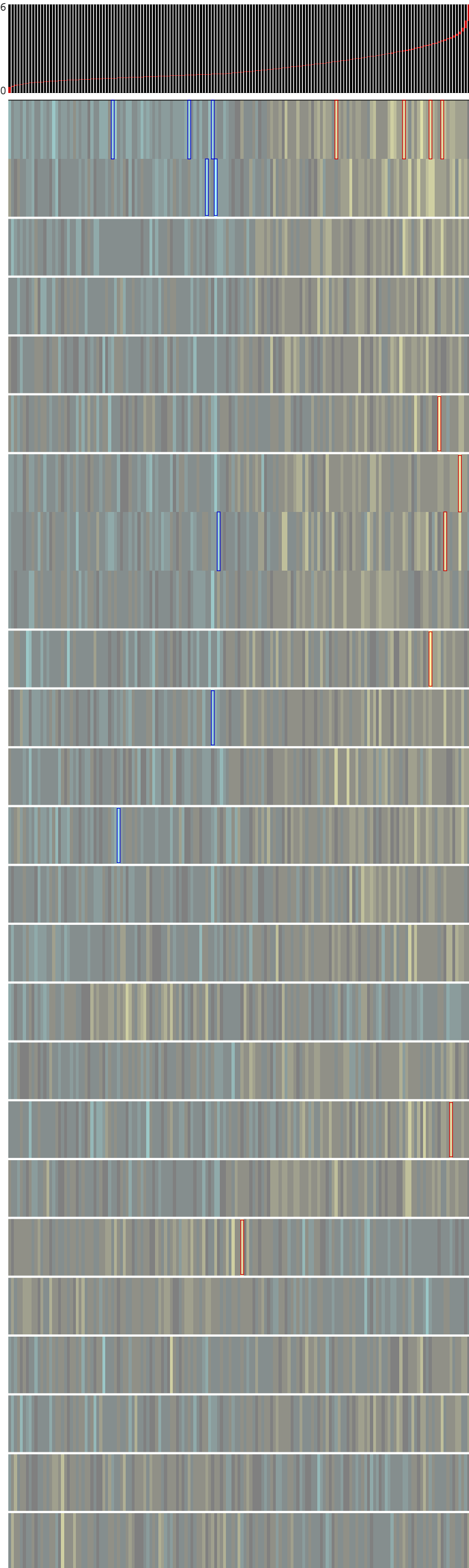
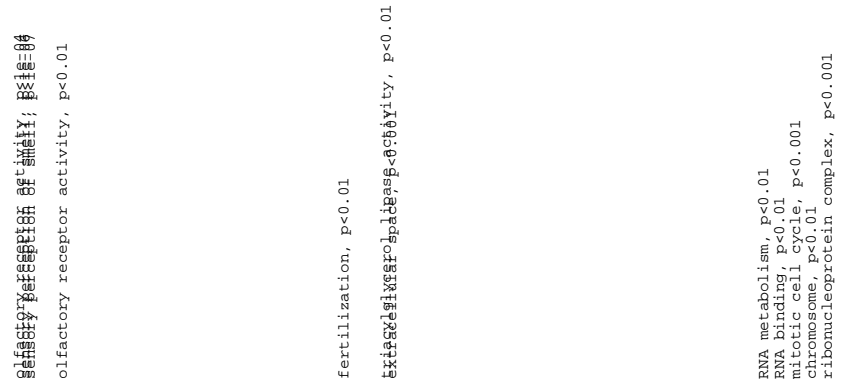


over-representation

under-representation

20

-20



olfactory receptor activity, p<0.01

fertilization, p<0.01

exchange rate apolipoprotein, p<0.01

RNA metabolism, p<0.01
 RNA binding, p<0.01
 mitotic cell cycle, p<0.001
 chromosome, p<0.01
 ribonucleoprotein complex, p<0.001

bits	Optimized motif	location	MI (bits)	z-score	Robustness	Position bias	orientation bias	conservation bias	seed	Motif name
1.8	CCGGAA	5'	0.038	38.8	10/10	Y	-	1.00	CCGGAAG	ELK4
1.8	UUUUU	3'UTR	0.017	12.3	10/10	-	→	1.00	CUUUUUU	-
1.8	TCATCG	5'	0.022	18.0	10/10	Y	-	1.00	CCTGCGC	-
1.8	ATGCG	5'	0.018	13.5	10/10	-	-	0.99	ATGGCGG	bZIP911
1.8	ACTAGC	5'	0.017	12.3	10/10	-	-	0.69	ACTACGG	-
1.8	AGTTC	5'	0.017	12.3	10/10	-	-	0.75	ACGTCCG	-
1.8	CAATCA	5'	0.017	11.8	10/10	-	-	1.00	CCAATCA	NF-Y
1.8	AAAGC	5'	0.016	11.2	10/10	-	-	0.99	CTCGCGA	AhR
1.8	CTAGC	5'	0.015	9.3	9/10	-	-	0.85	CTACCCG	-
1.8	AGTACG	5'	0.016	11.2	10/10	-	-	0.97	AGTGACG	CRE-BP1
1.8	AATCG	5'	0.016	10.5	10/10	-	←	0.67	AGTTCCG	-
1.8	CTTAG	5'	0.015	10.0	10/10	-	-	0.83	CTTCACG	Tax_CREB
1.8	CAAGC	5'	0.015	9.8	9/10	-	-	0.57	CACGACG	-
1.8	TGTAGC	5'	0.015	9.5	10/10	-	←	0.71	TCGTCCG	-
1.8	AGCCAAA	5'	0.015	9.5	10/10	-	→	0.74	TCGCCGA	-
1.8	AGGCC	3'UTR	0.015	8.1	6/10	-	→	0.48	CCGCCCC	-
1.8	AAGCC	5'	0.014	8.6	9/10	-	←	0.55	AACGCCG	-
1.8	CAGGA	5'	0.014	8.5	9/10	-	-	0.71	CGACGGA	-
1.8	GCGAC	5'	0.014	8.4	9/10	-	←	0.92	CGCGAAC	-
1.8	AAGCAG	5'	0.014	8.5	8/10	-	←	0.84	CAGGCAG	-
1.8	AGAAGA	5'	0.013	7.8	9/10	-	→	0.74	AGACAGA	-
1.8	CGTTC	5'	0.013	7.6	8/10	-	←	0.20	CGTTTTC	-
1.8	AAGCG	5'	0.013	7.3	7/10	-	-	0.92	AACGGCG	-
1.8	CAACA	5'	0.013	6.8	6/10	-	-	0.22	ACACACA	-
1.8	CATTAC	5'	0.013	6.5	7/10	-	←	0.89	TATTTAC	Freac-3