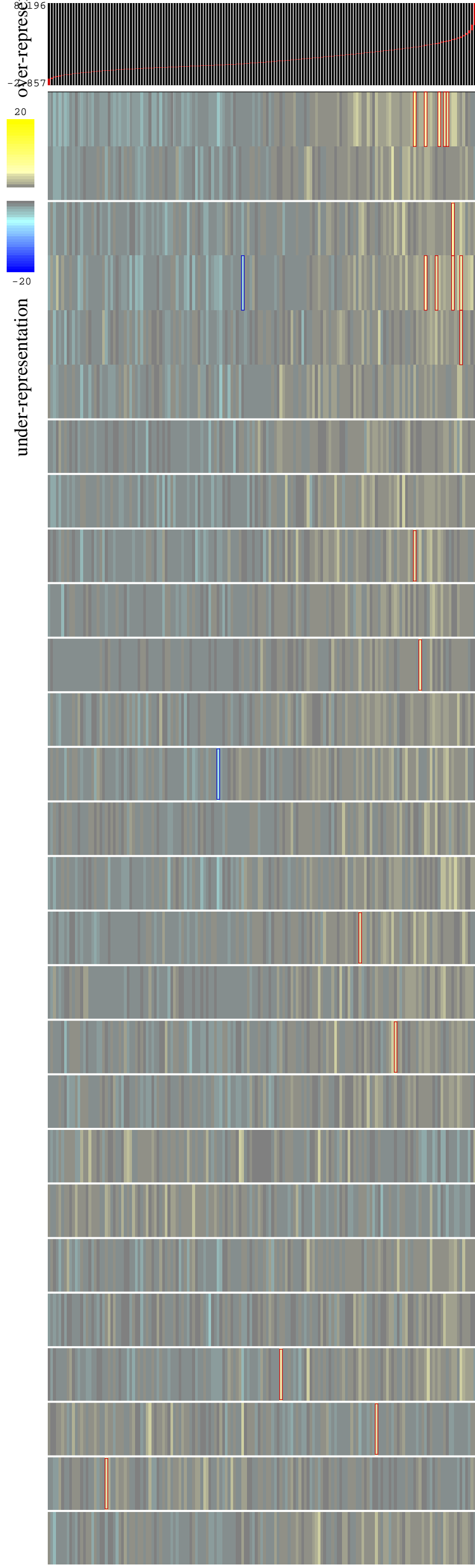


over-representation

under-representation



structural constituent of muscle, p<0.01
extracellular space, p<0.01

nuclear part, p<0.01

ribonucleoprotein complex, p<0.01
transcription factor activity, nucleic acid binding,
RNA binding, p<0.01
RNA binding, p<0.05
RNA binding, p<0.01

Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name
	5'	0.037	38.1	10/10	Y	-	1.00	CCGGAAG	NRF-2
	5'	0.020	16.4	10/10	-	-	1.00	CATGCGC	-
	5'	0.019	14.2	10/10	-	-	0.86	AACGGAA	v-Myb
	3'UTR	0.018	13.6	10/10	-	→	1.00	UUUGUAA	-
	5'	0.015	9.7	10/10	-	-	0.43	CGCTCTA	-
	5'	0.013	7.3	8/10	-	→	0.48	GACCGAC	-
	5'	0.017	12.5	10/10	-	-	0.93	CGTTTCC	-
	5'	0.017	11.8	10/10	-	-	1.00	CTCGCGA	StuAp
	5'	0.016	11.2	10/10	-	-	1.00	ATGGCGG	-
	5'	0.016	10.9	9/10	-	-	0.57	TTTCCGC	-
	5'	0.016	9.5	10/10	-	-	0.82	CGACTAC	-
	5'	0.016	10.2	10/10	-	→	0.74	ACCCGTA	-
	5'	0.015	9.7	8/10	-	←	0.96	CCCTTCG	-
	5'	0.015	9.1	9/10	-	←	0.30	AACGCAT	-
	5'	0.015	9.4	10/10	-	←	0.96	ACGTGAC	-
	5'	0.015	9.1	9/10	-	-	1.00	ACGTCAC	bZIP911
	5'	0.015	8.7	10/10	-	←	0.13	TAGCGGA	-
	5'	0.014	8.7	8/10	-	←	0.93	GCGAAAC	-
	5'	0.014	8.4	9/10	-	-	0.82	ACTACGG	-
	3'UTR	0.014	7.4	7/10	-	→	0.83	CCCCGGC	-
	5'	0.014	8.2	8/10	-	←	0.77	AGACAGA	-
	5'	0.014	7.8	8/10	-	→	0.78	ATTCCGC	-
	5'	0.013	7.7	7/10	-	-	0.18	TCGTTTC	-
	5'	0.013	7.4	9/10	-	←	0.58	CGATTCC	-
	5'	0.013	7.3	6/10	-	-	0.17	TCTCTCC	-
	3'UTR	0.013	6.0	6/10	-	→	0.45	UGCCGCC	-
	5'	0.012	6.1	6/10	-	-	0.72	ACGCAAC	-