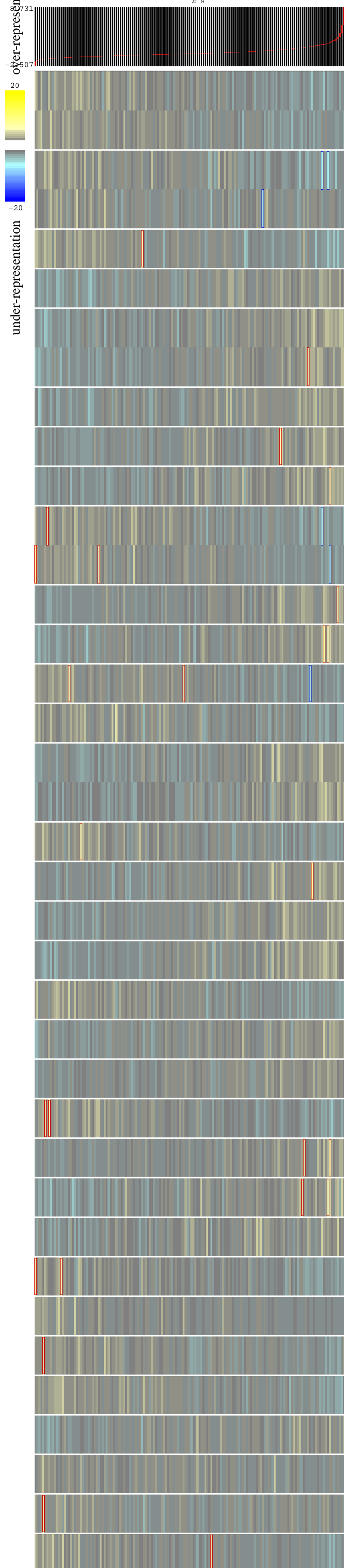


over-representation

under-representation

heme biosynthesis, p<0.01
response to other organism, p<0.01



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	3'UTR	0.017	11.9	10/10	-	→	0.99	UGUAUUAU	-
	3'UTR	0.016	10.2	10/10	-	→	0.99	UUUAUUAU	miR-181a/miR-181d/miR-181c/miR-181b
	3'UTR	0.016	11.1	10/10	-	→	0.98	UGAAUUAU	-
	5'	0.013	7.4	6/10	-	←	0.91	AAGCGCA	-
	3'UTR	0.016	10.8	10/10	-	→	0.94	AACUGUA	-
	3'UTR	0.016	10.6	9/10	-	→	0.53	GUCCUGU	-
	3'UTR	0.016	10.6	9/10	-	→	0.77	CUGCCGC	-
	3'UTR	0.015	9.7	10/10	-	→	0.87	UCCUCCC	-
	3'UTR	0.016	10.4	10/10	-	→	0.84	CUCUGCU	-
	3'UTR	0.016	10.3	10/10	-	→	0.68	UGGCUCC	-
	3'UTR	0.015	9.6	10/10	-	→	0.44	GGUCUGG	-
	3'UTR	0.015	10.2	10/10	-	→	0.96	UAAUUUG	-
	3'UTR	0.014	8.1	10/10	-	→	0.97	UUGUAUG	-
	3'UTR	0.015	9.2	8/10	-	→	0.93	GGACCCA	-
	3'UTR	0.015	9.7	10/10	-	→	0.90	UGUGCCC	-
	5'	0.015	10.1	9/10	-	→	0.99	AAAATAA	MEF-2
	3'UTR	0.015	9.1	9/10	-	→	0.95	UACUGAU	-
	3'UTR	0.015	8.7	8/10	-	→	0.40	CUGGUGC	-
	3'UTR	0.015	8.4	7/10	-	→	0.33	AGGCCCG	-
	3'UTR	0.015	9.0	10/10	-	→	0.95	AUGUUUAU	-
	3'UTR	0.015	9.3	10/10	-	→	0.71	CACCUCU	-
	3'UTR	0.015	9.0	9/10	-	→	0.73	CUUCCCC	-
	3'UTR	0.015	8.7	9/10	-	→	0.51	CCCCAGA	-
	3'UTR	0.015	8.8	9/10	-	→	0.99	UUUGAUA	-
	3'UTR	0.015	8.9	10/10	-	→	0.85	GCCAGAG	-
	3'UTR	0.015	8.2	7/10	-	→	0.34	GUCCUGC	-
	3'UTR	0.015	9.1	10/10	-	→	0.97	GUUUUGU	-
	3'UTR	0.014	7.3	8/10	-	→	0.49	CCGCAGC	-
	3'UTR	0.014	8.4	7/10	-	→	0.56	GGCCUUG	-
	3'UTR	0.014	7.8	9/10	-	→	0.49	CUCACCC	-
	3'UTR	0.014	7.1	6/10	-	→	0.59	CUUAAUA	-
	3'UTR	0.014	6.5	8/10	-	→	0.84	AUCUAUA	-
	3'UTR	0.013	7.4	8/10	-	→	0.84	ACUUAAA	-
	3'UTR	0.013	7.6	6/10	-	→	0.98	UCAUGAA	-
	3'UTR	0.013	7.1	6/10	-	→	0.85	CAUGGCC	-
	5'	0.013	7.1	7/10	-	→	0.34	TAAGTAC	-
	5'	0.013	7.3	8/10	-	→	0.99	ACTTCCG	-
	3'UTR	0.013	6.3	7/10	-	→	0.87	AAUAUGA	-