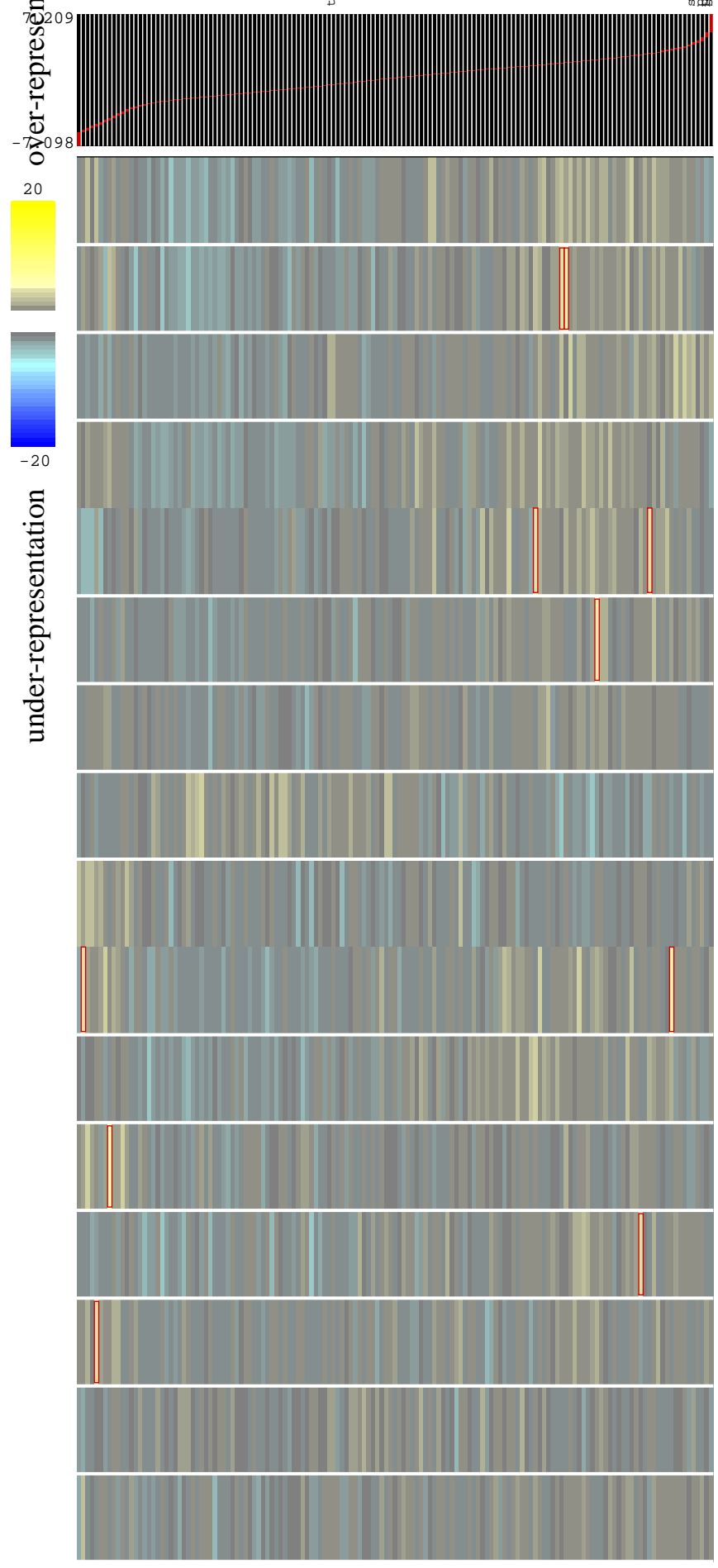


over-representation

under-representation



transcription regulator activity, $p < 0.01$

structural constituent of cuticle, $p < 1e-08$
structural constituent of cuticle, $p < 1e-09$

bits	Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
bits 0 1 2 1 2 3 4 5 6 7 8 9 UCACCCUC	3'UTR	0.019	13.3	10/10	-	→	1.00	UCCCCC	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 UCUUUU	3'UTR	0.018	12.3	10/10	-	→	0.99	UUUUUU	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 TCTTATC	5'	0.016	10.7	10/10	Y	-	1.00	TCTTATC	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 UCCUUUU	3'UTR	0.016	10.4	10/10	-	→	0.98	UCCUUUU	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 TACGCGC	5'	0.014	8.4	7/10	-	→	0.99	TACGCGC	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 GCGAGAC	5'	0.015	9.6	9/10	-	←	0.94	GCGAGAC	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 AAACGAG	5'	0.015	9.0	9/10	-	←	0.97	AAACGAG	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 GCUGAAA	3'UTR	0.015	8.9	7/10	-	→	0.97	GCUGAAA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 ATCGAAG	5'	0.015	8.5	9/10	-	-	0.88	ATCGAAG	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 UAUUUUAU	3'UTR	0.013	7.5	6/10	-	→	1.00	UAUUUUAU	miR-79	
bits 0 1 2 1 2 3 4 5 6 7 8 9 TTCGCAA	5'	0.015	8.5	9/10	-	→	0.98	TTCGCAA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 CTTCTCG	5'	0.014	8.5	10/10	-	-	0.93	CTTCTCG	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 CTGCGTA	5'	0.014	7.7	7/10	-	→	1.00	CTGCGTA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 CTCCTCG	5'	0.014	7.7	8/10	-	-	0.98	CTCCTCG	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 TAGTAGA	5'	0.013	6.9	7/10	-	-	0.19	TAGTAGA	-	
bits 0 1 2 1 2 3 4 5 6 7 8 9 AGAGAAA	5'	0.013	6.8	9/10	-	←	0.83	AGAGAAA	-	