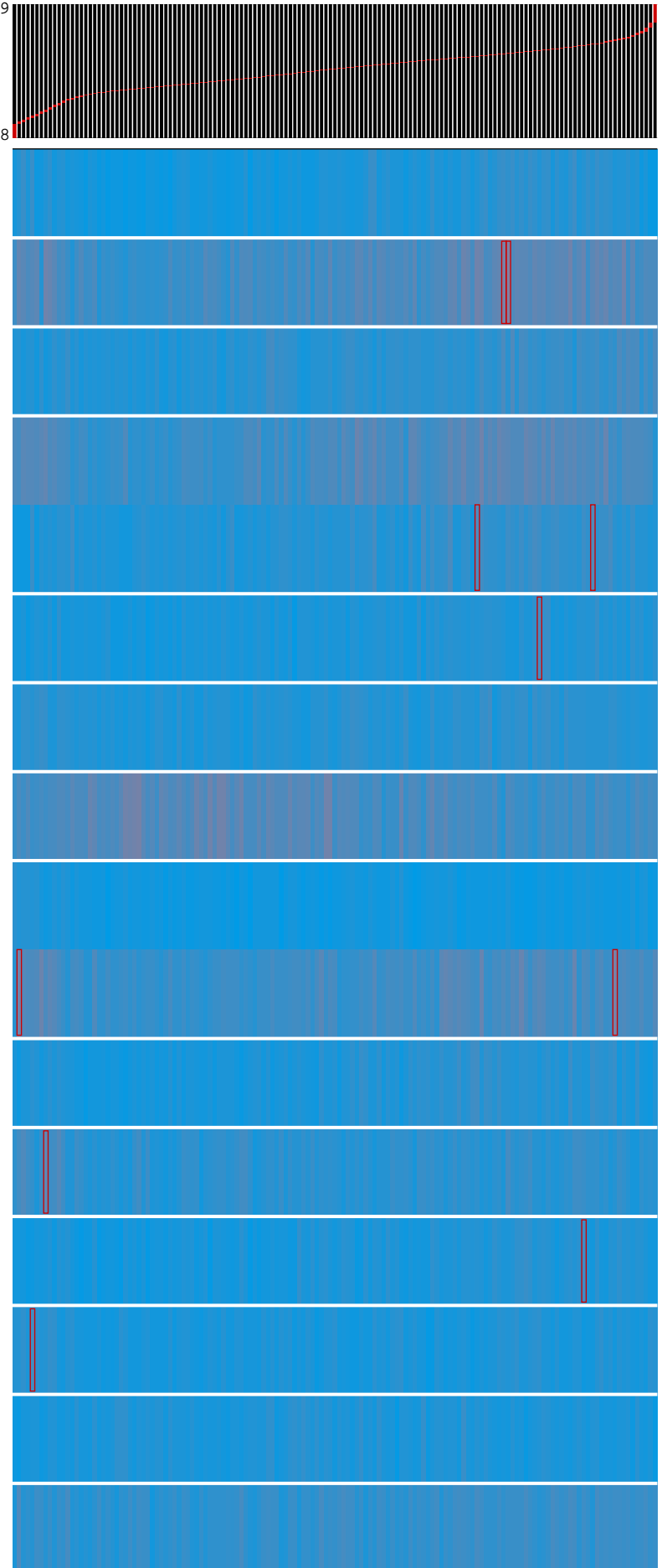


over-representation



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
	UCCCCC	3'UTR	0.019	13.3	10/10	-	→	1.00	UCCCCC	-
	UUUCUUU	3'UTR	0.018	12.3	10/10	-	→	0.99	UUUCUUU	-
	TCTTATC	5'	0.016	10.7	10/10	Y	-	1.00	TCTTATC	-
	UCCUUUU	3'UTR	0.016	10.4	10/10	-	→	0.98	UCCUUUU	-
	TACGCGC	5'	0.014	8.4	7/10	-	→	0.99	TACGCGC	-
	GCGAGAC	5'	0.015	9.6	9/10	-	←	0.94	GCGAGAC	-
	AAACGAG	5'	0.015	9.0	9/10	-	←	0.97	AAACGAG	-
	GCUGAAA	3'UTR	0.015	8.9	7/10	-	→	0.97	GCUGAAA	-
	ATCGAAG	5'	0.015	8.5	9/10	-	-	0.88	ATCGAAG	-
	UAUUUUAU	3'UTR	0.013	7.5	6/10	-	→	1.00	UAUUUUAU	miR-79
	TTCGCAA	5'	0.015	8.5	9/10	-	→	0.98	TTCGCAA	-
	CTCTCTG	5'	0.014	8.5	10/10	-	-	0.93	CTCTCTG	-
	CTGCGTA	5'	0.014	7.7	7/10	-	→	1.00	CTGCGTA	-
	CTCCTCG	5'	0.014	7.7	8/10	-	-	0.98	CTCCTCG	-
	TAGTAGA	5'	0.013	6.9	7/10	-	-	0.19	TAGTAGA	-
	AGAGAAA	5'	0.013	6.8	9/10	-	←	0.83	AGAGAAA	-