

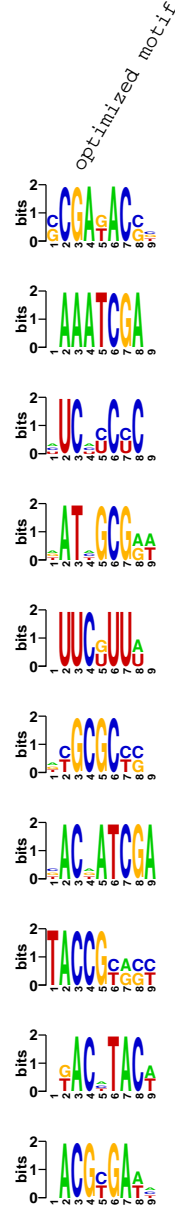
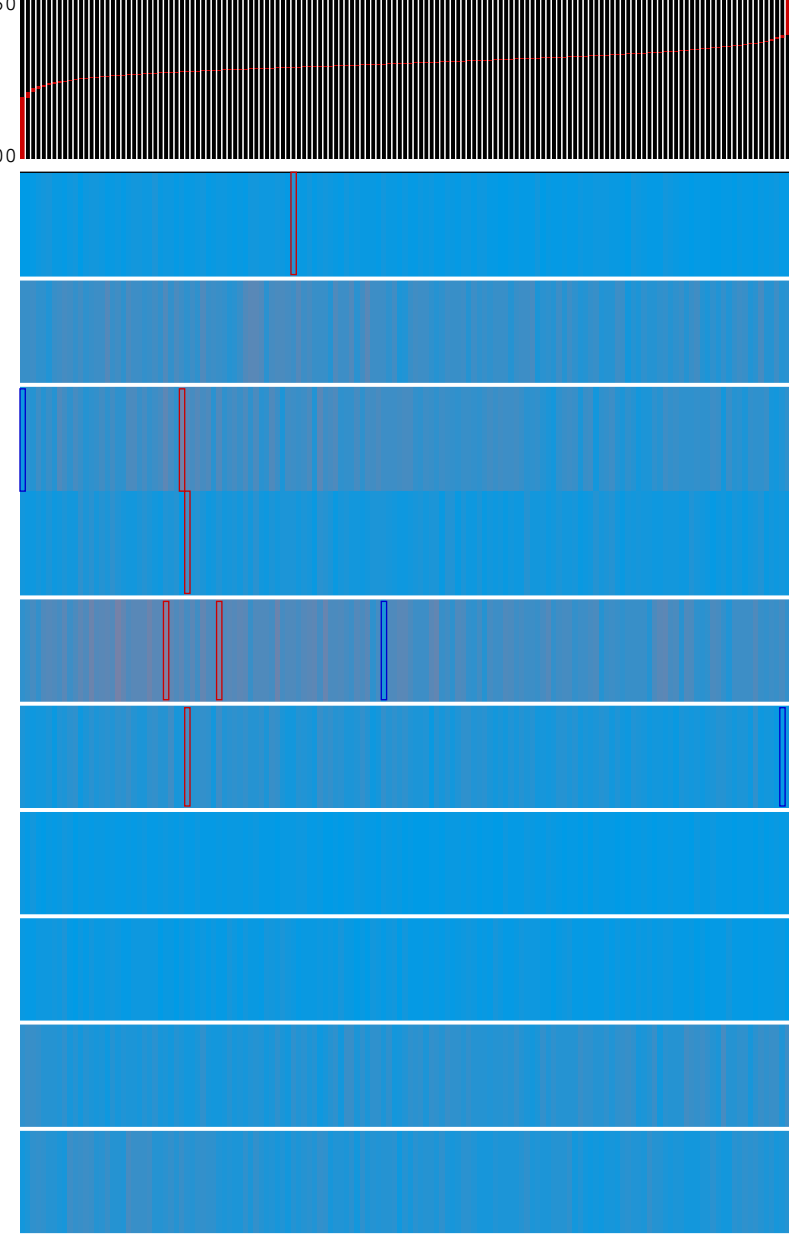
over-representation



under-representation



transferase_mechanism_activity, p=0.0001
 morphogenesis, p<0.01
 lipid metabolism, p<0.001



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
5' C G A G A C C	5'	0.016	9.3	10/10	-	-	0.99	CGAGACC	-
5' A A A T C G A	5'	0.015	9.8	10/10	-	-	0.99	AAATCGA	-
3' UTR U C A U C U C	3'UTR	0.015	9.1	10/10	-	→	1.00	UCAUCUC	-
5' A T G C G A A	5'	0.013	7.0	6/10	-	-	0.97	ATTGCGA	-
3' UTR U U C U U U U	3'UTR	0.014	8.2	6/10	-	→	0.96	UUCUUUU	-
5' C C C C C C C	5'	0.014	7.8	8/10	-	→	1.00	CGCGCTC	-
5' A C A T G A	5'	0.014	6.6	8/10	-	←	0.70	ACGATCG	-
5' T A C C C A C C	5'	0.013	6.7	6/10	-	←	0.92	ACCGCAG	-
5' T A C T A C	5'	0.013	6.7	7/10	-	←	0.55	TACATAC	-
5' A G G G A A	5'	0.013	6.4	7/10	-	-	0.94	ACGTGAA	-