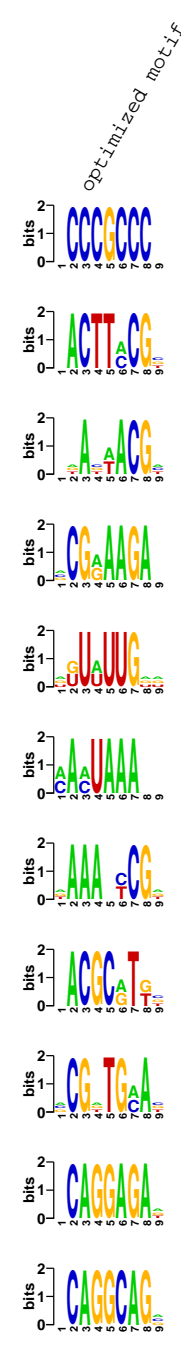
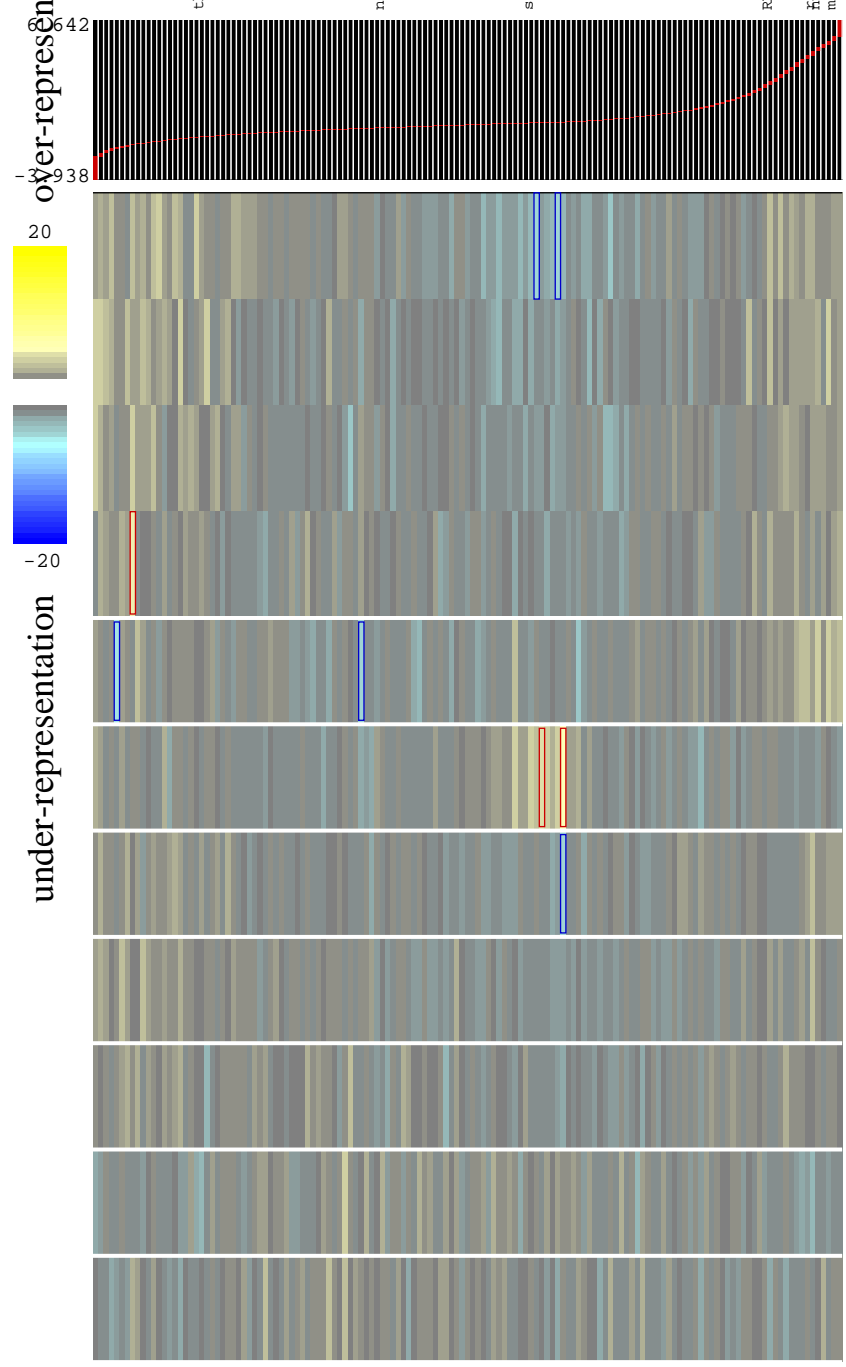


over-representation

under-representation



Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name
CCCCCCC	5'	0.029	26.0	10/10	-	-	1.00	CCCCCC	Sp1
ACTTCCG	5'	0.026	21.5	10/10	Y	-	1.00	ACTTCCG	NRF-2
AACAACG	5'	0.017	11.4	10/10	-	-	0.83	AACAACG	-
CGGAAGA	5'	0.015	9.0	9/10	-	→	0.91	CGGAAGA	NRF-2
GUUUUGU	3'UTR	0.015	9.5	10/10	-	→	0.99	GUUUUGU	-
AAUAAAA	3'UTR	0.014	8.2	7/10	-	→	1.00	AAUAAAA	-
AAAACCG	5'	0.014	7.8	6/10	-	-	0.55	AAAACCG	-
ACGCGTG	5'	0.014	7.4	6/10	-	-	0.41	ACGCGTG	-
CGGTGCA	5'	0.014	7.4	7/10	-	-	0.37	CGGTGCA	-
CAGGAGA	5'	0.013	7.0	7/10	-	→	0.68	CAGGAGA	RAV1
CAGGCAG	5'	0.013	6.2	6/10	-	-	0.49	CAGGCAG	-

thyroid hormone receptor binding, p<0.01
neurite development, p<0.001
serine-type endopeptidase activity, p<0.01
RNA processing, p<0.001
regulation of DNA metabolic process, p<0.001
mitotic cell cycle, p<0.01