

;TFM Explorer

;Date : Wed May 13 06:26:21 2020
 ;Scanned location : -3000:300
 ;Scanned sequences : None (8 sequences)
 ;Scanned matrices : (130 matrices)
 ;Parameters : minsize= 30, maxsize= 1500, ratio=3.0, top=25

; headers

; 1	rank	window rank
; 2	matrix	matrix name
; 3	tf	transcription factor name
; 4	info	information of content of the matrix
; 5	gc	gc content of the matrix (G+C)%
; 6	location	location of the window (relatively to TSS)
; 7	pvalue	pvalue of the window

1 MA0003.1 TFAP2A 7.8120920509 0.800000024164 -1678:-640
 1.78361128641e-05

list of hits

GRM8	-1676	-1667	-	6.51	GCTCCAGGC
GRM8	-1297	-1288	+	7.05	GCCCTAGGG
GRM8	-0970	-961	-	6.86	CCCTCAGGC
GRM8	-0901	-892	-	6.51	GCTCCCGGC
GRM8	-0882	-873	+	7.04	GCCTGGGGC
GRM8	-0796	-787	-	6.37	GCGCCGGGC
GRM8	-0698	-689	+	6.39	GCCCGGCGG
GRIK2	-1002	-993	+	6.02	GCCGCCAGC
GRIK2	-0892	-883	+	6.03	GCCGCCAGG
NEB	-1678	-1669	+	6.31	GCCTGAAGC
CCDC148	-1453	-1444	+	7.06	GCCCCGCGC
CCDC148	-1406	-1397	+	6.87	GCCCCGAGC
CCDC148	-1265	-1256	-	6.57	CCCGGCGGC
CCDC148	-1158	-1149	-	6.94	GCTCCGGGC
CCDC148	-0955	-946	+	6.95	GCCCCGAGG
CCDC148	-0930	-921	+	7.42	GCCCCGGGG
CCDC148	-0913	-904	-	6.31	GCGCGGGGC
CCDC148	-0826	-817	-	6.45	GCTGGGGGC
CCDC148	-0708	-699	+	7.06	GCCGGGGGG
CCDC148	-0640	-631	+	6.45	GCCGCGAGG
ANK1	-1175	-1166	+	6.52	GCCGGGAGG
ANK1	-1074	-1065	+	6.28	GCCCTCAGC
ANK1	-0704	-695	-	6.99	CCCCGAGGC
KAT6A	-1522	-1513	-	6.70	GCTCAGGGC
KAT6A	-1470	-1461	-	6.70	GCTCAGGGC
KAT6A	-1003	-994	+	6.26	GCCTCAAGG
KAT6A	-0663	-654	+	6.31	GCCCCGCGC

2 MA0139.1 CTCF 17.2051081365 0.644893727864 -852:-443
 1.83288295322e-05

list of hits

GRM8	-0852	-833	+	9.09	CCGCCTCTAGATGGAACTT
GRM8	-0690	-671	-	3.63	GCTCTCCATCGGCTGGAGG
GRM8	-0576	-557	-	8.36	CCGCGCCCCCTTCTGCGCA
MIR592	-0841	-822	+	5.15	GTTCCTCAAGGTGACAGTT
GRIK2	-0584	-565	+	5.92	TGCACAGCGGGTGGTGGTG
GRIK2	-0519	-500	+	5.02	ACGCCAGTAGGTGGACTAA
NEB	-0784	-765	-	3.98	CATTATCTTCTCCTGGTAA
NEB	-0725	-706	-	4.35	TTGAACCCTCTTGTGCCTG
NEB	-0528	-509	-	3.79	TAATTACACCCTGTGGATA
RIF1	-0450	-431	+	4.07	TCACCTAAAGTAGGCACTA
CCDC148	-0642	-623	+	4.52	CGGCCGCGAGGCGGTGGGG
CCDC148	-0591	-572	-	5.56	CGGCGCCCCCTCGCAGGCAG
ANK1	-0555	-536	+	3.60	CGAGCGGCGGGGGGAACAG
ANK1	-0498	-479	-	7.38	CGGCGCCCCCGGCCGACC
ANK1	-0443	-424	+	8.93	CCGCCGCCCCGGGGGCGCCC
KAT6A	-0635	-616	+	4.29	CCTACAGCAGGGGTGAGCA
KAT6A	-0447	-428	-	3.48	AAACGCCATCAAGAGTTCA

3	MA0024.1	E2F1	13.8381257118	0.625	-830:288	3.69804597541e-05
	list of hits					
	GRM8	-0415	-407	-	8.82	GCGGCCAAA
	GRM8	+0134	142	+	4.20	GTGGGCGC
	GRM8	+0288	296	+	4.20	CTGGGCGC
	MIR592	-0360	-352	-	4.20	GAGCCAAA
	GRIK2	-0830	-822	+	4.20	TTCGGCGC
	GRIK2	-0733	-725	-	10.19	GCGCCAAA
	GRIK2	-0542	-534	+	8.41	TTTCCCGC
	GRIK2	-0210	-202	+	3.80	TCTCGCGC
	GRIK2	-0202	-194	+	3.80	TTTCGCTC
	NEB	+0177	185	+	4.20	TTTGGGGC
	RIF1	-0072	-64	+	4.20	TTCGGCGC
	RIF1	+0180	188	-	3.80	GCGCGAAC
	RIF1	+0286	294	-	6.24	CCGGGAAA
	CCDC148	-0745	-737	-	6.24	CCGGGAAA
	CCDC148	-0012	-4	-	3.80	GAGCGAAA
	CCDC148	+0040	48	+	4.20	TTGGGCGC
	CCDC148	+0166	174	-	4.42	GCGTCAAA
	ANK1	-0532	-524	+	6.24	TTTCCCGG
	KAT6A	-0325	-317	+	6.24	TTTCCCGG
	KAT6A	-0159	-151	+	6.24	TTTCCCGG
	KAT6A	+0058	66	+	4.20	TTTGGGGC

4 MA0158.1 HOXA5 8.75888972496 0.319270834327 -2508:-2167
4.30556116033e-05

list of hits					
GRM8	-2167	-2159	-	7.09	CATTACTG
MIR592	-2403	-2395	+	7.02	CACAAATG
MIR592	-2389	-2381	-	6.87	AATTTGAG
MIR592	-2191	-2183	-	7.09	AATTTCTG
NEB	-2342	-2334	-	6.54	CATTACAG
RIF1	-2303	-2295	-	6.94	AATTAACG
CCDC148	-2467	-2459	+	6.69	CAGAAATG
CCDC148	-2335	-2327	-	6.72	AATTAAAG
CCDC148	-2295	-2287	-	7.09	CATTACTG
KAT6A	-2508	-2500	+	7.09	CAGTAATG
KAT6A	-2340	-2332	+	7.42	CACAAATT

5	MA0003.1	TFAP2A	7.8120920509	0.800000024164	121:262	4.71030171077e-05
	list of hits					
	GRM8	+0205	214	+	6.98	GCCGCGGGC
	GRM8	+0229	238	+	5.88	GCCGCGCGC
	GRM8	+0253	262	+	5.81	GCCGGTGGG
	GRIK2	+0126	135	-	7.06	CCCCCGGC
	GRIK2	+0143	152	-	6.51	GCTCCCGGC
	GRIK2	+0262	271	-	6.87	GCTCGGGGC
	RIF1	+0213	222	-	6.45	CCTCGCGGC
	RIF1	+0250	259	+	5.90	GCCCCCGG
	CCDC148	+0258	267	-	6.79	CCCTGAGGC
	ANK1	+0121	130	-	5.96	GCGGCGGGC
	ANK1	+0133	142	+	5.79	GCCCAGAGC
	ANK1	+0144	153	-	5.52	GTCCCGGGC
	ANK1	+0198	207	-	6.32	CCGCGGGGC
	ANK1	+0223	232	+	5.72	GCCCTCCGC
	KAT6A	+0124	133	+	5.91	GCCGAGGGG
	KAT6A	+0135	144	+	6.99	GCCCCCGGC
	KAT6A	+0145	154	+	7.41	GCCCCGGGC
	KAT6A	+0160	169	+	7.28	GCCCGAGGC
	KAT6A	+0175	184	+	7.42	GCCCCGGGG
	KAT6A	+0195	204	+	5.89	GCCTCGCGG
	KAT6A	+0257	266	-	5.94	GCGCCAGGC

6 MA0092.1 Hand1::Tcf2a 10.1435823018 0.506896541268 -2108:-2072
7.15140387838e-05

list of hits					
GRM8	-2072	-2062	-	5.88	CTTGCAGACC
CCDC148	-2108	-2098	-	7.04	GTACCAGACA
ANK1	-2096	-2086	+	5.84	GAGCTGGAAT

ANK1	-2086	-2076	-	7.26	TAGCCAGACT
KAT6A	-2074	-2064	+	5.85	TTTCTGGATC