

;TFM Explorer

```
;Date      : Wed May 13 06:33:31 2020
;Scanned location : -3275:0
;Scanned sequences : None (178 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 MA0089.1      NFE2L1::MafG      7.93814372721    0.421568617371  -486:-313
2.80696885964e-10
```

list of hits

MIR331	-0471	-465	+	6.66	CATGAC	
MIR135A-2		-0334	-328	-	6.66	GTCATG
ART4	-0485	-479	+	6.66	CATGAC	
GRI.2B	-0380	-374	+	6.66	CATGAC	
GSG1	-0444	-438	+	6.57	GATGAC	
MIR9170	-0321	-315	+	6.66	CATGAC	
PIP5K1B	-0313	-307	-	6.66	GTCATG	
TJP2	-0391	-385	+	6.66	CATGAC	
TJP2	-0313	-307	-	6.66	GTCATG	
MAMDC2	-0364	-358	+	6.66	CATGAC	
LOC100052901		-0476	-470	-	6.57	GTCATC
LOC100052951		-0458	-452	-	6.57	GTCATC
LOC100052951		-0397	-391	-	6.57	GTCATC
LOC100052638		-0397	-391	-	6.57	GTCATC
LOC100052638		-0336	-330	-	6.57	GTCATC
LOC100052689		-0412	-406	-	6.57	GTCATC
LOC100052689		-0351	-345	-	6.57	GTCATC
_LOC100049805		-0469	-463	-	6.57	GTCATC
LOC100052229		-0414	-408	-	6.57	GTCATC
LOC100052292		-0486	-480	-	6.57	GTCATC
SPRYD7	-0374	-368	+	6.57	GATGAC	
R.ASEH2B		-0410	-404	-	6.57	GTCATC
PSMB2	-0336	-330	-	6.57	GTCATC	
ZMYM4	-0473	-467	+	6.66	CATGAC	
ZMYM4	-0464	-458	-	6.66	GTCATG	
ZBTB6	-0349	-343	-	6.66	GTCATG	
OR1K1	-0428	-422	+	6.66	CATGAC	
LOC100071189		-0367	-361	+	6.66	CATGAC
LOC100071189		-0360	-354	-	6.66	GTCATG
LOC100071244		-0444	-438	+	6.66	CATGAC
LOC100067520		-0442	-436	+	6.66	CATGAC
LOC100071251		-0387	-381	+	6.66	CATGAC
LOC100071227		-0439	-433	+	6.66	CATGAC
LOC100071264		-0348	-342	+	6.66	CATGAC
LOC100071264		-0339	-333	+	6.57	GATGAC
_LOC100071297		-0354	-348	-	6.57	GTCATC
OR1.1	-0459	-453	+	6.57	GATGAC	
LOC100071407		-0428	-422	+	6.66	CATGAC
LOC100071445		-0336	-330	-	6.57	GTCATC
LOC100071469		-0465	-459	-	6.57	GTCATC

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2 MA0130.1      ZNF354C 8.95800882514    0.614583333333  -707:-634
1.05430731724e-09
```

list of hits

PLX.C1	-0686	-680	+	6.86	CTCCAC	
TMCC3	-0638	-632	+	6.86	CTCCAC	
SLC01C1	-0650	-644	-	7.01	GTGGAT	
LOC100065342		-0677	-671	-	6.86	GTGGAG
DGKD	-0668	-662	+	7.01	ATCCAC	

EIF4E2	-0663	-657	+	7.01	ATCCAC	
CHR.G	-0707	-701	-	6.86	GTGGAG	
SOX5	-0672	-666	-	6.86	GTGGAG	
SMCO3	-0695	-689	+	6.86	CTCCAC	
ART4	-0638	-632	-	7.01	GTGGAT	
MGP	-0680	-674	+	7.01	ATCCAC	
H4-16	-0651	-645	+	7.01	ATCCAC	
FOXP1	-0648	-642	-	7.01	GTGGAT	
DMRT3	-0641	-635	-	6.86	GTGGAG	
FOXD4	-0634	-628	+	7.01	ATCCAC	
APBA1	-0668	-662	-	6.86	GTGGAG	
MAMDC2	-0636	-630	-	6.86	GTGGAG	
SMC2	-0698	-692	+	6.86	CTCCAC	
LOC100052951		-0679	-673	+	6.86	CTCCAC
LOC100052638		-0662	-656	+	6.86	CTCCAC
LOC100052689		-0674	-668	+	6.86	CTCCAC
LOC100052689		-0634	-628	+	6.86	CTCCAC
_LOC100049805		-0691	-685	+	6.86	CTCCAC
LOC100052229		-0679	-673	+	6.86	CTCCAC
LOC100052229		-0639	-633	+	6.86	CTCCAC
VPS36	-0695	-689	+	6.86	CTCCAC	
.EK5	-0683	-677	-	6.86	GTGGAG	
WDFY2	-0645	-639	+	6.86	CTCCAC	
R.ASEH2B		-0672	-666	+	7.01	ATCCAC
TE.M4	-0690	-684	-	6.86	GTGGAG	
AGO4	-0695	-689	-	7.01	GTGGAT	
AGO1	-0664	-658	-	6.86	GTGGAG	
_CSF3R	-0650	-644	-	6.86	GTGGAG	
STK40	-0700	-694	-	6.86	GTGGAG	
LSM10	-0644	-638	+	7.01	ATCCAC	
CLSP.	-0660	-654	-	7.01	GTGGAT	
TFAP2E	-0699	-693	+	6.86	CTCCAC	
ZBTB6	-0652	-646	+	7.01	ATCCAC	
RC3H2	-0704	-698	-	6.86	GTGGAG	
_LOC100071170		-0668	-662	-	6.86	GTGGAG
LOC100071338		-0666	-660	+	6.86	CTCCAC
LOC100071486		-0706	-700	+	7.01	ATCCAC
FBXO5	-0651	-645	+	6.86	CTCCAC	

3 MA0031.1 FOXD1 11.9264176032 0.27500000177 -1242:-1137
1.991759584e-08

list of hits

.DUFAl2	-1228	-1220	+	6.85	GTAAATAT	
MIR135A-2		-1171	-1163	+	5.88	GTAAATAG
SLCO1A2	-1241	-1233	-	6.80	ATGTTGAC	
SLCO1A2	-1167	-1159	-	6.72	TTGCTTAC	
IAPP	-1157	-1149	+	6.91	ATAAACAT	
.EU2	-1161	-1153	+	6.91	TTAAACAT	
.EU2	-1153	-1145	-	5.88	CTGGTTAC	
.EU2	-1145	-1137	-	6.72	TTGCTTAC	
SOX5	-1198	-1190	+	5.94	CTAAACAG	
ERP27	-1237	-1229	-	6.91	ATGTTTAC	
H2AJ	-1208	-1200	-	6.72	TTATTTAC	
PLBD1	-1173	-1165	-	6.72	TTTTTTAC	
PROK2	-1171	-1163	-	9.69	ATGTTTAC	
DMRT2	-1142	-1134	+	6.85	GTAACCAT	
_KA.K1	-1223	-1215	-	5.94	CTGTTTAT	
DOCK8	-1230	-1222	-	6.72	TTATTTAC	
DOCK8	-1193	-1185	+	6.72	GTAACCAA	
LOC100052901		-1152	-1144	-	6.72	TTTTTTAC
LOC100052638		-1165	-1157	-	5.94	CTGTTTAC
LOC100052689		-1212	-1204	-	6.91	ATGTTTAC
LOC100052689		-1176	-1168	-	5.94	CTGTTTAC
LOC100147522		-1233	-1225	-	5.94	CTGTTTAC
CKAP2	-1215	-1207	-	6.72	TTTTTTAC	
.EK3	-1225	-1217	-	6.72	TTTTTTAC	
.EK3	-1181	-1173	-	6.80	ATGTTGAC	
ATP7B	-1213	-1205	+	6.85	GTAAAAAT	
ATP7B	-1192	-1184	-	6.85	ATTTTTAC	

CCDC70	-1150	-1142	-	6.77	TTGTTTAA	
DHRS12	-1190	-1182	+	8.72	GTAAACAG	
_I.TS6	-1164	-1156	-	5.94	CTGTTTAT	
KC.RG	-1162	-1154	+	9.56	GTAAACAA	
MIR15A	-1187	-1179	-	5.94	CTGTTTAT	
DLEU7	-1137	-1129	+	5.88	GTAAATAG	
_CSF3R	-1137	-1129	+	6.77	ATAAACAA	
SH3D21	-1232	-1224	+	6.91	ATAAACAT	
SH3D21	-1181	-1173	+	6.85	GTAAAAAT	
AGO3	-1220	-1212	+	6.77	CTAAACAA	
PDCL	-1233	-1225	+	6.72	GTAAAAAA	
LOC100071212		-1193	-1185	+	6.77	TTAAACAA
LOC100071244		-1187	-1179	-	6.91	ATGTTTAA
LOC100067520		-1235	-1227	-	6.91	ATGTTTAT
LOC100071251		-1167	-1159	-	6.91	ATGTTTAT
OR1B1	-1137	-1129	+	5.94	TTAAACAG	
LOC100071332		-1166	-1158	+	6.85	GTAAATAT
LOC100071407		-1225	-1217	-	6.91	ATGTTTAT
LOC100071420		-1152	-1144	-	6.72	TTATTTAC
LOC100071420		-1138	-1130	+	6.91	TTAAACAT
LOC100071469		-1158	-1150	-	6.91	ATGTTTAT
MTRF1L	-1223	-1215	+	6.72	GTAACCAA	
VIP	-1166	-1158	-	6.77	TTGTTTAA	
RGS17	-1242	-1234	-	6.85	ATATTTAC	

4 MA0095.1 YY1 8.10118848971 0.509803925951 -199:-141
5.01648758677e-08

list of hits

MIR135A-2	-0186	-180	+	6.58	GCCATC
C6H12orf60	-0199	-193	+	6.58	GCCATC
C6H12orf60	-0173	-167	+	6.58	GCCATC
TMEM252	-0157	-151	+	6.58	GCCATC
APBA1	-0169	-163	-	6.42	GATGGT
LOC100052951	-0150	-144	+	6.42	ACCATC
_LOC100049805	-0166	-160	+	6.42	ACCATC
ADPRHL2	-0159	-153	+	6.58	GCCATC
OR1K1	-0156	-150	+	6.58	GCCATC
LOC100071212	-0159	-153	+	6.58	GCCATC
LOC100071244	-0198	-192	+	6.58	GCCATC
LOC100071244	-0141	-135	+	6.42	ACCATC
LOC100071218	-0159	-153	+	6.58	GCCATC
LOC100067520	-0198	-192	+	6.58	GCCATC
LOC100067520	-0141	-135	+	6.58	GCCATC
LOC100071251	-0142	-136	+	6.58	GCCATC
LOC100071227	-0198	-192	+	6.58	GCCATC
LOC100071227	-0141	-135	+	6.58	GCCATC
OR1Q1	-0171	-165	+	6.58	GCCATC
LOC100071311	-0153	-147	+	6.58	GCCATC
LOC100071407	-0187	-181	+	6.58	GCCATC
LOC100071420	-0144	-138	+	6.42	ACCATC
LOC100071448	-0144	-138	+	6.42	ACCATC

5 MA0070.1 PBX1 14.6408950838 0.310185187496 -53:-17 6.40650017578e-08

list of hits

MIR135A-2	-0043	-31	-	4.39	GTTGATTCATCT
PDE3A	-0017	-5	+	4.89	ATATGAATCATA
MGP	-0021	-9	+	4.30	CCATCAATTTAA
LOC100052689	-0025	-13	+	5.95	TGATCCATCCAT
LOC100052526	-0050	-38	-	4.18	TTTGGTTGTTGT
LOC100052229	-0023	-11	+	6.13	CCATCCATCCAC
MIR3613	-0050	-38	+	6.29	AGCACAAATCAAA
MIR3613	-0018	-6	+	3.68	CCCACAATCTTT
MIR16-2	-0041	-29	-	5.95	ATTGAATGAGAT
MIR15A	-0031	-19	-	5.76	TTTTATTGATAA
THRAP3	-0025	-13	+	3.27	CAACCACTCAAA
STRBP	-0051	-39	-	3.89	ATTGTTTGTGTTGT
GPR21	-0029	-17	+	5.76	AGATGAATCAAA
_LOC100071297	-0036	-24	-	5.49	TATGCTGGATGC
LOC100071311	-0018	-6	-	3.66	TATGCTGGGTGT

LOC100071329	-0053	-41	+	3.44	TAAACATGCAAA
LOC100071329	-0037	-25	+	7.84	GGATCAATCCAT
LOC100071329	-0021	-9	-	3.66	TATGCTGGGTGT
LOC100071346	-0025	-13	+	4.86	AAGTCCATCAAG
LOC100071365	-0037	-25	+	5.11	GAGTCAATCCAT
LOC100071402	-0033	-21	+	4.23	CAGTCAATCCTC
LOC100071469	-0021	-9	+	4.65	TCACCAATCTGT
MYCT1	-0047	-35	-	3.44	ACTGCATGATTT

6 MA0063.1 Nkx2-5 8.26972553332 0.218487398433 -2735:-2636
2.37774186268e-07

list of hits

CEP83	-2715	-2708	+	6.35	TTAATAG
CEP83	-2637	-2630	-	7.00	CACTTAA
TMCC3	-2717	-2710	-	6.18	CAATTGA
MIR135A-2		-2685	-2678	-	6.06 AAATTAA
SLCO1C1	-2733	-2726	-	7.35	CAATTAA
.EU2	-2657	-2650	+	6.18	TCAATTG
SOX5	-2658	-2651	-	7.00	CACTTAA
SOX5	-2636	-2629	-	6.75	CACTTAT
WBP11	-2723	-2716	+	6.10	ATAATAG
ART4	-2670	-2663	-	6.75	CACTTAT
H2AJ	-2638	-2631	-	7.00	CACTTAA
ATF7IP	-2721	-2714	-	7.00	CACTTAA
GRI.2B	-2641	-2634	-	5.99	CTCTTAA
PGM5	-2735	-2728	-	6.75	CACTTAT
TMEM252	-2717	-2710	+	6.35	TTAATAG
FAM122A	-2733	-2726	+	7.00	TTAAGTG
APBA1	-2723	-2716	-	7.00	CACTTAA
APBA1	-2642	-2635	-	6.10	CTATTAT
C23H9orf135		-2673	-2666	-	7.00 CACTTAA
C23H9orf135		-2643	-2636	-	6.35 CTATTAA
MAMDC2	-2706	-2699	-	6.06	AAATTAA
SMC2	-2641	-2634	-	6.06	AAATTAA
_KA.K1	-2697	-2690	-	6.06	AAATTAA
DOCK8	-2667	-2660	-	7.00	CACTTAA
LOC100052901		-2683	-2676	+	6.06 TTAATTT
CKAP2	-2706	-2699	+	6.06	TTAATTT
WDFY2	-2694	-2687	-	7.00	CACTTAA
SERPI.E3		-2656	-2649	-	6.06 AAATTAA
DLEU7	-2704	-2697	+	5.99	TTAAGAG
DLEU7	-2643	-2636	+	5.93	ACAATTG
C1H15orf41		-2673	-2666	+	5.93 ACAATTG
TE.M4	-2657	-2650	-	6.06	AAATTAA
C2H1orf216		-2695	-2688	+	7.10 ATAATTG
PSMB2	-2704	-2697	-	6.06	AAATTAA
STRBP	-2646	-2639	-	6.06	AAATTAA
ZBTB6	-2700	-2693	-	6.18	CAATTGA
ZBTB26	-2648	-2641	-	6.06	AAATTAA
LOC100071212		-2686	-2679	+	5.93 ACAATTG
LOC100067520		-2715	-2708	-	7.00 CACTTAA
LOC100071251		-2695	-2688	+	7.35 TTAATTG
OR1B1	-2658	-2651	-	7.35	CAATTAA
LOC100071270		-2683	-2676	-	6.06 AAATTAA
LOC100071270		-2653	-2646	+	6.35 TTAATAG
_LOC100071297		-2642	-2635	-	5.99 CTCTTAA
LOC100071346		-2665	-2658	-	6.06 AAATTAA
LOC100071358		-2727	-2720	+	6.06 TTAATTT
LOC100071358		-2682	-2675	-	5.99 CTCTTAA
LOC100071407		-2731	-2724	-	6.35 CTATTAA
LOC100071486		-2679	-2672	-	5.93 CAATTGT

7 MA0047.2 Foxa2 13.2676175109 0.315129053384 -1814:-1777
4.73018047045e-07

list of hits

CEP83	-1810	-1798	+	5.11	TCTTTACATTTA
CEP83	-1780	-1768	+	4.98	TATTTATTTGAG
MIR135A-2		-1793	-1781	-	5.47 GGTGAGCCAACA
SOX5	-1800	-1788	-	7.75	GAAGAATAAACA

GRI.2B	-1791	-1779	-	5.43	GAAAAGAAAACA
GSG1	-1810	-1798	+	4.99	TAATTACACAGG
_PTAR1	-1791	-1779	-	5.74	GTTAAGTAAAAA
C23H9orf135		-1795	-1783	-	8.18 GTAAAAATAAACA
C23H9orf135		-1783	-1771	-	5.92 CATGAACAAACA
_KA.K1	-1811	-1799	-	6.44	TTTGTGTACACA
DOCK8	-1779	-1767	-	7.04	CCTTAGTACACA
.EK5	-1814	-1802	-	4.99	AGGGTGTAAACA
CCDC70	-1792	-1780	-	6.12	TTTGTGCAAATA
EBPL	-1809	-1797	-	6.91	TAACGTGTAAATA
ClH15orf41		-1791	-1779	+	4.92 TGTTGAAACTGG
DPH6	-1810	-1798	-	5.77	ATTTGGTAAATA
AGO4	-1787	-1775	-	5.67	CATTTGTACACA
.CD.	-1796	-1784	+	10.47	TGTTTACTTAAT
GPR21	-1812	-1800	-	4.98	GATCTATCAACA
ZBTB6	-1795	-1783	+	7.40	TATTTATTTATT
RC3H2	-1798	-1786	+	10.75	TGTTTACATAAG
OR1K1	-1812	-1800	+	5.92	TATTTGCAGAGA
LOC100071212		-1795	-1783	-	5.63 AATATGTAAAGA
LOC100071258		-1801	-1789	-	5.59 TCAATACAAATA
LOC100071258		-1786	-1774	-	7.40 AATAAAATAAATA
_LOC100071297		-1793	-1781	+	5.54 TATTGACTTGTC
_LOC100071297		-1777	-1765	+	5.01 TATTGGCTGTGT
LOC100071346		-1813	-1801	+	5.93 TGTTTGTTTAAT
LOC100071420		-1806	-1794	+	9.36 TATTTACATAAT
LOC100071420		-1790	-1778	-	5.42 CTAACGTAAATA
LOC100071420		-1777	-1765	+	8.90 TGTTTACTGAAG
LOC100071445		-1791	-1779	+	8.32 TATTGACTTATC
MTRF1L	-1785	-1773	+	5.68	TGTTTTCATTTG

8 MA0027.1 En1 6.42106531013 0.445454545184 -1667:-1565
1.03926279007e-06

list of hits

PLX.C1	-1570	-1559	+	6.35	TGGTGGTGCTC
.R2C1	-1606	-1595	-	5.61	AACCATAACTT
PDE3A	-1566	-1555	+	6.42	AAGTTATTGCC
SLC01A2	-1653	-1642	-	5.66	GAAAACAACCC
IAPP	-1577	-1566	+	6.64	ACGTGGTGGTC
SLC01B3	-1613	-1602	-	6.30	GGACTCTACTC
SLC01C1	-1643	-1632	-	5.89	GCCAACCACTT
USP40	-1667	-1656	+	6.64	AGGTGGTGTCC
I.PP5D	-1605	-1594	-	5.86	GAAC TTCACTT
.EU2	-1637	-1626	+	5.61	AAGTTATGTTT
.GEF	-1571	-1560	+	5.61	AAAGAGTGCCC
KC.J13	-1653	-1642	-	6.45	GAACACTCCTT
MGP	-1643	-1632	+	5.73	GAGTTATTTCC
PGM5	-1646	-1635	+	5.89	CAGTGGTTTCC
FAM189A2		-1616	-1605	+	5.90 AAGTAATGACC
C23H9orf135		-1627	-1616	+	7.83 AAGTAGTGGTC
LOC100052526		-1589	-1578	+	5.79 ACATGGTGCTC
VPS36	-1580	-1569	+	6.17	TAGTAGTTCCT
CKAP2	-1628	-1617	-	5.61	GACCATTCCTT
MIR3613	-1664	-1653	+	5.86	AAATAATTGCC
MIR3613	-1632	-1621	-	5.86	GGAATCTATTT
AGO4	-1660	-1649	-	5.61	AAAAATTACTT
AGO4	-1588	-1577	+	6.01	GAATTGTGTCC
_CSF3R	-1617	-1606	-	5.88	AGGAACAAC TA
STK40	-1635	-1624	-	5.61	AGGCATCACTT
C2H1orf216		-1667	-1656	+	6.17 AAGTGGTTTTT
PDCL	-1602	-1591	+	6.30	AAGTAGAATCC
LOC100071244		-1656	-1645	+	5.77 AAGTTGTGGCA
LOC100071244		-1614	-1603	-	5.77 GAGTACTCCTT
LOC100071258		-1622	-1611	-	6.35 GGCAACTACCA
OR1B1	-1659	-1648	-	6.86	GAGCACCACCTC
_LOC100071297		-1565	-1554	-	5.73 GAGAATAACTC
LOC100071329		-1624	-1613	+	6.18 TAGTAGTGGGC
LOC100071358		-1628	-1617	-	5.79 GAAACTATCT
LOC100071438		-1619	-1608	-	6.17 AGCAACAACCTT
LOC100071445		-1566	-1555	-	5.73 GAGAATAACTC

LOC100071460	-1568	-1557	-	6.42	GAAAAATCACTT
MTRF1L	-1588	-1577	+	5.86	AAATAATTTCC
VIP	-1657	-1646	-	6.42	GAGAACCATTT

9 MA0089.1 NFE2L1::MafG 7.93814372721 0.421568617371 -2886:-2737
1.55300729324e-06

list of hits

TMCC3	-2886	-2880	-	6.66	GTCATG
TMCC3	-2756	-2750	+	6.66	CATGAC
TMCC3	-2747	-2741	-	6.66	GTCATG
FGD6	-2826	-2820	+	6.66	CATGAC
LOC100065342	-2806	-2800	+	6.57	GATGAC
CHR.D	-2753	-2747	+	6.57	GATGAC
PRSS56	-2781	-2775	+	6.66	CATGAC
EIF4E2	-2885	-2879	+	6.57	GATGAC
ARHGDIB	-2860	-2854	+	6.66	CATGAC
MGP	-2853	-2847	+	6.66	CATGAC
GRI.2B	-2839	-2833	+	6.66	CATGAC
DMRT3	-2738	-2732	-	6.57	GTCATC
SMC2	-2802	-2796	+	6.66	CATGAC
DOCK8	-2884	-2878	+	6.57	GATGAC
LOC100052689	-2747	-2741	-	6.66	GTCATG
LOC100052292	-2787	-2781	+	6.57	GATGAC
LOC100147522	-2783	-2777	-	6.57	GTCATC
.EK3	-2838	-2832	+	6.66	CATGAC
.EK5	-2822	-2816	+	6.66	CATGAC
_I.TS6	-2846	-2840	+	6.66	CATGAC
EBPL	-2775	-2769	+	6.57	GATGAC
STK40	-2876	-2870	-	6.57	GTCATC
STK40	-2787	-2781	+	6.57	GATGAC
AGO3	-2875	-2869	-	6.57	GTCATC
AGO3	-2791	-2785	-	6.66	GTCATG
AGO3	-2769	-2763	-	6.66	GTCATG
MAP7D1	-2880	-2874	-	6.66	GTCATG
CLSP.	-2737	-2731	+	6.57	GATGAC
C2H1orf216	-2778	-2772	+	6.57	GATGAC
C2H1orf216	-2767	-2761	+	6.57	GATGAC
.CD.	-2849	-2843	+	6.57	GATGAC
RABGAP1	-2842	-2836	+	6.66	CATGAC
RC3H2	-2757	-2751	+	6.66	CATGAC
LOC100071189	-2851	-2845	-	6.66	GTCATG
LOC100071189	-2801	-2795	-	6.57	GTCATC
LOC100071212	-2860	-2854	+	6.57	GATGAC
_LOC100071297	-2878	-2872	+	6.57	GATGAC
LOC100071332	-2821	-2815	-	6.66	GTCATG
LOC100071402	-2800	-2794	-	6.57	GTCATC
LOC100071420	-2774	-2768	-	6.66	GTCATG
LOC100071445	-2882	-2876	+	6.57	GATGAC
MTRF1L	-2743	-2737	+	6.66	CATGAC

10 MA0152.1 NFATC2 9.85861508532 0.346153842592 -2799:-2758
2.85459229986e-06

list of hits

PLX.C1	-2791	-2784	-	7.20	AGGAAAA
USP40	-2797	-2790	-	8.69	TGGAAAA
ATG16L1	-2766	-2759	+	8.69	TTTTCCA
PLBD1	-2772	-2765	-	8.69	TGGAAAA
PLBD1	-2758	-2751	+	6.81	ATTTCCA
CBWD1	-2792	-2785	-	7.20	AGGAAAA
FOX4	-2786	-2779	+	6.92	TTTTCCC
PGM5	-2784	-2777	+	6.42	GTTTCCA
C23H9orf135	-2798	-2791	-	7.20	AGGAAAA
C23H9orf135	-2764	-2757	+	7.20	TTTTCCT
LOC100052526	-2799	-2792	+	6.81	ATTTCCA
LOC100052526	-2790	-2783	+	8.69	TTTTCCA
LOC100052526	-2777	-2770	+	6.81	ATTTCCA
.EK5	-2762	-2755	+	6.37	TCTTCCA
ATP7B	-2758	-2751	-	6.92	GGGAAAA
_I.TS6	-2790	-2783	-	6.42	TGGAAAC

TRIM13	-2799	-2792	+	6.37	TGTTCCA
DLEU7	-2776	-2769	+	6.92	TTTTCCC
ClH15orf41		-2783	-2776	+	6.92 TTTTCCC
OSCP1	-2799	-2792	-	6.92	GGGAAAA
AGO1	-2758	-2751	+	6.37	TGTTCCA
PSMB2	-2798	-2791	-	6.92	GGGAAAA
RABGAP1	-2789	-2782	-	6.37	TGGAAGA
LOC100071251		-2791	-2784	+	6.37 TCTTCCA
OR1Q1	-2774	-2767	+	7.20	TTTTCCCT
LOC100071270		-2770	-2763	-	6.42 TGGA AAC
_LOC100071297		-2791	-2784	-	6.92 GGGAAAA
_LOC100071297		-2759	-2752	-	8.69 TGGA AAA
LOC100071346		-2778	-2771	-	6.92 GGGAAAA
LOC100071365		-2760	-2753	+	6.92 TTTTCCC
LOC100071420		-2781	-2774	-	7.20 AGGAAAA
LOC100071445		-2794	-2787	-	7.20 AGGAAAA
FBXO5	-2796	-2789	+	7.20	TTTTCCCT
FBXO5	-2761	-2754	-	8.69	TGGA AAA
MYCT1	-2777	-2770	-	6.37	TGGAAGA

11 MA0148.1 FOXA1 12.5328023695 0.332119902252 -2939:-2901
3.26060686909e-06

list of hits

PLX.C1	-2937	-2926	-	9.06	AAGGGTAAACA
CEP83	-2936	-2925	+	5.44	TGTTTGTAATT
TMCC3	-2923	-2912	-	5.73	ATGAATCAACA
PDE3A	-2923	-2912	+	6.55	TGTTTCCTCTC
LOC100065342		-2930	-2919	-	6.22 AATAATAAACA
GUCY2C	-2907	-2896	+	5.23	TGTTTGCAGGT
PDE6H	-2917	-2906	+	6.21	TATTTTCTCTT
H2AJ	-2926	-2915	+	6.44	TGGTTACTTAG
GRI.2B	-2902	-2891	+	7.53	TATTTACTGAG
EMP1	-2933	-2922	-	10.18	GAAAGTAAACA
PROK2	-2939	-2928	+	5.31	TGTCTACCCTG
_KA.K1	-2903	-2892	+	5.80	TATTTACAAAT
_LOC100049805		-2929	-2918	-	6.62 AAAGACAAACA
.EK3	-2938	-2927	+	6.28	TGTTAGCTCAG
ATP7B	-2901	-2890	+	5.41	TGTTTACCTCT
MIR16-2	-2911	-2900	-	6.52	ATGGATAAACA
_RCBTB1	-2918	-2907	+	7.90	TGTTTGTTTAT
R.ASEH2B		-2913	-2902	+	5.35 TTTTTCATAT
LSM10	-2907	-2896	-	11.37	CAGAGTAAACA
THRAP3	-2906	-2895	+	6.52	TGTTTGATCTG
CLSP.	-2937	-2926	+	5.85	TGTTTCTAAT
CLSP.	-2920	-2909	-	5.91	TAAGGAAAACA
C2Hlorf216		-2928	-2917	-	5.45 CTAAATACACA
.CD.	-2911	-2900	+	8.77	TATTTACATAG
ZMYM4	-2914	-2903	-	5.21	ACAAGCCAACA
STRBP	-2915	-2904	-	5.60	GAAAGCAAAAA
ZBTB26	-2930	-2919	-	6.39	AAAAGCAAACCT
PDCL	-2932	-2921	-	6.28	ATGAGTAAACT
PDCL	-2921	-2910	+	9.67	TGTTTGATAT
OR1B1	-2905	-2894	+	7.40	TGTTGACCTAG
_LOC100071297		-2904	-2893	+	5.44 TGTTTGTAATT
LOC100071338		-2939	-2928	+	9.91 TGTTTGATTT
OR1.1	-2913	-2902	-	6.12	GTAATAAACA
LOC100071445		-2908	-2897	+	5.44 TGTTTGTAATT
MYCT1	-2925	-2914	+	5.46	TGTTTATTAAC
RGS17	-2921	-2910	-	7.07	AAGAGGAAACA

12 MA0006.1 Arnt::Ahr 9.53241699429 0.715277771155 -455:-418
4.636342681e-06

list of hits

GIGYF2	-0455	-449	-	7.05	CACGCG
ARHGDIB	-0429	-423	-	7.05	CACGCG
RYBP	-0448	-442	+	7.05	CGCGTG
PROK2	-0453	-447	+	7.05	CGCGTG
FOXP1	-0450	-444	+	7.37	TGCGTG
FAM122A	-0453	-447	-	7.05	CACGCG

APBA1	-0418	-412	-	7.05	CACGCG
DOCK8	-0436	-430	-	7.05	CACGCG
ALG11	-0423	-417	-	7.05	CACGCG
_I.TS6	-0452	-446	+	7.05	CGCGTG
FAM124A	-0419	-413	-	7.37	CACGCA
TE.M4	-0418	-412	+	7.37	TGCGTG
AGO4	-0426	-420	-	7.37	CACGCA
MRPS15	-0435	-429	-	7.37	CACGCA
TFAP2E	-0445	-439	+	7.37	TGCGTG
STRBP	-0431	-425	+	7.05	CGCGTG
RGS17	-0418	-412	-	7.05	CACGCG

13 MA0031.1 FOXD1 11.9264176032 0.27500000177 -2939:-2902
4.91922843776e-06

list of hits

PLX.C1	-2933	-2925	+	9.69	GTAAACAT
FGD6	-2924	-2916	-	5.88	CTGGTTAC
SLCO1A2	-2924	-2916	+	5.94	CTAAACAG
LOC100065342	-2926	-2918	+	6.77	ATAAACAA
I.PP5D	-2921	-2913	+	6.77	ATAAACAA
CHR.G	-2922	-2914	+	6.77	TTAAACAA
GRI.2B	-2922	-2914	+	6.72	GTAAAAAA
GRI.2B	-2903	-2895	-	6.85	ATATTTAC
EMP1	-2929	-2921	+	9.56	GTAAACAA
_KA.K1	-2904	-2896	-	6.85	ATATTTAC
CKAP2	-2909	-2901	+	6.91	TTAAACAT
ATP7B	-2902	-2894	-	9.69	ATGTTTAC
WDFY2	-2934	-2926	+	6.77	TTAAACAA
SERPI.E3	-2939	-2931	+	6.91	ATAAACAT
MIR16-2	-2907	-2899	+	6.77	ATAAACAA
_RCBTB1	-2915	-2907	-	6.77	TTGTTTAT
DPH6	-2935	-2927	+	5.88	GTAACCAG
LSM10	-2903	-2895	+	9.56	GTAAACAA
.CD.	-2912	-2904	-	6.85	ATATTTAC
GPR21	-2937	-2929	-	6.72	TTTTTTTAC
OR1B1	-2906	-2898	-	6.80	ATGTTGAC
LOC100071346	-2924	-2916	-	5.94	CTGTTTAT
OR1.1	-2909	-2901	+	6.91	ATAAACAT
MYCT1	-2926	-2918	-	6.91	ATGTTTAT

14 MA0083.1 SRF 17.9647717767 0.465579714133 -2988:-2923
7.1966303339e-06

list of hits

EFHD1	-2976	-2964	+	4.10	TCCCAAAGATGG
GUCY2C	-2948	-2936	-	2.99	TTATATGTGGGA
DMRT3	-2946	-2934	+	3.25	GTCCCTATAGGG
PGM5	-2955	-2943	-	2.67	GCAACTATGGGC
FAM189A2	-2927	-2915	+	3.67	TGCCACATTTGG
APBA1	-2944	-2932	-	3.12	GCAAATTTGGGT
LOC100052526	-2964	-2952	+	5.25	TCCAATATAAAG
LOC100052292	-2988	-2976	-	4.40	CTTTATCAGGGC
LOC100052292	-2969	-2957	+	4.44	GACCACATAGGG
OSCP1	-2956	-2944	-	10.33	TCTTATAAGGGC
TRAPPC3	-2927	-2915	+	3.41	TCCCAAAGAAGG
MAP7D1	-2926	-2914	-	3.41	CCTTCTTTGGGA
ADPRHL2	-2951	-2939	-	3.41	CCTTATTTGTGA
STRBP	-2958	-2946	+	5.92	GCCCCATTTTGA
GPR21	-2962	-2950	+	3.05	TCCAATATCTGG
ZBTB6	-2927	-2915	+	3.64	ATCCAAATATGA
RC3H2	-2973	-2961	+	4.26	TGCCATATTTAG
LOC100071258	-2939	-2927	+	3.19	GACCATAAAAAA
OR1B1	-2923	-2911	+	2.49	AACATCATATGG
LOC100071438	-2982	-2970	-	3.28	CCTTCTATGCTC
LOC100071448	-2983	-2971	-	4.59	GCTAATAGGGGC

15 MA0140.1 Tal1::Gata1 11.2966184617 0.45067769915 -3108:-3030
7.57917797919e-06

list of hits

FGD6	-3033	-3015	-	6.10	TTTATCATAAGTCTGAAT
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PRSS56	-3108	-3090	+	6.75	GGTTCGAACTCAGATAAA
GUCY2C	-3054	-3036	+	6.04	TTTTATGAGGAAGATTAG
PDE6H	-3093	-3075	+	6.35	CGTGACACCATAGATAGG
C6H12orf60		-3095	-3077	-	6.80 CTTATCTGCAAAGTTCTT
MGP	-3046	-3028	-	5.98	ATTATCTAAAACCCAAAT
H2AJ	-3094	-3076	+	9.00	GTGGCCCCCACAGATAAT
EMP1	-3069	-3051	-	5.62	TTTATCTTTCAAAAATAT
PIP5K1B	-3030	-3012	-	6.22	CGTATCACCTCCCTTCAG
FX.	-3104	-3086	+	7.06	GTGAAGTGGGGTGATAGG
FX.	-3044	-3026	-	5.78	ATTATCTGGAGGTAGACA
LOC100052901		-3047	-3029	+	6.96 CCGTGTTATTTAGATAAC
LOC100052951		-3108	-3090	+	7.14 CTAGCAACAAAAGATAAA
LOC100052951		-3055	-3037	+	6.66 CTGTGTACTAAAGATAGT
LOC100052689		-3071	-3053	+	6.27 CAACAGCCAAAAGATAAG
LOC100052582		-3035	-3017	-	8.52 TCTATCTCCTGCCACCAA
LOC100052526		-3077	-3059	-	6.14 CCTATCAGTAGTTGCATG
_LOC100049805		-3060	-3042	+	5.87 TTGTGTACTAAAGATAGT
LOC100052292		-3068	-3050	-	6.71 TCTATCTCCATGTCCCCA
_I.TS6	-3100	-3082	-	6.31	TTTATCTAGGGACCACTG
KP.A3	-3035	-3017	+	6.40	TTGCTCCCCAGAGATTAA
MIR15A	-3059	-3041	-	6.76	ATTATCAAAAAAAAAACAG
_CSF3R	-3060	-3042	+	6.58	ACCCCTGTGGCAGATAAG
THRAP3	-3102	-3084	-	5.90	CTAATCTTCCTCAAAAAT
THRAP3	-3031	-3013	+	5.68	GGTAGAATTTTCAGATAAA
CLSP.	-3090	-3072	+	5.94	GTGTGATATAATGATAGA
_LOC100071297		-3053	-3035	-	8.00 CTTATCTGAAAAATAGAG
LOC100071338		-3056	-3038	-	5.84 TTTATCTTTATTCTAATA
LOC100071407		-3093	-3075	+	8.20 AGTGAAACTGCAGATAAG
LOC100071445		-3060	-3042	-	8.00 CTTATCTGAAAAATAGAG
LOC100071469		-3032	-3014	-	6.35 CTAATCTTTCTCAAAAAA

16 MA0081.1 SPIB 9.06007130057 0.466472323191 -2920:-2872
8.68057919725e-06

list of hits

.DUFA12	-2913	-2906	-	7.28	TTCCCTCA
PDE3A	-2920	-2913	-	7.82	TTCCCTCT
SLC01B3	-2912	-2905	-	7.82	TTCCCTCT
.EU2	-2880	-2873	+	7.82	AGAGGAA
EFHD1	-2881	-2874	-	7.82	TTCCCTCT
CHR.D	-2879	-2872	+	7.09	ACAGGAA
CHR.G	-2907	-2900	-	7.82	TTCCCTCT
C6H12orf60		-2872	-2865	-	6.55 TTCCTGA
ART4	-2901	-2894	-	7.82	TTCCCTCT
PLBD1	-2905	-2898	+	6.60	AGGGGAA
PROK2	-2880	-2873	-	7.09	TTCCCTGT
DMRT2	-2910	-2903	-	6.55	TTCCCTGA
FOXO4	-2912	-2905	-	6.60	TTCCCCCT
PIP5K1B	-2904	-2897	+	6.55	TCAGGAA
C23H9orf135		-2903	-2896	+	7.28 TGAGGAA
C23H9orf135		-2895	-2888	+	7.09 ACAGGAA
WDFY2	-2894	-2887	+	7.28	TGAGGAA
TRIM13	-2902	-2895	-	7.82	TTCCCTCT
SPRYD7	-2898	-2891	-	7.28	TTCCCTCA
EBPL	-2919	-2912	+	7.09	ACAGGAA
AGO1	-2890	-2883	-	7.09	TTCCCTGT
STK40	-2899	-2892	+	7.82	AGAGGAA
THRAP3	-2872	-2865	-	7.82	TTCCCTCT
TRAPPC3	-2875	-2868	-	6.60	TTCCCCCT
LOC100071189		-2901	-2894	+	6.60 AGGGGAA
_LOC100071297		-2872	-2865	+	7.82 AGAGGAA
LOC100071332		-2916	-2909	-	6.55 TTCCTGA
LOC100071420		-2898	-2891	+	6.60 AGGGGAA
LOC100071445		-2876	-2869	+	7.82 AGAGGAA
RGS17	-2920	-2913	+	7.82	AGAGGAA

17 MA0070.1 PBX1 14.6408950838 0.310185187496 -511:-446
1.12664644452e-05

list of hits

MIR135A-2		-0461	-449	-	4.80 GTTGAAGGATAA
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PDE3A	-0484	-472	-	7.32	TTTGCTTGAGGA
CHR.G	-0493	-481	-	6.35	AAAGATGGATGG
WBP11	-0490	-478	+	6.75	GTGTCAATCAAC
ARHGDIB	-0472	-460	+	4.45	ATATCACTCAAG
PDE6H	-0466	-454	-	6.19	ATTGATTGTGTG
ATF7IP	-0484	-472	+	7.32	ACCTCATTCAAA
DMRT2	-0460	-448	-	6.97	AATGATTGAGTC
FOXD4	-0478	-466	-	6.19	CTGGATTGTTGG
MAMDC2	-0491	-479	-	7.32	TTTGCTTGAGGA
THSD1	-0460	-448	+	5.95	TCATCAAGCCAC
VPS36	-0488	-476	-	4.30	TTTAATTGGTGG
TRIM13	-0511	-499	+	7.38	ACAACAATCCAA
EBPL	-0500	-488	+	3.99	AAATCAAGCCTC
LSM10	-0450	-438	-	6.17	AAAGCTTGATGA
SH3D21	-0507	-495	-	6.69	CTTGAATGATTC
CLSP.	-0454	-442	+	4.83	CGCCAATCCAA
PSMB2	-0508	-496	+	5.95	TCCTCAAGCAAG
_LOC100071170	-0459	-447	-	3.89	ATGGTTTGATGA
LOC100071227	-0499	-487	+	4.12	ACAACAATGAAA
LOC100071270	-0491	-479	+	7.67	TCCTCAATCAGA
_LOC100071297	-0502	-490	+	6.85	TCATCAATAAAAA
LOC100071365	-0491	-479	-	5.05	CTAGATGGATGC
LOC100071358	-0458	-446	+	5.82	ATATCTATCAAA
LOC100071358	-0446	-434	+	4.06	ACATGCATCAAA
LOC100071486	-0449	-437	-	3.83	ATTAATTGAGGA
VIP	-0500	-488	-	4.46	TATGCTTGGTAC

18 MA0077.1 SOX9 9.07881468797 0.358187139655 -2665:-2593
1.19689911211e-05

list of hits

.DUFA12	-2593	-2584	+	7.54	ATACAATGG
FGD6	-2630	-2621	+	9.56	GAACAATGG
PDE3A	-2594	-2585	-	6.46	CTATTGGTC
I.PP5D	-2644	-2635	-	6.07	CCATTATTC
.EU2	-2659	-2650	+	5.74	TATCAATTG
GIGYF2	-2665	-2656	-	5.95	GGATTGTTC
CHR.D	-2595	-2586	-	6.57	CCATGGTTT
CHR.G	-2626	-2617	-	6.92	CCATTGGTC
WBP11	-2600	-2591	+	6.98	TAACAATGA
C6H12orf60	-2599	-2590	+	6.00	AAACAATAT
EMP1	-2665	-2656	-	5.94	CCTTTGTTA
FOXP1	-2646	-2637	+	5.98	AAACAATTC
CBWD1	-2634	-2625	+	6.71	GAACAATGT
FX.	-2615	-2606	+	6.28	GAACAAAAG
_PTAR1	-2598	-2589	+	7.77	AAACAATTG
ALG11	-2593	-2584	+	7.81	AATCAATGG
MIR3613	-2608	-2599	-	6.25	CAATTGTAC
DLEU7	-2645	-2636	+	7.77	AAACAATTG
AGO1	-2657	-2648	-	5.83	CCAATGTTT
THRAP3	-2617	-2608	+	5.83	AAACACTGG
KIAA0319L	-2605	-2596	-	6.23	TAATTGTTC
STRBP	-2640	-2631	+	7.52	AAACAATGC
RABGAP1	-2665	-2656	+	6.02	AATCAATGA
LOC100071212	-2615	-2606	+	6.65	AAACTATAG
LOC100071264	-2620	-2611	+	7.06	AAACAATAC
_LOC100071297	-2638	-2629	+	5.94	TAACAAAGG
LOC100071329	-2653	-2644	+	6.30	CAACAATGC
LOC100071329	-2608	-2599	-	5.75	GCATTGTCC
LOC100071346	-2657	-2648	+	7.00	TTACAATGG
LOC100071438	-2648	-2639	-	6.46	ACATTGTTT
LOC100071420	-2647	-2638	-	6.02	CTTTTGTTT
LOC100071445	-2643	-2634	+	5.94	TAACAAAGG
LOC100071469	-2634	-2625	-	6.68	CTATTGTGT
VIP	-2640	-2631	-	5.83	CCAATGTTT
VIP	-2624	-2615	-	6.02	CTTTTGTTT

19 MA0108.2 TBP 10.0863285279 0.376692369239 -2342:-2300
1.33914105896e-05

list of hits

.R2C1	-2342	-2327	-	6.61	TCTGCCCTATTTATCC
SLC01C1	-2310	-2295	+	6.29	GTTTAAAAATGCTTG
SOX5	-2340	-2325	+	6.62	TTATAAAATTCAGGC
GUCY2C	-2338	-2323	-	7.69	GGGGGCCCTTTTATCG
H4-16	-2314	-2299	-	6.87	AGCAGTATTTTATAC
GSG1	-2308	-2293	-	6.58	ATTGGCCTTTTATGT
EIF4E3	-2330	-2315	+	7.08	ATATAAAAATGCTTA
EIF4E3	-2303	-2288	+	6.60	TTATAAAAAGAAAATG
FAM189A2		-2342	-2327	+	6.08 GTATAAACTATCTA
FAM189A2		-2302	-2287	-	6.21 TCTGTTCTATATAC
APBA1	-2335	-2320	+	6.65	CCATATAAAAAGAGCG
_KA.K1	-2319	-2304	+	9.51	CTATAAAAAGGAATG
LOC100052951		-2317	-2302	-	7.70 TGATTCCCTTTTATAT
LOC100052689		-2308	-2293	-	5.86 TTGGAGTATATATAT
_LOC100049805		-2324	-2309	-	7.70 TGATTCCCTTTTATAT
LOC100052229		-2329	-2314	+	8.81 CTATAAAAAGAATGA
FAM124A	-2335	-2320	-	6.04	AGGGGCCATTTGTAC
ZMYM4	-2323	-2308	+	7.61	CTATAAATCCCTCTG
LOC100071264		-2341	-2326	+	7.58 CTATAAAATGAAGAC
LOC100071346		-2329	-2314	+	8.08 CTATATAAAACAGCA
LOC100071346		-2304	-2289	+	7.65 CCATAAAAAGAAGGA
OR1.1	-2318	-2303	+	8.56	CTATAAAAGAAAGTG
LOC100071420		-2338	-2323	+	7.11 GTTTAAAAACACAGT
RGS17	-2300	-2285	-	6.21	TGGTTGTATTTAAAG

20 MA0153.1 HNF1B 16.8212281893 0.22222222512 -1028:-962
1.5201192336e-05

list of hits					
PLX.C1	-0971	-959	-	5.10	AATAAATATTAG
FGD6	-1016	-1004	+	3.13	TTAGTGAGTATC
MIR331	-1024	-1012	-	5.57	GTTTAACATGAA
PDE3A	-1009	-997	-	3.73	GTCAAATTTGAA
MGP	-1028	-1016	-	7.46	GTTAATTATCAA
FOXP1	-0962	-950	+	4.23	CTAGTTGTTAAC
DMRT2	-1012	-1000	+	6.04	TTAAAGGTTAAC
CBWD1	-0997	-985	-	3.41	GTTATCCATGGA
LOC100052951		-1007	-995	-	10.72 GTTAATTAGTAG
LOC100052689		-0963	-951	-	7.97 GTCAATTAGTGG
_LOC100049805		-1019	-1007	-	7.97 GTCAATTAGTGG
LOC100052229		-0968	-956	-	7.97 GTCAATTAGTGG
VPS36	-1026	-1014	-	5.69	GTTATACATGAA
.EK5	-1025	-1013	+	3.18	CTAGTATTTATT
WDFY2	-0991	-979	-	8.82	GTTAACATATGGG
EBPL	-0967	-955	-	4.20	GTTCCTATTAA
GPR21	-1004	-992	+	7.28	TCAATATTTAAG
ZBTB6	-0971	-959	+	2.78	TCAGTAAGTCAC
LOC100071264		-1020	-1008	-	3.82 GATAATCACTGG
LOC100071264		-0977	-965	-	4.88 GCTACACATTGA
LOC100071332		-1024	-1012	-	2.65 TTTACTTATGAG
LOC100071338		-1013	-1001	+	4.10 TTAATGGTTGAG
LOC100071460		-1027	-1015	-	3.47 TTTAATTAGGAA
LOC100071469		-0992	-980	-	3.73 AACAAATATTAA
MTRF1L	-1020	-1008	+	4.53	CCCATATTTTAC
SY.E1	-0967	-955	-	4.37	GATACTCATTGA
MYCT1	-0990	-978	+	3.98	TTACTATGTTAC
RGS17	-0964	-952	+	7.46	TTAATAATTCAC

21 MA0063.1 Nkx2-5 8.26972553332 0.218487398433 -2488:-2449
1.58384961451e-05

list of hits					
MIR331	-2487	-2480	+	7.00	TTAAGTG
SLC01B3	-2486	-2479	+	7.10	ATAATTG
DGKD	-2456	-2449	+	7.35	TTAATTG
GSG1	-2481	-2474	+	6.06	TTAATTT
GSG1	-2460	-2453	+	6.75	ATAAGTG
RYBP	-2449	-2442	-	7.00	CACTTAA
EIF4E3	-2465	-2458	-	7.10	CAATTAT
FOXP1	-2486	-2479	-	7.35	CAATTAA
APBA1	-2453	-2446	-	6.06	AAATTAA

_KA.K1	-2473	-2466	-	6.06	AAATTAA
ARL11	-2477	-2470	-	6.10	CTATTAT
TE.M4	-2449	-2442	+	6.18	TCAATTG
RC3H2	-2458	-2451	+	6.06	TTAATTT
_LOC100071297		-2483	-2476	+	6.18 TCAATTG
LOC100071329		-2477	-2470	+	7.00 TTAAGTG
LOC100071329		-2458	-2451	+	6.10 ATAATAG
LOC100071358		-2488	-2481	+	7.00 TTAAGTG
LOC100071407		-2487	-2480	-	5.99 CTCCTAA
LOC100071438		-2458	-2451	+	6.18 TCAATTG
LOC100071420		-2478	-2471	+	6.35 TTAATAG
LOC100071445		-2488	-2481	+	6.18 TCAATTG
LOC100071448		-2480	-2473	+	5.99 TTAAGAG
MTRF1L	-2473	-2466	-	7.00	CACTTAA

22 MA0136.1 ELF5 8.69309550562 0.429292928841 -1290:-1231
1.76063872487e-05

list of hits

.R2C1	-1241	-1232	-	6.19	AAGGAAGAG
SLC01A2	-1261	-1252	+	6.70	GATTTCCCTT
KC.J13	-1278	-1269	-	6.47	AAGGAATTA
PDE6H	-1233	-1224	-	6.26	AAGGATGAA
MGP	-1233	-1224	+	6.27	CATTTCCGG
ATF7IP	-1289	-1280	+	7.41	AATTTCCCTG
EIF4E3	-1265	-1256	-	6.56	CCGGAATTT
FOXP1	-1256	-1247	+	7.15	TGTTTCCTT
PGM5	-1249	-1240	-	8.56	AAGGAAATA
FAM122A	-1269	-1260	+	6.13	CATTTCCCTA
PIP5K1B	-1290	-1281	-	6.20	GAGGAAACA
PIP5K1B	-1265	-1256	-	6.98	AAGGAAGAA
STXBP6	-1287	-1278	+	6.82	TTTTTCCTT
LOC100052638		-1250	-1241	-	6.81 GAGGAAATG
LOC100052689		-1261	-1252	-	6.81 GAGGAAATG
CKAP2	-1284	-1275	+	6.18	TTTTTCCTG
CKAP2	-1231	-1222	+	7.93	CACTTCCTT
ATP7B	-1258	-1249	+	6.93	TATTTCCCTA
SERPI.E3		-1236	-1227	-	6.30 TAGGAAGTG
KC.RG	-1246	-1237	-	6.33	AAGGAAAGA
MIR708	-1246	-1237	+	7.35	TAGTTCCTT
EVA1B	-1245	-1236	+	7.10	AATTTCCCTC
AGO3	-1288	-1279	-	6.69	CAGGATATT
C2H1orf216		-1285	-1276	+	6.34 TTCTTCCTG
C2H1orf216		-1239	-1230	+	6.09 AACTTCCCT
PSMB2	-1257	-1248	-	6.12	AAGGATCTT
RABGAP1	-1270	-1261	+	6.97	CACTTCCTC
RABGAP1	-1236	-1227	+	6.33	TCTTTCCTT
ZBTB6	-1237	-1228	+	6.20	AAGTTCCTG
LOC100071189		-1285	-1276	-	6.15 ATGGATGTA
LOC100071189		-1238	-1229	+	6.64 AGTTTCCTT
LOC100071270		-1273	-1264	-	7.57 CAGGAAGTT
LOC100071438		-1238	-1229	+	7.87 TACTTCCGT
LOC100071420		-1271	-1262	+	6.88 TATATCCTC
FBXO5	-1276	-1267	-	6.33	AAGGAAAGA
SY.E1	-1257	-1248	-	6.67	CAGGAAGCA

23 MA0087.1 Sox5 10.8307137621 0.198757763952 -2646:-2530
1.92617159936e-05

list of hits

FGD6	-2630	-2623	+	7.41	GAACAAT
I.PP5D	-2566	-2559	-	8.38	ATTGTTT
.EU2	-2627	-2620	-	8.38	ATTGTTT
WBP11	-2600	-2593	+	8.38	TAACAAT
ARHGDIB	-2555	-2548	+	7.69	CAACAAT
C6H12orf60		-2599	-2592	+	8.38 AAACAAT
SMCO3	-2543	-2536	+	7.41	GAACAAT
FOXP1	-2646	-2639	+	8.38	AAACAAT
CBWD1	-2634	-2627	+	7.41	GAACAAT
PGM5	-2554	-2547	+	7.69	CAACAAT
_PTAR1	-2598	-2591	+	8.38	AAACAAT

DOCK8	-2532	-2525	-	8.38	ATTGTTT	
FAM124A	-2557	-2550	-	7.41	ATTGTTC	
MIR16-2	-2593	-2586	+	7.69	CAACAAT	
DLEU7	-2645	-2638	+	8.38	AAACAAT	
AGO1	-2530	-2523	+	8.38	TAACAAT	
TEKT2	-2624	-2617	+	8.38	TAACAAT	
KIAA0319L		-2603	-2596	-	7.41	ATTGTTC
ZMYM4	-2551	-2544	+	7.69	CAACAAT	
STRBP	-2640	-2633	+	8.38	AAACAAT	
_LOC100071170		-2548	-2541	+	7.69	CAACAAT
LOC100071189		-2536	-2529	-	8.38	ATTGTTT
LOC100071258		-2604	-2597	-	7.41	ATTGTTC
LOC100071227		-2625	-2618	-	8.38	ATTGTTT
LOC100071264		-2620	-2613	+	8.38	AAACAAT
LOC100071358		-2600	-2593	-	8.38	ATTGTTA
LOC100071358		-2586	-2579	-	8.38	ATTGTTA
LOC100071438		-2646	-2639	-	8.38	ATTGTTT
LOC100071448		-2557	-2550	+	7.41	GAACAAT
LOC100071460		-2576	-2569	-	7.69	ATTGTTG
FBXO5	-2586	-2579	+	8.38	AAACAAT	

24 MA0113.1 NR3C1 14.7489180922 0.432098770583 -317:-282
1.97336073377e-05

list of hits

.DUFA12	-0308	-290	+	6.79	GGGAACCTTCTGTCGTGG
SLC01B3	-0311	-293	+	5.93	GAAAGCAGCTTTTACTGC
ERP27	-0282	-264	-	5.77	TGGGAACAGTTTGATCCC
ARHGDIB	-0283	-265	-	11.18	TTAGAACATTTTTTTTTTT
SMCO3	-0294	-276	+	9.41	GAGAAAATAAAATTTCTGT
TMEM252	-0301	-283	+	5.94	GAGAGCATTCCTCCCCAG
LOC100052292		-0289	-271	-	4.87 CCTGGTCTTATTGGCCTT
CKAP2	-0317	-299	-	5.31	TCTGAACATTTTCGTTTT
CCDC70	-0314	-296	+	4.69	GGTAACAATCATTTCTGA
MIR15A	-0298	-280	-	5.99	GCAGCACATAATGGTTTG
DLEU7	-0304	-286	-	4.52	CTCCAAAGTAATTTCCCTT
RC3H2	-0313	-295	-	5.99	CTAGGTCGGGATCCCTCC
LOC100071251		-0295	-277	-	6.36 CTTGATCAAATTGTCCTT
_LOC100071297		-0309	-291	+	5.88 GGAAACCACATGTCCAGT
LOC100071329		-0285	-267	+	4.64 CAGAGCAGTGTGTCCAAG
LOC100071346		-0286	-268	+	5.28 GGGAGAAAACATGAAGTAG
LOC100071338		-0284	-266	-	6.33 AAAGAACATTCTTCCTCT
LOC100071402		-0285	-267	+	4.35 CAGAGCAGAGTGTCCAAG
LOC100071438		-0294	-276	+	7.60 AGAATCAACCAGTCCAGT
LOC100071448		-0307	-289	-	4.69 CTTGAAAGGATTTTATCT

25 MA0078.1 Sox17 10.5018372033 0.383512551426 -2872:-2781
1.98290157695e-05

list of hits

FGD6	-2835	-2826	-	7.13	AACAATGGA	
SLC01C1	-2788	-2779	-	7.87	GACAATAGA	
CHR.G	-2870	-2861	+	6.24	CTCATTGGC	
PDE6H	-2842	-2833	+	8.03	TCCATTGTG	
SMCO3	-2859	-2850	+	7.44	TTCATTGTT	
GSG1	-2850	-2841	+	8.03	TCCATTGTG	
PROK2	-2835	-2826	+	8.10	ATCATTGTG	
PGM5	-2781	-2772	+	8.56	TCCATTGTC	
SMC2	-2865	-2856	+	7.63	AGCATGTG	
_KA.K1	-2831	-2822	-	6.75	AACAATAAA	
LOC100052951		-2796	-2787	-	7.95	CACAATGAC
LOC100147522		-2816	-2807	-	6.94	CACAATATC
ATP7B	-2863	-2854	-	6.19	AACAATATT	
ATP7B	-2800	-2791	-	6.75	AACAATAAA	
TRIM13	-2866	-2857	+	7.09	ACTATTGTG	
KC.RG	-2836	-2827	+	6.26	GGTATTGTG	
MIR16-2	-2831	-2822	-	6.44	AACAATATG	
R.ASEH2B		-2805	-2796	-	7.95	CACAATGAC
OSCP1	-2785	-2776	+	8.35	TTCATTGTG	
AGO1	-2864	-2855	+	8.03	TCCATTGTG	
C2H1orf216		-2786	-2777	-	7.13	AACAATGGG

RABGAP1	-2826	-2817	+	6.58	CTAATTGTG
ZBTB6	-2832	-2823	-	6.75	AACAATAAA
LOC100071189		-2791	-2782	-	7.13 AACAATGGA
LOC100071244		-2782	-2773	+	6.58 CTAATTGTG
LOC100071218		-2805	-2796	+	6.54 ACAATTGTC
OR1Q1	-2855	-2846	-	6.39	GACAATTGC
OR1Q1	-2814	-2805	-	7.10	GACAATTAG
OR1B1	-2781	-2772	-	7.34	CACAATATA
LOC100071338		-2872	-2863	-	7.87 GACAATATG
LOC100071338		-2810	-2801	-	6.50 AACAATAAT
LOC100071407		-2848	-2839	-	6.44 AACAATATA
LOC100071438		-2834	-2825	-	7.34 CACAATAGG
LOC100071420		-2820	-2811	-	7.44 AACAATGAA