

```
;TFM Explorer
;Date           : Wed May 13 06:35:17 2020
;Scanned location : -3280:0
;Scanned sequences : None (193 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
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1   MA0003.1          TFAP2A  7.8120920509    0.800000024164  -437:-278
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## list of hits

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DUSP5	-0392	-383	-	7.00	CCCGGGGGGC
DUSP5	-0374	-365	+	6.75	GCCCCGAAGG
XP.PEP1	-0378	-369	+	6.31	GCCCCGCGC
SMC3	-0402	-393	+	6.45	GCCGCGAGG
SMC3	-0322	-313	+	6.01	GCCCTTGCGG
SMC3	-0285	-276	+	6.15	GCCCTGCGG
RBM20	-0402	-393	+	6.63	GCCGGCGGC
RBM20	-0345	-336	-	5.94	GCGCCCCGGC
RBM20	-0329	-320	-	6.29	CCTGAGGGC
ADK	-0341	-332	+	6.32	GCCAGGGGC
KAT6B	-0329	-320	+	6.39	GCCGTCGGC
SAMD8	-0316	-307	-	6.28	CCTCAAGGC
COMTD1	-0373	-364	+	5.97	GCCCCGCCG
VDAC2	-0394	-385	-	7.00	CCCGGGGGGC
VDAC2	-0301	-292	+	6.01	GCCCCGGGT
DUPD1	-0423	-414	+	5.91	GCCAGCGGG
LOC100068320	-0430	-421	+	6.16	GCCCCTGGC
KLHL2	-0335	-326	+	6.99	GCCGCGGGG
CPE	-0417	-408	+	5.94	GCCGGGCGC
CPE	-0375	-366	-	6.34	CCCCTGGGC
CPE	-0348	-339	+	5.97	GCCCCGCCG
LOC106780946	-0433	-424	-	6.64	CCCGCCGGC
LOC106780946	-0396	-387	-	6.37	GCGCCGGGC
LOC106780946	-0369	-360	+	7.06	GCCCCGCGC
LOC106780946	-0345	-336	-	6.87	GCTCGGGGC
EPB41L3	-0409	-400	+	6.63	GCCGGCGGC
EPB41L3	-0358	-349	-	6.31	GCGCGGGGC
L3MBTL4	-0434	-425	+	6.70	GCCCTGAGC
L3MBTL4	-0382	-373	+	6.70	GCCCTGAGC
TMEM200C	-0410	-401	+	6.87	GCCCCGAGC
TMEM200C	-0386	-377	+	6.98	GCCGCGGGC
TMEM200C	-0359	-350	+	6.37	GCCCCGCGC
TMEM200C	-0322	-313	+	6.64	GCCGGCGGG
TMEM200C	-0309	-300	+	6.99	GCCGCGGGG
TMEM200C	-0296	-287	+	6.98	GCCGCGGGC
.R2E1	-0330	-321	+	6.13	GCCAGAGGG
FOXO3	-0293	-284	+	6.98	GCCGCGGGC
ARMC2	-0366	-357	-	6.10	CCTGCCGGC
SES.1	-0410	-401	-	5.94	GCGCCCCGGC
CEP57L1	-0393	-384	-	6.86	CCCTCCGGC
CEP57L1	-0360	-351	-	5.88	GCGCGCGGC
CEP57L1	-0280	-271	+	7.06	GCCTGGGGG
OSTM1	-0413	-404	-	5.88	GCGCGAGGC
OSTM1	-0391	-382	+	5.97	GCCCCGCCG
OSTM1	-0374	-365	-	6.51	GCTCCCGGC
OSTM1	-0348	-339	+	5.88	GCCGCGCGC
OSTM1	-0302	-293	-	6.44	GCTCGCGGC
OSTM1	-0279	-270	+	6.31	GCCGGAAGC

PPIL6	-0432	-423	-	6.05	GCCTGTGGC	
PPIL6	-0376	-367	+	6.39	GCCGTCGGC	
PPIL6	-0363	-354	-	6.33	CCCCCTGGC	
PPIL6	-0339	-330	-	6.34	CCCCTGGGC	
PPIL6	-0316	-307	-	6.99	CCCCGCGGC	
PPIL6	-0278	-269	+	5.89	GCCGCGCGG	
SMPD2	-0427	-418	+	6.99	GCCGCGGGG	
SMPD2	-0404	-395	+	6.34	GCCCAGGGG	
SMPD2	-0380	-371	+	6.33	GCCAGGGGG	
SMPD2	-0367	-358	-	6.39	GCCGACGGC	
SMPD2	-0311	-302	+	6.05	GCCACAGGC	
MICAL1	-0437	-428	+	6.99	GCCCCCGGC	
MICAL1	-0319	-310	+	5.94	GCCGGGCGC	
ZBTB24	-0353	-344	+	7.04	GCCGGGGGC	
ZBTB24	-0304	-295	-	6.51	GCTCCCCGC	
FIG4	-0348	-339	-	6.69	CCTTGGGGC	
WASF1	-0412	-403	-	6.52	CCTCCCCGC	
CDC40	-0434	-425	+	6.52	GCCGGGAGG	
METTL24	-0405	-396	+	6.18	GCCCGACGC	
METTL24	-0388	-379	+	5.92	GCCCACGGG	
METTL24	-0356	-347	+	6.39	GCCCGGCGG	
METTL24	-0335	-326	-	6.09	GCTGCCGGC	
METTL24	-0315	-306	+	7.41	GCCCCGGGC	
AK9	-0315	-306	+	6.69	GCCCCAAGG	
SLC22A16		-0413	-404	+	6.14	GCCCTGCGC
SLC22A16		-0298	-289	+	6.52	GCCCGCAGC
SLC22A16		-0284	-275	-	5.88	GC GCGCGGC
RBFOX3	-0362	-353	+	6.86	GCCGGAGGG	
E.GASE	-0333	-324	+	6.45	GCCCCCAGC	
E.GASE	-0292	-283	+	6.98	GCCGCGGGC	
C1QT.F1	-0343	-334	+	5.97	GCCCGCCGG	
CA.T1	-0436	-427	+	6.86	GCCTGAGGG	
CA.T1	-0285	-276	+	6.51	GCCGGGAGC	
LGALS3BP		-0425	-416	+	6.81	GCCTTGGGC
LGALS3BP		-0372	-363	+	7.21	GCCCCAGGC
TIMP2	-0383	-374	+	6.51	GCCGGGAGC	
TIMP2	-0357	-348	+	6.02	GCCGCCAGC	
TIMP2	-0291	-282	+	6.52	GCCCGCAGC	
CYTH1	-0401	-392	+	7.06	GCCTGGGGG	
CYTH1	-0319	-310	-	5.96	GCGGCGGGC	
CYTH1	-0305	-296	+	6.32	GCCCCGCGG	
CYTH1	-0286	-277	+	6.63	GCCGGCGGC	
SOCS3	-0335	-326	+	6.56	GCCGCCGGC	
SOCS3	-0290	-281	-	5.96	CCGCCCCGC	
SOCS3	-0279	-270	+	6.34	GCCCAGGGG	
TMEM235	-0384	-375	-	5.89	CCGCGCGGC	
AFMID	-0281	-272	+	5.91	GCCCACGGC	
CA4	-0338	-329	+	6.33	GCCAGGGGG	
Z.HIT3	-0334	-325	+	5.88	GCCGCGCGC	
GG.BP2	-0351	-342	-	5.96	CCGCCCCGC	
GG.BP2	-0285	-276	-	6.26	CCCCGTGGC	
DHRS11	-0405	-396	-	6.37	GCGCCGGGC	
DHRS11	-0373	-364	+	6.32	GCCAGGGGC	
DHRS11	-0331	-322	+	6.51	GCCGGGAGC	
DHRS11	-0322	-313	-	6.11	GCGTGGGGC	
LHX1	-0348	-339	-	5.91	CCCCTCGGC	
LHX1	-0324	-315	-	7.06	CCCCCAGGC	
AATF	-0282	-273	+	6.74	GCCCGAAGC	
ACACA	-0405	-396	+	6.02	GCCGCCAGC	
ACACA	-0383	-374	+	6.14	GCCCAAGGG	
ACACA	-0322	-313	+	5.96	GCCCGCCGC	
ACACA	-0310	-301	-	5.91	CCCCTCGGC	
USP32	-0408	-399	+	6.52	GCCGGGAGG	
SPTB.1	-0428	-419	+	6.31	GCCCCGCGC	
SPTB.1	-0320	-311	+	6.31	GCCCCGCGC	
ACYP2	-0326	-317	-	6.02	GCTGGCGGC	
PSME4	-0391	-382	+	6.56	GCCGCCGGC	
PSME4	-0381	-372	+	6.99	GCCGCGGGG	
GPR75	-0292	-283	+	6.81	GCCTTGGGC	

C15H2orf73	-0403	-394	+	5.96	GCCCGCCGC
C15H2orf73	-0341	-332	-	7.06	CCCCCAGGC
C15H2orf73	-0316	-307	-	5.94	GCGCCCGGC
KC.S3	-0313	-304	-	6.95	CCTCCGGGC
GE.1	-0331	-322	-	6.57	CCCGGAGGC
SMC6	-0395	-386	-	6.31	GCTTCCGGC
SMC6	-0327	-318	-	5.97	CCGGCGGGC
VS.L1	-0279	-270	-	6.02	GCTGGAGGC
RDH14	-0296	-287	+	5.80	GCCGGTGGC
.OL10	-0377	-368	-	6.52	CCTCCCGGC
ODC1	-0319	-310	-	6.18	GCGTCGGGC
ODC1	-0284	-275	-	5.96	GCGGCGGGC
HPCAL1	-0432	-423	+	7.04	GCCGGGGGC
HPCAL1	-0415	-406	+	7.06	GCCTGGGGG
HPCAL1	-0387	-378	+	6.53	GCCCCGAGG
HPCAL1	-0358	-349	+	5.88	GCCGCGCGC
HPCAL1	-0346	-337	+	6.99	GCCCCCGGC
HPCAL1	-0333	-324	+	6.57	GCCTCCGGG
RRM2	-0368	-359	-	6.94	GCTCCGGGC
RRM2	-0356	-347	+	5.97	GCCCCGCCG
RRM2	-0309	-300	-	6.32	CCGCGGGGC
RRM2	-0288	-279	+	5.75	GCCGCTGGG
RRM2	-0278	-269	+	7.04	GCCGGGGGC
KLF11	-0434	-425	+	6.09	GCCGGCAGC
KLF11	-0396	-387	-	5.94	GCGCCCGGC
KLF11	-0339	-330	-	6.99	CCCCGCGGC
KLF11	-0298	-289	+	6.45	GCCGCGAGG
GRHL1	-0390	-381	-	6.52	CCTCCCGGC
GRHL1	-0355	-346	+	6.02	GCCGCCAGC
TAF1B	-0294	-285	-	6.99	CCCCGCGGC
ADAM17	-0384	-375	+	5.89	GCCGCGCGG
ADAM17	-0369	-360	-	6.31	GCTTCCGGC
ADAM17	-0327	-318	+	6.31	GCCGGAAGC
CYS1	-0378	-369	+	6.99	GCCCCCGGC
CYS1	-0297	-288	+	5.94	GCCGGGCGC
RPS7	-0345	-336	+	6.32	GCCCAGGGC
ADI1	-0435	-426	+	6.31	GCCCCGCGC
ADI1	-0402	-393	-	6.87	GCTCGGGGC
ADI1	-0317	-308	+	5.97	GCCCCGCCG
TRAPPC12	-0379	-370	-	6.88	CCTCGGGGC
TRAPPC12	-0329	-320	-	6.09	GCTGCCGGC
PDZR.3	-0421	-412	-	6.52	CCTCCCGGC
PPP4R2	-0417	-408	-	6.45	CCTCGCGGC
PPP4R2	-0369	-360	-	5.88	GCGCGCGGC
PPP4R2	-0319	-310	+	5.94	GCCGGGCGC
GXYLT2	-0404	-395	+	5.97	GCCCCGCCG
GXYLT2	-0393	-384	+	6.87	GCCCCGAGC
GXYLT2	-0348	-339	+	5.88	GCCGCGCGC
GXYLT2	-0317	-308	-	5.96	CCGCCCCGC
GXYLT2	-0280	-271	+	7.49	GCCCCGGGG
SHQ1	-0336	-327	-	6.11	GCGTGGGGC
SHQ1	-0289	-280	+	6.31	GCCGGAAGC
RYBP	-0435	-426	-	5.94	GCGCCCCGC
RYBP	-0317	-308	-	6.28	GCTGAGGGC
GXYLT2	-0404	-395	+	5.97	GCCCCGCCG
GXYLT2	-0393	-384	+	6.87	GCCCCGAGC
GXYLT2	-0348	-339	+	5.88	GCCGCGCGC
GXYLT2	-0317	-308	-	5.96	CCGCCCCGC
GXYLT2	-0280	-271	+	7.49	GCCCCGGGG
PROK2	-0408	-399	-	6.31	GCGCGGGGC
PROK2	-0394	-385	-	5.89	GCGGGGGGC
PROK2	-0371	-362	+	7.28	GCCCCAGGC
PROK2	-0350	-341	+	5.88	GCCGCGCGC
PROK2	-0313	-304	-	5.90	GCCGCTGGC
DIPK2A	-0422	-413	+	6.45	GCCCCCAGC
DIPK2A	-0388	-379	-	5.88	GCGCGCGGC
DIPK2A	-0356	-347	+	6.87	GCCCCGAGC
TASP1	-0333	-324	-	6.31	GCTTCCGGC
ISM1	-0371	-362	+	6.37	GCCCCGCGC

ISM1	-0341	-332	+	6.15	GCCCTGCGG
LOC100034197	-0364	-355	+	7.22	GCCCCAGGG
LOC100056127	-0338	-329	+	7.42	GCCCCGGGG
SLC31A2	-0418	-409	+	6.32	GCCCCGCGG
SLC31A2	-0357	-348	+	7.21	GCCCCAGGC
PRPF4	-0293	-284	+	6.18	GCCCCCTGGG
R.F183	-0412	-403	+	6.70	GCCCTGAGC
WDR31	-0345	-336	+	6.18	GCCCCCTGGG
WDR31	-0311	-302	+	6.09	GCCGGCAGC
WDR31	-0292	-283	+	6.95	GCCCCGAGG
BSPRY	-0334	-325	+	6.64	GCCGGGCGGG
BSPRY	-0301	-292	+	5.90	GCCCCCCC
HDHD3	-0356	-347	-	5.89	GCGGGGGGC
ALAD	-0396	-387	+	5.97	GCCCCCGCG
ALAD	-0362	-353	+	6.44	GCCTCGAGC
ALAD	-0301	-292	+	6.29	GCCCTCAGG
POLE3	-0404	-395	-	6.64	CCCGCCGCG
Z.F618	-0437	-428	+	7.04	GCCGGGGGC
Z.F618	-0340	-331	+	5.89	GCCCCCCC
Z.F618	-0329	-320	+	5.89	GCCCCCCC
Z.F618	-0314	-305	+	5.90	GCCCCCCC
AMBP	-0326	-317	+	6.82	GCCTTGGGG
COL27A1	-0291	-282	+	5.85	GCCTTCAGC
AK.A	-0356	-347	+	6.98	GCCTCGGGC
TEX48	-0373	-364	-	6.31	GCTTCCGGC
TEX48	-0289	-280	+	6.86	GCCGGAGGG
LOC100050034	-0394	-385	+	6.24	GCCTCAAGC
DCK	-0431	-422	+	7.24	GCCCTGGGG
DCK	-0373	-364	-	5.88	GCGCGCGGC
DCK	-0353	-344	-	5.89	CCGCGCGGC
DCK	-0314	-305	+	5.94	GCCGGGCGC
DCK	-0290	-281	+	6.74	GCCCCGAAGC
MOB1B	-0432	-423	-	6.32	CCGCGGGGC
MOB1B	-0373	-364	+	6.86	GCCGGAGGG
MOB1B	-0317	-308	-	5.89	GCGGGGGGC
GRSF1	-0428	-419	-	6.08	ACCCCGGGC
GRSF1	-0414	-405	+	6.34	GCCCAGGGG
GRSF1	-0400	-391	+	7.41	GCCCCGGGC
GRSF1	-0388	-379	+	6.69	GCCCCAAGG
GRSF1	-0337	-328	+	5.89	GCCTCGCGG
GRSF1	-0292	-283	-	6.52	CTTCCCGGC
RUFY3	-0426	-417	+	6.34	GCCCAGGGG
RUFY3	-0398	-389	+	6.86	GCCGGAGGG
RUFY3	-0322	-313	+	6.78	GCCGCAGGC
RUFY3	-0298	-289	+	6.09	GCCGGCAGC
UTP3	-0414	-405	+	6.45	GCCCCCAGC
Z.F572	-0285	-276	+	6.57	GCCTCCGGG
SOLE	-0380	-371	-	6.02	GCTGGCGGC
SOLE	-0352	-343	-	6.31	GCGCGGGGC
WASHC5	-0307	-298	+	6.32	GCCAGGGGC
.SMCE2	-0366	-357	+	6.16	GCCCCCTGGC
PLEKHH2	-0284	-275	-	5.79	GCTCTGGGC
ABCG8	-0343	-334	-	6.09	CCCCATGGC
ABCG8	-0315	-306	-	6.09	CCCCATGGC
ABCG8	-0287	-278	-	6.09	CCCCATGGC
LRPPRC	-0342	-333	-	5.94	GCGCCCGGC
LRPPRC	-0319	-310	-	6.37	GCGCCGGGC
PPM1B	-0379	-370	+	5.84	GCCCTGGGT
KLHL29	-0427	-418	+	7.47	GCCCCGGGC
KLHL29	-0359	-350	+	6.16	GCCCCCTGGC
PLCB1	-0400	-391	+	6.57	GCCGCCGGG
PLCB1	-0349	-340	+	5.79	GCCAGGAGG
TMX4	-0355	-346	-	6.08	ACCCCGGGC
COX20	-0431	-422	+	7.47	GCCCCGGGC
COX20	-0412	-403	+	6.32	GCCGGAAGG
COX20	-0386	-377	+	7.21	GCCCCAGGC
COX20	-0335	-326	+	7.06	GCCCCGCGC
CATSPERE	-0311	-302	+	6.99	GCCGCGGGG
CATSPERE	-0295	-286	-	5.88	GCGCGCGGC

ZBTB18	-0424	-415	+	6.99	GCCCCCGGC
ZBTB18	-0343	-334	+	6.09	GCCATGGGG
ZBTB18	-0289	-280	+	5.91	GCCAGCGGG
ADSS2	-0395	-386	+	6.99	GCCGCGGGG
ADSS2	-0371	-362	-	6.64	CCCGCCGGC
ADSS2	-0348	-339	-	6.53	CCTGCGGGC
ADSS2	-0319	-310	-	5.88	GCGCGAGGC
ADSS2	-0280	-271	-	6.31	GCGCGGGGC
DESI2	-0419	-410	-	6.79	CCCTGCGGC
H.R.PU	-0415	-406	+	5.89	GCCGCGCGG
H.R.PU	-0398	-389	+	6.37	GCCCCGGCGC
H.R.PU	-0379	-370	+	5.94	GCCGGGCGC
H.R.PU	-0364	-355	-	6.51	GCTCCCCGGC

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list of hits					
DUSP5	-0392	-381	+	7.98	CCCGGGGGCGT
ADD3	-0366	-355	-	4.55	CCTCCCACAGC
XP.PEP1	-0340	-329	+	5.44	GATGGGGGCGG
XP.PEP1	-0298	-287	+	4.46	GGCGTGGCCGG
MXI1	-0301	-290	-	6.71	ACACTCACACA
SMC3	-0421	-410	-	4.56	CCCCCTACGCT
SMC3	-0370	-359	-	7.20	CCGCCTCCACG
RBM20	-0431	-420	-	5.38	CCGCTCCCGGG
RBM20	-0278	-267	-	4.51	CCGCGCCCGCG
ADK	-0412	-401	-	4.25	CCTCCTACAGT
ADK	-0401	-390	+	5.96	CGGGTGGGCGG
ADK	-0330	-319	+	7.00	TGTGTGGGAGA
COMTD1	-0324	-313	-	4.38	CCGCCGCCGCT
VDAC2	-0492	-481	-	4.58	CCGCCCCCTCG
VDAC2	-0425	-414	-	4.15	CGCCCCCGCT
VDAC2	-0394	-383	+	7.98	CCCGGGGGCGG
LOC100061588	-0471	-460	-	5.32	CCACCCACTCA
LOC100068208	-0500	-489	+	6.02	GGTGGGGGTGG
MSMO1	-0472	-461	-	6.60	CCGCCTCCGGG
KLHL2	-0333	-322	+	4.44	CGCGGGGGCCG
TMEM192	-0270	-259	+	8.29	AGTGGGGGCGG
APELA	-0362	-351	+	5.32	AGTGGAGGAGG
APELA	-0343	-332	+	5.03	GCCGGGGGAGG
LOC100066472	-0377	-366	+	5.62	GGTGTAGGAGT
LOC100068041	-0442	-431	+	4.92	TGAGTGGGAGG
LOC106780946	-0478	-467	-	4.38	CCGCCGCCGCT
LOC106780946	-0366	-355	+	4.66	CGCGGCGGCGG
EPB41L3	-0473	-462	+	4.58	TGTGTGCGCGT
EPB41L3	-0395	-384	+	6.47	GGCGGGAGCGG
EPB41L3	-0366	-355	-	4.44	CCGCCCGCGG
TMEM200C	-0391	-380	-	4.66	CCGCCGCCGCG
TMEM200C	-0279	-268	+	4.38	AGCGGCGGCGG
S.X3	-0400	-389	-	7.16	CCGCCTCCGGA
AFG1L	-0328	-317	-	6.41	CCTCCCACGGC
FOXO3	-0481	-470	+	4.38	AGCGGCGGCGG
FOXO3	-0344	-333	-	7.48	CCTCCCCCGCC
FOXO3	-0328	-317	-	4.44	CCGCCCGGCGG
ARMC2	-0332	-321	+	8.86	TGCGTGGGAGA
CEP57L1	-0444	-433	-	6.37	CCGCCCAGGCA
CEP57L1	-0279	-268	+	6.13	CCTGGGGGCGT
OSTM1	-0464	-453	-	4.05	CCACCTCCGGC
PPIL6	-0440	-429	-	4.87	CCTCTCCCGCC
PPIL6	-0330	-319	-	5.44	CCGCCCCCATC
PPIL6	-0290	-279	+	10.15	AGCGGGGGCGG
SMPD2	-0455	-444	-	10.15	CCGCCCCCGCT
SMPD2	-0415	-404	+	5.44	GATGGGGGCGG
SMPD2	-0305	-294	+	4.87	GGCGGGAGAGG
MICAL1	-0448	-437	+	10.45	GGCGTGGGCGG
ZBTB24	-0314	-303	+	4.66	CGCGCAGGCGG
WASF1	-0352	-341	+	4.58	CGAGGGGGCGG
CDC40	-0496	-485	-	4.58	CCGCCCCCTCG
METTL24	-0292	-281	+	6.23	CGCGGGAGAGG

SLC22A16	-0322	-311	+	9.07	GGCGGGGGCGG
E.GASE	-0335	-324	-	4.77	CCGCCCCCAGC
CA.T1	-0502	-491	-	4.46	CCGCCCTCCAGT
CA.T1	-0480	-469	-	4.11	TCACCCCCACC
CA.T1	-0317	-306	-	4.51	CCGCGCCCGCG
CA.T1	-0285	-274	+	4.02	GCCGGGAGCGT
LGALS3BP	-0402	-391	-	7.22	ACGCCCACAGT
TIMP2	-0295	-284	-	5.06	CCGCGCCCGCA
USP36	-0314	-303	+	6.14	GCTGTGGGCGT
CYTH1	-0429	-418	+	6.04	CGCGCGGGCGG
CYTH1	-0400	-389	+	6.13	CCTGGGGGCGG
CYTH1	-0329	-318	+	6.04	CGCGCGGGCGG
CYTH1	-0274	-263	+	4.44	CGCGGGGGCCGG
SOCS3	-0361	-350	-	4.66	CCGCCGCCGCG
SOCS3	-0296	-285	-	7.16	TCGCCCCCGCC
TMEM235	-0286	-275	-	4.09	ACTCTCCCACT
Z.HIT3	-0293	-282	+	4.53	GGCGTGC GCGT
MYO19	-0491	-480	+	8.58	CGTGGGGGCGG
GG.BP2	-0304	-293	-	5.75	CCGCCCTCGCT
LHX1	-0327	-316	-	4.53	CCTCCCCCAGG
AATF	-0407	-396	-	4.03	ACGCGCACACG
AATF	-0339	-328	-	5.84	ACGCCCCCAGT
AATF	-0310	-299	-	4.44	CCTCCCGCGCG
ACACA	-0423	-412	-	7.46	CCTCCTCCGCG
ACACA	-0401	-390	-	4.62	CCAGCCACGCG
ACACA	-0314	-303	-	4.58	CCGCCCCCTCG
USP32	-0305	-294	+	4.61	GGTGGGAGCGG
USP32	-0281	-270	+	5.42	CATGGAGGCGG
ACYP2	-0316	-305	-	5.00	CCTCCCTCGCA
PSME4	-0363	-352	+	7.46	CGCGGAGGAGG
PSME4	-0317	-306	+	4.08	AGGGTGGGAGG
PSME4	-0269	-258	+	5.96	CGGGTGGGCGG
ERLEC1	-0365	-354	+	6.62	TCCGTAGGCGA
ERLEC1	-0288	-277	+	5.84	GGTGGAGGCGG
KC.S3	-0345	-334	+	9.24	CGCGGGGGTGG
GE.1	-0495	-484	-	6.04	CCGCCCCGCGCG
SMC6	-0349	-338	-	5.88	CCGCGCACGCG
SMC6	-0316	-305	+	7.22	GGTGGGGGCGG
ODC1	-0502	-491	-	4.66	CCGCCGCCGCG
HPCAL1	-0462	-451	+	9.07	GGCGGGGGCGG
HPCAL1	-0432	-421	+	6.62	GCCGGGGGCGG
HPCAL1	-0414	-403	+	6.13	CCTGGGGGCGT
HPCAL1	-0398	-387	+	8.95	AGCGGGGGTGG
HPCAL1	-0348	-337	-	6.62	CCGCCCCCGGC
HPCAL1	-0335	-324	-	6.60	CCGCCCTCCGGG
HPCAL1	-0322	-311	-	6.04	CCGCCCCGCGG
KLF11	-0386	-375	-	4.44	CCGCCCCGCGG
KLF11	-0343	-332	-	10.43	CCGCCCCCGCG
KLF11	-0271	-260	+	6.04	CGCGCGGGCGG
GRHL1	-0462	-451	-	4.68	CCGCCCCGCGCC
GRHL1	-0434	-423	-	4.99	CCGCCCCGGCA
YWHAQ	-0295	-284	+	4.06	CGTGGGAGCGA
ADAM17	-0355	-344	+	6.14	GCTGTGGGCGG
CYS1	-0496	-485	-	7.70	CCGCCCCCGGT
CYS1	-0478	-467	-	4.25	CCTCCCCCAGT
CYS1	-0434	-423	-	4.25	CCTCCCCCAGT
CYS1	-0406	-395	-	7.70	CCGCCCCCGGT
CYS1	-0363	-352	-	4.16	CCTCCCGCGCT
CYS1	-0346	-335	-	4.16	CCTCCCGCGCT
ALLC	-0377	-366	+	6.94	TCCGGGGGAGG
RPS7	-0374	-363	-	5.00	ACTCCCACGAA
TRAPPC12	-0432	-421	+	5.44	GATGGGGGCGG
TRAPPC12	-0273	-262	+	10.99	TGCGGGGGCGG
PDZR.3	-0396	-385	+	4.60	GGGGTGGGCGG
PPP4R2	-0491	-480	+	9.07	GGCGGGGGCGG
PPP4R2	-0473	-462	+	9.07	GGCGGGGGCGG
PPP4R2	-0455	-444	+	7.94	TGTGGGGGTGG
PPP4R2	-0408	-397	-	7.70	ACGCCCTCCGCC
GXYLT2	-0419	-408	-	4.33	CCTCCTCCGTC

GXYLT2	-0364	-353	+	4.33	GACGGAGGAGG
GXYLT2	-0268	-257	-	4.66	CCGCCGCCGCG
SHQ1	-0318	-307	-	6.25	TCTCTCACGCA
RYBP	-0498	-487	-	9.07	CCGCCCCCGCC
RYBP	-0405	-394	+	7.70	GGCGGAGGCGG
RYBP	-0360	-349	+	4.38	AGCGGCGGCGG
RYBP	-0301	-290	+	8.84	CGCGGGGGAGG
GXYLT2	-0419	-408	-	4.33	CCTCCTCCGTC
GXYLT2	-0364	-353	+	4.33	GACGGAGGAGG
GXYLT2	-0268	-257	-	4.66	CCGCCGCCGCG
PROK2	-0365	-354	+	9.07	GGCGGGGGCGT
PROK2	-0276	-265	+	5.06	TGCGGGGCGCGG
DIPK2A	-0444	-433	-	4.38	CCGCCGCCGCT
DIPK2A	-0405	-394	+	5.88	CGCGTGCGCGT
TASP1	-0346	-335	+	4.18	CAGGTGGGCGT
TASP1	-0329	-318	-	4.04	CCGGCCACGTG
TASP1	-0286	-275	-	7.04	TCACCCCCGCT
ISM1	-0501	-490	-	4.68	CCGCCGACGCC
ISM1	-0455	-444	-	6.62	ACGCCCCCGGC
ISM1	-0423	-412	+	9.61	TGCGGAGGCGG
SPTLC3	-0380	-369	+	4.38	CATGTGAGTGT
ZFP37	-0311	-300	+	5.43	GCCGGGGGTGG
FKBP15	-0461	-450	-	4.30	CCGCCCCCCT
FKBP15	-0427	-416	+	4.44	CGCAGGGGCGT
SLC31A1	-0353	-342	-	4.44	ACGCCCCTGCG
SLC31A1	-0319	-308	+	4.30	AGGGGGGGCGG
PRPF4	-0269	-258	+	5.26	AGCGGAGGAGA
ALAD	-0497	-486	-	9.39	CCTCCCCCGCA
ALAD	-0347	-336	+	12.37	TGCGTGGGCGG
RGS3	-0428	-417	-	4.34	ACACCCATGCT
POLE3	-0461	-450	-	4.02	CCGCTCCCGGC
POLE3	-0379	-368	-	8.86	TCTCCCACGCA
Z.F618	-0437	-426	+	6.62	GCCGGGGGCGG
Z.F618	-0420	-409	+	10.43	CGCGGGGGCGG
Z.F618	-0382	-371	+	4.66	CGCGGCGGCGG
Z.F618	-0293	-282	+	6.10	GGCGGAGGAGG
Z.F618	-0281	-270	+	4.38	AGCGGCGGCGG
AMBP	-0446	-435	-	5.03	CCTCCCCCGGC
COL27A1	-0273	-262	-	4.77	CCGCCCCCAGC
AK.A	-0469	-458	-	9.61	CCGCCTCCGCA
AK.A	-0457	-446	+	5.44	GATGGGGGCGT
AK.A	-0345	-334	+	4.52	TGTTTGGGCGG
ATP6V1G1		-0357	-346	-	6.10 CCTCCTCCGCC
T.FSF8	-0494	-483	-	7.40	CCACCCACACC
T.FSF8	-0451	-440	-	6.30	CCTCCCACATT
DCK	-0398	-387	-	4.66	CCGCCCCCGAG
MOB1B	-0419	-408	+	5.96	TCCGGAGGTGT
MOB1B	-0327	-316	+	5.44	GATGGGGGCGG
GRSF1	-0354	-343	-	5.78	TCGCCTCCGCC
RUFY3	-0465	-454	+	4.44	CGCCGGGGCGG
UTP3	-0500	-489	-	6.10	ACTCCCCCGGT
UTP3	-0416	-405	-	4.77	ACGCCCCCAGC
R.PC3	-0346	-335	-	5.68	ACTCCTCCGTG
COL11A1	-0385	-374	+	5.96	CGAGTGGGCGG
SQLE	-0503	-492	-	8.29	ACGCCCCACT
SQLE	-0339	-328	+	4.60	GGGGTGGGCGG
WASHC5	-0464	-453	-	7.75	TCGCCCACACT
TRIB1	-0480	-469	-	4.58	CCGCCCCCCC
TRIB1	-0336	-325	+	6.10	GGCGGAGGAGG
LRPPRC	-0327	-316	-	4.32	TCTCTCCCGCG
PREPL	-0468	-457	-	4.34	ACAACCACGCT
SLC3A1	-0355	-344	+	7.40	GGTGTGGGTGT
KLHL29	-0412	-401	-	5.62	CCTCCCCCACC
KLHL29	-0399	-388	-	7.88	CCACCCCCGCC
KLHL29	-0334	-323	-	5.00	CCTCCCTCGCA
PLCB1	-0373	-362	+	4.56	AGCGAGGGTGG
C25H9orf43		-0503	-492	-	7.70 CCGCCTCCGCC
COX20	-0272	-261	+	10.15	AGCGGGGGCGG
CATSPERE		-0277	-266	+	9.07 GGCGTAGGCGG

ZBTB18	-0472	-461	+	5.24	TGCGTGCGTG
ZBTB18	-0453	-442	-	9.07	CCGCCCCCGCC
ZBTB18	-0441	-430	-	9.07	CCGCCCCCGCC
ZBTB18	-0426	-415	-	6.62	CCGCCCCCGGC
ZBTB18	-0286	-275	+	10.15	AGCGGGGGCGG
ADSS2	-0481	-470	+	5.96	CGGGTGGGCGG
ADSS2	-0441	-430	-	7.16	TCGCCCCCGCC
ADSS2	-0391	-380	+	4.58	CGGGGGGGCGT
DESI2	-0494	-483	+	4.99	TGCGGGGGCTT
DESI2	-0345	-334	-	9.06	CCGCTCCGCG
DESI2	-0322	-311	+	4.56	AGCGGGGGGGG
H.R.PU	-0392	-381	+	10.43	CGCGGGGGCGG
H.R.PU	-0358	-347	+	9.07	GGCGGGGGCGG
H.R.PU	-0336	-325	+	6.44	TGCGTGCGCGG
H.R.PU	-0323	-312	-	4.44	CCGCCCCTGCG

3 MA0079.2 SP1 11.1288627426 0.820000010729 -398:-322  
2.72407069304e-23

## list of hits

DUSP5	-0368	-358	-	8.96	AGGGGCGGGG
ADD3	-0326	-316	+	5.80	CCCTGCTTCC
XP.PEP1	-0389	-379	+	8.11	CCCTGCCTCC
XP.PEP1	-0353	-343	-	9.67	GTGGGCGGGG
XP.PEP1	-0337	-327	-	11.09	GGGGGCGGGG
SMC3	-0372	-362	+	8.00	CTCCGCCTCC
ADK	-0398	-388	-	6.94	GTGGGCGGGA
KAT6B	-0392	-382	-	6.51	AGGAGAGGGG
KAT6B	-0350	-340	+	6.75	CCCCGCCCC
SAMD8	-0351	-341	+	7.69	CCCCGCTTCC
SAMD8	-0322	-312	+	7.39	CCCTGCCCTC
VDAC2	-0391	-381	-	11.09	GGGGGCGGGG
LOC100068191	-0349	-339	+	8.11	CCCAGCCTCC
TMEM192	-0337	-327	+	9.13	CCCTCCCTC
CPE	-0328	-318	+	6.51	CCCTCTCTCT
APELA	-0388	-378	-	6.34	CGGGAGGGGG
APELA	-0378	-368	-	8.01	GGGGGGGGAG
APELA	-0359	-349	-	9.86	GGAGGAGGGG
APELA	-0346	-336	-	6.03	GAGGCCGGGG
LOC106780946	-0363	-353	-	5.72	GGCGGCGGCG
EPB41L3	-0329	-319	-	9.28	GAGGGCGGGG
L3MBTL4	-0362	-352	+	5.66	CCCATCTTCC
TMEM200C	-0393	-383	+	5.72	CGCCGCCGCC
RIT2	-0347	-337	-	6.47	GGGGGCAGGA
SYT4	-0364	-354	-	6.64	GGGAGAGGAG
SYT4	-0344	-334	-	7.55	GGAAGAGGGG
S.X3	-0355	-345	-	5.72	GGCGGCGGCG
AFG1L	-0363	-353	+	7.97	CCCTTCCTCC
AFG1L	-0335	-325	+	8.96	CCCCGCCCT
FOXO3	-0393	-383	-	5.72	GGCGGCGGCG
FOXO3	-0351	-341	+	7.43	CCCCGTCCCT
FOXO3	-0340	-330	+	6.90	CCCCGCCGCA
FOXO3	-0330	-320	+	8.96	CCCCGCCCCG
ARMC2	-0383	-373	+	7.54	CTCCTCCAC
SES.1	-0372	-362	-	9.28	GAGGGCGGGG
SES.1	-0353	-343	-	9.86	GGAGGAGGGG
CEP57L1	-0398	-388	+	9.28	CCCCGCCCTC
OSTM1	-0359	-349	-	8.96	TGGGGCGGGG
OSTM1	-0338	-328	-	9.56	GGGGACGGGG
PPIL6	-0368	-358	+	11.09	CCCCGCCCCC
PPIL6	-0355	-345	+	8.96	CCCCGCCCCA
PPIL6	-0345	-335	+	6.38	TCCCACCCCC
PPIL6	-0332	-322	+	7.71	GCCCCCCCCC
SMPD2	-0389	-379	-	8.96	TGGGGCGGGG
SMPD2	-0376	-366	-	11.09	GGGGGCGGGG
MICAL1	-0342	-332	+	6.58	CCCACTCCCC
ZBTB24	-0372	-362	+	8.96	CCCCGCCCCG
ZBTB24	-0362	-352	+	8.96	CCCCGCCCCG
FIG4	-0363	-353	+	9.09	CTCCGCCCCC
FIG4	-0345	-335	-	8.96	TGGGGCGGGG



FIG4	-0327	-317	-	8.02	GGAGGTGGGG
WASF1	-0349	-339	-	11.09	GGGGGCGGGG
METTL24	-0393	-383	+	5.71	CCCCGGCCCA
AK9	-0337	-327	+	8.02	CCCCACCTCC
SLC22A16		-0373	-363	-	5.97 AGAGGCTGGG
SLC22A16		-0363	-353	-	10.00 GGGGGGGGGG
SLC22A16		-0348	-338	-	6.90 CGCGGCGGGG
SLC22A16		-0325	-315	-	6.90 AGCGGCGGGG
E.GASE	-0392	-382	+	5.95	CCCAGGCCCC
E.GASE	-0368	-358	+	9.28	CCCCGCCCTC
E.GASE	-0352	-342	+	8.96	CCCCGCCCCA
E.GASE	-0337	-327	+	11.09	CCCCGCCCCC
E.GASE	-0325	-315	+	7.97	CCCTTCCTCC
C1QT.F1	-0369	-359	-	6.47	GGAGGAGGGC
CA.T1	-0376	-366	+	7.86	CTCCTCCTCC
LGALS3BP		-0383	-373	-	5.83 AGAGGAAGGG
TIMP2	-0395	-385	-	8.81	CGGGGAGGGG
TIMP2	-0343	-333	-	8.00	GGAGGCGGAG
USP36	-0350	-340	-	7.43	CGGGACGGGG
CYTH1	-0397	-387	-	9.09	GGGGGCGGAG
CYTH1	-0323	-313	-	5.72	GGCGGCGGCG
SOCS3	-0375	-365	+	5.72	CGCCGCCGCC
SOCS3	-0363	-353	+	5.72	CGCCGCCGCC
SOCS3	-0349	-339	+	5.84	CTCCGCCCCC
SOCS3	-0322	-312	+	6.89	CCCAGCTCCC
TMEM235	-0374	-364	+	8.78	CCCCGCTCCC
TMEM235	-0361	-351	+	6.89	CCCTGCTCCC
TMEM235	-0347	-337	+	7.87	CCCCGCCTCT
TMEM235	-0331	-321	+	7.25	CCCCGTTCCT
CA4	-0388	-378	-	6.79	GGGAGCGGAG
CA4	-0355	-345	-	7.72	AGAGGAGGGG
CA4	-0334	-324	-	8.95	GGGGGAGGAG
MYO19	-0391	-381	-	5.73	AGAGGAGGAG
GG.BP2	-0363	-353	-	10.00	GGAGGCGGGG
GG.BP2	-0334	-324	+	7.00	CCCTCCCTTG
GG.BP2	-0324	-314	+	7.30	CCCCACCCTC
DHRS11	-0370	-360	-	8.96	AGGGGCGGGG
DHRS11	-0350	-340	-	8.96	AGGGGCGGGG
LHX1	-0372	-362	+	6.54	TCCCGCCCTC
LHX1	-0362	-352	+	6.06	CCCTCCCGCC
LHX1	-0352	-342	+	6.19	CTCCCCCCTC
LHX1	-0341	-331	+	5.82	GCCTGCCCCC
LHX1	-0330	-320	+	8.47	CCCCCTCCCC
ACACA	-0322	-312	+	5.65	GCCCGCCGCC
USP32	-0396	-386	-	6.19	GAGGGGGGAG
USP32	-0360	-350	-	7.00	AAGGGAGGGG
USP32	-0325	-315	-	9.13	GAGGGAGGGG
SPTB.1	-0360	-350	+	6.40	TCCCTCCCTC
PSME4	-0360	-350	-	6.54	GGAGGAGGCG
PSME4	-0345	-335	-	6.51	CGGAGAGGGG
PSME4	-0333	-323	-	7.84	GGGGCCGGGG
C15H2orf73		-0347	-337	+	8.36 TCCCGCCCCC
KC.S3	-0362	-352	-	8.36	GGGGGCGGGA
KC.S3	-0343	-333	-	5.98	CGGGGGTGGG
GE.1	-0376	-366	-	6.22	TGGGGCGGGA
SMC6	-0387	-377	+	7.72	CCCTTCCTCT
RDH14	-0360	-350	+	5.64	CGCCGCCCTT
.OL10	-0384	-374	+	6.92	CCCTTCCCCT
ODC1	-0363	-353	+	6.11	CTCAGCCTCC
ODC1	-0351	-341	+	5.72	CGCCGCCGCC
HPCAL1	-0396	-386	-	5.98	CGGGGGTGGG
HPCAL1	-0350	-340	+	11.09	CCCCGCCCCC
HPCAL1	-0337	-327	+	10.00	CCCCGCCTCC
HPCAL1	-0324	-314	+	6.54	TCCCGCCCTC
KLF11	-0388	-378	+	8.96	CCCCGCCCCG
KLF11	-0345	-335	+	11.09	CCCCGCCCCC
GRHL1	-0395	-385	+	6.62	GCCCGCCTCC
GRHL1	-0374	-364	+	6.08	TCCCTCCCCG
TAF1B	-0349	-339	-	7.40	CTGGGAGGGG

YWHAQ	-0398	-388	+	6.22	TCCCGCCCCG
YWHAQ	-0387	-377	+	7.37	CCCCCTCGCC
YWHAQ	-0336	-326	-	7.27	GGAGGCGGGA
CYS1	-0391	-381	+	7.40	CCCCTCCCAG
CYS1	-0376	-366	+	7.84	CCCCGGCCCC
CYS1	-0353	-343	+	6.22	TCCCGCCCCCT
ALLC	-0375	-365	-	5.98	CGGGGGAGGG
ALLC	-0349	-339	+	6.49	CCCCATCTCC
COLEC11	-0327	-317	+	10.00	CCCCCCCCC
ADI1	-0328	-318	+	9.67	CCCCGCCAC
TRAPPC12		-0397	-387	+	9.56 CCCCCGTCCCC
TRAPPC12		-0365	-355	+	9.67 CCCCCGCCAC
DCDC2C	-0380	-370	+	8.64	CCCCCTCTCCC
PDZR.3	-0393	-383	-	6.94	GTGGGCGGGA
PPP4R2	-0348	-338	-	9.04	GGCGGCGGGG
GXYLT2	-0328	-318	+	9.04	CCCCGCCGCC
SHQ1	-0384	-374	+	6.44	CCCTTTCTCC
SHQ1	-0356	-346	+	5.74	TCCCGTCTCC
SHQ1	-0333	-323	-	6.22	TGGGGCGGGA
RYBP	-0357	-347	-	5.72	GGCGGCGGCG
GXYLT2	-0328	-318	+	9.04	CCCCGCCGCC
MIR9170	-0393	-383	-	6.25	GTGGACAGGG
PROK2	-0368	-358	-	7.87	CGAGGCGGGG
DIPK2A	-0371	-361	+	5.92	CCCCGCACTC
DIPK2A	-0361	-351	+	6.75	CCCCCGCCCC
DIPK2A	-0332	-322	-	7.95	GGCGGGGGGG
TASP1	-0365	-355	-	9.09	GGGGGCGGAG
ISM1	-0376	-366	+	5.71	CCCCGGCCCCG
ISM1	-0361	-351	+	6.90	CCCCGCCGCG
ISM1	-0327	-317	-	8.78	GGGAGCGGGG
SPTLC3	-0338	-328	+	7.12	CTCCACCCCC
LOC100034197		-0384	-374	-	7.54 GTGGGAGGAG
LOC100056127		-0358	-348	-	7.54 GTGGGAGGAG
SLC31A1	-0322	-312	-	5.64	GGCAGGGGGG
PRPF4	-0396	-386	+	6.90	CTCCTCCGCC
WDR31	-0368	-358	-	6.05	CAAGGCGGGG
BSPRY	-0322	-312	-	5.71	CGGGCCGGGG
HDHD3	-0380	-370	-	6.06	GGCGGGAGGG
HDHD3	-0368	-358	-	6.96	CGGGGCGGAG
HDHD3	-0353	-343	-	11.09	GGGGGCGGGG
HDHD3	-0328	-318	-	11.09	GGGGGCGGGG
ALAD	-0344	-334	-	9.67	GTGGGCGGGG
POLE3	-0324	-314	-	6.92	TGGGGAAGGG
Z.F618	-0397	-387	-	5.64	AGGGGCGGCG
Z.F618	-0379	-369	-	9.04	GGCGGCGGGG
AMBP	-0386	-376	+	5.95	CCCTGGCCCC
COL27A1	-0391	-381	+	6.65	CCCCCACCC
ATP6V1G1		-0359	-349	+	7.12 TCCCTCCTCC
ATP6V1G1		-0348	-338	+	8.96 CCCCCCCCCCT
T.FSF15	-0331	-321	+	7.70	CCCCACCCAC
T.C	-0398	-388	-	6.89	GGGAGCAGGG
TEX48	-0392	-382	+	6.25	CCCAGTCCAC
DCK	-0365	-355	+	8.96	CCCCGCCCT
DCK	-0345	-335	+	9.09	CTCCGCCCCC
MOB1B	-0368	-358	-	8.96	AGGGGCGGGG
MOB1B	-0324	-314	-	7.77	GGGGGCGGCG
GRSF1	-0392	-382	+	8.96	CCCCGCCCA
GRSF1	-0341	-331	+	7.87	CCCCGCCCTCG
RUFY3	-0344	-334	+	7.77	CGCCGCCCCC
COL11A1	-0382	-372	-	7.68	GTGGGCGGAG
SQLE	-0367	-357	-	9.67	GTGGGCGGGG
SQLE	-0336	-326	-	9.67	GTGGGCGGGG
WASHC5	-0340	-330	+	6.96	CTCCGCCCT
.SMCE2	-0334	-324	-	6.96	AGGGGCGGAG
TRIB1	-0339	-329	-	8.00	GGAGGCGGAG
PPM1B	-0325	-315	+	6.05	CCCCGCCTTT
PREPL	-0349	-339	-	5.89	TGAGGTGGGG
KLHL29	-0395	-385	+	9.67	CCCCGCCAC
KLHL29	-0339	-329	+	6.62	CCCCGCCCTCC

PLCB1	-0394	-384	-	6.33	GGGGGAAGGA
PLCB1	-0362	-352	-	6.92	CGGGGAAGGG
PLCB1	-0345	-335	-	7.86	GGAGGAGGAG
PLCB1	-0332	-322	-	7.14	GAGGGAGGAG
HAO1	-0379	-369	-	5.73	TGAGGAGGAG
HAO1	-0366	-356	-	5.71	GAGGAAAGGG
COX20	-0344	-334	+	6.96	CTCCGCCCCG
ADSS2	-0393	-383	-	5.82	CGCGGGGGGG
DESI2	-0347	-337	+	8.00	CTCCGCCCTCC
DESI2	-0322	-312	-	5.82	AGCGGGGGGG
H.R.PU	-0389	-379	-	11.09	GGGGGCGGGG
H.R.PU	-0355	-345	-	11.09	GGGGGCGGGG

4 MA0039.2 Klf4 12.6183576774 0.771222760739 -371:-312  
1.66990586527e-12

## list of hits

DUSP5	-0367	-357	+	7.75	GGGGCGGGGA
XP.PEP1	-0352	-342	+	10.68	TGGGCGGGGC
XP.PEP1	-0336	-326	+	10.13	GGGGCGGGGC
SMC3	-0314	-304	+	7.12	GGGGAGGGGT
KAT6B	-0350	-340	-	7.85	CCCCCGCCCC
KAT6B	-0319	-309	-	7.25	GCAACGCCCA
LOC100061588	-0326	-316	+	5.66	AAGGTGTGGT
MSMO1	-0317	-307	+	6.37	GAGGCGGGGC
TMEM192	-0343	-333	-	7.53	GACACGCCCC
EPB41L3	-0328	-318	+	8.11	AGGGCGGGGA
SYT4	-0338	-328	+	5.94	GGGGAGGGGG
.R2E1	-0324	-314	+	5.35	GGGGTGTGTG
AFG1L	-0336	-326	-	10.13	GCCCCGCCCC
FOXO3	-0336	-326	-	7.06	GCCGCACCCC
SES.1	-0371	-361	+	8.11	AGGGCGGGGA
SES.1	-0347	-337	+	9.02	GGGGCGGGGT
OSTM1	-0358	-348	+	10.13	GGGGCGGGGC
PPIL6	-0369	-359	-	10.13	GCCCCGCCCC
PPIL6	-0356	-346	-	10.13	GCCCCGCCCC
PPIL6	-0346	-336	-	5.78	ATCCCACCCC
PPIL6	-0333	-323	-	6.84	GGCCCCGCCCC
MICAL1	-0342	-332	-	5.88	CCCACTCCCC
ZBTB24	-0363	-353	-	10.13	GCCCCGCCCC
FIG4	-0364	-354	-	7.48	GCTCCGCCCC
FIG4	-0344	-334	+	10.13	GGGGCGGGGC
FIG4	-0326	-316	+	5.37	GAGGTGGGGT
WASF1	-0348	-338	+	10.13	GGGGCGGGGC
WASF1	-0316	-306	-	9.02	ACCCCGCCCC
DDO	-0327	-317	+	6.19	AGGGTGGGCT
AK9	-0338	-328	-	5.37	ACCCACCTC
AK9	-0320	-310	-	10.13	GCCCCGCCCC
SLC22A16	-0357	-347	+	5.65	GGGGGGGGGC
SLC22A16	-0318	-308	+	10.13	GGGGCGGGGC
LOC102147786	-0355	-345	+	7.58	GGGGTGGAGC
E.GASE	-0369	-359	-	10.49	GCCCCGCCCT
E.GASE	-0353	-343	-	10.13	GCCCCGCCCC
E.GASE	-0338	-328	-	10.13	GCCCCGCCCC
CYTH1	-0315	-305	+	7.71	CGGGCGGGGC
SOCS3	-0328	-318	-	5.57	GCCCGGCCCA
CA4	-0333	-323	+	5.57	GGGGAGGAGC
GG.BP2	-0362	-352	+	6.37	GAGGCGGGGC
GG.BP2	-0335	-325	-	8.59	GCCCCCTCCCT
GG.BP2	-0325	-315	-	10.60	GCCCCACCTT
DHRS11	-0369	-359	+	10.13	GGGGCGGGGC
DHRS11	-0349	-339	+	10.13	GGGGCGGGGC
DHRS11	-0318	-308	+	10.13	GGGGCGGGGC
LHX1	-0336	-326	-	7.85	CCCCCGCCCC
AATF	-0342	-332	-	6.71	GCAACGCCCA
AATF	-0318	-308	-	10.13	GCCCCGCCCC
USP32	-0359	-349	+	6.21	AGGGAGGGGA
USP32	-0337	-327	+	6.72	AGGGCGGAGT
USP32	-0324	-314	+	6.21	AGGGAGGGGA
USP32	-0312	-302	+	9.02	GGGGCGGGGT

SPTB.1	-0361	-351	-	5.24	GTCCCTCCCT
SPTB.1	-0320	-310	-	5.48	GCCCCGCGCA
PSME4	-0339	-329	+	7.95	GGGGTGGGGG
C15H2orf73		-0348	-338	-	6.79 GTCCCGCCCC
KC.S3	-0341	-331	+	7.70	GGGGTGGGTC
SMC6	-0323	-313	+	6.60	CGGGCGGGGT
SMC6	-0312	-302	+	10.13	GGGGCGGGGC
HPCAL1	-0351	-341	-	10.13	GCCCCGCCCC
HPCAL1	-0325	-315	-	7.15	GTCCCGCCCT
RRM2	-0361	-351	-	7.71	GCCCCGCCCC
RRM2	-0333	-323	-	10.61	GCCACGCCCA
KLF11	-0351	-341	-	6.95	GCCGCGCCCC
KLF11	-0332	-322	-	7.42	GCCGCACCTT
KLF11	-0314	-304	-	10.13	GCCCCGCCCC
TAF1B	-0348	-338	+	6.48	TGGGAGGGGG
ADAM17	-0351	-341	+	7.32	TGGGCGGTGC
CYS1	-0371	-361	-	10.13	GCCCCGCCCC
CYS1	-0349	-339	-	5.81	GCCCCTCCCC
ADI1	-0359	-349	-	5.81	GCCCCTCCCC
ADI1	-0334	-324	-	6.84	GGCCCGCCCC
TRAPPC12		-0366	-356	-	10.68 GCCCCGCCCA
DCDC2C	-0371	-361	+	5.17	CGGGCGGGTC
SHQ1	-0332	-322	+	6.79	GGGGCGGGAC
PROK2	-0361	-351	+	7.78	GGGGCGTGGG
DIPK2A	-0361	-351	-	7.85	CCCCCGCCCC
TASP1	-0312	-302	-	6.20	AGCACGCCCA
ISM1	-0357	-347	-	7.49	GCCGCGGCCA
SPTLC3	-0339	-329	-	5.20	TCTCCACCCC
LOC100034197		-0313	-303	+	5.78 GGGGAGTGGA
SLC31A1	-0356	-346	-	5.12	CCTACGCCCC
SLC31A1	-0315	-305	+	10.13	GGGGCGGGGC
WDR31	-0367	-357	+	6.73	AAGGCGGGGC
HDHD3	-0352	-342	+	10.13	GGGGCGGGGC
HDHD3	-0327	-317	+	10.13	GGGGCGGGGC
ALAD	-0343	-333	+	10.68	TGGGCGGGGC
Z.F618	-0319	-309	-	7.85	CCCCCGCCCC
AK.A	-0364	-354	+	5.15	TTGGCGGGGC
AK.A	-0341	-331	+	5.73	TGGGCGGAGG
ATP6V1G1		-0354	-344	-	5.19 CCTCCGCCCC
T.FSF15	-0332	-322	-	10.78	GCCCCACCCA
DCK	-0366	-356	-	10.13	GCCCCGCCCC
DCK	-0346	-336	-	7.48	GCTCCGCCCC
MOB1B	-0367	-357	+	9.02	GGGGCGGGGT
GRSF1	-0342	-332	-	6.37	GCCCCGCCCT
SQLE	-0366	-356	+	10.68	TGGGCGGGGC
SQLE	-0335	-325	+	10.68	TGGGCGGGGC
WASHC5	-0353	-343	-	10.43	GCCACGCCCT
.SMCE2	-0321	-311	+	10.43	AGGGCGTGGC
ABCG5	-0353	-343	-	7.24	GGCACACCTT
SLC3A1	-0357	-347	+	7.89	GGGGTGTGGG
SLC3A1	-0345	-335	+	5.80	TGGGTGTGTA
PLCB1	-0312	-302	+	8.20	AGGGCGGGGG
TMX4	-0325	-315	+	10.07	GGGGCGTGGC
COX20	-0345	-335	-	5.19	CCTCCGCCCC
H.R.PU	-0354	-344	+	10.13	GGGGCGGGGC
H.R.PU	-0326	-316	-	5.90	GCGCCGCCCC

5 MA0006.1 Arnt::Ahr 9.53241699429 0.715277771155 -530:-303  
3.42488344196e-11

list of hits					
RBM20	-0369	-363	-	7.05	CACGCG
MSM01	-0491	-485	-	7.05	CACGCG
LOC100068026		-0346	-340	-	7.37 CACGCA
LOC100068026		-0346	-340	-	7.37 CACGCA
EPB41L3	-0467	-461	+	7.05	CGCGTG
.R2E1	-0426	-420	+	7.05	CGCGTG
ARMC2	-0332	-326	+	7.37	TGCGTG
SES.1	-0481	-475	-	7.37	CACGCA
CEP57L1	-0331	-325	-	7.37	CACGCA

CEP57L1	-0325	-319	+	7.37	TGCGTG	
PPIL6	-0508	-502	-	7.05	CACGCG	
LOC102147786		-0513	-507	-	7.37	CACGCA
USP36	-0386	-380	+	7.37	TGCGTG	
CYTH1	-0528	-522	+	7.37	TGCGTG	
CYTH1	-0477	-471	+	7.05	CGCGTG	
CYTH1	-0435	-429	+	7.37	TGCGTG	
CYTH1	-0375	-369	+	7.05	CGCGTG	
CYTH1	-0363	-357	+	7.05	CGCGTG	
CYTH1	-0345	-339	+	7.05	CGCGTG	
AFMID	-0387	-381	+	7.05	CGCGTG	
GG.BP2	-0456	-450	-	7.05	CACGCG	
DHRS11	-0323	-317	+	7.05	CGCGTG	
AATF	-0422	-416	-	7.05	CACGCG	
AATF	-0408	-402	-	7.05	CACGCG	
ACACA	-0396	-390	-	7.05	CACGCG	
ACACA	-0390	-384	-	7.05	CACGCG	
ACACA	-0372	-366	+	7.37	TGCGTG	
ACACA	-0334	-328	+	7.37	TGCGTG	
GE.1	-0488	-482	+	7.05	CGCGTG	
GE.1	-0308	-302	-	7.37	CACGCA	
SMC6	-0524	-518	+	7.37	TGCGTG	
SMC6	-0344	-338	-	7.05	CACGCG	
.OL10	-0416	-410	+	7.05	CGCGTG	
ODC1	-0416	-410	-	7.05	CACGCG	
HPCAL1	-0508	-502	+	7.05	CGCGTG	
KLF11	-0460	-454	-	7.05	CACGCG	
GRHL1	-0496	-490	-	7.05	CACGCG	
GRHL1	-0481	-475	-	7.05	CACGCG	
PDZR.3	-0365	-359	+	7.37	TGCGTG	
PPP4R2	-0394	-388	-	7.05	CACGCG	
SHQ1	-0313	-307	-	7.37	CACGCA	
RYBP	-0448	-442	+	7.05	CGCGTG	
PROK2	-0453	-447	+	7.05	CGCGTG	
PROK2	-0379	-373	+	7.37	TGCGTG	
DIPK2A	-0405	-399	+	7.05	CGCGTG	
CDC26	-0519	-513	+	7.05	CGCGTG	
PRPF4	-0498	-492	+	7.37	TGCGTG	
ALAD	-0457	-451	-	7.05	CACGCG	
ALAD	-0347	-341	+	7.37	TGCGTG	
POLE3	-0374	-368	-	7.37	CACGCA	
COL27A1	-0528	-522	-	7.05	CACGCG	
COL27A1	-0317	-311	+	7.05	CGCGTG	
T.FSF8	-0515	-509	-	7.37	CACGCA	
T.FSF8	-0478	-472	-	7.37	CACGCA	
DCK	-0304	-298	-	7.37	CACGCA	
COL11A1	-0451	-445	+	7.05	CGCGTG	
SOLE	-0486	-480	-	7.37	CACGCA	
SOLE	-0395	-389	+	7.37	TGCGTG	
.SMCE2	-0485	-479	-	7.05	CACGCG	
DY.C2LI1		-0304	-298	-	7.37	CACGCA
PREPL	-0490	-484	-	7.37	CACGCA	
TMX4	-0487	-481	-	7.05	CACGCG	
TMX4	-0453	-447	-	7.05	CACGCG	
HAO1	-0489	-483	+	7.37	TGCGTG	
COX20	-0322	-316	-	7.05	CACGCG	
ZBTB18	-0476	-470	+	7.05	CGCGTG	
ZBTB18	-0468	-462	+	7.37	TGCGTG	
ADSS2	-0525	-519	-	7.37	CACGCA	
DESI2	-0530	-524	+	7.37	TGCGTG	
H.R.PU	-0336	-330	+	7.37	TGCGTG	
H.R.PU	-0303	-297	+	7.37	TGCGTG	

6 MA0161.1 NFIC 6.98267924778 0.5685040611 -1507:-1417  
1.32023656629e-09  
list of hits  
VDAC2 -1432 -1426 + 6.73 TTGGCA  
LOC100068208 -1480 -1474 + 6.73 TTGGCA  
LOC100068026 -1446 -1440 + 6.73 TTGGCA

LOC100068026	-1423	-1417	-	6.73	TGCCAA
LOC100068026	-1446	-1440	+	6.73	TTGGCA
LOC100068026	-1423	-1417	-	6.73	TGCCAA
RIT2	-1465	-1459	-	5.83	TGCCAG
SYT4	-1482	-1476	-	6.73	TGCCAA
SES.1	-1417	-1411	-	5.91	AGCCAA
OSTM1	-1506	-1500	+	6.73	TTGGCA
PPIL6	-1439	-1433	+	5.83	CTGGCA
PPIL6	-1432	-1426	-	5.91	AGCCAA
CD164	-1502	-1496	+	5.91	TTGGCT
CIQT.F1	-1498	-1492	+	5.91	TTGGCT
CA4	-1455	-1449	+	6.73	TTGGCA
PIGW	-1492	-1486	-	5.83	TGCCAG
LHX1	-1488	-1482	-	5.91	AGCCAA
USP32	-1457	-1451	+	5.91	TTGGCT
ERLEC1	-1424	-1418	+	5.83	CTGGCA
SMC6	-1426	-1420	+	5.91	TTGGCT
LOC100056590	-1481	-1475	+	5.91	TTGGCT
.OL10	-1441	-1435	-	5.83	TGCCAG
ODC1	-1418	-1412	+	5.83	CTGGCA
GRHL1	-1483	-1477	+	5.83	CTGGCA
TAF1B	-1457	-1451	+	5.91	TTGGCT
COLEC11	-1454	-1448	-	5.83	TGCCAG
TRAPPC12	-1423	-1417	+	5.83	CTGGCA
RYBP	-1455	-1449	-	5.91	AGCCAA
PROK2	-1507	-1501	+	6.73	TTGGCA
SPTLC3	-1502	-1496	+	5.91	TTGGCT
LOC100056127	-1492	-1486	+	6.73	TTGGCA
FKBP15	-1432	-1426	+	5.91	TTGGCT
SLC31A1	-1473	-1467	+	6.73	TTGGCA
PRPF4	-1468	-1462	-	5.91	AGCCAA
RGS3	-1451	-1445	+	5.91	TTGGCT
RGS3	-1427	-1421	+	5.91	TTGGCT
ATP6V1G1	-1445	-1439	+	5.83	CTGGCA
T.FSF15	-1461	-1455	+	6.73	TTGGCA
LOC100050100	-1489	-1483	+	5.91	TTGGCT
GC	-1420	-1414	+	6.73	TTGGCA
JCHAI.	-1425	-1419	+	5.83	CTGGCA
SLC4A4	-1466	-1460	-	6.73	TGCCAA
SLC4A4	-1449	-1443	-	6.73	TGCCAA
WASHC5	-1423	-1417	+	5.83	CTGGCA
TRIB1	-1469	-1463	+	5.83	CTGGCA
LRPPRC	-1492	-1486	+	5.83	CTGGCA
SLC3A1	-1460	-1454	+	6.73	TTGGCA
TMX4	-1500	-1494	-	5.83	TGCCAG
C25H9orf43	-1443	-1437	+	5.91	TTGGCT
DESI2	-1490	-1484	+	5.83	CTGGCA
H.R.PU	-1425	-1419	-	5.83	TGCCAG

7 MA0104.2 Mycn 11.1040870395 0.698630136997 -617:-448  
2.92984293472e-09

list of hits

XP.PEP1	-0600	-590	-	5.70	GCCACGTTCC
KAT6B	-0538	-528	-	6.05	GGCATGTGGG
VDAC2	-0606	-596	+	7.42	CCCACGCGGG
DUPD1	-0544	-534	+	5.80	TCCACGTGAT
LOC100068320	-0558	-548	-	6.05	GGCATGTGGG
CPE	-0482	-472	+	6.63	TTCACGTGGT
FOXO3	-0616	-606	-	5.97	GCCCCGTGCG
PPIL6	-0510	-500	+	6.64	GGCACGCGGG
SMPD2	-0466	-456	+	6.17	ACCGCGCGGC
CD164	-0489	-479	+	6.06	GTCACGTGGG
USP36	-0487	-477	+	6.72	CCCACGTGCG
CYTH1	-0544	-534	-	5.82	GCAGCGTGCC
CYTH1	-0479	-469	-	5.69	CGCGCGTGCG
AFMID	-0617	-607	+	5.79	ACCACGGGGC
AFMID	-0568	-558	-	5.56	GCCACGTTGA
GG.BP2	-0552	-542	+	6.20	CCCGCGCGGC
AATF	-0471	-461	+	7.67	TCCACGTGCC

ACACA	-0592	-582	+	7.37	CCCGCGTGCC
ACACA	-0450	-440	-	7.15	GCCTCGTGCC
C15H2orf73		-0559	-549	-	6.20 GCCGCGCGGG
KC.S3	-0586	-576	-	5.95	GCCACATGCC
GE.1	-0490	-480	-	5.69	CGCGCGTGCG
ODC1	-0604	-594	-	6.10	TGCGCGTGCG
HPCAL1	-0510	-500	+	5.92	CCCGCGTGGA
KLF11	-0511	-501	+	7.09	AACACGTGCC
KLF11	-0462	-452	+	7.63	ATCACGCGGC
GRHL1	-0498	-488	+	6.91	GCCACGCGGA
GRHL1	-0483	-473	+	6.91	GCCACGCGGA
ADAM17	-0593	-583	+	7.55	CGCACGCGCC
DCDC2C	-0590	-580	-	6.48	GCCACGTTGG
RYBP	-0587	-577	-	5.65	GGCACGCGCG
PROK2	-0520	-510	+	9.10	AGCACGTGGA
PROK2	-0455	-445	-	7.55	GGCGCGTGCG
ZFP37	-0572	-562	+	8.96	AACACGTGGC
CDC26	-0521	-511	-	5.80	GGCGCGTGAG
ALAD	-0459	-449	+	7.42	CCCGCGCGGG
COL27A1	-0587	-577	+	6.91	TCCACGCGGA
COL27A1	-0530	-520	+	6.50	TCCACGCGCC
AK.A	-0612	-602	+	8.59	CCCGCGTGGG
AK.A	-0599	-589	+	5.55	CCCGCGCGCG
TEX48	-0568	-558	+	5.68	GCCACGCTGC
GRSF1	-0548	-538	+	6.13	GCCACGTGTT
COL11A1	-0617	-607	+	7.27	AGCACGCGTC
SQLE	-0448	-438	-	5.59	GCCGCGTGCG
.SMCE2	-0487	-477	+	6.10	CGCACGCGCA
TRIB1	-0573	-563	-	5.84	GCCACCTGCA
PREPL	-0465	-455	+	6.56	ACCACGCTGC
KLHL29	-0601	-591	-	7.52	GCCACGCGCG
PLCB1	-0569	-559	+	5.70	GGAACGTGGC
TMX4	-0489	-479	+	5.96	CACACGCGCC
TMX4	-0455	-445	+	6.54	CACACGCGGT
C25H9orf43		-0567	-557	+	6.15 CTCACGTTGC
COX20	-0600	-590	+	6.35	CGCGCGCGGC
COX20	-0485	-475	-	7.88	GCCATGTGGT
ZBTB18	-0478	-468	-	9.42	GCCGCGTGCG

8 MA0147.1 Myc 11.157239362 0.685903085415 -617:-455  
3.06174041938e-09

## list of hits

DUSP5	-0467	-457	+	5.91	AGCACACGGA
XP.PEP1	-0600	-590	-	6.63	GCCACGTTCC
KAT6B	-0538	-528	+	5.57	GGCATGTGGG
VDAC2	-0606	-596	+	7.11	CCCGCGCGGG
DUPD1	-0544	-534	-	7.11	TCCACGTGAT
LOC100068320		-0558	-548	+	5.57 GGCATGTGGG
CPE	-0482	-472	+	6.37	TTCACGTGGT
APELA	-0605	-595	+	5.32	TGCATGTGGG
LOC106780946		-0460	-450	+	5.61 CGCCCCGCGGC
PPIL6	-0510	-500	+	7.03	GGCACGCGGG
CD164	-0489	-479	+	5.88	GTCACGTGGG
TIMP2	-0488	-478	-	6.46	GCCAGGTGCG
USP36	-0487	-477	+	6.13	CCCGCGTGCG
CYTH1	-0544	-534	-	5.39	GCAGCGTGCC
CYTH1	-0479	-469	-	5.65	CGCGCGTGCG
SOCS3	-0547	-537	+	5.61	CGCCCCGCGGC
AFMID	-0568	-558	-	5.49	GCCACGTTGA
MYO19	-0574	-564	-	6.11	GCCAGGTGCT
LHX1	-0531	-521	-	6.01	GCCACGGGCC
LHX1	-0485	-475	+	6.46	CGCACCTGGC
AATF	-0471	-461	+	6.39	TCCACGTGCC
ACACA	-0592	-582	+	6.28	CCCGCGTGCC
KC.S3	-0586	-576	-	7.04	GCCACATGCC
GE.1	-0490	-480	-	5.65	CGCGCGTGCG
ODC1	-0604	-594	-	6.27	TGCGCGTGCG
HPCAL1	-0510	-500	+	5.43	CCCGCGTGGA
KLF11	-0511	-501	+	6.81	AACACGTGCC

KLF11	-0462	-452	+	6.60	ATCACGCGGC
GRHL1	-0498	-488	+	6.76	GCCACGCGGA
GRHL1	-0483	-473	+	6.76	GCCACGCGGA
YWHAQ	-0476	-466	+	5.73	ACCCCGTGGC
ADAM17	-0593	-583	+	7.13	CGCACGCGCC
DCDC2C	-0590	-580	-	6.71	GCCACGTTGG
MIR9170	-0544	-534	+	5.49	GGCACTTGGC
PROK2	-0520	-510	+	9.63	AGCACGTGGA
PROK2	-0455	-445	-	7.13	GGCGCGTGCG
ISM1	-0616	-606	-	5.80	CCCATGTGCA
ZFP37	-0572	-562	+	9.16	AACACGTGGC
ALAD	-0459	-449	+	7.11	CCCACGCGGG
COL27A1	-0587	-577	+	6.51	TCCACGCGGA
AK.A	-0612	-602	+	8.47	CCCACGTGGG
AK.A	-0599	-589	-	5.70	CCCACGCGCG
LOC100050034	-0496	-486	-	5.47	TCCACATGTT
LOC100051562	-0512	-502	-	5.47	TCCACATGTT
LOC100050100	-0501	-491	-	5.47	TCCACATGTT
GRSF1	-0548	-538	+	6.35	GCCACGTGTT
JCHAI.	-0539	-529	+	5.91	AAAACGTGGC
COL11A1	-0617	-607	+	7.22	AGCACGCGTC
.SMCE2	-0487	-477	+	6.27	CGCACGCGCA
TRIB1	-0573	-563	-	5.54	GCCACCTGCA
KLHL29	-0601	-591	-	7.18	GCCACGCGCG
PLCB1	-0569	-559	+	6.63	GGAACGTGGC
TMX4	-0489	-479	+	5.80	CACACGCGCC
TMX4	-0455	-445	+	7.41	CACACGCGGT
COX20	-0600	-590	+	5.81	CGCGCGCGGC
COX20	-0485	-475	+	5.42	GCCATGTGGT
ZBTB18	-0478	-468	-	9.48	GCCGCGTGCG

9 MA0003.1 TFAP2A 7.8120920509 0.800000024164 -668:-633  
8.14016173123e-08

## list of hits

DUSP5	-0653	-644	+	6.45	GCCCCCAGC
RBM20	-0658	-649	+	7.05	GCCCTAGGG
ADK	-0652	-643	+	6.28	GCCGTGAGG
COMTD1	-0648	-639	+	7.22	GCCCCAGGG
LOC100067994	-0661	-652	-	6.11	GCGTGCGGC
LOC106780946	-0664	-655	-	6.39	GCCGACGGC
LOC106780946	-0638	-629	-	6.45	CCTCGCGGC
FOXO3	-0661	-652	+	7.25	GCCCTGGGG
SES.1	-0653	-644	+	6.31	GCCCCGCGC
CEP57L1	-0642	-633	-	6.31	GCGCGGGGC
AK9	-0664	-655	-	6.62	CCCTACGGC
CYTH1	-0667	-658	+	6.87	GCCCCGAGC
SOC3	-0658	-649	+	6.57	GCCGCCGGG
SOC3	-0637	-628	-	6.64	CCCGCCGGC
CA4	-0644	-635	+	6.86	GCCGGAGGG
ACACA	-0647	-638	+	6.99	GCCGCGGGG
ACACA	-0634	-625	+	6.34	GCCCAGGGG
SPTB.1	-0663	-654	+	7.29	GCCCGAGGG
ASB3	-0656	-647	+	6.32	GCCTGAAGG
PSME4	-0668	-659	+	7.00	GCCCCCGGG
GE.1	-0645	-636	-	6.47	CCTGGGGGC
ODC1	-0643	-634	+	6.51	GCCTGGAGC
HPCAL1	-0658	-649	+	6.57	GCCTCCGGG
HPCAL1	-0638	-629	-	6.64	CCCGCAGGC
RRM2	-0667	-658	+	6.64	GCCGGCGGG
GRHL1	-0652	-643	-	6.82	GCCGAGGGC
CYS1	-0663	-654	+	6.16	GCCCCCTGGC
CYS1	-0651	-642	+	6.99	GCCCCCGGC
DCDC2C	-0642	-633	+	6.79	GCCGCAGGG
DIPK2A	-0665	-656	-	6.64	CCCGCCGGC
DIPK2A	-0653	-644	+	6.99	GCCCCCGGC
SLC31A2	-0633	-624	+	7.04	GCCTGGGGC
AK.A	-0657	-648	+	6.64	GCCGGCGGG
DCK	-0640	-631	-	6.52	CCTCCAGGC
TRIB1	-0660	-651	+	7.41	GCCCCGGGC



TRIB1	-0649	-640	+	6.86	GCCGGAGGG
C25H9orf43		-0650	-641	+	6.78 GCCTCAGGC
COX20	-0634	-625	-	7.07	CCCGCGGGC

10 MA0076.1 ELK4 14.1232301212 0.5833333336645 -345:-246  
1.34472905636e-07

list of hits

SAMD8	-0342	-333	-	5.68	CCTTCCGGT
SAMD8	-0271	-262	-	8.59	AGTTCCGGT
S.X3	-0311	-302	+	5.76	GCCGGAACC
OSTM1	-0279	-270	+	8.42	GCCGGAAGC
ZBTB24	-0289	-280	-	7.75	GCTTCCGGG
FIG4	-0309	-300	+	6.44	TCCGGAAC
AK9	-0255	-246	+	5.09	CCCGGAACC
USP36	-0247	-238	-	5.73	GTATCCGGC
TMEM235	-0307	-298	+	5.09	CCCGGAACC
AATF	-0296	-287	+	8.52	CCCGGAAGT
CHAC2	-0345	-336	+	5.36	GCCGGAACAA
CHAC2	-0263	-254	-	3.88	ACAGCCGGT
ERLEC1	-0341	-332	+	7.14	CCCGGATGT
ERLEC1	-0317	-308	+	6.44	CCCGGAAC
C15H2orf73		-0254	-245	-	4.69 TTTTCCGGG
RDH14	-0277	-268	+	8.52	CCCGGAAGT
LOC100056590		-0249	-240	+	3.94 ACAGGAAAT
.OL10	-0332	-323	-	6.00	TCTTCCGGG
.OL10	-0314	-305	-	7.11	GTTTCCGGC
.OL10	-0304	-295	+	8.52	CCCGGAAGT
ADAM17	-0327	-318	+	8.42	GCCGGAAGC
ADAM17	-0286	-277	-	7.75	GCTTCCGGG
ADAM17	-0255	-246	-	8.73	TCTTCCGGT
RPS7	-0259	-250	-	8.73	TCTTCCGGT
TRAPPC12		-0345	-336	+	9.17 ACCGGAAC
SHQ1	-0289	-280	+	8.42	GCCGGAAGC
TASP1	-0333	-324	-	8.42	GCTTCCGGC
TASP1	-0247	-238	-	11.25	ACTTCCGGT
LOC100034197		-0282	-273	-	5.25 ACTCCCGGT
LOC100056127		-0257	-248	-	5.25 ACTCCCGGT
FKBP15	-0286	-277	-	3.88	ACATCCCGT
PRPF4	-0320	-311	+	3.94	ACCGCAAAT
ALAD	-0246	-237	-	7.75	GCTTCCGGG
LOC100050034		-0337	-328	+	4.31 ACCGGATGG
LOC100050034		-0276	-267	-	5.25 ACTTCCGTT
LOC100050100		-0342	-333	+	7.35 ACCGGATGA
LOC100050100		-0281	-272	-	5.25 ACTTCCGTT
UTP3	-0304	-295	+	4.77	ACCGGAATC
CAMKMT	-0301	-292	+	9.94	ACCGGAAAT
ABCG5	-0296	-287	-	4.01	TGTTCCGGC

11 MA0162.1 Egr1 14.4555832005 0.739393945445 -663:-597  
8.5752756276e-07

list of hits

KLHL2	-0626	-615	-	4.02	CCGCTCCCGGC
LOC100067994		-0641	-630	+	4.65 ACTGGGGGTGG
LOC106780946		-0601	-590	+	8.52 CGCGGGGCGA
TMEM200C		-0654	-643	+	6.59 TGCGAGGCGG
TMEM200C		-0617	-606	-	6.04 CCGCCCTCGCG
FOXO3	-0632	-621	+	7.48	GGCGGGGAGG
LOC102147786		-0612	-601	+	4.78 TGCCCTGGGAGG
CYTH1	-0626	-615	+	9.06	CGCGGAGGCGG
AFMID	-0633	-622	-	6.50	CCACCCCGGT
ACACA	-0604	-593	-	7.54	CCTCCCCACA
USP32	-0651	-640	+	9.95	CGTGTGGGCGG
USP32	-0602	-591	+	6.04	CGCGGGGCGG
SPTB.1	-0632	-621	+	6.51	TGGGTGGGCGG
PSME4	-0610	-599	-	4.73	CCTCCTCCGGT
ERLEC1	-0617	-606	-	7.06	CCGCTCACACT
C15H2orf73		-0605	-594	+	4.44 CGCCGGGGCGG
GE.1	-0645	-634	+	6.13	CCTGGGGGCGT
SMC6	-0626	-615	-	6.44	TCTCCACACG

ODC1	-0654	-643	+	5.88	CGCGTGCGCGG
ODC1	-0602	-591	+	5.88	CGCGTGCGCGT
HPCAL1	-0660	-649	-	6.60	CCGCCCTCCGGG
KLF11	-0600	-589	-	10.43	CCGCCCCCGCG
GRHL1	-0662	-651	+	4.18	CAAGTGGGCGG
YWHAQ	-0614	-603	+	6.63	CGCGGGAGTGG
CYS1	-0653	-642	-	6.62	CCGCCCCCGGC
ADI1	-0661	-650	-	8.37	CCGCCCCCGTT
ADI1	-0634	-623	-	6.10	ACACCCCCGTC
TRAPPC12		-0612	-601	+	4.78 TGC GTGGCAGG
PROK2	-0630	-619	-	6.79	ACACCCCCGGG
DIPK2A	-0655	-644	-	6.62	CCGCCCCCGGC
ISM1	-0659	-648	-	7.54	CCGCTCCCGCT
LOC100034197		-0662	-651	+	4.21 GATGTGAGCGT
LOC100056127		-0638	-627	+	4.21 GATGTGAGCGG
AK.A	-0615	-604	-	6.52	TCTCCACGTG
LOC100051420		-0597	-586	-	7.48 CCTCCCCCGCC
LOC100050034		-0661	-650	-	4.11 TCACCCCCACC
LOC100051562		-0663	-652	-	7.48 CCTCCCCCGCC
LOC100050100		-0652	-641	-	5.62 CCTCCCCCACC
TRIB1	-0613	-602	+	7.98	CCCGGGGGCGT
ABCG5	-0618	-607	-	4.74	CCACTTACGGA
C25H9orf43		-0658	-647	-	4.59 TCACCTCCGCC
C30H1orf100		-0597	-586	-	4.78 CCACTCCCACG

12 MA0109.1 Hltf 7.46926527425 0.397046551108 -2165:-2133  
1.72088122308e-06

## list of hits

DUSP5	-2164	-2154	+	5.70	GCCCTTATCA
LOC100068208		-2149	-2139	+	6.18 AACCATATGC
LOC100068320		-2138	-2128	-	5.98 TCATAAGGAC
MSMO1	-2156	-2146	+	5.61	ATACATATAG
LOC100066472		-2155	-2145	+	5.73 ATCCATAGAT
LOC100066472		-2141	-2131	-	5.78 GGATAAGGGA
LOC100068026		-2154	-2144	+	5.84 TTCCTTTTAC
LOC100068026		-2154	-2144	+	5.84 TTCCTTTTAC
MICAL1	-2147	-2137	+	5.66	GAACATATCC
WASF1	-2145	-2135	-	5.75	ACCTAAGTTA
CA.T1	-2134	-2124	+	5.76	AACCTTATTG
CYTH1	-2162	-2152	-	5.92	TGAAAAGGTC
C15H2orf73		-2164	-2154	+	5.68 TAACATTTGT
GE.1	-2144	-2134	+	5.75	TAACCTTAGGT
TRAPPC12		-2154	-2144	+	5.66 ACACATATGT
DCDC2C	-2140	-2130	+	5.74	ATACTTTTGC
GXYLT2	-2156	-2146	+	5.68	GTACTTTTCT
SHQ1	-2163	-2153	+	5.76	GACCTTAGAA
GXYLT2	-2156	-2146	+	5.68	GTACTTTTCT
LOC100034197		-2133	-2123	-	6.38 CTATAAGGTT
LOC100056127		-2156	-2146	+	5.81 TAACATATAC
CDC26	-2165	-2155	+	5.75	ACACTTTTAT
PRPF4	-2157	-2147	-	5.87	CTAAAAGGAT
POLE3	-2156	-2146	+	5.63	ATCCATATTT
Z.F618	-2165	-2155	-	5.69	GCCTAAGGTC
ATP6V1G1		-2151	-2141	+	5.77 ACCCTTTTAA
LOC100051420		-2134	-2124	-	6.38 CTATAAGGTT
RUFY3	-2136	-2126	-	5.81	GTAAAAGGTC
DY.C2LI1		-2150	-2140	-	5.71 AGAAAAGGGA
ABCG5	-2138	-2128	+	5.80	AACCTTGTC
PREPL	-2153	-2143	-	5.85	CTAAAAGTTT
PREPL	-2143	-2133	-	5.66	GCAAATGTTT
PLCB1	-2146	-2136	+	5.66	TTCCTTTTAC
C25H9orf43		-2155	-2145	+	6.17 AAACATATGT

13 MA0056.1 MZF1\_1-4 8.58551308885 0.724999990314 -2180:-2114  
2.89031386155e-06

## list of hits

ADD3	-2167	-2161	-	7.05	TCCCCA
KAT6B	-2118	-2112	+	7.05	TGGGGA
DUSP13	-2169	-2163	-	7.05	TCCCCA

COMTD1	-2155	-2149	+	7.05	TGGGGA	
LOC100067994	-2157	-2151	+	7.05	TGGGGA	
LOC100146977	-2156	-2150	-	7.05	TCCCCA	
FOXO3	-2114	-2108	+	7.05	TGGGGA	
FIG4	-2129	-2123	-	7.05	TCCCCA	
RBFOX3	-2174	-2168	-	7.05	TCCCCA	
D.AH17	-2136	-2130	-	7.05	TCCCCA	
CA4	-2145	-2139	-	7.05	TCCCCA	
SPTB.1	-2151	-2145	+	7.05	TGGGGA	
SPTB.1	-2140	-2134	+	7.05	TGGGGA	
CHAC2	-2172	-2166	+	7.05	TGGGGA	
CHAC2	-2162	-2156	+	7.05	TGGGGA	
KC.S3	-2133	-2127	+	7.05	TGGGGA	
RDH14	-2180	-2174	-	7.05	TCCCCA	
.OL10	-2119	-2113	+	7.05	TGGGGA	
GRHL1	-2158	-2152	-	7.05	TCCCCA	
YWHAQ	-2139	-2133	+	7.05	TGGGGA	
CYS1	-2173	-2167	+	7.05	TGGGGA	
CYS1	-2126	-2120	-	7.05	TCCCCA	
PPP4R2	-2175	-2169	-	7.05	TCCCCA	
BSPRY	-2143	-2137	-	7.05	TCCCCA	
KIF12	-2134	-2128	+	7.05	TGGGGA	
COL27A1	-2119	-2113	-	7.05	TCCCCA	
T.FSF8	-2180	-2174	+	7.05	TGGGGA	
TEX48	-2158	-2152	-	7.05	TCCCCA	
GRSF1	-2135	-2129	-	7.05	TCCCCA	
TRIB1	-2165	-2159	-	7.05	TCCCCA	
TRIB1	-2116	-2110	+	7.05	TGGGGA	
C25H9orf43	-2174	-2168	+	7.05	TGGGGA	

14 MA0004.1 Arnt 10.9916749403 0.641666668778 -2118:-1953  
9.70150131415e-06

list of hits

LOC100067994	-2112	-2106	-	6.62	CACGTT	
S.X3	-1953	-1947	-	6.62	CACGTT	
METTL24	-2118	-2112	+	8.00	CACGTG	
DDO	-2085	-2079	+	8.00	CACGTG	
RBFOX3	-2046	-2040	+	6.62	AACGTG	
LGALS3BP	-2084	-2078	-	6.62	CACGTT	
LGALS3BP	-2077	-2071	-	6.62	CACGTT	
TIMP2	-2051	-2045	+	6.62	AACGTG	
CYTH1	-2072	-2066	+	6.62	AACGTG	
MRM1	-2029	-2023	+	8.00	CACGTG	
KC.S3	-2011	-2005	+	8.00	CACGTG	
ODC1	-2110	-2104	+	8.00	CACGTG	
RRM2	-2013	-2007	+	8.00	CACGTG	
TASP1	-1961	-1955	+	6.62	AACGTG	
LOC100056127	-2028	-2022	+	6.62	AACGTG	
HDHD3	-1962	-1956	-	6.62	CACGTT	
RGS3	-1976	-1970	+	6.62	AACGTG	
KIF12	-2044	-2038	-	6.62	CACGTT	
WASHC5	-2079	-2073	+	6.62	AACGTG	
ABCG8	-2028	-2022	-	6.62	CACGTT	
ABCG8	-2017	-2011	+	6.62	AACGTG	
PREPL	-1987	-1981	+	6.62	AACGTG	
COX20	-2092	-2086	+	6.62	AACGTG	

15 MA0035.2 Gata1 10.8778685237 0.372818182556 -2790:-2747  
1.03175348622e-05

list of hits

XP.PEP1	-2786	-2775	+	7.06	GGTGATAAGTG	
VDAC2	-2780	-2769	+	6.12	GGAGATAGAGG	
DUPD1	-2749	-2738	-	8.50	CTCTTATCTAT	
LOC100061588	-2773	-2762	-	6.50	CTTTTATCATA	
LOC100066359	-2756	-2745	+	8.65	TAAGATAAGGA	
EPB41L3	-2752	-2741	-	7.30	CTGTTATCTAT	
RIT2	-2761	-2750	+	8.11	CCAGATAAAGA	
SYT4	-2790	-2779	-	8.32	CCCTTATCAGA	
FIG4	-2748	-2737	+	8.30	CCTGATAAGGA	

SLC22A16	-2758	-2747	-	7.19	TTGTTATCACA
ClQT.F1 -2771	-2760	-	6.35	TTCTAATCTCT	
C15H2orf73	-2752	-2741	-	8.36	TTCTTATCAGG
ADAM17 -2785	-2774	-	8.62	TCTTTATCTCC	
ADAM17 -2761	-2750	-	7.19	TGTTTATCTTA	
SHQ1 -2788	-2777	-	8.62	TGTTTATCTGT	
PROK2 -2748	-2737	+	6.18	CAAGATAGGAA	
SPTLC3 -2748	-2737	+	6.41	ACTGATAATAC	
RGS3 -2754	-2743	-	5.95	ACATTATCTGG	
GRSF1 -2785	-2774	-	7.76	TCCTTATCAAC	
LOC100049851	-2779	-2768	+	6.82	TGAGATAAACT
SQLE -2747	-2736	-	6.41	GTATTATCAGT	
WASHC5 -2787	-2776	-	6.70	TATTTATCTCA	
.SMCE2 -2759	-2748	+	6.12	TAAGATAATAG	
PPM1B -2763	-2752	-	8.11	TCTTTATCTGG	
TMX4 -2785	-2774	-	6.70	TATTTATCTCA	

16 MA0048.1 NHLH1 14.131557299 0.674382714037 -244:-211  
1.38923056368e-05

## list of hits

XP.PEP1 -0231	-219	+	7.69	GATCAGCTGGTC	
SMC3 -0212	-200	+	5.65	AAGCAGGTGAGG	
ADK -0219	-207	+	8.43	CAGCAGCTGAGG	
KAT6B -0243	-231	+	4.95	GGGCAGCTTCTC	
SAMD8 -0242	-230	-	6.94	GCGCGGCTGAGA	
VDAC2 -0213	-201	+	9.13	CCGCAGCTGCAG	
TMEM192 -0214	-202	+	5.11	GCGCAGGTGGAG	
LOC100066444	-0229	-217	-	5.93	CTACAGCTGAGT
S.X3 -0231	-219	+	5.42	TCTCAGCCGGGC	
ZBTB24 -0244	-232	+	5.53	CAGAAGCTGGGG	
METTL24 -0233	-221	+	5.71	GCGCTGCTGCTC	
CYTH1 -0230	-218	+	4.60	GGCCAGGTGCGG	
ACACA -0236	-224	-	4.95	GAGCAGCTTCCC	
ACYP2 -0219	-207	+	4.74	CCCCAGCTGCCC	
VS.L1 -0215	-203	-	6.00	GCGCGCCTGCGC	
LOC100034197	-0239	-227	-	4.70	ATGAAGCTGCTG
LOC100056127	-0214	-202	-	4.70	ATGAAGCTGCTG
SLC31A2 -0211	-199	+	7.32	GAGAAGCTGCGG	
AMBP -0241	-229	+	5.31	TCTCAGCTGCCT	
KIF12 -0224	-212	+	5.12	CCGGAGCTGCTG	
ABCG5 -0220	-208	+	6.87	GAGCAGGTGGGG	
LRPPRC -0237	-225	-	5.42	GCCCTGCTGAGA	
HAO1 -0212	-200	+	5.48	ACGCAGCTTTGA	
CATSPERE	-0238	-226	-	6.04	GCGCTGCTGTGG
CATSPERE	-0224	-212	+	4.88	GCTGAGCTGCGG
DESI2 -0232	-220	-	4.58	CCGAGGCTGCGC	

17 MA0004.1 Arnt 10.9916749403 0.641666668778 -1132:-1054  
1.65716648912e-05

## list of hits

LOC100068208	-1068	-1062	+	6.62	AACGTG
LOC100066501	-1067	-1061	+	6.62	AACGTG
LOC100067994	-1054	-1048	-	6.62	CACGTT
ARMC2 -1114	-1108	+	6.62	AACGTG	
CEP57L1 -1066	-1060	-	6.62	CACGTT	
AATF -1102	-1096	+	8.00	CACGTG	
ODC1 -1116	-1110	+	6.62	AACGTG	
SHQ1 -1060	-1054	-	6.62	CACGTT	
RYBP -1102	-1096	+	8.00	CACGTG	
ALAD -1101	-1095	+	6.62	AACGTG	
ALAD -1075	-1069	-	6.62	CACGTT	
AMBP -1132	-1126	-	6.62	CACGTT	
T.FSF15 -1087	-1081	+	8.00	CACGTG	
LOC100051562	-1126	-1120	+	6.62	AACGTG
RUFY3 -1095	-1089	-	6.62	CACGTT	
LRPPRC -1122	-1116	+	8.00	CACGTG	

18 MA0032.1 FOXC1 6.50807164809 0.4453125 -2707:-2650  
2.067367994e-05

## list of hits

ADD3	-2652	-2644	-	5.72	TACTTTCC
SMC3	-2668	-2660	-	5.54	TACTCACG
KAT6B	-2651	-2643	+	5.43	GGGAAGTA
LOC100066472	-2684	-2676	+	5.54	GCAAAGTA
L3MBTL4	-2686	-2678	-	5.94	TACTTACC
MICAL1	-2677	-2669	+	5.72	GGAAAGTA
CA.T1	-2650	-2642	+	5.54	AGTGAGTA
PIGW	-2653	-2645	-	5.54	TACTCACG
ACACA	-2707	-2699	-	5.72	TACTTACT
SPTLC3	-2662	-2654	+	5.72	GGCAAGTA
CDC26	-2676	-2668	+	5.50	AGAAAGTA
R.F183	-2700	-2692	-	5.54	TACTCACG
HDHD3	-2670	-2662	-	5.54	TACTTAGT
WASHC5	-2704	-2696	-	5.94	TACTTACC
PPM1B	-2694	-2686	-	5.72	TACTTACT
SLC3A1	-2702	-2694	-	5.50	TACTTGCT
COX20	-2684	-2676	+	5.54	ACTAAGTA
ZBTB18	-2677	-2669	-	5.50	TACTTTCT

19 MA0145.1 Tcfcp2l1 11.6502911816 0.609628129495 -252:-218  
2.15932001258e-05

## list of hits

RBM20	-0249	-235	-	5.83	CAGGACCTCACCGG
COMTD1	-0221	-207	+	6.81	CCGGCCTCTTCCTG
MSMO1	-0241	-227	-	5.76	CTGGGAGAGGCAGG
CPE	-0232	-218	+	9.16	GCAGCTCCAGCCAG
D.AH17	-0223	-209	+	5.87	CTAGAAGAGGCCAG
MYO19	-0248	-234	-	5.64	CTGGAGAAAACCGC
PIGW	-0227	-213	+	6.05	CCTGCTCAAGCCTC
GG.BP2	-0227	-213	+	6.09	CCCGCCAGGCCAG
DHRS11	-0229	-215	-	5.94	CAGGATGGAGCCGG
GE.1	-0227	-213	-	6.72	CCGGAAGAGGCAGG
RRM2	-0245	-231	+	5.97	CCTGTCTGAACCGC
CYS1	-0224	-210	-	5.96	CCGGCGGGGCTGG
GXYLT2	-0218	-204	+	5.78	CCTGCTCGCGCTGG
GXYLT2	-0218	-204	+	5.78	CCTGCTCGCGCTGG
LOC100034197	-0243	-229	-	7.30	CAGGATGAAGCTGC
LOC100056127	-0218	-204	-	7.30	CAGGATGAAGCTGC
ALAD	-0252	-238	+	5.65	GCAGCTGCTTCCGG
Z.F618	-0224	-210	-	6.20	CCGGGAGGAGCAGG
AMBP	-0235	-221	-	6.63	CTGCCCTCCAGCAGG
T.C	-0236	-222	+	6.42	CTGGCCACAGCCTG
RUFY3	-0229	-215	-	6.98	CTGGCTCGGACTCG
E.AM	-0223	-209	-	7.13	CTGGTACATACAGG
CAMKMT	-0237	-223	-	7.03	CAGGTCTTGACAGG
LRPPRC	-0235	-221	+	7.56	CCTGCTGAGACCTG
C25H9orf43	-0246	-232	-	6.67	GTGGACTGAGCCGG
ADSS2	-0251	-237	-	6.90	CCGGCGGGGGCAGG

20 MA0125.1 Nobox 9.57325016988 0.25986841647 -3240:-3200  
2.50110282093e-05

## list of hits

SMC3	-3218	-3210	-	6.08	TGCAATTA
SAMD8	-3232	-3224	-	8.20	ACTAATTA
LOC100068320	-3240	-3232	-	8.20	ACTAATTA
LOC100068041	-3214	-3206	-	6.71	AATAATTA
AK9	-3213	-3205	+	8.17	TAATTGCT
SLC22A16	-3213	-3205	+	7.09	TAATTGAT
DHRS11	-3239	-3231	-	6.10	TCTAATTA
ACYP2	-3202	-3194	-	7.09	AACAATTA
CHAC2	-3209	-3201	+	8.20	TAATTAGT
GPR75	-3223	-3215	+	7.79	TAATTACT
C15H2orf73	-3223	-3215	-	7.09	ATCAATTA
YWHAQ	-3234	-3226	-	8.20	ACTAATTA
DCDC2C	-3230	-3222	+	6.44	TAATTAAC
WDR31	-3229	-3221	+	8.31	TAATTGGC
JCHAI.	-3200	-3192	-	6.71	ATTAATTA
R.PC3	-3224	-3216	-	6.06	CTCAATTA

R.PC3	-3205	-3197	-	6.82	GACAATTA
CAMKMT	-3200	-3192	-	6.71	AATAATTA
SLC3A1	-3227	-3219	-	6.06	CTCAATTA

21 MA0139.1 CTF 17.2051081365 0.644893727864 -926:-892  
2.55083011703e-05

list of hits

ADK	-0906	-887	-	7.39	TACCGCTCCCTTCCGGCCC
LOC100068208	-0892	-873	+	5.20	CAACCCCCGGGGGTACAA
LOC100067994	-0919	-900	-	3.75	TTGTTCCCACTTGAGGGAG
AFG1L	-0924	-905	-	4.05	TGCCAGCCTCTTCTGAACA
FOXO3	-0918	-899	-	3.47	GGGGGCCCCCCTCCGCCGGGAG
SES.1	-0907	-888	+	5.50	AGCCCGCCGGAGGGCGGGG
CEP57L1	-0924	-905	-	3.09	CCCCGCCCTCCGCCGCTCC
PPIL6	-0896	-877	+	4.11	TCACCAGCAGTTGAGGCTG
CDC40	-0912	-893	-	5.25	CGCCGCCCCCACC GCCC
SOC3	-0917	-898	+	4.41	GGGCCTCCTGGGGCCGCGA
TMEM235	-0926	-907	+	4.18	GGACCAACAGGGGCCCTGCC
AFMID	-0925	-906	+	7.05	GGGCCACCGGAGGACAGGG
MRM1	-0926	-907	+	5.39	CCCCACTAGGGGCTAGAA
GPR75	-0904	-885	-	4.12	CAATTCTTCTGCTGCAAA
MSG.1	-0905	-886	-	7.30	CACAGCCACCTTGGGGCTA
ODC1	-0919	-900	+	4.27	AGGGCAGAAGGGGCCAGAG
ISM1	-0892	-873	-	3.90	GGCCCCCATCTGGAGCCGG
RGS3	-0920	-901	-	4.47	GTCTTCCCTCTCTGAGAA
AMBP	-0895	-876	-	3.96	CAACTCCACTTCTTGGCTG
AK.A	-0922	-903	+	4.42	GATCCTCCAGAGGCCACGC
LOC100050034	-0904	-885	+	3.77	TGGACTGTTGAGGACACAG
UTP3	-0897	-878	-	5.71	CGGTGCCCTTCTGAGCCAC
SOLE	-0912	-893	-	5.70	TCCTTTCTTCTTCTGGCAA
TRIB1	-0923	-904	-	3.81	CAGCTCCAACCGGAGGTCC
C25H9orf43	-0894	-875	+	3.78	GGCGCGGGAGATGGCGCTC
COX20	-0903	-884	-	4.31	CGCGCCCCGCCCTTGGCAC

22 MA0062.2 GABPA 13.3349243401 0.647453861192 -570:-532  
2.77112231052e-05

list of hits

LOC100061588	-0542	-531	-	7.49	GTCACCTTCCTC
LOC100068208	-0568	-557	-	6.53	GGGGCTTCCTG
KLHL2	-0545	-534	+	4.73	GAGGAAGGGGA
SES.1	-0550	-539	+	5.13	CCGGAATCGGC
SLC22A16	-0553	-542	+	4.54	CCCGAAGCGCC
SLC22A16	-0542	-531	-	6.53	GGGGCTTCCTG
CD164	-0537	-526	-	7.96	ACAACCTCCGC
CYTH1	-0553	-542	+	6.04	CGGGAAGCGGC
DHRS11	-0568	-557	-	6.08	TTCTCTTCCTG
PSME4	-0570	-559	+	11.43	CCGGAAGTGAC
PSME4	-0548	-537	+	6.61	CCGGAACCGCT
KC.S3	-0548	-537	+	5.02	GCGGAACCTACA
MSG.1	-0562	-551	+	4.59	GCGGAAAGGAG
RRM2	-0537	-526	-	5.34	GCCGCTCCCGG
COLEC11	-0559	-548	+	8.64	CAGGAAGTGGT
TRAPPC12	-0535	-524	+	4.72	CAGGAAGAAAA
DCDC2C	-0567	-556	-	5.07	CTCCCTTCCGT
RYBP	-0532	-521	-	4.62	CCCACGTCCGC
POLE3	-0563	-552	+	7.29	CCGAAAAGGC
AMBP	-0564	-553	-	7.35	TCAGCTTCCGC
MOB1B	-0539	-528	-	5.77	CCCACTTCCTT
GRSF1	-0544	-533	-	6.52	CGTGTTTCCGG
E.AM	-0534	-523	-	5.30	GTCATTTCTC
CATSPERE	-0538	-527	-	4.73	ATCACTTACGG
ZBTB18	-0570	-559	-	5.00	GCCGCTTTCGG

23 MA0161.1 NFIC 6.98267924778 0.5685040611 -2359:-2329  
2.89684028946e-05

list of hits

DUSP13	-2359	-2353	-	6.73	TGCCAA
SMPD2	-2337	-2331	+	6.73	TTGGCA
LOC102147786	-2348	-2342	+	6.73	TTGGCA

TMEM235	-2354	-2348	-	6.73	TGCCAA
GG.BP2	-2353	-2347	+	6.73	TTGGCA
PSME4	-2329	-2323	+	6.73	TTGGCA
ISM1	-2354	-2348	-	6.73	TGCCAA
ALAD	-2356	-2350	-	6.73	TGCCAA
T.C	-2357	-2351	-	6.73	TGCCAA
GC	-2348	-2342	+	6.73	TTGGCA
LOC100049851		-2339	-2333	-	6.73 TGCCAA
R.PC3	-2354	-2348	-	6.73	TGCCAA
TRIB1	-2333	-2327	+	6.73	TTGGCA

24 MA0109.1 Hltf 7.46926527425 0.397046551108 -1917:-1878  
3.04110693034e-05

## list of hits

SMC3	-1882	-1872	-	6.03	TCATAAGTAT
RBM20	-1878	-1868	-	5.76	GCATATGGAA
LOC100066444		-1879	-1869	+	5.97 AACCTTAGGA
LOC100066472		-1912	-1902	-	5.66 ACATATGTGT
LOC106780946		-1909	-1899	+	6.42 AACCTTTTGT
CEP57L1	-1881	-1871	+	6.11	TTACTTATAT
ZBTB24	-1883	-1873	+	5.88	AAACATTTGT
E.GASE	-1906	-1896	-	5.69	CTACAAGGTT
LGALS3BP		-1914	-1904	+	5.66 AAACATTTCC
USP36	-1884	-1874	+	6.02	CACCTTATGA
ACACA	-1917	-1907	+	5.66	ATACATTTGT
.OL10	-1903	-1893	-	5.77	ACCTAAGGAA
KLF11	-1883	-1873	+	5.73	AAACATTTAC
ADAM17	-1889	-1879	-	5.76	ATATATGGGA
RPS7	-1881	-1871	+	5.76	TTACTTTTCT
ADI1	-1901	-1891	-	5.74	ACACAAGGTC
PDZR.3	-1913	-1903	+	6.27	AACCTTTTAA
PDZR.3	-1883	-1873	+	6.09	ATCCTTATGG
DIPK2A	-1907	-1897	+	5.83	TCACTTATAT
ZFP37	-1896	-1886	-	5.66	CTAAAAGGAA
PRPF4	-1901	-1891	-	5.84	TTAAAAGGAA
POLE3	-1888	-1878	+	5.69	AACCTTTGGA
POLE3	-1878	-1868	-	5.72	AGACATGGTT
T.FSF8	-1899	-1889	+	5.70	GCCCTTTTAT
T.C	-1892	-1882	-	5.68	TCAAAAGTTC
TEX48	-1912	-1902	-	5.79	ACACAAGTTT
TEX48	-1888	-1878	+	6.00	TTCCTTTTCT
LOC100050100		-1879	-1869	+	6.00 TTCCTTTTGT
GC	-1907	-1897	-	5.97	GGAAAAGTTT
UTP3	-1899	-1889	-	5.79	AGACAAGTTT
SLC4A4	-1916	-1906	+	5.80	AAACTTAGAC
SLC4A4	-1891	-1881	-	5.75	ATAAAAGTAC
LOC100049851		-1891	-1881	+	5.83 TACCTTAGAA
SLC3A1	-1903	-1893	+	5.79	CTCCATATAT
ZBTB18	-1917	-1907	-	5.69	TGCAAAGGTT

25 MA0060.1 NFYA 12.9251246242 0.522629311625 -3255:-3198  
3.13629191277e-05

## list of hits

DUSP13	-3201	-3185	-	4.96	GCTTCCATTGGAGCCT
SAMD8	-3225	-3209	-	6.81	AGGCTTATTGGTCTGT
LOC100068191		-3233	-3217	-	7.39 GTGTTTATTGGCCATC
LOC100066501		-3245	-3229	+	5.26 TTTGGCAAATCAAAAG
MICAL1	-3255	-3239	-	5.42	CTAATGATTGGATATT
ZBTB24	-3239	-3223	-	5.64	GAGTCCATTGGAGGAG
ZBTB24	-3200	-3184	-	9.11	TTTTTCATTGGCTGAA
CD164	-3207	-3191	+	11.49	ATTGGCCAATCAGAAG
D.AH17	-3253	-3237	+	5.34	AGCAGCCGATGAGCCT
MRM1	-3253	-3237	-	6.49	CCCATCATTTGGTCTCT
LHX1	-3200	-3184	-	4.85	CGCTCGATTGGACCAG
ACACA	-3255	-3239	-	4.84	TTTCCCATTTGGGTAC
KLF11	-3235	-3219	+	7.83	TTCGGCCAATAGCATC
WDR31	-3233	-3217	-	8.94	GTCTAATTGGCTGAC
AMBP	-3217	-3201	+	5.58	CTGCCCCAATGGGGTG
COL27A1	-3236	-3220	-	6.29	TCTGTTATTGGATGTT

LOC100051562	-3252	-3236	-	6.12	TAAATCATTGGTCATT
PPM1B	-3224	-3208	+	5.70	GATTACCAATGACCAA
C25H9orf43	-3217	-3201	-	5.55	TCACTCATTTGTCAAC
ZBTB18	-3198	-3182	-	6.11	AACATTATTGGCTCTT