



Jump to: [Multiple Alignment](#) [Motif Tree](#) [Motif Matching](#)

Input file: 20 motifs loaded

Settings: Metric=PCC, Alignment=SWU, Gap-open=1000, Gap-extend=1000, -nooverlapalign

Multiple Alignment=IR, Tree=UPGMA, Matching against: TRANSFAC

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Multiple Alignment

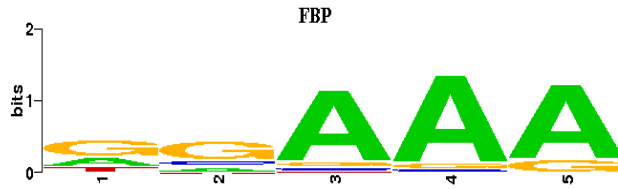
(Consensus sequence representations shown, but multiple alignment was carried out on the matrices)

```

M0 :          GGGGGTGGGGG-----
M1 :          ----AAAAAAAAA-----
M2 :          -----CAAACAAA
M3 :          -----GGRAGGGA--
M4 :          -----TTTAAAA-----
M5 :          -----GAAAGAAA-----
M6 :          -----AGGAAGGA---
M7 :          -----AAGGAAAA-----
M8 :          -----GGGGAGAG----
M9 :          -----AAAACACA-
M10 :         -----CMAAGGAG-
M11 :         ----TCCCAGA-----
M12 :         ----TCTGAGRA-----
M13 :         -----AAATAAAT
M14 :         -----GCAAAGGC--
M15 :         -----AAAGGGSAA
M16 :         -----TATTTAAA-----
M17 :         ----AGGGCTGA-----
M18 :         -----RGGGAAAT-----
M19 :         -----AAAACAAC

```

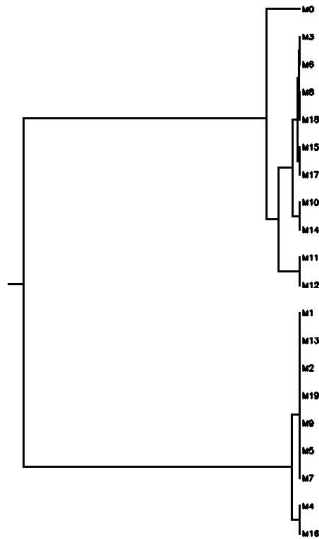
Familial Profile:
[\(click for matrix\)](#)



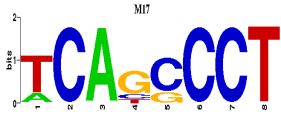



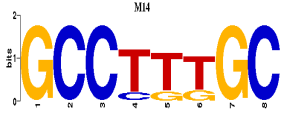











Motif Tree

Tree (drawn by **Phylip**)

[Click here for Newick-format tree \(viewable with MEGA\)](#)

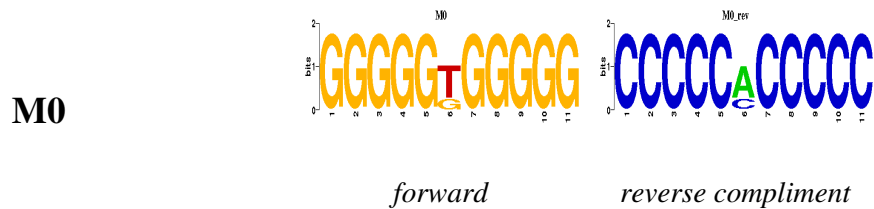


Input Motif	Best match in TRANSFAC
<p>M0</p>	<p>ZNF219_M01122 (E val: 8.4828e-11)</p>
<p>M3</p>	<p>MAZ_M00649 (E val: 3.9536e-09)</p>
<p>M6</p>	<p>Ets_M00971 (E val: 4.6392e-07)</p>
<p>M8</p>	<p>MAZ_M00649 (E val: 6.6442e-07)</p>
<p>M18</p>	<p>STAT1_M00492 (E val: 4.2865e-08)</p>
<p>M15</p>	<p>PBF_M01130 (E val: 3.2142e-06)</p>

 <p>M17</p>	 <p>Dde_M00304 (E val: 5.1823e-06)</p>
 <p>M10</p>	 <p>alpha-CP1_M00687 (E val: 2.7034e-06)</p>
 <p>M14</p>	 <p>LEF1_M00805 (E val: 4.4761e-06)</p>
 <p>M11</p>	 <p>SREBP-1_M00749 (E val: 1.9150e-05)</p>
 <p>M12</p>	 <p>Alx-4_M00619 (E val: 3.2878e-07)</p>
 <p>M1</p>	 <p>STE11_M01005 (E val: 2.4553e-07)</p>
 <p>M13</p>	 <p>Croc_M00266 (E val: 1.8847e-10)</p>
 <p>M2</p>	 <p>HNF3alpha_M00724 (E val: 8.8463e-09)</p>

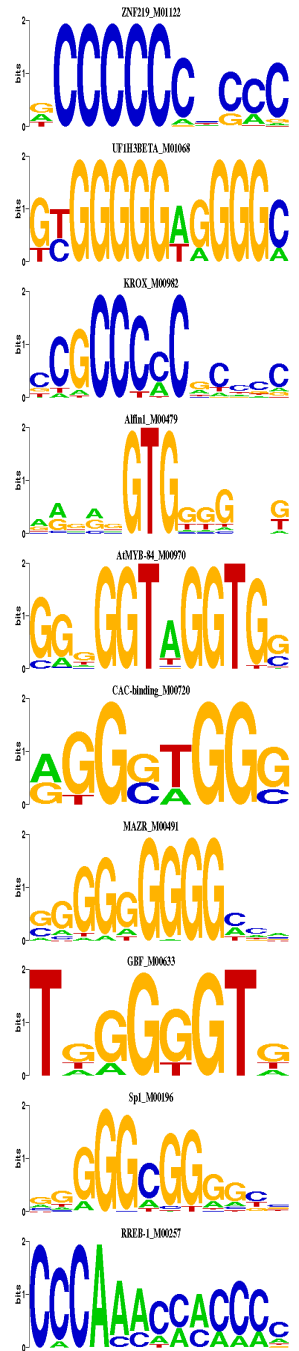
<p>M19</p>	<p>FOXP1_M00987 (E val: 2.0794e-07)</p>
<p>M9</p>	<p>FOXP1_M00987 (E val: 1.7821e-06)</p>
<p>M5</p>	<p>STE11_M01005 (E val: 2.1378e-08)</p>
<p>M7</p>	<p>Helios_M01004 (E val: 1.8061e-11)</p>
<p>M4</p>	<p>MEF-2_M00405 (E val: 9.5438e-08)</p>
<p>M16</p>	<p>avian_M00311 (E val: 4.0122e-08)</p>

Motif Similarity Matches



Name E value Alignment Motif

ZNF219_M01122	8.4828e-11	GGGGGTGGGGG-- -GGNGGGGGGGN
UF1H3BETA_M01068	9.1526e-11	CCCCCACCCTCC-- GCCCTCCCCRC
KROX_M00982	7.0908e-10	GGGGGTGGGGG--- -GNNGNGGGGGCGG
Alfin1_M00479	7.3393e-10	--CCCCCACCCTCC-- MNNCCCCACNYYN
AtMYB-84_M00970	1.6616e-08	GGGGGTGGGGG-- GGNGGTAGGTGS
CAC-binding_M00720	8.0690e-08	CCCCCACCCTCC-- --CCASCCY--
MAZR_M00491	1.0964e-07	GGGGGTGGGGG-- -SGGGGGGGGMNN
GBF_M00633	1.6981e-07	CCCCCACCCTCC-- ----NACCCNA
Sp1_M00196	2.1850e-06	-CCCCCACCCTCC-- NNCCCCGCCCN
RREB-1_M00257	2.6808e-06	--GGGGGTGGGGG GGGGTGGTTTGGG



M3



forward


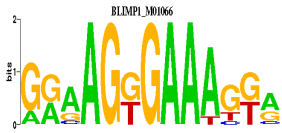


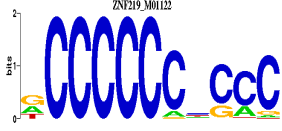



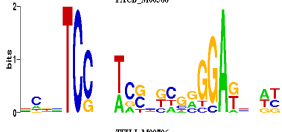

reverse complement

Name

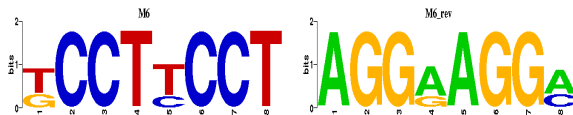
E value

Alignment

Motif

MAZ_M00649	3.9536e-09	TCCCTYCC -CCCTCCC	
BLIMP1_M01066	1.7848e-08	-----TCCCTYCC YMCTTTCMCTTYC	
UF1H3BETA_M01068	8.5527e-06	-TCCCTYCC----- GCCCTCCCCRC	
Sp3_M00665	6.7152e-05	-----GGRAGGGA SMCTTGGSRRGG-	
ZNF219_M01122	9.8320e-05	GGRAGGGA--- GGNGGGGGGN	
Tra-1_M01048	1.1530e-04	TCCCTYCC -ACCWCCC	
Sp1_M00933	1.9981e-04	--GGRAGGGA NGGGGMGG-	
c-Ets-1_M00339	2.0732e-04	----TCCCTYCC-- NNMNNNACTTCTG	
FACB_M00388	2.7417e-04	-----GGRAGGGA----- NNNNMTCCNNNNNSNANNGGANNNN	
TFII-I_M00706	2.8604e-04	--TCCCTYCC CCTMCNTC--	

M6



forward








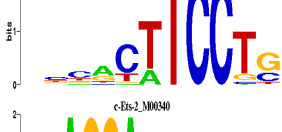


reverse complement

Name

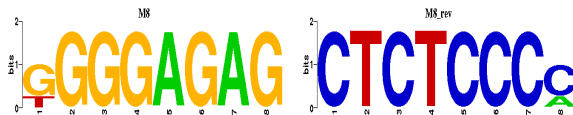
E value

Alignment

Motif

Ets_M00971	4.6392e-07	-AGGAAGGA NAGGAAG--	
Tel-2_M00678	5.8506e-07	-AGGAAGGA CAGGAAGTA	
PU.1_M00658	6.2041e-07	TCCTTCCT- --CTTCCTC	
PEA3_M00655	2.2421e-06	AGGAAGGA MGGAWG--	
c-Ets-1_M00743	3.2659e-06	TCCTTCCT -GCTTCCK	
TFII-I_M00706	1.9366e-05	TCCTTCCT- -CCTMCNTC	
GCR1_M00046	3.8978e-05	-AGGAAGGA GWGGAAGC-	
Ets_M00771	7.0099e-05	-AGGAAGGA-- CAGGAAGYNNN	
c-Ets-2_M00340	9.1291e-05	--AGGAAGGA--- RCAGGAAGTNNNT	
MAZ_M00649	2.0413e-04	TCCTTCCT CCCTCCC-	

M8



forward

reverse complement

Name

E value

Alignment

Motif

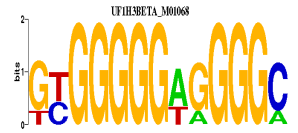
MAZ_M00649 6.6442e-07

CTCTCCCC
CCCTCCC-



UF1H3BETA_M01068 4.4895e-06

--CTCTCCCC--
GCCCTCCCCRC



Lyf-1_M00141 2.8132e-05

CTCTCCCC-
-YCTCCCAA



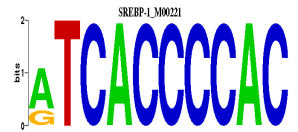
Sp1_M00933 1.1217e-04

-GGGGAGAG
NGGGGMGG



SREBP-1_M00221 1.3747e-04

--GGGGAGAG
GTGGGTGAT



Nrf-2_M00108 1.7707e-04

CTCTCCCC-
SNCTTCCGG



MZF1_M00083 2.5381e-04

CTCTCCCC--
---TCCCCNN



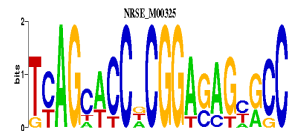
Sp3_M00665 3.3581e-04

CTCTCCCC-----
CCCYSCCAAGKS



NRSE_M00325 4.9339e-04

----CTCTCCCC-----
GGCRCTCTCCGNGGTGCTGA



Sp1_M00196 1.0685e-03

---CTCTCCCC-
NNCCCCGCCCN



M18



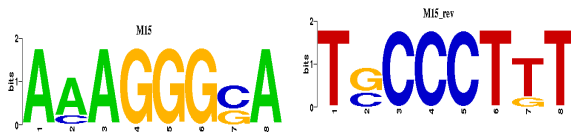
forward



reverse complement

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STAT1_M00492	4.2865e-08	RGGGAAAT -SGGAANT	
BLIMP1_M01066	4.7937e-06	---RGGGAAAT-- GRAAGKGAAAGKR	
NF-kappaB_M00052	1.1648e-05	RGGGAAAT--- --GGAAANTCC	
STAT3_M00225	1.7000e-05	-----RGGGAAAT--- NNNCATTTCCSGGAAATNNN	
MAF_M00648	2.1318e-05	--RGGGAAAT----- NGRRGGAAGTKKNSN	
STAT1_M00224	4.1814e-05	----ATTTCCTY----- NSNCANTTCCCGGAANNNNN	
E2F_M01114	4.5247e-05	ATTTCCTY-- NTTTCCTCGCN	
RBP-Jkappa_M01112	1.5560e-04	ATTTCCTY--- -KTTCCACGN	
c-Rel_M00053	1.9400e-04	RGGGAAAT--- --GGAAWNYCC	
Nanog_M01123	2.1613e-04	RGGGAAAT----- --GGMAATGGNCC	

M15

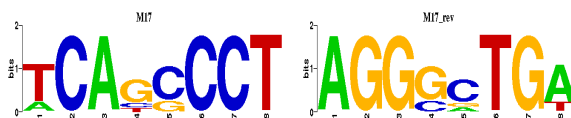


forward

reverse compliment

Name	E value	Alignment	Motif
PBF_M01130	3.2142e-06	TSCCCTTT ---CCTTT	
PPAR_M00528	9.9015e-06	TSCCCTTT----- TGACCTTTGNCCNNNN	
PPAR,_M00762	1.0970e-05	TSCCCTTT---- TGACCTTTGNCC	
KR_M01089	3.4362e-05	--AAAGGSA- NNAAAGGTNN	
PPARgamma-RXRalpha_M00512	3.7094e-05	----TSCCCTTT----- NNNNTGACCTTTGACCYCNN	
PPARalpha-RXRalpha_M00242	5.6434e-05	TSCCCTTT----- TGACCTTTGNCCCTAGWTYW	
HNF4alpha1_M00411	5.6488e-05	-TSCCCTTT----- NTGACCTTTGNCCY	
SED_M01128	6.0706e-05	-AAAGGSA NAAAGNNNA	
HNF4_M00134	1.0389e-04	---TSCCCTTT----- NNNTGNMCTTTGNNCYNN	
COUPTF_M01036	1.3617e-04	-----AAAGGSA----- NKNNRNGKNNAAAGGTCANNNN	

M17

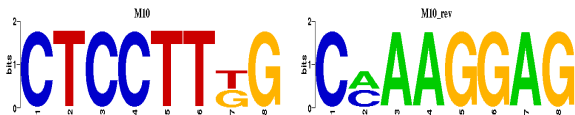


forward

reverse compliment

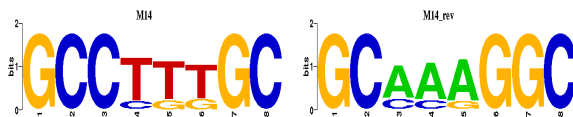
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Dde_M00304	5.1823e-06	AGGGCTGA-- --GGCTGAGC	
ZBRK1_M01105	3.7071e-05	--AGGGCTGA---- AAANNCTGCKSCC	
SREBP-1_M00221	8.1864e-05	-AGGGCTGA- GTGGGGTGAT	
SREBP_M00776	2.2898e-04	---TCAGCCCT NNNTCACCCYA	
CDC5_M00361	2.6784e-04	--TCAGCCCT SCTCAGCGSN	
TBX5_M01044	3.7852e-04	-AGGGCTGA AAGGTGTGA	
SZF1-1_M01109	4.2306e-04	AGGGCTGA----- -CNGCTGWTACCCTG	
bZIP910_M00357	5.9885e-04	---TCAGCCCT ACGTCAGCAYS	
LMAF_M01139	9.1644e-04	AGGGCTGA- -CTGCTGAS	
CAC-binding_M00720	2.1494e-03	-TCAGCCCT CCCASCCY-	

M10



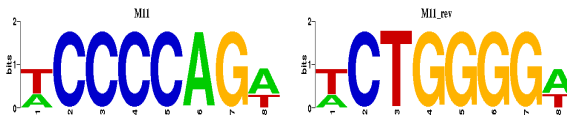
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
alpha-CP1_M00687	2.7034e-06	CTCCTTKG-- CTCATTGGCT	
LEF1_M00805	5.1130e-05	CTCCTTKG ---CTTGG	
PBF_M01130	6.3640e-05	CTCCTTKG --CCTT-	
LUN-1_M00480	6.9255e-05	---CMAAGGAG----- TCCCAAAGTAGCTGGG	
COUP_M00765	6.2145e-04	----CMAAGGAG GGGNCAAAGGTC	
PPAR_M00763	6.9591e-04	----CMAAGGAG NGGNCAAAGGTC	
PPAR,_M00762	7.0363e-04	---CMAAGGAG- GGNCAAAGGTCA	
TFIIA_M00707	1.0553e-03	--CMAAGGAG- MTNNRAGGRNS	
STE11_M01005	1.3355e-03	CTCCTTKG--- TTTCTTTGTTC	
HNF4alpha1_M00411	1.5391e-03	--CTCCTTKG---- NTGACCTTTGNCCY	


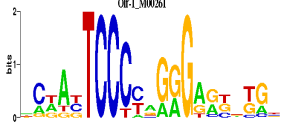








M14



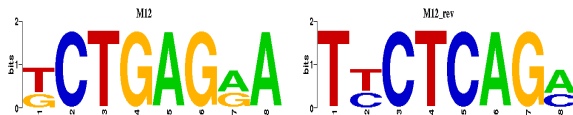
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LEF1_M00805	4.4761e-06	GCCTTTGC --CTTTG--	
PBF_M01130	6.1626e-06	GCCTTTGC -CCTTT--	
PPAR_M00528	9.5805e-06	--GCCTTTGC----- TGACCTTTGNCCNNNN	
HNF4alpha1_M00411	1.3131e-05	---GCCTTTGC--- NTGACCTTTGNCCY	
HNF4_M01031	1.9746e-05	--GCAAAGGC--- GNNCAAAGKYCAN	
COUPTF_M01036	5.0284e-05	-----GCAAAGGC----- NKNNRNGKNNAAAGTCAANNNN	
COUP_M00765	7.7962e-05	-GCCTTTGC--- GACCTTTGNCCC	
PPAR,_M00762	1.0780e-04	--GCCTTTGC-- TGACCTTTGNCC	
PPAR_M00763	1.3156e-04	---GCAAAGGC- NGGNCAAAGGTC	
ARP-1_M00155	1.7690e-04	--GCCTTTGC----- GARCCYTTGAMCCYW	











M11



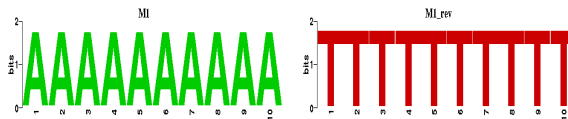
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SREBP-1_M00749	1.9150e-05	TCTGGGGA --TGGSGT	
Olf-1_M00261	2.9874e-05	-----TCTGGGGA----- NCMNNYTCCCNRRGGANTNGN	
MIG1_M00061	7.5110e-05	-TCCCCAGA----- NNCCCCRSNTTTWNN	
BRK_M01096	2.0178e-04	TCTGGGGA -NTGGCG-	
EBF_M00977	2.0690e-04	--TCTGGGGA NCYCWRGGGA	
AP-2_M00915	2.2176e-04	--TCCCCAGA-- NNNCCNCNGGCN	
MZF1_M00083	5.0169e-04	TCCCCAGA TCCCCNN-	
SREBP-1_M00221	9.3126e-04	TCTGGGGA--- -GTGGGGTGAT	
STAT_M00777	1.0241e-03	TCCCCAGA----- -TCCNAGAANNNN	
GBF_M00633	1.2206e-03	--TCCCCAGA NACCCNA--	

M12



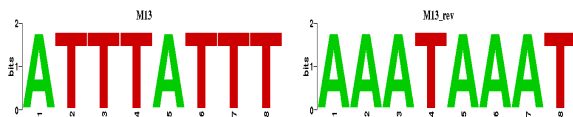
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Alx-4_M00619	3.2878e-07	-----TYCTCAGA GATTATTCTCAG-	
Dde_M00304	1.2850e-04	TYCTCAGA- -GCTCAGCC	
CDC5_M00361	8.7487e-04	TYCTCAGA--- -SCTCAGCGSN	
STAT_M00777	9.3528e-04	TYCTCAGA----- -TCCNAGAANNNN	
GATA-1_M00346	2.2813e-03	--TYCTCAGA NNTTATCNN-	
AP-1_M00173	2.8622e-03	--TYCTCAGA NTGACTNMNW	
MAF_M00983	2.9368e-03	--TYCTCAGA NTGACTCANC	
NF-E2_M00037	3.1296e-03	TCTGAGRA-- GCTGAGTCAY	
XPF-1_M00684	3.7179e-03	--TYCTCAGA GKTSNYCNG-	
Ik-3_M00088	5.4799e-03	TCTGAGRA---- NYNGGGAATACC	

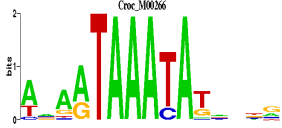








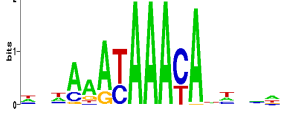
M1



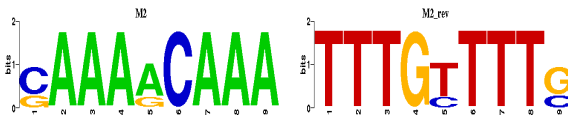
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	2.4553e-07	TTTTTTTTTT- TTTCTTTGTTT	
FOXP1_M00987	5.4934e-07	AAAAAAAAAA----- ATAAAAAACAACACAAATA	
HFH1_M00129	4.6005e-06	-TTTTTTTTTT AWGTTTATWT	
FOXD3_M00130	4.8858e-06	-TTTTTTTTTT AWGTTTNTTT	
STE11_M00274	8.0941e-06	-----AAAAAAAA-- WNNNNAACAAAGAAANW	
Antp_M01084	9.0724e-06	-TTTTTTTTTT NTWATKNNTWT	
HSF_M00163	1.3117e-05	-AAAAAAAAAAA--- GAANAGAANAGAAN	
Hb_M00022	1.7080e-05	-TTTTTTTTTT NTTTTTNYK--	
BR-C_M00091	1.9985e-05	-----TTTTTTTTTT--- NNNWYTTGYTATNANN	
FOX_M00809	2.4352e-05	-AAAAAAAAAAA- WAAAYAAACANT	




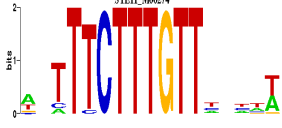






M13



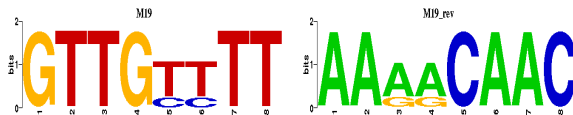
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Croc_M00266	1.8847e-10	-----ATTTATTT- NNNNMTATTTATNT	
POU1F1_M00744	1.0935e-07	ATTTATTT- WTTTATNCA	
Lentiviral_M00318	1.4526e-07	AAATAAAT -AATAAAG	
TBP_M00471	1.8156e-07	AAATAAAT- --ATAAATW	
HFH1_M00129	2.1963e-07	---ATTTATTT AWTGTTTATWT	
HFH3_M00289	2.4693e-07	---ATTTATTT- NNRTRTTTRWTN	
HNF3beta_M00131	3.2719e-07	-AAATAAAT----- WAARYAAAYANTNC	
Freac-3_M00291	3.3493e-07	-ATTTATTT----- TGTTTATTTACNNN	
HNF6_M00639	6.6661e-07	--ATTTATTT- NTATTGATTTN	
FOXJ2_M00422	6.7850e-07	-----ATTTATTT--- NNNNNTGTTTATTTNN	

M2



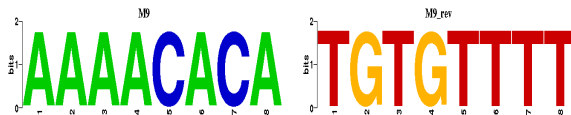
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HNF3alpha_M00724	8.8463e-09	CAAAACAAA- NWRARCAAAY	
SOX_M01014	2.6364e-07	--TTTGTTTTG- TCTTTGTTANGN	
HFH4_M00742	9.5858e-07	CAAAACAAA---- -TAAACAAACAMW	
STE11_M00274	1.7447e-06	-----TTTGTTTTG-- WNTTTCITTTGTTNNNNW	
SRY_M00148	2.3678e-06	CAAAACAAA ---AACANM	
FOX_M00809	2.8454e-06	----TTTGTTTTG ANTGTTTRITTW-	
FOXD3_M00130	1.0405e-05	CAAAACAAA---- --AAANAAACAWT	
HFH3_M00289	1.4066e-05	CAAAACAAA---- -NAWAYAAAYANN	
FOXP1_M00987	1.9172e-05	-----CAAAACAAA-- ATAAAAAACAACACAAATA	
BR-C_M00094	2.5296e-05	--CAAAACAAA- WWRTAASAWAA	

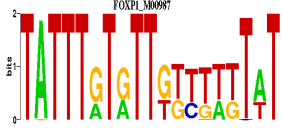
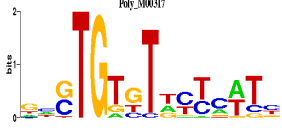

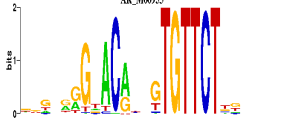



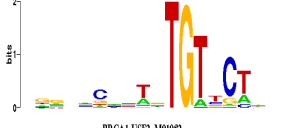
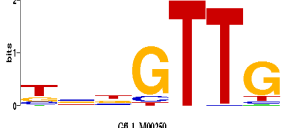
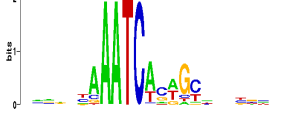
M19



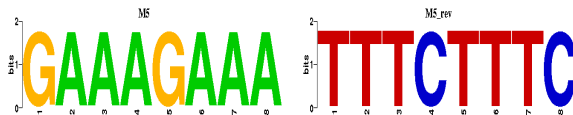
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
FOXP1_M00987	2.0794e-07	-----GTTGTTTT----- TATTTGTTGTTTTTTTAT	
FOXO4_M00476	2.8400e-07	----AAAACAAC-- NANGTAAACAACN	
HNF3alpha_M00724	2.4133e-06	-AAAACAAC- NWRARCAAAY	
ID1_M01021	2.7681e-06	AAAACAAC-- AWAASGACAA	
FOXP3_M00992	3.7385e-06	----AAAACAAC----- NTMTGNNAACNNNW	
MEF-2_M00006	3.9374e-06	----AAAACAAC--- TCTAAAATAACYCY	
MEF-2_M00406	5.4311e-06	----AAAACAAC--- KCTAAAATAACCCN	
Mat1-Mc_M00276	2.8944e-05	--GTTGTTTT CNATTGTYN-	
core-binding_M00722	3.3858e-05	GTTGTTTT GTGGTNW-	
FOXO3A_M01137	4.4692e-05	--GTTGTTTT- NNNTTGTITAY	











M9



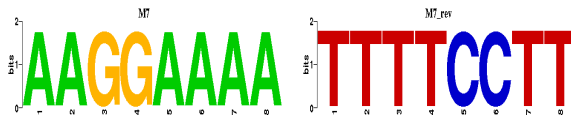
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
FOXP1_M00987	1.7821e-06	-----AAAACACA----- ATAAAAAACAACACAAATA	
Poly_M00317	6.7081e-06	---TGTGTTTT--- NNSGTGKTNYMWTN	
HFH4_M00742	1.0603e-05	TGTGTTTT--- WKTGTTTGTTTA	
AR_M00953	1.9883e-05	-----AAAACACA----- NNNNNNAGAACACNNTGTNCYNNNNN	
AML_M00769	3.4660e-05	--AAAACACA--- NNWRACCACANNNN	
HNF3alpha_M00724	3.7192e-05	-AAAACACA- NWRARCAAAY	
core-binding_M00722	3.8180e-05	TGTGTTTT -GTGGTNW	
GR_M00192	5.3141e-05	--AAAACACA----- NNAGNACANWNNNNNNNN	
BRCA1-USF2_M01082	1.1080e-04	AAAACACA -CAACNNN	
Gfi-1_M00250	2.2788e-04	-----TGTGTTTT----- NNNNNNNRCWNTGATTTNNNNNN	



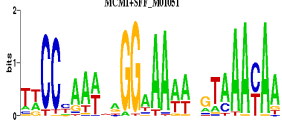

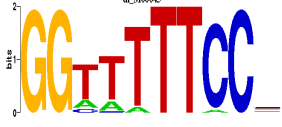





M5



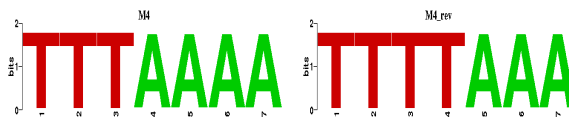
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	2.1378e-08	TTTCTTTC--- TTTCTTTGTC	
STE11_M00274	3.9973e-07	-----GAAAGAAA-- WNNNNAACAAAGAAANW	
Rim101p_M01030	1.5075e-06	TTTCTTTC TTNCTTG-	
HSF_M00163	5.6859e-06	-GAAAGAAA----- GAANAGAANAGAAN	
HSF_M00164	5.6859e-06	-GAAAGAAA----- GAANAGAANNITCT	
BPC1_M01126	1.4372e-05	TTTCTTTC ---NTTTC	
BR-C_M00094	1.8167e-05	-TTTCTTTC--- TTWSTTTAYWW	
PEND_M01015	1.4491e-04	GAAAGAAA- --AGAAGT	
SRY_M00148	3.1174e-04	GAAAGAAA --AACANM	
HFH4_M00742	3.4180e-04	GAAAGAAA----- TAAACAAACAMW	

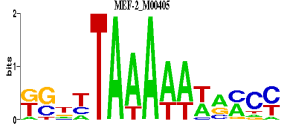

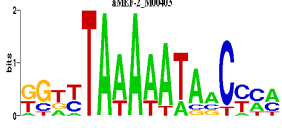

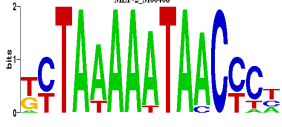




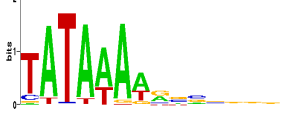
M7



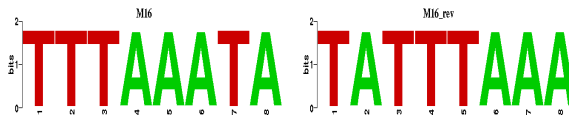
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Helios_M01004	1.8061e-11	-TTTTCCTT- NTTTCCTWN	
AG_M01133	3.0607e-07	-----AAGGAAAA TWNCAAAAAWGGNAAN	
MCM1+SFF_M01051	6.2552e-06	-----AAGGAAAA----- TNCNAAWNNGGNAAWANNNTAAAYAA	
BLIMP1_M01066	9.8459e-06	--AAGGAAAA-- GRAAGKGAAAGKR	
dI_M00043	1.4825e-05	AAGGAAAA--- -NGGAAAAACC	
ID1_M01021	7.3578e-05	--AAGGAAAA AWAASGACAA	
HSF_M00163	7.6010e-05	--AAGGAAAA----- GAANAGAANAGAAN	
STE11_M01005	1.7979e-04	TTTTCCTT---- -TTCCTTGTTC	
dI_M00120	1.9333e-04	---TTTTCCTT NGNTTTCYC-	
Ets_M00971	1.9799e-04	AAGGAAAA NAGGAAG-	


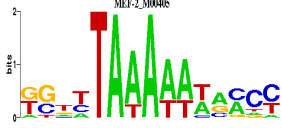


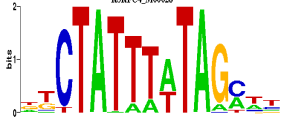
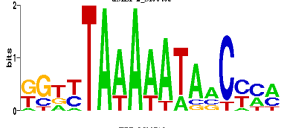

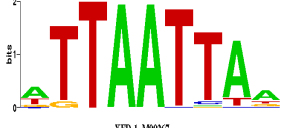

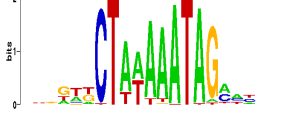
M4



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MEF-2_M00405	9.5438e-08	-----TTTTAAA-- RGKNWTTTTTANNM	
TATA_M00216	6.1097e-07	-TTTTAAA- NTTTTATAG	
aMEF-2_M00403	8.4162e-07	-----TTTTAAA-- KKRGNTATTTTTARNM	
Abd-B_M01094	8.4859e-06	TTTTAAA TTTTAT-	
MEF-2_M00406	1.0591e-05	-----TTTTAAA NGGGTTATTTTTAGM	
Nkx6-1_M00424	1.5888e-05	TTTTAAA----- WTTTAATTGNTT	
MEF-2_M00006	2.4566e-05	-----TTTTAAA RGRGTTATTTTTAGA	
Cdc5_M00478	1.0457e-04	---TTTTAAA- NTAYGTTAAMN	
Muscle_M00320	1.7409e-04	-----TTTTAAA-- SSNNNNGNTTTATANN	
TATA_M00252	1.7957e-04	TTTTAAA----- TATAAAWRNNNNNN	

M16



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
avian_M00311	4.0122e-08	-TTTAAATA GCTTAWATA	
MEF-2_M00405	1.3006e-06	-----TATTTAAA-- RGKNWTTTTTANNM	
GT-1_M00635	3.8240e-06	TATTTAAA TWTNNA--	
TEF_M00672	9.8571e-06	-TATTTAAA-- TTATNTNANCA	
RSRFC4_M00026	1.1864e-05	----TTTAAATA---- NNKCTATAAATAGMN	
aMEF-2_M00403	1.3081e-05	-----TATTTAAA-- KKRGNATTTTTARNCM	
TBP_M00713	1.3168e-05	TATTTAAA- -ATATAAAN	
Lhx3_M00510	3.0435e-05	TTTAAATA- WTTAATTAN	
XFD-1_M00267	3.1042e-05	-TTTAAATA---- AWGTAAATAWWRY	
MEF-2_M00232	4.0632e-05	-----TTTAAATA----- NNNNWKCTAWAAATAGMNNNN	

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