

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

Input file: 58 motifs loaded

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

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

Note: All results files are removed nightly at midnight EST. Please save your results by saving "Webpage, complete".

[Download results as a PDF](#)

[Click here to run STAMP again.](#)

Multiple Alignment

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

```

M0 : -----AAAGAAAAAAAAAAAAAAAAAAAA
M1 : ----TTTTTAAAAA-----
M2 : TGTGTGTGTGTG-----
M3 : -----GGGAGGGAGG-----
M4 : -----AAAGAAAGAAAA-----
M5 : -----AAAAAGAAAAG-----
M6 : -----CCCCAGCCC-----
M7 : ---GGGGCGGGGC-----
M8 : -----AAGGAAAAAAAA-----
M9 : -----GAAGGAAGC-----
M10 : -----CAGAGGCAG-----
M11 : -----AAAAACAAAACAAAA-----
M12 : ----AAACAAACAAA-----
M13 : -----AGGAGGMAG-----
M14 : -----TGGGAAAGA-----
M15 : -----GGGAGGGGGMGGGG-----
M16 : -----AAAACAAAACAAAA-----
M17 : -----AGGAGACAG-----
M18 : -----TATGCAAATG-----
M19 : -----GAGGAAAGA-----
M20 : -----GGGGYGGAG-----
M21 : -----GCGCAKCGC-----
M22 : -----GGAGGAG-----

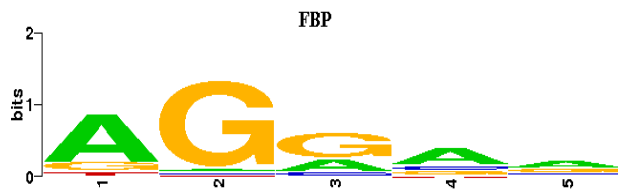
```

Stamp Results

04/30/14

M23: -----CCCAGCCC-----
M24: -----AGAGARAG-----
M25: -----GGGAAGG-----
M26: -----AGAAGAAA-----
M27: -----AGAAAAG-----
M28: -----AGGCAGA-----
M29: -----CAGAGCAG-----
M30: -----GGAGGCTG-----
M31: -----GGGAGAG-----
M32: -----TGCAGRG-----
M33: -----GCCCAGG-----
M34: -----GGCGGCGG-----
M35: -----SCAGGCAG-----
M36: -----AGAAAAAG-----
M37: -----TGGGGAG-----
M38: -----CAGGAAA-----
M39: -----AAATAAAT-----
M40: -----AGGMCAG-----
M41: -----GGGTGTG-----
M42: -----ATTAAAA-----
M43: -----AAATATTT-----
M44: -----SAGAAGCC-----
M45: -----GCCAGAGC-----
M46: -----CTGAGGAA-----
M47: -----GNGCTCAG-----
M48: -----MAAGGAGG-----
M49: -----ACCCAGA-----
M50: -----GCAGGGAC-----
M51: -----CTGAAAGG-----
M52: -----GGGAAAA-----
M53: -----GGCAGAAG-----
M54: -----CAGRGTCC-----
M55: -----CAGGTGAG-----
M56: -----AGAAACTT-----
M57: -----TGTCTGGR-----

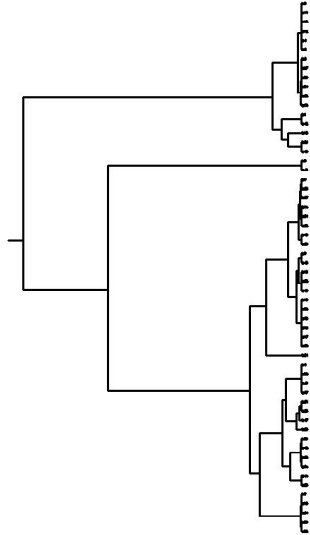
Familial Profile:
[\(click for matrix\)](#)



Motif Tree

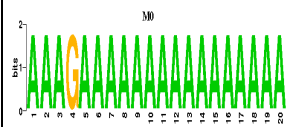


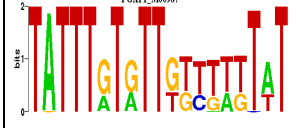

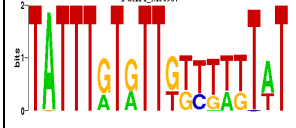






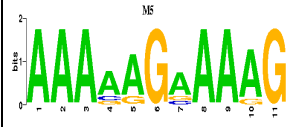

Tree (drawn by **Phylip**)

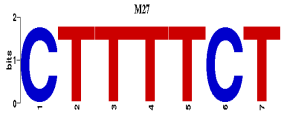

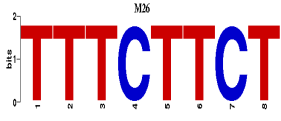

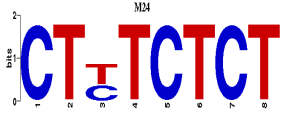
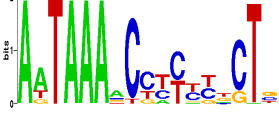

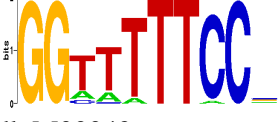



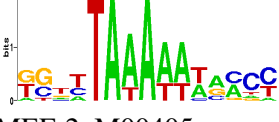




[Click here for Newick-format tree \(viewable with MEGA\)](#)


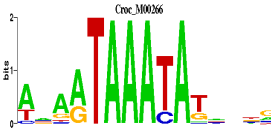

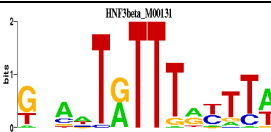



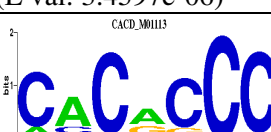
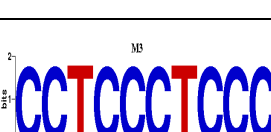


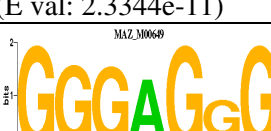

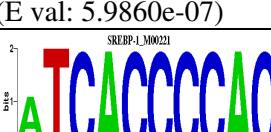
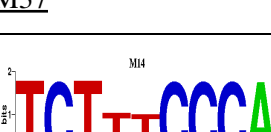





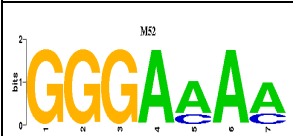

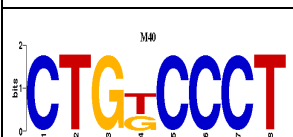

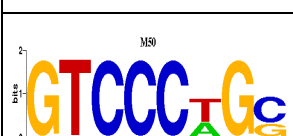





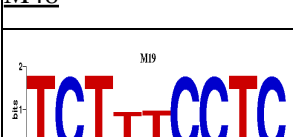
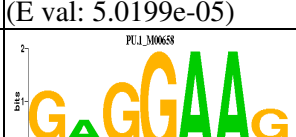


Input Motif

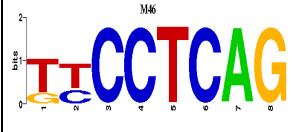

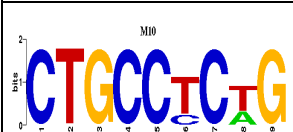
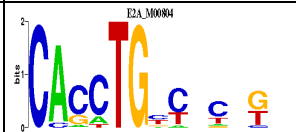



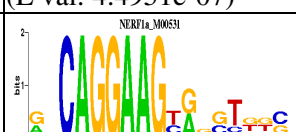
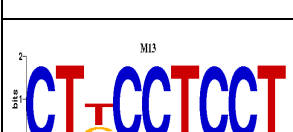
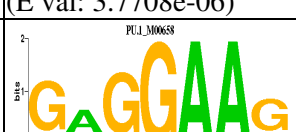




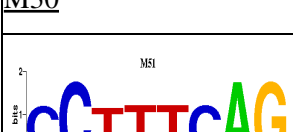

Best match in TRANSFAC








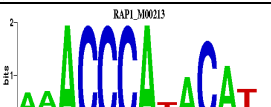



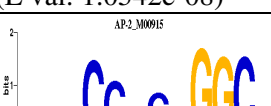



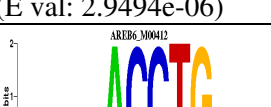
 <p>M0</p>	 <p>FOXPL_M00987 (E val: 2.4128e-08)</p>
 <p>M11</p>	 <p>FOXPL_M00987 (E val: 1.5239e-12)</p>
 <p>M16</p>	 <p>FOXPL_M00987 (E val: 1.6808e-11)</p>
 <p>M12</p>	 <p>HFH4_M00742 (E val: 9.9920e-16)</p>
 <p>M4</p>	 <p>STE11_M01005 (E val: 2.0663e-09)</p>
 <p>M8</p>	 <p>Helios_M01004 (E val: 5.9779e-08)</p>
 <p>M5</p>	 <p>HSF_M00163 (E val: 3.2114e-11)</p>

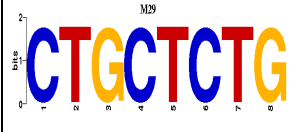
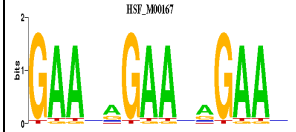
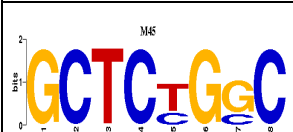
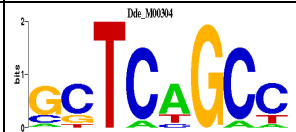


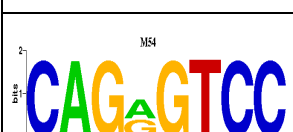

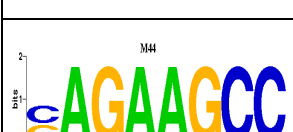
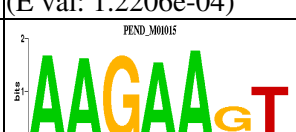
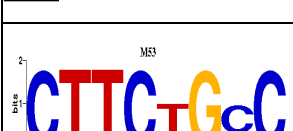
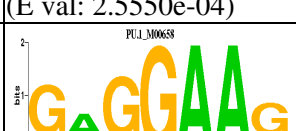
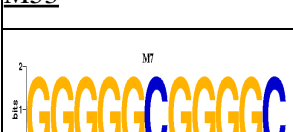
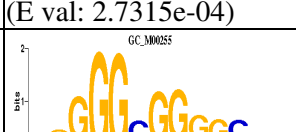
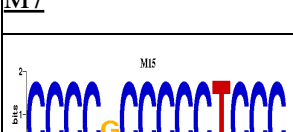
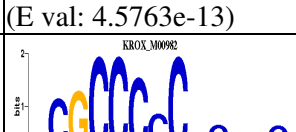
<p>M27</p>  <p>CTTTTTCT</p>	<p>HSF_M00163</p>  <p>GAAAGAAAGAA</p> <p>HSF_M00163 (E val: 8.5599e-08)</p>
<p>M26</p>  <p>TTTTCTTCT</p>	<p>Rim101p_M01030</p>  <p>CAAGAA</p> <p>Rim101p_M01030 (E val: 1.5075e-06)</p>
<p>M24</p>  <p>CT-TCTCT</p>	<p>Retroviral_M00212</p>  <p>CT-TCTCT</p> <p>Retroviral_M00212 (E val: 1.7006e-05)</p>
<p>M36</p>  <p>AGAAAAAG</p>	<p>d1_M00043</p>  <p>GGTTTTC</p> <p>d1_M00043 (E val: 1.7481e-05)</p>
<p>M56</p>  <p>AGTTTCT</p>	<p>HSF1_M01023</p>  <p>TTCTTCT</p> <p>HSF1_M01023 (E val: 1.9223e-07)</p>
<p>M1</p>  <p>TTTTAAAAA</p>	<p>MEF-2_M00405</p>  <p>TTTTAAAAA</p> <p>MEF-2_M00405 (E val: 2.9868e-07)</p>
<p>M42</p>  <p>ATTAAAAA</p>	<p>Nkx6-1_M00424</p>  <p>TTTAAAAA</p> <p>Nkx6-1_M00424 (E val: 2.1085e-07)</p>
<p>M18</p>  <p>TATGCAAATG</p>	<p>OCT-x_M00210</p>  <p>TATGCAATG</p> <p>OCT-x_M00210 (E val: 1.1102e-16)</p>

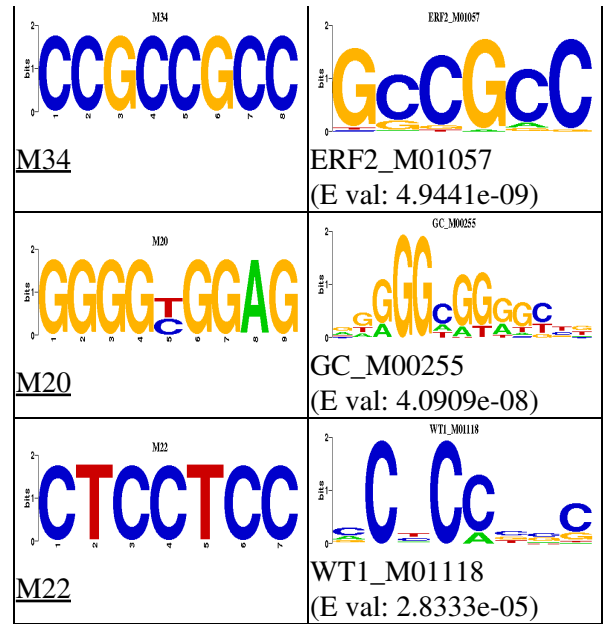
 <p>M39</p>	 <p>Croc_M00266 (E val: 1.8847e-10)</p>
 <p>M43</p>	 <p>HNF3beta_M00131 (E val: 7.6547e-09)</p>
 <p>M2</p>	 <p>HFH4_M00742 (E val: 3.4597e-06)</p>
 <p>M41</p>	 <p>CACD_M01113 (E val: 2.1652e-11)</p>
 <p>M3</p>	 <p>TFII-I_M00706 (E val: 2.3344e-11)</p>
 <p>M25</p>	 <p>MAZ_M00649 (E val: 5.9860e-07)</p>
 <p>M37</p>	 <p>SREBP-1_M00221 (E val: 1.6557e-06)</p>
 <p>M14</p>	 <p>Lyf-1_M00141 (E val: 3.8983e-06)</p>

 <p>M31</p>	 <p>MAZ_M00649 (E val: 1.2667e-07)</p>
 <p>M52</p>	 <p>dl_M00120 (E val: 9.1139e-08)</p>
 <p>M40</p>	 <p>BLIMP1_M01066 (E val: 5.2274e-05)</p>
 <p>M50</p>	 <p>Ttk_M00009 (E val: 5.7867e-04)</p>
 <p>M9</p>	 <p>c-Ets-1_M00743 (E val: 1.7743e-08)</p>
 <p>M48</p>	 <p>PBF_M01130 (E val: 5.0199e-05)</p>
 <p>M19</p>	 <p>PU.1_M00658 (E val: 6.4223e-06)</p>
 <p>M38</p>	 <p>STAT5B_M00459 (E val: 4.1717e-07)</p>

<p>M46</p>  <p>M46</p>	<p>XPF-1_M00684</p>  <p>XPF-1_M00684 (E val: 4.4160e-07)</p>
<p>M10</p>  <p>M10</p>	<p>E2A_M00804</p>  <p>E2A_M00804 (E val: 3.1630e-06)</p>
<p>M28</p>  <p>M28</p>	<p>SMAD3_M00701</p>  <p>SMAD3_M00701 (E val: 4.4951e-07)</p>
<p>M35</p>  <p>M35</p>	<p>NERF1a_M00531</p>  <p>NERF1a_M00531 (E val: 3.7708e-06)</p>
<p>M13</p>  <p>M13</p>	<p>PU.1_M00658</p>  <p>PU.1_M00658 (E val: 3.4259e-09)</p>
<p>M17</p>  <p>M17</p>	<p>ARF_M00438</p>  <p>ARF_M00438 (E val: 1.7356e-06)</p>
<p>M30</p>  <p>M30</p>	<p>SMAD4_M00733</p>  <p>SMAD4_M00733 (E val: 4.8026e-05)</p>
<p>M51</p>  <p>M51</p>	<p>PBF_M01130</p>  <p>PBF_M01130 (E val: 3.6754e-06)</p>

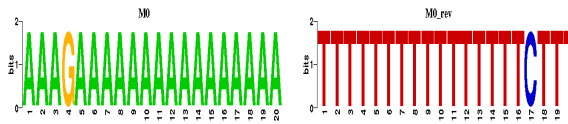
<p>M6</p>  <p>M6</p>	<p>CAC-binding_M00720</p>  <p>CAC-binding_M00720 (E val: 4.6486e-08)</p>
<p>M23</p>  <p>M23</p>	<p>CAC-binding_M00720</p>  <p>CAC-binding_M00720 (E val: 7.5184e-09)</p>
<p>M49</p>  <p>M49</p>	<p>RAP1_M00213</p>  <p>RAP1_M00213 (E val: 1.5257e-05)</p>
<p>M57</p>  <p>M57</p>	<p>RAP1_M00213</p>  <p>RAP1_M00213 (E val: 1.1768e-05)</p>
<p>M21</p>  <p>M21</p>	<p>Nrf-1_M00652</p>  <p>Nrf-1_M00652 (E val: 1.0542e-08)</p>
<p>M33</p>  <p>M33</p>	<p>AP-2_M00915</p>  <p>AP-2_M00915 (E val: 7.2559e-05)</p>
<p>M47</p>  <p>M47</p>	<p>Dde_M00304</p>  <p>Dde_M00304 (E val: 2.9494e-06)</p>
<p>M55</p>  <p>M55</p>	<p>AREB6_M00412</p>  <p>AREB6_M00412 (E val: 1.2319e-06)</p>

<p>M29</p>  <p>M29</p>	<p>HSF_M00167</p>  <p>HSF_M00167 (E val: 5.8941e-06)</p>
<p>M45</p>  <p>M45</p>	<p>Dde_M00304</p>  <p>Dde_M00304 (E val: 1.9571e-05)</p>
<p>M32</p>  <p>M32</p>	<p>Eve_M00629</p>  <p>Eve_M00629 (E val: 1.6856e-05)</p>
<p>M54</p>  <p>M54</p>	<p>SF1_M00727</p>  <p>SF1_M00727 (E val: 1.2206e-04)</p>
<p>M44</p>  <p>M44</p>	<p>PEND_M01015</p>  <p>PEND_M01015 (E val: 2.5550e-04)</p>
<p>M53</p>  <p>M53</p>	<p>PU.1_M00658</p>  <p>PU.1_M00658 (E val: 2.7315e-04)</p>
<p>M7</p>  <p>M7</p>	<p>GC_M00255</p>  <p>GC_M00255 (E val: 4.5763e-13)</p>
<p>M15</p>  <p>M15</p>	<p>KROX_M00982</p>  <p>KROX_M00982 (E val: 4.5445e-12)</p>



Motif Similarity Matches

M0



forward

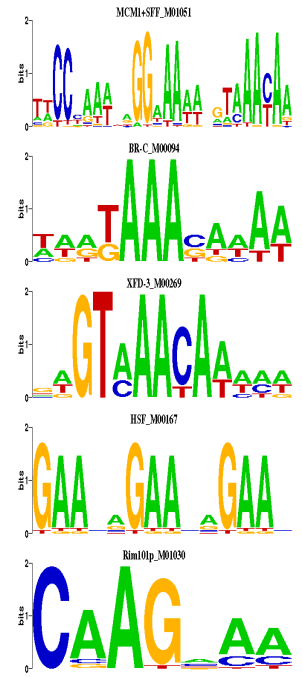
reverse compliment

Name	E value	Alignment	Motif
FOXP1_M00987	2.4128e-08	AAAGAAAAAAAAAAAAAAAAAA -ATAAAAAACAACACAAATA	
HSF_M00163	4.2848e-08	TTTTTTTTTTTTTTTTCTTT ---NTTCTNTTCTNTTC---	
STE11_M00274	7.0725e-08	AAAGAAAAAAAAAAAAAAAAAA- ----WNNNNAACAAAGAAANW	
BR-C_M00092	1.5064e-07	AAAGAAAAAAAAAAAAAAAAAA ----RANAAATAGNWNNNN-	
STE11_M01005	5.6586e-07	TTTTTTTTTTTTTTTTCTTT -----TTTCTTTGTTC---	

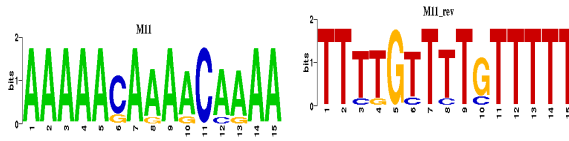
Stamp Results

04/30/14

MCM1+SFF_M01051	6.3557e-07	TTTTTTTTTTTTTTTTCTTT----- -TTRTTANNTWTINCCNNWTTNGNA
BR-C_M00094	6.0444e-05	TTTTTTTTTTTTTTTTCTTT -----TTWTSTTTAYWW
XFD-3_M00269	6.3144e-05	TTTTTTTTTTTTTTTTCTTT -----WKWTTGTTTACWN-
HSF_M00167	2.1274e-04	TTTTTTTTTTTTTTTTCTTT ---NTTCNNTTCNNTTC---
Rim101p_M01030	2.2806e-04	TTTTTTTTTTTTTTTTCTTT -----TTNCTTG



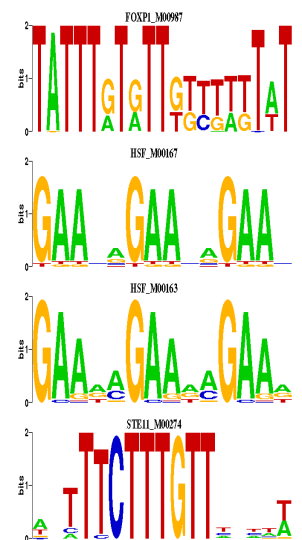
M11



forward

reverse compliment

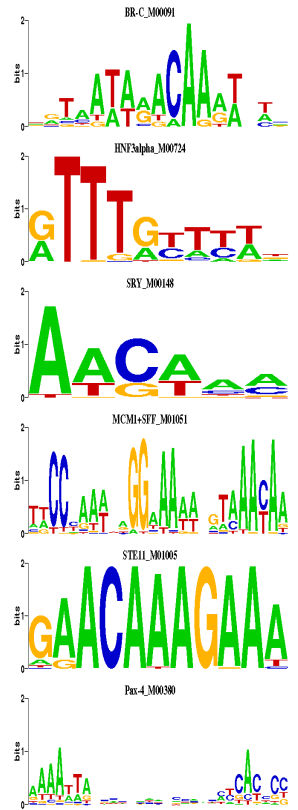
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
FOXP1_M00987	1.5239e-12	---AAAAACAAAACAAA- ATAAAAACAACACAATA
HSF_M00167	5.0875e-08	-TTTTGTTTGTTTTT NTTCNNTTCNNTTC--
HSF_M00163	2.9159e-07	TTTGTTTTGTTTTT -NTTCNNTTCNNTTC
STE11_M00274	8.3279e-07	--AAAAACAAAACAAA WNNNNAACAAGAAANW



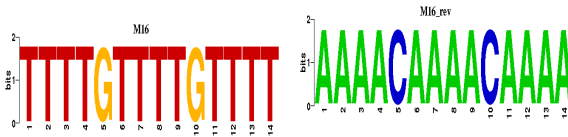
Stamp Results

04/30/14

BR-C_M00091	2.1757e-06	TTTTGTTTTGTTTT---- --NNNWTGTYTATNANN
HNF3alpha_M00724	4.7664e-06	AAAAACAAAACAAAA -----NWRARCAAAY
SRY_M00148	1.2022e-05	AAAAACAAAACAAAA ---AACANM-----
MCM1+SFF_M01051	1.6375e-05	TTTTGTTTTGTTTT----- --TTRTTANNWTTNCCNNWTTNGNA
STE11_M01005	1.6928e-05	TTTTGTTTTGTTTTT --TTCTTTGTTC--
Pax-4_M00380	1.9804e-05	AAAAACAAAACAAAA----- NAAAWTANNNNNNNNNNNNNNNNNNNCACNCN



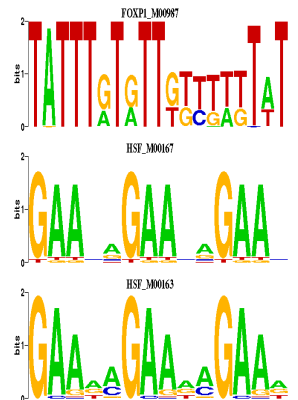
M16

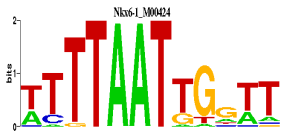








forward

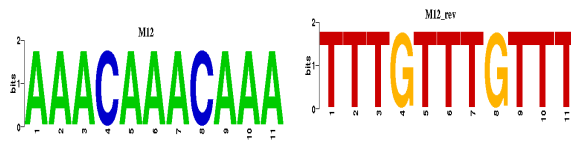
reverse complement

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
FOXP1_M00987	1.6808e-11	----AAAACAAAACAAAA- ATAAAAAACAACACAAATA
HSF_M00167	3.4479e-08	-TTTTGTTTTGTTTT NTTCNNTTCNNTTC-
HSF_M00163	3.2647e-07	TTTTGTTTTGTTTT- -NTTCNNTTCNNTTC



Nkx6-1_M00424	5.9337e-06	AAAACAAAACAAAA --AANCAATTAAAW	
STE11_M00274	6.6882e-06	---AAAACAAAACAAAA WNNNNAACAAAGAAANW	
HNF3alpha_M00724	7.1859e-06	-AAAACAAAACAAAA NWRARCAAAY-----	
SRY_M00148	1.0084e-05	AAAACAAAACAAAA --AACANM-----	
STE11_M01005	1.6322e-05	AAAACAAAACAAAA -GAACAAAGAAA--	
DMRT3_M01148	2.3770e-05	AAAACAAAACAAAA NNAATGTAWCAAWN	
HFH1_M00129	3.4584e-05	TTTTGTTTTGTTTT -AWTGTTTATWT--	

M12

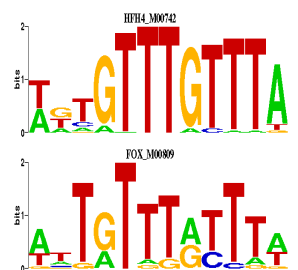


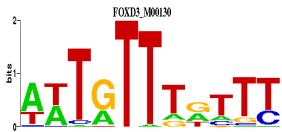







forward

reverse compliment

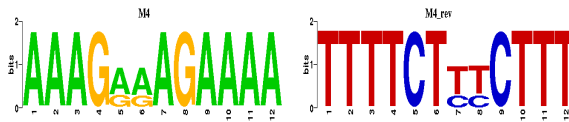
Name	E value	Alignment
HFH4_M00742	9.9920e-16	TTTGTTTGTTT- WKTGTTTGTTTA
FOX_M00809	1.1049e-12	TTTGTTTGTTT- AN TGTTTRTTTW

Motif




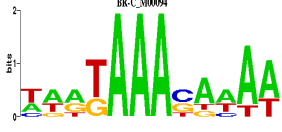
FOXD3_M00130	1.5716e-12	AAACAAACAAA AAANAAACAWT	
STE11_M00274	4.8669e-11	----AAACAAACAAA-- WNNNNAACAAAGAAANW	
STE11_M01005	6.0396e-11	TTTGTTTGTTT TTTCTTTGTTC	
HFH1_M00129	1.0247e-09	AAACAAACAAA AWATAAACAWT	
HFH3_M00289	8.5781e-09	TTTGTTTGTTT- NNRTRTTTRTWN	
BR-C_M00094	2.0655e-07	-TTTGTTTGTTT TTWSTTTAYWW	
HNF3alpha_M00724	5.5731e-07	--AAACAAACAAA NWRARCAAAY---	
Freac-3_M00291	9.5431e-07	TTTGTTTGTTT----- --TGTTTATTTACNNNN	

M4

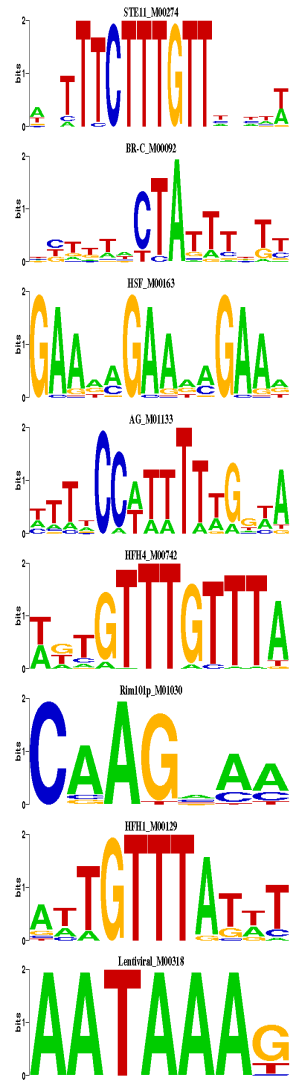


forward

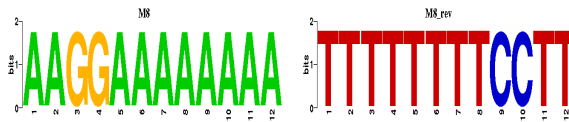
reverse compliment

Name	E value	Alignment	Motif
STE11_M01005	2.0663e-09	TTTTCTTTCTTT -TTTTCTTTGTTC	
BR-C_M00094	3.1638e-09	TTTTCTTTCTTT TTWSTTTAYWW	

STE11_M00274	4.4358e-09	----AAAGAAAGAAAA-- WNNNNAACAAAGAAANW
BR-C_M00092	5.1229e-06	-AAAGAAAGAAAA-- RANAAATAGNWNWNN
HSF_M00163	2.1186e-05	TTTTCTTTCTTT-- NTTCTNTTCTNTTC
AG_M01133	3.5983e-05	----AAAGAAAGAAAA TWNCAAAAAGGGNAAN
HFH4_M00742	3.9044e-05	-AAAGAAAGAAAA TAAACAAACAMW-
Rim101p_M01030	5.0411e-05	TTTTCTTTCTTT -TTNCTTG----
HFH1_M00129	1.3970e-04	TTTTCTTTCTTT -AWTGTTTATWT
Lentiviral_M00318	1.8142e-04	AAAGAAAGAAAA -AATAAG----



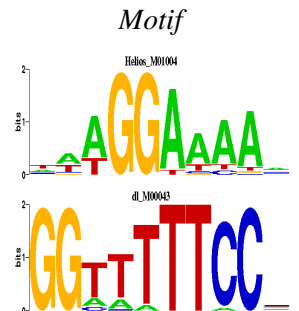
M8



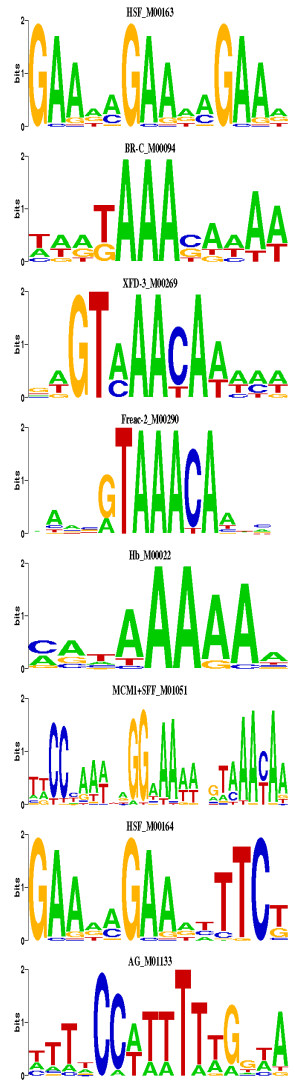
forward

reverse compliment

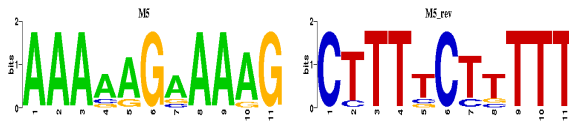
Name	E value	Alignment
Helios_M01004	5.9779e-08	TTTTTTTTCCTT- ---NTTTCCTWN
dl_M00043	6.7611e-06	AAGGAAAAAAAAA -NGGAAAAACC-



HSF_M00163	7.9016e-06	TTTTTTTTCCTT-- NNTCTNNTCTNTTC
BR-C_M00094	1.5453e-05	TTTTTTTTCCTT TTWTSITTTAYWW
XFD-3_M00269	3.0542e-05	AAGGAAAAAAAAA-- NWTGTAACAAMWW
Freac-2_M00290	6.0293e-05	--TTTTTTTTCCTT-- NNNNTGTTTACNNTN
Hb_M00022	7.7592e-05	-TTTTTTTTCCTT NTTTTTNYK----
MCM1+SFF_M01051	1.1619e-04	-----TTTTTTTTCCTT----- TTRITTTANNWTTNCCNNWTTNGGNA
HSF_M00164	1.4714e-04	-----TTTTTTTTCCTT AGAANNTTCTNTTC---
AG_M01133	6.1230e-04	-----AAGGAAAAAAAAA TWNCAAAAAWGGNAAN-----



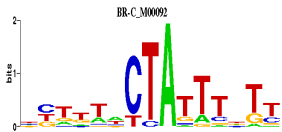
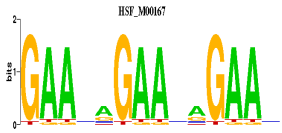

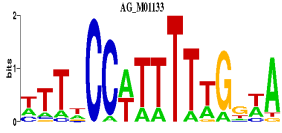




M5



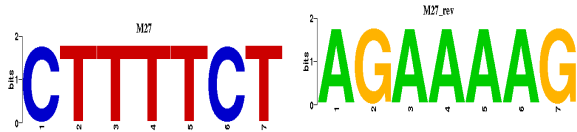
forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HSF_M00163	3.2114e-11	---CTTTTCTTTTT NNTCTNNTCTNTTC	
STE11_M01005	1.8093e-07	CTTTTCTTTTT-- --TTTCTTTGTTC	

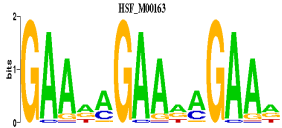
BR-C_M00092	3.6026e-07	---AAAAGAAAAG-- RANAAATAGNWNNNN	
HSF_M00167	6.0907e-07	---CTTTTCTTTTT NTTCNNTTCNNTTC	
ID1_M01021	1.3272e-06	AAAAGAAAAG AWAASGACAA-	
AG_M01133	2.7212e-06	-----AAAAGAAAAG TWNCAAAAAGGNAAN	
STE11_M00274	1.0555e-05	-----AAAAGAAAAG WNNNAACAAAGAAANW	
HSF_M00164	1.4647e-05	---CTTTTCTTTTT AGAANNITCTNTTC	
Rim101p_M01030	2.3729e-05	CTTTTCTTTTT --TTNCTTG--	
BR-C_M00094	2.5188e-05	CTTTTCTTTTT-- -TTWTSTTTAYWW	

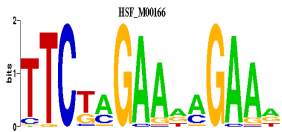








M27



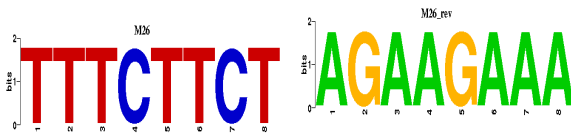
forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HSF_M00163	8.5599e-08	---CTTTTCT--- NTTCNNTTCNNTTC	

HSF_M00166	8.5599e-08	---CTTTTCT--- NTTCTNTTCTAGAA	
GATA-1_M00347	1.7081e-05	-CTTTTCT- YNTTATCTN	
GATA-2_M00349	2.3319e-05	-AGAAAAG- SAGATAANA	
HSF_M00167	2.4623e-05	---CTTTTCT--- NTTCNNTTCNNTTC	
HSF_M00170	2.4623e-05	---CTTTTCT--- NTTCNNTTCNNGAA	
dI_M00120	2.9020e-05	--CTTTTCT- NGNTTTTCYC	
GATA-3_M00350	3.2048e-05	-CTTTTCT- TNTTATCTY	
GATA-2_M00348	3.4530e-05	-CTTTTCT- NSTTATCWN	
BR-C_M00092	3.8151e-05	-----AGAAAAG- RANAAATAGNWNNNN	

M26



forward











reverse compliment

Name

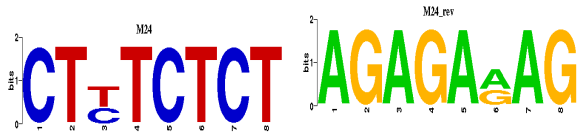
E value

Alignment

Motif

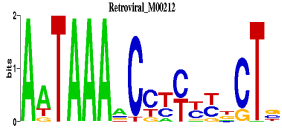






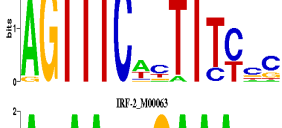


Rim101p_M01030	1.5075e-06	TTTCTTCT TTNCTTG-	
Elf-1_M00746	9.2030e-06	-TTTCTTCT-- AYTTCCTCTTN	
STE11_M01005	2.6067e-05	TTTCTTCT--- TTTCTTTGTTC	
HSF_M00163	2.6422e-05	-----TTTCTTCT- NTTCTNTTCTNTTC	
HSF_M00164	2.6422e-05	-----TTTCTTCT- AGAANNTTCTNTTC	
PEND_M01015	1.4491e-04	AGAAGAAA- --AAGAAGT	
STE11_M00274	2.3229e-04	-----AGAAGAAA-- WNNNNAACAAAGAAANW	
XPF-1_M00684	2.5882e-04	TTTCTTCT- GKTSNYCNG	
Alx-4_M00619	2.8911e-04	---AGAAGAAA- CTGAGAATAATC	
SRY_M00148	3.1174e-04	AGAAGAAA --AACANM	

M24

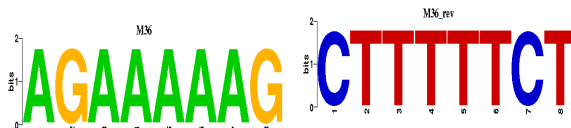


forward

reverse complement

Name	E value	Alignment	Motif
Retroviral_M00212	1.7006e-05	-AGAGARAG----- NAGNRRRRRGNTTTATT	
GAGA_M00723	1.8980e-05	-AGAGARAG- SWGAGMGNRA	
BLIMP1_M01066	4.2631e-05	--CTYTCTCT--- YMCTTTCMCTTYC	
PU.1_M00658	4.2824e-05	CTYTCTCT CTTCCTC-	
Elf-1_M00746	5.9211e-05	-CTYTCTCT-- AYTTCCTCTTN	
BPC1_M01126	1.2778e-04	CTYTCTCT NTTTC---	
IRF_M00972	2.3947e-04	CTYTCTCT-- NTTTCWNTTT	
ISGF-3_M00258	2.5042e-04	-----AGAGARAG- GNGAAANWGAAACT	
IRF-2_M00063	3.7418e-04	-CTYTCTCT--- RSTTTCRCTTTT	
SMAD3_M00701	8.3647e-04	AGAGARAG AGNCAGAC	

M36

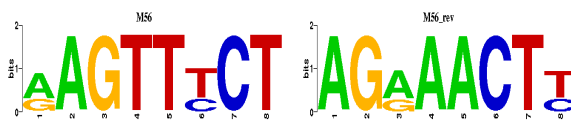


forward

reverse compliment

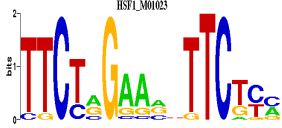




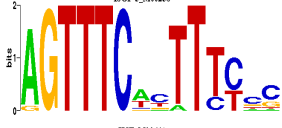
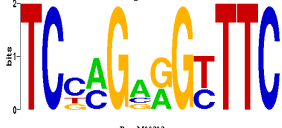

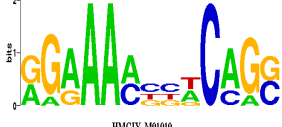
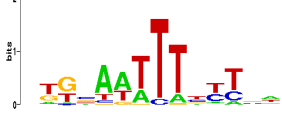
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
dl_M00043	1.7481e-05	-AGAAAAAG- -NGGAAAAACC	
Dof_M01136	2.3094e-05	AGAAAAAG--- -NAAAAAGNNN	
Helios_M01004	1.7258e-04	CTTTTTCT-- NTTTTCTWN	
dl_M00120	1.9333e-04	-CTTTTTCT- -NGNTTTTCYC	
Retroviral_M00212	2.1346e-04	-AGAAAAAG----- NAGNRRRRRGNTTTATT	
Abd-B_M01094	2.3230e-04	CTTTTTCT --TTTTAT	
Alx-4_M00619	2.8911e-04	---AGAAAAAG- CTGAGAATAATC	
BPC1_M01126	3.2435e-04	CTTTTTCT --NTTTC-	
Hb_M00022	5.8844e-04	CTTTTTCT- NTTTTTNYK	
CIZ_M00734	6.1244e-04	--CTTTTTCT NNNTTTT--	

M56

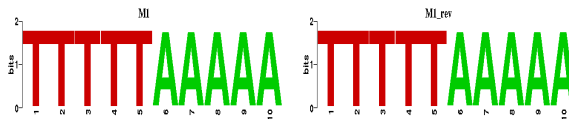


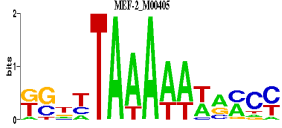
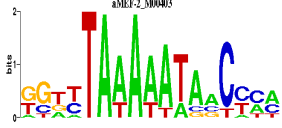
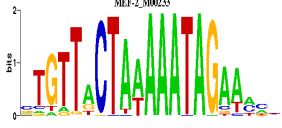
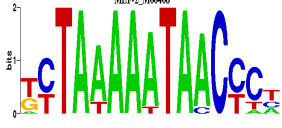
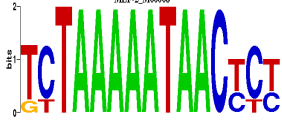


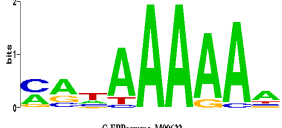


forward

reverse compliment

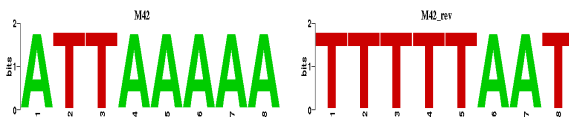
Name	E value	Alignment	Motif
HSF1_M01023	1.9223e-07	--AGAACTT----- KRAGAANN TTCYAGAA	
HSF_M00164	3.2868e-06	--AAGTTTCT---- AGAANN TTCNTTC	
HSF_M00165	3.2868e-06	-----AGAACTT- NTTCTAGAANN TTC	
STE12_M00664	3.6061e-05	AAGTTTCT --GTTTCA	
ICSBP_M00699	5.4858e-05	AAGTTTCT--- CAGTTTCA YTT	
ISGF-3_M00258	6.1855e-05	-----AGAACTT GNGAAANWGAACT-	
HSF_M00641	7.7469e-05	AGAACTT----- -GAARCYNCKNGA	
Pax_M00808	1.3258e-03	--AAGTTTCT GTKAGTTCCA	
PTF1-beta_M00657	1.3990e-03	-----AAGTTTCT SCTGWNNKTTTCY	
HMG1Y_M01010	2.0885e-03	--AGAACTT---- NNRRNAAAWTNMNN	



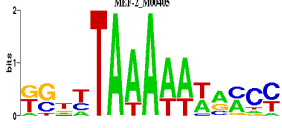

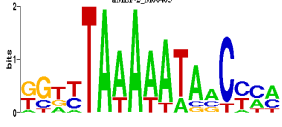

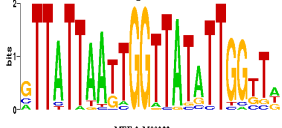
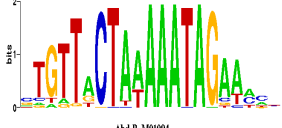


M1



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MEF-2_M00405	2.9868e-07	-----TTTTTAAAAA RGKNWTTTTTANNM	
aMEF-2_M00403	3.1767e-06	-----TTTTTAAAAA KKRGNTATTTTTARNM	
MEF-2_M00233	1.9584e-05	-----TTTTTAAAAA--- NNNTTCTATTTTTAGTAACAN	
MEF-2_M00406	2.5426e-05	-----TTTTTAAAAA NGGGTTATTTTTAGM--	
MEF-2_M00006	4.9225e-05	-----TTTTTAAAAA RGRGTTATTTTTAGA--	
TATA_M00216	7.5424e-05	TTTTTAAAAA NTTTTATAG-	
Abd-B_M01094	8.7874e-05	TTTTTAAAAA -TTTTAT---	
Hb_M00022	1.2639e-04	-TTTTTAAAAA NTTTTTNYK--	
C-EBPgamma_M00622	1.8426e-04	-TTTTTAAAAA- TNATTTCARAAW	
GT-1_M00635	3.0590e-04	TTTTTAAAAA TWNNA----	











M42



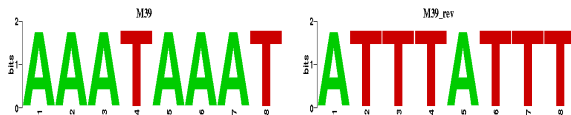
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Nkx6-1_M00424	2.1085e-07	TTTTTAAT----- -WTTTAATTGNTT	
unc-86_M00689	4.0348e-07	ATTAAAAA- ATWMRAAAT	
MEF-2_M00405	3.8447e-06	-----TTTTTAAT-- RGKNWTTTTTANNSM	
D-Type_M00334	4.8477e-06	TTTTTAAT-- -GTTTAATGG	
aMEF-2_M00403	5.7778e-06	-----TTTTTAAT-- KKRGNATTTTTARNCM	
Hb_M00022	1.0406e-05	-TTTTTAAT NTTTTTNYK	
AIRE_M01000	1.6942e-05	-----ATTAATAA- NAMCCAATATAACCAATTAATAAN	
MEF-2_M00233	2.2347e-05	-----TTTTTAAT----- NNNTTCTATTTTAGTAACAN	
Abd-B_M01094	2.3381e-05	TTTTTAAT -TTTTAT-	
OTX_M01117	2.6242e-05	TTTTTAAT -ANNTAAT	

M18

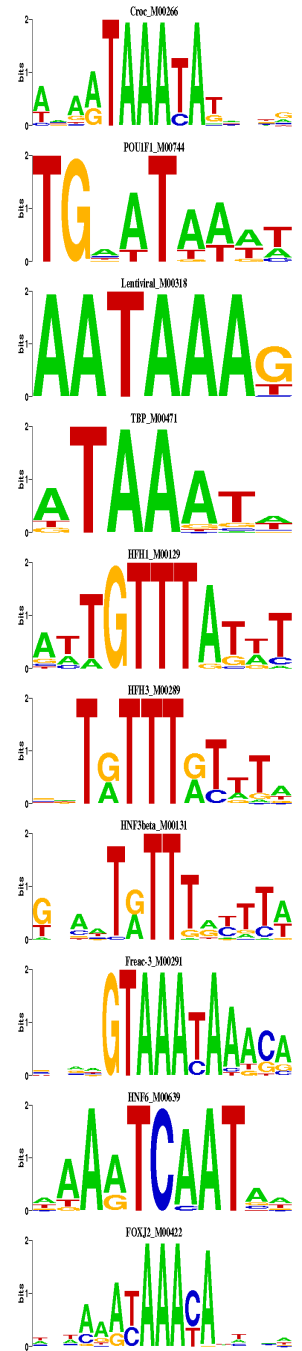


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
OCT-x_M00210	1.1102e-16	-TATGCAAATG- RTATGCAAATNA	
Oct-1_M00930	5.1525e-13	TATGCAAATG NATGNAAATN	
Oct-1_M00161	3.2148e-12	--TATGCAAATG- RRTATGCAAATNM	
Oct-1_M00342	2.3365e-11	CATTTCATA NATTTGCAT-	
Oct-1_M00135	9.7410e-11	----CATTTCATA---- NNNANATTTGCATANNNN	
Octamer_M00795	4.1979e-10	TATGCAAATG NATGCAAATN	
Oct-4_M01125	1.1209e-09	CATTTCATA----- -ATTTGCATNASAAW	
Oct-1_M00195	3.8802e-08	--TATGCAAATG-- NNNATGCAAATNAN	
Oct-1_M00248	5.1471e-08	CATTTCATA- AATTANCATAN	
POU3F2_M00464	5.7902e-08	CATTTCATA -ATTARCATA	

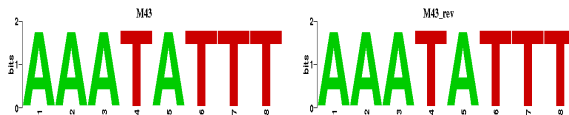
M39

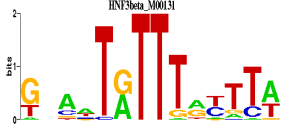



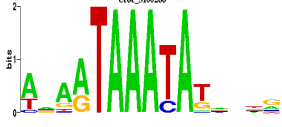
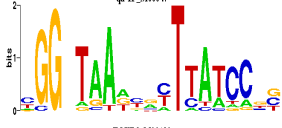






	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
Croc_M00266	1.8847e-10	-----ATTTATTT- NNNNMTATTTATNT
POU1F1_M00744	1.0935e-07	ATTTATTT- WTTTATNCA
Lentiviral_M00318	1.4526e-07	AAATAAAT -AATAAAG
TBP_M00471	1.8156e-07	AAATAAAT- --ATAAATW
HFH1_M00129	2.1963e-07	---ATTTATTT 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

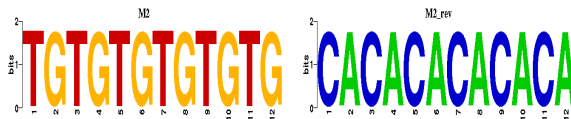


M43



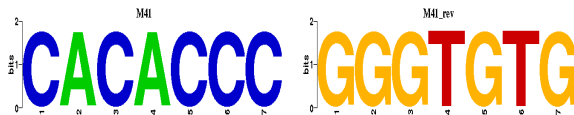
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HNF3beta_M00131	7.6547e-09	-----AAATATTT- WAARYAAAYANTNC	
FOXJ2_M00423	1.7597e-07	---AAATATTT-- YMATAATATTTKN	
ATHB-5_M00503	1.5696e-05	AAATATTT AATNATTG	
XFD-1_M00267	1.1196e-04	-AAATATTT---- RYWWTATTTACWT	
Croc_M00266	2.3517e-04	--AAATATTT----- NNNNMTATTTATNT	
qa-1F_M00047	2.5721e-04	-----AAATATTT----- NGGNTAANNYYTTATCCNN	
FOXD3_M00130	3.1709e-04	-----AAATATTT AAANAAACAWT-	
Athb-1_M00089	4.7447e-04	--AAATATTT--- TNCAATAATTNNN	
Nkx6-2_M00489	4.9920e-04	---AAATATTT NNNAWTTANYW	
POU1F1_M00744	5.5191e-04	AAATATTT- WWTATNCA	

M2



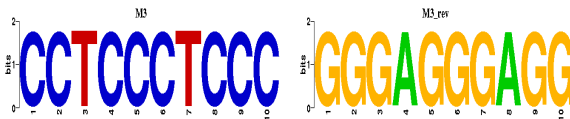
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HFH4_M00742	3.4597e-06	TGTGTGTGTGTG WKTGTTTTGTTA	
RAP1_M00213	1.1714e-05	--TGTGTGTGTGTG NRTGTATGGGTKY-	
Egr-3_M00245	7.8585e-05	CACACACACACA -ACGCCACGCA	
Egr-1_M00243	1.0858e-04	TGTGTGTGTGTG TGCGTGGGCGK-	
Egr-2_M00246	1.9169e-04	TGTGTGTGTGTG TGCGTGGGCGK-	
CACD_M01113	1.9889e-04	TGTGTGTGTGTG -GGGYGTG----	
NGFI-C_M00244	2.2546e-04	CACACACACACA -CCRCCCACGCA	
GBF_M00633	1.5577e-03	TGTGTGTGTGTG TNGGGGTN----	
Hmx3_M00433	1.6752e-03	CACACACACACA CACGCACTT---	
FOXP1_M00987	1.9878e-03	----TGTGTGTGTGTG--- TATTTGTGTTGTTTTTTAT	

M41



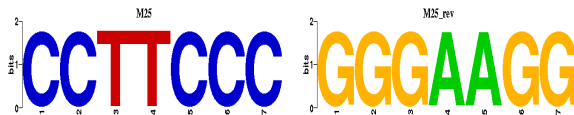
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CACD_M01113	2.1652e-11	GGGTGTG GGGYGTG	
CACCC-binding_M00721	9.6046e-08	-CACACCC----- CCNCACCCWNNKNGT	
TBX5_M01044	5.1971e-07	-GGGTGTG- AAGGTGTGA	
GBF_M00633	1.1743e-06	CACACCC- NACCCNA	
CAC-binding_M00720	4.4394e-05	CACACCC- CCCASCCY	
Brachyury_M00150	5.2431e-05	-----GGGTGTG----- NNNTSACACCTAGGTGTGAAATT	
AR_M00481	5.8280e-05	--CACACCC----- AGNACANNNTGTWC	
Tax-CREB_M00115	7.0741e-05	--GGGTGTG----- GGGGRTATGCGTCA	
TBX5_M01019	1.4485e-04	---CACACCC- NNTNACACCTN	
TBX5_M01020	1.6968e-04	-CACACCC- NMACACCNN	










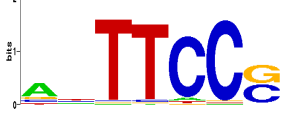
M3



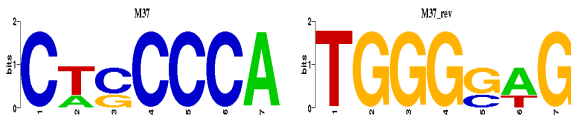
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
TFII-I_M00706	2.3344e-11	CCTCCCTCCC CCTMCNTC--	
MAZ_M00649	3.6118e-10	CCTCCCTCCC ---CCCTCCC	
ZNF219_M01122	8.4691e-10	GGGAGGGAGG- GGGNGGGGGGN	
VDR_M00444	8.3957e-06	---CCTCCCTCCC- TSWCCYNYNTMCC	
Tra-1_M01048	1.6910e-05	-CCTCCCTCCC ACCWCCC----	
UF1H3BETA_M01068	1.8036e-05	---CCTCCCTCCC GCCCTCCCCRC	
PU.1_M00658	3.1639e-05	GGGAGGGAGG --GAGGAAG-	
CAC-binding_M00720	7.6359e-05	CCTCCCTCCC- ---CCCASCCY	
MAF_M00648	1.1749e-04	-----CCTCCCTCCC NSNMMACTTCCYYCN-	
Sp1_M00933	1.1790e-04	--GGGAGGGAGG NGGGMGGG---	






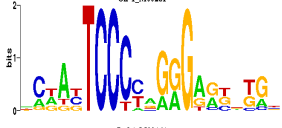




M25



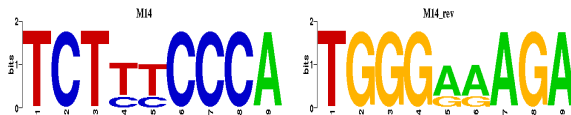
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MAZ_M00649	5.9860e-07	CCTTCCC CCCTCCC	
UF1H3BETA_M01068	1.8486e-05	--CCTTCCC---- GCCCCCTCCCCRC	
MAF_M00648	4.7375e-05	---GGGAAGG----- NGRRGGAAGTKKNSN	
AtMYB-84_M00970	4.9379e-05	--GGGAAGG--- GGNGGTAGGTGS	
PU.1_M00658	7.2251e-05	CCTTCCC- -CTTCCTC	
Ets_M00971	7.2561e-05	-GGGAAGG NAGGAAG-	
c-Ets-1_M00743	7.4398e-05	CCTTCCC GCTTCK	
PEA3_M00655	1.2717e-04	GGGAAGG MGGAWG-	
GCR1_M00046	1.8673e-04	-GGGAAGG GWGGAAGC	
STAT1_M00492	3.1752e-04	CCTTCCC ANTTCCS	

M37



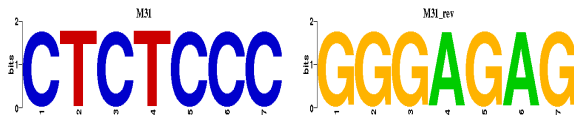
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SREBP-1_M00221	1.6557e-06	-TGGGGAG-- GTGGGGTGAT	
Sp3_M00665	2.8268e-06	--CTCCCCA---- CCCYSCCCAAGKS	
SREBP_M00776	8.6562e-06	----CTCCCCA NNNTCACCXYA	
UF1H3BETA_M01068	2.0706e-05	----CTCCCCA-- GCCCTCCCCRC	
SREBP-1_M00749	5.1320e-05	CTCCCCA -ACSCCA	
Olf-1_M00261	6.8219e-05	-----TGGGGAG----- NCMNNYTCCCNRRGGANTNGN	
Lyf-1_M00141	8.9836e-05	-CTCCCCA YCTCCCAA	
MAZ_M00649	2.7550e-04	--CTCCCCA CCCTCCC--	
MZF1_M00083	2.8630e-04	CTCCCCA- -TCCCCNN	
Tra-1_M01048	3.4665e-04	--CTCCCCA ACCWCCC--	




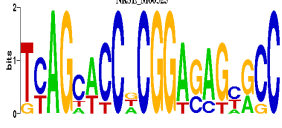


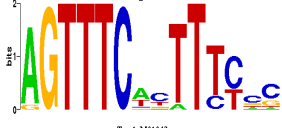

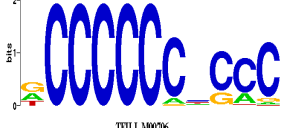

M14



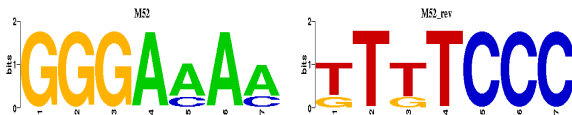
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Lyf-1_M00141	3.8983e-06	-TGGGAAAGA TTGGGAGR--	
RBP-Jkappa_M01112	4.0112e-06	TCTTTCCCA--- --KTTCACGN	
ISGF-3_M00258	6.8938e-06	TGGGAAAGA----- -GNGAAANWGAAACT	
BLIMP1_M01066	2.9051e-05	-TCTTTCCCA--- YMCTTTCMCTTYC	
Su_H_M00234	4.1846e-05	TCTTTCCCA--- NGKTTCACRN	
BPC1_M01126	7.7414e-05	TCTTTCCCA -NTTTC---	
STAT1_M00492	1.8724e-04	TCTTTCCCA -ANTTCCS-	
NF-kappaB_M00208	2.5804e-04	---TCTTTCCCA GGGAYTTTCCN-	
E2F_M01114	4.1641e-04	TCTTTCCCA-- -NTTTCACGN	
HOXA5_M00023	4.2672e-04	-----TGGGAAAGA----- NGRNNNNNNNANTAAATGRNGNNNNNNNGC	

M31



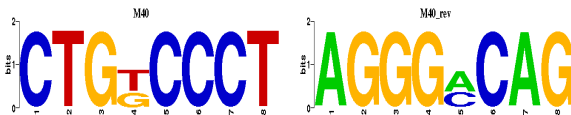
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MAZ_M00649	1.2667e-07	CTCTCCC CCCTCCC	
Lyf-1_M00141	5.1614e-06	CTCTCCC-- -YCTCCCAA	
Nrf-2_M00108	3.2163e-05	CTCTCCC-- SNCTTCCGG	
NRSE_M00325	1.2900e-04	----CTCTCCC----- GGCRCTCTCCGNGGTGCTGA	
UF1H3BETA_M01068	1.3968e-04	--CTCTCCC---- GCCCTCCCCRC	
BLIMP1_M01066	4.0728e-04	--CTCTCCC---- YMCTTTCMCTTYC	
ISGF-3_M00258	4.7677e-04	GGGAGAG----- GNGAAANWGAAACT	
Tra-1_M01048	5.1032e-04	GGGAGAG GGGWGGT	
ZNF219_M01122	7.5710e-04	GGGAGAG---- GGNGGGGGGN	
TFII-I_M00706	1.0160e-03	CTCTCCC-- -CCTMCNTC	









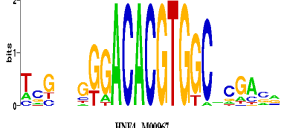

M52



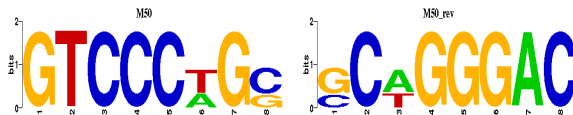
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
dl_M00120	9.1139e-08	---TTTTCCC NGNTTTTTCYC	
Helios_M01004	4.0235e-06	-TTTTCCC-- NTTTTTCTWN	
dl_M00043	5.0263e-06	GGGAAAA--- NGGAAAAACC	
E2F_M01114	7.8333e-06	TTTTCCC--- NTTTCCCGCN	
STAT1_M00492	1.3361e-05	GGGAAAA SGGAANT	
E2F_M00024	3.0884e-05	---TTTTCCC--- YMNTTTTCGCGCNN	
RBP-Jkappa_M01112	3.6075e-05	TTTTCCC---- -KTCCCACGN	
BLIMP1_M01066	6.0941e-05	--TTTTCCC--- YMCTTTCMCTTYC	
ISGF-3_M00258	7.2249e-05	GGGAAAA----- GNGAAANWGAAACT	
PTF1-beta_M00657	1.3715e-04	-----TTTTCCC SCTGWNNKTTTCY-	

M40



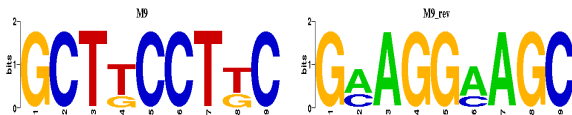
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
BLIMP1_M01066	5.2274e-05	---AGGGMCAG--- GRAAGKGAAGKR	
NRSF_M00256	1.1223e-04	-----AGGGMCAG----- TCAGCACCACGGACAGCRSC	
NRSF_M01028	1.9387e-04	-----AGGGMCAG----- TCAGCACCRYGGACAGNR	
LF-A1_M00646	3.5308e-04	CTGKCCCT YWGASCC-	
BRK_M01096	9.2499e-04	CTGKCCCT NTGGCG--	
ID1_M01021	1.7068e-03	CTGKCCCT-- TTGTCSTTWT	
TEIL_M00502	1.9046e-03	AGGGMCAG AGRTWCA-	
ARF_M00438	2.0268e-03	AGGGMCAG -GAGACAA	
ABF1_M00399	2.7444e-03	-----CTGKCCCT----- NNTCNGCCACGTGTCCCNNNNW	
HNF4_M00967	3.1494e-03	CTGKCCCT NTGGACYT	









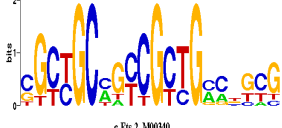

M50



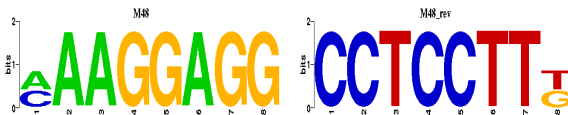
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Ttk_M00009	5.7867e-04	GTCCCTGC -GTCCCTGC	
HEB_M00698	1.0166e-03	--GCAGGGAC CAGCWGG---	
Pax-6_M00979	1.3643e-03	--GTCCCTGC--- KAGTTCCAGGTCA	
CAC-binding_M00720	1.5481e-03	GTCCCTGC-- --CCCASCCY	
LXR_M00766	1.8997e-03	--GTCCCTGC----- GGGTACTNCCGGTC	
Ik-3_M00088	2.0149e-03	----GTCCCTGC GGTATTCCNRN	
EBF_M00977	2.1311e-03	---GCAGGGAC TCCCYWGRGN-	
Gfi1b_M01058	2.2075e-03	--GTCCCTGC- AAATCACKGCW	
PCF5_M00952	2.3345e-03	--GTCCCTGC TGGNCCNN-	
NRSF_M00256	2.8221e-03	-----GTCCCTGC----- GSYGCTGTCCGTGGTGCTGA	

M9



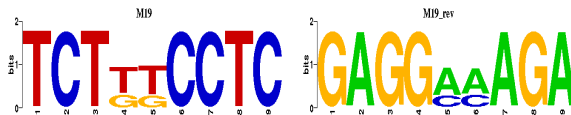
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
c-Ets-1_M00743	1.7743e-08	GCTTCCTTC GCTTCCK--	
GCR1_M00046	1.9851e-07	GAAGGAAGC -GWGGAAGC	
Ets_M00971	1.5476e-06	GAAGGAAGC -NAGGAAG-	
PU.1_M00658	2.0340e-06	GAAGGAAGC -GAGGAAG-	
PEA3_M00655	5.4837e-06	GAAGGAAGC --MGGAWG-	
NERF1a_M00531	6.8087e-06	-----GCTTCCTTC- SNNASNYRCTTCCTGNY	
Tel-2_M00678	1.1612e-05	GAAGGAAGC- -CAGGAAGTA	
MAF_M00648	2.0820e-05	----GCTTCCTTC- NSNMMACTTCCYYCN	
Adf-1_M00923	9.1144e-05	-----GCTTCCTTC- SGCYGCMGYCGCTGMMNKYG	
c-Ets-2_M00340	1.3895e-04	GAAGGAAGC---- RCAGGAAGTNNNT	






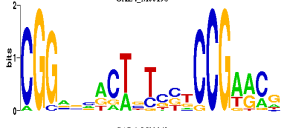
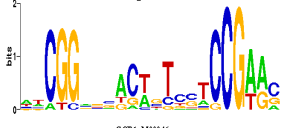



M48



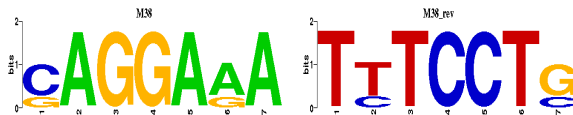
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PBF_M01130	5.0199e-05	CCTCCTTK ---CCTTT	
TFIIA_M00707	1.7385e-04	---MAAGGAGG MTNNRAGGRNS	
MAZ_M00649	2.1983e-04	-CCTCCTTK CCCTCCC--	
VDR_M00444	4.3595e-04	---CCTCCTTK--- TSWCCYNYTNMCC	
ETF_M00695	4.5350e-04	MAAGGAGG --NGGCGG	
TFII-I_M00706	4.6433e-04	MAAGGAGG GANGKAGG	
Barbie_M00238	7.2682e-04	---CCTCCTTK--- CMNNCNSCTTTNNN	
alpha-CP1_M00687	1.1113e-03	CCTCCTTK--- -CTCATTGGCT	
Tra-1_M01048	1.2740e-03	-CCTCCTTK ACCWCCC--	
PU.1_M00658	1.7957e-03	MAAGGAGG -GAGGAAG	











M19



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	6.4223e-06	GAGGAAAGA GAGGAAG--	
Elf-1_M00746	3.6769e-05	TCTTTCCTC--- -AYTTCCTCTTN	
STE11_M01005	1.0360e-04	--TCTTTCCTC TTTCTTTGTTC	
GATA-2_M00349	1.0422e-04	TCTTTCCTC TNTTATCTS	
BPC1_M01126	1.5633e-04	TCTTTCCTC -NTTTC---	
GAL4_M00198	1.6881e-04	-----GAGGAAAGA----- NGYTTCGNNNANAGNNNNCCG	
GAL4_M00049	3.0719e-04	-----GAGGAAAGA----- STTCGGASNANWGTNNNCCGNN	
GCR1_M00046	4.7074e-04	GAGGAAAGA GWGGAAGC-	
Helios_M01004	5.0638e-04	TCTTTCCTC- NTTTTCTWN	
HSF_M00167	9.8787e-04	--TCTTTCCTC--- NTTCNNTTCNNTTC	








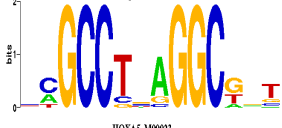
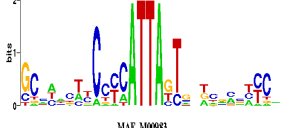

M38



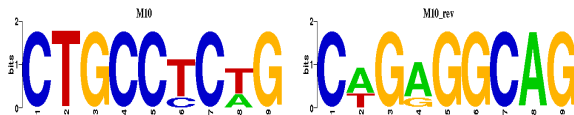
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STAT5B_M00459	4.1717e-07	-TTTCCTG----- NWTTCNNGGAANYN	
Tel-2_M00678	1.7946e-06	CAGGAAA-- CAGGAAGTA	
c-Ets-2_M00340	3.1404e-06	-CAGGAAA----- RCAGGAAGTNNNT	
STAT5A_M00457	4.1362e-06	--TTTCCTG----- NRNTTCNNGAANY	
Helios_M01004	5.4892e-06	--TTTCCTG- NTTTTCTWN	
Elf-1_M00746	6.1119e-06	-TTTCCTG--- AYTTCCTCTTN	
Ets_M00771	8.7445e-06	CAGGAAA----- CAGGAAGYNNN	
PU.1_M00658	1.6281e-05	TTTCCTG CTTCCTC	
Rim101p_M01030	1.6631e-05	TTTCCTG TTNCTTG	
c-Ets-1_M00339	3.1122e-05	-----TTTCCTG NNMNNNACTTCCTG	

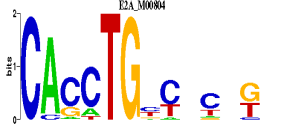









M46



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
XPF-1_M00684	4.4160e-07	-TTCCTCAG GKTSNYCNG	
PU.1_M00658	1.9105e-06	CTGAGGAA- --GAGGAAG	
GCR1_M00046	1.4435e-04	CTGAGGAA-- --GWGGAAGC	
Elf-1_M00746	1.5282e-04	--TTCCTCAG- AYTTCCTCTTN	
Alx-4_M00619	6.9183e-04	----TTCCTCAG GATTATTCTCAG	
Ets_M00971	8.3323e-04	CTGAGGAA- --NAGGAAG	
Dde_M00304	9.0539e-04	--CTGAGGAA GGCTGAGC--	
AP-2alphaA_M01047	9.8974e-04	----CTGAGGAA- ANMGCCTNAGGCKN	
HOXA5_M00023	1.2052e-03	-----CTGAGGAA----- NGRNNNNNNNNNANTAATGRNGNNNNNNNGC	
MAF_M00983	1.3898e-03	-TTCCTCAG- NTGACTCANC	

M10



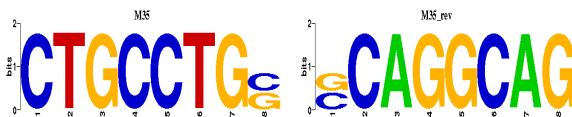
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
E2A_M00804	3.1630e-06	---CTGCCTCTG- CACCTGNCNCNKN	
PU.1_M00658	1.3006e-05	CTGCCTCTG CTTCCTC--	
v-Maf_M00035	1.5919e-05	-----CAGAGGCAG----- NNNTGCNNNGTCAGCANN	
MAF_M00983	5.1054e-05	CTGCCTCTG- NTGACTCANC	
Elf-1_M00746	1.4615e-04	-CTGCCTCTG- AYTTCCTCTTN	
Nrf-2_M00821	1.6587e-04	-CTGCCTCTG-- NNTGACTCAGCA	
NF-E2_M00037	1.8281e-04	CTGCCTCTG- RTGACTCAGC	
AP-1_M00173	1.9530e-04	-CAGAGGCAG WNKNAGTCAN	
TFII-I_M00706	2.6843e-04	-CTGCCTCTG CCTMCNTC--	
XPF-1_M00684	4.4395e-04	CAGAGGCAG CNGRNSAMC	



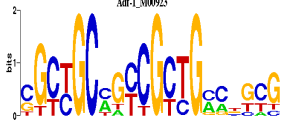
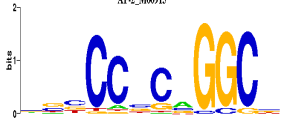


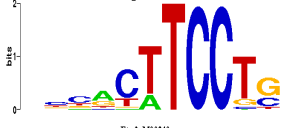



M28



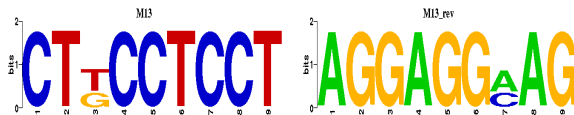
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SMAD3_M00701	4.4951e-07	AGGCAGA- AGNCAGAC	
Dde_M00304	4.0214e-04	AGGCAGA-- -GGCTGAGC	
Ets_M00971	5.7503e-04	-AGGCAGA NAGGAAG-	
SMAD4_M00733	5.9147e-04	-----TCTGCCT-- RGNTGKCTGNMYSN	
PU.1_M00658	7.0533e-04	-AGGCAGA GAGGAAG-	
TAL1_M00993	8.2649e-04	AGGCAGA--- -RNCAGNTGG	
E2A_M00973	1.2191e-03	AGGCAGA- -RNCAGNT	
c-Ets-1_M00743	2.2213e-03	TCTGCCT GCTTCK	
Tel-2_M00678	2.4637e-03	-AGGCAGA- CAGGAAGTA	
E2A_M00804	2.4647e-03	--TCTGCCT---- CACCTGNCNCNK	

M35



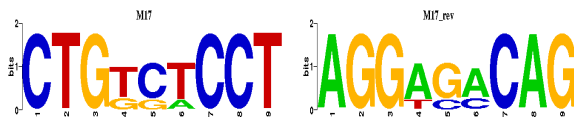
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
NERF1a_M00531	3.7708e-06	-SCAGGCAG----- RNCAGGAAGYRNSTNNS	
Tel-2_M00678	4.9645e-05	SCAGGCAG-- -CAGGAAGTA	
Adf-1_M00923	1.2380e-04	-----CTGCCTGS- SGCYGCMGYCGCTGMMNKYG	
AP-2_M00915	1.6718e-04	CTGCCTGS----- -NGCCNGNGGNNN	
AP-2_M00800	2.3799e-04	---SCAGGCAG--- SCSSCRGGCNRNRNN	
Ttk_M00009	4.4373e-04	CTGCCTGS -GTCCTGC	
Ets_M00771	4.9584e-04	----CTGCCTGS NNNRCTTCTG-	
c-Ets-2_M00340	1.0147e-03	SCAGGCAG----- RCAGGAAGTNNNT	
SMAD3_M00701	1.0174e-03	SCAGGCAG-- --AGNCAGAC	
Ets_M00971	1.4922e-03	SCAGGCAG -NAGGAAG	

M13



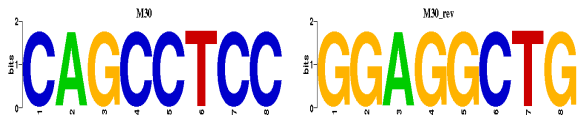
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	3.4259e-09	AGGAGGMAG --GAGGAAG	
GCR1_M00046	7.6565e-07	-CTKCCTCCT GCTTCCWC--	
Elf-1_M00746	2.1140e-06	-CTKCCTCCT- AYTTCCTCTTN	
Ets_M00971	5.6671e-06	AGGAGGMAG --NAGGAAG	
MAF_M00648	6.7893e-06	AGGAGGMAG----- NGRRGGAAGTKKNSN	
PEA3_M00655	2.0469e-05	AGGAGGMAG ---MGGAWG	
c-Ets-1_M00743	3.1957e-05	-CTKCCTCCT GCTTCK---	
Tel-2_M00678	1.2592e-04	AGGAGGMAG-- --CAGGAAGTA	
MZF1_M00084	1.6171e-04	CTKCCTCCT---- -TTNCCCCTCNNN	
NERF1a_M00531	4.0532e-04	-----CTKCCTCCT SNNASNYRCTTCTGNY	







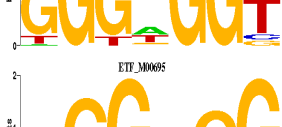


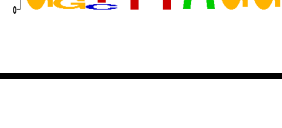
M17



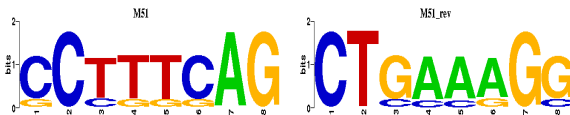
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ARF_M00438	1.7356e-06	AGGAGACAG --GAGACAA	
SMAD3_M00701	7.8447e-05	AGGAGACAG-- ---AGNCAGAC	
YY1_M00069	7.2844e-04	-----CTGTCTCCT NNCNGCCATCTTGNNTSNW	
SMAD4_M00733	1.1199e-03	--CTGTCTCCT-- RGNTGKCTGNMYSN	
T3R_M00963	1.5102e-03	-AGGAGACAG NAGGWCAN--	
ABF1_M00399	2.3181e-03	-----CTGTCTCCT-- NNTCNNGCCACGTGTCCCNNNW	
NF-E2_M00037	2.9520e-03	-CTGTCTCCT GCTGAGTCAY	
Poly_M00211	4.4865e-03	-CTGTCTCCT GTGGTCTC--	
E2A_M00804	4.7546e-03	---CTGTCTCCT- CACCTGNCNCNKN	
BRK_M01096	1.0110e-02	CTGTCTCCT NTGGCG---	

M30



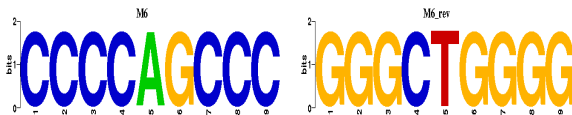
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SMAD4_M00733	4.8026e-05	-----CAGCCTCC-- NSRKNCAGMCANCY	
ERF2_M01057	2.1881e-04	GGAGGCTG GGCGGC--	
MAZ_M00649	2.1983e-04	CAGCCTCC-- --CCCTCCC	
CAC-binding_M00720	5.0895e-04	--CAGCCTCC CCCASCCY--	
Dde_M00304	9.3263e-04	GGAGGCTG--- ---GGCTGAGC	
repressor_M00014	1.0303e-03	-----GGAGGCTG-- NNYNTNGGCGGCTANN	
Tra-1_M01048	1.2740e-03	CAGCCTCC-- --ACCWCCC	
ETF_M00695	1.6054e-03	-GGAGGCTG NGGCGG---	
KROX_M00982	2.0308e-03	CAGCCTCC----- CCGCCCCCNCNNC	
TFII-I_M00706	2.1533e-03	---GGAGGCTG GANGKAGG---	







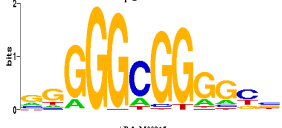



M51



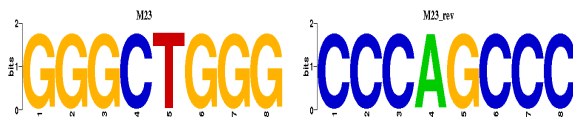
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PBF_M01130	3.6754e-06	CCTTTCAG CCTTT---	
BPC1_M01126	1.5876e-05	CCTTTCAG -NTTTC--	
TGIF_M00418	2.5540e-05	CCTTTCAG-- GCTGTCANNW	
STE12_M00664	3.0015e-05	CCTTTCAG -GTTTCA-	
TFIIA_M00707	5.3136e-05	---CCTTTCAG SNYCCTYNNAK	
BLIMP1_M01066	1.0792e-04	-CCTTTCAG---- YMCTTTCMCTTYC	
COUP_M00765	1.9901e-04	--CCTTTCAG-- GACCTTTGNCCC	
PPAR_M00763	3.0032e-04	--CTGAAAGG-- NGGNCAAAGGTC	
PPAR,_M00762	3.2175e-04	---CCTTTCAG- TGACCTTTGNCC	
C-EBPgamma_M00622	3.5869e-04	---CTGAAAGG- WTTYTGAAATNA	










M6



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CAC-binding_M00720	4.6486e-08	GGGCTGGGG RGGSTGGG-	
KROX_M00982	5.3723e-08	---CCCCAGCCC- CCGCCCCCNCNNC	
Sp1_M00931	3.8973e-07	CCCCAGCCC NCCCCGCC	
Alfin1_M00479	9.0084e-07	---CCCCAGCCC-- MNNCCCCACNYYN	
UF1H3BETA_M01068	4.9751e-06	-CCCCAGCCC--- GCCCTCCCCRC	
Sp1_M00932	9.5369e-06	-CCCCAGCCC-- NNCCCCGCCNN	
Sp1_M00196	1.0727e-05	--GGGCTGGGG- NGGGCGGGGNN	
AP-2_M00915	2.1345e-05	GGGCTGGGG--- NGCCNGNGGNNN	
GC_M00255	7.1714e-05	--CCCCAGCCC-- NNGCCCCGCCNN	
Dde_M00304	8.2373e-05	GGGCTGGGG -GGCTGAGC	



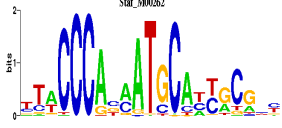






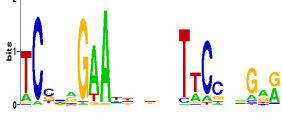
M23



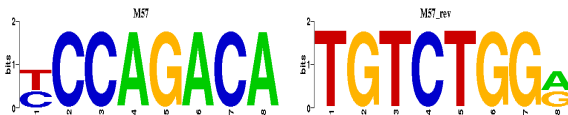
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CAC-binding_M00720	7.5184e-09	GGGCTGGG RGGSTGGG	
Sp1_M00931	4.9457e-08	-CCCAGCCC NCCCCGCC	
Sp1_M00932	9.1985e-07	--CCCAGCCC-- NNCCCCGCCNN	
Sp1_M00196	1.0547e-06	--GGGCTGGG-- NNGGGCGGGNN	
KROX_M00982	3.5572e-06	----CCCAGCCC-- CCGCCCCCNCNN	
GC_M00255	7.7874e-06	---CCCAGCCC-- NNGCCCCGCCNN	
Dde_M00304	2.5348e-05	GGGCTGGG- -GGCTGAGC	
Alfin1_M00479	4.3469e-05	----CCCAGCCC-- MNNCCCCACNYNYN	
Sp1_M00008	4.5569e-05	-CCCAGCCC WCCCYGCCY	
MTF-1_M00650	5.9973e-05	-----CCCAGCCC NTGCACNCGGCC	

M49



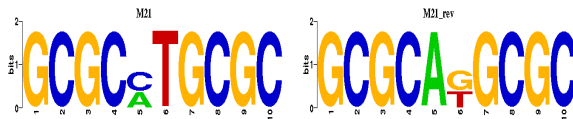
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
RAP1_M00213	1.5257e-05	----TCTGGGT-- NRTGTATGGGTKY	
CP2_M00072	1.6291e-05	TCTGGGT---- -CTGGKTNNG	
Staf_M00262	6.6463e-05	-----TCTGGGT-- NNGCYRNTGCATKNTGGGWAN	
STAT_M00777	7.2900e-05	ACCAGA----- TCCNAGAANNNN	
GLI_M01037	2.2459e-04	-----ACCCAGA NGACCACCCAN-	
RCS1_M00753	3.0528e-04	-TCTGGGT---- AANTGGGTGCAK	
CP2-LBP-1c-LSF_M00947	6.2235e-04	-----ACCCAGA CNRGNNNNANCCAG-	
STATx_M00223	7.0839e-04	ACCAGA- TCCCRKAA	
Grainyhead-Elf-1-NTF-1_M00951	8.2697e-04	-ACCCAGA AAACCRG-	
STAT5A_M00460	8.2766e-04	-----TCTGGGT YNCNNGGAANNNNNTTCNNNGA	

M57



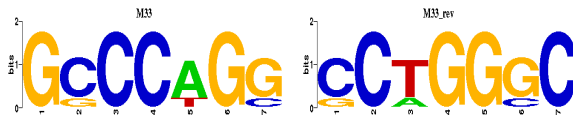
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
RAP1_M00213	1.1768e-05	---YCCAGACA-- RMACCCATACAYN	
SMAD_M00974	3.8483e-05	-TGCTGGR- NWGCTGNNN	
ARF_M00438	2.0738e-04	YCCAGACA- --GAGACAA	
Hand1-E47_M00222	3.8360e-04	---YCCAGACA---- NNWNCCAGAYNCNNN	
TGIF_M00418	4.0153e-04	--TGCTGGR GCTGTCANNW	
RP58_M00532	4.3269e-04	---TGCTGGR NAACATCTGGA	
SMAD3_M00701	8.1985e-04	-YCCAGACA AGNCAGAC-	
HSF_M00641	1.7305e-03	----TGCTGGR GAARCYNCKNGA	
SMAD4_M00733	2.5498e-03	---TGCTGGR--- RGNTGKCTGNMYSN	
ABF1_M00400	3.0767e-03	-----YCCAGACA NNCNNYNCCACGTGGCCNCGACA	

M21



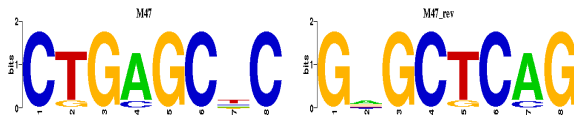
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Nrf-1_M00652	1.0542e-08	-GCGCMTGCGC YGC GCAYGC--	
Egr-2_M00246	1.7368e-05	GCGCMTGCGC- MCGCCCACGCA	
Egr-3_M00245	3.3621e-05	GCGCMTGCGC- ACGCCCACGCA	
AP-2_M00189	4.3040e-05	--GCGCAKGC GC NCCCSCNGGCG-	
Egr-1_M00243	5.7329e-05	-GCGCAKGC GC TGC GTGGCGK	
NGFI-C_M00244	2.4894e-04	GCGCMTGCGC- CCRCCCACGCA	
E12_M00693	5.5002e-04	--GCGCMTGCGC NNNCACCTGY--	
HEN1_M00058	5.9622e-04	-----GCGCMTGCGC----- NNNGGNCGCAGCTGCGNCCNN	
AP-2_M00800	5.9711e-04	-GCGCAKGC GC----- SCSSCRGGCNRNRNN	
myogenin_M00712	1.0375e-03	GCGCMTGCGC -CASCTGN--	

M33



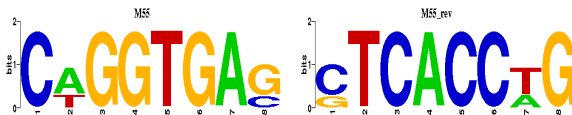
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AP-2_M00915	7.2559e-05	--CCTGGGC--- NGCCNGNGGNNN	
Egr-3_M00245	8.0740e-05	--GCCCAGG-- ACGCCACGCA	
Egr-1_M00243	1.0686e-04	--GCCCAGG-- MCGCCCACGCA	
Egr-2_M00246	1.3709e-04	--GCCCAGG-- MCGCCCACGCA	
NGFI-C_M00244	1.7687e-04	--GCCCAGG-- CCRCCCACGCA	
PCF2_M00948	8.1500e-04	---GCCCAGG NGNCCCAC-	
p53_M00034	8.4847e-04	-----CCTGGGC----- RGACATGCCCGGCATGTC	
MEF-3_M00319	8.9846e-04	GCCCAGG----- GSTCAGGTTWCN	
EBF_M00977	9.2049e-04	GCCCAGG--- NCYCWRGGGA	
AP-2alpha_M00469	9.4325e-04	GCCCAGG- SCNNGG	











M47



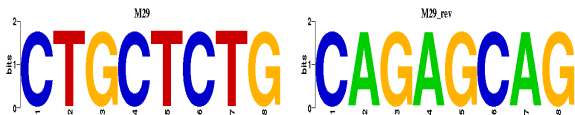
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Dde_M00304	2.9494e-06	GNGCTCAG-- --GCTCAGCC	
CDC5_M00361	2.8443e-05	----CTGAGCNC NSCGCTGAGS--	
PXR_M01153	3.3444e-05	CTGAGCNC -TGAACTN	
Pax_M00808	3.1533e-04	--GNGCTCAG TGGAACMAC	
HEN1_M00068	6.7507e-04	-----CTGAGCNC-- NNNGGNCNCAGCTGNGNCCNN	
GATA-2_M00349	8.8328e-04	-CTGAGCNC TNTTATCTS	
LF-A1_M00646	8.8423e-04	CTGAGCNC YWGASCC-	
MEF-3_M00319	1.9004e-03	-----CTGAGCNC NGWAACCTGASC--	
RXR_M01152	2.2190e-03	CTGAGCNC -TGAACTN	
AR_M00962	3.0463e-03	CTGAGCNC NNNTGCTC	











M55



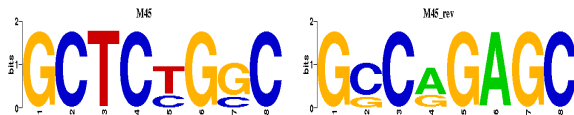
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AREB6_M00412	1.2319e-06	---CAGGTGAG- RNWCAGGTRNRN	
USF_M00796	5.2501e-06	-CTCACCTG-- NSTCACGTGNN	
myogenin_M00712	9.9914e-06	CTCACCTG- --CASCTGN	
MyoD_M00184	1.7463e-05	--CAGGTGAG GNCAGNTGN-	
Stra13_M00985	3.0631e-05	--CTCACCTG--- NNNTCACGTGANN	
E12_M00693	3.0776e-05	-CAGGTGAG- RCAGGTGNNN	
SREBP-1_M00220	4.8799e-05	--CAGGTGAG NTCACGTGAT	
AREB6_M00414	5.4021e-05	---CAGGTGAG NNMCAGGTGYN	
RAV1_M00344	5.8071e-05	----CAGGTGAG NNNCAGGTGN-	
MyoD_M00001	7.4536e-05	--CAGGTGAG- NNCAGGTGNYN	

M29



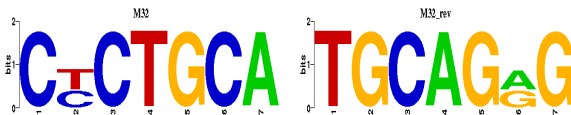
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HSF_M00167	5.8941e-06	---CTGCTCTG--- NTTCNNTTCNNTTC	
Eve_M00629	6.3835e-05	-CAGAGCAG GCNGNSSWN	
LMAF_M01139	7.0501e-04	CTGCTCTG CTGCTGAS	
XPF-1_M00684	8.2279e-04	-CTGCTCTG GKTSNYCNG	
AR_M00962	1.0230e-03	--CTGCTCTG NNNTGCTC--	
GR_M00205	1.1014e-03	-----CTGCTCTG GTACANNNTGTYCTK	
HSF_M00170	1.1650e-03	---CTGCTCTG--- NTTCNNTTCNNGAA	
Dde_M00304	1.5392e-03	--CAGAGCAG GGCTGAGC--	
Pax-1_M00326	1.5757e-03	-----CAGAGCAG----- ATATCTAGAGCGGAACG	
GR_M00921	1.8057e-03	CAGAGCAG -AGNACAN	











M45



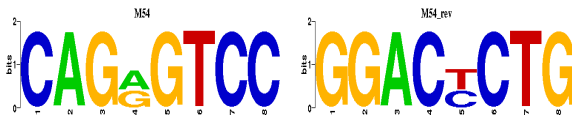
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Dde_M00304	1.9571e-05	GCCAGAGC GGCTGAGC	
BRK_M01096	5.2336e-05	-GCCAGAGC CGCCAN----	
Eve_M00629	2.9803e-04	GCCAGAGC-- -GCNGNSSWN	
HAC1_M00730	6.3960e-04	---GCTCTGGC GACACGCTGKC	
Hand1-E47_M00222	1.2470e-03	---GCCAGAGC---- NNWNCCAGAYNCNNN	
ZID_M00085	1.3644e-03	---GCCAGAGC- GRIGATRGAGCC	
AP-4_M00005	2.0352e-03	---GCCAGAGC----- MNGNCNNCAGCTGNNNN	
GC_M00255	2.6556e-03	--GCTCTGGC--- NNGCCCCGCCCN	
ZBRK1_M01105	2.9213e-03	-----GCTCTGGC- AAANNNCTGCKSCC	
Zta_M00711	3.0524e-03	---GCCAGAGC- TGWGYCANNNTN	

M32



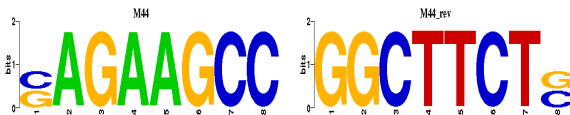
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Eve_M00629	1.6856e-05	TGCAGRG--- -GCNGNSSWN	
Nrf-2_M00821	3.0495e-04	-----CYCTGCA NNTGACTCAGCA	
v-Maf_M00035	6.1649e-04	---TGCAGRG----- NNNTGCNNNGTCAGCANN	
COUPTF_M01036	1.0509e-03	TGCAGRG----- NKNNRNGKNNAAAGGTCANNNN	
Ttk_M00009	1.2118e-03	TGCAGRG- -GCAGGAC	
MAZ_M00649	1.8034e-03	TGCAGRG GGGAGGG	
Dde_M00304	2.6414e-03	TGCAGRG- GGCTGAGC	
HSF_M00641	2.7229e-03	-----CYCTGCA GAARCYNCKNGA	
KAISO_M01119	4.2511e-03	--TGCAGRG NTNGCAGGA	
E2A_M00973	5.0154e-03	TGCAGRG RNCAGNT	

M54



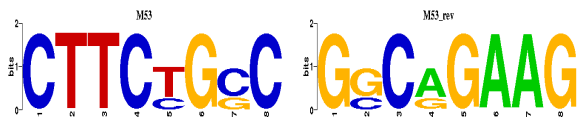
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SF1_M00727	1.2206e-04	CAGRGTCC CAAGGTC-	
SF1_M01132	5.4356e-04	-CAGRGTCC NCAAGGTN-	
NF-kappaB_M00208	5.8508e-04	--CAGRGTCC- NGGAAARTCCC	
MAF_M00983	6.6460e-04	-GGACYCTG- NTGACTCANC	
COUPTF_M01036	9.1467e-04	--CAGRGTCC----- NKNNRNGKNNAAAGGTCANNNN	
HNF4_M01031	1.0050e-03	--GGACYCTG--- NTGRMCTTTGNNC	
HNF4_M00967	1.0496e-03	--GGACYCTG NTGGACYT--	
NF-E2_M00037	1.3854e-03	-GGACYCTG- RTGACTCAGC	
Nrf-2_M00821	1.4252e-03	--GGACYCTG-- NNTGACTCAGCA	
SZF1-1_M01109	1.5413e-03	-----GGACYCTG CNGCTGWTACCCCTG	








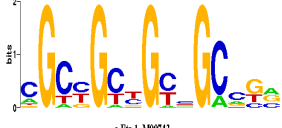


M44



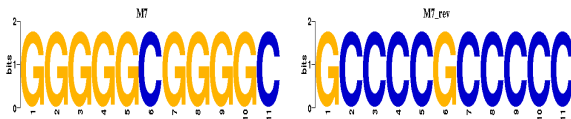
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PEND_M01015	2.5550e-04	GGCTTCTS -ACTTCTT	
GCR1_M00337	2.9491e-04	GGCTTCTS----- GGCTTCCACTWTT	
c-Ets-1_M00743	6.4588e-04	GGCTTCTS -GCTTCK	
GCR1_M00046	8.2414e-04	GGCTTCTS- -GCTTCCWC	
Sry-beta_M00666	8.6661e-04	-SAGAAGCC AGWGATGC-	
CCAAT_M00200	1.2654e-03	-----SAGAAGCC----- ANNWGNNGNRRGNNGNTGATTGG	
GZF1_M01069	1.3885e-03	--SAGAAGCC- TATAGANGCGC	
HSF_M00641	4.0282e-03	SAGAAGCC----- --GAARCYNCKNGA	
p53_M00761	4.1045e-03	SAGAAGCC- GRCAWGNCN	
dl_M00043	5.3029e-03	--SAGAAGCC NGGAAAAACC	

M53



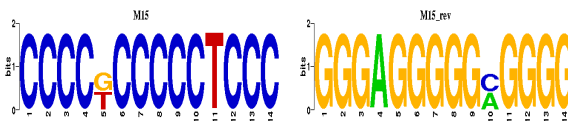
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	2.7315e-04	CTTCTGCC CTTCTC-	
TAL1_M00993	2.7607e-04	GGCAGAAG- RNCAGNTGG	
Nrf-2_M00108	3.6743e-04	--CTTCTGCC SNCTTCCGG-	
PEND_M01015	3.9337e-04	-CTTCTGCC ACTTCTT--	
GABP_M00341	5.9623e-04	GGCAGAAG---- -CCGGAAGNGCR	
LMAF_M01139	1.5478e-03	CTTCTGCC CTGCTGAS	
Ttk_M00009	1.6555e-03	GGCAGAAG -GCAGGAC	
Adf-1_M00171	2.8662e-03	-----GGCAGAAG-- NMNGCNRCRGCRGCG	
c-Ets-1_M00743	4.3288e-03	-CTTCTGCC GCTTCCK--	
Dde_M00304	4.6719e-03	CTTCTGCC GCTCAGCC	

M7



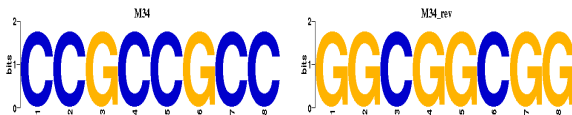
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
GC_M00255	4.5763e-13	GGGGGCGGGGC-- NNGGGCGGGGCNN	
UF1H3BETA_M01068	2.0896e-12	GCCCCGCCCC-- GCCCCCTCCCCRC	
ZNF219_M01122	1.2592e-11	GGGGGCGGGGC GGGNGGGGGGN	
Sp1_M00196	3.9909e-11	-GCCCCGCCCC NNCCCCGCCCCN	
Sp1_M00931	1.7229e-10	GCCCCGCCCC NCCCCGCC--	
Sp1_M00933	3.1431e-10	GCCCCGCCCC --CCCKCCCN	
KROX_M00982	3.4872e-10	---GCCCCGCCCC CCGCCCCCNCNNC-	
MAZR_M00491	1.7190e-08	GGGGGCGGGGC-- -SGGGGGGGGMNN	
Alfin1_M00479	2.1254e-08	--GCCCCGCCCC-- MNNCCCCACNYNYN	
ABI4_M00958	6.1750e-08	GGGGGCGGGGC-- --GGGCGGTGCN	

M15



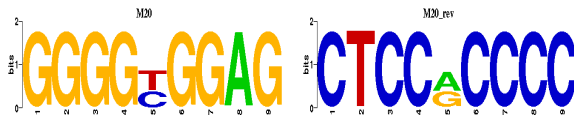
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
KROX_M00982	4.5445e-12	-GGGAGGGGGMGGGG GNNGNNGGGGGCGG--	
UF1H3BETA_M01068	1.5344e-10	-CCCCKCCCCCTCCC GCCCTCCCCRC--	
MAZ_M00649	3.8481e-09	CCCCKCCCCCTCCC -----CCCTCCC	
Sp1_M00933	1.1989e-08	CCCCKCCCCCTCCC -CCCKCCCN-----	
Sp1_M00931	1.4549e-08	-CCCCKCCCCCTCCC NCCCCGCC-----	
Sp1_M00196	1.6412e-08	--CCCCKCCCCCTCCC NNCCCCGCCCN----	
ZNF219_M01122	1.6709e-08	GGGAGGGGGMGGGG GGGNNGGGGGN---	
MAZR_M00491	9.8834e-08	CCCCKCCCCCTCCC --NNKCCCCCCCCS	
GC_M00255	3.9822e-07	---CCCCKCCCCCTCCC NNGCCCCGCCCN----	
Sp1_M00932	5.9741e-06	--CCCCKCCCCCTCCC NNCCCCGCCCN----	

M34



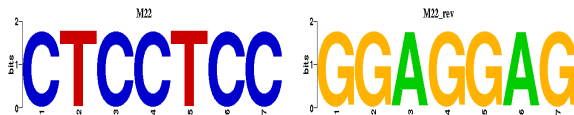
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ERF2_M01057	4.9441e-09	GGCGGCGG GGCGGC--	
Adf-1_M00171	1.2268e-07	--GGCGGCGG----- NMNGCNRCRGRGCG	
ETF_M00695	1.6885e-06	CCGCCGCC CCGCCN--	
KROX_M00982	3.1966e-06	-----GGCGGCGG GNNGNNGGGGCGG	
Adf-1_M00923	1.4126e-05	--CCGCCGCC----- SGCYGCMGYCGCTGMMNKYG	
ABI4_M00958	1.5780e-05	-GGCGGCGG- GGGCGGTGCN	
AP-2_M00189	2.2821e-05	-GGCGGCGG-- CGCCNGSGGGN	
Egr_M00807	4.9841e-05	-CCGCCGCC- NYYGCSCCCA	
Sp1_M00931	6.6760e-05	CCGCCGCC- NCCCCGCC	
Sp1_M00933	1.0988e-04	GGCGGCGG- NGGGMGGG	

M20



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
GC_M00255	4.0909e-08	---CTCCRCCCC-- NNGCCCCGCCNN	
Sp1_M00196	7.6821e-08	--CTCCRCCCC-- NNCCCCGCCCN	
KROX_M00982	8.9319e-08	GGGGYGGAG---- GNNNGGGGGGCGG	
Sp1_M00933	1.2274e-06	-GGGGYGGAG NGGGGMGGG-	
Sp1_M00931	2.7865e-06	-CTCCRCCCC NCCCCGCC-	
Alfin1_M00479	1.3092e-05	---CTCCRCCCC-- MNNCCCCACNYNYN	
Sp1_M00932	4.0840e-05	--CTCCRCCCC-- NNCCCCGCCNN	
ABI4_M00958	5.2311e-05	GGGGYGGAG-- -GGGCGGTGCN	
UF1H3BETA_M01068	6.2238e-05	-CTCCRCCCC--- GCCCTCCCCRC	
Zic2_M00449	6.2954e-05	CTCCRCCCC NACCACC-	

M22



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
WT1_M01118	2.8333e-05	GGAGGAG- GNNGGNGN	
Nrf-2_M00108	3.2163e-05	CTCCTCC-- SNCTTCCGG	
MAZ_M00649	7.0083e-05	CTCCTCC- -CCCTCCC	
PU.1_M00658	1.0018e-04	-CTCCTCC CTTCTC-	
GAL4_M00198	1.0090e-04	-----GGAGGAG----- NGYTCCGNNNANAGNNNNCCG	
UF1H3BETA_M01068	1.3968e-04	-CTCCTCC----- GCCCTCCCCRC	
GAL4_M00049	1.8919e-04	-----CTCCTCC----- NNCGGNNACWNTNSTCCGAAS	
Tra-1_M01048	4.8305e-04	CTCCTCC- -ACCWCCC	
Ttk_M00009	5.3972e-04	GGAGGAG GCAGGAC	
TFII-I_M00706	6.9259e-04	---GGAGGAG GANGKAGG--	

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