

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

Input file: 68 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".

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Multiple Alignment

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

```

M0 : -----GGGGGGGGGGGG-----
M1 : -----AAAGAAAAAAAAAAAAAAAA
M2 : -----GGAGGAGGG-----
M3 : -----CACACACACACA-----
M4 : -----GGAGGSAGGG-----
M5 : -----AGAGAGAGA-----
M6 : -----AGGGGAGGG-----
M7 : -----AAGGAAGGAAG-----
M8 : -----CCCCACCCACCCC-----
M9 : -----CCCCACCCACC-----
M10 : -----AGAAGGAAGA-----
M11 : -----AGAGGAAGA-----
M12 : -----TTTTTAAAAA-----
M13 : -----AAGGMAGGC-----
M14 : -----AAAAGAAAGAAAAAAAAA-----
M15 : -----GGTGGGGGA-----
M16 : -----AAAGAAAGAAA-----
M17 : -----AAAAACAAAAGA-----
M18 : -----CAGAGGNAG-----
M19 : -----AAAAGAAAAGAAA-----
M20 : AAAAAAAAACAAAACAAAAAAAAA-----
M21 : -----AAACAAACAAAAAAAA-----
M22 : -----AGAACAAAG-----

```

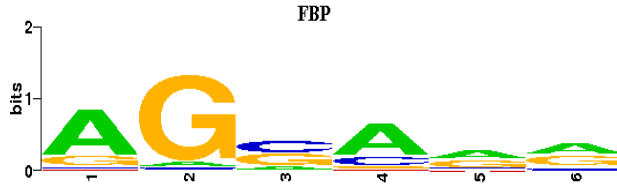
Stamp Results

04/30/14

M23: -----CCAGAGCTT-----
M24: -----AGGAMAGAG-----
M25: -----CAGCCTYCC-----
M26: -----AAACAAACAAA-----
M27: -----CCCAGCC-----
M28: -----GGAGGAG-----
M29: -----GGAGAGG-----
M30: -----AGGCAGA-----
M31: -----AGAGCAG-----
M32: -----CAGGCAG-----
M33: -----CACAGCA-----
M34: -----AGCCCAG-----
M35: -----CTGGGAR-----
M36: -----CAGCAGRG-----
M37: -----CCCAGRGC-----
M38: -----CTGCAGCC-----
M39: -----GSAGAGGG-----
M40: -----AGCAGCT-----
M41: -----AGGGCAG-----
M42: -----CAGAGCC-----
M43: -----GGAAGCA-----
M44: -----AGGAAAG-----
M45: -----CAGAGAG-----
M46: -----CTGGAGA-----
M47: -----CAGAGAA-----
M48: -----GGAGCCAG-----
M49: -----CTGGGGA-----
M50: -----AGCCACAG-----
M51: -----CCACACCC-----
M52: -----GAGAAAG-----
M53: -----GGGAGAG-----
M54: -----AGGAAAA-----
M55: -----AAAAGGAA-----
M56: -----GGCCCCAG-----
M57: -----CAGCCACA-----
M58: -----RAGCCAGG-----
M59: -----RGGGAGA-----
M60: -----CAGCTGGM-----
M61: -----CCAGAGGA-----
M62: -----CCASCAG-----
M63: -----AAAGCCTG-----
M64: -----CTGAGGGG-----
M65: -----AAAGAAGA-----

M66: -----CTCTGAGM-----
 M67: -----AAAAGAAG-----

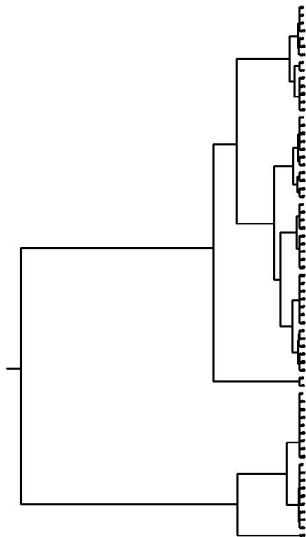
Familial Profile:
 (click for matrix)



Motif Tree

Tree (drawn by **Phylip**)



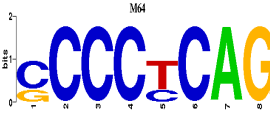



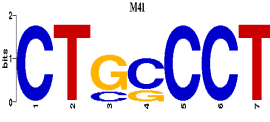








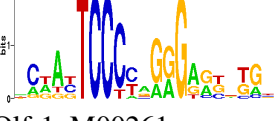
[Click here for Newick-format tree \(viewable with MEGA\)](#)


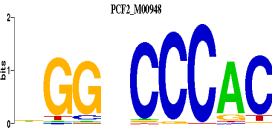
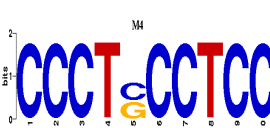



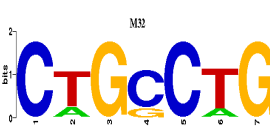






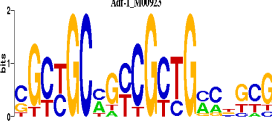




















Input Motif

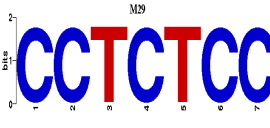
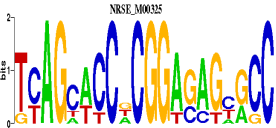


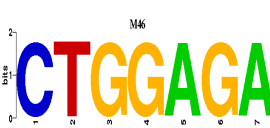



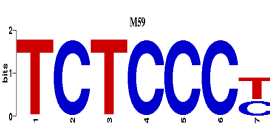

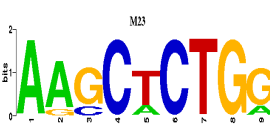


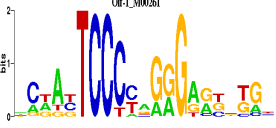


Best match in TRANSFAC



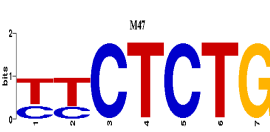



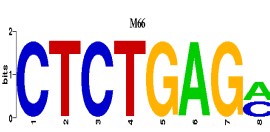









 M0	 ZNF219_M0112 (E val: 8.7019e-13)
 M8	 UF1H3BETA_M01068 (E val: 4.2744e-14)
 M9	 SREBP-1_M00221 (E val: 5.1144e-09)
 M15	 UF1H3BETA_M01068 (E val: 1.3191e-08)
 M2	 UF1H3BETA_M01068 (E val: 4.1818e-08)

<p>M28</p>  <p>CTCCTCC</p>	<p>WT1_M01118</p>  <p>C Cc c</p> <p>(E val: 2.8333e-05)</p>
<p>M64</p>  <p>CCCCAG</p>	<p>AP-2alphaA_M01045</p>  <p>GCC T AGG</p> <p>(E val: 6.4687e-05)</p>
<p>M6</p>  <p>AGGGAGGG</p>	<p>MAZ_M00649</p>  <p>GGGAGGG</p> <p>(E val: 2.6799e-10)</p>
<p>M41</p>  <p>CTGcCCT</p>	<p>HNF4_M01033</p>  <p>G CA</p> <p>(E val: 3.6901e-05)</p>
<p>M27</p>  <p>CCCAGCC</p>	<p>CAC-binding_M00720</p>  <p>AGG GT GGG</p> <p>(E val: 2.1814e-08)</p>
<p>M34</p>  <p>GCCCCAG</p>	<p>PCF2_M00948</p>  <p>GG CCCAc</p> <p>(E val: 3.3511e-04)</p>
<p>M35</p>  <p>CTGGGAAG</p>	<p>Ik-3_M00088</p>  <p>CT GGAAT ACC</p> <p>(E val: 6.1248e-07)</p>
<p>M49</p>  <p>TCCCCAG</p>	<p>Olf-1_M00261</p>  <p>CAA T C C G G A G T T G</p> <p>(E val: 9.3953e-07)</p>






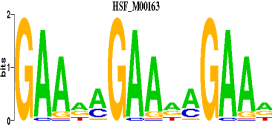




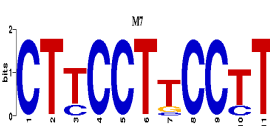



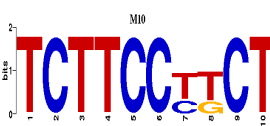

<p>M56</p> 	<p>PCF2_M00948</p>  <p>(E val: 6.9345e-06)</p>
<p>M4</p> 	<p>TFII-I_M00706</p>  <p>(E val: 3.9667e-09)</p>
<p>M30</p> 	<p>SMAD3_M00701</p>  <p>(E val: 4.4951e-07)</p>
<p>M32</p> 	<p>Tel-2_M00678</p>  <p>(E val: 1.7490e-05)</p>
<p>M48</p> 	<p>BRK_M01096</p>  <p>(E val: 2.1022e-05)</p>
<p>M58</p> 	<p>Grainyhead-Elf-1-NTF-1_M00951</p>  <p>(E val: 1.9076e-05)</p>
<p>M38</p> 	<p>Adf-1_M00923</p>  <p>(E val: 1.6376e-06)</p>
<p>M43</p> 	<p>c-Ets-1_M00743</p>  <p>(E val: 5.9273e-07)</p>


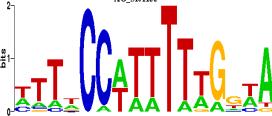





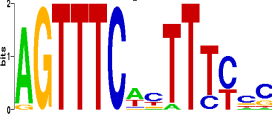


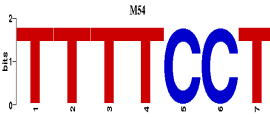


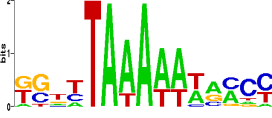
 <p>M25</p>	 <p>MAZ_M00649 (E val: 1.0625e-05)</p>
 <p>M63</p>	 <p>MEF-3_M00319 (E val: 2.5590e-04)</p>
 <p>M50</p>	 <p>Zta_M00711 (E val: 1.7146e-05)</p>
 <p>M57</p>	 <p>SMAD4_M00733 (E val: 2.5726e-04)</p>
 <p>M5</p>	 <p>GAGA_M00723 (E val: 2.4246e-08)</p>
 <p>M52</p>	 <p>PU.1_M00658 (E val: 1.2666e-06)</p>
 <p>M11</p>	 <p>PU.1_M00658 (E val: 1.0558e-09)</p>
 <p>M18</p>	 <p>PU.1_M00658 (E val: 2.0225e-08)</p>

 <p>M29</p>	 <p>NRSE_M00325 (E val: 1.2900e-04)</p>
 <p>M39</p>	 <p>UF1H3BETA_M01068 (E val: 1.8340e-05)</p>
 <p>M46</p>	 <p>BRK_M01096 (E val: 8.3786e-05)</p>
 <p>M53</p>	 <p>MAZ_M00649 (E val: 1.2667e-07)</p>
 <p>M59</p>	 <p>TFII-I_M00706 (E val: 4.2388e-06)</p>
 <p>M23</p>	 <p>HSF_M00641 (E val: 6.6151e-07)</p>
 <p>M37</p>	 <p>Olf-1_M00261 (E val: 2.4985e-05)</p>
 <p>M42</p>	 <p>NRSF_M00256 (E val: 1.3233e-05)</p>

 <p>M45</p>	 <p>GAGA_M00723 (E val: 2.4747e-05)</p>
 <p>M47</p>	 <p>STE11_M01005 (E val: 1.0035e-04)</p>
 <p>M61</p>	 <p>HSF_M00641 (E val: 3.3803e-06)</p>
 <p>M66</p>	 <p>CDC5_M00361 (E val: 5.5766e-05)</p>
 <p>M31</p>	 <p>HSF_M00167 (E val: 1.6673e-04)</p>
 <p>M40</p>	 <p>LBP-1_M00644 (E val: 2.0512e-08)</p>
 <p>M33</p>	 <p>Nrf-2_M00821 (E val: 1.8411e-05)</p>
 <p>M36</p>	 <p>HEB_M00698 (E val: 4.0040e-07)</p>

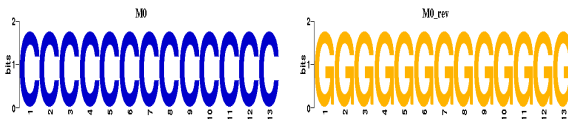
<p>M62</p>	<p>LMAF_M01139 (E val: 3.0422e-06)</p>
<p>M60</p>	<p>HEB_M00698 (E val: 1.2426e-10)</p>
<p>M3</p>	<p>HFH4_M00742 (E val: 3.4597e-06)</p>
<p>M51</p>	<p>CACD_M01113 (E val: 2.1371e-10)</p>
<p>M1</p>	<p>FOXP1_M00987 (E val: 2.4128e-08)</p>
<p>M14</p>	<p>STE11_M01005 (E val: 5.6541e-08)</p>
<p>M20</p>	<p>FOXP1_M00987 (E val: 1.1102e-16)</p>
<p>M16</p>	<p>STE11_M00274 (E val: 4.8669e-11)</p>








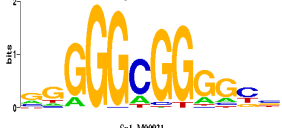

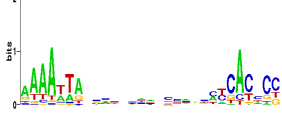
 <p>M21</p>	 <p>HFH4_M00742 (E val: 1.5711e-12)</p>
 <p>M26</p>	 <p>HFH4_M00742 (E val: 9.9920e-16)</p>
 <p>M17</p>	 <p>HSF_M00163 (E val: 1.5244e-09)</p>
 <p>M19</p>	 <p>HSF_M00163 (E val: 1.1102e-16)</p>
 <p>M22</p>	 <p>STE11_M01005 (E val: 1.2978e-10)</p>
 <p>M7</p>	 <p>PU.1_M00658 (E val: 4.5163e-06)</p>
 <p>M13</p>	 <p>Ets_M00971 (E val: 1.4402e-05)</p>
 <p>M10</p>	 <p>MAF_M00648 (E val: 1.5750e-07)</p>

 <p>M55</p>	 <p>AG_M01133 (E val: 5.3568e-08)</p>
 <p>M65</p>	 <p>PEND_M01015 (E val: 2.6717e-07)</p>
 <p>M67</p>	 <p>PEND_M01015 (E val: 2.6717e-07)</p>
 <p>M24</p>	 <p>ISGF-3_M00258 (E val: 3.6409e-05)</p>
 <p>M44</p>	 <p>NF-kappaB_M00208 (E val: 1.1677e-05)</p>
 <p>M54</p>	 <p>Helios_M01004 (E val: 6.4796e-10)</p>
 <p>M12</p>	 <p>MEF-2_M00405 (E val: 2.9868e-07)</p>

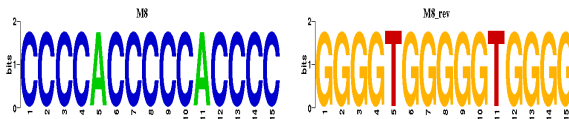
Motif Similarity Matches

M0



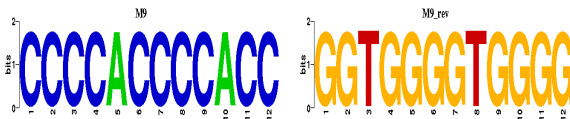
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ZNF219_M01122	8.7019e-13	GGGGGGGGGGGGGG GGGNGGGGGGN--	
KROX_M00982	4.4263e-12	GGGGGGGGGGGGGG GNNNGGGGGGCGG	
MAZR_M00491	2.8460e-09	---GGGGGGGGGGGGG SGGSGGGGGGGMNN-	
UF1H3BETA_M01068	1.1918e-08	-CCCCCCCCCCCCC GCCCTCCCCRC-	
RREB-1_M00257	1.3559e-07	GGGGGGGGGGGGGG GGGGTGGTTTGGG	
AtMYB-84_M00970	2.9390e-06	GGGGGGGGGGGGGG GGNGGTAGGTGS-	
Alfin1_M00479	1.5311e-05	CCCCCCCCCCCCC- MNNCCCCACNYYN	
Sp1_M00196	1.5434e-05	--CCCCCCCCCCCCC NNCCCCGCCCN---	
Sp1_M00931	4.0043e-05	-CCCCCCCCCCCCC NCCCCGCC-----	
Pax-4_M00380	6.1908e-05	-----CCCCCCCCCCCCC NAAAWTANNNNNNNNNNNNNNNNNNNCACNCN	



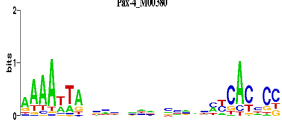







M8



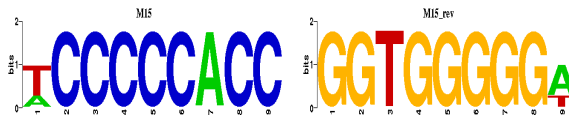
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
UF1H3BETA_M01068	4.2744e-14	-CCCCACCCCCACCCC GCCCTCCCCRC---	
KROX_M00982	2.2382e-13	GGGGTGGGGTGGGG GNNNGGGGGCGG--	
GBF_M00633	2.6601e-10	CCCCACCCCCACCCC ---NACCCNA----	
Alfin1_M00479	5.3896e-10	CCCCACCCCCACCCC-- ---MNNCCCCACNYNYN	
ZNF219_M01122	1.1492e-08	GGGGTGGGGTGGGG GGNGGGGGGN----	
RREB-1_M00257	6.6020e-08	GGGGTGGGGTGGGG -GGGGTGGTTTGGG-	
CAC-binding_M00720	2.7398e-07	GGGGTGGGGTGGGG RGGSTGGG-----	
Pax-4_M00380	1.2184e-06	GGGGTGGGGTGGGG----- NGNGTGNNNNNNNNNNNNNNNTAWTTN	
Egr_M00807	1.2324e-05	CCCCACCCCCACCCC -NYYGCSCCA----	
AtMYB-84_M00970	1.2987e-05	GGGGTGGGGTGGGG -GGNGGTAGGTGS--	

M9



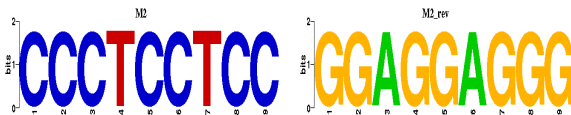
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SREBP-1_M00221	5.1144e-09	GGTGGGGTGGGG -GTGGGGTGAT-	
RREB-1_M00257	3.1302e-08	--GGTGGGGTGGGG GGGGTGGTTTGGG-	
Pax-4_M00380	6.2570e-08	--GGTGGGGTGGGG----- NGNGTGNNNNNNNNNNNNNNNNNTAWTTTN	
CAC-binding_M00720	6.6711e-08	GGTGGGGTGGGG ---RGGSTGGG-	
Alfin1_M00479	7.8685e-08	---CCCCACCCCACC MNNCCCCACNYNYN-	
UF1H3BETA_M01068	1.9404e-07	-CCCCACCCCACC GCCCTCCCCRC	
SREBP-1_M00749	6.8090e-07	GGTGGGGTGGGG --TGSGT----	
KROX_M00982	1.1711e-06	----CCCCACCCCACC CCGCCCCNCNNC---	
Sp1_M00196	2.4110e-06	--CCCCACCCCACC NNCCCCGCCCN--	
ROM_M00700	3.3121e-06	CCCCACCCCACC --CCACSTCA--	

M15



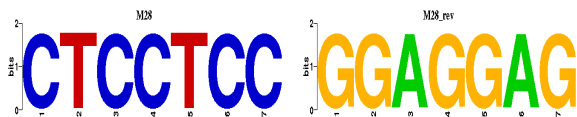
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
UF1H3BETA_M01068	1.3191e-08	GGTGGGGGA----- -GYGGGGGAGGGGC	
KROX_M00982	2.4459e-06	--GGTGGGGGA-- GNNGNNGGGGGCGG	
ZNF219_M01122	3.3785e-06	-GGTGGGGGA- GGGNNGGGGGGN	
Alfin1_M00479	3.5856e-06	-TCCCCCACC----- MNNCCCCACNYYN	
MAZR_M00491	5.1481e-06	-GGTGGGGGA-- SGGGGGGGGMNN	
GBF_M00633	8.8926e-06	-TCCCCCACC NACCCNA--	
SREBP-1_M00221	6.7051e-05	GGTGGGGGA-- -GTGGGGTGAT	
MZF1_M00084	7.6101e-05	-TCCCCCACC-- TTNCCCCTCNNN	
CAC-binding_M00720	7.6852e-05	TCCCCCACC-- ---CCCASCCY	
MOVO-B_M01104	1.2357e-04	TCCCCCACC -CCCCN--	





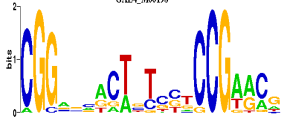

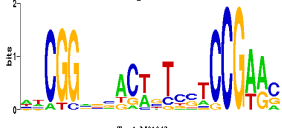



M2



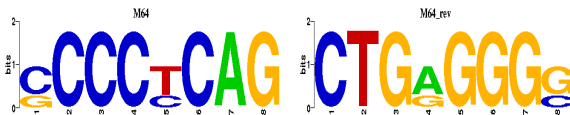
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<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
UF1H3BETA_M01068	4.1818e-08	--CCCTCCTCC-- GCCCTCCCCRC	
ZNF219_M01122	1.9528e-07	-GGAGGAGGG- GGNGGGGGGN	
MAZ_M00649	7.4906e-07	CCCTCCTCC CCCTCCC--	
PU.1_M00658	1.5920e-05	GGAGGAGGG -GAGGAAG-	
Alfin1_M00479	3.3233e-05	----CCCTCCTCC- MNNCCCCACNYNYN	
MAZR_M00491	1.1248e-04	GGAGGAGGG--- SGGGGGGGMNN	
Sp1_M00933	1.4123e-04	GGAGGAGGG NGGGGMGGG	
VDR_M00444	1.6743e-04	---CCCTCCTCC-- TSWCCYYNYTNMCC	
ROM_M00700	1.7947e-04	GGAGGAGGG TGASGTGG-	
WT1_M01118	3.6148e-04	GGAGGAGGG GNNGGNGN-	





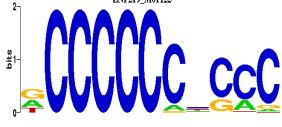




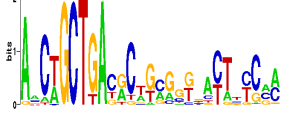
M28



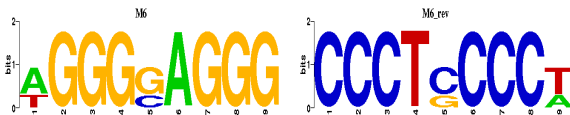
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
WT1_M01118	2.8333e-05	GGAGGAG- GNNGGNGN	
Nrf-2_M00108	3.2163e-05	CTCCTCC-- SNCTTCCGG	
MAZ_M00649	7.0083e-05	CTCCTCC- -CCCTCCC	
PU.1_M00658	1.0018e-04	-CTCCTCC CTTCTC-	
GAL4_M00198	1.0090e-04	-----GGAGGAG-----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

M64

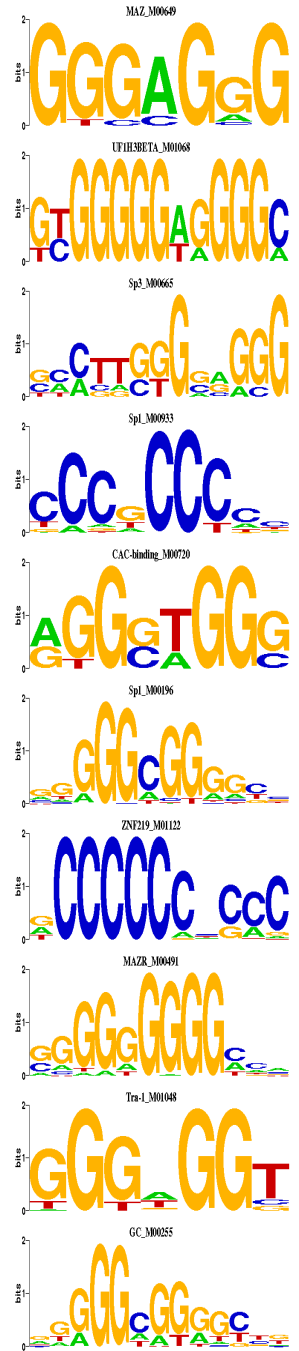


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AP-2alphaA_M01045	6.4687e-05	----CTGAGGGG-- NNGCCTNAGGSNNN	
STRE_M00308	7.0946e-05	-CCCCTCAG NCCCCT----	
GBF_M00633	1.6224e-04	-CCCCTCAG NACCCNA-	
ROM_M00700	1.6306e-04	CTGAGGGG- -TGASGTGG	
ZNF219_M01122	2.2196e-04	CTGAGGGG--- GGNGGGGGGN	
AP-2alphaA_M01047	3.9161e-04	----CTGAGGGG- ANMGCTNAGGCKN	
MZF1_M00084	4.1594e-04	---CCCCTCAG- TTNCCCCTCINN	
MAZ_M00649	4.6624e-04	CTGAGGGG GGGAGGG-	
STRE_M00154	5.2540e-04	-CCCCTCAG NCCCCTN--	
Bel-1_M00312	5.2545e-04	-----CCCCTCAG----- KNGRNAGTNMCKCWGYRTCAGCAGNT	

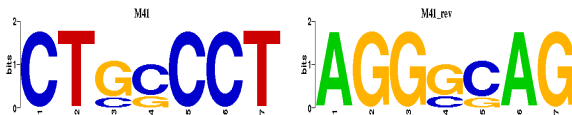
M6

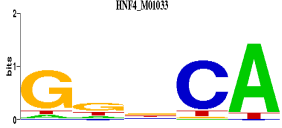

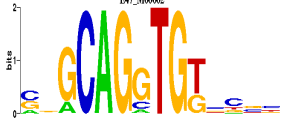

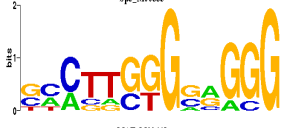


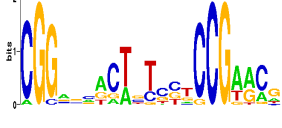


	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
MAZ_M00649	2.6799e-10	AGGGGAGGG --GGGAGGG
UF1H3BETA_M01068	8.3321e-09	--CCCTCCCCT-- GCCCCCCCCRC
Sp3_M00665	8.6491e-09	----AGGGGAGGG SMCTTGGGSRGGG
Sp1_M00933	1.6633e-07	CCCTCCCCT CCCKCCCN
CAC-binding_M00720	4.1609e-07	AGGGGAGGG -RGGSTGGG
Sp1_M00196	5.6366e-06	---CCCTCCCCT NNCCCCGCCCN
ZNF219_M01122	1.2451e-05	AGGGGAGGG---- --GGGNGGGGGGN
MAZR_M00491	1.8276e-05	AGGGGAGGG---- -SGGGGGGGGMNN
Tra-1_M01048	2.3694e-05	CCCTCCCCT ACCWCCC--
GC_M00255	3.6690e-05	----CCCTCCCCT NNGCCCCGCCNN

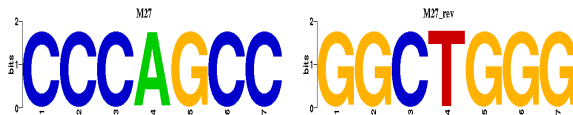








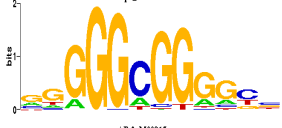



M41



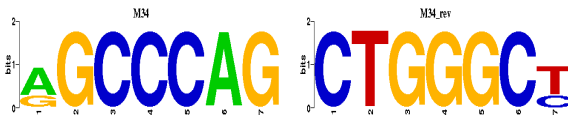
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HNF4_M01033	3.6901e-05	CTGCCCT -TGNNC-	
SMAD4_M00733	4.9535e-04	-----CTGCCCT- RGNTGKCTGNMYSN	
COUPTF_M01036	1.5654e-03	-----AGGGCAG----- NKNNRNGKNNAAAGGTCANNNN	
E47_M00002	1.8265e-03	-----CTGCCCT NNNNACACCTGCNS-	
E2A_M00973	2.4783e-03	AGGGCAG-- --RNCAGNT	
Sp3_M00665	2.7963e-03	--CTGCCCT---- CCCYSCCAAGKS	
MAF_M00648	2.8373e-03	--AGGGCAG----- NGRRGGAAGTKKNSN	
BRK_M01096	3.7078e-03	CTGCCCT NTGGCG-	
Eve_M00629	4.0886e-03	--AGGGCAG GCNGNSSWN	
GAL4_M00198	4.3799e-03	-----AGGGCAG----- NGYTCGGNNNANAGNNNNCCG	

M27



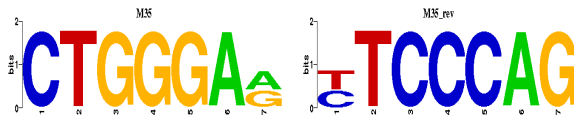
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CAC-binding_M00720	2.1814e-08	CCCAGCC- CCCASCCY	
Dde_M00304	4.5915e-06	GGCTGGG- GGCTGAGC	
Sp1_M00008	6.7548e-06	-CCCAGCC- WCCCYGCCY	
Sp1_M00931	7.8495e-06	-CCCAGCC- NCCCCGCC	
LUN-1_M00480	1.4639e-05	-----GGCTGGG TCCCAAAGTAGCTGGG	
Sp1_M00932	5.5489e-05	--CCCAGCC-- NNCCCCGCCCN	
Sp1_M00196	5.8793e-05	---GGCTGGG-- NGGGGCGGGGN	
AP-2_M00915	1.2904e-04	-GGCTGGG---- NGCCNGNGGNN	
KROX_M00982	1.6540e-04	--GGCTGGG---- GNNGNGGGGGCGG	
HEB_M00698	2.0498e-04	-GGCTGGG CAGCWGG-	








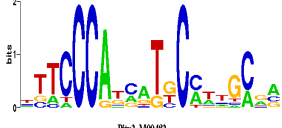


M34



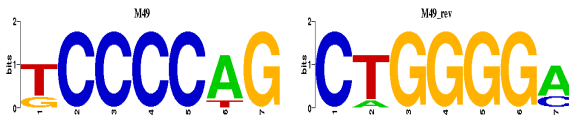
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PCF2_M00948	3.3511e-04	--AGCCCAG NGGNCCCAC	
YY1_M00069	5.9713e-04	---AGCCCAG----- WNSANNCAAGATGGCNGNN	
SREBP-1_M00749	6.0365e-04	CTGGGCT -TGGSGT	
Pitx2_M00482	7.8462e-04	CTGGGCT--- NTGGGATTAN	
Dde_M00304	1.8434e-03	--CTGGGCT GGCTGAGC-	
Egr-3_M00245	1.8933e-03	---CTGGGCT- TGGTGGGCGT	
Egr-1_M00243	2.0090e-03	-AGCCCAG--- MCGCCCACGCA	
Poly_M00211	2.0727e-03	-AGCCCAG GAGACCAC	
HEN1_M00068	2.4911e-03	-----CTGGGCT--- NNNGGNCNCAGCTGNGNCCNN	
CP2_M00072	2.5155e-03	CTGGGCT--- CTGGKTNGNG	

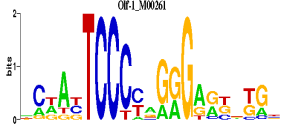


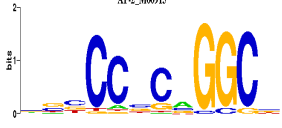






M35



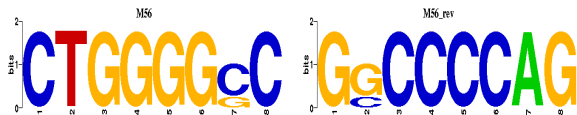
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Ik-3_M00088	6.1248e-07	----YTCCCAG-- GGTATTCCCNRN	
Lyf-1_M00141	8.3004e-07	-YTCCCAG YCTCCCAA	
RBP-Jkappa_M01112	1.0207e-05	-YTCCCAG-- KTTCCCACGN	
RBP-Jkappa_M01111	5.1589e-05	-CTGGGAR NGTGGGA-	
STAT_M00777	8.0079e-05	YTCCCAG----- -TCCNAGAANNNN	
Su_H_M00234	8.4276e-05	---YTCCCAG-- NGKTTCCCACRN	
Ik-1_M00086	8.6389e-05	----YTCCCAG-- NNNATTCCCANN	
Staf_M00264	9.1777e-05	-----CTGGGAR-- NNGCANNKGNANNNNTGGGANN	
Pitx2_M00482	1.8446e-04	CTGGGAR--- NTGGGATTAN	
Alx-4_M00619	3.3172e-04	-----YTCCCAG GATTATTCTCAG	

M49



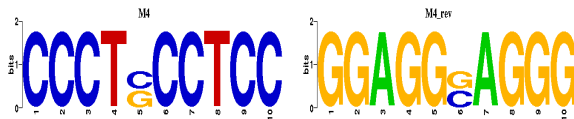
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Olf-1_M00261	9.3953e-07	-----TCCCCAG----- NCNANTCCCYNGGGGARNNKGN	
EBF_M00977	8.5188e-06	TCCCCAG--- TCCCYWGRGN	
SREBP-1_M00749	4.1201e-05	CTGGGGA -TGGSGT	
AP-2_M00915	4.3245e-05	---CTGGGGA-- NGCCNGNGGNNN	
MZF1_M00083	7.8038e-05	TCCCCAG TCCCCNN	
BRK_M01096	9.8255e-05	CTGGGGA NTGGCG-	
XPF-1_M00684	1.4290e-04	--TCCCCAG GKTSNYCNG	
GBF_M00633	3.9480e-04	--TCCCCAG NACCCNA-	
Ik-3_M00088	4.0789e-04	-CTGGGGA---- NYNGGGAATACC	
Sp3_M00665	6.9739e-04	---TCCCCAG--- CCCYSCCAAGKS	

M56



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PCF2_M00948	6.9345e-06	-GGCCCCAG NGGNCCCAC	
Alfin1_M00479	1.0315e-05	-GGCCCCAG----- MNNCCCCACNYNYN	
Muscle_M00324	2.7069e-05	-----CTGGGGCC--- KSCNSYKGNRTGRNGNCNNN	
Muscle_M00323	6.1325e-05	-----CTGGGGCC--- KSCNSCTGNRTGGNGNCNNN	
Egr_M00807	6.4737e-05	---GGCCCCAG NYYGCSCCCA-	
SREBP-1_M00749	9.3983e-05	CTGGGGCC -TGSGT-	
BRK_M01096	2.0178e-04	CTGGGGCC NTGGCG--	
AP-2_M00915	2.2176e-04	-GGCCCCAG--- NNNCCNCNGGCN	
HEN1_M00058	2.4059e-04	-----CTGGGGCC-- NNNGGNCGCAGCTGCGNCCNN	
ZBRK1_M01105	2.7431e-04	-----CTGGGGCC AAANNCTGCKSCC	

M4



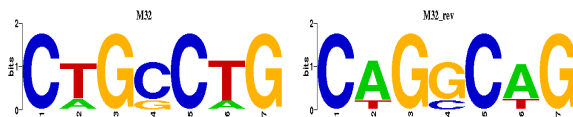
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
TFII-I_M00706	3.9667e-09	CCCTSCCTCC -CTMCNTC-	
MAZ_M00649	7.3910e-09	CCCTSCCTCC CCCTCCC---	
CAC-binding_M00720	9.6761e-08	CCCTSCCTCC CCCASCCY--	
UF1H3BETA_M01068	5.2698e-06	--CCCTSCCTCC- GCCCCTCCCCRC	
ZNF219_M01122	1.4883e-05	-GGAGGSAGGG GGGNGGGGGGN	
Sp3_M00665	1.3467e-04	---GGAGGSAGGG SMCTTGGGSRGGG	
PU.1_M00658	1.4083e-04	CCCTSCCTCC --CTTCCTC-	
E2A_M00804	2.1128e-04	--GGAGGSAGGG- NMNGNGNCAGGTG	
Tra-1_M01048	2.7249e-04	GGAGGSAGGG ---GGGWGGT	
Sp1_M00008	4.3466e-04	-CCCTSCCTCC WCCCYGCCY--	


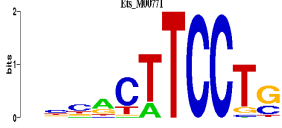
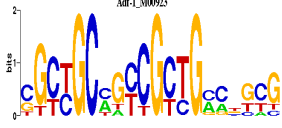







M30



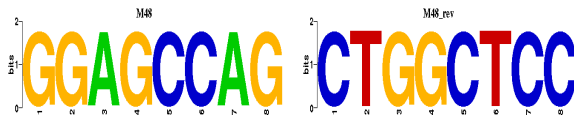
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SMAD3_M00701	4.4951e-07	AGGCAGA- AGNCAGAC	
Dde_M00304	4.0214e-04	AGGCAGA-- -GGCTGAGC	
Ets_M00971	5.7503e-04	-AGGCAGA NAGGAAG-	
SMAD4_M00733	5.9147e-04	-----TCTGCCT-- RGNTGKCTGNMYSN	
PU.1_M00658	7.0533e-04	-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---- CACCTGNCNCNKN	


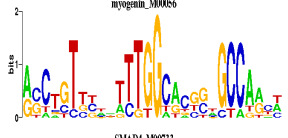

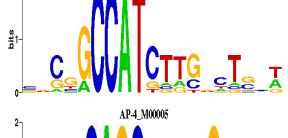






M32



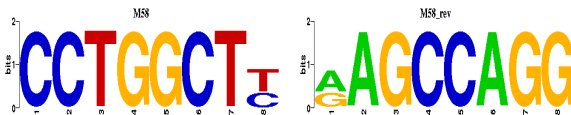
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Tel-2_M00678	1.7490e-05	--CTGCCTG TACTTCCTG	
Ets_M00771	8.9017e-05	----CTGCCTG NNNRCTTCCTG	
Adf-1_M00923	1.3899e-04	--CAGGCAG----- CRMNKKCAGCGRCKGCRGCS	
c-Ets-2_M00340	2.1612e-04	----CTGCCTG- ANNNACTTCCTGY	
c-Ets-1_M00339	2.3445e-04	-----CTGCCTG NNMNNNACTTCCTG	
NERF1a_M00531	2.6254e-04	-----CTGCCTG-- SNNNASNYRCTTCCTGNY	
Ets_M00971	8.9926e-04	CAGGCAG NAGGAAG	
SMAD3_M00701	1.2672e-03	CAGGCAG-- -AGNCAGAC	
SMAD4_M00733	1.5469e-03	-CAGGCAG----- NSRKNCAGMCANCY	
PU.1_M00658	1.6773e-03	CAGGCAG GAGGAAG	

M48



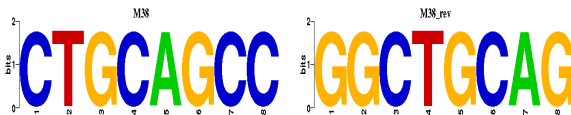
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
BRK_M01096	2.1022e-05	CTGGCTCC NTGGCG--	
myogenin_M00056	5.1107e-05	--CTGGCTCC----- NNYTGGCNSNGTGCCAAANNNNACAGST	
SMAD4_M00733	1.3521e-04	--CTGGCTCC---- RGNTGKCTGNMYSN	
YY1_M00069	2.9776e-04	-----CTGGCTCC- NNCNGCCATCTTGNNTSNW	
AP-4_M00005	3.6755e-04	-----CTGGCTCC MNGNCNNCAGCTGNNNN-	
ZID_M00085	6.3058e-04	-----GGAGCCAG GRTGATRGAGCC--	
ARF_M00438	1.2769e-03	GGAGCCAG -GAGACAA	
Zta_M00711	1.6689e-03	GGAGCCAG---- TGWGYCANNNTN	
v-Maf_M00035	1.6936e-03	-----GGAGCCAG----- NNNTGCNNNGTCAGCANN	
Grainyhead-Elf-1-NTF-1_M00951	2.0741e-03	CTGGCTCC CYGGTTT-	

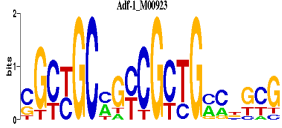


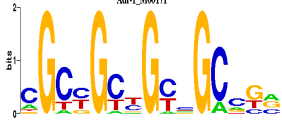



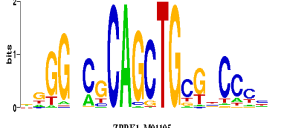


M58



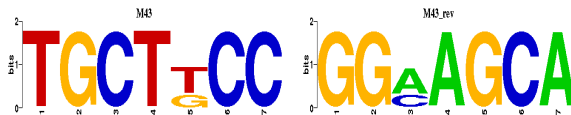
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Grainyhead-Elf-1-NTF-1_M00951	1.9076e-05	RAGCCAGG AAACCRG-	
BRK_M01096	2.1022e-05	CCTGGCTY -NTGGCG-	
E2A_M00804	7.4707e-04	---RAGCCAGG-- NMNGNGNCAGGTG	
PPARalpha-RXRalpha_M00242	1.1803e-03	-RAGCCAGG----- WRAWCTAGGNCAAAGGTCA	
CP2-LBP-1c-LSF_M00947	1.3677e-03	CCTGGCTY----- -CTGGNTNNNNCYNG	
CP2_M00072	1.3718e-03	CCTGGCTY--- -CTGGKTINGNG	
E2A_M00973	2.0739e-03	RAGCCAGG- --RNCAGNT	
CCAAT_M00200	2.1088e-03	-----CCTGGCTY----- CCAATCANCNNNCYNNCNCWNNT	
AP-4_M00005	2.7747e-03	RAGCCAGG----- NNNNCAGCTGNNGNCNK	
alpha-CP1_M00687	3.2264e-03	---CCTGGCTY CTCATTGGCT-	

M38



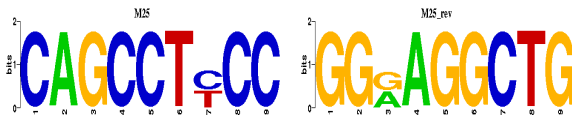
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Adf-1_M00923	1.6376e-06	-----GGCTGCAG-- CRMNKKCAGCGRCKGCRGCS	
RCS1_M00753	8.7287e-05	----GGCTGCAG AANTGGGTGCAK	
LBP-1_M00644	9.9357e-05	CTGCAGCC --SCAGCN	
Adf-1_M00171	1.0112e-04	--GGCTGCAG----- NMNGCNRCRGCRGCG	
ERF2_M01057	2.6381e-04	GGCTGCAG GGCGGC--	
SMAD4_M00733	2.9034e-04	----GGCTGCAG-- RGNTGKCTGNMYSN	
LMAF_M01139	3.3754e-04	CTGCAGCC CTGCTGAS	
HEN1_M00058	4.7353e-04	-----CTGCAGCC-- NNNGGNCGCAGCTGCGNCCNN	
ZBRK1_M01105	5.7072e-04	-----CTGCAGCC AAANNCTGCKSCC	
Dde_M00304	9.3263e-04	GGCTGCAG GGCTGAGC	

M43



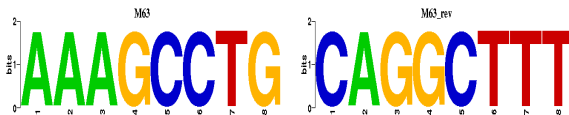
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
c-Ets-1_M00743	5.9273e-07	TGCTTCC-- -GCTTCK	
GCR1_M00046	6.9523e-07	--GGAAGCA GWGGAAGC-	
Tel-2_M00678	1.9045e-05	--GGAAGCA CAGGAAGTA	
GCR1_M00337	3.6874e-05	-----GGAAGCA AAWAGTGGGAAGCC	
c-Ets-2_M00340	1.1139e-04	---TGCTTCC--- ANNNACTTCCTGY	
NERF1a_M00531	1.2349e-04	-----TGCTTCC----- SNNNASNYRCTTCCTGNY	
PU.1_M00658	1.7081e-04	TGCTTCC-- --CTTCCTC	
Ets_M00971	1.7151e-04	--GGAAGCA NAGGAAG--	
PEA3_M00655	3.0524e-04	-GGAAGCA MGGAWG--	
HEN1_M00058	3.2338e-04	---GGAAGCA----- NNNGGNCGCAGCTGCGNCCNN	


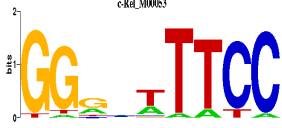

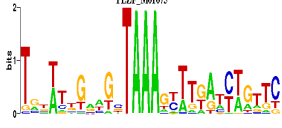

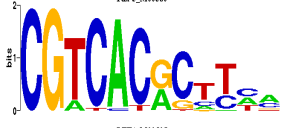


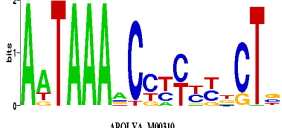
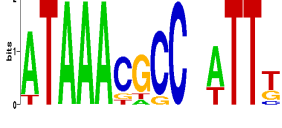
M25



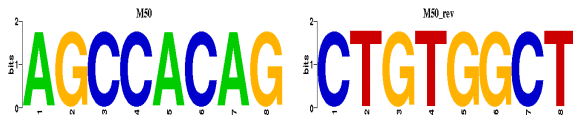
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MAZ_M00649	1.0625e-05	CAGCCTYCC --CCCTCCC	
Tra-1_M01048	1.0114e-04	GGRAGGCTG GGGWGGT--	
TFII-I_M00706	6.3417e-04	CAGCCTYCC-- ---CCTMCNTC	
SMAD4_M00733	7.6183e-04	GGRAGGCTG----- RGNTGKCTGNMYSN	
CAC-binding_M00720	1.2712e-03	--CAGCCTYCC CCCASCCY---	
Lyf-1_M00141	1.8750e-03	CAGCCTYCC-- ---YCTCCCAA	
Dde_M00304	2.2027e-03	GGRAGGCTG--- ----GGCTGAGC	
Tra-1_M01049	3.3286e-03	CAGCCTYCC --ACCNCCC	
ERF2_M01057	3.7153e-03	GGRAGGCTG -GGCGGC--	
UF1H3BETA_M01068	4.0080e-03	CAGCCTYCC----- GCCCCTCCCCRC	

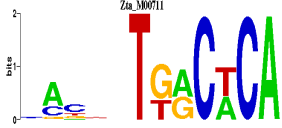
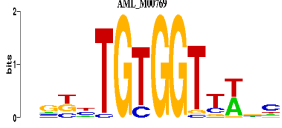








M63



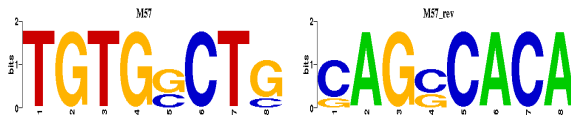
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MEF-3_M00319	2.5590e-04	-AAAGCCTG--- NGWAACCTGASC	
c-Rel_M00053	9.3059e-04	--AAAGCCTG GGAAWNYCC-	
Barbie_M00238	1.1094e-03	---CAGGCTTT--- CMNNCNSCTTTNNN	
PLZF_M01075	1.7622e-03	-----CAGGCTTT----- GANCWRNTMAARNTTTANCNNCNRWNA	
PBF_M01130	1.7687e-03	CAGGCTTT ---CCTTT	
Pax-3_M00360	1.9053e-03	---CAGGCTTT- CGTCACRCTTMM	
LEF1_M00805	1.9804e-03	CAGGCTTT- ----CTTTG	
SZF1-1_M01109	3.3167e-03	-----AAAGCCTG CNGCTGWTACCCTG	
Retroviral_M00212	3.5940e-03	-----CAGGCTTT--- NAGNRRRRRGNTTTATT	
APOLYA_M00310	4.1333e-03	---CAGGCTTT--- MAATNGGCGTTTAT	

M50



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Zta_M00711	1.7146e-05	--AGCCACAG-- TGWGYCANNNTN	
AML_M00769	4.6002e-05	---AGCCACAG--- NNWRACCACANNNN	
SEF-1_M00214	1.5224e-04	-----CTGTGGCT ACACGGATATCTGTGGTY	
Osf2_M00731	1.9997e-04	-CTGTGGCT KNTGTGG--	
RAV1_M00343	2.2816e-04	---CTGTGGCT NNWNIGTTGCN	
PEBP_M00984	3.6840e-04	----CTGTGGCT-- NNNNYTGTGGTNAN	
TRAB1_M00507	5.5343e-04	AGCCACAG--- -GNCACRCGTM	
alpha-CP1_M00687	7.2537e-04	AGCCACAG-- AGCCAATGAG	
core-binding_M00722	1.0556e-03	-AGCCACAG WNACCAC--	
ZBRK1_M01105	1.3794e-03	-----CTGTGGCT AAANNNTGCKSCC	




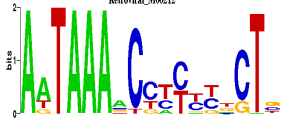

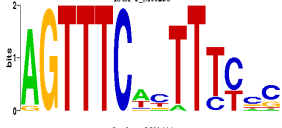



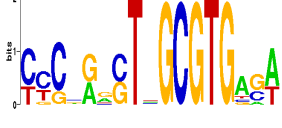
M57



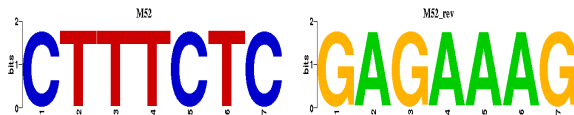
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SMAD4_M00733	2.5726e-04	-----CAGCCACA- NSRKN CAGMCANCY	
Alfin1_M00479	2.6759e-04	CAGCCACA----- MNNCCCCACNYNYN	
Osf2_M00731	5.6407e-04	--TGTGGCTG KNTGTGG---	
TRAB1_M00507	7.5697e-04	CAGCCACA----- --GNCACRCGTM	
AML_M00769	1.6552e-03	--CAGCCACA----- NNWRACCACANNNN	
Hmx3_M00433	1.7222e-03	CAGCCACA- CACGCACTT	
LUN-1_M00480	2.4169e-03	-----TGTGGCTG-- TCCCAAAGTAGCTGGG	
core-binding_M00722	2.6318e-03	CAGCCACA WNACCAC-	
GBF_M00633	3.0577e-03	CAGCCACA NACCCNA	
Dde_M00304	3.2643e-03	TGTGGCTG---- ---GGCTGAGC	





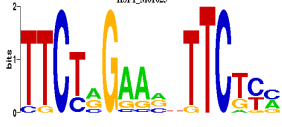





M5



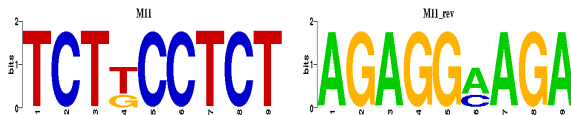
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
GAGA_M00723	2.4246e-08	TCTCTCTCT- TYNCKCTCWS	
SMAD3_M00701	1.1231e-04	AGAGAGAGA AGNCAGAC-	
TFII-I_M00706	4.7197e-04	TCTCTCTCT CCTMCNTC-	
Retroviral_M00212	5.8363e-04	-AGAGAGAGA----- NAGNRRRRRRGNTTTATT	
ARF_M00438	2.5373e-03	AGAGAGAGA -GAGACAA-	
ISGF-3_M00258	4.2887e-03	-AGAGAGAGA---- GNGAAANWGAAACT	
Sry-beta_M00666	4.6982e-03	AGAGAGAGA AGWGATGC-	
MAZ_M00649	5.9581e-03	TCTCTCTCT -CCCTCCC-	
IRF_M00972	6.0867e-03	-TCTCTCTCT NNTTCWNNTT	
AhR_M00139	7.9551e-03	TCTCTCTCT----- TSTCACGCNASNYNGRG	











M52



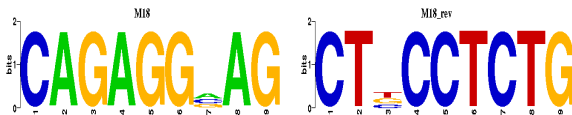
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	1.2666e-06	GAGAAAG GAGGAAG	
BPC1_M01126	6.7139e-06	CTTTCTC NTTTC--	
dl_M00120	4.0734e-05	---CTTTCTC NGNTTTTCYC	
GCR1_M00046	5.3099e-05	GAGAAAG- GWGGAAGC	
HSF1_M01023	1.2703e-04	-----CTTTCTC- TTCTRGAANNTTCTYM	
BLIMP1_M01066	2.8271e-04	--CTTTCTC---- YMCTTTCMCTTYC	
Rim101p_M01030	3.0992e-04	CTTTCTC- -TTNCTTG	
Elf-1_M00746	4.5791e-04	-CTTTCTC---- AYTTCCTCTTN	
ISGF-3_M00258	4.7677e-04	GAGAAAG----- GNGAAANWGAAACT	
ARF_M00438	4.8424e-04	GAGAAAG GAGACAA	

M11



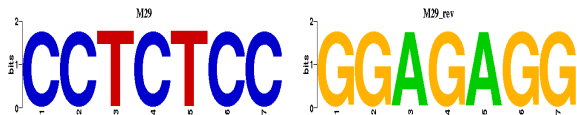
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	1.0558e-09	AGAGGAAGA -GAGGAAG-	
Elf-1_M00746	2.1188e-08	TCTTCCTCT-- AYTTCCTCTTN	
GCR1_M00046	2.9617e-07	AGAGGAAGA -GWGGAAGC	
Ets_M00971	2.2756e-06	AGAGGAAGA -NAGGAAG-	
PEA3_M00655	8.1174e-06	AGAGGAAGA --MGGAWG-	
c-Ets-1_M00743	1.3805e-05	TCTTCCTCT GCTTCCK--	
GCR1_M00337	1.6420e-05	---AGAGGAAGA- AAWAGTGGAAGCC	
c-Ets-2_M00340	2.8194e-05	----TCTTCCTCT ANNNACTTCCTGY	
Tel-2_M00678	6.1347e-05	AGAGGAAGA- -CAGGAAGTA	
Nrf-2_M00108	1.0671e-04	-TCTTCCTCT SNCTTCGG-	

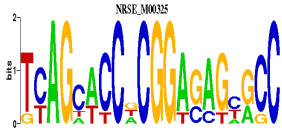

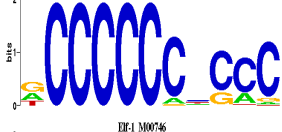






M18



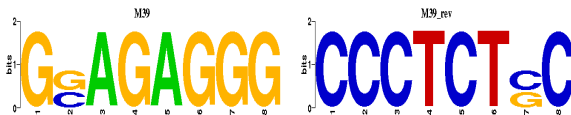
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	2.0225e-08	CTNCCTCTG CTTCCTC--	
Elf-1_M00746	2.4422e-07	-CTNCCTCTG- AYTTCCTCTTN	
GCR1_M00046	3.1835e-06	-CTNCCTCTG GCTTCCWC--	
Ets_M00971	2.2098e-05	CAGAGGNAG --NAGGAAG	
XPF-1_M00684	4.6370e-05	CTNCCTCTG GKTSNYCNG	
PEA3_M00655	8.0502e-05	CAGAGGNAG ---MGGAWG	
GCR1_M00337	1.0455e-04	--CAGAGGNAG-- AAWAGTGGAAGCC	
c-Ets-1_M00743	1.1115e-04	-CTNCCTCTG GCTTCCK---	
c-Ets-2_M00340	1.7024e-04	-----CTNCCTCTG ANNNACTTCTCTGY-	
TFII-I_M00706	3.2570e-04	-CTNCCTCTG CCTMCNTC--	

M29



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
NRSE_M00325	1.2900e-04	---CCTCTCC----- GGCRCTCTCCGNGGTGCTGA	
UF1H3BETA_M01068	1.3968e-04	-CCTCTCC----- GCCCCTCCCCRC	
MAZ_M00649	1.6991e-04	-GGAGAGG GGGAGGG-	
ZNF219_M01122	7.5143e-04	-GGAGAGG--- GGNGGGGGGN	
Elf-1_M00746	1.6053e-03	----CCTCTCC AYTTCCTCTTN	
Lyf-1_M00141	1.8218e-03	CCTCTCC--- --YCTCCCAA	
BLIMP1_M01066	1.9349e-03	-CCTCTCC----- YMCTTTCMCTTYC	
NF-kappaB_M00208	2.5053e-03	---CCTCTCC- GGGAYTTTCN	
Tra-1_M01048	2.8842e-03	-CCTCTCC ACCWCCC-	
Sp3_M00665	2.9186e-03	-CCTCTCC----- CCCYSCCCAAGKS	






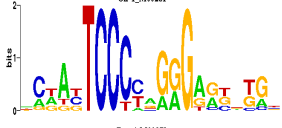




M39



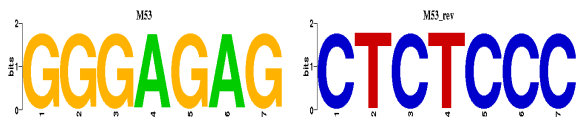
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
UF1H3BETA_M01068	1.8340e-05	---GSAGAGGG-- GYGGGGGAGGGGC	
ZNF219_M01122	2.1811e-05	-GSAGAGGG-- GGGNGGGGGGN	
MAZ_M00649	2.6267e-05	CCCTCTSC CCCTCCC-	
TAL1_M00993	5.6918e-05	-GSAGAGGG RNCAGNTGG	
COUPTF_M01036	1.1905e-04	-GSAGAGGG----- NKNNRNGKNNAAGGTCANNNN	
Sp1_M00933	5.8623e-04	-GSAGAGGG NGGGGMGG	
Sp3_M00665	9.5016e-04	CCCTCTSC----- CCCYSCCAAGKS	
GAGA_M00723	1.3647e-03	---CCCTCTSC TYNCKCTCWS-	
NRSE_M00325	2.5161e-03	--CCCTCTSC----- GGCRCTCTCCGNGGTGCTGA	
Eve_M00629	2.9106e-03	GSAGAGGG- GCNGNSSWN	




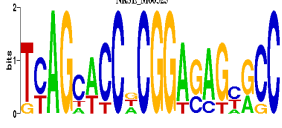


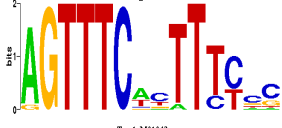

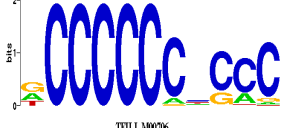

M46



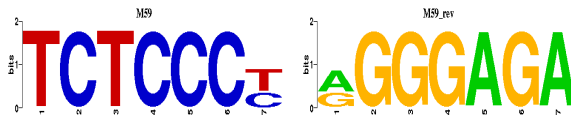
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
BRK_M01096	8.3786e-05	CTGGAGA NTGGCG-	
XPF-1_M00684	1.8966e-04	--TCTCCAG GKTSNYCNG	
Barbie_M00238	7.1460e-04	TCTCCAG----- CMNNCNSCTTTNNN	
NF-kappaB_M00208	1.7980e-03	CTGGAGA----- -NGGAAARTCCC	
Lyf-1_M00141	1.8218e-03	TCTCCAG- YCTCCCAA	
Olf-1_M00261	2.1072e-03	-----CTGGAGA----- NCMNNYTCCCNRRGGANTNGN	
Pax-6_M00979	2.1150e-03	--TCTCCAG---- KAGTTCCAGGTCA	
RP58_M00532	2.2228e-03	TCTCCAG----- --TCCAGATGTTN	
HP1_M00725	2.6314e-03	CTGGAGA---- CTGTTGAAWAT	
NF-AT_M00935	3.0899e-03	---TCTCCAG NWNITTCCW-	

M53



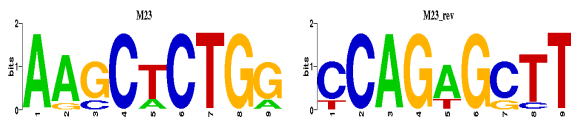
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MAZ_M00649	1.2667e-07	CTCTCCC CCCTCCC	
Lyf-1_M00141	5.1614e-06	CTCTCCC-- -YCTCCCAA	
Nrf-2_M00108	3.2163e-05	CTCTCCC-- SNCTTCCGG	
NRSE_M00325	1.2900e-04	----CTCTCCC----- GGCRCTCTCCGNGGTGCTGA	
UF1H3BETA_M01068	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	










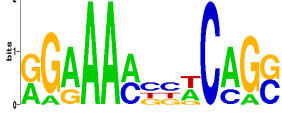
M59



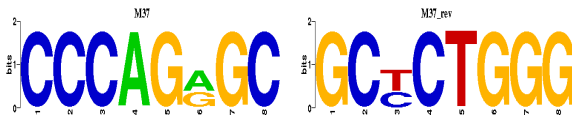
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
TFII-I_M00706	4.2388e-06	TCTCCCY- CCTMCNTC	
Lyf-1_M00141	5.1614e-06	TCTCCCY- YCTCCCA	
MAZ_M00649	6.1607e-05	-TCTCCCY CCCTCCC-	
SREBP_M00776	9.0026e-05	---TCTCCCY- NNNTCACCCYA	
VDR_M00444	1.2148e-04	-----RGGGAGA GGKNARNRRGGWSA	
MZF1_M00084	1.7853e-04	----RGGGAGA- NNGAGGGGNAA	
Tra-1_M01048	5.1032e-04	RGGGAGA- -GGWGGT	
SREBP-1_M00221	5.1591e-04	--RGGGAGA- GTGGGTGAT	
CAC-binding_M00720	5.6444e-04	-TCTCCCY CCASCY	
EBF_M00977	6.6977e-04	-----RGGGAGA NCYCWRGGGA--	

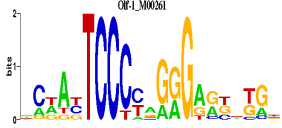




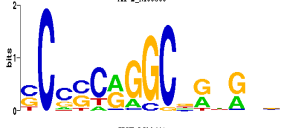




M23



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HSF_M00641	6.6151e-07	--AAGCTCTGG-- GAARCYNCKNGA	
RP58_M00532	2.1054e-05	-CCAGAGCTT- TCCAGATGTTN	
Eve_M00629	9.2971e-05	AAGCTCTGG NWSSNCNGC	
AP-4_M00005	5.9054e-04	----CCAGAGCTT---- MNGNCNNCAGCTGNNNN	
Nkx2-2_M00485	1.4924e-03	AAGCTCTGG AASYACTTA	
TBX5_M01044	1.9225e-03	CCAGAGCTT TCACACCTT	
Gfi1b_M01058	2.7868e-03	-CCAGAGCTT- WGCMGTGATT	
Dde_M00304	3.8073e-03	-CCAGAGCTT GGCTGAGC--	
Sry-beta_M00666	5.6314e-03	CCAGAGCTT- --AGWGATGC	
PTF1-beta_M00657	6.4293e-03	CCAGAGCTT---- SCTGWNNKTTTCY	

M37

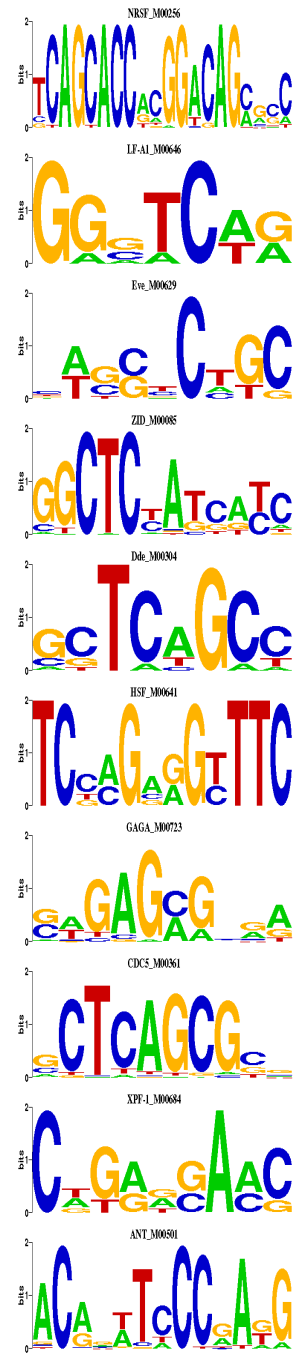


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Olf-1_M00261	2.4985e-05	-----GCYCTGGG----- NCMNNYTCNCRGGGANTNGN	
EBF_M00977	1.9689e-04	GCYCTGGG-- NCYCWRGGGA	
Eve_M00629	2.3116e-04	CCCAGRGC-- -GCNGNSSWN	
CACCC-binding_M00721	4.9581e-04	-----CCCAGRGC-- CCNCACCCWNNKGNT	
AP-2alpha_M00469	1.1481e-03	GCYCTGGG SCNNNNGG	
AP-2_M00800	1.9182e-03	-CCCAGRGC----- SCSSCRGGCNRNRNN	
HSF_M00641	1.9593e-03	----GCYCTGGG GAARCYNCKNGA	
STAT_M00777	2.0763e-03	-CCCAGRGC--- TCCNAGAANNNN	
CDC5_M00361	2.5480e-03	-GCYCTGGG- NSCGCTGAGS	
LUN-1_M00480	3.0298e-03	-CCCAGRGC----- TCCCAAAGTAGCTGGG	

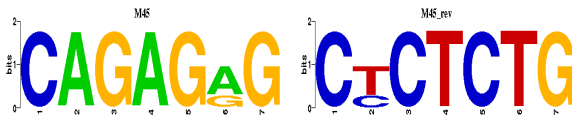
M42


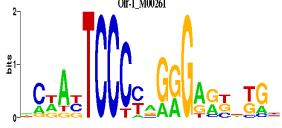

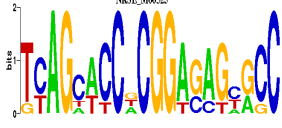


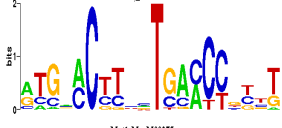

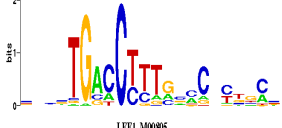



	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
NRSF_M00256	1.3233e-05	GGCTCTG----- GSYGCTGTCCGTGGTGCTGA
LF-A1_M00646	1.5442e-05	CAGAGCC YWGASCC
Eve_M00629	6.6369e-05	-CAGAGCC- GCNGNSSWN
ZID_M00085	1.2909e-04	GGCTCTG----- GGCTCYATCAYC
Dde_M00304	4.7473e-04	--CAGAGCC GGCTGAGC-
HSF_M00641	2.8999e-03	---GGCTCTG-- GAARCYNCKNGA
GAGA_M00723	3.3196e-03	---GGCTCTG TYNCKCTCWS
CDC5_M00361	3.8697e-03	----CAGAGCC NSCGCTGAGS-
XPF-1_M00684	4.3285e-03	--GGCTCTG GKTSNYCNG
ANT_M00501	4.5321e-03	-CAGAGCC----- ACANWTCCCRAKG

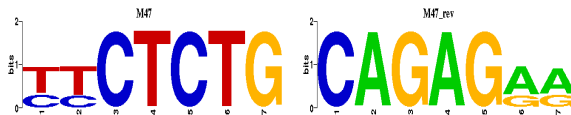




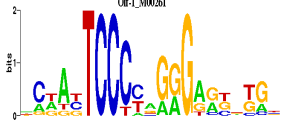
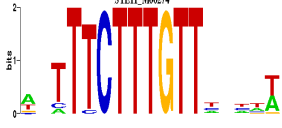






M45



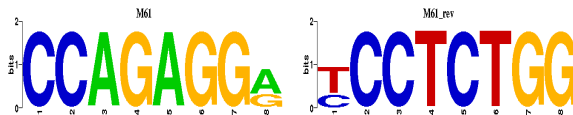
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
GAGA_M00723	2.4747e-05	---CTCTCTG TYNCKCTCWS	
Olf-1_M00261	3.8182e-04	-----CAGAGAG----- NCNANTCCCYNGGGARNNKGN	
Sry-beta_M00666	1.4639e-03	CAGAGAG-- -AGWGATGC	
NRSE_M00325	1.7198e-03	---CTCTCTG----- GGCRCTCTCCGNGGTGCTGA	
SMAD3_M00701	2.4662e-03	CAGAGAG-- -AGNCAGAC	
MAZ_M00649	3.5098e-03	CTCTCTG CCCTCCC	
VDR_M00966	5.0664e-03	-----CAGAGAG----- ANNNGGKTCANNARGKNCAAY	
Mat1-Mc_M00275	5.2375e-03	---CTCTCTG----- GRYNTCTTTGTTNNKYN	
COUPTF_M01036	6.3449e-03	-----CTCTCTG-- NNNNTGACCTTTNNMCNYYNMMN	
LEF1_M00805	6.6593e-03	CTCTCTG --CTTTG	







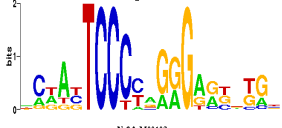


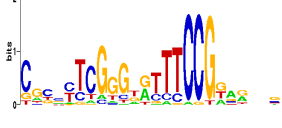
M47



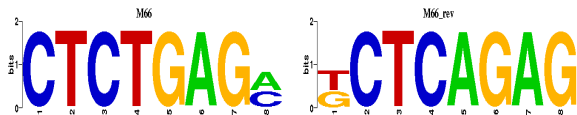
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	1.0035e-04	-TTCTCTG--- TTTCTTTGTTC	
Alx-4_M00619	1.5961e-04	-----TTCTCTG GATTATTCTCAG	
Olf-1_M00261	2.9344e-04	-----TTCTCTG----- NCMNNYTCCCNRRGGGANTNGN	
STE11_M00274	4.9559e-04	-----CAGAGAA--- WNNNNAACAAAGAAANW	
PR_M00960	5.1212e-04	---TTCTCTG NTGYCNNW-	
GATA-1_M00346	5.5666e-04	--TTCTCTG NNTTATCNN	
GAGA_M00723	5.8413e-04	---TTCTCTG TYNCKCTCWS	
Sry-beta_M00666	1.4865e-03	CAGAGAA-- -AGWGATGC	
Elf-1_M00746	1.9245e-03	---TTCTCTG- AYTTCCTCTTN	
Mat1-Mc_M00275	2.1554e-03	-----CAGAGAA--- NRMNNAACAAAGANRYC	

M61



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HSF_M00641	3.3803e-06	---TCCTCTGG- GAARCYNCKNGA	
Elf-1_M00746	9.6924e-05	---TCCTCTGG AYTTCCTCTTN	
XPF-1_M00684	1.6852e-04	--TCCTCTGG GKTSNYCNG-	
RP58_M00532	2.2357e-04	--TCCTCTGG- NAACATCTGGA	
EBF_M00977	4.4489e-04	--CCAGAGGA NCYCWRGGGA	
PU.1_M00658	6.7475e-04	CCAGAGGA-- ---GAGGAAG	
Olf-1_M00261	2.1275e-03	-----TCCTCTGG----- NCMNNYTCCCNRRGGANTNGN	
Nrf-2_M00108	2.2405e-03	-TCCTCTGG SNCTTCCGG	
ANT_M00501	4.9673e-03	TCCTCTGG----- -CMTYGGGAWNTGT	
DEAF1_M01001	5.7317e-03	-----CCAGAGGA-- NNNNNNCGGAAAYNCCCGARNNG	

M66

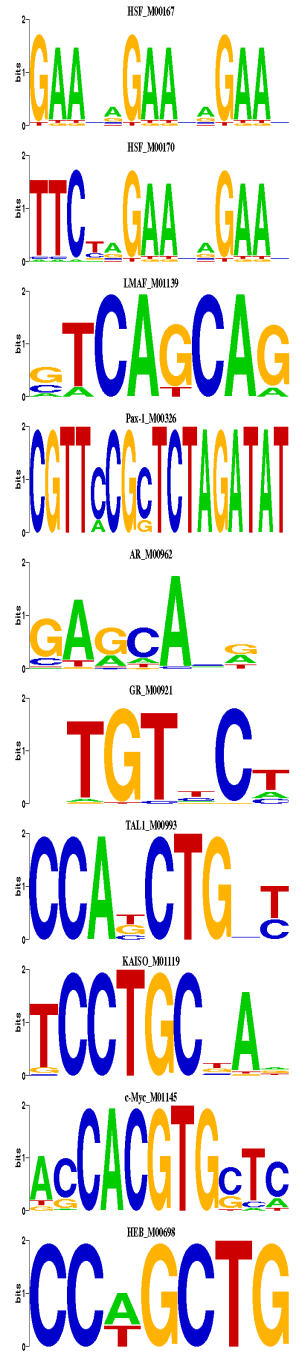


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CDC5_M00361	5.5766e-05	--CTCTGAGM NSCGCTGAGS	
Dde_M00304	1.8750e-04	CTCTGAGM GGCTGAGC	
Alx-4_M00619	3.2659e-04	-----KCTCAGAG GATTATTCTCAG--	
AP-1_M00173	5.9898e-04	CTCTGAGM--- -WNKNAGTCAN	
STAT_M00777	1.1578e-03	KCTCAGAG---- TCCNAGAANNNN	
TCF-4_M00671	1.2890e-03	KCTCAGAG -WTCAAAG	
NRSE_M00325	1.9504e-03	-----KCTCAGAG----- GGCRCTCTCCGNGGTGCTGA	
MAF_M00983	4.7152e-03	---KCTCAGAG NTGACTCANC-	
NF-E2_M00037	4.9564e-03	---KCTCAGAG RTGACTCAGC-	
dTCF_M00362	5.4375e-03	CTCTGAGM-- CTTTGATCTT	

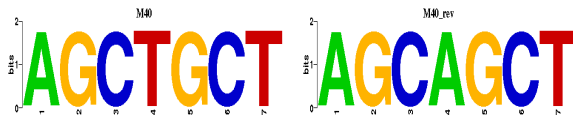
M31



	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
HSF_M00167	1.6673e-04	---CTGCTCT--- NTTCNNTTCNNTTC
HSF_M00170	1.6673e-04	---CTGCTCT--- NTTCNNTTCNNGAA
LMAF_M01139	1.9491e-04	CTGCTCT- CTGCTGAS
Pax-1_M00326	2.1259e-04	-----AGAGCAG----- ATATCTAGAGCGGAACG
AR_M00962	2.9727e-04	--CTGCTCT NNTTGCTC-
GR_M00921	7.0967e-04	AGAGCAG AGNACAN
TAL1_M00993	1.2297e-03	AGAGCAG----- --RNCAGNTGG
KAISO_M01119	1.2495e-03	--CTGCTCT TCCTGCNAN
c-Myc_M01145	2.1149e-03	-----CTGCTCT ACCACGTGCTC-
HEB_M00698	2.2929e-03	AGAGCAG- -CAGCWGG

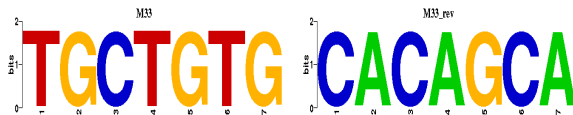



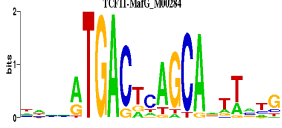


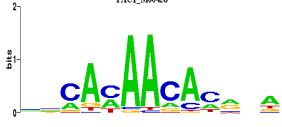





M40



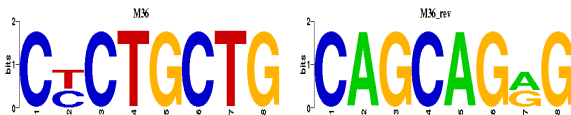
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LBP-1_M00644	2.0512e-08	AGCAGCT -SCAGCN	
TAL1_M00993	4.6591e-08	AGCAGCT-- RNCAGNTGG	
AP-4_M00927	6.1530e-07	--AGCTGCT NCAGCTGY-	
myogenin_M00712	2.2484e-06	AGCAGCT- -NCAGSTG	
HEN1_M00068	2.8573e-05	-----AGCTGCT----- NNGGNCNCAGCTGNGCCNNN	
HEN1_M00058	3.4193e-05	-----AGCAGCT----- NNNGGNCGCAGCTGCGNCCNN	
FACB_M00389	1.1943e-04	-----AGCTGCT--- ANNNGCNRNGMNAAMNCTGCNNNN	
LUN-1_M00480	1.3639e-04	-----AGCAGCT--- TCCCAAAGTAGCTGGG	
LMAF_M01139	1.9491e-04	AGCTGCT--- --CTGCTGAS	
HEB_M00698	2.0498e-04	-AGCTGCT CAGCWGG-	

M33



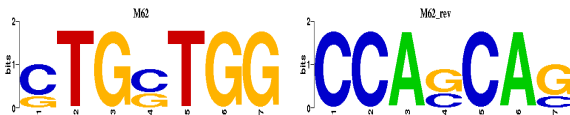
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Nrf-2_M00821	1.8411e-05	-----CACAGCA NNTGACTCAGCA	
TCF11-MafG_M00284	8.2461e-05	-----CACAGCA----- NNNNATGACNCAGCANNTNNG	
LMAF_M01139	1.8001e-04	-TGCTGTG CTGCTGAS	
v-Maf_M00035	3.6175e-04	---TGCTGTG----- NNNTGCNNNGTCAGCANN	
FAC1_M00456	4.0909e-04	----TGCTGTG-- NNNNTGTTKTGNN	
AP-4_M00005	7.0518e-04	-----CACAGCA----- MNGNCNNCAGCTGNNNN	
CACD_M01113	9.5750e-04	CACAGCA CACRCC	
TGIF_M00418	1.0295e-03	TGCTGTG---- -GCTGTCANNW	
bZIP910_M00357	1.1013e-03	--CACAGCA-- ACGTCAGCAYS	
Dde_M00304	1.5949e-03	-CACAGCA GCTCAGCC	








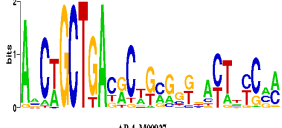


M36



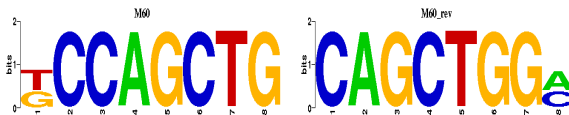
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HEB_M00698	4.0040e-07	CYCTGCTG -CCWGCTG	
LMAF_M01139	1.4112e-06	CYCTGCTG-- --CTGCTGAS	
Eve_M00629	1.0464e-04	---CYCTGCTG NWSSNCNGC--	
KAISO_M01119	3.0617e-04	CYCTGCTG- TCCTGCNAN	
HEN1_M00068	4.6530e-04	-----CYCTGCTG----- NNGGNCNCAGCTGNGNCCNNN	
TAL1_M00993	9.3674e-04	CAGCAGRG-- -RNCAGNTGG	
GATA-4_M00632	1.2341e-03	--CAGCAGRG- GATANMAGRSA	
Bel-1_M00312	1.6172e-03	-----CAGCAGRG KNGRNAGTNMNCKCWGYRTCAGCAGNT	
BRCA1-USF2_M01082	1.9754e-03	CAGCAGRG CAACNNN-	
AP-4_M00927	2.3836e-03	-CAGCAGRG RCAGCTGN-	

M62



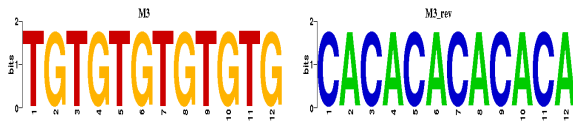
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LMAF_M01139	3.0422e-06	CTGSTGG- CTGCTGAS	
HEB_M00698	1.8223e-05	CTGSTGG CAGCWGG	
ACAAT_M00309	2.8891e-05	CCASCAG- CCACCAAT	
AP-4_M00176	9.4103e-05	-CCASCAG- NNCAGCTGN	
TAL1_M00993	3.7920e-04	--CTGSTGG RNCAGNTGG	
CAC-binding_M00720	5.2635e-04	-CCASCAG CCCASCCY	
myogenin_M00712	8.8394e-04	CCASCAG- -CASCTGN	
Bel-1_M00312	9.5757e-04	-----CCASCAG-- KNGRNAGTNMCKCWGYRTCAGCAGNT	
AP-4_M00927	1.7070e-03	CCASCAG- RCAGCTGN	
LBP-1_M00644	2.1058e-03	CCASCAG SCAGCN-	

M60

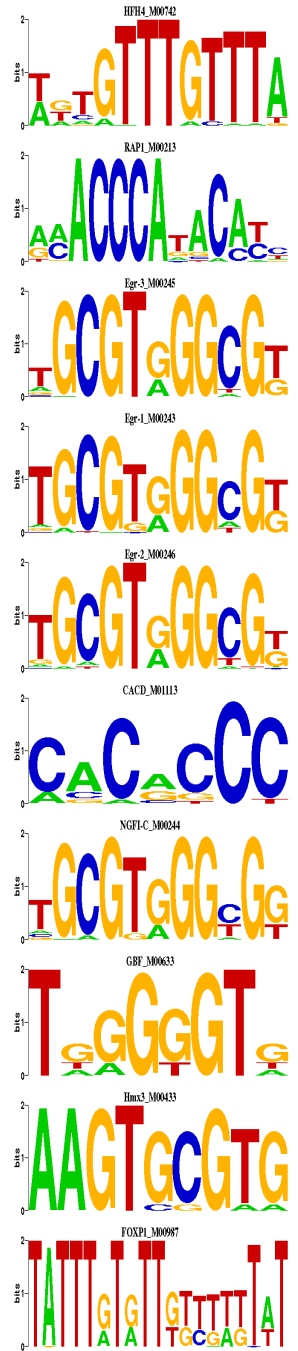


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HEB_M00698	1.2426e-10	CAGCTGGM CAGCWGG-	
AP-4_M00176	6.6226e-09	KCCAGCTG- NNCAGCTGN	
TAL1_M00993	1.0818e-07	--CAGCTGGM RNCAGNTGG-	
RP58_M00532	6.3502e-07	---CAGCTGGM NAACATCTGGA	
AP-4_M00927	1.9637e-06	KCCAGCTG- -RCAGCTGN	
LBP-1_M00644	3.1650e-06	KCCAGCTG -SCAGCN-	
myogenin_M00712	4.3111e-06	KCCAGCTG- --CASCTGN	
AP-4_M00175	9.7933e-06	KCCAGCTG- NNCAGCTGN	
AP-4_M00005	1.4550e-05	-----CAGCTGGM-- MNGNCNNCAGCTGNNNN	
HEN1_M00068	9.2487e-05	-----CAGCTGGM----- NNNGNCNCAGCTGNGCCNN	

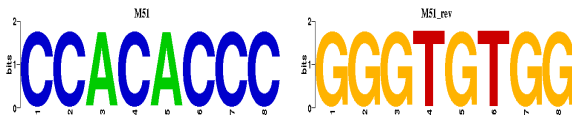
M3




	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</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

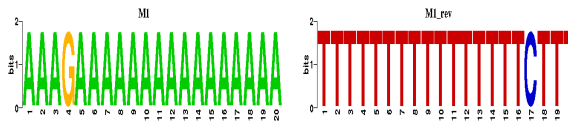


M51



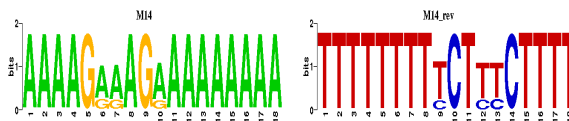
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CACD_M01113	2.1371e-10	GGGTGTGG GGYGTTG-	
CACCC-binding_M00721	1.2121e-09	CCACACCC----- CCNCACCCWNNKGNT	
TBX5_M01044	4.8477e-06	-GGGTGTGG AAGGTGTGA	
Alfin1_M00479	5.6578e-06	---CCACACCC--- MNNCCCCACNYNYN	
GBF_M00633	7.5091e-06	CCACACCC- -NACCCNA	
KROX_M00982	2.9149e-05	----CCACACCC- CCGCCCCNCNNC	
Sp1_M00931	1.4327e-04	-CCACACCC NCCCCGCC	
RREB-1_M00257	1.4521e-04	----GGGTGTGG- GGGGTGGTTGGG	
CAC-binding_M00720	1.9046e-04	CCACACCC- -CCCASCCY	
UF1H3BETA_M01068	1.9896e-04	-CCACACCC---- GCCCTCCCCRC	






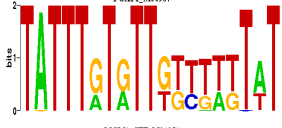
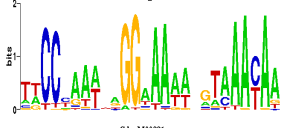
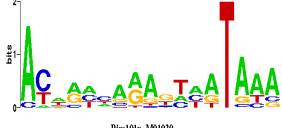
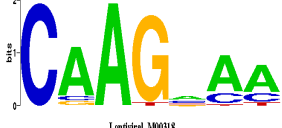

M1



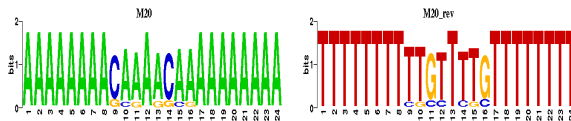
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
FOXP1_M00987	2.4128e-08	AAAGAAAAAAAAAAAAAAAAAA -ATAAAAAACAACACAAATA	
HSF_M00163	4.2848e-08	TTTTTTTTTTTTTTTTTCTTT ---NTTCTNTTCTNTTC---	
STE11_M00274	7.0725e-08	AAAGAAAAAAAAAAAAAAAAAA- ----WNNNNAACAAAGAAANW	
BR-C_M00092	1.5064e-07	AAAGAAAAAAAAAAAAAAAAAA ----RANAAATAGNWNNNN-	
STE11_M01005	5.6586e-07	TTTTTTTTTTTTTTTTTCTTT -----TTCTTTGTC---	
MCM1+SFF_M01051	6.3557e-07	TTTTTTTTTTTTTTTTTCTTT----- -TTRTTTANNTWTTNCCNNWTTNGNA	
BR-C_M00094	6.0444e-05	TTTTTTTTTTTTTTTTTCTTT -----TTWTSTTTAYWW	
XFD-3_M00269	6.3144e-05	TTTTTTTTTTTTTTTTTCTTT -----WKWTTGTTTACWN-	
HSF_M00167	2.1274e-04	TTTTTTTTTTTTTTTTTCTTT ---NTTCNNTTCNNTTC---	
Rim101p_M01030	2.2806e-04	TTTTTTTTTTTTTTTTTCTTT -----TTNCTTG	

M14



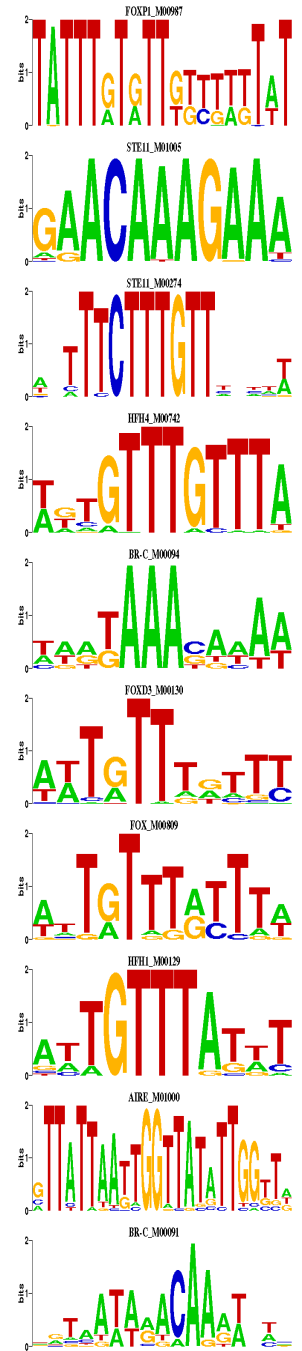
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	5.6541e-08	TTTTTTTTTCTTTCTTT -----TTCCTTTGTTC-	
BR-C_M00094	1.2533e-07	AAAAGAAAGAAAAAAAAA -WWR TAAASAWAA-----	
STE11_M00274	5.7107e-07	---AAAAGAAAGAAAAAAAAA WNNNNAACAAAGAAANW----	
HSF_M00163	8.0991e-07	TTTTTTTTTCTTTCTTT -NTTCNTTCTNTTC---	
BR-C_M00092	1.4611e-06	AAAAGAAAGAAAAAAAAA RANAAATAGNWNNNN---	
FOXP1_M00987	7.9865e-06	AAAAGAAAGAAAAAAAAA- ATAAAAAACAACACAAATA	
MCM1+SFF_M01051	9.8422e-05	--TTTTTTTTTCTTTCTTT----- TTRTTTANNTWTTNCCNNWTTNGNA	
Cdx_M00991	2.1682e-04	TTTTTTTTTCTTTCTTT- --TTTATNNNTYTNNYNRT	
Rim101p_M01030	3.4742e-04	TTTTTTTTTCTTTCTTT -----TTNCTTG-----	
Lentiviral_M00318	3.4882e-04	AAAAGAAAGAAAAAAAAA --AATAAG-----	

M20

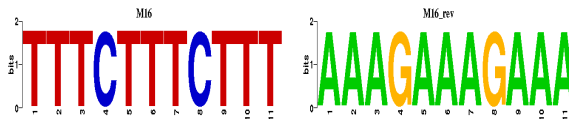


forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
FOXP1_M00987	1.1102e-16	AAAAAAAACAAACAAAAAAAAAA ATAAAAAACAACACAAATA-----
STE11_M01005	1.0256e-07	TTTTTTTTTTGTTTTGTTTTTTTT ---TTTCTTTGTTT-----
STE11_M00274	1.6535e-07	TTTTTTTTTTGTTTTGTTTTTTTT -----WNTTCTTTGTTNNNNW-
HFH4_M00742	1.2038e-06	AAAAAAAACAAACAAAAAAAAAA -----TAAACAAACAMW---
BR-C_M00094	1.7376e-06	TTTTTTTTTTGTTTTGTTTTTTTT -----TTWTSITTTAYWW-
FOXD3_M00130	1.8989e-06	TTTTTTTTTTGTTTTGTTTTTTTT -----AWTGTNTNTTT-
FOX_M00809	1.9459e-06	AAAAAAAACAAACAAAAAAAAAA WAAAYAAACANT-----
HFH1_M00129	1.9551e-06	AAAAAAAACAAACAAAAAAAAAA -AWATAACAAT-----
AIRE_M01000	2.0362e-06	-TTTTTTTTTTGTTTTGTTTTTTTT NTTATTAATTGGTTATATTGGKTN-
BR-C_M00091	2.6742e-06	-AAAAAAAACAAACAAAAAAAAAA NNTNATARACAARWNNN-----

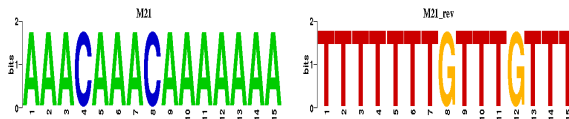


M16

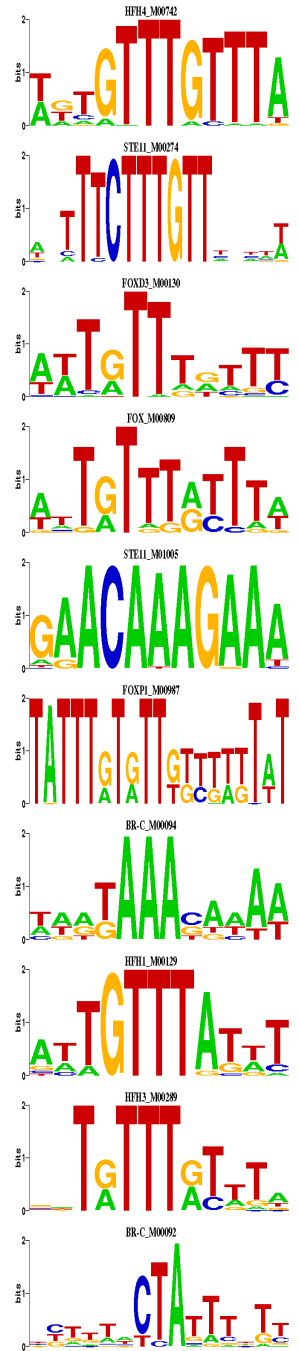


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M00274	4.8669e-11	---AAAGAAAGAAA-- WNNNNAACAAAGAAANW	
STE11_M01005	6.0396e-11	TTTCTTTCTTT TTTCTTTGTTT	
BR-C_M00094	6.1152e-08	-TTTCTTTCTTT TTWISTTTAYWW	
HSF_M00163	1.7056e-06	-TTTCTTTCTTT-- NTTCTNTTCTNTTC	
HFH4_M00742	3.6404e-06	-AAAGAAAGAAA TAAACAAACAMW	
HFH1_M00129	1.7339e-05	TTTCTTTCTTT AWTGTTTATWT	
Rim101p_M01030	1.7912e-05	TTTCTTTCTTT TTNCTTG----	
Lentiviral_M00318	2.9807e-05	AAAGAAAGAAA -AATAAAG---	
BR-C_M00092	3.6465e-05	-AAAGAAAGAAA--- RANAAATAGNWNNNN	
Cdx_M00991	4.3941e-05	TTTCTTTCTTT----- TTTATNNNTYTNNYNRT	

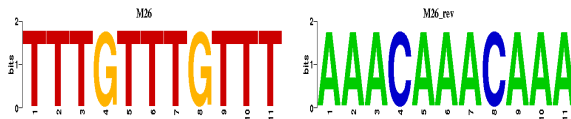
M21






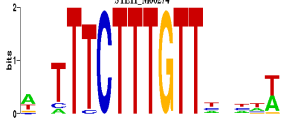




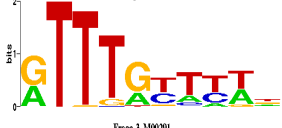

	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
HFH4_M00742	1.5711e-12	TTTTTTTGTGGTTT- ----WKTGTTTGTTTA
STE11_M00274	2.1871e-12	AAACAAACAAAAAA-- WNNNNAACAAAGAAANW
FOXD3_M00130	2.5347e-10	AAACAAACAAAAAA AAANAAACAWT----
FOX_M00809	5.3763e-10	TTTTTTTGTGGTTT- ----ANTGTTTRTTTW
STE11_M01005	5.8657e-09	TTTTTTTGTGGTTT TTTCTTGTTC----
FOXP1_M00987	8.3650e-09	----AAACAAACAAAAAA ATAAAAAACAACACAAATA
BR-C_M00094	6.2051e-08	AAACAAACAAAAAA WVRTAAASAWAA---
HFH1_M00129	6.6256e-08	AAACAAACAAAAAA AWATAAACAWT----
HFH3_M00289	8.2084e-07	TTTTTTTGTGGTTT- ----NNTRTTTRTWTN
BR-C_M00092	1.0202e-06	AAACAAACAAAAAA- -RANAAATAGNWNNNN



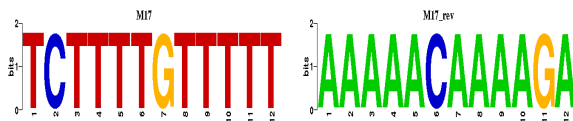
M26



forward *reverse compliment*

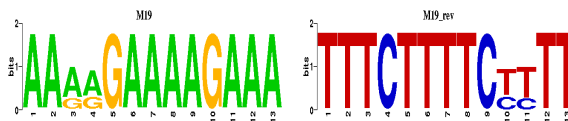
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HFH4_M00742	9.9920e-16	TTTGTGGTTT- WKTGTTTGTTTA	
FOX_M00809	1.1049e-12	TTTGTGGTTT- ANTGTTTRTTTW	
FOXD3_M00130	1.5716e-12	AAACAAACAAA AAANAAACAWT	
STE11_M00274	4.8669e-11	----AAACAAACAAA-- WNNNNAACAAAGAAANW	
STE11_M01005	6.0396e-11	TTTGTGGTTT TTTCTTTGTTT	
HFH1_M00129	1.0247e-09	AAACAAACAAA AWATAAACAWT	
HFH3_M00289	8.5781e-09	TTTGTGGTTT- NNRTRTTTRTWN	
BR-C_M00094	2.0655e-07	-TTTGTGGTTT TTWTSITTAAYWW	
HNF3alpha_M00724	5.5731e-07	--AAACAAACAAA NWRARCAAAY---	
Freac-3_M00291	9.5431e-07	TTTGTGGTTT----- --TGTTTATTTACNNNN	









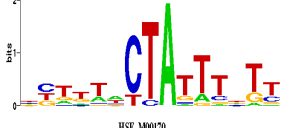

M17



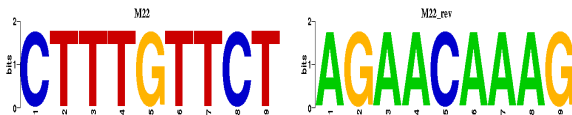
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HSF_M00163	1.5244e-09	--TCTTTTGT TTTT NTTCTNTTCTNTTC	
HNF3alpha_M00724	2.1636e-06	AAAAACAAAAGA NWRARCAAAY--	
BR-C_M00094	2.3105e-06	--AAAAACAAAAGA WVRTAAASAWAA--	
STE11_M00274	2.5112e-06	--AAAAACAAAAGA--- WNNNNAACAAAGAAANW	
SRY_M00148	5.9169e-06	AAAAACAAAAGA ---AACANM---	
FOXP1_M00987	6.7681e-06	---AAAAACAAAAGA---- ATAAAAAACAACACAAATA	
Mat1-Mc_M00276	8.9043e-06	TCTTTTGT TTTT -CNATTGTYN--	
ROX1_M00728	1.1453e-05	AAAAACAAAAGA ---ACAATRS-	
IRF-2_M00063	1.4443e-05	TCTTTTGT TTTT RSTTTCRCTTTT	
BR-C_M00091	1.5061e-05	-TCTTTTGT TTTT---- NNNWYTTGTYTATNANN	

M19



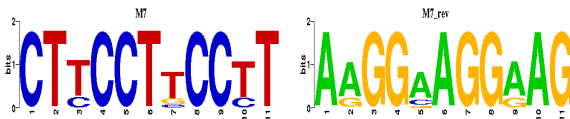
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HSF_M00163	1.1102e-16	TTTCTTTTCTTTT- NTTCNTTTCNTTC	
HSF_M00167	2.9746e-10	TTTCTTTTCTTTT- NTTCNNTTCNNTTC	
STE11_M00274	7.4353e-08	--TTTCTTTTCTTTT-- WNTTCTTTGTTNNNNW	
Evi-1_M00081	1.3827e-07	-AAAAGAAAAGAAA GATANGANAAGATA	
HSF_M00164	3.9124e-07	AAAAGAAAAGAAA----- ----GAANAGAANNTTCT	
HSF_M00166	5.3177e-07	-AAAAGAAAAGAAA TTCTAGAANAGAAN	
Evi-1_M00078	3.8114e-06	-TTTCTTTTCTTTT- TTATCTTATCTTRTC	
STE11_M01005	4.8925e-06	TTTCTTTTCTTTT TTTCTTTGTTTC--	
BR-C_M00092	7.6119e-06	AAAAGAAAAGAAA--- -RANAAATAGNWNNNN	
HSF_M00170	1.1913e-05	TTTCTTTTCTTTT- NTTCNNTTCNNGAA	

M22



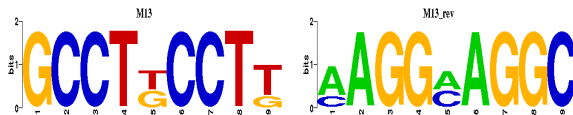
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	1.2978e-10	---CTTTGTTCT TTTCTTTGTTCT	
dTCF_M00362	4.5616e-10	CTTTGTTCT- CTTTGATCTT	
STE11_M00274	4.4181e-08	---AGAACAAAG----- WNNNNAACAAAGAAANW	
SOX_M01014	7.1998e-08	-CTTTGTTCT-- TCTTTGTTANGN	
SRY_M00148	1.1038e-06	AGAACAAAG --AACANM-	
GR_M00921	1.6691e-06	AGAACAAAG AGNACAN--	
LEF1_M00978	2.0703e-06	CTTTGTTCT- CTTTGATSNN	
HNF3alpha_M00724	2.2732e-06	-AGAACAAAG NWRARCAAA	
LEF1_M00805	4.2490e-06	CTTTGTTCT CTTTG----	
Mat1-Mc_M00275	6.1835e-06	---AGAACAAAG----- NRMNNAACAAAGANRYC	

M7



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	4.5163e-06	CTTCCTTCCTT ----CTTCCTC	
Ets_M00971	5.2455e-06	AAGGAAGGAAG ----NAGGAAG	
Tel-2_M00678	6.8003e-06	AAGGAAGGAAG CAGGAAGTA--	
MAF_M00648	7.3031e-06	-----CTTCCTTCCTT NSNMMACTTCCYYCN--	
PEA3_M00655	1.4003e-05	AAGGAAGGAAG ----MGGAWG	
c-Ets-1_M00743	2.9483e-05	-CTTCCTTCCTT GCTTCCK-----	
c-Ets-2_M00340	3.1997e-05	-CTTCCTTCCTT- ANNNACTTCCTGY	
NERF1a_M00531	1.1810e-04	-----CTTCCTTCCTT SNNASNYRCTTCCTGNY--	
c-Ets-1_M00339	3.0416e-04	---CTTCCTTCCTT NNMNNNACTTCCTG	
GCR1_M00046	4.0291e-04	AAGGAAGGAAG- ----GWGGAAGC	






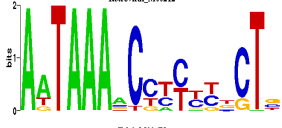




M13



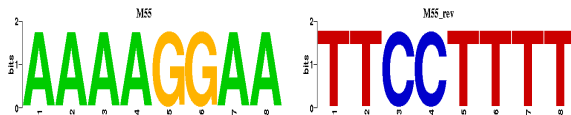
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Ets_M00971	1.4402e-05	AAGGMAGGC NAGGAAG--	
PU.1_M00658	1.8440e-05	GCCTKCCTT --CTTCCTC	
PEA3_M00655	5.2399e-05	AAGGMAGGC -MGGAWG--	
c-Ets-1_M00743	7.5151e-05	GCCTKCCTT -GCTTCCK-	
Tel-2_M00678	1.7947e-04	AAGGMAGGC CAGGAAGTA	
E2A_M00973	4.5593e-04	AAGGMAGGC --RNCAGNT	
GCR1_M00046	6.7233e-04	AAGGMAGGC GWGGAAGC-	
Ets_M00771	1.5935e-03	AAGGMAGGC-- CAGGAAGYNNN	
SMAD3_M00701	1.6028e-03	AAGGMAGGC -AGNCAGAC	
TFII-I_M00706	2.3643e-03	AAGGMAGGC GANGKAGG-	

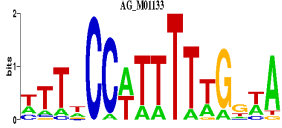








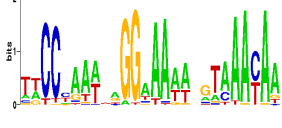
M10



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MAF_M00648	1.5750e-07	-----TCTTCCTTCT NSNMMACTTCCYYCN	
PU.1_M00658	2.7308e-06	TCTTCCTTCT -CTTCCTC--	
Ets_M00971	5.6942e-06	AGAAGGAAGA --NAGGAAG-	
c-Ets-1_M00743	3.6165e-05	TCTTCCTTCT GCTTCCK---	
PEA3_M00655	4.0401e-05	AGAAGGAAGA ---MGGAWG-	
Retroviral_M00212	1.0353e-04	-AGAAGGAAGA----- NAGNRRRRRRGNTTTATT	
Tel-2_M00678	1.3180e-04	AGAAGGAAGA- --CAGGAAGTA	
NERF1a_M00531	1.3289e-04	AGAAGGAAGA----- RNCAGGAAGYRNSTNNS	
Nrf-2_M00108	1.3657e-04	AGAAGGAAGA- --CCGGAAGNS	
KAISO_M01119	2.7311e-04	--AGAAGGAAGA NTNGCAGGA---	

M55



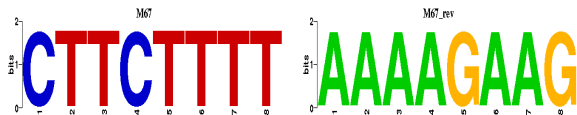
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AG_M01133	5.3568e-08	--TTCCTTTT----- NTTNC CWTTTTTIGNWA	
PBF_M01130	2.4789e-06	TTCCTTTT --CCTTT-	
MADS-A_M00408	3.1155e-06	-TTCCTTTT----- TTTCCATTTTTNNWN	
Elf-1_M00746	7.6058e-06	--TTCCTTTT- AYTTCCTCTTN	
MADS-B_M00404	1.5546e-05	-----AAAAGGAA- NCYAAAAATGSAAA	
SED_M01128	5.0296e-05	AAAAGGAA- NAAAGNNA	
HSF_M00163	5.1366e-05	-AAAAGGAA----- GAANAGAANAGAAN	
HSF_M00164	5.1366e-05	-AAAAGGAA----- GAANAGAANNTTCT	
ID1_M01021	6.3570e-05	AAAAGGAA-- AWAASGACAA	
MCM1+SFF_M01051	8.6338e-05	-----AAAAGGAA----- TNCNAAWNNGGNAAWANNTAAAYAA	

M65



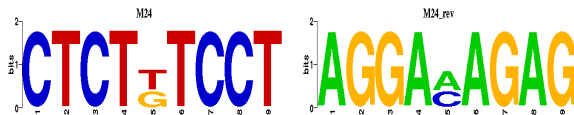
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PEND_M01015	2.6717e-07	AAAGAAGA -AAGAAGT	
HSF_M00163	1.0420e-06	----TCTTCTTT-- NTTCTNTTCTNTTC	
PR_M00960	7.0963e-06	AAAGAAGA- WNGRACAN	
STE11_M01005	2.5255e-05	TCTTCTTT---- -TTTCTTTGTTT	
Mat1-Mc_M00275	1.3223e-04	-----AAAGAAGA- NRMNNAACAAAGANRYC	
STE11_M00274	2.1678e-04	-----AAAGAAGA- WNNNNAACAAAGAAANW	
HSF_M00164	2.9535e-04	--AAAGAAGA---- GAANAGAANNTTCT	
HSF_M00166	5.2470e-04	-----AAAGAAGA TTCTAGAANAGAAN-	
Rim101p_M01030	6.4881e-04	TCTTCTTT -TTNCTTG	
Elf-1_M00746	7.0420e-04	---TCTTCTTT AYTTCCTCTTN	

M67



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PEND_M01015	2.6717e-07	AAAAGAAG- --AAGAAGT	
HSF_M00163	5.5585e-07	-AAAAGAAG----- GAANAGAANAGAAN	
HSF_M00164	5.5585e-07	-AAAAGAAG----- GAANAGAANNTTCT	
HSF_M00166	1.2274e-06	-----AAAAGAAG TTCTAGAANAGAAN	
STE11_M01005	2.5255e-05	CTTCTTTT--- TTTCTTTGTC	
Mat1-Mc_M00275	1.3223e-04	-----AAAAGAAG-- NRMNNAACAAAGANRYC	
HSF_M00167	1.8555e-04	CTTCTTTT----- NTTCNNTTCNNTTC	
HSF_M00168	1.8555e-04	-----CTTCTTTT- NGAANNNTTCNNTTC	
HSF_M00170	1.8555e-04	CTTCTTTT----- NTTCNNTTCNNGAA	
STE11_M00274	2.1678e-04	-----AAAAGAAG-- WNNNNAACAAAGAAANW	

M24



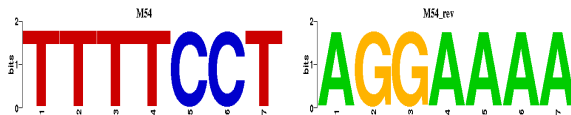
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ISGF-3_M00258	3.6409e-05	AGGAMAGAG----- GNGAAANWGAAACT	
NRSF_M00256	1.1739e-04	--CTCTKTCCT----- GSYGCTGTCCGTGGTGCTGA	
HSF_M00167	1.5676e-04	-CTCTKTCCT----- NTTCNNTTCNNTTC	
HSF_M00170	1.5676e-04	-CTCTKTCCT----- NTTCNNTTCNNGAA	
GAL4_M00198	2.1556e-04	-----AGGAMAGAG----- NGYTTCGGNNNANAGNNNNCCG	
SMAD3_M00701	2.7497e-04	AGGAMAGAG -AGNCAGAC	
BPC1_M01126	3.1360e-04	CTCTKTCCT --NTTTC--	
T3R_M00963	7.8583e-04	-AGGAMAGAG NAGGWCAN--	
Helios_M01004	8.2390e-04	CTCTKTCCT-- -NTTTCCTWN	
GAL4_M00049	9.7653e-04	-----AGGAMAGAG----- STTCGGASNANWGTNNNCCGNN	


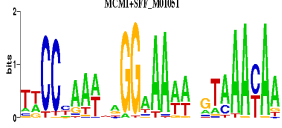
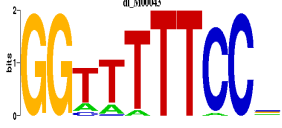
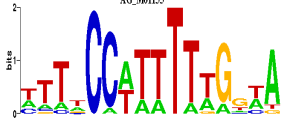






M44



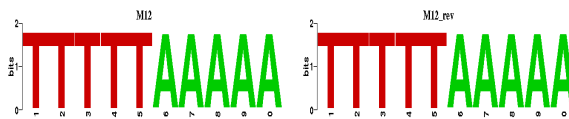
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
NF-kappaB_M00208	1.1677e-05	----CTTTCCT GGGAYTTTCCN	
Helios_M01004	1.4376e-05	-CTTTCCT-- NNTTTCCTWN	
BPC1_M01126	2.6871e-05	CTTTCCT NNTTC--	
NF-AT_M00302	7.8040e-05	--CTTTCCT-- NNNTTTCWNN	
Elf-1_M00746	1.2760e-04	CTTTCCT---- AYTTCCTCTTN	
ISGF-3_M00258	1.5981e-04	AGGAAAG----- GNCAAANWGAACT	
NF-kappaB_M00194	1.6897e-04	-AGGAAAG----- NNGGAAAKTCCCC	
BLIMP1_M01066	1.7273e-04	--CTTTCCT---- YMCTTTCMCTTYC	
Ets_M00971	2.3132e-04	-AGGAAAG NAGGAAG-	
PU.1_M00658	2.3867e-04	CTTTCCT- -CTTCCTC	

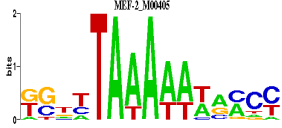
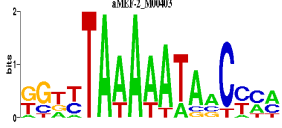
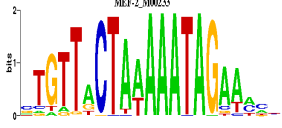
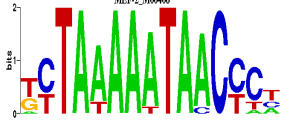
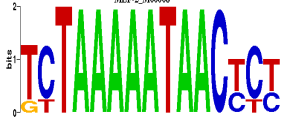


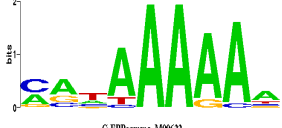


M54



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Helios_M01004	6.4796e-10	-TTTTCT-- NTTTCTWN	
MCM1+SFF_M01051	1.5158e-07	-----AGGAAA----- TNCNAAWNNGGNAAWANNNTAAAYAA	
dI_M00043	1.4412e-06	AGGAAA--- NGGAAAACC	
AG_M01133	1.2806e-05	-----AGGAAA TWNCAAAAAWGGNAAN	
NF-AT_M00302	2.8941e-05	--TTTTCT-- NNNTTCCWNN	
dI_M00120	2.9020e-05	---TTTTCT NGNTTTCYC	
Elf-1_M00746	4.2410e-05	TTTTCT---- AYTTCCTCTN	
Ets_M00971	6.2494e-05	-AGGAAA NAGGAAG-	
PU.1_M00658	7.9074e-05	TTTTCT- -CTTCCTC	
STAT5B_M00459	1.0214e-04	TTTTCT----- NWTTCNGGAANYN	

M12



	<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 RGKNWTTTTTTANNM	
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-----	

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