



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

Input file: 63 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 :                AAAAAAAAAAAAAAAAAA-----
M1 :                -----GGGGGGGGGGGG
M2 :                ----CACACACACACA-----
M3 :                -----TTTTTAAAAA-----
M4 :                ----GGGGGAGGGAGGGGG-----
M5 :                -----GGAGGGAGG-----
M6 :                -----TTCCAGGAA-----
M7 :                -----GGGGGAGGGGM-----
M8 :                ---CCCCACCCCCACCCC-----
M9 :                -----CAGCAGCAG-----
M10 :               -----AGAAAGAAA-----
M11 :               -----GGGGAGGAGG-----
M12 :               -----AGAAAAGAA-----
M13 :               -----AGGAAGGAAG-----
M14 :               -----CAGAGGCAG-----
M15 :               ---CCCCACCCCCA-----
M16 :               -----AGAAGGMAG-----
M17 :               -----AAACAAACAAA-----
M18 :               -AAAAAACAAAACAAAA-----
M19 :               -----AGGAAGCAG-----
M20 :               -----AGGAGACAG-----
M21 :               -----GGGGAGGGGGAGGGG-----
M22 :               -----GGAGGAG-----

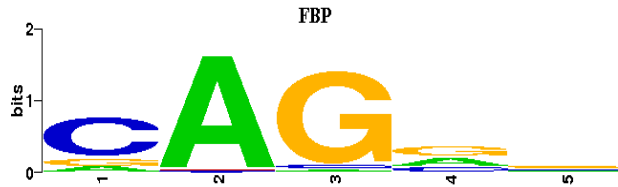
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Stamp Results

04/30/14

M23: -----CCCAGCC-----
M24: -----YTCCCAG-----
M25: -----AGGAAGG-----
M26: -----AGAGARAG-----
M27: -----GGCAGAG-----
M28: -----GGGAAGGG-----
M29: -----AGAGAGAG-----
M30: -----GGGGCAG-----
M31: -----GGCAGAG-----
M32: -----CAGAGNA-----
M33: -----CAGRGCTG-----
M34: -----CAGCCTCC-----
M35: -----GCAGCAG-----
M36: -----AGAAGAAA-----
M37: -----CAGGCTG-----
M38: -----CCAGRGC-----
M39: -----GAGCAGN-----
M40: -----CAGGCAG-----
M41: -----TCCCAGA-----
M42: -----AGCCACAG-----
M43: -----CAGCTCCT-----
M44: -----CTCCAGG-----
M45: -----AGGAGAGA-----
M46: -----CAGAGGGA-----
M47: -----CAGGGACA-----
M48: -----CACACCC-----
M49: -----GAGGCCA-----
M50: -----GAGGAAGA-----
M51: -----AAAACAGA-----
M52: -----CAGRAGCC-----
M53: -----CAGGAGAG-----
M54: -----CAGGCCTG-----
M55: -----TGGCAGC-----
M56: -----CTCAGCT-----
M57: -----CCTCAGCT-----
M58: -----RGCAGCCT-----
M59: -----AATTAAAA-----
M60: -----AAGCAGCT-----
M61: -----AGCAAAGA-----
M62: -----TGGCAGCT-----

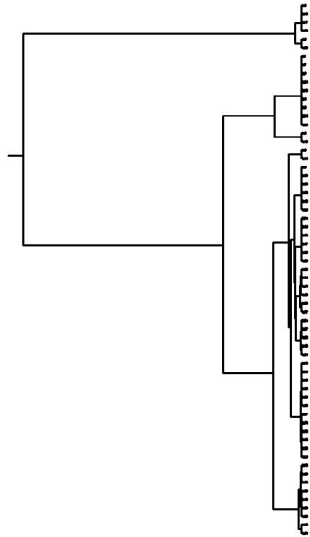
Familial Profile:
[\(click for matrix\)](#)



Motif Tree


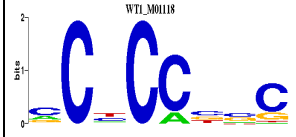

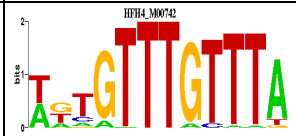

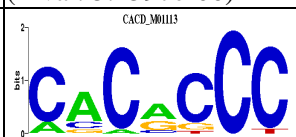
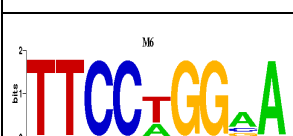
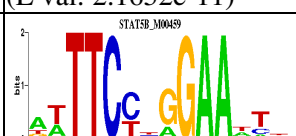
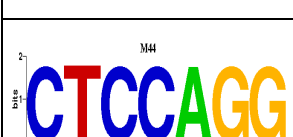
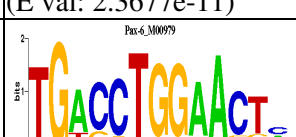



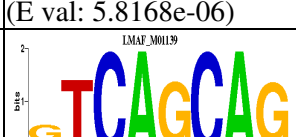


Tree (drawn by **Phylip**)



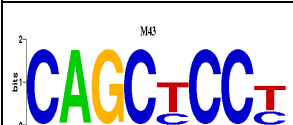



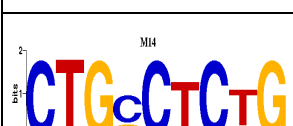




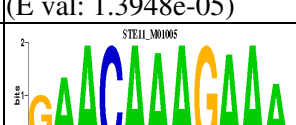
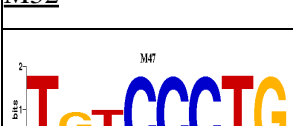
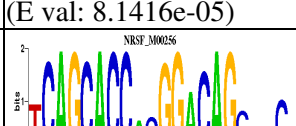

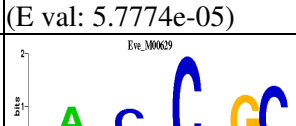
[Click here for Newick-format tree \(viewable with MEGA\)](#)








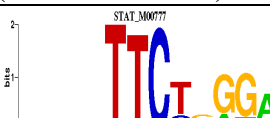

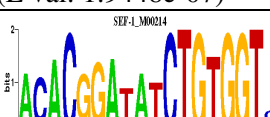





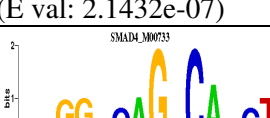







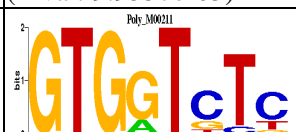
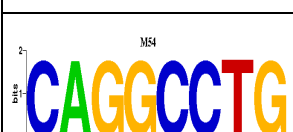
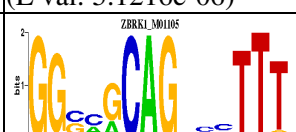
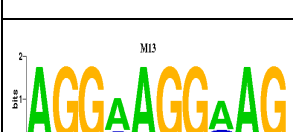


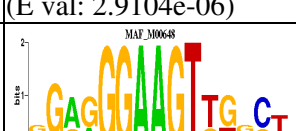




Input Motif	Best match in TRANSFAC
<p>M0</p>	<p>FOXP1_M00987 (E val: 7.1556e-10)</p>
<p>M18</p>	<p>FOXP1_M00987 (E val: 2.6645e-15)</p>
<p>M17</p>	<p>HFH4_M00742 (E val: 9.9920e-16)</p>
<p>M51</p>	<p>HSF_M00167 (E val: 4.8521e-06)</p>
<p>M3</p>	<p>MEF-2_M00405 (E val: 2.9868e-07)</p>
<p>M59</p>	<p>Nkx6-1_M00424 (E val: 7.1351e-11)</p>

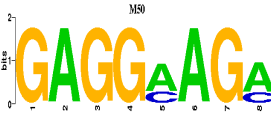












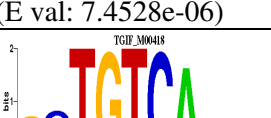

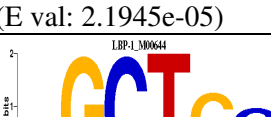
<p>M1</p>	<p>ZNF219_M0112</p>
<p>M7</p>	<p>UF1H3BETA_M01068</p>
<p>M8</p>	<p>UF1H3BETA_M01068</p>
<p>M21</p>	<p>KROX_M00982</p>
<p>M15</p>	<p>KROX_M00982</p>
<p>M4</p>	<p>TFII-I_M00706</p>
<p>M5</p>	<p>TFII-I_M00706</p>
<p>M11</p>	<p>ZNF219_M0112</p>
<p></p>	<p></p>

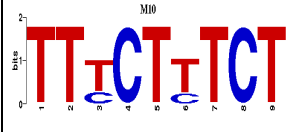

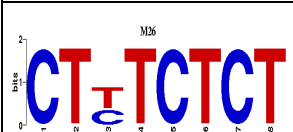
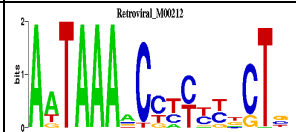






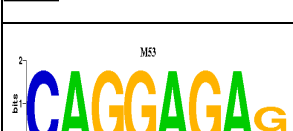

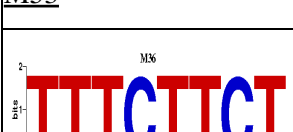


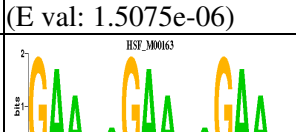
<p>M22</p>  <p>M22</p>	<p>WT1_M01118</p>  <p>WT1_M01118 (E val: 2.8333e-05)</p>
<p>M2</p>  <p>M2</p>	<p>HFH4_M00742</p>  <p>HFH4_M00742 (E val: 3.4597e-06)</p>
<p>M48</p>  <p>M48</p>	<p>CACD_M01113</p>  <p>CACD_M01113 (E val: 2.1652e-11)</p>
<p>M6</p>  <p>M6</p>	<p>STAT5B_M00459</p>  <p>STAT5B_M00459 (E val: 2.3677e-11)</p>
<p>M44</p>  <p>M44</p>	<p>Pax-6_M00979</p>  <p>Pax-6_M00979 (E val: 8.1790e-06)</p>
<p>M9</p>  <p>M9</p>	<p>LMAF_M01139</p>  <p>LMAF_M01139 (E val: 5.8168e-06)</p>
<p>M35</p>  <p>M35</p>	<p>LMAF_M01139</p>  <p>LMAF_M01139 (E val: 1.8121e-07)</p>
<p>M60</p>  <p>M60</p>	<p>LBP-1_M00644</p>  <p>LBP-1_M00644 (E val: 1.0779e-07)</p>

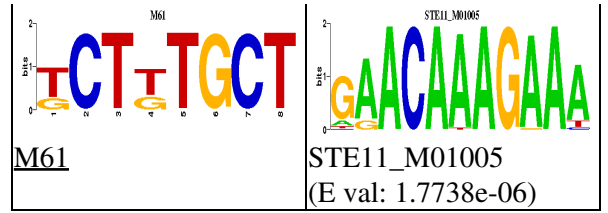
 <p>M39</p>	 <p>KAISO_M01119 (E val: 9.3506e-06)</p>
 <p>M43</p>	 <p>TAL1_M00993 (E val: 2.3829e-06)</p>
 <p>M52</p>	 <p>E12_M00693 (E val: 1.3612e-05)</p>
 <p>M14</p>	 <p>PU.1_M00658 (E val: 2.8819e-05)</p>
 <p>M46</p>	 <p>TFII-I_M00706 (E val: 1.3948e-05)</p>
 <p>M32</p>	 <p>STE11_M01005 (E val: 8.1416e-05)</p>
 <p>M47</p>	 <p>NRSF_M00256 (E val: 5.7774e-05)</p>
 <p>M33</p>	 <p>Eve_M00629 (E val: 3.1830e-06)</p>

<p>M38</p>  <p>M38</p>	<p>Eve_M00629</p>  <p>Eve_M00629 (E val: 5.6948e-05)</p>
<p>M23</p>  <p>M23</p>	<p>CAC-binding_M00720</p>  <p>CAC-binding_M00720 (E val: 2.1814e-08)</p>
<p>M24</p>  <p>M24</p>	<p>Ik-3_M00088</p>  <p>Ik-3_M00088 (E val: 2.5462e-07)</p>
<p>M41</p>  <p>M41</p>	<p>STAT_M00777</p>  <p>STAT_M00777 (E val: 1.9448e-07)</p>
<p>M42</p>  <p>M42</p>	<p>SEF-1_M00214</p>  <p>SEF-1_M00214 (E val: 5.7700e-05)</p>
<p>M56</p>  <p>M56</p>	<p>Dde_M00304</p>  <p>Dde_M00304 (E val: 4.8992e-07)</p>
<p>M57</p>  <p>M57</p>	<p>Dde_M00304</p>  <p>Dde_M00304 (E val: 2.1432e-07)</p>
<p>M34</p>  <p>M34</p>	<p>SMAD4_M00733</p>  <p>SMAD4_M00733 (E val: 4.8026e-05)</p>

<p>M37</p>  <p>M37</p>	<p>HAC1_M00730</p>  <p>HAC1_M00730 (E val: 1.0337e-04)</p>
<p>M58</p>  <p>M58</p>	<p>LBP-1_M00644</p>  <p>LBP-1_M00644 (E val: 9.9357e-05)</p>
<p>M49</p>  <p>M49</p>	<p>Poly_M00211</p>  <p>Poly_M00211 (E val: 5.1216e-06)</p>
<p>M54</p>  <p>M54</p>	<p>ZBRK1_M01105</p>  <p>ZBRK1_M01105 (E val: 5.2099e-04)</p>
<p>M13</p>  <p>M13</p>	<p>Ets_M00971</p>  <p>Ets_M00971 (E val: 2.9104e-06)</p>
<p>M16</p>  <p>M16</p>	<p>MAF_M00648</p>  <p>MAF_M00648 (E val: 9.2181e-07)</p>
<p>M19</p>  <p>M19</p>	<p>c-Ets-1_M00743</p>  <p>c-Ets-1_M00743 (E val: 4.8533e-08)</p>
<p>M25</p>  <p>M25</p>	<p>Ets_M00971</p>  <p>Ets_M00971 (E val: 1.2188e-07)</p>
<p></p>	<p></p>

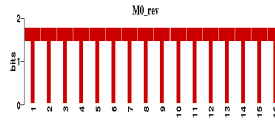
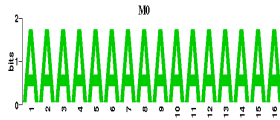
 <p>M50</p>	 <p>PU.1_M00658 (E val: 1.5497e-10)</p>
 <p>M28</p>	 <p>UF1H3BETA_M01068 (E val: 2.8231e-07)</p>
 <p>M27</p>	 <p>Dde_M00304 (E val: 6.5556e-07)</p>
 <p>M31</p>	 <p>Dde_M00304 (E val: 6.5556e-07)</p>
 <p>M30</p>	 <p>SMAD4_M00733 (E val: 6.9439e-06)</p>
 <p>M40</p>	 <p>Tel-2_M00678 (E val: 7.4528e-06)</p>
 <p>M55</p>	 <p>TGIF_M00418 (E val: 2.1945e-05)</p>
 <p>M62</p>	 <p>LBP-1_M00644 (E val: 7.4817e-08)</p>

 <p>M10</p>	 <p>STE11_M01005 (E val: 5.4699e-09)</p>
 <p>M26</p>	 <p>Retroviral_M00212 (E val: 1.8311e-05)</p>
 <p>M29</p>	 <p>GAGA_M00723 (E val: 2.3892e-06)</p>
 <p>M20</p>	 <p>ARF_M00438 (E val: 1.1955e-06)</p>
 <p>M45</p>	 <p>TBX5_M01044 (E val: 2.7763e-04)</p>
 <p>M53</p>	 <p>Ttk_M00009 (E val: 1.6619e-04)</p>
 <p>M36</p>	 <p>Rim101p_M01030 (E val: 1.5075e-06)</p>
 <p>M12</p>	 <p>HSF_M00163 (E val: 7.2365e-12)</p>



Motif Similarity Matches

M0



forward

reverse compliment

Name	E value	Alignment	Motif
FOXP1_M00987	7.1556e-10	---TTTTTTTTTTTTTTTT TATTTGTGTTGTTTTTAT	
STE11_M00274	9.8050e-10	AAAAAAAAAAAAAAAAA-- WNNNNAACAAAGAAANW	
BR-C_M00092	8.5197e-09	AAAAAAAAAAAAAAAAA RANAAATAGNWNNNN--	
HSF_M00163	1.8274e-06	-TTTTTTTTTTTTTTTT NTTCNTTCTNTTC---	
STE11_M01005	3.7220e-05	TTTTTTTTTTTTTTTT TTTCTTGTTC-----	
AG_M01133	6.3860e-05	-AAAAAAAAAAAAAAAAA TWNCAAAAAWGNAAN--	
MCM1+SFF_M01051	8.3305e-05	-----AAAAAAAAAAAAAAAA CCNAAWNNGGNAAWANNTAAAYAA--	
HFH4_M00742	1.3259e-04	-AAAAAAAAAAAAAAAAA TAAACAAACAMW-----	

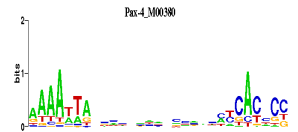
Stamp Results

04/30/14

Pax-4_M00380

1.8938e-04

-AAAAAAAAAAAAAAAAA-----
N-AAAWTANNNNNNNNNNNNNNNNNNNCACCNCN



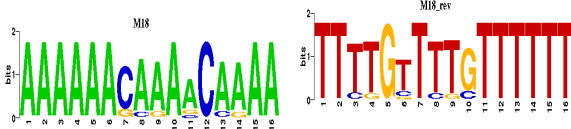
FOX_M00809

2.1294e-04

TTTTTTTTTTTTTTTTT
ANTGTTTRITTTW----



M18



forward

reverse compliment

Name

E value

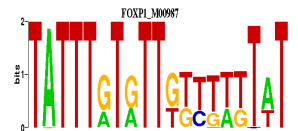
Alignment

Motif

FOXP1_M00987

2.6645e-15

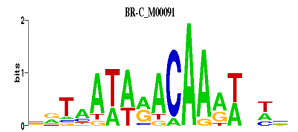
--AAAAACAAAACAAA--
ATAAAAACAACACAAATA



BR-C_M00091

3.4503e-08

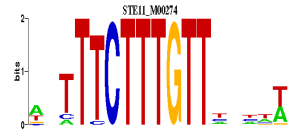
TTTGTTTTGTTTTT---
--NNWYTTGYTATNANN



STE11_M00274

6.0225e-08

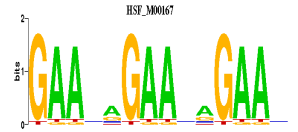
TTTGTTTTGTTTTT-
WNITTCTTTGTNNNNW



HSF_M00167

1.1999e-07

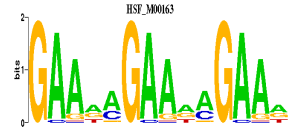
-TTTTGTTTGTTTTTT
NTTCNNTTCNNTTC---



HSF_M00163

6.0738e-07

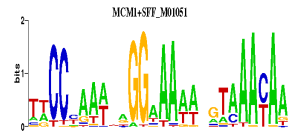
TTTTGTTTGTTTTTT
-NTTCNNTTCNNTTC-



MCM1+SFF_M01051

6.3690e-07

TTTTGTTTGTTTTTT-----
--TTRTTANNTWTTNCCNNWTTNGGNA



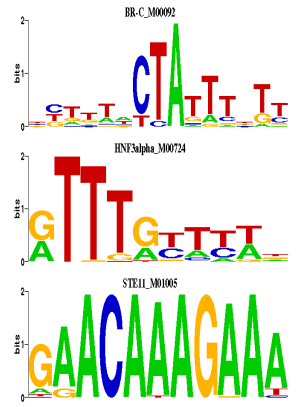
BR-C_M00094

7.3604e-07

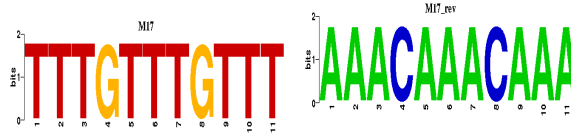
-AAAAACAAAACAAA
WVRTAAASAWAA-----



BR-C_M00092	1.3253e-06	AAAAAACAAAACAAAA RANAAATAGNWNNNN-
HNF3alpha_M00724	8.5335e-06	AAAAAACAAAACAAAA -----NWRARCAAAY
STE11_M01005	1.5336e-05	TTTTGTTTTGTTTTT- -----TTTCTTTGTTC



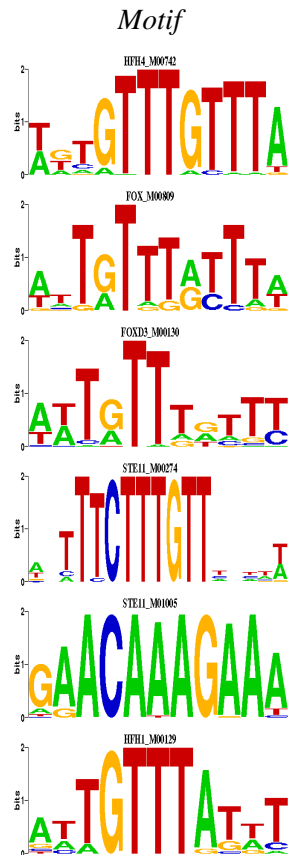
M17



forward

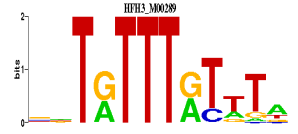
reverse complement

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
HFH4_M00742	9.9920e-16	TTTGTTTGTTT- WKTGTTTGTTTA
FOX_M00809	1.1049e-12	TTTGTTTGTTT- ANIGTTTTRTTWT
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



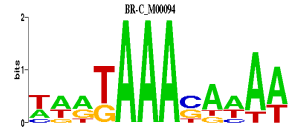
HFH3_M00289 8.5781e-09

TTTGTTTGTTT-
NNRTRTTTRTWN



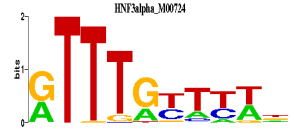
BR-C_M00094 2.0655e-07

-TTTGTTTGTTT
TTWISTTTAYWW



HNF3alpha_M00724 5.5731e-07

--AAACAAACAAA
NWRARCAAAY---

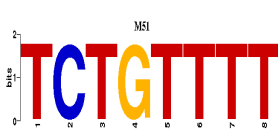


Freac-3_M00291 9.5431e-07

TTTGTTTGTTT-----
--TGTTTATTTACNNNN



M51



forward

reverse compliment

Name

E value

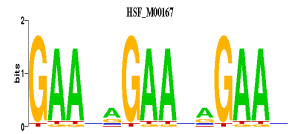
Alignment

Motif

HSF_M00167

4.8521e-06

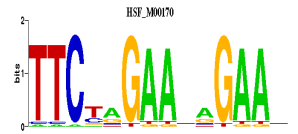
--TCTGTTTT-----
NTTCNNTTCNNTTC



HSF_M00170

4.8521e-06

--TCTGTTTT-----
NTTCNNTTCNNGAA



Grainyhead-Elf-1-NTF-1_M00951 6.1483e-06

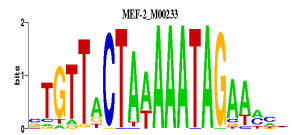
AAAACAGA
AAACCRG-



MEF-2_M00233

1.3665e-05

-----TCTGTTTT-----
NNNTTCTATTTTTAGTAACAN




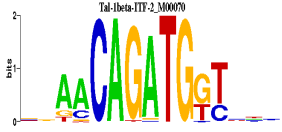



SMAD3_M00701

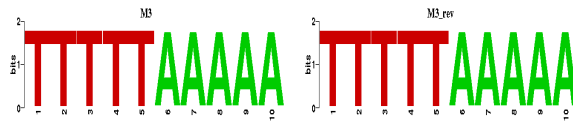
3.5568e-05

-TCTGTTTT
GTCGNCT-



HNF3alpha_M00724	4.5987e-05	-AAAACAGA- NWRARCAAA	
BRCA1-USF2_M01082	4.8334e-05	AAAACAGA -CAACNNN	
RAV1_M00343	1.3206e-04	--TCTGTTTT- NNWNTGTTGCN	
Tal-1beta-ITF-2_M00070	1.7679e-04	-----TCTGTTTT NNNACCATCTGTTNN	
HSF_M00168	1.8208e-04	-----TCTGTTTT NGAANN TTCNNTTC-	

M3

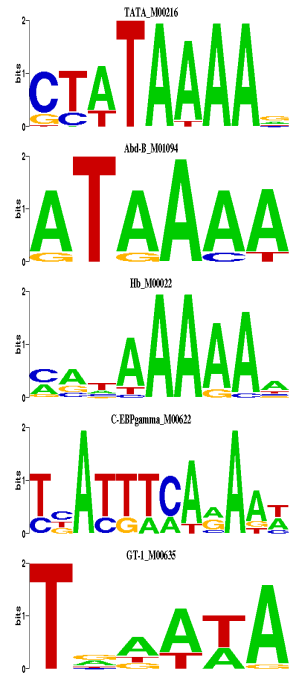


forward

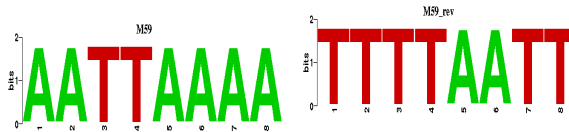
reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MEF-2_M00405	2.9868e-07	-----TTTTTAAAAA RGKNWTTTTTANNSM	
aMEF-2_M00403	3.1767e-06	-----TTTTTAAAAA KKRGNTATTTTTARNCM	
MEF-2_M00233	1.9584e-05	-----TTTTTAAAAA---- NNNTTCTATTTTTAGTAACAN	
MEF-2_M00406	2.5426e-05	-----TTTTTAAAAA NGGTTATTTTTAGM--	
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 TWTNNA----



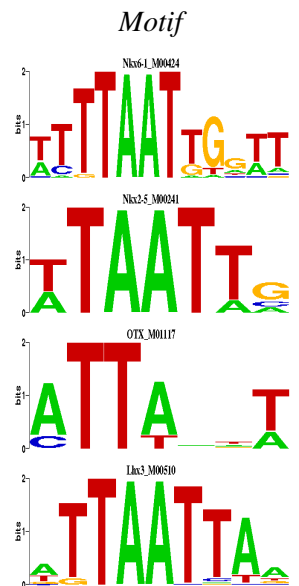
M59



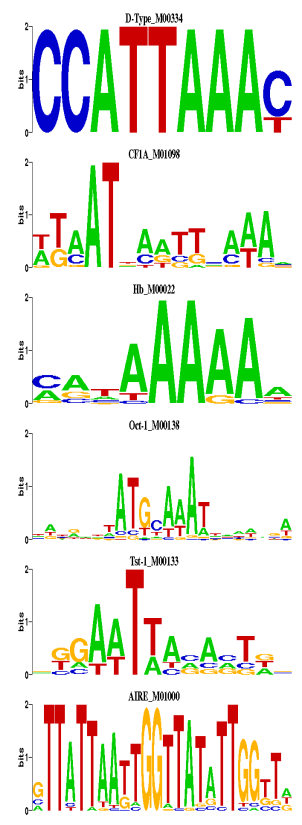
forward

reverse compliment

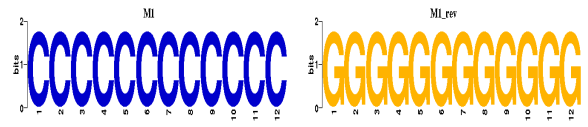
Name	E value	Alignment
Nkx6-1_M00424	7.1351e-11	TTTTAATT----- WTTTAATTGNTT
Nkx2-5_M00241	1.0763e-06	-AATTAAAA NAATTAW--
OTX_M01117	2.2532e-06	AATTAAAA ANNNTAAT-
Lhx3_M00510	3.0296e-06	TTTTAATT-- -WTTAATTAN



D-Type_M00334	4.8477e-06	TTTTAATT- GTTTAATGG
CF1A_M01098	5.6626e-06	-----AATTAAAA- WTAATNARTTNAAN
Hb_M00022	7.7490e-06	-TTTTAATT NTTTTTNYK
Oct-1_M00138	1.2647e-05	--TTTTAATT----- WNNNNNNATTTNCATNNNNNNN
Tst-1_M00133	1.4004e-05	---TTTTAATT--- NNANTNTAATTTCMN
AIRE_M01000	1.7321e-05	-----AATTAAAA-- NAMCCAATATAACCAATTAATAAN

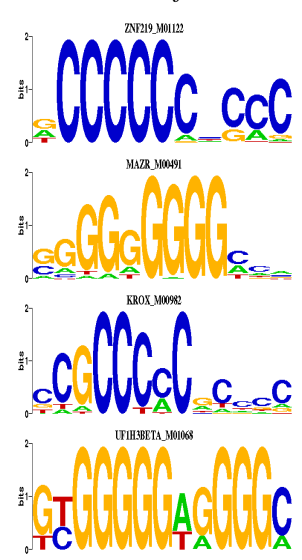


M1

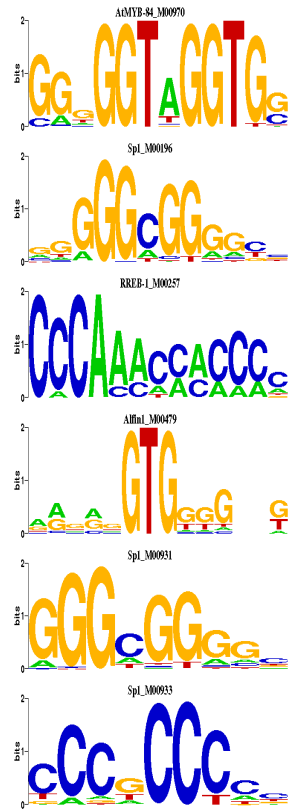


forward *reverse complement*

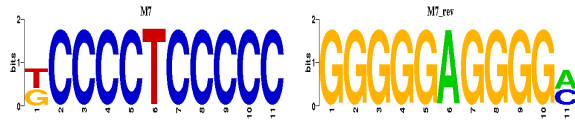
Name	E value	Alignment
ZNF219_M01122	2.4247e-13	GGGGGGGGGGGG GGGNGGGGGGN-
MAZR_M00491	7.3591e-10	---GGGGGGGGGGG SGGSGGGGGGGMNN
KROX_M00982	1.4426e-09	-CCCCCCCCCCCC CCGCCCCCNCNCC
UF1H3BETA_M01068	2.4590e-09	-CCCCCCCCCCCC GCCCTCCCCRC



AtMYB-84_M00970	1.0881e-06	GGGGGGGGGGGG GGNGGTAGGTGS
Sp1_M00196	6.2691e-06	--CCCCCCCCCCCC NNCCCCGCCCCN--
RREB-1_M00257	1.3239e-05	-GGGGGGGGGGGG GGGGTGGTTGGG
Alfin1_M00479	1.7336e-05	---CCCCCCCCCCCC MNNCCCCACNYNYN-
Sp1_M00931	2.3343e-05	-CCCCCCCCCCCC NCCCCGCC----
Sp1_M00933	4.6608e-05	-CCCCCCCCCCCC C-CCKCCCCN---



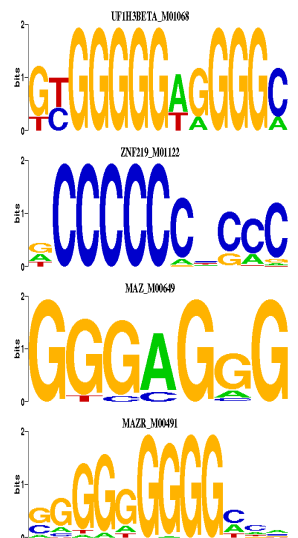
M7



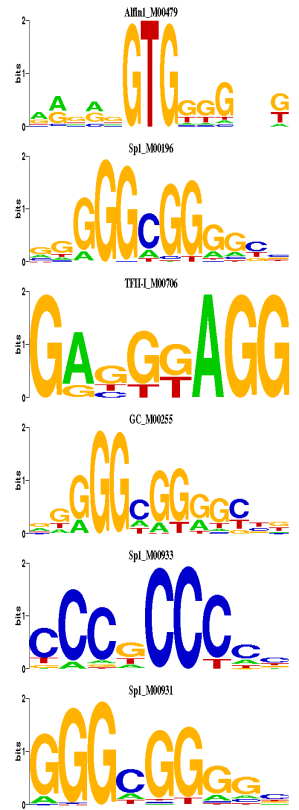
forward

reverse compliment

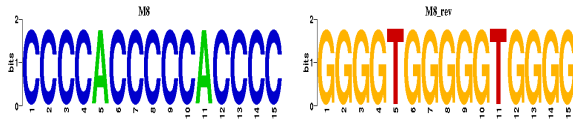
Name	E value	Alignment
UF1H3BETA_M01068	0.0000e+00	KCCCTCCCCC-- GCCCTCCCCRC
ZNF219_M01122	7.4369e-11	GGGGGAGGGGM GGNGGGGGGN
MAZ_M00649	8.6829e-10	KCCCTCCCCC --CCCTCC--
MAZR_M00491	1.7966e-09	GGGGGAGGGM-- -SGGGGGGGMNN



Alfin1_M00479	6.7900e-08	--KCCCCTCCCC-- MNNCCCCACNYYN
Sp1_M00196	1.8742e-07	-KCCCCTCCCC NNCCCCGCCCCN
TFII-I_M00706	4.9626e-07	KCCCCTCCCC ---CCTMCNTC
GC_M00255	7.3207e-07	--KCCCCTCCCC NNGCCCCGCCCCN
Sp1_M00933	8.1515e-07	KCCCCTCCCC --CCCKCCCN
Sp1_M00931	1.3356e-06	KCCCCTCCCC NCCCCGCC--



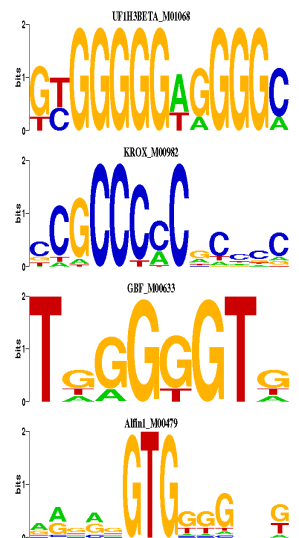
M8

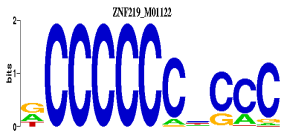
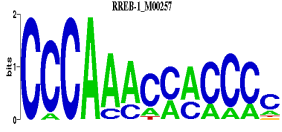

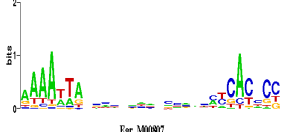




forward

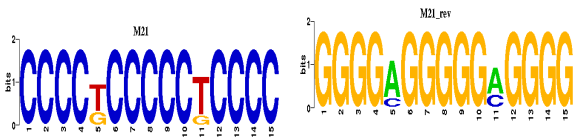
reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
UF1H3BETA_M01068	4.2744e-14	-CCCCACCCCCACCCC GCCCTCCCCRC---
KROX_M00982	2.2382e-13	GGGGTGGGGGTGGGG GNNGNGGGGCGG--
GBF_M00633	2.6601e-10	CCCCACCCCCACCCC ---NACCCNA----
Alfin1_M00479	5.3896e-10	CCCCACCCCCACCCC-- ---MNNCCCCACNYYN



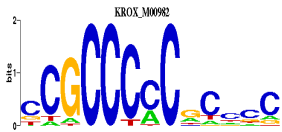


ZNF219_M01122	1.1492e-08	GGGGTGGGGGTGGGG GGGNGGGGGGN----	
RREB-1_M00257	6.6020e-08	GGGGTGGGGGTGGGG -GGGGTGGTTTGGG-	
CAC-binding_M00720	2.7398e-07	GGGGTGGGGGTGGGG RGGSTGGG-----	
Pax-4_M00380	1.2184e-06	GGGGTGGGGGTGGGG----- NGNGTGNNNNNNNNNNNNNNNNNTAWTTTN	
Egr_M00807	1.2324e-05	CCCCACCCCCACCCC -NYYGCSCCCA----	
AtMYB-84_M00970	1.2987e-05	GGGGTGGGGGTGGGG -GGNGGTAGGTGS--	

M21

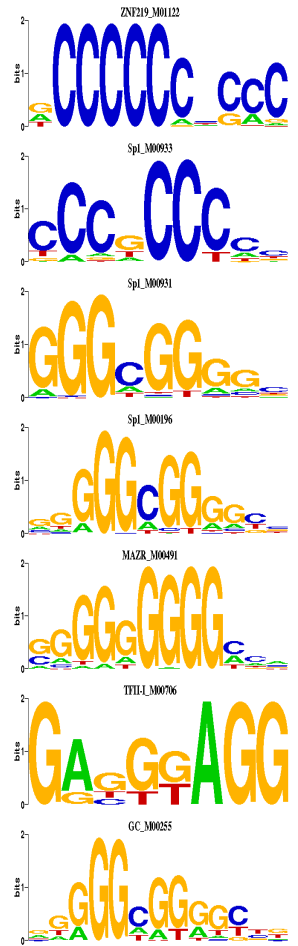


forward

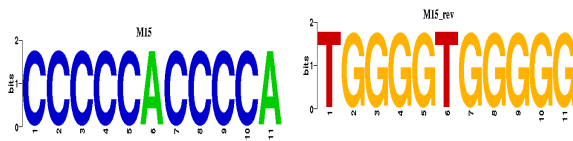
reverse compliment

Name	E value	Alignment	Motif
KROX_M00982	3.2419e-14	GGGGAGGGGGAGGGG GNNGNGGGGGCGG--	
UF1H3BETA_M01068	1.6388e-11	-CCCCTCCCCCTCCCC GCCCTCCCCRC---	
MAZ_M00649	5.4655e-09	CCCCTCCCCCTCCCC -----CCCTCCC-	

ZNF219_M01122	9.7580e-08	GGGGAGGGGGAGGGG GGGNGGGGGGN-----
Sp1_M00933	3.6342e-07	CCCCTCCCCCTCCCC -CCCKCCCN-----
Sp1_M00931	5.5228e-07	-CCCCTCCCCCTCCCC NCCCCGCC-----
Sp1_M00196	5.7542e-07	--CCCCTCCCCCTCCCC NNCCCCGCCCN-----
MAZR_M00491	2.5310e-06	GGGGAGGGGGAGGGG -SGGGGGGGMNN--
TFII-I_M00706	8.5108e-06	CCCCTCCCCCTCCCC --CCTMCNTC-----
GC_M00255	8.7440e-06	---CCCCTCCCCCTCCCC NNGCCCCGCCCN-----



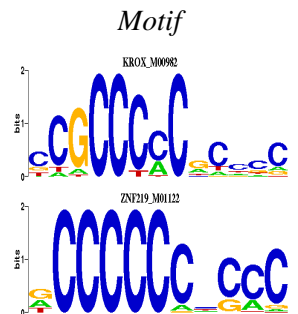
M15



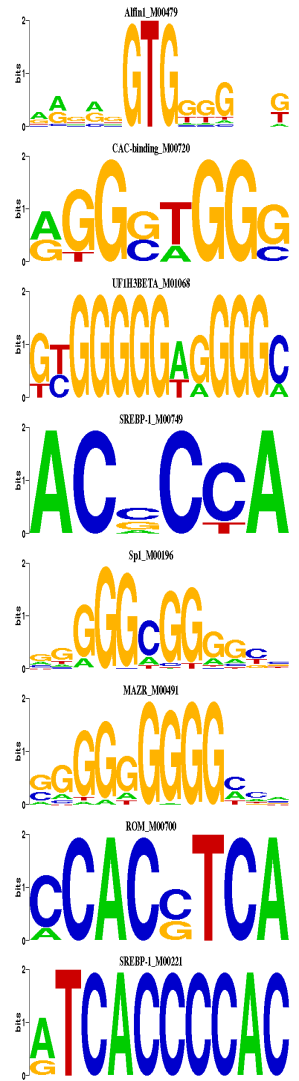
forward

reverse compliment

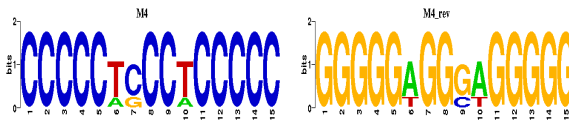
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
KROX_M00982	1.4302e-10	TGGGGTGGGGG--- -GNNGNGGGGGCGG
ZNF219_M01122	1.4636e-09	TGGGGTGGGGG- -GGGNGGGGGGN



Alfin1_M00479	1.0670e-08	--CCCCACCCCA-- MNNCCCCACNYNYN
CAC-binding_M00720	3.0003e-08	TGGGGTGGGGG -RGGSTGGG--
UF1H3BETA_M01068	4.4831e-08	CCCCACCCCA-- GCCCTCCCCRC
SREBP-1_M00749	4.1163e-07	TGGGGTGGGGG TGGSGT-----
Sp1_M00196	6.2171e-07	-CCCCACCCCA NNCCCCGCCCN
MAZR_M00491	1.0151e-06	TGGGGTGGGGG-- -SGGGGGGGMNN
ROM_M00700	1.6926e-06	CCCCACCCCA ---CCACSTCA
SREBP-1_M00221	1.9466e-06	-TGGGGTGGGGG GTGGGGTGAT--



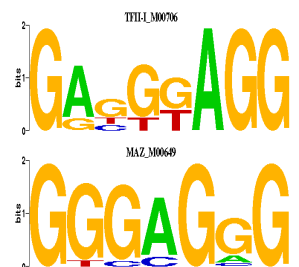
M4



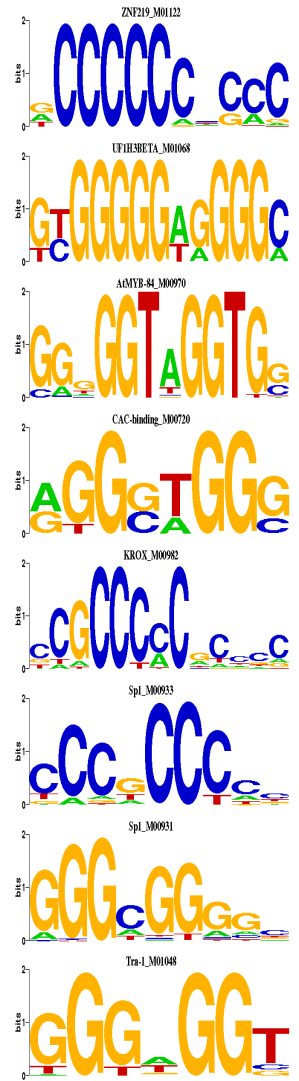
forward

reverse compliment

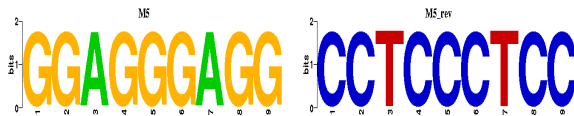
Name	E value	Alignment
TFII-I_M00706	1.1053e-08	CCCCCTCCCTCCCC ---CCTMCNTC----
MAZ_M00649	1.5734e-08	CCCCCTCCCTCCCC --CCCTCCC-----



ZNF219_M01122	3.2359e-08	GGGGGAGGGAGGGGG-- -----GGGNGGGGGGN
UF1H3BETA_M01068	8.8377e-08	CCCCCTCCCTCCCC-- ----GCCCCCTCCCCRC
AtMYB-84_M00970	9.1729e-07	CCCCCTCCCTCCCC ---SCACCTACCNCC
CAC-binding_M00720	9.5898e-07	GGGGGAGGGAGGGGG -----RGGSTGG--
KROX_M00982	9.6387e-07	GGGGGAGGGAGGGGG -GNNGNGGGGGCGG-
Sp1_M00933	2.0280e-05	CCCCCTCCCTCCCC -----CCCKCCCN
Sp1_M00931	3.3839e-05	CCCCCTCCCTCCCC NCCCCGCC-----
Tra-1_M01048	4.1230e-05	CCCCCTCCCTCCCC -----ACCWCC--



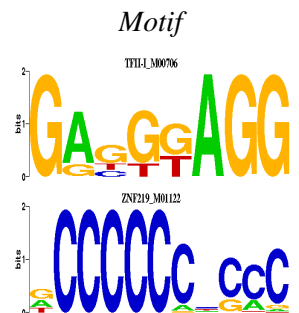
M5











forward

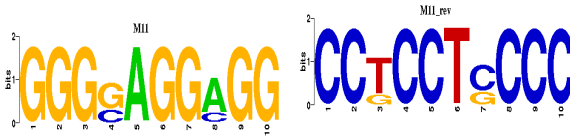
reverse compliment

Name	E value	Alignment
TFII-I_M00706	4.6796e-12	CCTCCCTCC CCTMCNTC-
ZNF219_M01122	1.9528e-07	-GGAGGGAGG- GGGNGGGGGGN



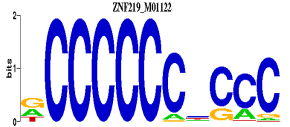
MAZ_M00649	7.4906e-07	-CCTCCCTCC CCCTCCC---	
Tra-1_M01048	8.2984e-06	-CCTCCCTCC ACCWCCC---	
PU.1_M00658	1.5920e-05	GGAGGGAGG -GAGGAAG-	
MAF_M00648	2.0859e-05	-----CCTCCCTCC NSNMMACTTCCYYCN	
UF1H3BETA_M01068	3.0630e-05	---CCTCCCTCC- GCCCCTCCCCRC	
AtMYB-84_M00970	6.4851e-05	GGAGGGAGG--- GGNGGTAGGTGS	
MAZR_M00491	9.8929e-05	GGAGGGAGG--- SGGGGGGGGMNN	
CAC-binding_M00720	1.0235e-04	-CCTCCCTCC CCCASCCY--	

M11










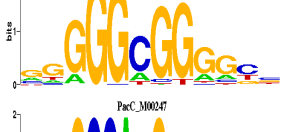

forward

reverse compliment

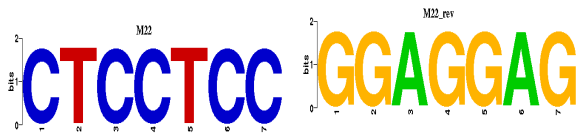
Name	E value	Alignment	Motif
ZNF219_M01122	2.2800e-06	GGGGAGGAGG-- -GGNGGGGGGN	

Stamp Results

04/30/14

UF1H3BETA_M01068	2.2887e-06	CCTCCTCCCC--- GCCCCTCCCCRC	
VDR_M00444	2.3572e-06	----CCTCCTCCCC TSWCCYYNYTNMCC	
MAZ_M00649	3.3211e-06	CCTCCTCCCC --CCCTCCC-	
AtMYB-84_M00970	1.2395e-05	--GGGGAGGAGG GGNGGTAGGTGS	
KROX_M00982	1.9338e-05	GGGGAGGAGG--- GNNGNGGGGGCGG	
PU.1_M00658	4.0782e-05	GGGGAGGAGG ---GAGGAAG	
Tra-1_M01048	5.2628e-05	CCTCCTCCCC --ACCWCCC-	
Sp1_M00196	1.2264e-04	-CCTCCTCCCC- NNCCCCGCCCN	
PacC_M00247	1.4114e-04	----CCTCCTCCCC-- NNNNNNKCYTGCCNGN	

M22



forward

reverse compliment

Name

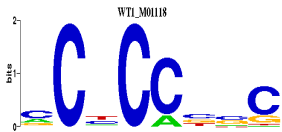





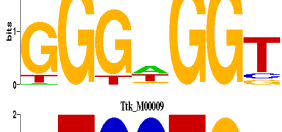


E value

Alignment

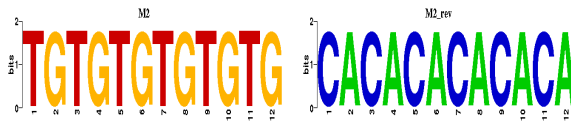
Motif

Stamp Results

04/30/14

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----- NGYTTCGNNNANAGNNNNCCG	
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--	

M2



forward

reverse complement

Name

E value

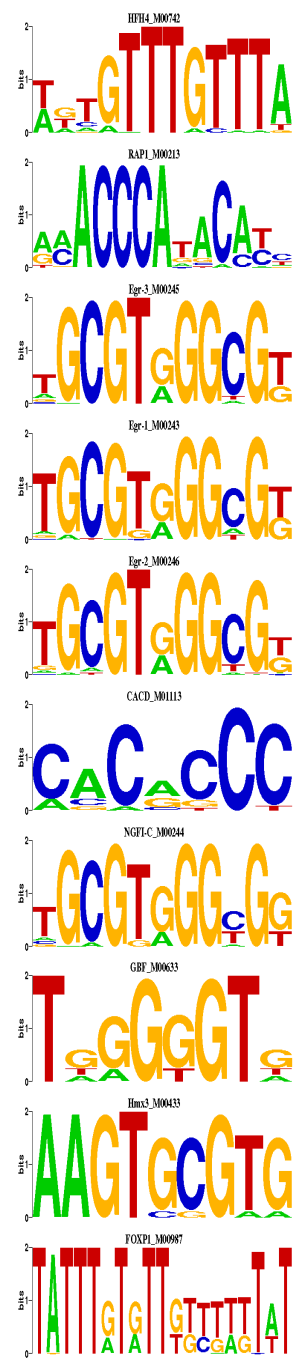
Alignment

Motif

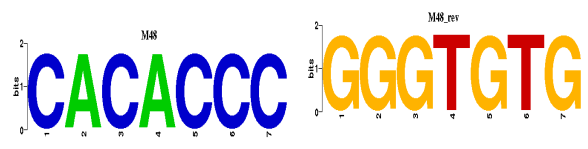
Stamp Results

04/30/14

HFH4_M00742	3.4597e-06	TGTGTGTGTGTG WKTGTTTGTTTA
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 -GGYG TG----
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






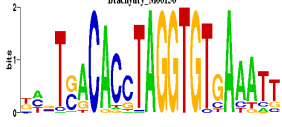






M48

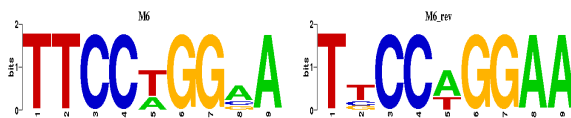


forward

reverse complement

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CACD_M01113	2.1652e-11	GGGTGTG GGYGTTG	
CACCC-binding_M00721	9.6046e-08	-CACACCC----- CCNCACCCWNNKGNT	
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	

M6

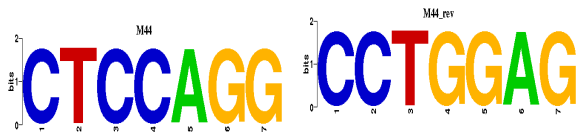


forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STAT5B_M00459	2.3677e-11	--TTCCTGGAA--- NWTTCNNGGAANYN	
STAT5A_M00457	2.8932e-11	---TTCCTGGAA-- NRNTTCNNGAANY	
STATx_M00223	1.9760e-06	TTCCAGGAA TTMYGGGA-	
STAT_M00259	5.2465e-06	-----TTCCTGGAA----- NNNNNTTTCSSGGAANNNN	
STAT1_M00224	6.2036e-06	-----TTCCAGGAA----- NNNNNTTCCGGAANTGNSN	
Pax-6_M00979	6.9324e-06	-TTCCTGGAA--- TGACCTGGAAC TM	
STAT3_M00225	1.0960e-05	-----TTCCTGGAA----- NNNCATTTCCSSGGAATNNN	
STAT5A_M00460	1.1451e-05	-----TTCCTGGAA----- TCNNNGAANNNNNTTCCNNGNR	
Tel-2_M00678	8.4076e-05	TTCCAGGAA--- ---CAGGAAGTA	
NERF1a_M00531	1.4384e-04	TTCCAGGAA----- -RNCAGGAAGYRNSTNNS	

M44

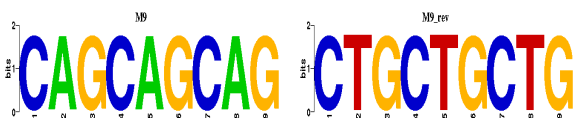


forward

reverse compliment





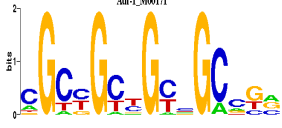

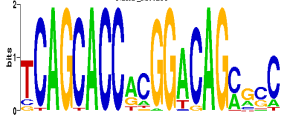



Name	E value	Alignment	Motif
Pax-6_M00979	8.1790e-06	---CTCCAGG--- KAGTTCCAGGTCA	
STAT5B_M00459	4.3863e-05	----CCTGGAG--- NWTTCNNGGAANYN	
BRK_M01096	8.3786e-05	CCTGGAG -NTGGCG	
AP-2_M00915	2.3914e-04	--CCTGGAG--- NGCCNNGGNNN	
Pax-5_M00144	2.6612e-04	-----CTCCAGG----- NNNRYNGTYMCGCTYNANNNNNNCNNNY	
STAT5A_M00457	5.3827e-04	----CCTGGAG-- NRNTTCNNGAANY	
STAT5A_M00460	6.0982e-04	-----CCTGGAG TCNNGAANNNNNNNTTCCNNGNR	
Barbie_M00238	7.1460e-04	-CTCCAGG----- CMNNCNSCTTTNNN	
RP58_M00532	2.2228e-03	CTCCAGG----- -TCCAGATGTTN	
ZAP1_M00754	2.4624e-03	-CCTGGAG-- ACCTTKAGGG	

M9

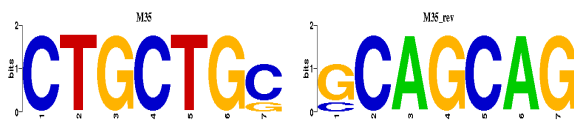


forward

reverse compliment








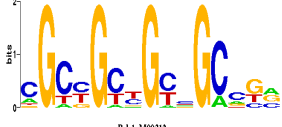
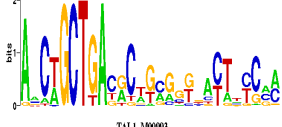

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LMAF_M01139	5.8168e-06	CTGCTGCTG CTGCTGAS-	
TAL1_M00993	2.9193e-05	CAGCAGCAG- -RNCAGNTGG	
HEB_M00698	5.4017e-05	CTGCTGCTG CWGCTG---	
AP-4_M00927	6.0222e-05	CAGCAGCAG- --RCAGCTGN	
Adf-1_M00171	9.2678e-05	--CTGCTGCTG---- CGCYGCGYNGCNKN	
NRSF_M01028	1.3541e-04	-----CTGCTGCTG- YNCCTGTCCRYGGTGCTGA	
NRSF_M00256	1.4391e-04	-CAGCAGCAG----- TCAGCACCACGGACAGCRSC	
myogenin_M00712	2.0052e-04	CAGCAGCAG --NCAGSTG	
LBP-1_M00644	2.0250e-04	CAGCAGCAG --SCAGCN-	
GAMYB_M01135	4.4905e-04	-CTGCTGCTG-- KNNGTTRYYSN	

M35

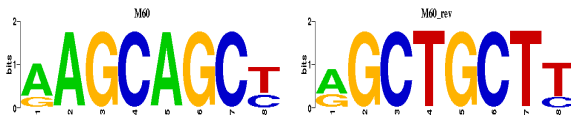


forward

reverse compliment

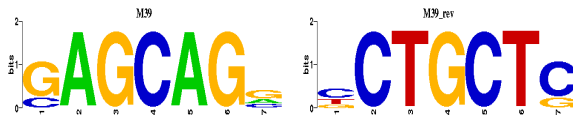
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LMAF_M01139	1.8121e-07	CTGCTGC- CTGCTGAS	
HEB_M00698	5.2380e-06	-CTGCTGC CCWGCTG-	
AP-4_M00927	9.0946e-06	GCAGCAG- RCAGCTGN	
LBP-1_M00644	1.4104e-05	GCAGCAG SCAGCN-	
myogenin_M00712	1.9983e-05	GCAGCAG NCAGSTG	
RAV1_M00343	7.1593e-05	-GCAGCAG--- NGCAACANWNN	
ZBRK1_M01105	8.4668e-05	-----CTGCTGC- AAANNCTGCKSCC	
Adf-1_M00171	1.1788e-04	-----GCAGCAG-- NMNGCNRCRGRGCG	
Bel-1_M00312	1.5935e-04	-----GCAGCAG-- KNGRNAGTNMNCKCWGYRTCAGCAGNT	
TAL1_M00993	1.6388e-04	-GCAGCAG- RNCAGNTGG	

M60



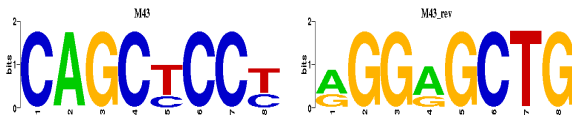
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LBP-1_M00644	1.0779e-07	AAGCAGCT --SCAGCN	
TAL1_M00993	1.6590e-06	AAGCAGCT-- -RNCAGNTGG	
HEN1_M00058	6.5955e-06	-----AAGCAGCT----- NNNGGNCGCAGCTGCGNCCNN	
LUN-1_M00480	1.1849e-05	-----AAGCAGCT--- TCCCAAAGTAGCTGGG	
AP-4_M00927	2.2622e-05	AAGCAGCT-- --RCAGCTGN	
myogenin_M00712	2.5009e-05	AAGCAGCT- --NCAGSTG	
HEN1_M00068	1.6175e-04	-----AAGCAGCT----- NNNGGNCNCAGCTGNGNCCNN	
NERF1a_M00531	3.1136e-04	---AGCTGCTT----- SNNASNYRCTTCTGNY	
LMAF_M01139	7.0501e-04	AGCTGCTT-- --CTGCTGAS	
HEB_M00698	1.2504e-03	-AGCTGCTT CAGCWGG--	

M39



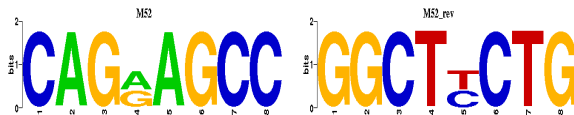
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
KAISO_M01119	9.3506e-06	-GAGCAGN- NTNGCAGGA	
HEB_M00698	1.7681e-05	GAGCAGN CAGCWGG	
E47_M00002	6.8686e-05	-----NCTGCTC NNNNACACCTGCNS	
TAL1_M00993	1.3952e-04	GAGCAGN--- -RNCAGNTGG	
AR_M00962	1.7782e-04	-NCTGCTC NNNTGCTC	
LMAF_M01139	1.9491e-04	NCTGCTC-- -CTGCTGAS	
Ttk_M00009	2.1429e-04	GAGCAGN-- --GCAGGAC	
c-Myc_M01145	2.7414e-04	GAGCAGN---- GAGCACGTGGT	
E2A_M00973	6.6961e-04	GAGCAGN- -RNCAGNT	
myogenin_M00712	1.7078e-03	GAGCAGN-- --NCAGSTG	

M43



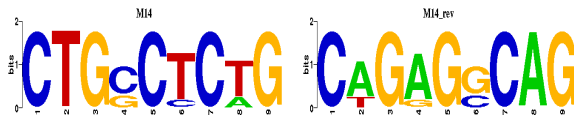
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
TAL1_M00993	2.3829e-06	-CAGCTCCT CCANCTGNY	
LUN-1_M00480	1.2977e-05	--CAGCTCCT----- CCCAGCTACTTTGGGA	
LBP-1_M00644	3.6801e-05	-CAGCTCCT SCAGCN---	
AP-4_M00927	6.7844e-05	-CAGCTCCT NCAGCTGY-	
myogenin_M00712	1.3636e-04	CAGCTCCT CASCTGN-	
HEB_M00698	9.0046e-04	AGGAGCTG- --CAGCWGG	
bZIP910_M00357	1.0260e-03	----CAGCTCCT ACGTCAGCAYS-	
NRSE_M00325	1.1426e-03	-----AGGAGCTG- GGCRCTCTCCGNGGTGCTGA	
ANT_M00501	1.3989e-03	----AGGAGCTG- CMTYGGGAWNTGT	
ZBRK1_M01105	1.6330e-03	-AGGAGCTG----- AAANNCTGCKSCC	

M52



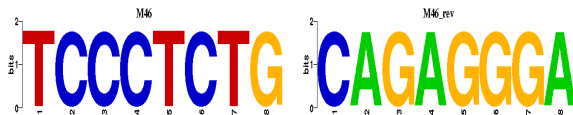
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
E12_M00693	1.3612e-05	-GGCTYCTG- NNNCACCTGY	
HES1_M01009	7.4150e-04	-----CAGRAGCC- NNNNSCACRAGNSN	
GCR1_M00337	1.8552e-03	-----CAGRAGCC AAWAGTGGAAGCC	
Ttk_M00009	2.1317e-03	-CAGRAGCC GCAGGAC--	
PEND_M01015	2.1726e-03	GGCTYCTG -ACTTCTT	
c-Ets-1_M00743	3.5550e-03	GGCTYCTG -GCTTCC	
AREB6_M00414	4.1921e-03	---CAGRAGCC NNMCAGGTGYN	
HSF_M00641	4.2450e-03	--GGCTYCTG-- GAARCYNCKNGA	
XPF-1_M00684	4.2832e-03	-GGCTYCTG GKTSNYCNG	
GCR1_M00046	4.7885e-03	GGCTYCTG- -GCTTCCWC	

M14



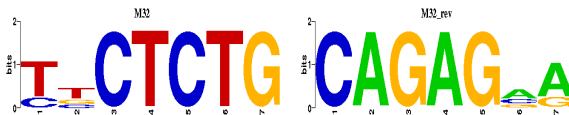
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	2.8819e-05	CTGCCTCTG CTTCCTC--	
E2A_M00804	3.9641e-05	-CAGAGGCAG--- NMNGNGNCAGGTG	
v-Maf_M00035	1.2626e-04	----CTGCCTCTG----- NNTGCTGACNNGCANNN	
Elf-1_M00746	1.4400e-04	-CTGCCTCTG- AYTTCCTCTTN	
XPF-1_M00684	3.7662e-04	CAGAGGCAG CNGRNSAMC	
MAF_M00983	5.0997e-04	-CAGAGGCAG GNTGAGTCAN	
TFII-I_M00706	6.7421e-04	-CTGCCTCTG CCTMCNTC--	
Pax-9_M00329	9.4591e-04	-----CTGCCTCTG NGNSNNCNCNCNNCNNTGSNTNW-	
Nrf-2_M00821	1.0920e-03	-CTGCCTCTG-- NNTGACTCAGCA	
AP-1_M00173	1.2707e-03	-CAGAGGCAG WKNAGTCAN	

M46



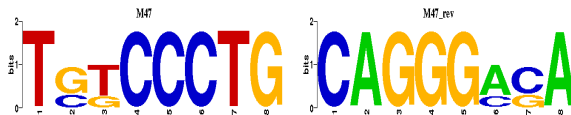
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
TFII-I_M00706	1.3948e-05	--TCCCTCTG CCTMCNTC--	
MAF_M00648	1.0257e-04	-----TCCCTCTG NSNMMACTTCCYYCN-	
MAZ_M00649	2.1493e-04	CAGAGGGA GGGAGGG-	
Elf-1_M00746	2.7420e-04	--TCCCTCTG- AYTTCCTCTTN	
COUPTF_M01036	4.7942e-04	-----TCCCTCTG-- NNNNTGACCTTTNMCYNNMN	
TAL1_M00993	5.9316e-04	TCCCTCTG-- -CCANCTGNY	
RBP-Jkappa_M01111	7.4997e-04	CAGAGGGA -NGTGGGA	
MZF1_M00084	8.0694e-04	-TCCCTCTG--- TTNCCCCTCINN	
HSF_M00641	1.0503e-03	--TCCCTCTG-- GAARCYNCKNGA	
XPF-1_M00684	1.4141e-03	-TCCCTCTG GKTSNYCNG	

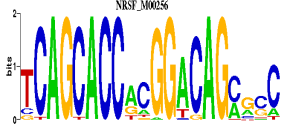




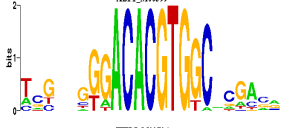


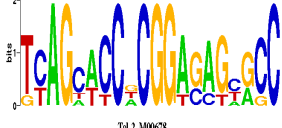

M32



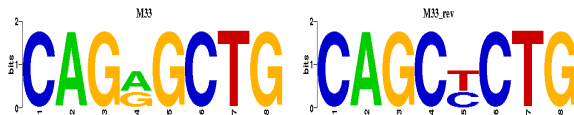
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	8.1416e-05	-TNCTCTG--- TTTCTTTGTTT	
Alx-4_M00619	1.2530e-04	-----TNCTCTG GATTATTCTCAG	
GAGA_M00723	1.5149e-04	---TNCTCTG TYNCKCTCWS	
STE11_M00274	4.3253e-04	-----CAGAGNA--- WNNNNAACAAAGAAANW	
GATA-1_M00346	4.4486e-04	--TNCTCTG NNTTATCNN	
Sry-beta_M00666	9.2861e-04	CAGAGNA-- -AGWGATGC	
Eve_M00629	1.2734e-03	-CAGAGNA- GCNGNSSWN	
PR_M00960	1.3644e-03	---TNCTCTG NTGTYCNNW-	
GATA-2_M00349	1.7154e-03	--TNCTCTG TNTTATCTS	
ARF_M00438	1.7905e-03	CAGAGNA GAGACAA	

M47



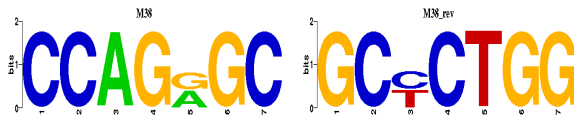
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
NRSF_M00256	5.7774e-05	-----TGTCCTG----- GSYGCTGTCCGTGGTGCTGA	
NRSF_M01028	7.7851e-05	-----CAGGGACA--- TCAGCACCRYGGACAGNR	
TEIL_M00502	7.7752e-04	CAGGGACA -AGRTWCA	
ARF_M00438	1.4539e-03	CAGGGACA- --GAGACAA	
ID1_M01021	1.5374e-03	-TGTCCTG- TTGTCSITWT	
ABF1_M00399	2.0191e-03	---CAGGGACA----- WNNNNGGGACACGTGGCNGANN	
TFII-I_M00706	2.1833e-03	TGTCCTG CCTMCNTC	
GATA-4_M00632	2.7117e-03	TGTCCTG----- --TSYCTKNTATC	
NRSE_M00325	4.4610e-03	-----TGTCCTG----- GGCRCTCTCCGNGGTGCTGA	
Tel-2_M00678	4.8958e-03	-TGTCCTG TACTTCTG	


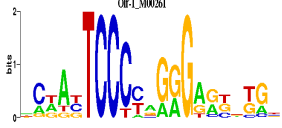



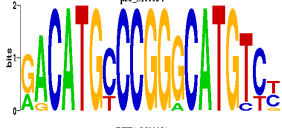




M33



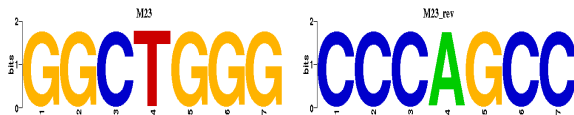
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Eve_M00629	3.1830e-06	-CAGRGCTG GCNGNSSWN	
ZBRK1_M01105	2.6641e-05	-CAGRGCTG----- AAANNCTGCKSCC	
LBP-1_M00644	9.6911e-05	-CAGCYCTG SCAGCN---	
Sry-beta_M00666	1.7429e-04	CAGRGCTG- -AGWGATGC	
AP-4_M00005	2.8274e-04	-----CAGRGCTG----- MNGNCNNCAGCTGNNNN	
HEB_M00698	2.7050e-03	CAGRGCTG- --CAGCWGG	
Alfin1_M00479	3.1417e-03	-----CAGCYCTG MNNCCCCACNYNYN	
AP-4_M00176	3.3546e-03	--CAGCYCTG NNCAGCTGN-	
AP-4_M00927	3.7384e-03	CAGRGCTG- -RCAGCTGN	
Dde_M00304	4.4962e-03	CAGRGCTG- ---GGCTGAGC	

M38



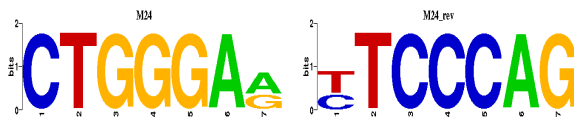
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Eve_M00629	5.6948e-05	CCAGRGC-- GCNGNSSWN	
Olf-1_M00261	4.6924e-04	-----GCYCTGG----- NCMNNYTCCCNRRGGANTNGN	
HSF_M00641	7.3316e-04	----GCYCTGG- GAARCYNCKNGA	
Pax-1_M00326	1.9406e-03	----CCAGRGC----- ATATCTAGAGCGGAACG	
Pax-6_M00979	2.1976e-03	----CCAGRGC- KAGTTCCAGGTCA	
p53_M00034	2.2016e-03	----CCAGRGC----- GACATGCCCGGGCATGTCY	
RFX1_M00281	2.7992e-03	----GCYCTGG----- NNGTTRCYANNGYNACN	
BRK_M01096	3.8269e-03	GCYCTGG-- ---NTGGCG	
Ttk_M00009	4.0925e-03	CCAGRGC GCAGGAC	
Dde_M00304	4.4609e-03	-CCAGRGC 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	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-	



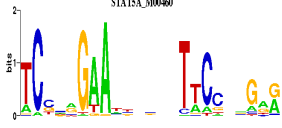


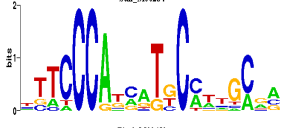




M24



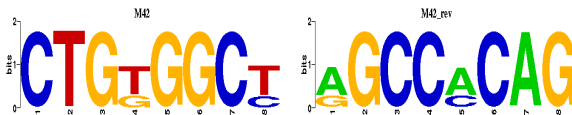
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Ik-3_M00088	2.5462e-07	----YTCCCAG- GGTATTCCCNRN	
Lyf-1_M00141	1.7896e-06	-YTCCCAG YCTCCCAA	
RBP-Jkappa_M01112	5.0647e-06	-YTCCCAG-- KTTCCCACGN	
Ik-1_M00086	4.1842e-05	----YTCCCAG- NNNATTCCANN	
Su_H_M00234	4.1902e-05	--CTGGGAR-- NYGTGGGAAMCN	
RBP-Jkappa_M01111	5.1589e-05	-CTGGGAR NGTGGGA-	
Staf_M00264	5.4289e-05	-----CTGGGAR- NNGCANNKGNANNNTGGGANN	
STAT_M00777	8.0079e-05	YTCCCAG----- -TCCNAGAANNNN	
Alx-4_M00619	1.7478e-04	----YTCCCAG GATTATTCTCAG	
Pitx2_M00482	1.8446e-04	CTGGGAR-- NTGGGATTAN	

M41

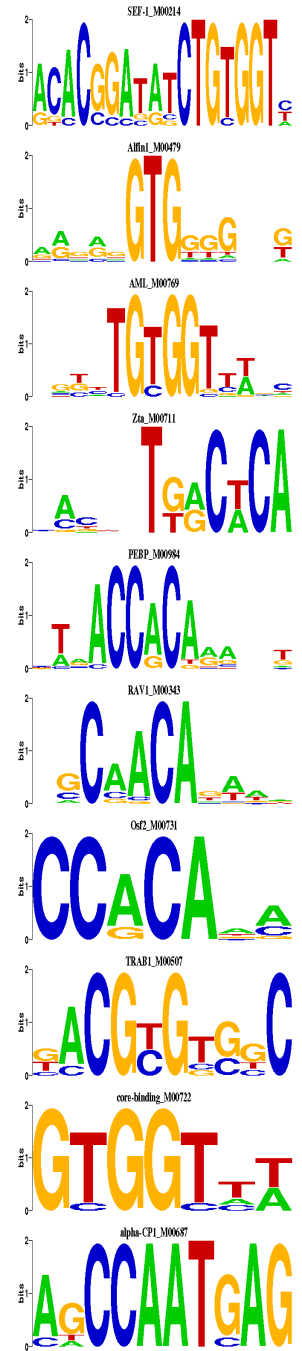


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STAT_M00777	1.9448e-07	TCCCAGA----- TCCNAGAANNNN	
STATx_M00223	2.5849e-06	-TCTGGGA TTMYGGGA	
STAT5A_M00460	6.9742e-06	-----TCTGGGA YNCNNGGAANNNNNTTCNNGA	
Ik-3_M00088	4.7839e-05	-----TCCCAGA GGTATTCCCNRN	
RBP-Jkappa_M01111	5.1589e-05	TCTGGGA NGTGGGA	
Staf_M00264	1.8060e-04	-----TCTGGGA-- NNGCNNKGNANNNNTGGGANN	
Pitx2_M00482	1.8446e-04	TCTGGGA----- -NTGGGATTAN	
Lyf-1_M00141	1.8799e-04	--TCCCAGA YCTCCCAA-	
LUN-1_M00480	3.4185e-04	TCCCAGA----- TCCCAAAGTAGCTGGG	
RBP-Jkappa_M01112	7.1608e-04	--TCCCAGA- KTTCCACGN	

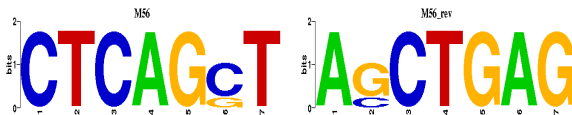
M42










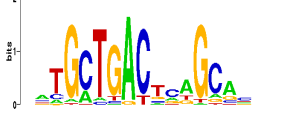


	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
SEF-1_M00214	5.7700e-05	AGCCACAG----- RACCACAGATATCCGTGT
Alfin1_M00479	7.1398e-05	-AGCCACAG----- MNNCCCCACNYNYN
AML_M00769	9.0558e-05	---AGCCACAG--- NNWRACCACANNNN
Zta_M00711	1.1508e-04	--AGCCACAG-- TGWGYCANNNTN
PEBP_M00984	2.8833e-04	----CTGTGGCT-- NNNNYTGTGGTNAN
RAV1_M00343	3.6391e-04	---CTGTGGCT NNWNIGTTGCN
Osf2_M00731	4.9023e-04	-CTGTGGCT KNTGTGG--
TRAB1_M00507	6.8044e-04	AGCCACAG--- -GNCACRCGTM
core-binding_M00722	1.9167e-03	-AGCCACAG WNACCAC--
alpha-CP1_M00687	2.1747e-03	AGCCACAG-- AGCCAATGAG

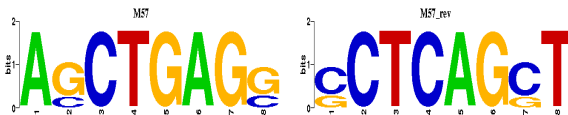


M56



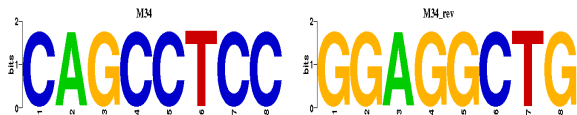
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Dde_M00304	4.8992e-07	-CTCAGCT GCTCAGCC	
CDC5_M00361	1.6450e-06	--AGCTGAG-- NSCGCTGAGS	
MAF_M00983	3.1837e-06	----CTCAGCT NTGACTCANC-	
NF-E2_M00037	8.3301e-06	AGCTGAG---- -GCTGAGTCAY	
AP-4_M00175	1.0390e-05	---AGCTGAG NNCAGCTGN-	
Nrf-2_M00821	1.0463e-05	-----CTCAGCT NNTGACTCAGCA	
LBP-1_M00644	1.9941e-05	CTCAGCT -SCAGCN	
HEN1_M00068	2.2133e-05	-----AGCTGAG----- NNNGGNCNCAGCTGNGNCCNN	
AP-4_M00176	2.7817e-05	---AGCTGAG NNCAGCTGN-	
v-Maf_M00035	5.0160e-05	---AGCTGAG----- NNNTGCNNNGTCAGCANN	

M57



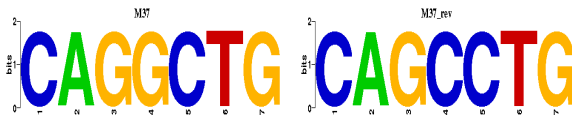
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Dde_M00304	2.1432e-07	AGCTGAGG GGCTGAGC	
CDC5_M00361	6.2604e-07	--AGCTGAGG NSCGCTGAGS	
HEN1_M00058	1.3891e-05	-----AGCTGAGG----- NNNGGNCGCAGCTGCGNCCNN	
MAF_M00983	2.9490e-05	---CCTCAGCT NTGACTCANC-	
LBP-1_M00644	5.3372e-05	CCTCAGCT --SCAGCN	
AP-4_M00175	6.7472e-05	---AGCTGAGG NNCAGCTGN--	
NF-E2_M00037	6.8225e-05	---CCTCAGCT RTGACTCAGC-	
Nrf-2_M00821	9.8866e-05	----CCTCAGCT NNTGACTCAGCA	
AP-4_M00176	1.5871e-04	---AGCTGAGG NNCAGCTGN--	
MEF-3_M00319	2.4578e-04	----AGCTGAGG NGWAACCTGASC	

M34



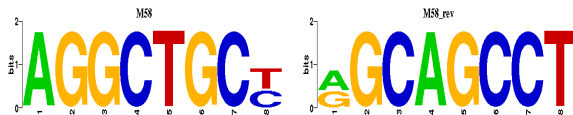
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SMAD4_M00733	4.8026e-05	-----CAGCCTCC-- NSRKNCAGMCANCY	
ERF2_M01057	2.1881e-04	GGAGGCTG GGCGGC--	
MAZ_M00649	2.1983e-04	CAGCCTCC-- --CCCTCCC	
CAC-binding_M00720	5.0895e-04	--CAGCCTCC CCCASCCY--	
Dde_M00304	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---	

M37



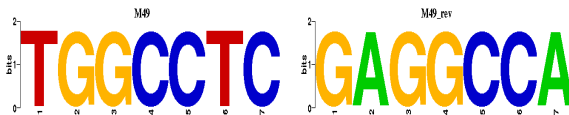
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HAC1_M00730	1.0337e-04	--CAGGCTG-- GACACGCTGKC	
CAC-binding_M00720	1.3477e-04	--CAGCCTG CCCASCCY-	
AP-2_M00800	2.1564e-04	----CAGCCTG---- NNYNYNGCCYGSSGS	
Dde_M00304	2.6766e-04	CAGGCTG--- --GGCTGAGC	
AP-2alphaA_M01047	4.4053e-04	-CAGCCTG----- ANMGCTNAGGCKN	
AR_M00481	1.0603e-03	----CAGCCTG--- AGNACANNNTGTWC	
SMAD4_M00733	1.2380e-03	-----CAGCCTG-- NSRKNCAGMCANCY	
AP-2_M00915	2.3030e-03	CAGCCTG----- -NGCCNGNGGNNN	
MEF-3_M00319	2.3795e-03	--CAGCCTG--- NGWAACCTGASC	
PEA3_M00655	3.1096e-03	CAGGCTG -MGGAWG	

M58



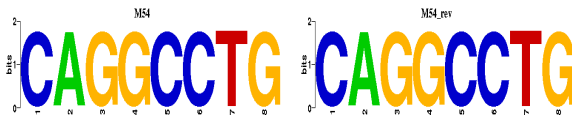
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LBP-1_M00644	9.9357e-05	RGCAGCCT -SCAGCN-	
TAL1_M00993	1.0696e-04	RGCAGCCT- RNCAGNTGG	
ERF2_M01057	2.6381e-04	AGGCTGCT -GGCGGC-	
CAC-binding_M00720	5.0895e-04	RGCAGCCT CCCASCCY	
SMAD4_M00733	8.5904e-04	---AGGCTGCT--- RGNTGKCTGNMYSN	
Dde_M00304	9.3263e-04	AGGCTGCT- -GGCTGAGC	
AP-4_M00927	1.3618e-03	-AGGCTGCT NCAGCTGCT-	
myogenin_M00712	3.0932e-03	AGGCTGCT CASCTGN-	
LMAF_M01139	3.8472e-03	AGGCTGCT--- ---CTGCTGAS	
Roaz_M00467	4.1460e-03	RGCAGCCT----- -KCACCCTGGGTG	

M49



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Poly_M00211	5.1216e-06	GAGGCCA- GAGACCAC	
NF-muE1_M00651	2.6938e-04	---TGGCCTC AGATGGCC--	
v-ErbA_M00239	4.8391e-04	-----TGGCCTC---- NNSNGTGACCTYANN	
PXR_M01153	7.0481e-04	TGGCCTC TGAACTN	
HNF4_M01033	7.2458e-04	TGGCCTC TGNNC--	
bZIP911_M00358	1.2031e-03	GAGGCCA----- --GCCACGTCAY	
HNF4_M00967	1.8830e-03	-TGGCCTC NTGGACYT	
PCF5_M00952	2.1662e-03	--GAGGCCA NNGGGNCCA	
COUPTF_M01036	2.4158e-03	----GAGGCCA----- NKNNRNGKNNAAAGGTCANNNN	
PPARalpha-RXRalpha_M00242	3.0134e-03	----GAGGCCA----- WRAWCTAGGNCAAAGGTCA	

M54



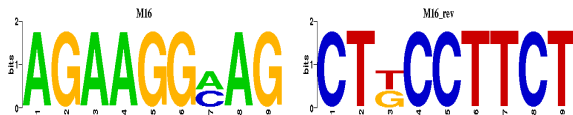
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ZBRK1_M01105	5.2099e-04	-CAGGCCTG----- AAANNCTGCKSCC	
Eve_M00629	7.2780e-04	-CAGGCCTG GCNGNSSWN	
Ttk_M00009	1.4089e-03	-CAGGCCTG GCAGGAC--	
p53_M00272	5.0646e-03	CAGGCCTG-- -RGRCAWGYC	
p53_M00034	6.8075e-03	---CAGGCCTG----- RGACATGCCCGGGCATGTC	
AP-2_M00915	8.7574e-03	CAGGCCTG----- --NGCCNGNGGNNN	
Staf_M00264	2.1613e-02	---CAGGCCTG----- NNGCCKGNANNNTGGGANN	
TBX5_M01044	2.2985e-02	CAGGCCTG- AAGGTGTGA	
E2A_M00973	2.3401e-02	--CAGGCCTG RNCAGNT---	
Pax-4_M00373	2.6040e-02	-----CAGGCCTG----- NNNSNNCACGCNTGAMNNC	











M13



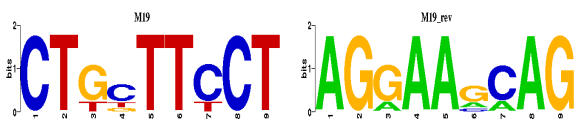
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Ets_M00971	2.9104e-06	-AGGAAGGAAG NAGGAAG----	
MAF_M00648	3.0744e-06	-----CTTCCTTCT NSNMMACTTCCYCN-	
PU.1_M00658	3.7936e-06	CTTCCTTCT- ----CTTCCTC	
Tel-2_M00678	5.7542e-06	-AGGAAGGAAG CAGGAAGTA--	
PEA3_M00655	8.6738e-06	AGGAAGGAAG MGGAWG----	
NERF1a_M00531	1.1372e-05	-----CTTCCTTCT SNNASNYRCTTCTGNY-	
c-Ets-2_M00340	1.3342e-05	-CTTCCTTCT-- ANNNACTTCTGY	
c-Ets-1_M00743	1.7193e-05	CTTCCTTCT ---GCTTCK	
GCR1_M00046	2.3397e-04	-AGGAAGGAAG GWGGAAGC---	
c-Ets-1_M00339	8.2530e-04	---CTTCCTTCT- NNMNNNACTTCTG	

M16



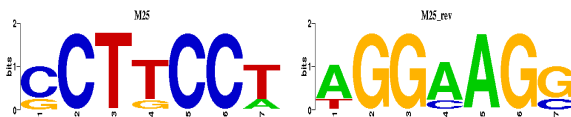
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MAF_M00648	9.2181e-07	AGAAGGMAG----- NGRRGGAAGTKKNSN	
Ets_M00971	1.4080e-05	AGAAGGMAG --NAGGAAG	
PU.1_M00658	1.8033e-05	CTKCCTTCT CTTCCTC--	
PEA3_M00655	5.1222e-05	AGAAGGMAG ---MGGAWG	
c-Ets-1_M00743	7.3612e-05	-CTKCCTTCT GCTTCK---	
Tel-2_M00678	2.5738e-04	AGAAGGMAG-- --CAGGAAGTA	
PEND_M01015	5.6976e-04	CTKCCTTCT- ---ACTTCTT	
NF-muE1_M00651	6.1074e-04	AGAAGGMAG AGATGGCC-	
GCR1_M00046	6.6091e-04	AGAAGGMAG- --GWGGAAGC	
NERF1a_M00531	7.6534e-04	-----CTKCCTTCT SNNASNYRCTTCTGNY	

M19



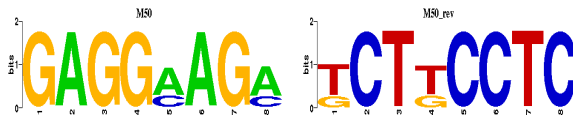
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
c-Ets-1_M00743	4.8533e-08	CTGCTTCCT --GCTTCCK	
NERF1a_M00531	1.6836e-07	-----CTGCTTCCT--- SNNASNYRCTTCCTGNY	
GCR1_M00046	2.0616e-07	CTGCTTCCT- --GCTTCWC	
Ets_M00971	9.6949e-07	-AGGAAGCAG NAGGAAG---	
PU.1_M00658	1.4832e-06	-AGGAAGCAG GAGGAAG---	
Tel-2_M00678	1.7837e-06	-AGGAAGCAG CAGGAAGTA-	
PEA3_M00655	4.7553e-06	AGGAAGCAG MGGAWG---	
c-Ets-2_M00340	2.1162e-05	--CTGCTTCCT-- ANNNACTTCCTGY	
HEN1_M00058	1.4490e-04	--AGGAAGCAG----- NNNGGNCGCAGCTGCGNCCNN	
Ets_M00771	2.7950e-04	-AGGAAGCAG- CAGGAAGYNNN	








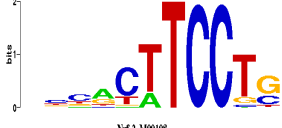


M25



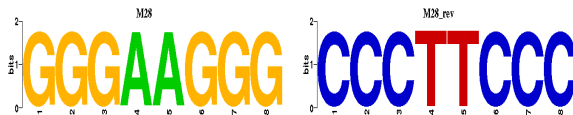
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Ets_M00971	1.2188e-07	-AGGAAGG NAGGAAG-	
PU.1_M00658	2.4781e-07	CCTTCCT- -CTTCCTC	
GCR1_M00046	1.0348e-06	-AGGAAGG GWGGAAGC	
PEA3_M00655	1.4244e-06	AGGAAGG MGGAWG-	
Tel-2_M00678	1.5356e-06	-AGGAAGG- CAGGAAGTA	
c-Ets-1_M00743	2.1653e-06	AGGAAGG MGGAAAGC	
Ets_M00771	9.2732e-06	-AGGAAGG--- CAGGAAGYNNN	
c-Ets-2_M00340	2.3363e-05	----CCTTCCT-- ANNNACTTCCTGY	
c-Ets-1_M00339	2.8448e-05	-----CCTTCCT- NNMNNNACTTCCTG	
NERF1a_M00531	2.9945e-05	-----CCTTCCT--- SNNASNYRCTTCCTGNY	

M50



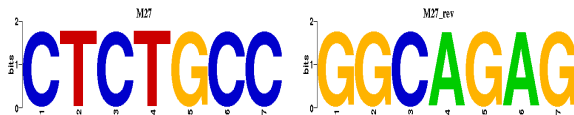
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PU.1_M00658	1.5497e-10	GAGGAAGA GAGGAAG-	
GCR1_M00046	8.5802e-09	GAGGAAGA GWGGAAGC	
Ets_M00971	5.6248e-07	GAGGAAGA NAGGAAG-	
Elf-1_M00746	1.9499e-06	TCTTCCTC--- AYTTCCTCTTN	
PEA3_M00655	2.7201e-06	GAGGAAGA -MGGAWG-	
c-Ets-1_M00743	3.9025e-06	TCTTCCTC GCTTCCK-	
Tel-2_M00678	1.1629e-05	GAGGAAGA- CAGGAAGTA	
Ets_M00771	4.3560e-05	GAGGAAGA--- CAGGAAGYNNN	
Nrf-2_M00108	5.9640e-05	-TCTTCCTC SNCTTCGG	
c-Ets-1_M00339	1.6744e-04	-----TCTTCCTC NNMNNNACTTCCTG	

M28



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
UF1H3BETA_M01068	2.8231e-07	-CCCTTCCC----- GCCCTTCCCCRC	
MAZ_M00649	2.7826e-06	CCCTTCCC -CCCTCCC	
BLIMP1_M01066	1.0080e-05	-----CCCTTCCC YMCTTTCMCTTYC-	
Sp3_M00665	1.7328e-05	CCCTTCCC----- CCCYSCCAAGKS	
ZNF219_M01122	2.5139e-05	GGGAAGGG--- GGNGGGGGGN	
Sp1_M00933	9.5238e-05	CCCTTCCC- CCCKCCCCN	
Sp1_M00931	1.4114e-04	-CCCTTCCC NCCCCGCC	
PU.1_M00658	2.2603e-04	CCCTTCCC- --CTTCTC	
Ets_M00971	2.2692e-04	-GGGAAGGG NAGGAAG--	
c-Ets-1_M00743	2.3215e-04	CCCTTCCC -GCTTCK	

M27



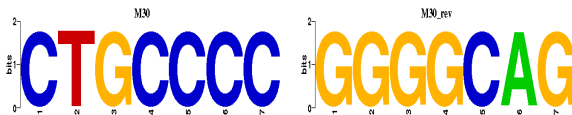
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Dde_M00304	6.5556e-07	GGCAGAG- GGCTGAGC	
Nrf-2_M00108	3.2163e-05	CTCTGCC-- SNCTTCCGG	
Eve_M00629	6.1383e-05	GGCAGAG--- -GCNGNSSWN	
SMAD3_M00701	3.5136e-04	-GGCAGAG AGNCAGAC	
HNF4_M01031	4.0579e-04	-----CTCTGCC- NTGRMCTTTGNNC	
MAZ_M00649	6.9329e-04	CTCTGCC CCCTCCC	
TAL1_M00993	8.2649e-04	GGCAGAG-- RNCAGNTGG	
HNF4alpha1_M00411	8.8092e-04	-----CTCTGCC-- NTGACCTTTGNCCY	
PPAR_M00528	9.5318e-04	----CTCTGCC----- TGACCTTTGNCCNNNN	
E2A_M00973	1.2191e-03	GGCAGAG RNCAGNT	




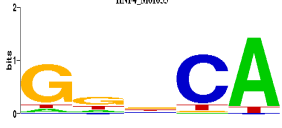

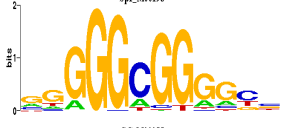




M31



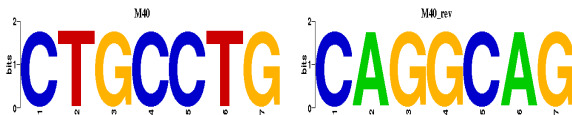
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Dde_M00304	6.5556e-07	GGCAGAG- GGCTGAGC	
Nrf-2_M00108	3.2163e-05	CTCTGCC-- SNCTTCCGG	
Eve_M00629	6.1383e-05	GGCAGAG--- -GCNGNSSWN	
SMAD3_M00701	3.5136e-04	-GGCAGAG AGNCAGAC	
HNF4_M01031	4.0579e-04	-----CTCTGCC- NTGRMCTTTGNNC	
MAZ_M00649	6.9329e-04	CTCTGCC CCCTCCC	
TAL1_M00993	8.2649e-04	GGCAGAG-- RNCAGNTGG	
HNF4alpha1_M00411	8.8092e-04	-----CTCTGCC-- NTGACCTTTGNCCY	
PPAR_M00528	9.5318e-04	----CTCTGCC----- TGACCTTTGNCCNNNN	
E2A_M00973	1.2191e-03	GGCAGAG RNCAGNT	


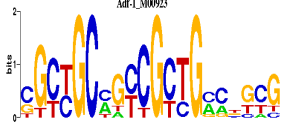








M30



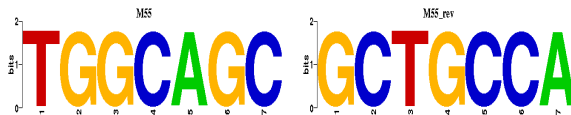
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SMAD4_M00733	6.9439e-06	-----CTGCCCC- RGNIGKCTGNMYSN	
Sp1_M00933	1.4138e-05	-GGGGCAG- NNGGGMGGG	
Egr_M00807	2.4738e-05	-CTGCCCC-- NYYGCSCCCA	
HNF4_M01033	5.0036e-05	CTGCCCC -TGNNC-	
AtMYB-84_M00970	5.6930e-05	----CTGCCCC- SCACCTACCNC	
Sp1_M00196	5.7185e-05	----CTGCCCC- NNCCCCGCCCN	
GC_M00255	5.8385e-05	-----CTGCCCC- NNGCCCCGCCNN	
KROX_M00982	8.7924e-05	-----GGGGCAG GNNNGGGGGCGG	
LF-A1_M00646	1.0344e-04	CTGCCCC YWGASCC	
UF1H3BETA_M01068	1.3968e-04	----CTGCCCC-- GCCCTCCCCRC	






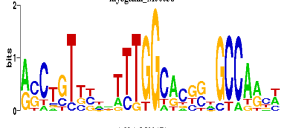
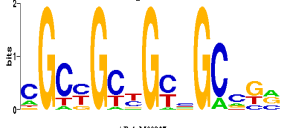
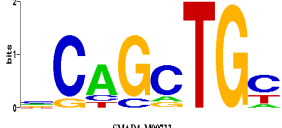


M40



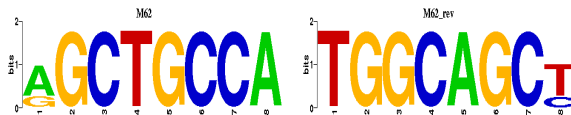
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Tel-2_M00678	7.4528e-06	CAGGCAG-- CAGGAAGTA	
Adf-1_M00923	3.3673e-05	--CAGGCAG----- CRMNKKCAGCGRCKGCRGCS	
Ets_M00771	7.7953e-05	----CTGCCTG NNNRCTTCTG	
NERF1a_M00531	1.4727e-04	-----CTGCCTG-- SNNASNYRCTTCTGNY	
c-Ets-2_M00340	1.5207e-04	-CAGGCAG----- RCAGGAAGTNNNT	
c-Ets-1_M00339	2.5526e-04	-----CTGCCTG NNMNNNACTTCTG	
SMAD3_M00701	2.9542e-04	CAGGCAG-- -AGNCAGAC	
Ets_M00971	5.7503e-04	CAGGCAG NAGGAAG	
SMAD4_M00733	5.9147e-04	-----CTGCCTG- RGNTGKCTGNMYSN	
PU.1_M00658	7.0533e-04	CAGGCAG GAGGAAG	

M55



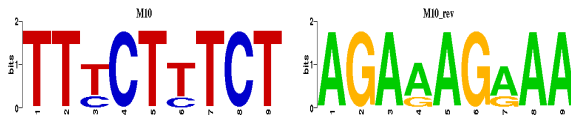
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
TGIF_M00418	2.1945e-05	---TGGCAGC WNNTGACAGC	
LBP-1_M00644	3.9422e-05	TGGCAGC- --SCAGCN	
GCR1_M00046	5.3099e-05	-TGGCAGC GWGGAAGC	
ERF2_M01057	8.2401e-05	TGGCAGC -GGCGGC	
GCR1_M00337	1.6821e-04	-----TGGCAGC- AAWAGTGGGAAGCC	
myogenin_M00056	2.7492e-04	---TGGCAGC----- NNYTGGCNSNGTGCCAAANNNNACAGST	
Adf-1_M00171	3.6973e-04	----GCTGCCA---- CGCYGCGYNGCNKN	
AP-4_M00927	4.1134e-04	---GCTGCCA NCAGCTGY--	
SMAD4_M00733	7.8378e-04	--TGGCAGC----- NSRKNCAGMCANCY	
TAL1_M00993	8.2649e-04	TGGCAGC--- -RNCAGNTGG	

M62



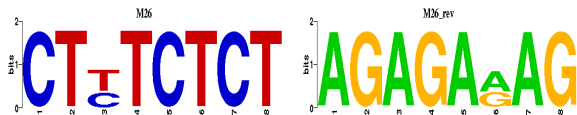
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LBP-1_M00644	7.4817e-08	TGGCAGCT --SCAGCN	
AP-4_M00927	1.1394e-05	TGGCAGCT-- --RCAGCTGN	
myogenin_M00712	1.5178e-05	-AGCTGCCA CASCTGN--	
TAL1_M00993	1.9652e-05	TGGCAGCT-- -RNCAGNTGG	
E2A_M00973	5.0084e-05	TGGCAGCT -RNCAGNT	
GCR1_M00337	7.1269e-05	-----TGGCAGCT AAWAGTGGGAAGCC	
TGIF_M00418	1.5235e-04	---TGGCAGCT WNNTGACAGC-	
ERF2_M01057	1.9865e-04	TGGCAGCT -GGCGGC-	
GCR1_M00046	2.2322e-04	-TGGCAGCT GWGGAAGC-	
repressor_M00014	3.6762e-04	-----TGGCAGCT--- NNYNTNGCGGCTANN	

M10

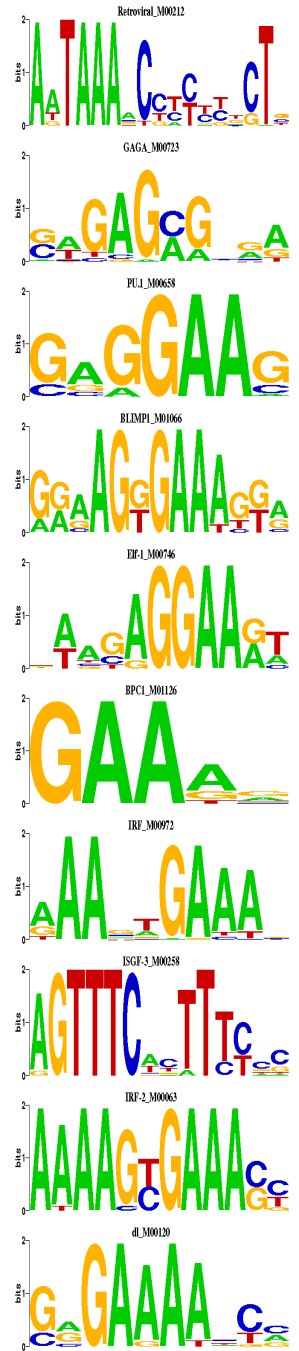


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	5.4699e-09	TTTCTTTCT-- TTTCTTTGTTC	
STE11_M00274	1.6130e-07	-----AGAAAGAAA-- WNNNNAACAAAGAAAANW	
BR-C_M00094	1.9673e-06	--AGAAAGAAA- WWR TAAASAWAA	
Rim101p_M01030	3.0613e-05	TTTCTTTCT TTNCTTG--	
BPC1_M01126	4.3302e-05	TTTCTTTCT ---NITTC-	
HSF_M00163	5.6933e-05	AGAAAGAAA----- GAANAGAANAGAAN	
HSF_M00164	5.6933e-05	AGAAAGAAA----- GAANAGAANNTTCT	
HSF_M00166	1.3852e-04	-TTTCTTTCT---- NTTCTNTTCTAGAA	
Lentiviral_M00331	1.9317e-04	-----TTTCTTTCT NCTTGC GGTANNCTNNTYTNT	
PR_M00960	3.3254e-04	--TTTCTTTCT NGTYCNNW--	

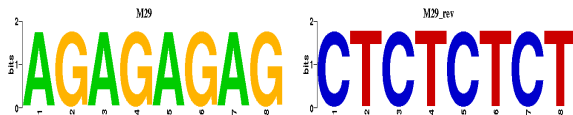
M26



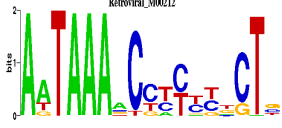





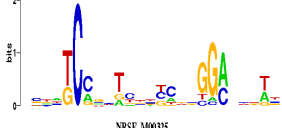
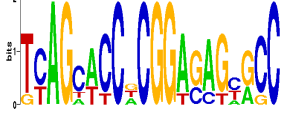


	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
Retroviral_M00212	1.8311e-05	-AGAGARAG----- NAGNRRRRRRGNTTTATT
GAGA_M00723	2.2712e-05	-CTYTCTCT- TYNCKTCTCWS
PU.1_M00658	3.6138e-05	AGAGARAG -GAGGAAG
BLIMP1_M01066	3.6410e-05	--CTYTCTCT--- YMCTTTCMCTTYC
Elf-1_M00746	5.0708e-05	-CTYTCTCT-- AYTTCCTCTTN
BPC1_M01126	1.0675e-04	CTYTCTCT NTTTC---
IRF_M00972	2.0579e-04	CTYTCTCT-- NTTTCWNITT
ISGF-3_M00258	2.1725e-04	-----AGAGARAG- GNGAAANWGAAACT
IRF-2_M00063	3.2621e-04	-CTYTCTCT--- RSTTTCRCITTT
dI_M00120	7.8025e-04	---CTYTCTCT NGNTTTTCYC-

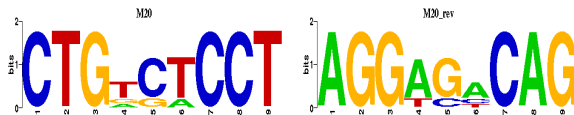


M29



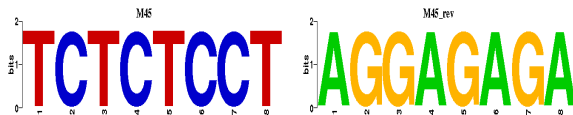
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
GAGA_M00723	2.3892e-06	-CTCTCTCT- TYNCKCTCWS	
SMAD3_M00701	3.5568e-05	AGAGAGAG AGNCAGAC	
Retroviral_M00212	8.3219e-05	-AGAGAGAG----- NAGNRRRRRGNTTTATT	
TFII-I_M00706	1.7134e-04	-CTCTCTCT CCTMCNTC-	
ARF_M00438	1.2769e-03	AGAGAGAG -GAGACAA	
Sry-beta_M00666	2.1533e-03	AGAGAGAG AGWGATGC	
ZID_M00085	2.7282e-03	--AGAGAGAG-- GRIGATRGAGCC	
MAZ_M00649	3.2152e-03	CTCTCTCT CCCTCCC-	
FACB_M00390	3.7322e-03	-----AGAGAGAG----- NWNNTCCNNNNNNNNNNKGANNNN	
NRSE_M00325	5.8362e-03	--CTCTCTCT----- GGCRCTCTCCGNGGTGCTGA	





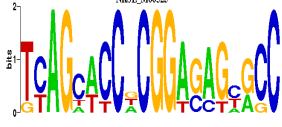

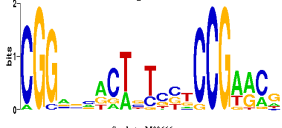



M20



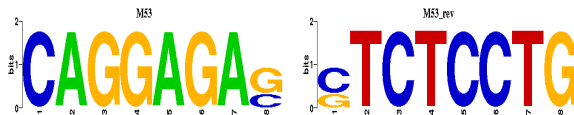
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ARF_M00438	1.1955e-06	AGGAGACAG --GAGACAA	
SMAD3_M00701	3.3213e-05	AGGAGACAG-- ---AGNCAGAC	
NF-E2_M00037	9.5667e-04	AGGAGACAG- RTGACTCAGC	
YY1_M00069	1.5208e-03	AGGAGACAG----- WNSANNCAAGATGGCNGNN	
SMAD4_M00733	1.7180e-03	--CTGTCTCCT-- RGNTGKCTGNMYSN	
ABF1_M00399	1.8300e-03	-----CTGTCTCCT-- NNTCNNGCCACGTGTCCCNNNNW	
T3R_M00963	1.9821e-03	-AGGAGACAG NAGGWCAN--	
Poly_M00211	3.6593e-03	AGGAGACAG- --GAGACCAC	
AP-1_M00173	5.3360e-03	CTGTCTCCT- NTGACTNMNW	
AP-1_M00925	5.9729e-03	AGGAGACAG NTNAGTCA-	

M45



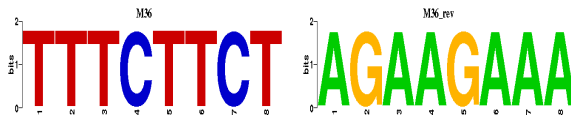
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
TBX5_M01044	2.7763e-04	TCTCTCCT- TCACACCTT	
MAZ_M00649	4.9286e-04	AGGAGAGA GGGAGGG-	
HSF_M00163	8.6330e-04	--TCTCTCCT---- NTTCTNTTCTNTTC	
HSF_M00166	8.6330e-04	--TCTCTCCT---- NTTCTNTTCTAGAA	
NRSE_M00325	1.0339e-03	---TCTCTCCT----- GGCRCTCTCCGNGGTGCTGA	
ARF_M00438	1.2769e-03	AGGAGAGA- --GAGACAA	
GAL4_M00198	1.8357e-03	-----AGGAGAGA----- NGYTCCGNNNANAGNNNCCG	
Sry-beta_M00666	2.1533e-03	AGGAGAGA--- ---AGWGATGC	
T3R_M00963	3.2067e-03	-AGGAGAGA NAGGWCAN-	
GAGA_M00723	3.7060e-03	----TCTCTCCT TYNCKCTCWS--	

M53



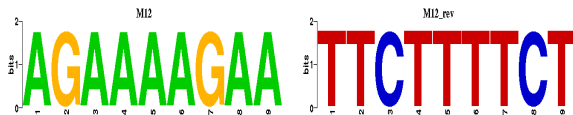
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Ttk_M00009	1.6619e-04	CTCTCCTG- --GTCCTGC	
Nrf-2_M00108	7.1918e-04	CTCTCCTG- SNCTTCCGG	
XPF-1_M00684	8.2279e-04	-CTCTCCTG GKTSNYCNG	
MAZ_M00649	1.1922e-03	CTCTCCTG CCCTCCC-	
KAISO_M01119	1.5352e-03	----CAGGAGAG NTNGCAGGA---	
LXR_M00965	1.6933e-03	---CTCTCCTG----- GNCCTNNNNTRACCYN	
Tel-2_M00678	1.7443e-03	CAGGAGAG- CAGGAAGTA	
USF_M00796	1.9406e-03	-CTCTCCTG-- NSTCACGTGNN	
AREB6_M00412	2.3379e-03	---CAGGAGAG- RNWCAGGTRNRN	
NRSE_M00325	2.8362e-03	----CTCTCCTG----- GGCRCTCTCCGNGGTGCTGA	











M36



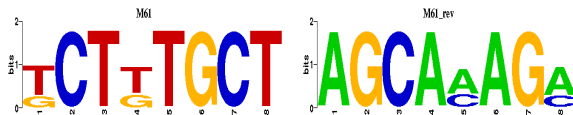
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Rim101p_M01030	1.5075e-06	TTTCTTCT TTNCTTG-	
Elf-1_M00746	9.2030e-06	-TTTCTTCT-- AYTTCCTCTTN	
STE11_M01005	2.6067e-05	TTTCTTCT--- TTTCTTTGTTT	
HSF_M00163	2.6422e-05	-----TTTCTTCT- NTTCTNTTCTNTTC	
HSF_M00164	2.6422e-05	-----TTTCTTCT- AGAANNTTCTNTTC	
PEND_M01015	1.4491e-04	AGAAGAAA- --AGAAGT	
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	




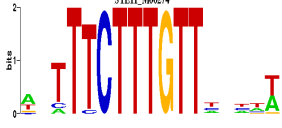
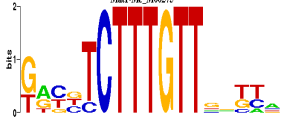
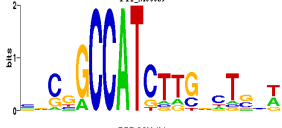




M12



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HSF_M00163	7.2365e-12	----AGAAAAGAA-- GAANAGAANAGAAN	
HSF_M00166	7.2365e-12	----AGAAAAGAA-- TTCTAGAANAGAAN	
HSF_M00167	5.4321e-09	-TTCTTTTCT---- NTTCNNTTCNNTTC	
HSF_M00170	5.4321e-09	-TTCTTTTCT---- NTTCNNTTCNNGAA	
HSF_M00164	1.7186e-08	-----TTCTTTTCT AGAANNITTCNTTC-	
GATA-2_M00349	1.1741e-06	-AGAAAAGAA SAGATAANA-	
GATA-3_M00350	1.8107e-06	TTCTTTTCT- -TNTTATCTY	
GATA-1_M00347	2.3500e-06	TTCTTTTCT- -YNTTATCTN	
HSF_M00168	4.7259e-06	-----TTCTTTTCT NGAANNITTCNNTTC-	
STE11_M01005	2.5560e-05	-TTCTTTTCT- TTCTTTTGTTCT	

M61



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	1.7738e-06	-AGCAAAGA-- GAACAAAGAAA	
SOX_M01014	4.3937e-06	TCTTTGCT---- TCTTTGTTANGN	
LEF1_M00805	6.2387e-06	TCTTTGCT -CTTTG--	
STE11_M00274	1.8692e-05	-----AGCAAAGA----- WNNNNAACAAAGAAANW	
Mat1-Mc_M00275	2.4671e-05	-----AGCAAAGA----- NRMNNAACAAAGANRYC	
YY1_M00069	6.7353e-05	---AGCAAAGA----- WNSANNCAAGATGGCNGNN	
DBP_M00624	1.9371e-04	TCTTTGCT -NWNTGC-	
HSF_M00167	2.0684e-04	--TCTTTGCT---- NTTCNNTTCNNTTC	
HSF_M00170	2.0684e-04	--TCTTTGCT---- NTTCNNTTCNNGAA	
dTCF_M00362	2.0895e-04	---AGCAAAGA AAGATCAAAG-	

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