

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

Input file: 13 motifs loaded

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

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

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

[Download results as a PDF](#)

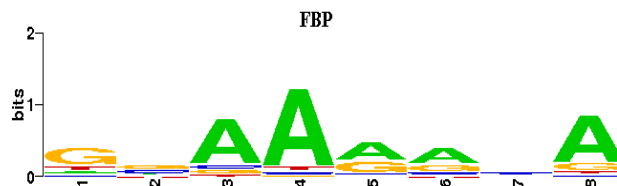
[Click here to run STAMP again.](#)

## Multiple Alignment

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

M0 :	-CCCCACCC---
M1 :	----AAAAA
M2 :	--GGAAGGGA--
M3 :	TTTTAAAA----
M4 :	--GAAAGAAA--
M5 :	-AGGAAGGA---
M6 :	AAGGAAAA----
M7 :	-TGGGAGAG---
M8 :	---CAAACAA-
M9 :	----AAAACACA
M10 :	-AACAAAAC---
M11 :	---CAAAGGAG-
M12 :	----AAGCTGGG

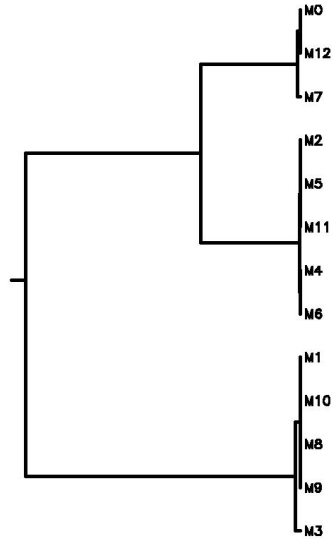
**Familial Profile:**  
([click for matrix](#))



# Motif Tree

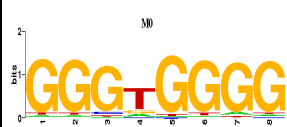

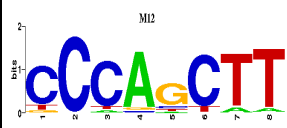

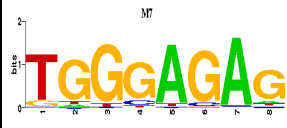

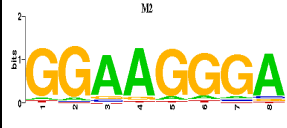

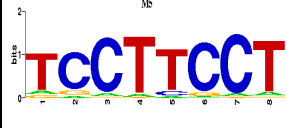

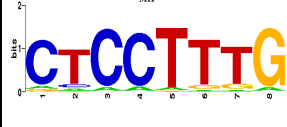



Tree (drawn by **Phylip**)

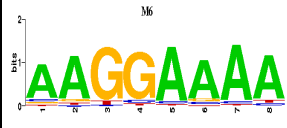
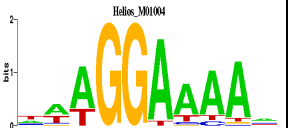
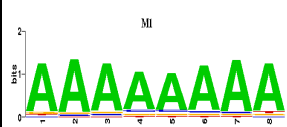

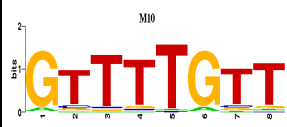

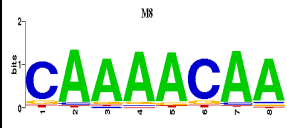

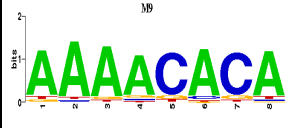

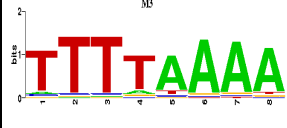
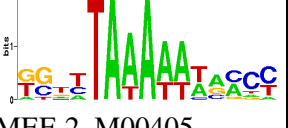
[Click here for Newick-format tree \(viewable with MEGA\)](#)



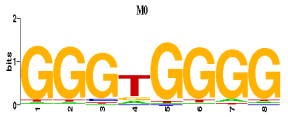
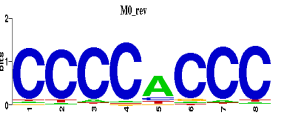
Input Motif

Best match in  
TRANSFAC

 <p><b>M0</b></p>	 <p>Alfin1_M00479 (E val: 2.6089e-09)</p>
 <p><b>M12</b></p>	 <p>LUN-1_M00480 (E val: 3.0511e-07)</p>
 <p><b>M7</b></p>	 <p>Lyf-1_M00141 (E val: 3.0076e-08)</p>
 <p><b>M2</b></p>	 <p>BLIMP1_M01066 (E val: 3.9308e-09)</p>
 <p><b>M5</b></p>	 <p>Tel-2_M00678 (E val: 7.9194e-08)</p>
 <p><b>M11</b></p>	 <p>LEF1_M00805 (E val: 2.3101e-06)</p>
 <p><b>M4</b></p>	 <p>STE11_M01005 (E val: 2.2404e-08)</p>

 <p><b>M6</b></p>	 <p>Helios_M01004 (E val: 2.1517e-11)</p>
 <p><b>M1</b></p>	 <p>Hb_M00022 (E val: 1.0595e-06)</p>
 <p><b>M10</b></p>	 <p>SRY_M00148 (E val: 4.2159e-07)</p>
 <p><b>M8</b></p>	 <p>HNF3alpha_M00724 (E val: 3.6663e-06)</p>
 <p><b>M9</b></p>	 <p>FOXP1_M00987 (E val: 1.9675e-06)</p>
 <p><b>M3</b></p>	 <p>MEF-2_M00405 (E val: 2.4796e-06)</p>

## Motif Similarity Matches

<b>M0</b>	 
	<i>forward</i> <i>reverse compliment</i>

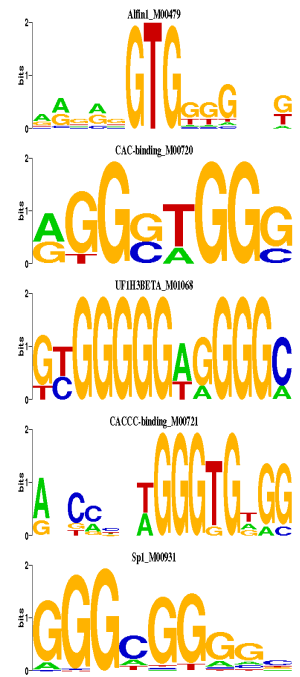
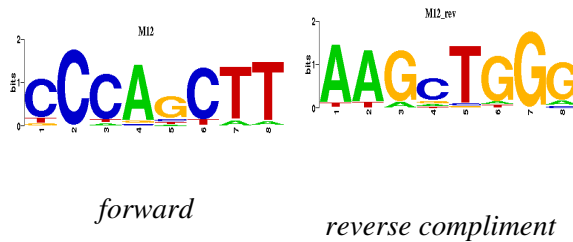
Name

E value

Alignment

Motif

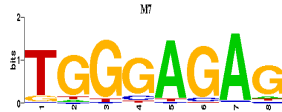
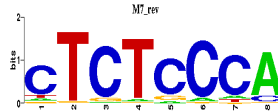
Alfin1_M00479	2.6089e-09	---CCCCACCC--- MNNCCCCACNYYN
CAC-binding_M00720	1.5006e-08	CCCCACCC- -CCCASCCY
UF1H3BETA_M01068	1.9542e-08	-CCCCACCC---- GCCCTCCCCRC
CACCC-binding_M00721	6.3357e-08	CCCCACCC----- CCNCACCCWNNKGNT
Sp1_M00931	6.8513e-08	-CCCCACCC NCCCCGCC

**M12**

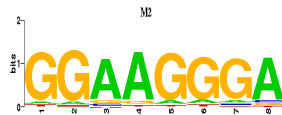
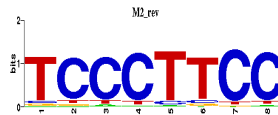
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LUN-1_M00480	3.0511e-07	-----AAGCTGGG TCCCAAAGTAGCTGGG	
Barbie_M00238	3.9907e-07	----AAGCTGGG-- NNNAAAGSNGNNKG	
HEB_M00698	1.1201e-06	CCCAGCTT -CCWGCTG	
LBP-1_M00644	4.5440e-06	CCCAGCTT -SCAGCN-	

AP-4\_M00176



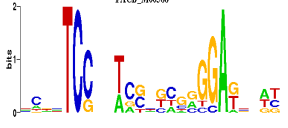

1.4139e-05

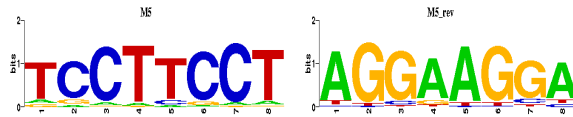
CCCAGCTT-  
NNCAGCTGN**M7***forward**reverse compliment*






<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Lyf-1_M00141	3.0076e-08	CTCTCCCA- -YCTCCCAA	<p>Sequence logo for Lyf-1_M00141. The y-axis represents 'bits' from 0 to 2. The x-axis shows positions 1 to 8. The sequence is TTGGGAGGA, with the 'T' at position 1 being the most conserved (approx. 1.8 bits).</p>
MAZ_M00649	7.1605e-07	TGGGAGAG -GGGAGGG	<p>Sequence logo for MAZ_M00649. The y-axis represents 'bits' from 0 to 2. The x-axis shows positions 1 to 6. The sequence is GGGAGGG, with the 'G' at position 1 being the most conserved (approx. 1.8 bits).</p>
UF1H3BETA_M01068	3.2473e-05	----CTCTCCCA- GCCCCCTCCCCRC	<p>Sequence logo for UF1H3BETA_M01068. The y-axis represents 'bits' from 0 to 2. The x-axis shows positions 1 to 10. The sequence is GTGGGGAGGGC, with the 'G' at position 2 being the most conserved (approx. 1.8 bits).</p>
RBP-Jkappa_M01111	1.8634e-04	--TGGGAGAG NGTGGGA---	<p>Sequence logo for RBP-Jkappa_M01111. The y-axis represents 'bits' from 0 to 2. The x-axis shows positions 1 to 5. The sequence is TCCCAc, with the 'T' at position 1 being the most conserved (approx. 1.8 bits).</p>
Nrf-2_M00108	3.4247e-04	-TGGGAGAG CCGGAAGNS	<p>Sequence logo for Nrf-2_M00108. The y-axis represents 'bits' from 0 to 2. The x-axis shows positions 1 to 6. The sequence is ccGGAAG, with the 'G' at position 3 being the most conserved (approx. 1.8 bits).</p>

**M2***forward**reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
BLIMP1_M01066	3.9308e-09	-----TCCCTTCC YMCTTTCMCTTYC	<p>Sequence logo for BLIMP1_M01066. The y-axis represents 'bits' from 0 to 2. The x-axis shows positions 1 to 10. The sequence is GGAGGAAAGGA, with the 'G' at position 2 being the most conserved (approx. 1.8 bits).</p>

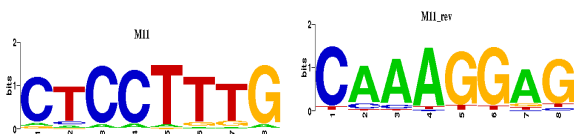
MAZ_M00649	2.7849e-06	TCCCTTCC -CCCTCCC	
c-Ets-1_M00339	2.3799e-05	----TCCCTTCC-- NNMNNNACTTCCTG	
FACB_M00388	2.8976e-05	----TCCCTTCC----- NNNNTCCNNTNSNNNNNGGAKNNNN	
UF1H3BETA_M01068	1.6788e-04	TCCCTTCC----- GCCCTTCCCCRC	

**M5***forward**reverse compliment*

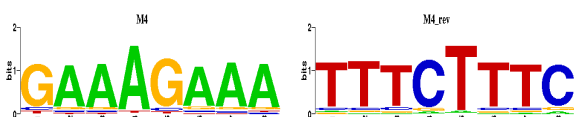
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Tel-2_M00678	7.9194e-08	-AGGAAGGA CAGGAAGTA	
Ets_M00971	3.1218e-07	-AGGAAGGA NAGGAAG--	
PU.1_M00658	5.1498e-07	TCCTTCCT- --CTTCCTC	
PEA3_M00655	1.0708e-06	AGGAAGGA MGGAWG--	
c-Ets-1_M00743	2.1967e-06	TCCTTCCT -GCTTCCK	

## Stamp Results

09/29/13

**M11***forward**reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LEF1_M00805	2.3101e-06	CTCCTTTG ---CTTTG	
LUN-1_M00480	2.5494e-06	---CAAAGGAG----- TCCCAAAGTAGCTGGG	
PBF_M01130	2.6299e-06	CTCCTTTG --CCTTT-	
COUP_M00765	7.1154e-05	----CAAAGGAG GGNCAAAGGTC	
PPAR_M00763	8.1110e-05	CTCCTTTG---- GACCTTTGNCCN	

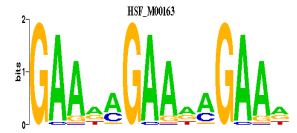
**M4***forward**reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	2.2404e-08	TTTC TTTC--- TTTC TTGTTC	
STE11_M00274	3.9894e-07	-----GAAAGAAA-- WNNNNAACAAAGAAANW	

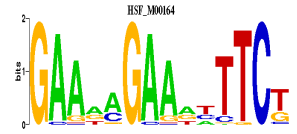
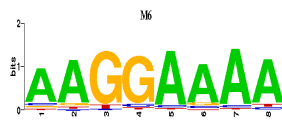
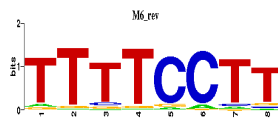
Rim101p\_M01030 1.7246e-06

TTTCTTTC  
TTNCTTG-

HSF\_M00163 5.5628e-06

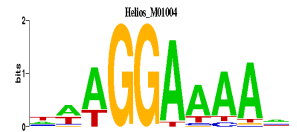
-----TTTCTTTC-  
NTTCTNTTCTNTTC

HSF\_M00164 5.5628e-06

-----TTTCTTTC-  
AGAANNTTCTNTTC**M6***forward**reverse compliment**Name**E value**Alignment**Motif*

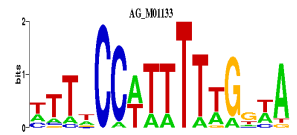
Helios\_M01004

2.1517e-11

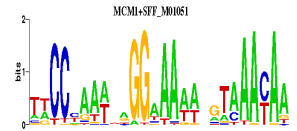
-TTTTCCTT-  
NTTTCCTWN

AG\_M01133

2.8728e-07

-----AAGGAAAA  
TWNCAAAAAWGGNAAN

MCM1+SFF\_M01051 5.4507e-06

-----TTTTCCTT-----  
TTRTTTANNTWTNCCNNWTTNGNA

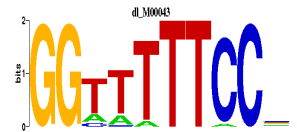
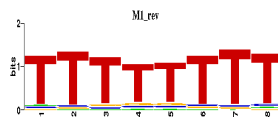
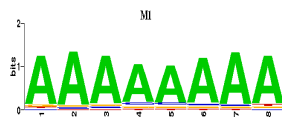
BLIMP1\_M01066

1.1505e-05


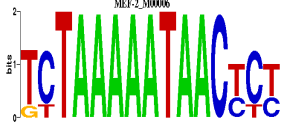
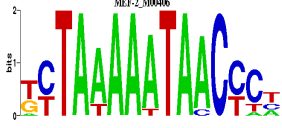
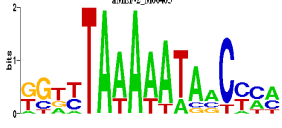
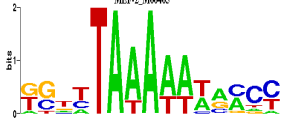
--AAGGAAAA--  
GRAAGKGAAAGKR

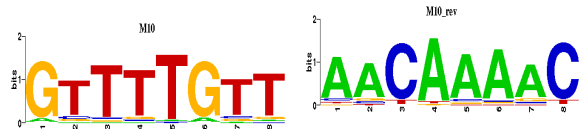
dl\_M00043



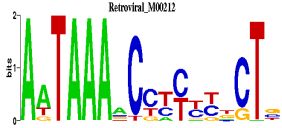
1.5055e-05

---TTTTCCTT  
GGTTTTTCN-**M1**

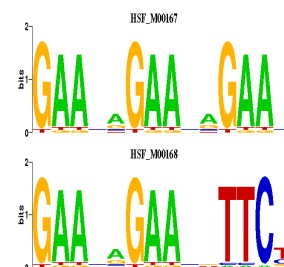
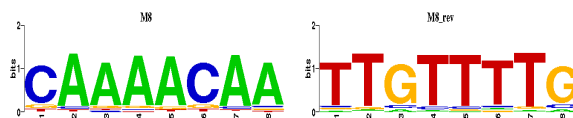


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Hb_M00022	1.0595e-06	-TTTTTTTT NTTTTTNYK	
MEF-2_M00006	2.2888e-06	---AAAAAAAA--- TCTAAAAATAACYCY	
MEF-2_M00406	3.0014e-06	---TTTTTTTT--- NGGGTTATTTTATAGM	
aMEF-2_M00403	4.3255e-06	---TTTTTTTT--- KKRGNTATTTTARNCM	
MEF-2_M00405	5.2687e-06	--TTTTTTTT--- RGKNWTTTTTANNSM	

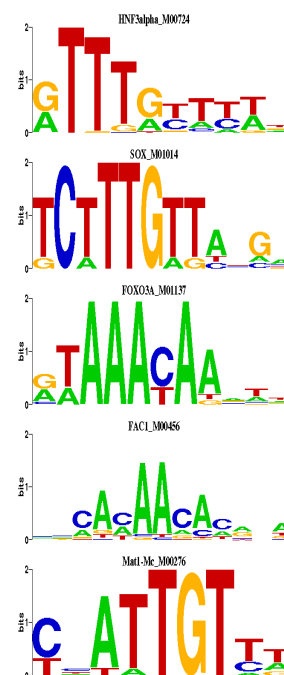
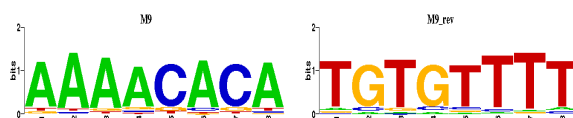
**M10**

	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SRY_M00148	4.2159e-07	GTTTGT --KNTGT	
BR-C_M00091	2.2028e-06	--GTTTGT----- NNNWYTTGTYTATNANN	
Retroviral_M00212	3.7255e-06	-----GTTTGT NAGNRRRRRGNTTTATT	

HSF_M00167	5.4167e-06	-----GTTTGTGTT- NTTCNNTTCNNTTC
HSF_M00168	5.4167e-06	-----GTTTGTGTT- NGAANNNTTCNNTTC

**M8***forward**reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HNF3alpha_M00724	3.6663e-06	CAAAACAA-- NWRARCAAAY	
SOX_M01014	7.2589e-06	---TTGTTTGTG- TCTTTGTTANGN	
FOXO3A_M01137	2.2362e-05	---TTGTTTGTG NNNTTGTTTAY	
FAC1_M00456	3.6136e-05	---TTGTTTGTG-- NNNNTGTTKTGNN	
Mat1-Mc_M00276	3.9966e-05	CAAAACAA--- --NRACAATNG	

**M9***forward**reverse compliment*

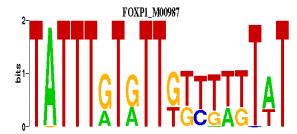
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
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# Stamp Results

09/29/13

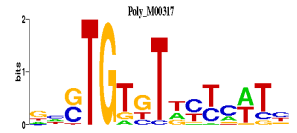
FOXP1\_M00987 1.9675e-06

-----AAAACACA-----  
ATAAAAAACAACACAAATA



Poly\_M00317 8.8246e-06

----AAAACACA---  
NAWKRRNAMACASNN



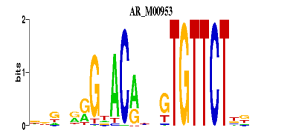
HFH4\_M00742 1.5592e-05

----AAAACACA  
TAAACAAACAMW



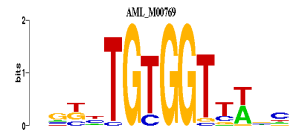
AR\_M00953 2.8895e-05

-----AAAACACA-----  
NNNNNNAGAACACNNTGTNCYNNNNN

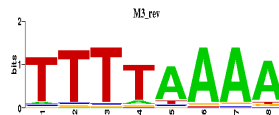
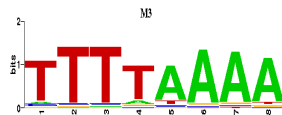


AML\_M00769 3.6018e-05

----TGTGTTTT--  
NNNTGTGGTYWNN



**M3**



*forward*

*reverse compliment*

*Name*

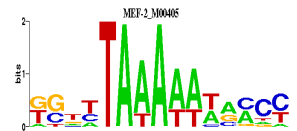
*E value*

*Alignment*

*Motif*

MEF-2\_M00405 2.4796e-06

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RGKNWTTTTTANNM



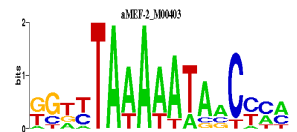
TATA\_M00216 5.8322e-06

-TTTTAAAA  
NTTTATAG



aMEF-2\_M00403 1.6840e-05

-----TTTTAAAA-  
KKGNTATTTTTARNM



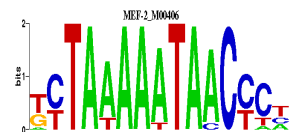
Abd-B\_M01094 2.4853e-05

TTTTAAAA  
TTTTAT--



MEF-2\_M00406 1.2717e-04

-----TTTTAAAA  
NGGGTTATTTTTAGM-



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