



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

Input file: 12 motifs loaded

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

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

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

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Multiple Alignment

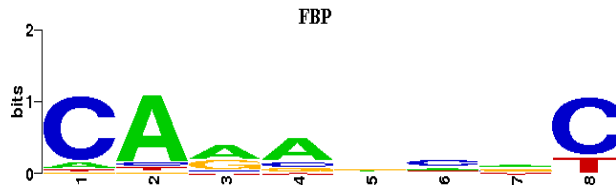
(Consensus sequence representations shown, but multiple alignment was carried out on the matrices)

```

Motif_1: -----TCAGAATTCAGTA-----
Motif_2: -----TTGANATGCAAA-----
Motif_3: -----GGAAAAGCGCCCAATTAGTGCCTCCCC
Motif_4: -----TCCNGATCCACACGCTACAAGGCA-----
Motif_5: -----CAATMCMNAGNACCAG-----
Motif_6: -----ACCN YCCKNNKKTNSCAAGCYGCGG-----
Motif_7: GCGAACCTCCGGAAGTGACAGTAACAGAGA-----
Motif_8: -----CAATAAYATGGATSTACACARCACATG-----
Motif_9: -----CAACAAAGANCGCGCCCNCTTTTC-----
Motif_10: -----AAWTGCAAAT-----
Motif_11: -----CCWCCNCCANCYCC-----
Motif_12: -----CACAYACRCANACACAMN-----

```

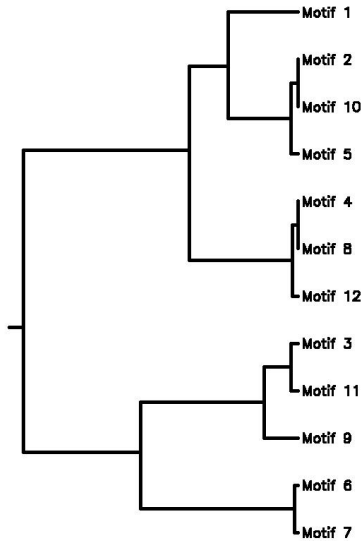
Familial Profile:
([click for matrix](#))



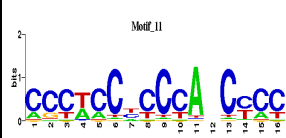
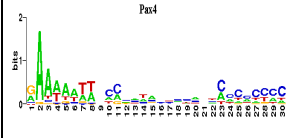
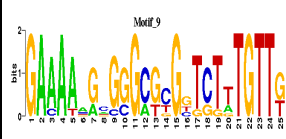



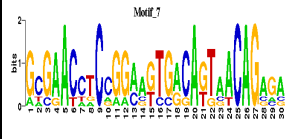

Motif Tree

Tree (drawn by [PhyIip](#))

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

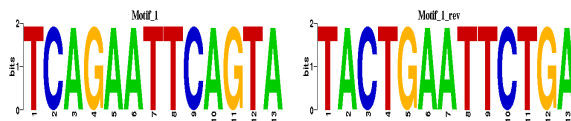


Input Motif	Best match in JASPAR
<p>Motif 1</p>	<p>NR2F1 (E val: 2.5413e-03)</p>
<p>Motif 2</p>	<p>HMG-IY (E val: 1.7118e-05)</p>
<p>Motif 10</p>	<p>HMG-IY (E val: 3.3314e-06)</p>
<p>Motif 5</p>	<p>REST (E val: 9.2402e-03)</p>
<p>Motif 4</p>	<p>ZNF354C (E val: 3.9705e-05)</p>
<p>Motif 8</p>	<p>Mycn (E val: 7.5450e-04)</p>
<p>Motif 12</p>	<p>CF2-II (E val: 5.0163e-03)</p>
<p>Motif 3</p>	<p>Pax4</p>

 <p>Motif 11</p>	 <p>Pax4 (E val: 4.8136e-11)</p>
 <p>Motif 9</p>	 <p>MNB1A (E val: 6.5278e-04)</p>
 <p>Motif 6</p>	 <p>Eip74EF (E val: 3.0567e-04)</p>
 <p>Motif 7</p>	 <p>ELK4 (E val: 2.2790e-06)</p>

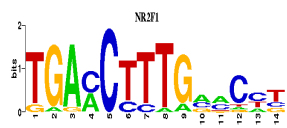
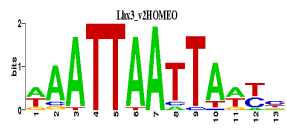

Motif Similarity Matches

Motif_1




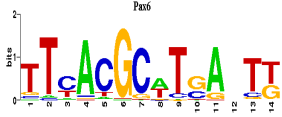
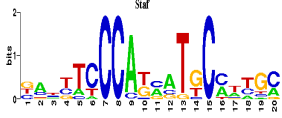

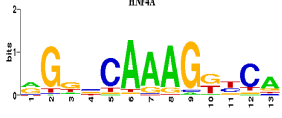
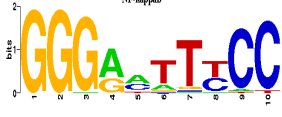

forward

reverse compliment

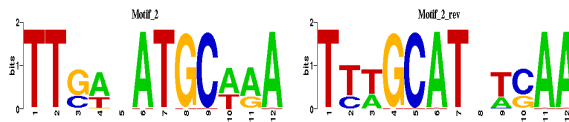
Name	E value	Alignment	Motif
NR2F1	2.5413e-03	----TCAGAATTCAGTA NNGKNCAAAGKTCA---	
Lhx3_v2HOMEO	7.9667e-03	TCAGAATTCAGTA--- ---WAATTAATTAWYN	
Prrx2	8.5980e-03	TCAGAATTCAGTA ---TAATT-----	

Stamp Results

04/16/09

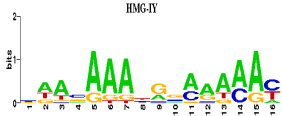

NKX3-1	9.7950e-03	TCAGAATTCAGTA- -----TAAGTAT	
Pax6	1.2029e-02	TACTGAATTCTGA- MANTSAWGCGTGAA	
Staf	1.2673e-02	-TACTGAATTCTGA----- KCNNKGMANNMTGGGANNNN	
Lhx3	1.5097e-02	-TACTGAATTCTGA WTAATTART-----	
HNF4A	2.0847e-02	TACTGAATTCTGA--- ---TGNMCTTTGNNCY	
NF-kappaB	3.2152e-02	TACTGAATTCTGA --GGAMTTYCC-	
Athb-1	3.3186e-02	TCAGAATTCAGTA -AATAATTN-----	

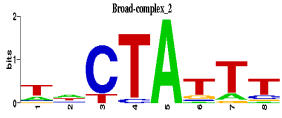

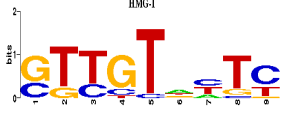
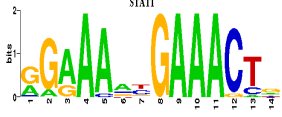



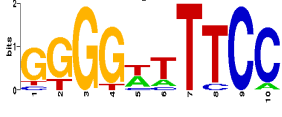
Motif_2



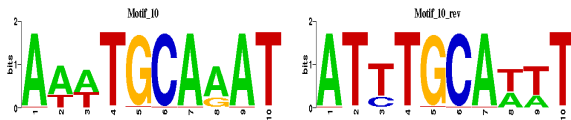
forward

reverse compliment

Name	E value	Alignment	Motif
HMG-IY	1.7118e-05	---TTTGCATNTCAA- RTTTYKNYNTTNTNN	
SQUA	1.0237e-03	-TTGANATGCAAA- MCAWAWATRGNAAN	


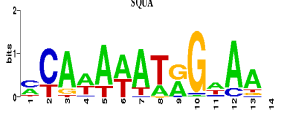
Broad-complex_2	3.4060e-02	TTGANATGCAAA ---AAATAGNW-	
NR2F1	3.4076e-02	-----TTTGCATNTCAA TGAMCTTTGNMCNN---	
HMG-1	3.9254e-02	TTTGCATNTCAA- ----GANNACAAC	
STAT1	3.9268e-02	TTGANATGCAAA-- RGAAANNGAAACTN	
RELA	4.2426e-02	TTTGCATNTCAA -GGGANTTTCC-	
NR1H2-RXRA	7.1076e-02	-TTTGCATNTCAA---- STTGACCTTTGACCTTT	
MNB1A	7.9661e-02	TTTGCATNTCAA ---NCTTT----	
DI_2	8.2895e-02	TTGANATGCAAA -GGAAAWCCCC-	

Motif_10



forward

reverse compliment

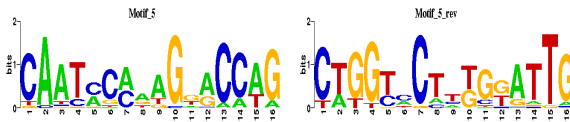
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HMG-IY	3.3314e-06	--ATTTGCAWTT---- RTTYKKNYNTTNTNN	
SQUA	9.4765e-05	----AAWTGCAAAT MCAWAWATRGNAAN	

Stamp Results

04/16/09

STAT1	8.7206e-04	-ATTTGCAWTT--- NAGTTTCNNTTTCY	
Pax4	1.4392e-03	-----AAWTGCAAAT----- RAAWAWWWNNMNNNNNNNNNNNNNNMNNNNNYMC	
Broad-complex_1	1.5224e-03	-ATTTGCAWTT--- NWYTTGTYYTATNAN	
Cebpa	1.4695e-02	ATTTGCAWTT-- TTNNNCAAYNNN	
HMG-1	1.7196e-02	AAWTGCAAAT GANNACAAC-	
Ddit3-Cebpa	2.2941e-02	--AAWTGCAAAT GSNATTGCAYNN	
NR2F1	2.4345e-02	----ATTTGCAWTT TGAMCTTTGNMCNN	
Foxa2	2.9932e-02	AAWTGCAAAT---- --AARYAAATANTN	

Motif_5



forward

reverse compliment

Name

E value

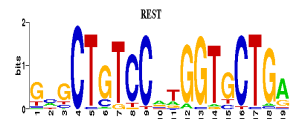
Alignment

Motif

REST

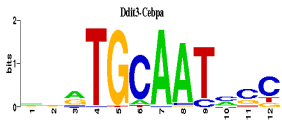
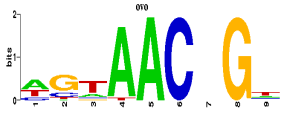

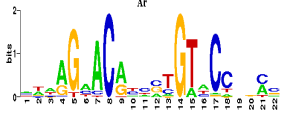
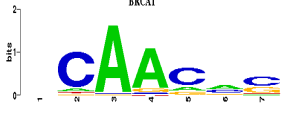
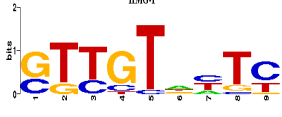
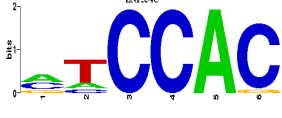

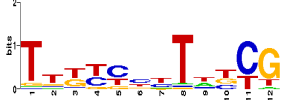
9.2402e-03

--CTGGTNCNTNKGKATTG-
GNGCTGTCCNWGGTGCTGA

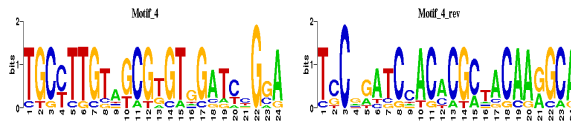


Stamp Results

04/16/09

Ddit3-Cebpa	1.3404e-02	CTGGTNCNTNKGKATTG----- -----GSNATTGCAYNN	
ovo	1.4403e-02	-CTGGTNCNTNKGKATTG NCNGTTACW-----	
NR1H2-RXRA	3.1690e-02	-CAATMCMNAGNACCAG AAAGGTCAAAGGTCAAS	
Ar	4.2602e-02	----CAATMCMNAGNACCAG-- NNNAGNACANNNTGTNCCNNMN	
BRCA1	4.3790e-02	CTGGTNCNTNKGKATTG- -----SNGTTGN	
HMG-1	4.6224e-02	CAATMCMNAGNACCAG GANNACAAC-----	
ZNF354C	4.6687e-02	CTGGTNCNTNKGKATTG -----GTGGAK--	
sna	4.7824e-02	CAATMCMNAGNACCAG -----CACCTG	
id1	5.0259e-02	CTGGTNCNTNKGKATTG TNKYNNNTNNCG----	

Motif_4



forward

reverse compliment

Name

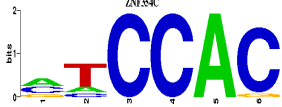
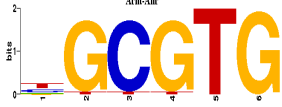
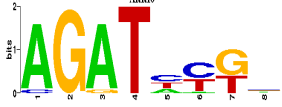




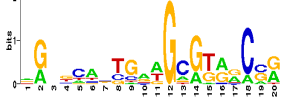


E value

Alignment

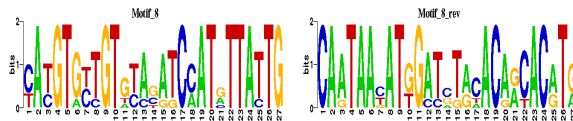
Motif

Stamp Results

04/16/09

ZNF354C	3.9705e-05	TGCCTTGTAGCGTGTGGATCNGGA -----GTGGAK-----	
Arnt-Ahr	2.5357e-03	TCCNGATCCACACGCTACAAGGCA -----CACGCN-----	
ARR10	6.9143e-03	TCCNGATCCACACGCTACAAGGCA -NMRNATCT-----	
MNB1A	1.2029e-02	TGCCTTGTAGCGTGTGGATCNGGA -NCTTT-----	
PBF	2.0724e-02	TCCNGATCCACACGCTACAAGGCA -----AAAGY-----	
Eip74EF	3.3313e-02	TGCCTTGTAGCGTGTGGATCNGGA -----YTCCGG-----	
Dof2	4.0010e-02	TGCCTTGTAGCGTGTGGATCNGGA NGCTTT-----	
Pax5	5.3635e-02	--TGCCTTGTAGCGTGTGGATCNGGA NGNNNNNYGNWGCGRRCR-----	
GATA2	5.5833e-02	TGCCTTGTAGCGTGTGGATCNGGA -----NGATN-----	
NFKB1	5.6928e-02	TCCNGATCCACACGCTACAAGGCA GGGGAATCCCC-----	

Motif_8

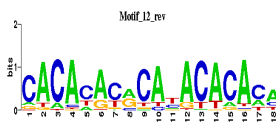
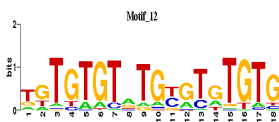


forward

reverse compliment

Name	E value	Alignment	Motif
Mycn	7.5450e-04	CATGTGYTGTGTASATCCATRTTATTG CACGTG-----	
Arnt	1.3445e-03	CAATAAYATGGATSTACACARCACATG -----CACGTG	
BRCA1	6.4320e-03	CATGTGYTGTGTASATCCATRTTATTG ---SNGTTGN-----	
USF1	6.6699e-03	CAATAAYATGGATSTACACARCACATG -----NCACGTG	
Athb-1	2.0170e-02	CATGTGYTGTGTASATCCATRTTATTG -----NAATTATT-	
MYC-MAX	2.0730e-02	--CATGTGYTGTGTASATCCATRTTATTG ACCACGTGSTN-----	
ZNF354C	2.2552e-02	CAATAAYATGGATSTACACARCACATG -----GTGGAK-----	
EMBP1	2.3024e-02	-CATGTGYTGTGTASATCCATRTTATTG CCACGTST-----	
sna	3.7716e-02	CAATAAYATGGATSTACACARCACATG -----CACCTG	
REST	4.1289e-02	CATGTGYTGTGTASATCCATRTTATTG- -----GNGCTGTCCNWGGTGCTGA	

Motif_12

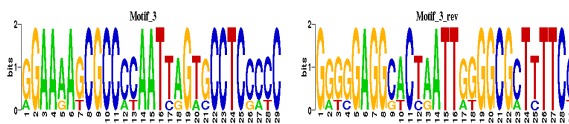


forward

reverse compliment

Name	E value	Alignment	Motif
CF2-II	5.0163e-03	CACAYACRCANACACAMN ---NTAYATATAY-----	
Arnt-Ahr	1.1257e-02	CACAYACRCANACACAMN ---CACGCN-----	
HMG-IY	1.1601e-02	-CACAYACRCANACACAMN NNANAAANRNMRAAA Y---	
RREB1	1.8612e-02	--NKTGTGTNTGYGTRTGTG NGKKKGKGGGTGKTTTGGG	
T	1.9860e-02	CACAYACRCANACACAMN --TTCACACCTAG-----	
Foxd3	3.0420e-02	CACAYACRCANACACAMN -AAANAAACAWTN-----	
FOXI1	3.4243e-02	---NKTGTGTNTGYGTRTGTG NNNTRTTTRTWT-----	
ZNF354C	5.0221e-02	NKTGTGTNTGYGTRTGTG ---GTGGAK-----	
Foxq1	6.9039e-02	-NKTGTGTNTGYGTRTGTG NATTGTTTATW-----	
Pax6	6.9676e-02	NKTGTGTNTGYGTRTGTG --MANTSAWGCGTGAA--	

Motif_3

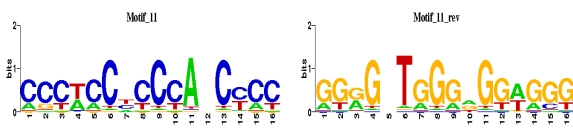


forward

reverse compliment

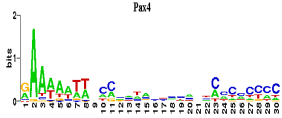
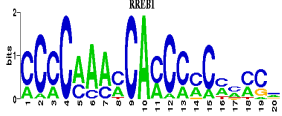
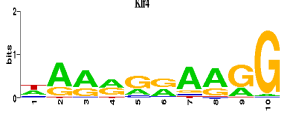

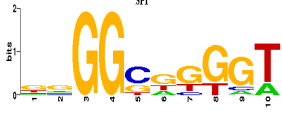
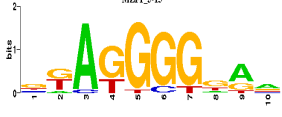
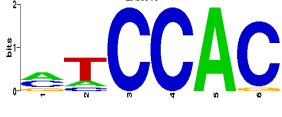
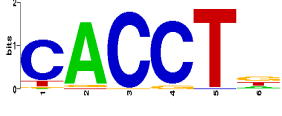
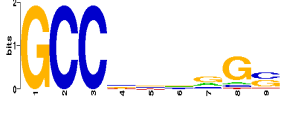

Name	E value	Alignment	Motif
Pax4	4.8136e-11	-GGGGAGGCACTAATTGGGGCGCTTTTCC GKRNNNNKNNNNNNNNNNKNNWWWWTWTTY	
Pdx1	6.0028e-06	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----AATTAG-----	
Prrx2	1.3008e-04	GGGGAGGCACTAATTGGGGCGCTTTTCC -----TAATT-----	
Dof3	1.8685e-04	GGGGAGGCACTAATTGGGGCGCTTTTCC -----NRCTTT-----	
MNB1A	2.2225e-04	GGGGAGGCACTAATTGGGGCGCTTTTCC -----NCTTT-----	
dl_1	3.1884e-04	GGGGAGGCACTAATTGGGGCGCTTTTCC- -----SGGGTTTTTCCN	
PBF	3.2872e-04	GGGGAGGCACTAATTGGGGCGCTTTTCC -----RCTTT-----	
Agamous	3.7219e-04	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----NCCNNWTTWGG-----	
Nkx2-5	4.7794e-04	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----CAMTTAW-----	
ATHB5	5.6424e-04	GGGGAGGCACTAATTGGGGCGCTTTTCC -----AATMATTGN-----	

Motif_11

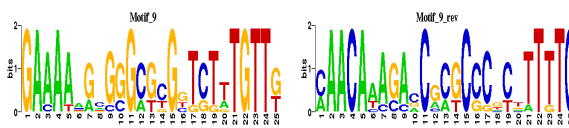


forward

reverse compliment

Name	E value	Alignment	Motif
Pax4	6.5278e-04	GGRGNTGGGNGGWGGG----- -GKRNNNNNKNNNNNNNNNNNNKNNWWWTWTTY	
RREB1	1.3388e-03	-----GGRGNTGGGNGGWGGG NGKKKGKGGGTGKTTTGGGG-	
Klf4	9.3992e-03	CCCWCCNCCCANCYCC CCTTYYYTTN-----	
MZF1_1-4	2.0693e-02	CCCWCCNCCCANCYCC ---TCCCN-----	
SP1	2.5923e-02	CCCWCCNCCCANCYCC -----ACCCNGCCNN	
MZF1_5-13	3.3083e-02	CCCWCCNCCCANCYCC --NTNCCCCTMN----	
ZNF354C	6.7150e-02	CCCWCCNCCCANCYCC --MTCCAC-----	
ZEB1	7.1363e-02	GGRGNTGGGNGGWGGG -----NAGGTG--	
TFAP2A	7.6314e-02	GGRGNTGGGNGGWGGG ---GCCNNNNGS----	
sna	8.2609e-02	GGRGNTGGGNGGWGGG -----CAGGTG--	

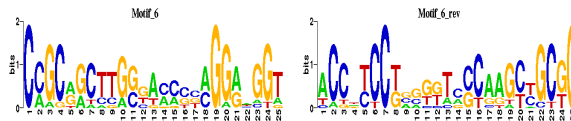
Motif_9



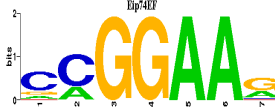


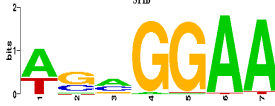

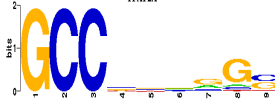
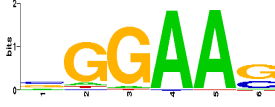

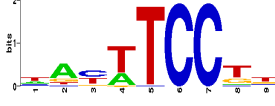

forward *reverse compliment*

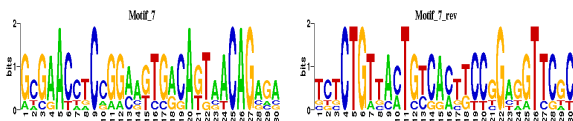
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MNB1A	3.1854e-04	CAACAAAGANCGCGCCNCNTTTTTC -----NCTTT---	
REST	6.5926e-04	----CAACAAAGANCGCGCCNCNTTTTTC TCAGCACCCWNGGACAGCNC-----	
Dof3	8.5118e-04	CAACAAAGANCGCGCCNCNTTTTTC -----NRCTTT---	
PBF	1.1530e-03	CAACAAAGANCGCGCCNCNTTTTTC -----RCTTT---	
Dof2	2.6836e-03	CAACAAAGANCGCGCCNCNTTTTTC -----NGCTTT---	
dl_1	7.0677e-03	CAACAAAGANCGCGCCNCNTTTTTC-- -----SGGGTTTTTCCN	
SP1	1.0486e-02	CAACAAAGANCGCGCCNCNTTTTTC -----ACCCNGCCNN-----	
Sox5	1.3638e-02	GAAAANGNGGGCGGNTCTTTGTTG -----ATTGTTN	
FOX11	1.9751e-02	CAACAAAGANCGCGCCNCNTTTTTC AWAYAAAAYANNN-----	
Foxd3	1.9823e-02	CAACAAAGANCGCGCCNCNTTTTTC AAANAAACAWTN-----	

Motif_6




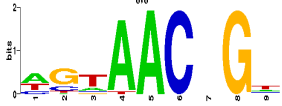

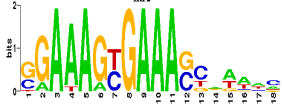
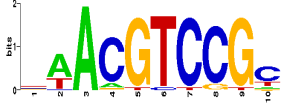
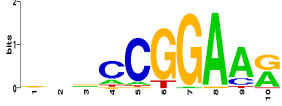
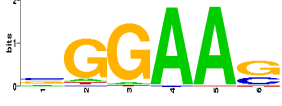



*forward**reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Eip74EF	3.0567e-04	ACCN ^Y CC ^K NN ^K KTNSCAAGCYGCGG --YTTCGG-----	
Roaz	4.4644e-04	ACCN ^Y CC ^K NN ^K KTNSCAAGCYGCGG GNMMCCYTRGGK ^K SC-----	
TEAD1	2.6430e-03	CCGCRGCTTGSNAMM ^N NMGGRNGGT- -----CNSW ^G GGAATGTR	
SPIB	1.2179e-02	ACCN ^Y CC ^K NN ^K KTNSCAAGCYGCGG ---TT ^C CKST-----	
NHLH1	1.5149e-02	CCGCRGCTTGSNAMM ^N NMGGRNGGT NCGCAGCTGCGN-----	
TFAP2A	1.6791e-02	ACCN ^Y CC ^K NN ^K KTNSCAAGCYGCGG ----SCN ^N NNNGGC-----	
SPI1	1.7288e-02	ACCN ^Y CC ^K NN ^K KTNSCAAGCYGCGG --STTCN-----	
ELK4	1.9825e-02	ACCN ^Y CC ^K NN ^K KTNSCAAGCYGCGG -ACTTCGGT-----	
ELF5	3.1065e-02	CCGCRGCTTGSNAMM ^N NMGGRNGGT -----NMGGAARTN	
PBF	3.9398e-02	CCGCRGCTTGSNAMM ^N NMGGRNGGT ----R ^C TTT-----	

Motif_7

forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ELK4	2.2790e-06	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----ACTTCCGGT-----	
Eip74EF	3.0442e-06	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----YTTCGG-----	
GABPA	4.9519e-06	GCGAACCTCCGGAAGTGACAGTAACAGAGA -----ACCGAAGNS-----	
ovo	1.1286e-05	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC --NCNGTTACW-----	
Spz1	2.2719e-04	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC --GCTGWTACCCT-----	
IRF2	4.8531e-04	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC ---NNWNRSTTTTCRITTCs-----	
MIZF	9.0722e-03	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----GCGGACGTTN--	
ELK1	9.6048e-03	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----YTTCGGNNN-----	
SPI1	1.8421e-02	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----STTCN-----	
IRF1	1.8953e-02	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----GGTTTCRNITTN-----	

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