



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: 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

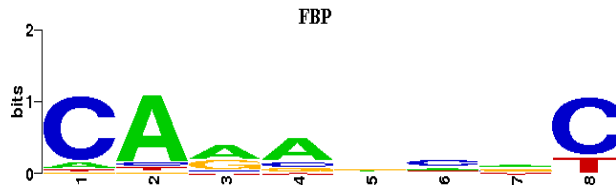
(Consensus sequence representations shown, but multiple alignment was carried out on the matrices)

```

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: -----CAACAAAGANCGCGCCNCNNTTTTC-----
Motif_10: -----AAWTGCAAAT-----
Motif_11: -----CCWCCNCCANCYCC-----
Motif_12: -----CACAYACRCANACACAMN-----

```

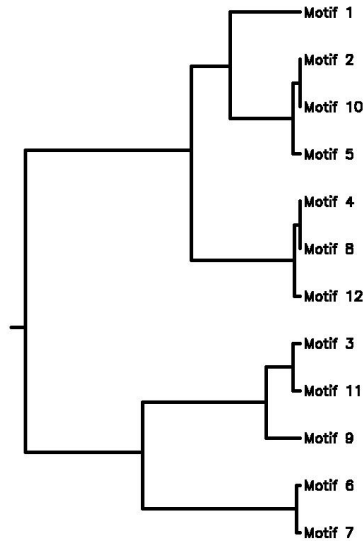
Familial Profile:
([click for matrix](#))

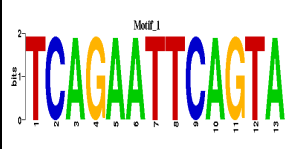
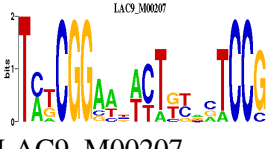
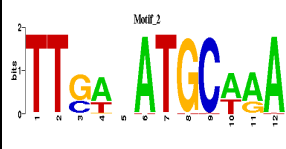

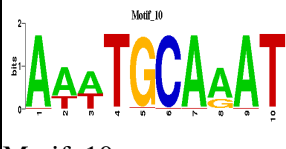

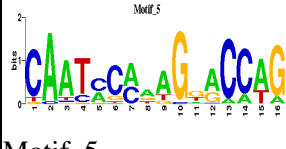

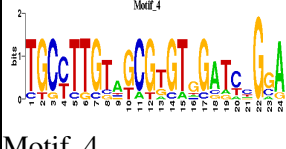

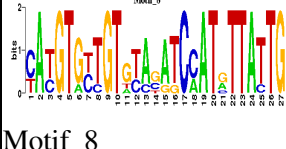
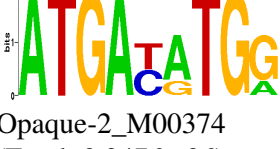
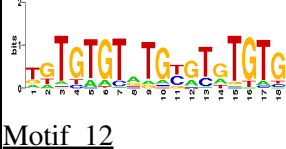
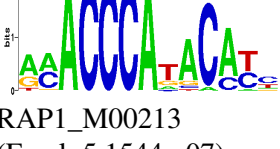
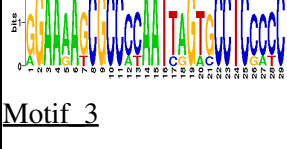



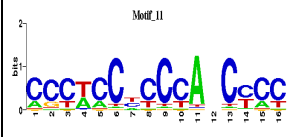

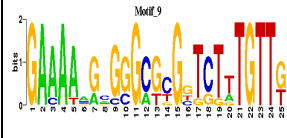

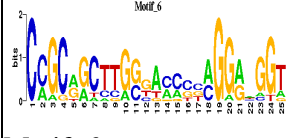

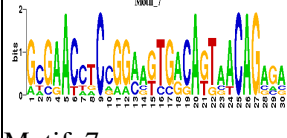

Motif Tree

Tree (drawn by [PhyIip](#))

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

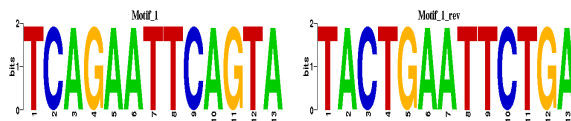


Input Motif	Best match in TRANSFAC
 <p>Motif 1</p>	 <p>LAC9_M00207 (E val: 8.9124e-06)</p>
 <p>Motif 2</p>	 <p>Oct-4_M01125 (E val: 4.4520e-14)</p>
 <p>Motif 10</p>	 <p>Oct-1_M00930 (E val: 1.0206e-11)</p>
 <p>Motif 5</p>	 <p>Pitx2_M00482 (E val: 7.7511e-05)</p>
 <p>Motif 4</p>	 <p>ARR10_M01050 (E val: 4.4376e-05)</p>
 <p>Motif 8</p>	 <p>Opaque-2_M00374 (E val: 3.9476e-06)</p>
 <p>Motif 12</p>	 <p>RAP1_M00213 (E val: 5.1544e-07)</p>
 <p>Motif 3</p>	 <p>En_M00696</p>

	(E val: 2.3193e-06)
 <p>Motif_11</p>	 <p>ZNF219_M01122 (E val: 5.1682e-07)</p>
 <p>Motif_9</p>	 <p>STE11_M01005 (E val: 1.2779e-05)</p>
 <p>Motif_6</p>	 <p>PEA3_M00655 (E val: 1.3863e-05)</p>
 <p>Motif_7</p>	 <p>BLIMP1_M01066 (E val: 8.8016e-09)</p>




Motif Similarity Matches

Motif_1



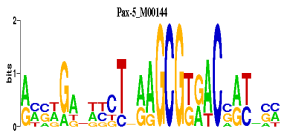

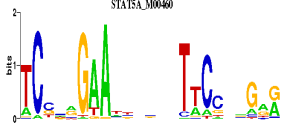




forward

reverse compliment

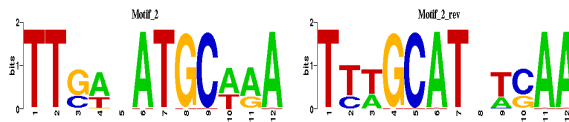
Name	E value	Alignment	Motif
LAC9_M00207	8.9124e-06	-----TACTGAATTCTGA-- NCGGANNRMAGWNWTCCGMKA	
PXR_M01153	2.8134e-04	TCAGAATTCAGTA ---NAGTTCA---	
HNF4alpha_M00638	3.0006e-04	--TCAGAATTCAGTA NKKCAAAGKTCA---	

Stamp Results

04/16/09

Pax-5_M00144	3.1125e-04	-----TCAGAATTCAGTA NNNRYNGTYMCGCTYNANNNNNNCNNNY	
WRKY_M00681	4.2784e-04	TCAGAATTCAGTA- ----TAYTYRGTC	
STAT5A_M00460	1.1024e-03	--TCAGAATTCAGTA----- TCNNNGAANNNNNNTTCCNNGNR	
CF1A_M01098	1.9102e-03	-TCAGAATTCAGTA- NTTNAAYTNATTAW	
HNF6_M00639	2.3155e-03	-TACTGAATTCTGA NTATTGATTTN---	
POU6F1_M00465	2.7103e-03	TACTGAATTCTGA --ATAAWTTATG-	
AP-3_M00690	2.9314e-03	TACTGAATTCTGA --CYMAATT----	

Motif_2

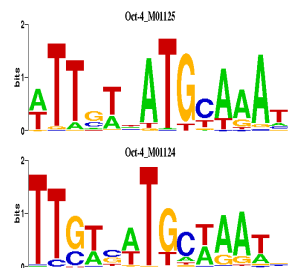



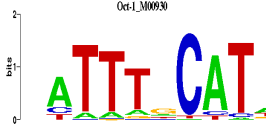

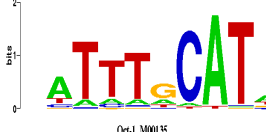
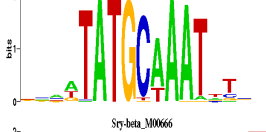



forward

reverse compliment

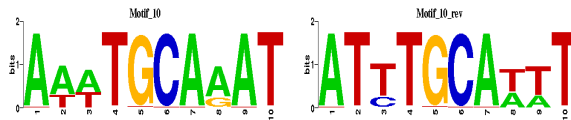
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
Oct-4_M01125	4.4520e-14	-TTGANATGCAAA- WTTSTNATGCAAAT
Oct-4_M01124	6.0190e-11	--TTTGCATNTCAA NWTTWGCAWNACAA

Motif



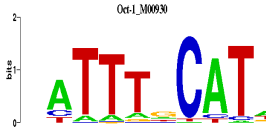

Oct-1_M00342	4.4049e-06	--TTTGCATNTCAA NATTTGCAT-----	
Oct-1_M00930	5.1738e-06	TTGANATGCAAA-- ----NATGNAAATN	
Oct-1_M00161	9.9342e-06	---TTTGCATNTCAA KNATTTGCATAYY--	
Octamer_M00795	2.1211e-05	--TTTGCATNTCAA NATTTGCATN-----	
Oct-1_M00135	4.9845e-05	-----TTTGCATNTCAA NNNANATTTGCATANNNN	
Sry-beta_M00666	7.1234e-05	TTGANATGCAAA -AGWGATGC---	
MADS-B_M00404	1.1431e-04	TTTGCATNTCAA-- TTTSCATTTTTTRGN	
MADS-A_M00408	1.1473e-04	TTTGCATNTCAA--- TTTCCATTTTTTNWN	

Motif_10

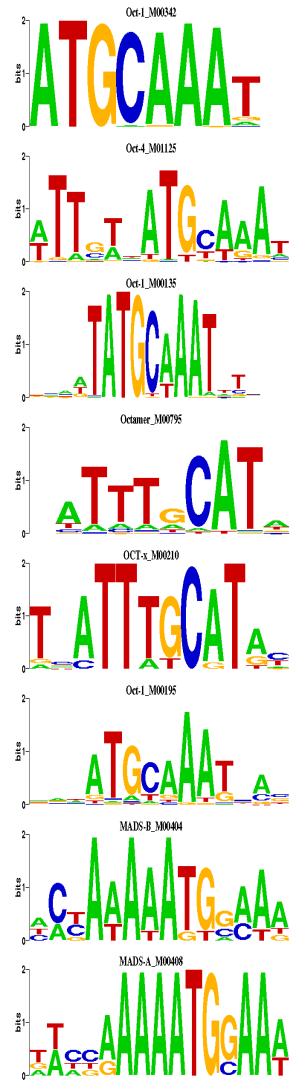


forward

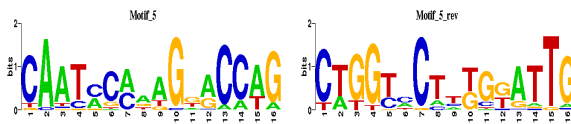
reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Oct-1_M00930	1.0206e-11	AAWTGCAAAT-- -NATGNAAATN	
Oct-1_M00161	4.5951e-11	-AAWTGCAAAT-- RRTATGCAAATNM	

Oct-1_M00342	2.9351e-10	AAWTGCAAAT- --ATGCAAATN
Oct-4_M01125	1.2209e-09	ATTTGCAWTT---- ATTTGCATNASAAW
Oct-1_M00135	2.0239e-09	---AAWTGCAAAT----- NNNNTATGCAAATNTNNN
Octamer_M00795	3.7860e-09	AAWTGCAAAT- -NATGCAAATN
OCT-x_M00210	3.9220e-08	AAWTGCAAAT-- RTATGCAAATNA
Oct-1_M00195	2.5267e-07	---ATTTGCAWTT- NTNATTTGCATNNN
MADS-B_M00404	6.1512e-07	ATTTGCAWTT----- -TTTSCATTTTTRGN
MADS-A_M00408	1.4312e-06	-----AAWTGCAAAT WNWNAAAAATGGAAA-

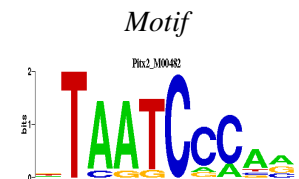









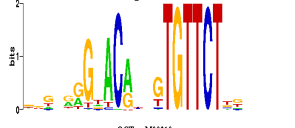

Motif_5



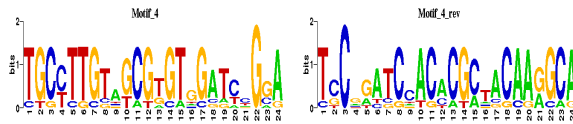
forward *reverse compliment*

Name	E value	Alignment
Pitx2_M00482	7.7511e-05	CTGGTNCTNKGKATTG- -----NTGGGATTAN



LUN-1_M00480	1.7159e-04	CAATMCMNAGNACCAG-- --TCCCAAAGTAGCTGGG	
MRF-2_M00454	2.6489e-04	CTGGTNCTNKGKATTG---- -----KNNGTATTGTNSW	
LEF1_M00805	5.3104e-04	CTGGTNCTNKGKATTG -----CTTTG-----	
PPARalpha-RXRalpha_M00518	8.5130e-04	--CAATMCMNAGNACCAG CNTSACCCCNATGACCNN	
EBF_M00977	1.1559e-03	CAATMCMNAGNACCAG ---NCYCWRGGGA---	
HOXA7_M01108	1.9510e-03	CTGGTNCTNKGKATTG -----AGATTG	
PBF_M01130	2.0304e-03	CAATMCMNAGNACCAG -----AAAG-----	
AR_M00953	3.2172e-03	-----CAATMCMNAGNACCAG--- NNNNNNAGAACACNNTGTNCYNNNNN	
OCT-x_M00210	4.7987e-03	CTGGTNCTNKGKATTG ----TNATTTGCATAY	

Motif_4



forward

reverse compliment

Name

E value

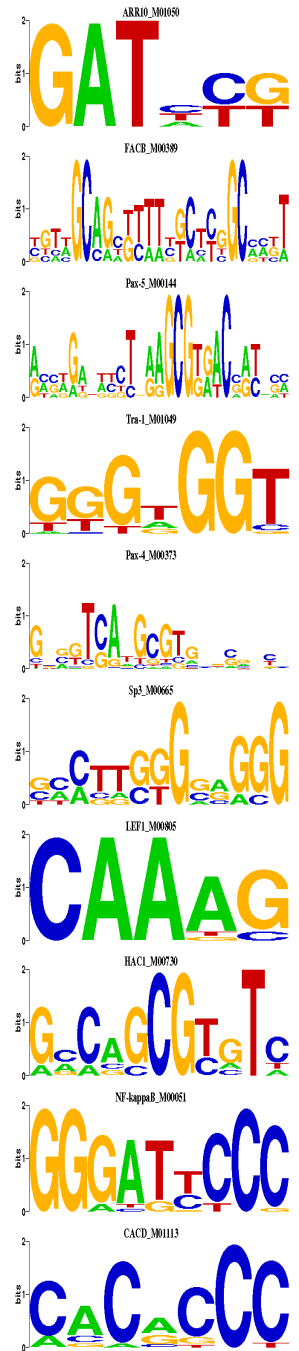
Alignment

Motif

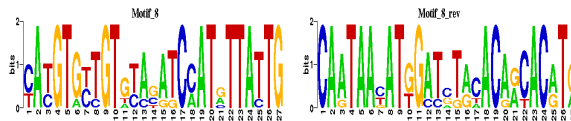
Stamp Results

04/16/09

ARR10_M01050	4.4376e-05	TCCNGATCCACACGCTACAAGGCA --MRNATC-----
FACB_M00389	1.0170e-04	---TCCNGATCCACACGCTACAAGGCA ANNNGCNRMNAAAMNCTGCNNNN--
Pax-5_M00144	2.8090e-03	-----TGCCTTGTAGCGTGTGGATCNGGA RNNNGNNNNNTNRAGCGKRACNRYNNN--
Tra-1_M01049	4.1863e-03	TGCCTTGTAGCGTGTGGATCNGGA -----GGNGGT-----
Pax-4_M00373	5.4883e-03	TGCCTTGTAGCGTGTGGATCNGGA -GNNKTCANGCGTGNSNNNN---
Sp3_M00665	6.7747e-03	TCCNGATCCACACGCTACAAGGCA -----CCCYSCCAAGKS-
LEF1_M00805	7.4009e-03	TGCCTTGTAGCGTGTGGATCNGGA --CTTIG-----
HAC1_M00730	7.5088e-03	TGCCTTGTAGCGTGTGGATCNGGA ----GMCAGCGTGTC-----
NF-kappaB_M00051	9.5336e-03	TGCCTTGTAGCGTGTGGATCNGGA -----GGGRATCCC--
CACD_M01113	1.1315e-02	TGCCTTGTAGCGTGTGGATCNGGA -----GGGYGTG-----



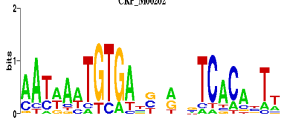



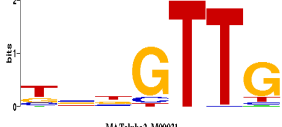





Motif_8

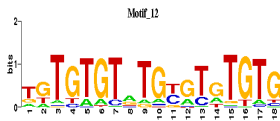


forward

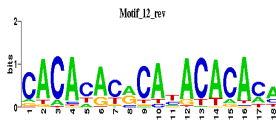
reverse compliment

Name	E value	Alignment	Motif
Opaque-2_M00374	3.9476e-06	CAATAAYATGGATSTACACARCACATG --ATGAYATGG-----	
TWI_M01103	1.3335e-05	CAATAAYATGGATSTACACARCACATG -----NNGCNNMACAYAT-	
CRP_M00202	4.3897e-05	CATGTGYTGTGTASATCCATRTTATTG -WANTGTGANNYNNTCACAWTWATT-	
TFE_M01029	1.4757e-04	CAATAAYATGGATSTACACARCACATG -----NCACATG	
ATHB-5_M00503	3.1301e-04	CAATAAYATGGATSTACACARCACATG CAATNATT-----	
bHLH66_M01054	5.8229e-04	CAATAAYATGGATSTACACARCACATG -----GCACGTG	
BRCA1-USF2_M01082	9.7729e-04	CAATAAYATGGATSTACACARCACATG -----CAACNNN--	
MATalpha2_M00031	1.6817e-03	CAATAAYATGGATSTACACARCACATG -NWNACAYG-----	
RITA-1_M00660	1.8787e-03	CAATAAYATGGATSTACACARCACATG -----SACGTR	
POU3F2_M00464	2.6381e-03	CAATAAYATGGATSTACACARCACATG -ATTARCATA-----	

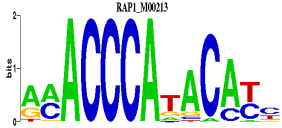

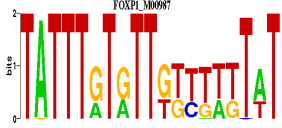



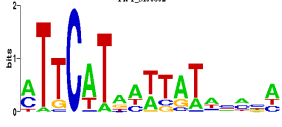



Motif_12



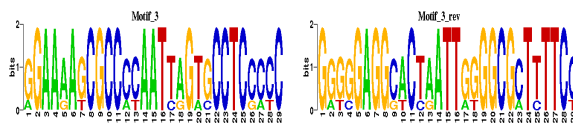
forward



reverse compliment

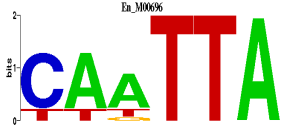
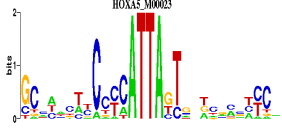


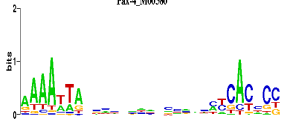





Name	E value	Alignment	Motif
RAP1_M00213	5.1544e-07	NKTGTGNTGYGTRTGTG --NRTGTATGGGTKY---	
Tax-CREB_M00115	4.3219e-05	NKTGTGNTGYGTRTGTG -GGGGRATGCGTCA---	
FOXP1_M00987	6.0635e-05	-CACAYACRCANACACAMN ATAAAAAACAACACAAATA	
NGFI-C_M00244	6.8421e-05	-CACAYACRCANACACAMN CCRCCCACGCA-----	
Egr-3_M00245	1.5210e-04	CACAYACRCANACACAMN -----ACGCCACGCA--	
Egr-2_M00246	2.0592e-04	CACAYACRCANACACAMN -----MCGCCCACGCA--	
Pit-1_M00802	2.0641e-04	CACAYACRCANACACAMN -MTTCATNNWTATNNNNN	
Egr-1_M00243	3.5130e-04	NKTGTGNTGYGTRTGTG --TGCGTGGGCGK-----	
CACD_M01113	6.4645e-04	CACAYACRCANACACAMN --CACRCCC-----	
HFH4_M00742	2.2067e-03	NKTGTGNTGYGTRTGTG --WKTGTTTGTTA-----	

Motif_3

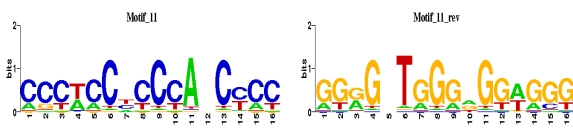


forward

reverse compliment

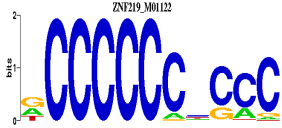









Name	E value	Alignment	Motif
En_M00696	2.3193e-06	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----CAATTA-----	
HOXA5_M00023	2.8121e-06	--GGGGGAGGCACTAATTGGGGCGCTTTTCC NGRNNNNNNNNNANTAATGRNGNNNNNNGC--	
HOXA4_M00640	4.2207e-06	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----CYAATTW-----	
TFII-I_M00706	5.4830e-06	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----CCTMCNTC-----	
Pax-4_M00380	1.5795e-05	-GGGGGAGGCACTAATTGGGGCGCTTTTCC NGNGTGNNNNNNNNNNNNNNNNTAWTTTN-	
ATHB-5_M00503	4.2772e-05	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----AATNATTG-----	
UF1H3BETA_M01068	7.4050e-05	--GGGGGAGGCACTAATTGGGGCGCTTTTCC GYGGGGGAGGGGC-----	
MAZ_M00649	1.0199e-04	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----CCCTCC--	
Nkx2-5_M00241	1.2150e-04	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----NAATTAW-----	
E2F-1_M00939	4.6967e-04	GGAAAAGCGCCCCAATTAGTGCCTCCCC -----CGCGCSAA-----	

Motif_11

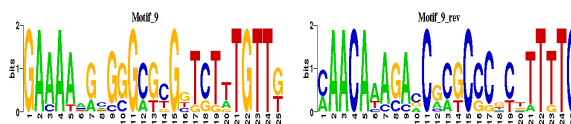


forward

reverse compliment

Name	E value	Alignment	Motif
ZNF219_M01122	5.1682e-07	-CCCWCCNCCCANCYCC NCCCCCNCCC-----	
VDR_M00444	1.4762e-06	CCCWCCNCCCANCYCC -TSWCCYYNYTNMCC-	
UF1H3BETA_M01068	3.3541e-06	--CCCWCCNCCCANCYCC GCCCTCCCCRC-----	
KROX_M00982	1.2985e-05	GGRGNTGGGNGGWGGG GNNGNGGGGGCGG---	
MAZ_M00649	1.6038e-05	CCCWCCNCCCANCYCC CCCTCC-----	
AtMYB-84_M00970	4.0469e-05	CCCWCCNCCCANCYCC ----SCACCTACCNC	
CAC-binding_M00720	7.2713e-05	GGRGNTGGGNGGWGGG -----RGGSTGG	
Lyf-1_M00141	1.6046e-04	CCCWCCNCCCANCYCC ----YCTCCCAA----	
Tra-1_M01048	2.1934e-04	GGRGNTGGGNGGWGGG -----GGWGGT----	
TFII-I_M00706	2.3594e-04	CCCWCCNCCCANCYCC -CCTMCNTC-----	

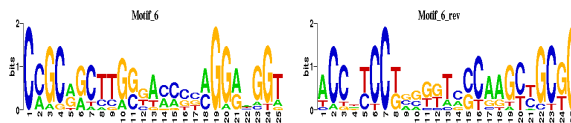
Motif_9









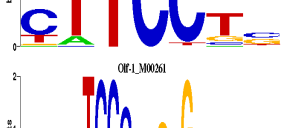



forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
STE11_M01005	1.2779e-05	CAACAAAGANCGCGCCNCNNTTTTC GAACAAAGAAA-----	
Mat1-Mc_M00275	3.3878e-05	----CAACAAAGANCGCGCCNCNNTTTTC NRMNNAACAAAGANRYC-----	
SRY_M00148	4.0988e-05	CAACAAAGANCGCGCCNCNNTTTTC -AACANM-----	
ZAP1_M00735	8.1564e-05	CAACAAAGANCGCGCCNCNNTTTTC -----TGACCGAGY-----	
SOX_M01014	1.1660e-04	---CAACAAAGANCGCGCCNCNNTTTTC NCNTAACAAAGA-----	
ZF5_M00333	1.8894e-04	CAACAAAGANCGCGCCNCNNTTTTC -----NWGCGGYNYNY-----	
LEF1_M00805	1.9076e-04	GAAAANGNGGGCGCGNTCTTTGTTG -----CTTTG---	
NRSF_M00256	2.1431e-04	----CAACAAAGANCGCGCCNCNNTTTTC TCAGCACCACGGACAGCRSC-----	
HFH4_M00742	3.2897e-04	-CAACAAAGANCGCGCCNCNNTTTTC TAAACAAACAMW-----	
KROX_M00982	6.9677e-04	GAAAANGNGGGCGCGNTCTTTGTTG ---GNNGNGGGGGCGG-----	

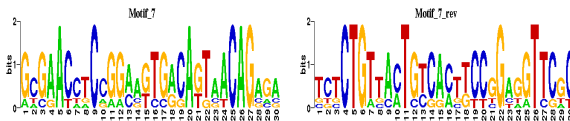
Motif_6








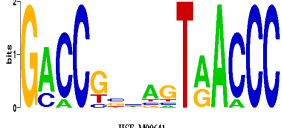

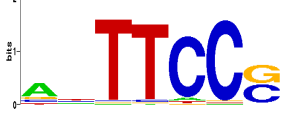


forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
PEA3_M00655	1.3863e-05	CCGCRGCTTGSNAMMNNMGGRRNGGT -----MGGAWG--	
Tra-1_M01048	5.2093e-05	ACCNYYCKNNKKTNSCAAGCYGCGG ACCWCC-----	
PU.1_M00658	3.8276e-04	ACCNYYCKNNKKTNSCAAGCYGCGG --CTTCTC-----	
LBP-1_M00644	3.8363e-04	CCGCRGCTTGSNAMMNNMGGRRNGGT --SCAGCN-----	
c-Ets-1_M00743	3.9782e-04	ACCNYYCKNNKKTNSCAAGCYGCGG -GCTTCK-----	
Tra-1_M01049	9.7222e-04	ACCNYYCKNNKKTNSCAAGCYGCGG ACCNCC-----	
Ets_M00971	1.1419e-03	CCGCRGCTTGSNAMMNNMGGRRNGGT -----NAGGAAG--	
Olf-1_M00261	3.1243e-03	---ACCNYYCKNNKKTNSCAAGCYGCGG NCMNNYTCCNRRGGANTNGN-----	
Tel-2_M00678	3.3696e-03	CCGCRGCTTGSNAMMNNMGGRRNGGT -----CAGGAAGTA	
c-Ets-1_p54_M00032	3.5880e-03	ACCNYYCKNNKKTNSCAAGCYGCGG NRCWTCCG-----	

Motif_7



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
BLIMP1_M01066	8.8016e-09	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----YMCTTTCMCTTYC-----	
GABP_M00341	1.3725e-07	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----YGCNCTTCCGG-----	
Nrf-2_M00108	4.2402e-07	GCGAACCTCCGGAAGTGACAGTAACAGAGA -----CCGGAAGNS-----	
c-Ets-1_p54_M00032	5.7446e-05	GCGAACCTCCGGAAGTGACAGTAACAGAGA -----CMGGAWGYN-----	
Tel-2_M00678	1.3932e-04	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----TACTTCTG-----	
ANT_M00501	1.4112e-04	GCGAACCTCCGGAAGTGACAGTAACAGAGA -----CMTYGGGAWN TGT-----	
SOX_M01014	1.4978e-04	GCGAACCTCCGGAAGTGACAGTAACAGAGA -----NCNTAACAAAGA	
LXR_M00766	2.4248e-04	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----GGGTACTNCCGGTC-----	
HSF_M00641	4.1429e-04	TCTCTGTTACTGTCACTTCCGGAGGTTTCGC -----TCNMGNRGYTT C-----	
STAT1_M00492	4.2149e-04	GCGAACCTCCGGAAGTGACAGTAACAGAGA -----SGGAANT-----	

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