Jump to: Multiple Alignment Motif Tree Motif Matching
Input file: 8 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".
Download results as a PDF
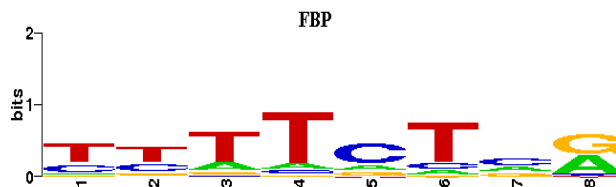Click here to run STAMP again.

Multiple Alignment

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

```
Motif1:               -------TCTAGCG-
Motif2:               -----TTTMTCACCC
Motif3:               CGCCTTTTCTC----
Motif4:               ----TCTTCAGGGA-
Motif5:               ------RACTG----
Motif6:               -CRRNGTTGCCA---
Motif7:               ----TTTTATA----
Motif8:               ---GCCATYT-----
```
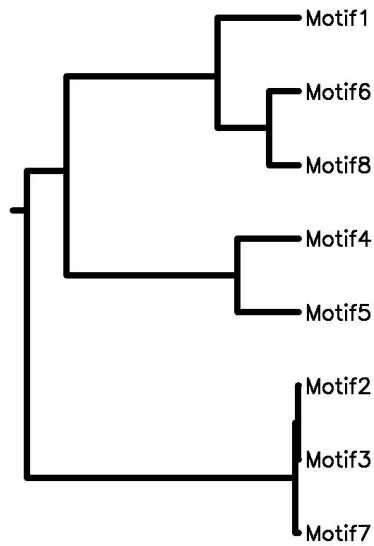
Familial Profile:
(click for matrix)

Motif Tree

| Tree (drawn by **Phylip**) Click here for Newick-format tree (viewable with MEGA)	Input Motif	Best match in JASPAR

| Motif1 | MA0266.1_ABF2 (E val: 5.5055e-05) |
Motif6	MA0365.1_RFX1 (E val: 2.1236e-06)
Motif8	MA0139.1_CTCF (E val: 4.1272e-05)
Motif4	MA0154.1_EBF1 (E val: 2.6654e-05)
Motif5	MA0092.1_Hand1_T (E val: 2.3608e-03)
Motif2	MA0009.1_T (E val: 1.7392e-04)
Motif3	MA0326.1_MAC1 (E val: 2.3800e-04)
Motif7	MA0108.1_TBP (E val: 6.1937e-09)

Motif Similarity Matches

Motif1
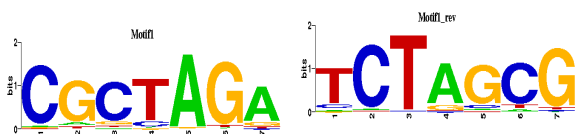
forward   *reverse compliment*

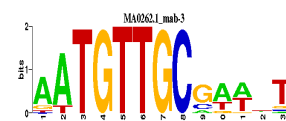| Name	E value	Alignment	Motif
MA0266.1_ABF2	5.5055e-05	CGCTAGA- -TCTAGAN	
MA0396.1_STP3	4.0666e-04	--CGCTAGA NGCGCTANN	
MA0397.1_STP4	4.0666e-04	--CGCTAGA NGCGCTANN	
MA0384.1_SNT2	1.1136e-03	---CGCTAGA- NGGCGCTAYCA	
MA0451.1_kni	2.9019e-03	----TCTAGCG- NTGCTCTANTTT	

Motif6
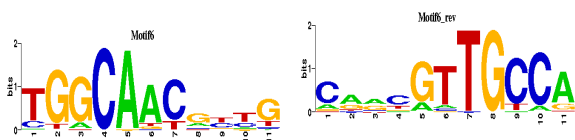
forward   *reverse compliment*

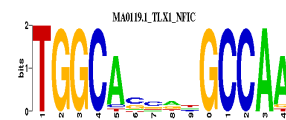| Name	E value	Alignment	Motif
MA0365.1_RFX1	2.1236e-06	TGGCAACNYYG TRGCAACN---	

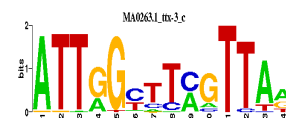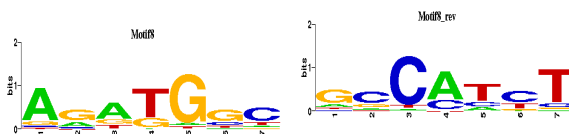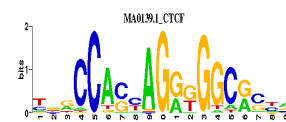|			
MA0262.1_mab-3	3.2509e-05	---TGGCAACNYYG ANWTCGCAACATT-	
MA0119.1_TLX1_NFIC	1.6004e-03	---CRRNGTTGCCA TTGGCNNNSTGCCA	
MA0097.1_bZIP911	2.9666e-03	--CRRNGTTGCCA GRTGACGTGGCC-	
MA0263.1_ttx-3_c	4.7794e-03	--TGGCAACNYYG- ATTGGYTTMGTTAR	

Motif8

forward   *reverse compliment*

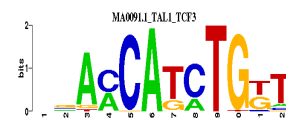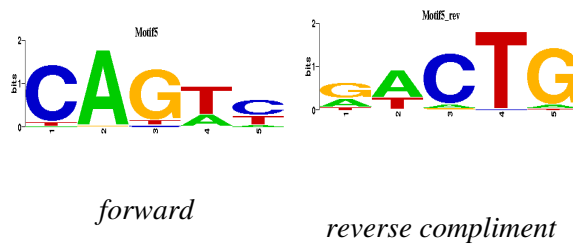| *Name*	*E value*	*Alignment*	*Motif*
MA0139.1_CTCF	4.1272e-05	----GCCATYT-------- NNSYGCCMCCTRSTGGNNR	
MA0373.1_RPN4	2.1959e-04	-GCCATYT CGCCACC-	
MA0091.1_TAL1_TCF3	6.2532e-04	---ARATGGC-- AMCAGATGKTNN	
MA0161.1_NFIC	5.5756e-03	ARATGGC- --TTGGCN	
MA0095.1_YY1	6.3864e-03	GCCATYT NCCATN-	
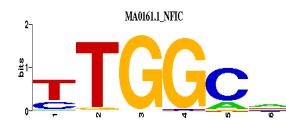
Motif4

forward   *reverse compliment*
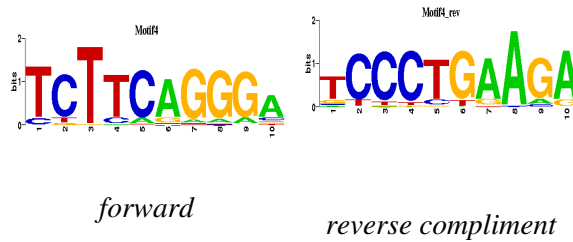
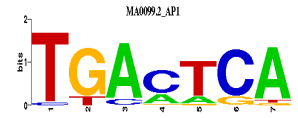| Name	E value	Alignment	Motif
MA0154.1_EBF1	2.6654e-05	TCCCTGAAGA TCCCTNGGGN	
MA0062.1_GABPA	2.6767e-05	-TCTTCAGGGA SNCTTCCGGT-	
MA0026.1_Eip74EF	5.3941e-05	TCTTCAGGGA -YTTCCGG--	
MA0413.1_USV1	1.0875e-04	----TCTTCAGGGA------ NNNNNNTTCAGGGGKANNNN	
MA0014.1_Pax5	3.2762e-04	-------TCTTCAGGGA--- YSGYYMCGCWNCRNNNNNCN	

Motif5

forward   *reverse compliment*

Name	E value	Alignment	Motif
MA0092.1_Hand1_T	2.3608e-03	-RACTG---- NRTCTGGNWN	
MA0145.1_Tcfcp2l1	4.3739e-03	--------RACTG- CYGGNTNNRNCYGG	

MA0272.1_ARG81	5.2434e-03	-CAGTY-- NGAGTCAN	
MA0099.2_AP1	7.5732e-03	-CAGTY- TGAGTCA	
MA0335.1_MET4	9.6118e-03	---CAGTY CCACAGNT	
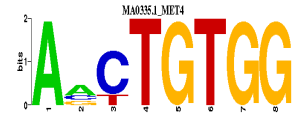
Motif2

forward
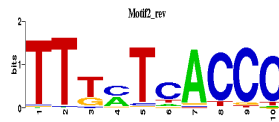
reverse compliment

Name	E value	Alignment	Motif
MA0009.1_T	1.7392e-04	--GGGTGAKAAA CTAGGTGTGAA-	
MA0326.1_MAC1	3.0091e-04	GGGTGAKAAA- ---YGAGCAAA	
MA0199.1_Optix	5.4325e-04	TTTMTCACCC --TATCA---	
MA0085.1_Su_H_	9.8180e-04	------TTTMTCACCC NNNNNGKTTCCCACRN	
MA0099.1_Fos	1.3079e-03	TTTMTCACCC TGANTCAC--	
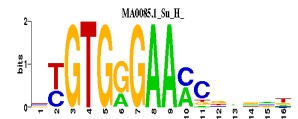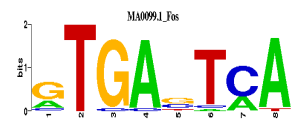
Motif3

forward

reverse compliment

Name	E value	Alignment	Motif
MA0326.1_MAC1	2.3800e-04	CGCCTTTTCTC- ----TTTGCTCR	
MA0459.1_tll	3.8584e-04	--CGCCTTTTCTC KTTGACTTTT---	
MA0243.1_sd	7.3799e-04	CGCCTTTTCTC-- -NWMATTYNNNRN	
MA0152.1_NFATC2	1.0981e-03	GAGAAAAGGCG TGGAAAA----	
MA0437.1_YPR196W	1.4835e-03	--GAGAAAAGGCG CGGRNAAAT----	

Motif7
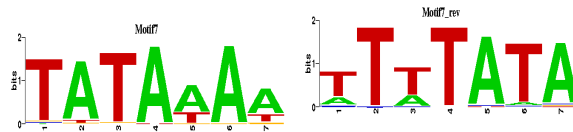
forward

reverse compliment

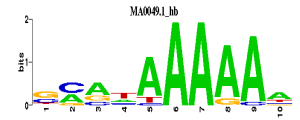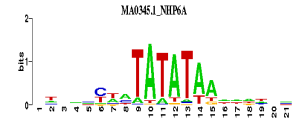| Name	E value	Alignment	Motif
MA0108.1_TBP	6.1937e-09	-------TTTTATA- NNNNNNYWTTTATAN	
MA0108.2_TBP	6.2153e-09	-------TTTTATA- NNNNNNYWTTTATAN	

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MA0052.1_MEF2A 4.9937e-06

```
-TATAAAA--
CTATAAATAG
```
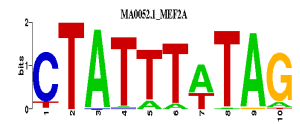

MA0049.1_hb   1.6534e-05

```
--TTTTATA-
NTTTTTNYKS
```


MA0345.1_NHP6A 2.7969e-05

```
------TTTTATA--------
NNNNNNTTATATANNRNNNNN
```


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