Jump to: Multiple Alignment Motif Tree Motif Matching
Input file: 3 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".
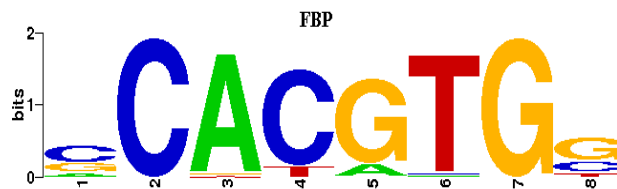Download results as a PDF
Click here to run STAMP again.

Multiple Alignment

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

```
cmyc_1h_merged:        SCACGTGG
cmyc_1h_ref_1_raw:     CCACGTGG
cmyc_1h_1_raw:         NCACGTGN
```

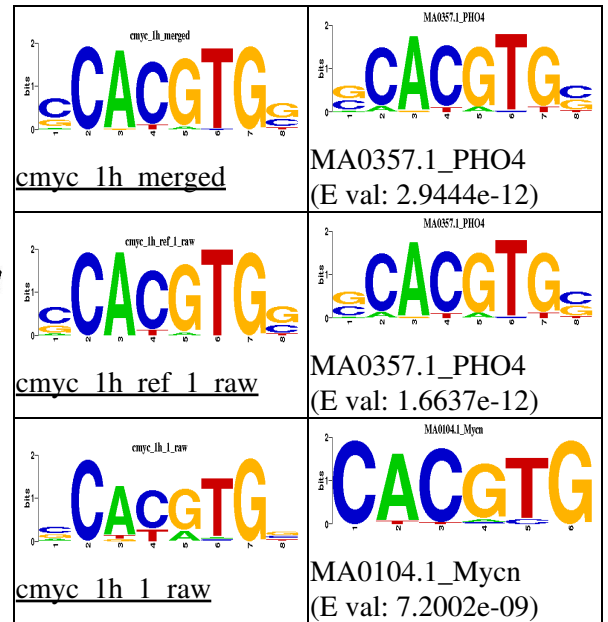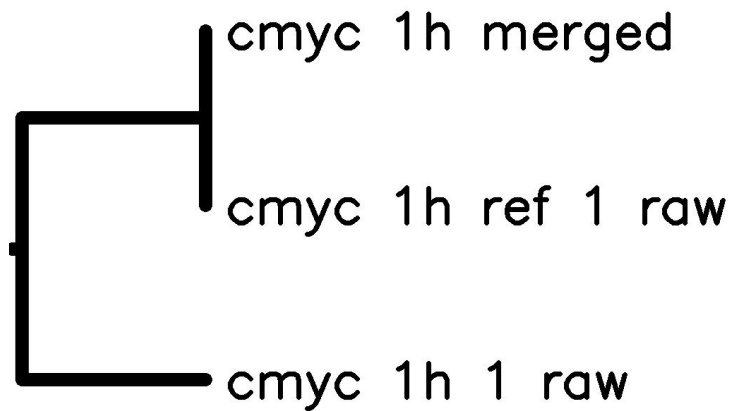**Familial Profile:**
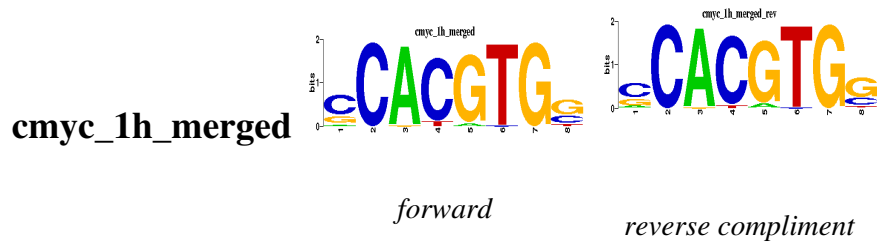**(click for matrix)**

Motif Tree

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

cmyc_1h_merged		MA0357.1_PHO4 (E val: 2.9444e-12)
cmyc_1h_ref_1_raw		MA0357.1_PHO4 (E val: 1.6637e-12)
cmyc_1h_1_raw		MA0104.1_Mycn (E val: 7.2002e-09)

Motif Similarity Matches

cmyc_1h_merged

forward   *reverse compliment*

Name	E value	Alignment	Motif
MA0357.1_PHO4	2.9444e-12	CCACGTGS SCACGTGS	
MA0059.1_MYC_MAX	1.3919e-11	-CCACGTGS-- ACCACGTGSTN	
MA0147.1_Myc	3.8932e-10	-CCACGTGS- NCCACGTGSN	
MA0128.1_EmBP-1	1.2868e-09	CCACGTGS CCACGTST	

MA0104.1_Mycn	3.9411e-09	CCACGTGS -CACGTG-

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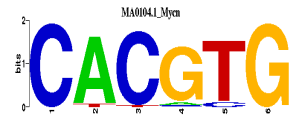
cmyc_1h_ref_1_raw

forward   *reverse compliment*

Name	E value	Alignment	Motif
MA0357.1_PHO4	1.6637e-12	CCACGTGG SCACGTGS	
MA0059.1_MYC_MAX	1.9283e-11	-CCACGTGG-- ACCACGTGSTN	
MA0147.1_Myc	5.0460e-10	-CCACGTGG- NCCACGTGSN	
MA0128.1_EmBP-1	1.6902e-09	CCACGTGG CCACGTST	
MA0104.1_Mycn	4.0150e-09	CCACGTGG -CACGTG-	
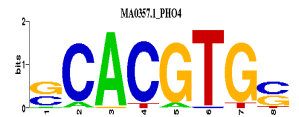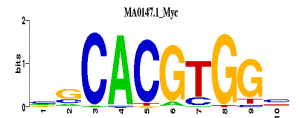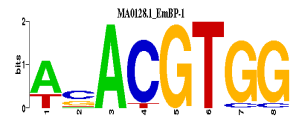
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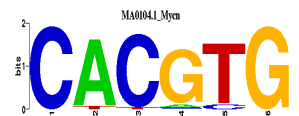
cmyc_1h_1_raw

forward   *reverse compliment*

Name	E value	Alignment	Motif

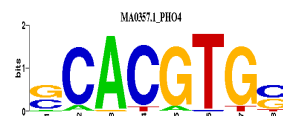|			
MA0104.1_Mycn	7.2002e-09	NCACGTGN -CACGTG-	
MA0004.1_Arnt	1.1549e-08	NCACGTGN -CACGTG-	
MA0093.1_USF1	2.4219e-07	NCACGTGN NCACGTG-	
MA0409.1_TYE7	3.4937e-07	NCACGTGN TCACGTG-	
MA0357.1_PHO4	1.7259e-06	NCACGTGN SCACGTGS	
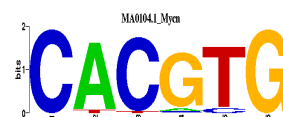
Sequence logo generation powered by weblogo
STAMP is written by Shaun Mahony