

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\_Fams

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

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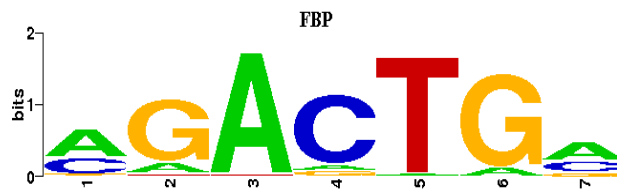
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## Multiple Alignment

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

GTCAGTCG:	-CGACTGA--
WGTCAGTH:	---ACTGANN
GCAGTCTT:	AAGACTGC--

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



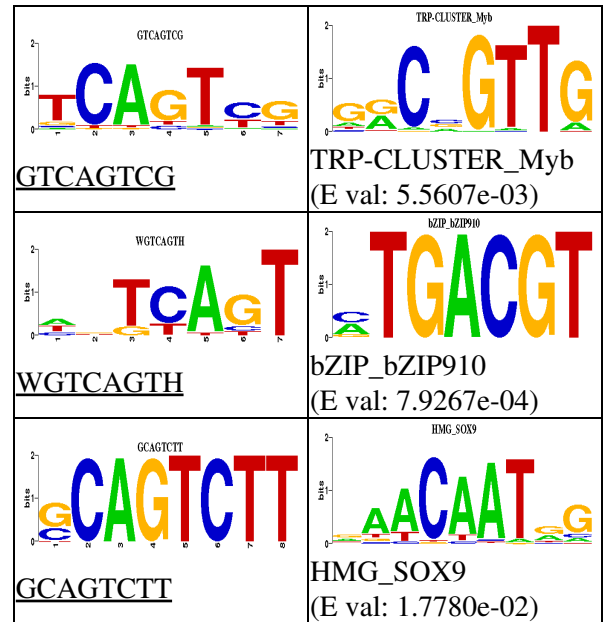
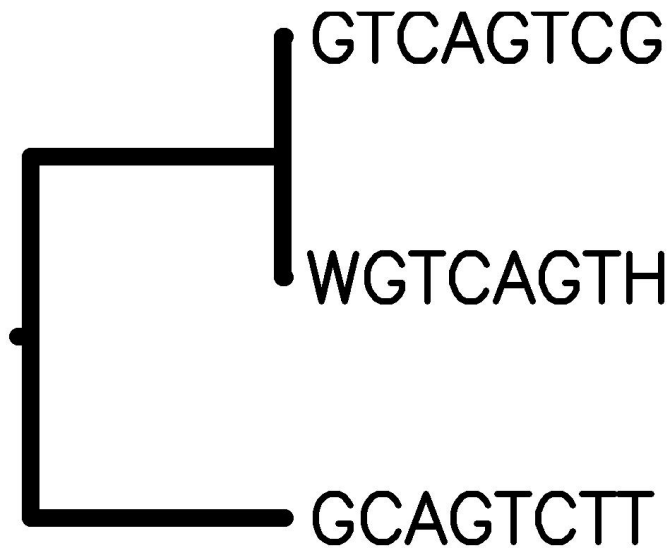
## Motif Tree

Tree (drawn by [Phylip](#))

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

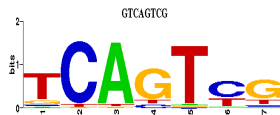
Input Motif

Best match in  
JASPAR\_Fams



## Motif Similarity Matches

GTCAGTCG



*forward*

*reverse compliment*

*Name*

*E value*

*Alignment*

*Motif*

TRP-CLUSTER\_Myb

5.5607e-03

CGACTGA-  
CAACNGYC



bZIP\_Fos

6.7298e-03

CGACTGA-  
TGANTCAC



ZN-FINGER\_C2H2\_sna 1.2481e-02

CGACTGA  
CACCTG-



HOMEOPB1

1.9282e-02

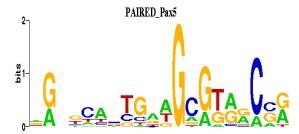
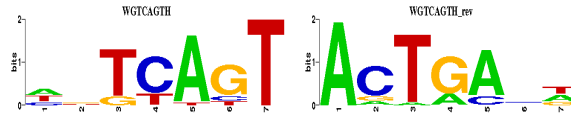
--CGACTGA--  
NTTGATTGATNN



PAIRED\_Pax5

2.3492e-02

-----TCAGTCG-----  
 YSGYYMCGCWNCRNNNNNCN

**WGTCAGTH***forward**reverse complement**Name**E value**Alignment**Motif*

bZIP\_bZIP910

7.9267e-04

-NNTCAGT  
 ACGTCAK-



bZIP\_TCF11-MafG

7.4938e-03

ACTGANN  
 NATGAC-



bZIP\_Fos

7.8534e-03

--ACTGANN  
 TGANTCAC-



bZIP\_TGA1a

1.9289e-02

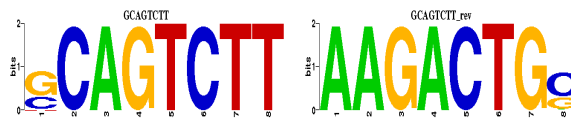
ACTGANN--  
 --TGACGTN



bHLH\_Hand1-Tcf2a

2.6448e-02

-NNTCAGT--  
 NWNCCAGAYN

**GCAGTCTT***forward**reverse complement**Name**E value**Alignment**Motif*

HMG\_SOX9

1.7780e-02

GCAGTCTT-  
 CYATTGTN



# Stamp Results

04/19/15

bZIP\_TCF11-MafG 2.8714e-02

GCAGTCTT-  
---GTCATN



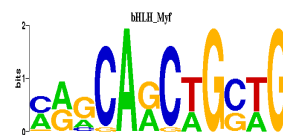
HOMEO\_NKX3-1 7.0672e-02

GCAGTCTT  
TAAGTAT-



bHLH\_Myf 8.0531e-02

--GCAGTCTT--  
CAGCAGYTGCYK



bZIP\_Ddit3-Cebpa 8.4274e-02

AAGACTGC----  
GSNATTGCAYNN



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