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[Input file: 4 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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Multiple Alignment

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

TGTCAAAA:	-TGTCAAAA-
ACGTTGCC:	--GGCAACGT
ATGGCAAC:	ATGGCAAC--
TGGCAACG:	-TGGCAACG-

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



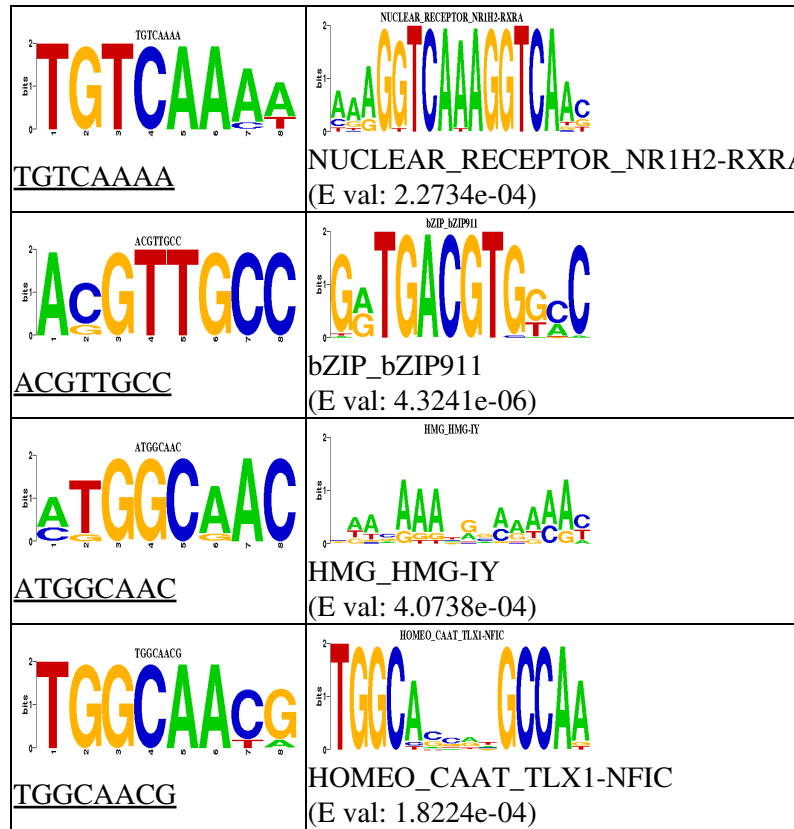
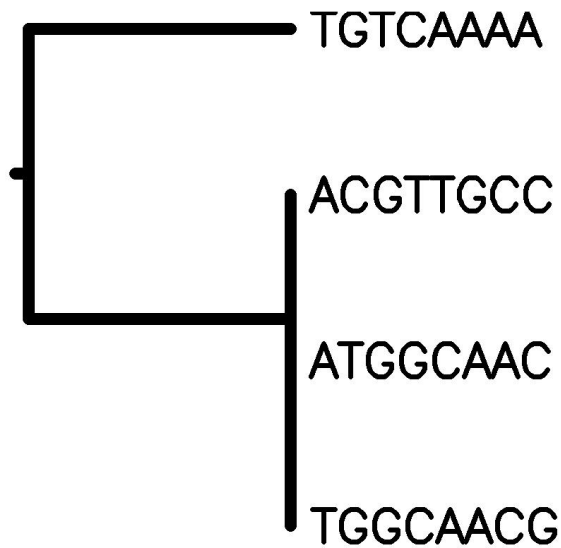
Motif Tree

Tree (drawn by [Phylip](#))

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

Input Motif

Best match in
JASPAR_Fams



Motif Similarity Matches

TGTCAAAA



forward



reverse compliment

Name

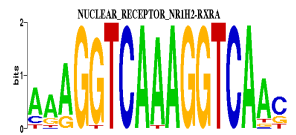
E value

Alignment

Motif

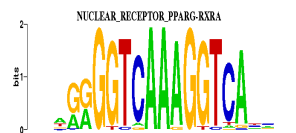
NUCLEAR_RECEPTOR_NRIH2-RXRA 2.2734e-04

-----TTTTGACA---
STTGACCTTTGACCTTT



NUCLEAR_RECEPTOR_PPARG-RXRA 4.1232e-04

-----TGTCAAAA-----
NNNGRGGTCAAAGGTCANN



NUCLEAR_RECEPTOR_HNF4A

6.3196e-03

----TTTTGACA-
TGNMCTTTGNNCY



Stamp Results

04/19/15

bZIP_TCF11-MafG

7.0363e-03

TGTCAAAA
-GTCATN-



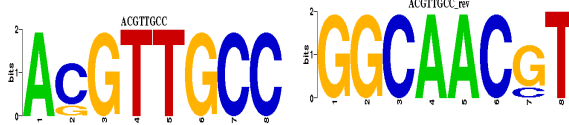
FORKHEAD_FOXD1

7.4041e-03

-TTTTGACA
NTGTTTAC-



ACGTTGCC



forward

reverse compliment

Name

E value

Alignment

Motif

bZIP_bZIP911

4.3241e-06

GGCAACGT----
GGCCACGTCAYC



HOME0_CAAT_TLX1-NFIC

7.1793e-04

--GGCAACGT----
TTGGCNNNSTGCCA



AP2_ABI4

3.3870e-03

---GGCAACGT
NGNNGCRSCG-



NUCLEAR_RECEPTOR_HNF4A

4.3568e-03

--GGCAACGT---
RGNNCAAAGKNCA



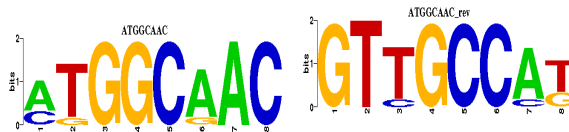
bZIP_EMBP1

4.5875e-03

GGCAACGT--
--CCACGTST



ATGGCAAC



forward

reverse compliment

TGGCAACG

forward

reverse complement

4

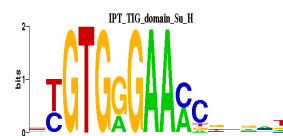
Stamp Results

04/19/15

IPT_TIG_domain_Su_H

1.2086e-02

-----CGTTGCCA---
NNNNNGKTTCCCACRN



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STAMP is written by Shaun Mahony