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Input file: 2 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".

[Download results as a PDF](#)

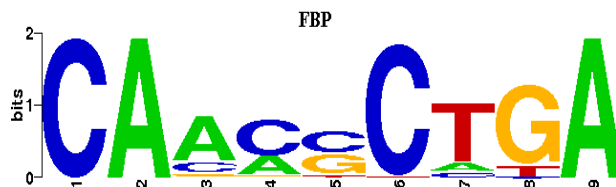
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Multiple Alignment

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

| | |
|-----------|-----------|
| TCAGCTKT: | -AMAGCWGA |
| CAACCCTG: | CAACCCTG- |

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

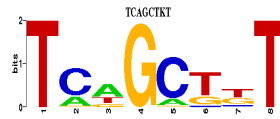
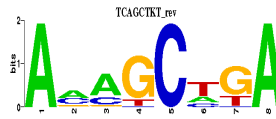


Motif Tree

NO TREE (too few input motifs)

Motif Similarity Matches

TCAGCTKT

*forward**reverse compliment**Name**E value**Alignment**Motif*

ZN-FINGER_DOF_MNB1A 4.3186e-05

AMAGCWGA
AAAGN---

ZN-FINGER_DOF_PBF 6.4789e-05

AMAGCWGA
AAAGY---

ZN-FINGER_DOF_Dof2 1.8384e-04

TCWGCCTKT
--NGCTTT

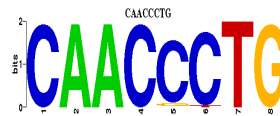
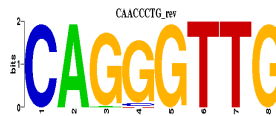
ZN-FINGER_DOF_Dof3 1.1016e-03

TCWGCCTKT
--NRCTTT

bZIP_MAF_Mafb 1.7065e-03

AMAGCWGA---
---GCTGANN

CAACCCTG

*forward**reverse compliment**Name**E value**Alignment**Motif*

ZN-FINGER_C2H2_Roaz 3.5880e-05

-CAACCCTG-----
GNMMCCYTRGGKKSC

-_BRCA1

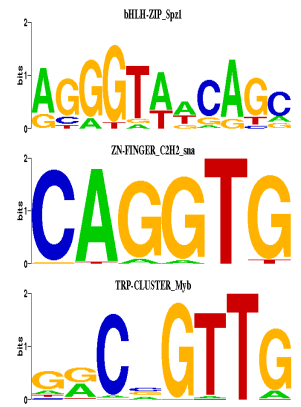
1.1482e-04

-CAACCCTG
NCAACNS--

Stamp Results

04/19/15

| | | |
|--------------------|------------|------------------------------|
| bHLH-ZIP_Spz1 | 3.4807e-03 | CAGGGTTG---- -AGGGTAWCAGC |
| ZN-FINGER_C2H2_sna | 6.5189e-03 | CAACCCTG --CACCTG |
| TRP-CLUSTER_Myb | 7.6999e-03 | CAGGGTTG GRCNGTTG |



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 STAMP is written by Shaun Mahony