

Jump to: [Multiple Alignment](#) [Motif Tree](#) [Motif Matching](#)

Input file: 9 motifs loaded

Settings: Metric=PCC, Alignment=SWU, Gap-open=1000, Gap-extend=1000, -nooverlapalign

Multiple Alignment=IR, Tree=UPGMA, Matching against: Place

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

[Download results as a PDF](#)

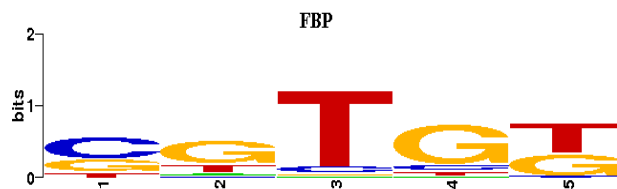
[Click here to run STAMP again.](#)

## Multiple Alignment

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

```
matrix:          --GNNACGTGTC-----
matrix_v2:       ---GNCGGNGNSG-----
matrix_v3:       GTCCCGGTTG-----
matrix_v4:       -----TTTTTWTITT--
matrix_v5:       --CTNMC GTGGC-----
matrix_v6:       -TTYTTTTTCT-----
matrix_v7:       ---RTACGTGTWC-----
matrix_v8:       -----ATATATATAT-
matrix_v9:       -----TGGCNGCAGC
```

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



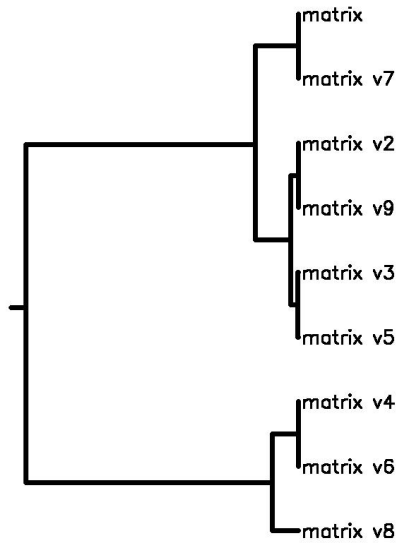
## Motif Tree

Input Motif

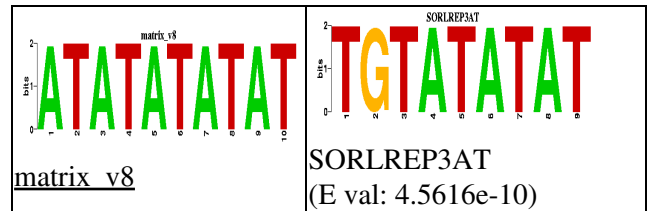
Best match in Place

Tree (drawn by **Phylip**)

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

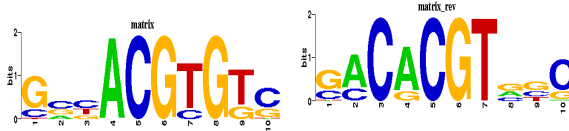


<p><u>matrix</u></p>	<p>ABRETAEM (E val: 2.1094e-14)</p>
<p><u>matrix v7</u></p>	<p>ZDNAFORMINGATCAB1 (E val: 2.2084e-09)</p>
<p><u>matrix v2</u></p>	<p>ABRECE1HVA22 (E val: 2.5130e-06)</p>
<p><u>matrix v9</u></p>	<p>GCCCORE (E val: 8.5150e-08)</p>
<p><u>matrix v3</u></p>	<p>ANAERO5CONSENSUS (E val: 1.8447e-06)</p>
<p><u>matrix v5</u></p>	<p>AUXRETGA2GMGH3 (E val: 5.9512e-09)</p>
<p><u>matrix v4</u></p>	<p>minus314MOTIFZMSBE1 (E val: 2.7167e-13)</p>
<p><u>matrix v6</u></p>	<p>TL1ATSAR (E val: 1.4861e-08)</p>



## Motif Similarity Matches

matrix



*forward*

*reverse compliment*

Name	E value	Alignment	Motif
ABRETAEM	2.1094e-14	GNNACGTGTC- GCCACGTGTCC	
ABREBNNAPA	1.2268e-13	-GACACGTNNC- GGACACGTGGCG	
HY5AT	1.2268e-13	-GNNACGTGTC- TGCCACGTGTCA	
GBOXLERBCS	2.1412e-12	GACACGTNNC -MCACGTGGC	
ACGTROOT1	8.2907e-12	GNNACGTGTC GCCACGTGGC	
SGBFGMGMAUX28	2.4035e-11	GNNACGTGTC TCCACGTGTC	
EMBP1TAEM	2.4583e-10	GACACGTNNC --CACGTGGC	
ABADESI2	4.0957e-10	GNNACGTGTC- GCCACGCGTCC	

ABREDISTBBNAPA 6.1192e-10

GACACGTNNC  
GACAAGTGGC

GBOX10NT

9.0524e-10

GACACGTNNC  
GCCACGTGCC

matrix\_v7



forward



reverse compliment

Name

E value

Alignment

Motif

ZDNAFORMINGATCAB1

2.2084e-09

RTACGTGTWC  
ATACGTGT--

WARBNEXTA

2.8132e-09

-----GWACACGTAY  
ACACGTTTTATAACACGTAC

ACGTOSGLUB1

2.9244e-09

GWACACGTAY  
---CACGTAC

ABREMOTIFAOSOSEM

1.7893e-08

GWACACGTAY  
-GACACGTA-

ACGTABREMOTIFAOSOSEM 1.7893e-08

GWACACGTAY  
-GACACGTA-

ABREATRD22

8.8772e-07

RTACGTGTWC  
RYACGTGGYR

ABRE2HVA22

1.0389e-06

GWACACGTAY-  
-GACACGTGCG

## Stamp Results

10/01/13

ACEATCHS

1.0557e-06

—RTACGTGTWC  
TCTACGTGTC—



GADOWNAT

1.2261e-06

GWACACGTAY  
—GACACGT—



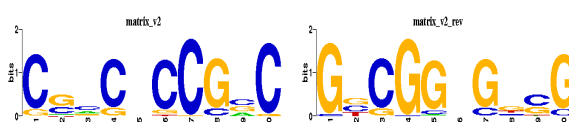
QARBNEXTA

1.2261e-06

GWACACGTAY  
—ACACGTT—



matrix\_v2

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

ABRECE1HVA22

2.5130e-06

GNCGGNGNSG  
—CCGGTGGCA



GCCCORE

8.0967e-06

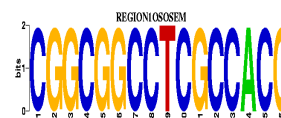
GNCGGNGNSG  
---GGCGGC—



REGION1OLOSEM

6.6354e-05

—GNCGGNGNSG-----  
CGGCGGCCTCGCCACG



DRECRTCOREAT

8.0771e-05

GNCGGNGNSG  
GTCGGY----



AGCBOXNPGLB

1.2282e-04

GNCGGNGNSG  
---GGCGGCT



BOXBPSAS1

5.0970e-04

—GNCGGNGNSG---  
AAACGGTGTCTGTTT



CBFHV

1.0175e-03

GNCGGNGNSG  
GTCGRY----



## Stamp Results

10/01/13

DRE2COREZMRAB17 1.5316e-03

GNCGGNGNSG  
GTCGGT----

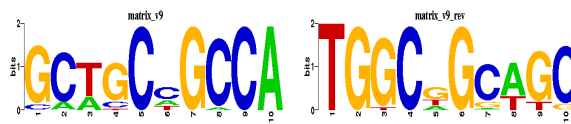
SORLIP1AT 2.0299e-03

GNCGGNGNSG  
----GTGGC-

GRAZMRAB28 2.1581e-03

GNCGGNGNSG--  
--GGCGGCATG

matrix\_v9

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

GCCCORE

8.5150e-08

TGGCNGCAGC  
-GGCGGC---

GRAZMRAB28

5.2396e-07

TGGCNGCAGC  
-GGCGGCATG

AGCBOXNPGLB

1.5180e-06

TGGCNGCAGC  
-GGCGGCT--

E2FAT

3.7631e-05

TGGCNGCAGC  
-GGCGGGARA

E2FBNTRNR

5.1427e-05

TGGCNGCAGC  
--GCGGCAAA

OCTAMOTIF2

5.1427e-05

TGGCNGCAGC  
-CGCGGCAT-

ANAERO2CONSENSUS 1.5638e-04

GCTGCNGCCA  
GCTGCT----

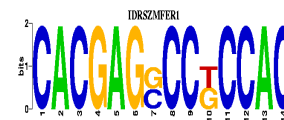
GREGIONNTPRB1B 1.9994e-04

TGGCNGCAGC-----  
TGGCGGCTCTTATCTCACGTGATG



IDRSZMFER1 2.3831e-04

---GCTGCNGCCA-  
CACGAGSCCKCCAC

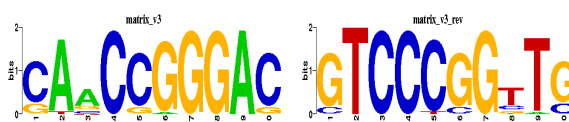


EREGCC 5.7907e-04

TGGCNGCAGC--  
-GGCGGCTCTTA



matrix\_v3

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

ANAERO5CONSENSUS 1.8447e-06

CAACCGGGAC  
-AACAGGGAA



DRE1COREZMRAB17 1.4875e-05

GTCCCGGTTG  
-TCTCGGT--



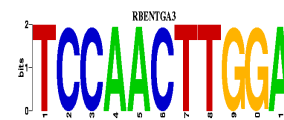
BOXCPSAS1\_2 7.1655e-05

-----CAACCGGGAC  
AAGAAGTGTGTACCGGGA-



RBENTGA3 1.8723e-04

--CAACCGGGAC  
TCCAAC TTGGA-



AMMORESVDCRNIA1 4.3532e-04

CAACCGGGAC-  
--CCCGGGGCC



ABRECE1HVA22 5.8898e-04

GTCCCGGTTG--  
---CCGGTGGCA






BS1EGCCR 6.2228e-04

CAACCGGGAC  
--AGCGGG--

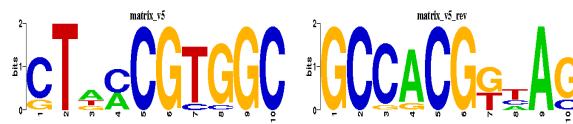









## Stamp Results

10/01/13

SITEIOSPCNA	9.3065e-04	CAACCGGGAC CCACCTGG--	
MYBPZM	1.0300e-03	GTCCCGGTTG-- -----GGTWGG	
VSF1PVGRP18	1.3089e-03	CAACCGGGAC CAACGGAGC-	

matrix\_v5

*forward**reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AUXRETGA2GMGH3	5.9512e-09	GCCACGKNAG GCCACGTCA-	
BOXIIPCCHS	6.9324e-08	GCCACGKNAG GCCACGT---	
ABREA2HVA1	5.6041e-07	GCCACGKNAG GCCACGTAGG	
ABREATCONSENSUS	1.0888e-06	GCCACGKNAG GCCACGTR--	
EMBP1TAEM	1.0888e-06	GCCACGKNAG GCCACGTG--	
HEXAT	1.0888e-06	GCCACGKNAG -CCACGTCA-	
LRENPCABE	1.0888e-06	-GCCACGKNAG TGCCACGT---	



## Stamp Results

10/01/13

UPRMOTIFIAT

1.0888e-06

CTNMC GTGGC  
-TGACGTGG-

ACGTABREMOTIFA2OSEM 1.8462e-06

CTNMC GTGGC  
---ACGTGKC

ABRE2HVA1

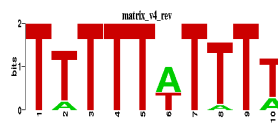
5.1126e-06

--GCCACGKNAG  
CCGCCACGTAGG

matrix\_v4



forward



reverse compliment

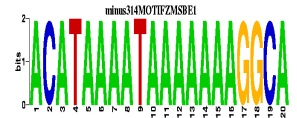
Name

E value

Alignment

Motif

minus314MOTIFZMSBE1 2.7167e-13

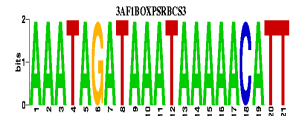
-----AAA WAAAAA-----  
ACATAAAATAAAAAAAGGCA

MARTBOX

1.1283e-10

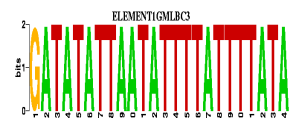
AAA WAAAAA  
AAWAAWAWAA

3AF1BOXPSRBCS3 9.8288e-10

-----AAA WAAAAA-----  
AAATAGATAAATAAAAAACATT

ELEMENT1GMLBC3

2.8420e-09

---AAA WAAAAA-----  
TATAAAATAAAATATTAATATATC

MARARS

2.2997e-08

AAA WAAAAA-  
WAAAYATAAAW

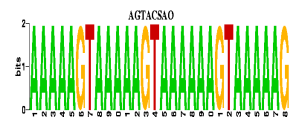
AT1BOX



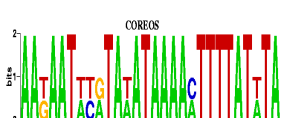
3.4320e-08

AAA WAAAAA-----  
--AATAAAATATT

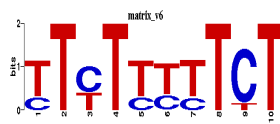
AGTACSAO


3.6489e-08

-TTTTTWTTTT-----  
CTTTTACTTTTTTACTTTTTACTTTTT

POLASIG1	2.0707e-07	AAAAWAAAAA --AATAAA--	
TATABOX5	2.0707e-07	AAAAWAAAAA -AAATAA---	
COREOS	4.9866e-07	-----AAAAWAAAAA----- AAKAATWYRTAWATAAAAAMTTTTATWTA	



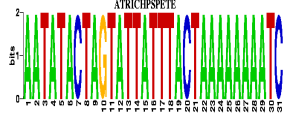
matrix\_v6

*forward**reverse compliment*

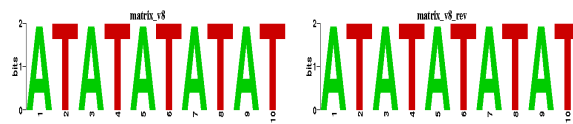
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
TL1ATSAR	1.4861e-08	-AGAAAAARAA CTGAAGAAGAA	
GT1GMSCAM4	3.1819e-07	AGAAAAARAA -GAAAAA---	
CTRMCAV35S	7.5055e-07	AGAAAAARAA AGAGAGAGA-	
PYRIMIDINEBOXHVEPB1	8.0887e-06	AGAAAAARAA GGAAAAA---	
XYLAT	1.2866e-05	TTYTTTTTCT TTCTTTGT--	
TCA1MOTIF	1.7997e-05	-AGAAAAARAA AAGAAGATGA-	
POLLEN1LELAT52	2.9155e-05	AGAAAAARAA AGAAA-----	


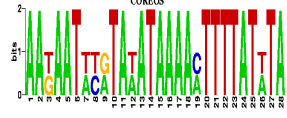





## Stamp Results

10/01/13

MARTBOX	4.0516e-05	AGAAAAARAA AAWAAWAWAA	
GAGA8HVBKN3	1.0550e-04	—AGAAAAARAA— GAGAGAGAGAGAGAGA	
ATRICHSPPETE	1.6844e-04	-----AGAAAAARAA-- AATATACTAGTATTATTACTAAAAAAATC	

## matrix\_v8

*forward**reverse compliment*

Name	E value	Alignment	Motif
SORLREP3AT	4.5616e-10	ATATATATAT ATATATAACA—	
COREOS	5.0932e-08	-----ATATATATAT----- TAWATAAAAKTTTTATWTAYRWATTMTT	
D2GMAUX28	6.0504e-08	ATATATATAT-- ATTTATATAAAT	
TATAPVTRNALEU	1.1300e-07	ATATATATAT —TATATAAA—	
SEF1MOTIF	3.6190e-07	ATATATATAT ATATTTA—	
AT1BOX	5.9575e-07	—ATATATATAT— AATATTTTTATT	
GLUTEBP2OS	1.1690e-06	--ATATATATAT----- ACTTATATCTATTGAGCAT	

# Stamp Results

10/01/13

TATABOX4 1.1714e-06

ATATATATAT  
TTATATA---



TATABOX1 4.7121e-06

ATATATATAT  
GTATTTATAG



TATABOX2 1.2359e-05

ATATATATAT  
ATTTATA---




---

Sequence logo generation powered by [weblogo](#)  
STAMP is written by Shaun Mahony