

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

Input file: 10 motifs loaded

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

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

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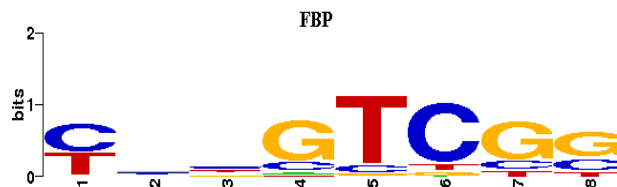
[Click here to run STAMP again.](#)

## Multiple Alignment

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

```
matrix:          -MCACGTGTC-----
matrix_v2:       -----GGNCGGYGSG--
matrix_v3:       -----TTTTTWTTTT
matrix_v4:       ---NCGCGTNGGC-----
matrix_v5:       -----GGGTCCCAC----
matrix_v6:       -----GTGTCGGYCN---
matrix_v7:       ---CTTAATCGCG-----
matrix_v8:       -----YYTYTCITTY----
matrix_v9:       CYNCTCCCTC-----
matrix_v10:      -----AGGTCGGTT----
```

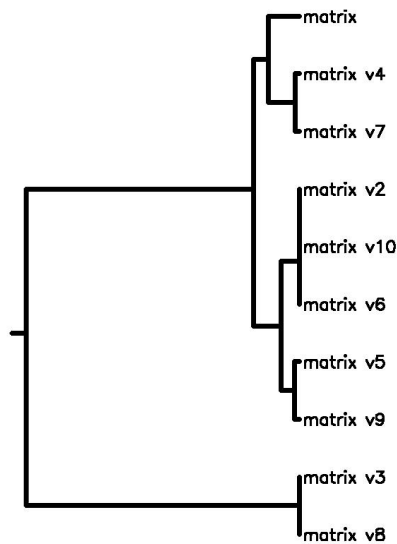
**Familial Profile:**  
([click for matrix](#))



## Motif Tree

Tree (drawn by **Phylip**)

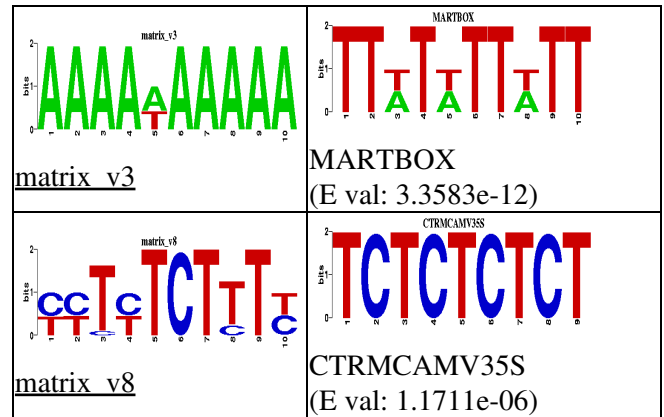
[Click here for Newick-format tree \(viewable with MEGA\)](#)



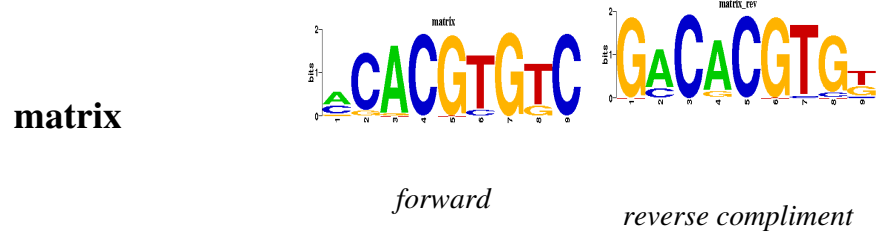
## Input Motif







## Best match in Place





<p><u>matrix</u></p>	<p>SGBFGMGMAUX28 (E val: 1.5404e-12)</p>
<p><u>matrix_v4</u></p>	<p>ABREMOTIFIHOSRAB16B (E val: 1.5608e-05)</p>
<p><u>matrix_v7</u></p>	<p>WUSATAg (E val: 9.4463e-06)</p>
<p><u>matrix_v2</u></p>	<p>ACIPVPAL2 (E val: 1.9914e-07)</p>
<p><u>matrix_v10</u></p>	<p>DRE2COREZMRAB17 (E val: 1.1768e-08)</p>
<p><u>matrix_v6</u></p>	<p>LTREATLTI78 (E val: 1.4904e-08)</p>
<p><u>matrix_v5</u></p>	<p>SITEIIBOSPCNA (E val: 1.0533e-11)</p>
<p><u>matrix_v9</u></p>	<p>BOXCPSAS1_3 (E val: 2.1774e-05)</p>



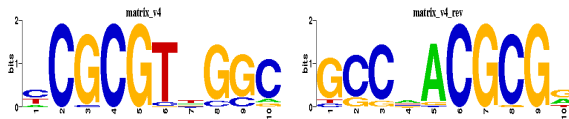
## Motif Similarity Matches









Name	E value	Alignment	Motif
SGBFGMGMAUX28	1.5404e-12	GACACGTGK- GACACGTGGA	
ABRETAEM	8.3442e-12	-GACACGTGK- GGACACGTGGC	
GBOXLERBCS	1.0828e-11	GACACGTGK GCCACGTGK	
ABREBNNAPA	2.7848e-11	-GACACGTGK-- GGACACGTGGCG	
HY5AT	2.7848e-11	-GACACGTGK-- TGACACGTGGCA	
ABRE2HVA22	3.5828e-11	GACACGTGK- GACACGTGCG	

GADOWNAT	1.1921e-10	GACACGTGK GACACGT--	
ACGTABREMOTIFA2OSEM	7.5927e-10	GACACGTGK GMCACGT--	
ABREMOTIFAOSOSEM	3.0232e-09	GACACGTGK GACACGTA-	
ACGTABREMOTIFAOSOSEM	3.0232e-09	GACACGTGK GACACGTA-	

matrix\_v4

*forward**reverse complement*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ABREMOTIFIHOSRAB16B	1.5608e-05	-NCGCGTNGGC GCCGCGTGGC-	
BP5OSWX	1.8434e-05	NCGCGTNGGC -CACGTTG--	
ABREA2HVA1	4.5325e-05	-NCGCGTNGGC GCCACGTAGG-	
NONAMERMOTIFTAH3H4	9.9426e-05	NCGCGTNGGC-- ---CGTTGGATG	
ABREAZMRAB28	1.3307e-04	GCCNACGCGN- -CCCACGTGGC	
CPRFPCCHS	1.8406e-04	NCGCGTNGGC CCACGTGGCC	

## Stamp Results

10/01/13

ABRE2HVA1

2.4331e-04

---NCGCGTNGGC  
CCGCCACGTAGG--



CE3OSOSEM

2.4436e-04

---NCGCGTNGGC  
GACACGCGTT---



GCAACREPEATZMZEIN

2.5373e-04

-NCGCGTNGGC  
GTTGCGTTGC-



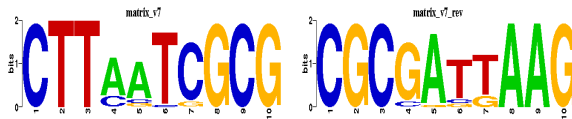
ABRERATCAL

3.5506e-04

NCGCGTNGGC  
NCRCGTK---



matrix\_v7

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

WUSATAg

9.4463e-06

CGCGATTAAAG  
--CCATTAA--



BOX2PVCHS15

1.3075e-04

---CTTAATCGCG-  
ATATTTAATCACAG



PE2FNTRNR1A

2.3589e-04

-CGCGATTAAAG  
GCGCGAAT---



GT1CORE

5.8490e-04

CTTAATCGCG  
-TTAACC---



POLASIG2

9.0088e-04

CTTAATCGCG  
TTTAATT---



TATABOX3

9.0088e-04

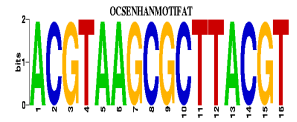
CTTAATCGCG  
ATTAATA---



TGA1ANTPR1A 1.0120e-03

CTTAATCGCG-----  
CGTCATCTCGATGACG

OCSENHANMOTIFAT 1.2506e-03

-----CGCGATTAAG-  
ACGTAAGCGCTTACGT

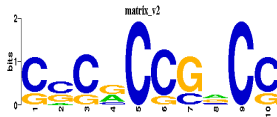
OCSGMHSP26A 2.7070e-03

---CTTAATCGCG-----  
TTACGTAATCTCTTACATCA

ANAERO3CONSENSUS 4.0073e-03

CGCGATTAAG  
-GTGATGA--

matrix\_v2

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

ACIPVPAL2

1.9914e-07

CSCRCCGNCC  
CCCACCTACC

DRECRTCOREAT

1.6957e-06

GGNCGGYGSG  
-GTCGGY---

CBFHV

3.8169e-05

GGNCGGYGSG  
-GTCGRY---

DRE2COREZMRAB17 1.1082e-04

GGNCGGYGSG  
-GTCGGT---

LTRECOREATCOR15 1.4883e-04

GGNCGGYGSG  
-GTCGG----

ACIPVPAL2

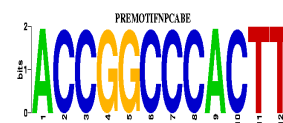
3.5592e-04

CSCRCCGNCC---  
-CCACCAACCCCC

## Stamp Results

10/01/13

PREMOTIFNPCABE 7.1929e-04

-CSCRCCGNCC-  
ACCGGCCCACTT

GCBP2ZMGAPC4 8.3980e-04

CSCRCCGNCC  
CGGGCCCAC-

ABRECE1HVA22 8.7808e-04

GGNCGGYGSG-  
--CCGGTGGCA

LTREATLTI78 9.8872e-04

GGNCGGYGSG  
TGTCGGT---

matrix\_v10

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

DRE2COREZMRAB17 1.1768e-08

AGGTCGGTT  
--GTCGGT-

DRECRTCOREAT 4.9478e-07

AGGTCGGTT  
--GTCGGY-

LTREATLTI78 5.1971e-07

AGGTCGGTT  
-TGTCGGT-

DREDR1ATRD29AB 1.6524e-06

AGGTCGGTT  
ATGTCGGTA

LTRECOREATCOR15 3.6033e-06

AGGTCGGTT  
--GTCGG--

CBFHV

1.3133e-05

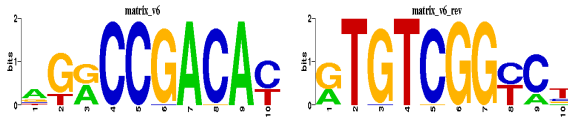
AGGTCGGTT  
--GTCGRY-







## Stamp Results

10/01/13

MYBPLANT	2.7252e-05	AGGTCGGTT -GKTWGGTK	
MREATCHS	4.6694e-05	AGGTCGGTT--- TGGTAGGTTAGA	
QELEMENTZM13	1.7163e-04	AACCGACCT ---TGACCT	
ACIPVPAL2	3.4248e-04	AGGTCGGTT-- -GGTAGGTGGG	

matrix\_v6

*forward**reverse complement*

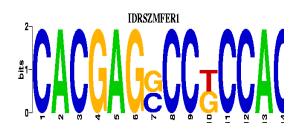
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
LTREATLTI78	1.4904e-08	GTGTCGGYCN -TGTCGGT--	
DRECRTCOREAT	2.5497e-08	GTGTCGGYCN --GTCGGY--	
DREDR1ATRD29AB	4.0169e-07	GTGTCGGYCN ATGTCGGTA-	
CBFHV	9.7835e-07	NGRCCGACAC --RYCGAC--	
DRE2COREZMRAB17	1.2719e-06	GTGTCGGYCN --GTCGGT--	
LTRECOREATCOR15	5.8448e-06	GTGTCGGYCN --GTCGG---	



IDRSZMFER1

1.2999e-05

----NGRCCGACAC  
CACGAGSCCKCCAC



CGTGTSPHZMC1

2.4069e-05

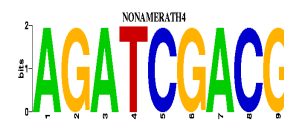
-----NGRCCGACAC-  
ATGCATGGACGACACG



NONAMERATH4

2.6972e-05

NGRCCGACAC  
AGATCGACG-



DRE1COREZMRAB17 1.8036e-04

GTGTCGGYCN  
-TCTCGGT--



matrix\_v5

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

SITEIIBOSPCNA

1.0533e-11

GTGGGACCC  
GTGGGACCA



GGTCCCATGMSAUR 6.2301e-09

GGGTCCAC  
-GGTCCAT



AUXREPSIAA4

1.8757e-07

GTGGGACCC  
ATGGGACM-



GCBP2ZMGAPC4

5.2051e-07

GGGTCCAC  
CGGGCCAC



BOXCPSAS1\_3

1.3303e-06

GTGGGACCC  
GTGGGAG--



NDEGMSAUR

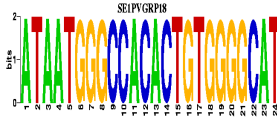


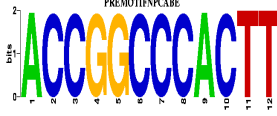
5.2314e-05

-----GGGTCCAC  
CCATATGCCATGTCTCTCAATTGGTCCCAT

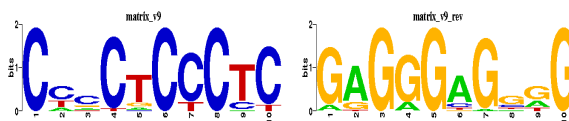








## Stamp Results





10/01/13

SE1PVGRP18	2.2912e-04	-----GGGTCCCAC----- ATAATGGGCCACACTGTGGGGCAT	
SITEIIAOSPCNA	2.5257e-04	-GGGTCCCAC ACGGGCCCA-	
RNFG2OS	3.2980e-04	---GGGTCCCAC--- CCAGGGGCACACTGG	
PREMOTIFNPCABE	1.8406e-03	--GTGGGACCC- AAGTGGGCCCGT	

matrix\_v9

*forward**reverse compliment*

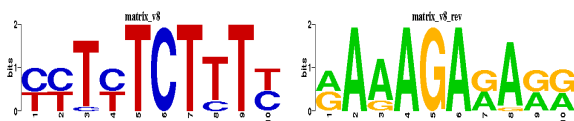
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
BOXCPSAS1_3	2.1774e-05	GAGGGAGNRG GTGGGAG---	
SORLIP5AT	2.7355e-05	CYNCTCCCTC ---CTCACTC	
SBOXATRBCS	6.5105e-05	GAGGGAGNRG --TGGAGGTG	
CTRMCAV35S	1.7976e-04	-GAGGGAGNRG AGAGAGAGA--	
AMMORESIIUDCRNIA1	7.2724e-04	CYNCTCCCTC ACCCTWCC--	
GAGA8HVBKN3	1.0952e-03	CYNCTCCCTC----- TCTCTCTCTCTCTCTC	

Protein	Information content (bits)	Sequence logo	Sequence logo (bits)
PALBOXAPC	1.2804e-03	GAGGGAGNRG ---GGACGG-	
GAGAGMGS1	1.8349e-03	CYNCTCCCTC----- TCTCTCTCTCTCTCTCTC	
ACIPVPAL2	3.2951e-03	GAGGGAGNRG-- --GGTAGGTGGG	
E2FAT	4.7123e-03	-GAGGGAGNRG GGCGGGARA--	



Name	E value	Alignment	Motif
MARTBOX	3.3583e-12	AAAAWAAAAA AAWAAWAWAA	
minus314MOTIFZMSBE1	4.4406e-12	-----TTTTTWTTTT----- TGCCTTTTTTTTATTTTATGT	
3AF1BOXPSRBCS3	1.6052e-08	----TTTTTWTTTT----- AATGTTTTTATTTATCTATTT	
ELEMENT1GMLBC3	2.8745e-08	---AAAWAAAAA----- TATAAAATAAAATATTAATATATC	
AGTACSAO	3.1090e-07	--AAAWAAAAA----- AAAAAAGTAAAAAGTAAAAAGTAAAAAG	
AT1BOX	4.1706e-07	AAAAWAAAAA----- --AATAAAAATATT	

## 10/01/13

**matrix\_v8**

*reverse compliment*

12

# Stamp Results

10/01/13

NODCON2GM 1.1141e-04

RAAAGARARR  
--AAGAG---



OSE2ROOTNODULE 1.1141e-04

RAAAGARARR  
--AAGAG---



POLLEN1LELAT52 2.0026e-04

YYTYTCTTTY  
--TTTCT---



XYLAT 2.5931e-04

YYTYTCTTTY-  
---TTCTTTGT




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STAMP is written by [Shaun Mahony](#)