



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

Input file: 40 motifs loaded

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

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

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Multiple Alignment

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

```

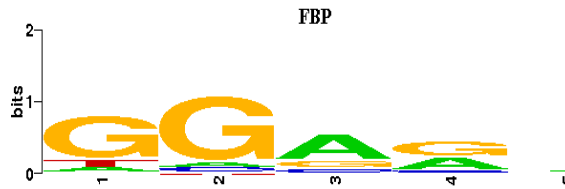
m1_c1_nGGAGGGAGn:   NGGAGGGAGN-----
m2_c2_rGGwGGGGmn:   ----NGGWGGGGAN--
m3_c3_nGGwGGGAAn:   NGGWGGGAAN-----
m4_c4_nyykGGGAGn:   NYTTGGGAGN-----
m5_c5_sCTGGGGrmn:   NCTGGGGRAN-----
m6_c5_nTkTGGrAn:    -NTKTGGGRAN----
m7_c6_nCAGGrArAn:   --NCAGGAGARN---
m8_c6_nCCTGGGmmn:   NCCTGGGMMN-----
m9_c7_nAAAAGAAAn:   -NAAAGAAAAN----
m10_c7_nCwTGGAAn:   -NCWTGGARAN----
m11_c8_nAGAGGrAGn:  NAGAGGRAGN-----
m12_c9_nwGGGGsTGn:  ---NTGGGGSTGN--
m13_c9_kGTGGGrGn:   -NGTGGGRGN-----
m14_c9_sCGGGGGCGs:  SCGGGGGCGN-----
m15_c10_nAGGCwGAGn: NAGGCwGAGN-----
m16_c10_sCGCGGGGn:  NCGCGGGGGN-----
m17_c10_nAGkGAGAmn: --NAGTGAGAMN---
m18_c11_nGrGsTsAGn: NGRGSTSAGN-----
m19_c11_nrrwGTGArn: NARWGTGAAN-----
m20_c11_nCGTGGGArn: NCGTGGGARN-----
m21_c12_nGCTGGGATk: NGCTGGGATN-----
m22_c12_nTTTTTAAAn: --NTTTAAAAAN---
m23_c13_nyyTCwGAGn: -NCTCWGARAN----

```

```

m24_c13_nrAGGrSAGn: --NGAGGRGAGN---
m25_c14_rGATGGGGr:  NGATGGGGN-----
m26_c14_nmTGGTGAAn: NMTGGTGAAN-----
m27_c14_nTTTCTGAAn: NTTCTGAAAN-----
m28_c15_nwmTGnAAAn: -NWMTGNAAAAN----
m29_c15_nAATkrrArn: NAATKRRARN-----
m30_c15_nAAGrGAArn: -NAAGRGAARN----
m31_c16_nCCTGGsCTs: -NCCTGGSCTN----
m32_c16_nCAGskGCmn: ----NKGCMCCTGN-
m33_c17_nTyTGTryTn: -NARCACARAN-----
m34_c17_CmTGTGCyn: ----NRGCACAAG--
m35_c18_nCAkGTGwsn: NCAGGTGWSN-----
m36_c19_nTktGGrsT:  -NTKTGGRNT-----
m37_c19_nGCTGGAGkn: -NGCTGGAGKN-----
m38_c19_nTGTGkGsCn: ----NGGCACACAN-
CSL_m1:                -YGTGGGAA-----
RelB-p52:              -----GGAAANCCCC
    
```

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

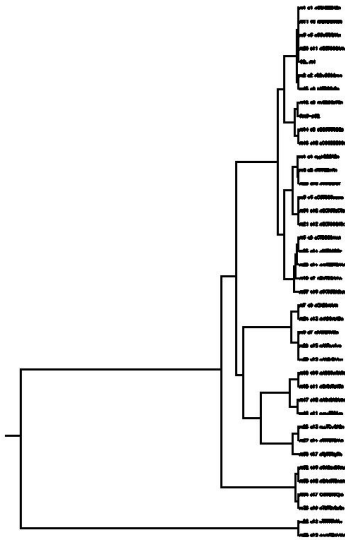


Motif Tree

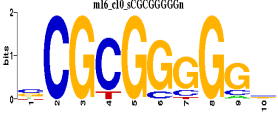







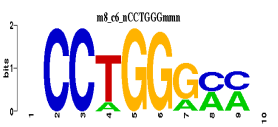

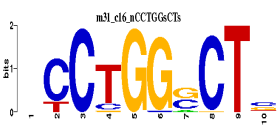

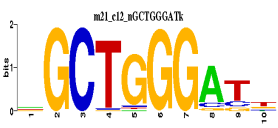



Tree (drawn by [Phylip](#))





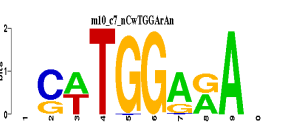

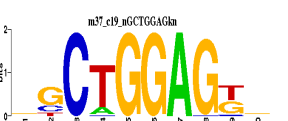









[Click here for Newick-format tree](#) (viewable with [MEGA](#))






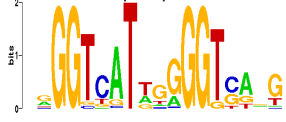









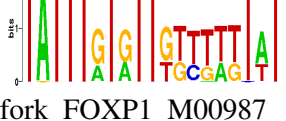
| Input Motif | Best match in TRANSFAC_Fams |
|--------------------------|--------------------------------------------------------------------------------------------------------------|
| <p>m1_c1_nGGAGGGAGn</p> | <p>CH_MAZ_M00649 CH_MAZ_M00649 (E val: 2.1096e-06)</p> |
| <p>m11_c8_nAGAGGrAGn</p> | <p>ETS_PU.1_M00658 ETS_PU.1_M00658 (E val: 1.2065e-06)</p> |









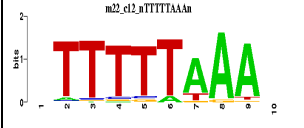
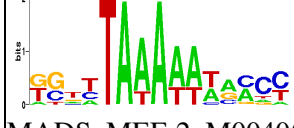




| | |
|-----------------------------------------------------|-------------------------------------------------------------------------|
| <p>m3_c3_nGGwGGGAAn</p> <p>m3_c3_nGGwGGGAAn</p> | <p>CH_MAZ_M00649</p> <p>CH_MAZ_M00649 (E val: 1.9191e-04)</p> |
| <p>m20_c11_nCGTGGGArn</p> <p>m20_c11_nCGTGGGArn</p> | <p>CH_Egr-1_M00243</p> <p>CH_Egr-1_M00243 (E val: 7.1141e-06)</p> |
| <p>CSL_m1</p> <p>CSL_m1</p> | <p>CH_Ik-1_M00086</p> <p>CH_Ik-1_M00086 (E val: 8.5834e-08)</p> |
| <p>m2_c2_rGGwGGGGmn</p> <p>m2_c2_rGGwGGGGmn</p> | <p>CH_MAZ_M00649</p> <p>CH_MAZ_M00649 (E val: 1.1250e-05)</p> |
| <p>m13_c9_kGTGGGrGn</p> <p>m13_c9_kGTGGGrGn</p> | <p>CH_KROX_M00982</p> <p>CH_KROX_M00982 (E val: 9.9241e-06)</p> |
| <p>m12_c9_nwGGGGsTGn</p> <p>m12_c9_nwGGGGsTGn</p> | <p>CC_GBF_M00633</p> <p>CC_GBF_M00633 (E val: 1.8441e-09)</p> |
| <p>RelB-p52</p> <p>RelB-p52</p> | <p>Rel_c-Rel_M00053</p> <p>Rel_c-Rel_M00053 (E val: 2.1716e-13)</p> |
| <p>m14_c9_sCGGGGGCGs</p> <p>m14_c9_sCGGGGGCGs</p> | <p>CH_KROX_M00982</p> <p>CH_KROX_M00982 (E val: 1.0876e-07)</p> |

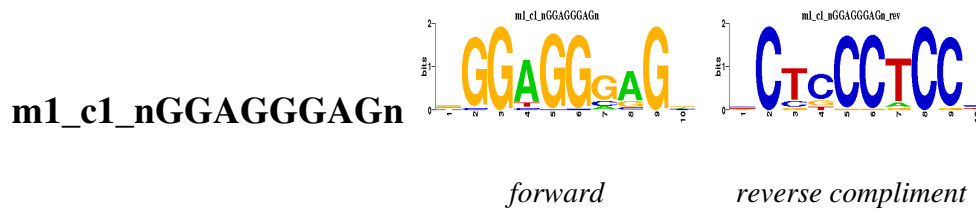
| | |
|-----------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|
|  <p>m16_c10_sCGCGGGGn</p> |  <p>CH_KROX_M00982 (E val: 4.0740e-05)</p> |
|  <p>m4_c4_nyykGGGAGn</p> |  <p>CH_Lyf-1_M00141 (E val: 1.4301e-07)</p> |
|  <p>m6_c5_nTkTGGrrAn</p> |  <p>CH_Ik-1_M00086 (E val: 1.2269e-05)</p> |
|  <p>m36_c19_nTkTGGrsT</p> |  <p>bHLH-ZIP_SREBP-1_M00221 (E val: 8.6209e-04)</p> |
|  <p>m8_c6_nCCTGGGmmn</p> |  <p>paired-homeo_Pax-6_M00979 (E val: 1.5669e-03)</p> |
|  <p>m31_c16_nCCTGGsCTs</p> |  <p>bHLH-ZIP_SREBP-1_M00749 (E val: 1.3772e-03)</p> |
|  <p>m21_c12_nGCTGGGATk</p> |  <p>homeo_Pitx2_M00482 (E val: 6.8928e-05)</p> |
|  <p>m5_c5_sCTGGGGrmn</p> |  <p>CC_GBF_M00633 (E val: 4.6637e-04)</p> |
| | |

| | |
|-----------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------|
|  <p>m25_c14_rGATGGGGr</p> |  <p>CH_MZF1_M00084 (E val: 1.5591e-04)</p> |
|  <p>m26_c14_nmTGGTGAAn</p> |  <p>bZIP_LMAF_M01139 (E val: 5.1437e-03)</p> |
|  <p>m10_c7_nCwTGGArAn</p> |  <p>Rel_NF-kappaB_M00208 (E val: 1.3809e-03)</p> |
|  <p>m37_c19_nGCTGGAGkn</p> |  <p>CH_ADR1_M00048 (E val: 9.8619e-04)</p> |
|  <p>m7_c6_nCAGGrrArn</p> |  <p>CH+homeo_AREB6_M00412 (E val: 9.7125e-04)</p> |
|  <p>m24_c13_nrAGGrsAGn</p> |  <p>C6_GAL4_M00198 (E val: 3.1534e-04)</p> |
|  <p>m9_c7_nAAAGAAAAn</p> |  <p>HMG_STE11_M01005 (E val: 4.6453e-06)</p> |
|  <p>m29_c15_nAATkrrArn</p> |  <p>MADS_MADS-B_M00404 (E val: 3.1774e-04)</p> |
| | |

| | |
|------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|
|  <p>m30_c15_nAAGrGAArn</p> |  <p>CH_BLIMP1_M01066 (E val: 1.9198e-05)</p> |
|  <p>m15_c10_nAGGCwGAGn</p> |  <p>SMAD_SMAD3_M00701 (E val: 1.4983e-04)</p> |
|  <p>m18_c11_nGrGsTsAGn</p> |  <p>CC_PPAlpha-RXRalpha_M00518 (E val: 1.2752e-04)</p> |
|  <p>m17_c10_nAGkGAGAmn</p> |  <p>trp_IRF-1_M00747 (E val: 9.2072e-04)</p> |
|  <p>m19_c11_nrrwGTGArn</p> |  <p>trp_IRF_M00972 (E val: 3.1354e-06)</p> |
|  <p>m23_c13_nyyTCwGAGn</p> |  <p>trp_CDC5_M00361 (E val: 1.2354e-02)</p> |
|  <p>m27_c14_nTTTCTGAAAn</p> |  <p>bZIP_C-EBPgamma_M00622 (E val: 1.0564e-04)</p> |
|  <p>m33_c17_nTyTGTryTn</p> |  <p>fork_FOXP1_M00987 (E val: 8.5327e-06)</p> |
| | |

| | |
|-----------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|
|  <p>m32_c16_nCAGskGCmn</p> |  <p>bHLH_E12_M00693 (E val: 1.7723e-07)</p> |
|  <p>m35_c18_nCAkGTGwsn</p> |  <p>bHLH_myogenin_M00712 (E val: 4.0585e-05)</p> |
|  <p>m34_c17_CmTGTGCyn</p> |  <p>bHLH-ZIP_TFE_M01029 (E val: 5.3933e-05)</p> |
|  <p>m38_c19_nTGTGkGsCn</p> |  <p>bHLH_PCF2_M00948 (E val: 4.3632e-05)</p> |
|  <p>m22_c12_nTTTTTAAAn</p> |  <p>MADS_MEF-2_M00405 (E val: 1.0861e-06)</p> |
|  <p>m28_c15_nwmTGnAAAn</p> |  <p>POU_Oct-1_M00930 (E val: 1.3241e-05)</p> |



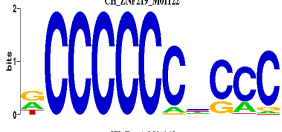


Motif Similarity Matches



Name E value Alignment Motif

Stamp Results

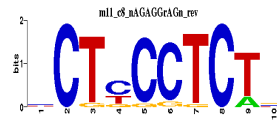
12/27/10

| | | | |
|---------------------|------------|---------------------------|-------------------------------------------------------------------------------------|
| CH_MAZ_M00649 | 2.1096e-06 | NCTCCCTCCN ---CCCTCCC |  |
| ETS_PU.1_M00658 | 3.2662e-05 | NGGAGGGAGN --GAGGAAG- |  |
| CH_ZNF219_M01122 | 2.6026e-04 | -NCTCCCTCCN NCCCCCNCCC |  |
| CH_Tra-1_M01048 | 3.2711e-03 | NCTCCCTCCN ---ACCWCCC |  |
| CC_Churchill_M00986 | 4.5470e-03 | NCTCCCTCCN -NNCCC---- |  |





m11_c8_nAGAGGrAGn



forward



reverse compliment

| <i>Name</i> | <i>E value</i> | <i>Alignment</i> | <i>Motif</i> |
|------------------|----------------|----------------------------|---------------------------------------------------------------------------------------|
| ETS_PU.1_M00658 | 1.2065e-06 | NCTYCCTCTN -CTTCCTC-- |  |
| ETS_Elf-1_M00746 | 2.1946e-05 | NCTYCCTCTN- AYTTCCTCTTN |  |
| ETS_Ets_M00971 | 4.4483e-04 | NAGAGGRAGN --NAGGAAG- |  |
| ETS_PEA3_M00655 | 1.3175e-03 | NAGAGGRAGN ---MGGAWG- |  |

Stamp Results

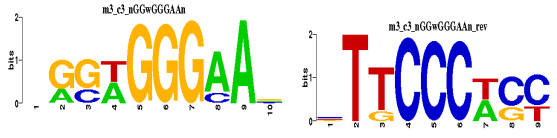
12/27/10

ETS_c-Ets-1_M00743 1.4650e-03

NCTYCCTCTN
GCTTCCK---



m3_c3_nGGwGGGAAn

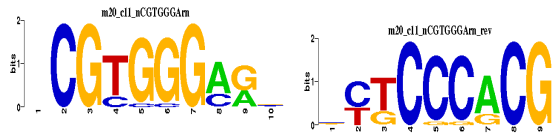


forward

reverse compliment

| Name | E value | Alignment | Motif |
|------------------------|------------|---------------------------------|-------|
| CH_MAZ_M00649 | 1.9191e-04 | NTTCCCWCCN ---CCCTCCC | |
| fork_E2F-1-DP-1_M00736 | 5.8666e-04 | NGGWGGGAAN --GCGSGAA- | |
| CH_BLIMP1_M01066 | 1.7067e-03 | ---NTTCCCWCCN YMCTTTCMCTTYC | |
| CH_Tra-1_M01048 | 3.2300e-03 | NTTCCCWCCN ---ACCWCCC | |
| CH_Ik-3_M00088 | 3.3224e-03 | NGGWGGGAAN--- -NYNGGGAATAACC | |

m20_c11_nCGTGGGArn

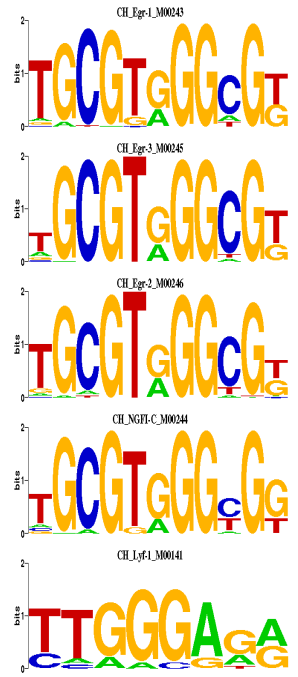


forward

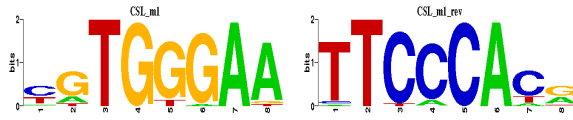
reverse compliment

Name *E value* *Alignment* *Motif*

| | | |
|------------------|------------|----------------------------|
| CH_Egr-1_M00243 | 7.1141e-06 | NYTCCCACGN- MCGCCCACGCA |
| CH_Egr-3_M00245 | 9.3079e-06 | NYTCCCACGN- ACGCCCACGCA |
| CH_Egr-2_M00246 | 1.8324e-05 | -NCGTGGGARN TGCGTGGGCGK |
| CH_NGFI-C_M00244 | 2.1539e-05 | -NCGTGGGARN TGCGTGGGYGG |
| CH_Lyf1_M00141 | 8.1234e-05 | NYTCCCACGN YCTCCCAA-- |



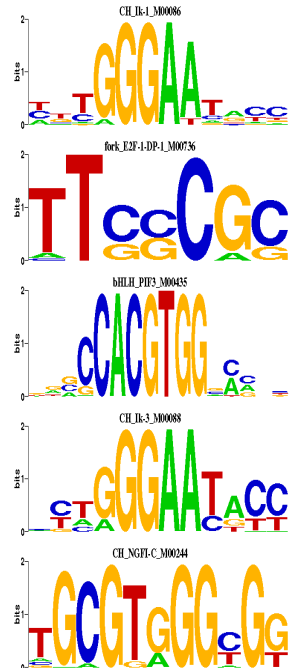
CSL_m1

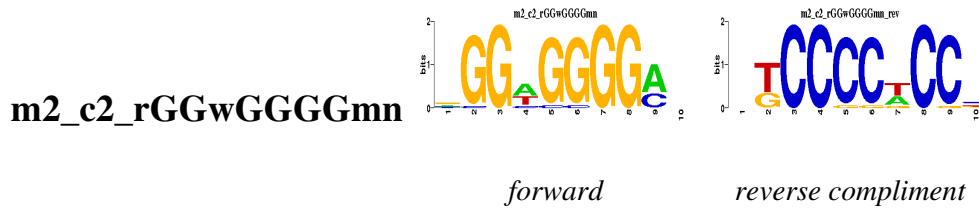


forward

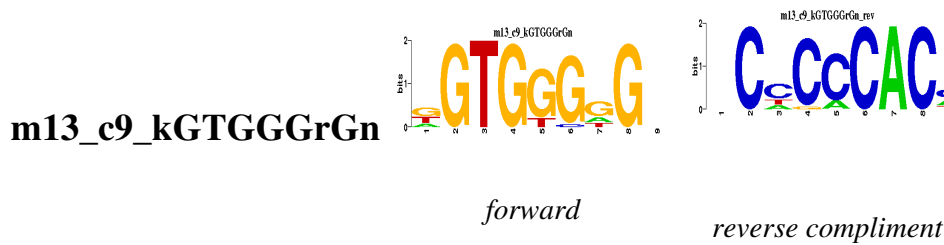
reverse compliment

| Name | E value | Alignment | Motif |
|------------------------|------------|------------------------------------|-------|
| CH_Ik-1_M00086 | 8.5834e-08 | ----TTCCACR NNNATTCCANN | |
| fork_E2F-1-DP-1_M00736 | 5.6778e-05 | YGTGGGAA -GCGSGAA | |
| bHLH_PIF3_M00435 | 6.0505e-05 | --TTCCACR----- NNNKNCCACGTGGNNN | |
| CH_Ik-3_M00088 | 1.0573e-04 | ----TTCCACR GGTATTCCNRN | |
| CH_NGFI-C_M00244 | 1.3815e-04 | --YGTGGGAA- TGCGTGGGYGG | |



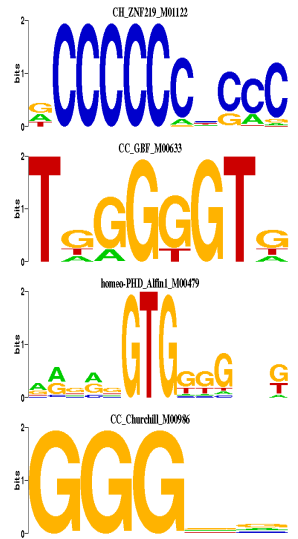


| Name | E value | Alignment | Motif |
|------------------------|------------|----------------------------------|-------|
| CH_MAZ_M00649 | 1.1250e-05 | NTCCCCWCCN ---CCCTCCC | |
| homeo-PHD_Alfm1_M00479 | 8.3578e-05 | ---NGGWGGGGAN- NRNRNGTGGGGNNK | |
| CH_Sp1_M00931 | 1.7219e-04 | NTCCCCWCCN -NCCCCGCC | |
| CH_STRE_M00308 | 3.2770e-04 | NTCCCCWCCN -NCCCCT--- | |
| CH_ZNF219_M01122 | 4.7770e-04 | NGGWGGGGAN- GGGNGGGGGGN | |

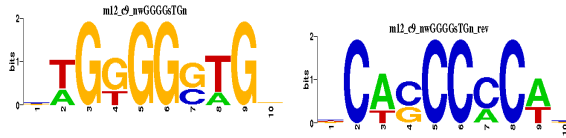


| Name | E value | Alignment | Motif |
|----------------|------------|-------------------------------|-------|
| CH_KROX_M00982 | 9.9241e-06 | --NGTGGGRGN-- GNNNGGGGGCGG | |

| | | |
|-------------------------|------------|----------------------------------|
| CH_ZNF219_M01122 | 1.3299e-05 | -NGTGGGRGN- GGGNGGGGGGN |
| CC_GBF_M00633 | 2.0496e-05 | -NCYCCCACN NACCCNA-- |
| homeo-PHD_Alf1n1_M00479 | 2.7348e-05 | ----NGTGGGRGN- NRNRNGTGGGGNNK |
| CC_Churchill_M00986 | 4.8254e-05 | NCYCCCACN -NNCC--- |



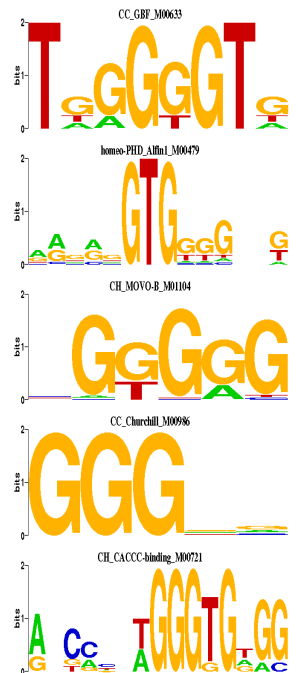
m12_c9_nwGGGGsTGn



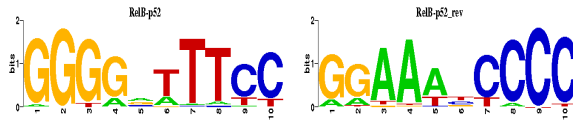
forward

reverse complement

| Name | E value | Alignment |
|-------------------------|------------|-----------------------------------|
| CC_GBF_M00633 | 1.8441e-09 | NCASCCCAN -NACCCNA- |
| homeo-PHD_Alf1n1_M00479 | 1.8018e-04 | NCASCCCAN----- -MNNCCCCACNYYN |
| CH_MOVO-B_M01104 | 3.8309e-04 | NTGGGGSTGN -NGGGG--- |
| CC_Churchill_M00986 | 1.0127e-03 | NCASCCCAN ---NNCC--- |
| CH_CACCC-binding_M00721 | 1.1710e-03 | ----NTGGGGSTGN ANCMNNWGGGTGNGG |



RelB-p52

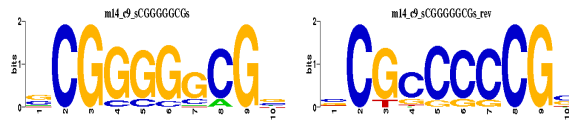


forward

reverse compliment

| Name | E value | Alignment | Motif |
|----------------------|------------|---------------------------------|-------|
| Rel_c-Rel_M00053 | 2.1716e-13 | GGAAANCCCC GGAAWNYCC- | |
| Rel_NF-kappaB_M00052 | 5.6348e-12 | GGAAANCCCC GGAAANTCC- | |
| Rel_NF-kappaB_M00054 | 4.0313e-09 | GGGGNTTTC -GGAMTTYCC | |
| Rel_NF-kappaB_M00194 | 1.3067e-08 | --GGAAANCCCC-- NNGGAAAKTCCCC | |
| Rel_NF-kappaB_M00774 | 1.9339e-08 | -GGGNTTTC----- NGGANTTTCNNNN | |

m14_c9_sCGGGGGCGs



forward

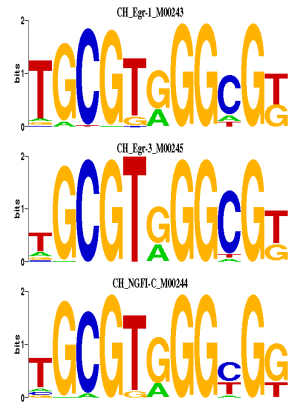
reverse compliment

| Name | E value | Alignment | Motif |
|----------------|------------|-------------------------------|-------|
| CH_KROX_M00982 | 1.0876e-07 | ---SCGGGGGCGN GNNNGGGGGCGG | |
| CH_Egr_M00807 | 1.0373e-05 | SCGGGGGCGN- -TGGGSGCRRN | |

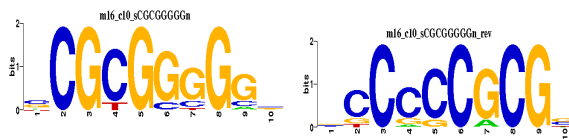
Stamp Results

12/27/10

| | | |
|------------------|------------|----------------------------|
| CH_Egr-1_M00243 | 2.7071e-05 | NCGCCCCCGS- MCGCCCACGCA |
| CH_Egr-3_M00245 | 6.8231e-05 | NCGCCCCCGS- ACGCCCACGCA |
| CH_NGFI-C_M00244 | 7.9829e-05 | NCGCCCCCGS- CCRCCCACGCA |



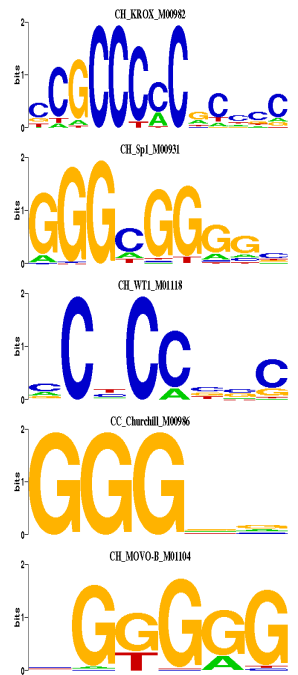
m16_c10_sCGCGGGGGn



forward

reverse compliment

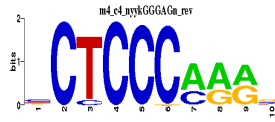
| <i>Name</i> | <i>E value</i> | <i>Alignment</i> |
|---------------------|----------------|--------------------------------|
| CH_KROX_M00982 | 4.0740e-05 | -NCGCGGGGGN-- GNNNGGGGGGCGG |
| CH_Sp1_M00931 | 1.2436e-04 | NCCCCGCGN -NCCCCGCC |
| CH_WT1_M01118 | 1.7136e-04 | NCGCGGGGGN --GNNGGNGN |
| CC_Churchill_M00986 | 1.7837e-04 | NCCCCGCGN -NNCCC---- |
| CH_MOVO-B_M01104 | 3.6042e-04 | NCCCCGCGN -CCCCN--- |



m4_c4_nyykGGGAGn



forward



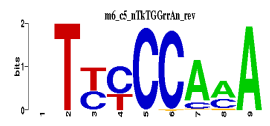
reverse compliment

| <i>Name</i> | <i>E value</i> | <i>Alignment</i> | <i>Motif</i> |
|--------------------|----------------|-------------------------------|--------------|
| CH_Lyf-1_M00141 | 1.4301e-07 | NYTTGGGAGN --TTGGGAGR | |
| CH_Ik-1_M00086 | 6.5338e-04 | ---NCTCCCAARN NNNATTCCANN- | |
| HLH_EBF_M00977 | 7.7704e-04 | NCTCCCAARN-- --NCYCWRGGGA | |
| CH_MAZ_M00649 | 8.2616e-04 | -NCTCCCAARN CCCTCCC---- | |
| homeo_Pitx2_M00482 | 1.0694e-03 | NYTTGGGAGN-- --NTGGGATTAN | |

m6_c5_nTkTGGrrAn



forward



reverse compliment

| <i>Name</i> | <i>E value</i> | <i>Alignment</i> | <i>Motif</i> |
|-----------------|----------------|--------------------------------|--------------|
| CH_Ik-1_M00086 | 1.2269e-05 | NTKTGGGRAN--- -NNTGGGAATNNN | |
| CH_Lyf-1_M00141 | 5.7369e-04 | NTYCCAMAN -YCTCCCAA- | |

bZIP_C-EBP_M00159 7.4680e-04

--NTYCCAMAN
NNNTNWN CAMAN



RING_LUN-1_M00480 1.0475e-03

NTYCCAMAN-----
--TCCCAAAGTAGCTGGG



Rel_NF-kappaB_M00208 3.4245e-03

NKKTGGGRAN----
---NGGAAARTCCC



m36_c19_nTkTGGrsT



forward

reverse compliment

Name

E value

Alignment

Motif

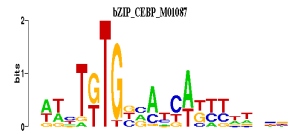
bHLH-ZIP_SREBP-1_M00221 8.6209e-04

NKKTGGRNT---
--GTGGGGTGAT



bZIP_CEBP_M01087 1.0832e-03

-----ANYCCAMAN---
NNNNNRMRMTRNTNNCAMANWWN



homeo_Pitx2_M00482 1.7704e-03

---ANYCCAMAN
NTAATCCCAN--



bHLH-ZIP_SREBP-1_M00749 2.3208e-03

NKKTGGRNT
---TGGSGT

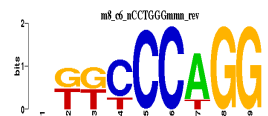


runt_Osf2_M00731 2.7090e-03

-NKKTGGRNT
KNTGTGG---



m8_c6_nCCTGGGmmn



forward *reverse compliment*

Name *E value* *Alignment* *Motif*

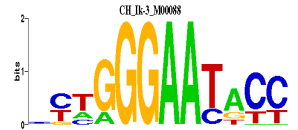
paired-homeo_Pax-6_M00979 1.5669e-03

-NKKCCCAGGN--
KAGTTCCAGGTCA



CH_Ik-3_M00088 2.9905e-03

---NKKCCCAGGN
GGTATTCCNRN-



bHLH_PIF3_M00435 3.1694e-03

-NKKCCCAGGN-----
NNNKNCACGTGGNNN



bHSH_AP-2_M00915 5.4977e-03

-NCCTGGGMMN-
NGCCNGNGGNNN

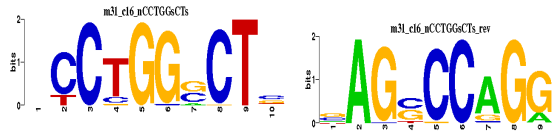


HLH_EBF_M00977 1.0663e-02

NKKCCCAGGN--
--NCYCWRGGGA



m31_c16_nCCTGGsCTs



forward

reverse compliment

Name *E value* *Alignment* *Motif*

bHLH-ZIP_SREBP-1_M00749 1.3772e-03

NCCTGGSCTN
---TGGSGT-



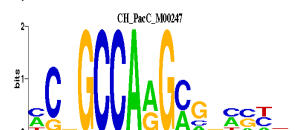
bHSH_AP-2alpha_M00469 7.9938e-03

NAGSCCAGGN
--SCNNNGG



CH_PacC_M00247 8.0734e-03

-----NCCTGGSCTN
NNNNNNKCYTGCCNGN



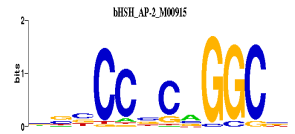
Stamp Results

12/27/10

bHSH_AP-2_M00915

1.2488e-02

-NCCTGGSCTN-
NGCCNGNGGNNN



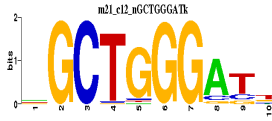
CH_Egr-3_M00245

1.5428e-02

NAGSCCAGGN-
ACGCCACGCA



m21_c12_nGCTGGGATk



forward

reverse compliment

Name

E value

Alignment

Motif

homeo_Pitx2_M00482

6.8928e-05

NGCTGGGATN--
--NTGGGATTAN



bHLH_HEB_M00698

2.2175e-03

-NGCTGGGATN
CAGCWGG----



bHLH-ZIP_SREBP-1_M00749 2.3365e-03

NGCTGGGATN
---TGGSGT-



CH_Lyf-1_M00141

3.1111e-03

NATCCCAGCN
YCTCCCAA--



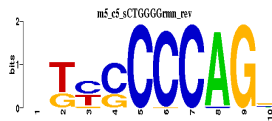
RING_LUN-1_M00480

3.4783e-03

-----NGCTGGGATN
TCCCAAAGTAGCTGGG---



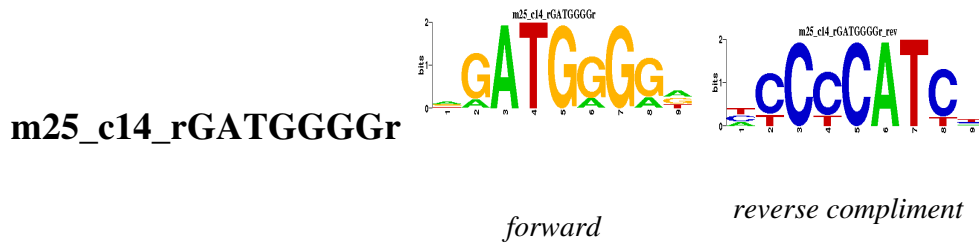
m5_c5_sCTGGGGrmn



forward

reverse compliment

| <i>Name</i> | <i>E value</i> | <i>Alignment</i> | <i>Motif</i> |
|-------------------------|----------------|------------------------------|--------------|
| CC_GBF_M00633 | 4.6637e-04 | NTYCCCCAGN NACCCNA-- | |
| bHSH_AP-2_M00189 | 5.4095e-04 | NTYCCCCAGN-- -NCCCSCNGGCG | |
| bHLH-ZIP_SREBP-1_M00749 | 6.1121e-04 | NCTGGGGRAN --TGGSGT-- | |
| CC_Churchill_M00986 | 6.6581e-04 | NTYCCCCAGN --NNCC--- | |
| CH_Egr_M00807 | 1.5104e-03 | --NTYCCCCAGN NYYGCSCCA-- | |



| <i>Name</i> | <i>E value</i> | <i>Alignment</i> | <i>Motif</i> |
|-------------------------|----------------|--------------------------------------------------------|--------------|
| CH_MZF1_M00084 | 1.5591e-04 | -NCCCCATCN-- TTNCCCCTCANN | |
| bHLH-ZIP_SREBP-1_M00749 | 2.7983e-04 | NGATGGGN ---TGGSGT | |
| homeo_HOXA5_M00023 | 3.0295e-04 | -----NCCCCATCN----- GCNNNNNNNCNYCATTANTNNNNNNNNNYCN | |
| CC_GBF_M00633 | 4.2463e-04 | --NCCCCATCN NACCCNA--- | |

CC_Churchill_M00986

6.1232e-04

NCCCCATCN
NNCCC----



m26_c14_nmTGGTGAAn



forward

reverse compliment

Name

E value

Alignment

Motif

bZIP_LMAF_M01139

5.1437e-03

NMTGGTGAAN
-CTGCTGAS-



runt_AML1_M00751

7.0782e-03

NTTACCAKN
----ACCAC-



runt_AML1a_M00271

7.3701e-03

NTTACCAKN
----ACCAC-



bZIP_OSBZ8_M00654

1.1359e-02

-NMTGGTGAAN--
GWNTSGCGACACG

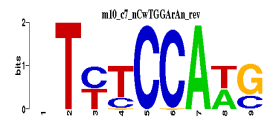
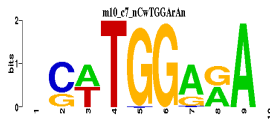


bHLH-ZIP_SREBP-1_M00221 1.8693e-02

-NMTGGTGAAN
GTGGGTGAT-



m10_c7_nCwTGGArAn



forward

reverse compliment

Name

E value

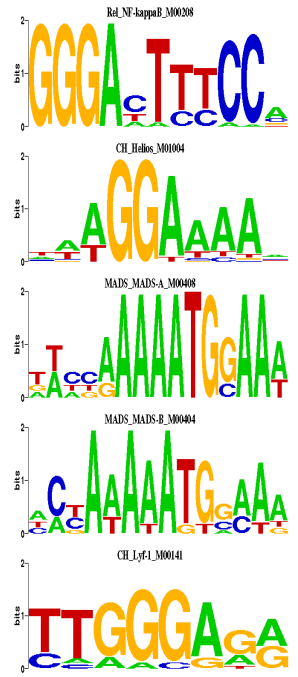
Alignment

Motif

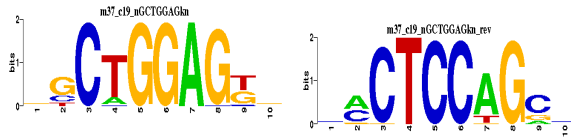
Stamp Results

12/27/10

| | | |
|----------------------|------------|------------------------------------|
| Rel_NF-kappaB_M00208 | 1.3809e-03 | NCWTGGARAN----- ---NGGAAARTCCC |
| CH_Helios_M01004 | 3.1774e-03 | -NTYTCCAWGN NTTTTCTWN- |
| MADS_MADS-A_M00408 | 3.7654e-03 | NTYTCCAWGN----- -TTTCCATTTTNNWN |
| MADS_MADS-B_M00404 | 8.0205e-03 | NTYTCCAWGN----- -TTTSCATTTTTRGN |
| CH_Lyf-1_M00141 | 1.1521e-02 | NTYTCCAWGN -YCTCCCAA- |



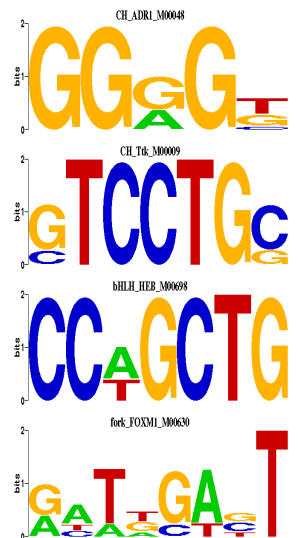
m37_c19_nGCTGGAGkn



forward

reverse compliment

| Name | E value | Alignment |
|-------------------|------------|----------------------------|
| CH_ADR1_M00048 | 9.8619e-04 | NMCTCCAGCN -MCCC----- |
| CH_Ttk_M00009 | 1.6003e-03 | NGCTGGAGKN -GCAGGAC-- |
| bHLH_HEB_M00698 | 1.6336e-03 | -NGCTGGAGKN CAGCWGG---- |
| fork_FOXM1_M00630 | 2.0990e-03 | NMCTCCAGCN -ANTCNANY- |

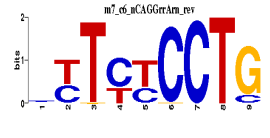


Grainyhead_LBP-1_M00644 5.0607e-03

NMCTCCAGCN
 ----SCAGCN



m7_c6_nCAGGrrArn



forward

reverse compliment

Name

E value

Alignment

Motif

CH+homeo_AREB6_M00412 9.7125e-04

--NCAGGAGARN
 RNWCAGGTRNRN



CH_Ttk_M00009

1.8701e-03

NCAGGAGARN
 GCAGGAC---



CH_Helios_M01004

2.1551e-03

NYTCTCCTGN
 NTTTTCTWN



CH_Evi-1_M00011

6.9968e-03

NCAGGAGARN
 -CAAGATAA-



HLH_EBF_M00977

7.8428e-03

--NCAGGAGARN
 NCYCWRGGGA--



m24_c13_nrAGGrsAGn



forward

reverse compliment

Name

E value

Alignment

Motif

Stamp Results

12/27/10

C6_GAL4_M00198 3.1534e-04

-----NGAGGRGAGN-----
 NGYTCGGNNNANAGNNNNCCG



C6_GAL4_M00049 1.4934e-03

-----NGAGGRGAGN-----
 STTCGGASNANWGTNNNCCGNN



CH_STRE_M00308 2.4718e-03

NCTCYCCTCN
 --NCCCCT--



CH_MAZ_M00649 1.1966e-02

NGAGGRGAGN-
 ----GGGAGGG

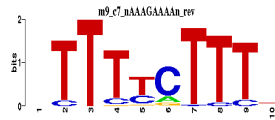


CH_ADR1_M00048 1.2825e-02

NCTCYCCTCN
 --MCCCC--



m9_c7_nAAAGAAAAn



forward

reverse compliment

Name

E value

Alignment

Motif

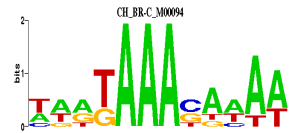
HMG_STE11_M01005 4.6453e-06

NTTTTCTTTN---
 --TTTCTTTGTTT



CH_BR-C_M00094 2.1451e-05

NTTTTCTTTN---
 -TTWTSTTTAYWW



CC_PR_M00960 7.1700e-05

NTTTTCTTTN
 NTGYCNNW-



CH_Rim101p_M01030 7.7254e-05

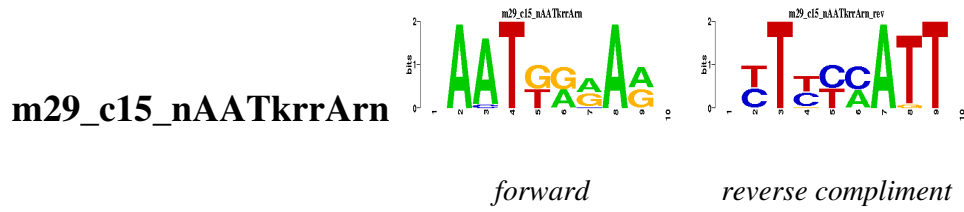
NAAAGAAAAN
 -CAAGNAA--



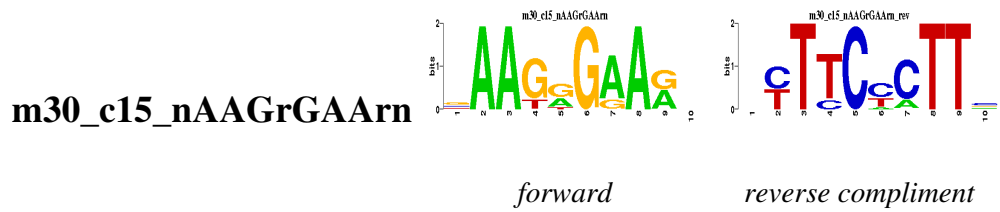
HMG_STE11_M00274 9.5434e-05

-----NAAAGAAAAN
 WNNNNAACAAAGAAAANW



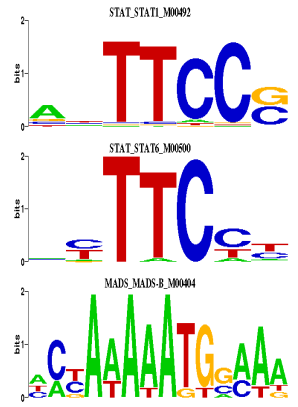


| Name | E value | Alignment | Motif |
|------------------------|------------|-----------------------------------------------------------|-------|
| MADS_MADS-B_M00404 | 3.1774e-04 | NYTYYMATTN----- -TTTSCATTTTTTRGN | |
| homeo_HOXA4_M00640 | 4.4525e-04 | NYTYYMATTN ---CYAATTW | |
| MADS_MADS-A_M00408 | 1.5265e-03 | NYTYYMATTN----- -TTTCCATTTTTNNWN | |
| NK-2-Nkx_Nkx6-1_M00424 | 2.3879e-03 | ---NAATKRRARN AANCAATTAAAW- | |
| homeo_HOXA5_M00023 | 7.4518e-03 | -----NAA TKRRARN----- NGRNNNNNNNNNANTAA TGRNGNNNNNNNGC | |

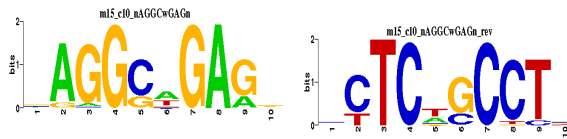


| Name | E value | Alignment | Motif |
|------------------|------------|--------------------------------|-------|
| CH_BLIMP1_M01066 | 1.9198e-05 | --NYTTCYCTTN- YMCTTTCMCTTYC | |
| trp_IRF_M00972 | 2.0378e-04 | NYTTCYCTTN NTTTCWNTTT | |

| | | |
|--------------------|------------|------------------------------------|
| STAT_STAT1_M00492 | 7.8156e-04 | NAAGRGAARN ---SGGAANT |
| STAT_STAT6_M00500 | 8.8383e-04 | NYTTCYCTTN NYTTCYY--- |
| MADS_MADS-B_M00404 | 1.3843e-03 | -----NAAGRGAARN NCYAAAAATGSAAA- |



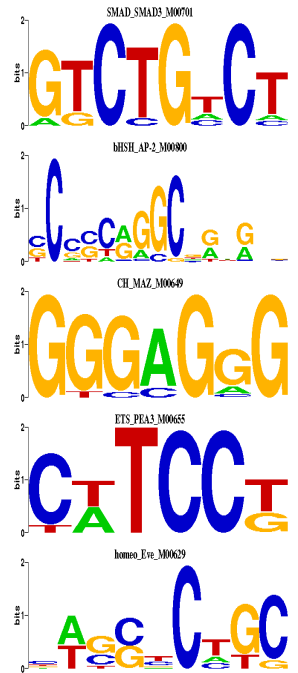
m15_c10_nAGGCwGAGn



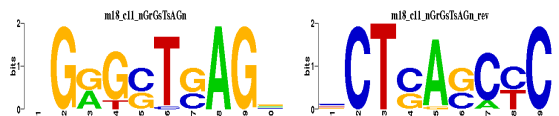
forward

reverse compliment

| <i>Name</i> | <i>E value</i> | <i>Alignment</i> |
|-------------------|----------------|------------------------------------|
| SMAD_SMAD3_M00701 | 1.4983e-04 | NAGGCWGAGN -AGNCAGAC- |
| bHSH_AP-2_M00800 | 3.3136e-03 | -NCTCWGCCTN---- NNYNYNGCCYGSSGS |
| CH_MAZ_M00649 | 5.0866e-03 | NAGGCWGAGN --GGGAGGG- |
| ETS_PEA3_M00655 | 5.8217e-03 | NAGGCWGAGN -MGGAWG--- |
| homeo_Eve_M00629 | 6.0690e-03 | NAGGCWGAGN-- ---GCNGNSSWN |

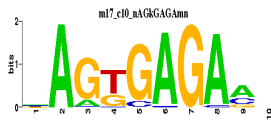



m18_c11_nGrGsTsAGn



| | <i>forward</i> | <i>reverse compliment</i> | |
|---------------------------|----------------|---------------------------------------|--------------|
| <i>Name</i> | <i>E value</i> | <i>Alignment</i> | <i>Motif</i> |
| CC_PPAlpha-RXAlpha_M00518 | 1.2752e-04 | NCTSASCYCN----- CNTSACCCCNATGACCNN | |
| bHLH-ZIP_SREBP-1_M00221 | 5.4211e-04 | -NGRGSTSAGN GTGGGTGAT- | |
| trp_CDC5_M00361 | 8.9105e-04 | NGRGSTSAGN NSCGCTGAGS | |
| bHLH-ZIP_SREBP_M00776 | 9.7152e-04 | NGRGSTSAGN- TRGGGTGANNN | |
| CC_VDR_M00444 | 5.8870e-03 | -----NGRGSTSAGN GGKNARNRRGGWSA-- | |

m17_c10_nAGkGAGAmn

forward *reverse compliment*

| <i>Name</i> | <i>E value</i> | <i>Alignment</i> | <i>Motif</i> |
|--------------------|----------------|----------------------------------|--------------|
| trp_IRF-1_M00747 | 9.2072e-04 | NAGTGAGAMN AANTGA---- | |
| homeo_Alx-4_M00619 | 3.1726e-03 | ----NKTCTCACTN GATTATTCTCAG-- | |
| CH_MZF1_M00084 | 4.2056e-03 | ---NAGTGAGAMN NNGAGGGGNAA- | |

Stamp Results

12/27/10

trp_IRF_M00972 4.9499e-03

NKTCTCACTN-
-NTTTCWNTTT



CH_Lyf-1_M00141 1.0429e-02

NKTCTCACTN
--YCTCCCAA



m19_c11_nrrwGTGArn



forward

reverse compliment

Name E value Alignment Motif

trp_IRF_M00972 3.1354e-06

NARWGTGAAN-
-AAANWGAAAN



trp_IRF-1_M00747 1.2348e-04

NARWGTGAAN
--AANTGA--



trp_IRF-2_M00063 1.4856e-04

NARWGTGAAN--
AAAAGYGAAASY



CH_BLIMP1_M01066 1.8839e-04

NARWGTGAAN---
GRAAGKGAAAGKR



trp_IRF-1_M00062 2.1500e-04

NARWGTGAAN--
AAAAGYGAAACC



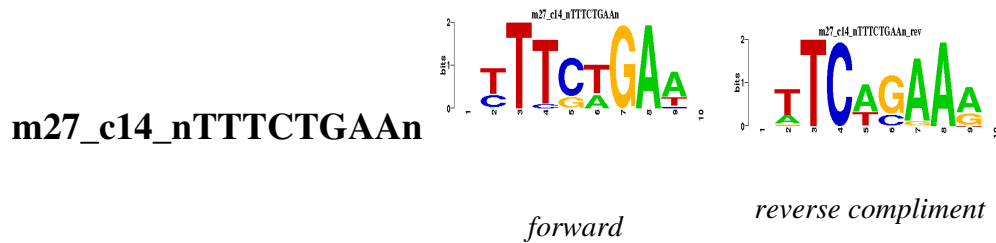
m23_c13_nyyTCwGAGn



forward

reverse compliment

| Name | E value | Alignment | Motif |
|------------------------|------------|-----------------------------------------------|-------|
| trp_CDC5_M00361 | 1.2354e-02 | NTYTCWGAGN NSCGCTGAGS | |
| fork_FOXP3_M00992 | 2.1003e-02 | NCTCWGARAN----- -NTMTGNNANAACNNNW | |
| HMG_TCF-4_M00671 | 2.1599e-02 | NTYTCWGAGN --WTCAAAG- | |
| bZIP_AP-1_M00173 | 2.6093e-02 | NTYTCWGAGN--- ---WNKNAGTCAN | |
| bZIP_TCF11-MafG_M00284 | 2.9516e-02 | ----NTYTCWGAGN----- CNNANN TGCTGNGTCATNNNN | |



| Name | E value | Alignment | Motif |
|------------------------|------------|-----------------------------------------------------|-------|
| bZIP_C-EBPgamma_M00622 | 1.0564e-04 | NTTCAGAAAN-- WTTYTGAAATNA | |
| paired_Pax-5_M00144 | 3.1478e-03 | -----NTTTCTGAAN----- RNNNGNNNNNTNRAGCGKRACNRYNNN | |
| CC_VDR,_M00966 | 3.6741e-03 | ----NTTCAGAAAN---- ANNNGGKTCANNARGKNCA Y | |
| homeo_TGIF_M00418 | 5.8488e-03 | NTTTCTGAAN-- --WNNTGACAGC | |

Stamp Results

12/27/10

bZIP_LMAF_M01139

9.0203e-03

NTTTCTGAAN
-CTGCTGAS-



m33_c17_nTyTGTryTn



forward

reverse compliment

Name

E value

Alignment

Motif

fork_FOXP1_M00987 8.5327e-06

-NTYTGTGYTN-----
TATTTGTGTTGTTTTTAT



runt_Osf2_M00731 1.0411e-04

NTYTGTGYTN
-KNTGTGG--



HMG_STE11_M01005 1.3030e-03

-NTYTGTGYTN
TTTCTTTGTTC



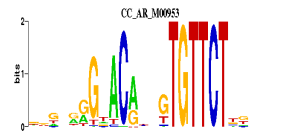
runt_PEBP_M00984 1.6083e-03

--NTYTGTGYTN--
NNNNYTGTGTTNAN



CC_AR_M00953 1.7018e-03

-----NTYTGTGYTN-----
NNNNNRGNACANNGTGTTCTNNNNN



m32_c16_nCAGskGCmn



forward


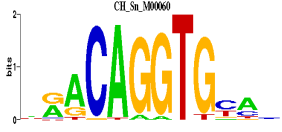



reverse compliment

Name


E value

Alignment


Motif

| | | | |
|----------------------|------------|-------------------------------|-------------------------------------------------------------------------------------|
| bHLH_E12_M00693 | 1.7723e-07 | NKGCMCCTGN NNNCACCTGY |  |
| CH_Sn_M00060 | 7.3846e-06 | --NCAGGKGC MN NRACAGGTGYMN |  |
| bHLH_myogenin_M00712 | 1.2618e-05 | NKGCMCCTGN ---CASCTGN |  |
| bHLH-ZIP_AP-4_M00927 | 2.1095e-05 | NKGCMCCTGN --RCAGCTGN |  |
| LIM_Lmo2_M00277 | 5.1628e-05 | NKGCMCCTGN- NNNCACCTGNN |  |






m35_c18_nCAkGTGwsn

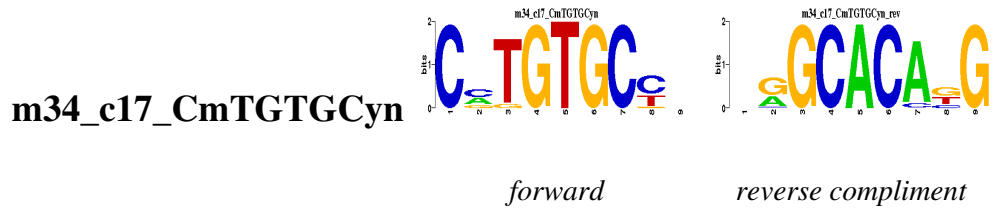


forward

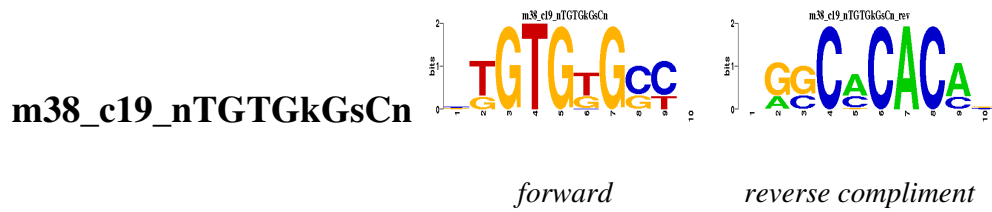


reverse compliment

| <i>Name</i> | <i>E value</i> | <i>Alignment</i> | <i>Motif</i> |
|-----------------------|----------------|------------------------------|---------------------------------------------------------------------------------------|
| bHLH_myogenin_M00712 | 4.0585e-05 | NSWCACCTGN ---CASCTGN |  |
| T-box_TBX5_M01044 | 2.6108e-04 | NSWCACCTGN TCACACCTT- |  |
| bHLH_MyoD_M00184 | 2.6417e-04 | -NCAGGTGWSN GNCAGNTGN-- |  |
| bHLH_E12_M00693 | 4.6466e-04 | NSWCACCTGN NNNCACCTGY |  |
| CH+homeo_AREB6_M00412 | 4.8403e-04 | --NCAGGTGWSN RNWCAGGTRNRN |  |



| Name | E value | Alignment | Motif |
|----------------------|------------|----------------------------------|-------|
| bHLH-ZIP_TFE_M01029 | 5.3933e-05 | NRGCACA --NCACATG | |
| bHLH_E12_M00693 | 4.5439e-04 | NRGCACA NNNCACCTGY | |
| bHLH_TAL1_M00993 | 6.0237e-04 | -CMTGTGCYN CCANCTGNY- | |
| bHLH_CBF1_M00303 | 1.5448e-03 | -CMTGTGCYN NCACGTGAY- | |
| CC_HNF4alpha1_M00411 | 3.1085e-03 | ----CMTGTGCYN- NTGACCTTTGNCCY | |



| Name | E value | Alignment | Motif |
|-------------------|------------|----------------------------|-------|
| bHLH_PCF2_M00948 | 4.3632e-05 | NTGTGTGCCN- --GTGGGNCCN | |
| bZIP_TRAB1_M00507 | 1.2560e-03 | -NTGTGTGCCN KACGYGTGNC- | |

bZIP_DBP_M00624 3.5396e-03

NTGTGTGCCN
--NWNTGC--



T-box_TBX5_M01044 1.0621e-02

-NTGTGTGCCN
AAGGTGTGA--

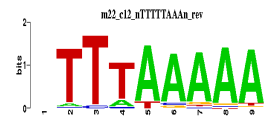
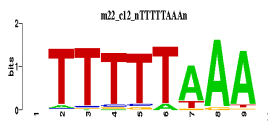


runt_Osf2_M00731 1.2717e-02

NGGCACACAN
--CCACANM-



m22_c12_nTTTTTAAAn



forward

reverse complement

Name

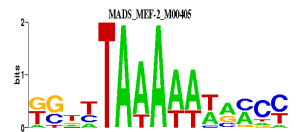
E value

Alignment

Motif

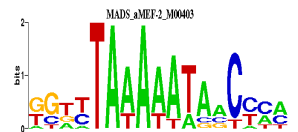
MADS_MEF-2_M00405 1.0861e-06

----NTTTTTAAAN-
RGKNWTTTTTANNM



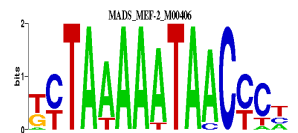
MADS_aMEF-2_M00403 4.6999e-06

-NTTTAAAAAN-----
KGN YTAAAAATANCYMM



MADS_MEF-2_M00406 2.5857e-05

-----NTTTTTAAAN
NGGGTTATTTTTAGM-



MADS_MEF-2_M00006 4.5147e-05

-----NTTTTTAAAN
RGRGTTATTTTTAGA-

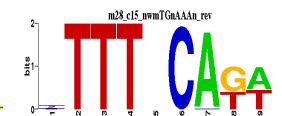


CH_Hb_M00022 9.0216e-05

NTTTTTAAAN
NTTTTTNYK-

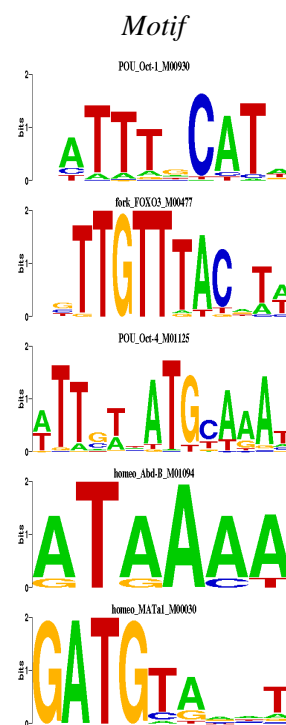


m28_c15_nwmTGnAAAn



*forward**reverse compliment*

| <i>Name</i> | <i>E value</i> | <i>Alignment</i> |
|--------------------|----------------|----------------------------------|
| POU_Oct-1_M00930 | 1.3241e-05 | NWMTGNAAAN- -NATGNAAATN |
| fork_FOXO3_M00477 | 4.7143e-05 | ----NTTNC AKWN NNTTGTTTACNTW- |
| POU_Oct-4_M01125 | 3.1231e-04 | NTTNC AKWN---- ATTTGCATNASAAW |
| homeo_Abd-B_M01094 | 4.1397e-04 | NTTNC AKWN TTTTAT---- |
| homeo_MATa1_M00030 | 6.5072e-04 | NWMTGNAAAN -GATGTANNT |



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