



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

Number of files:	2
Number of top significant motifs:	10
Number of best matches:	10
Similarity cutoff >=	0.75
Matching motif database:	UniProbe Mus Musculus
Motif tree:	Yes
Combined similar motifs:	Yes
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
MEME-ChIP_DM721.txt	11	1
PScanChIP_DM721.txt	37	2

RESULTS

Top 10 Significant Motifs - Global Matching (Highest to Lowest)

Dataset #: 1 Motif ID: 4 Motif name: Motif 4

Original motif Consensus sequence: CTCTGY



Reverse complement motif Consensus sequence: KCAGAG



Best Matches for Top Significant Motif ID 4 (Highest to Lowest)

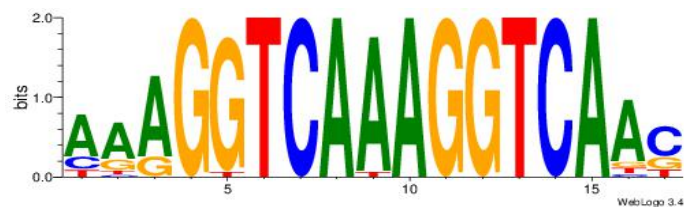
Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.012269

Alignment:

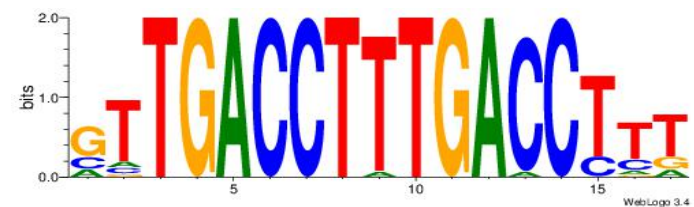
AAAGGTCAAAGGTCAAC

-----KCAGAG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

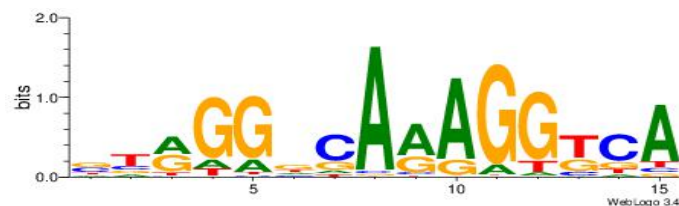


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0140102

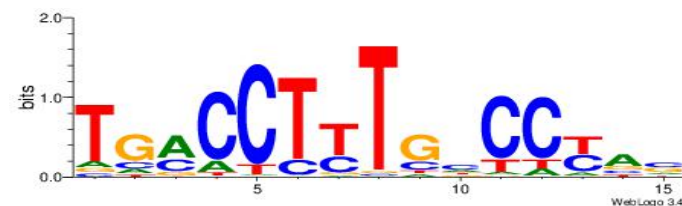
Alignment:

BTRGGDCARAGGKCA
 -----KCAGAG-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5

Number of overlap: 6
Similarity score: 0.0186793

Alignment:
AKGY YCAAAGRTCA
----KCAGAG----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA

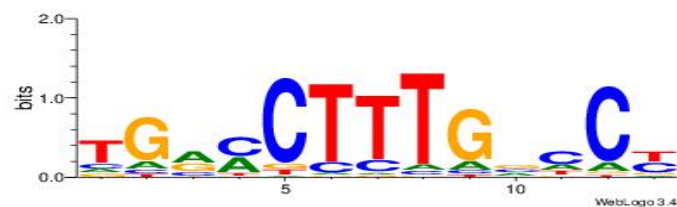
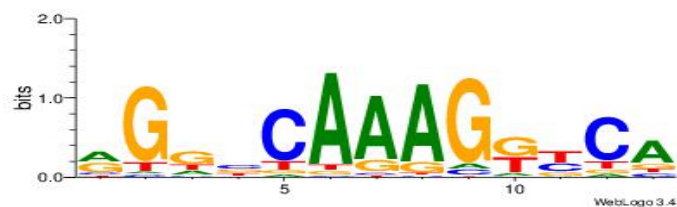


Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020602

Alignment:
RGGBCAAAGKYCA
---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGM YCTTTGBCCK



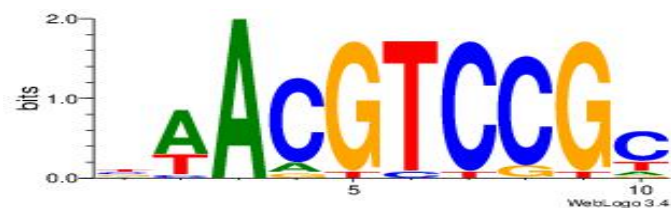
Dataset #: 2
 Motif ID: 37
 Motif name: MIZF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0221665

Alignment:

BAACGTCCGC

----CTCTGY

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



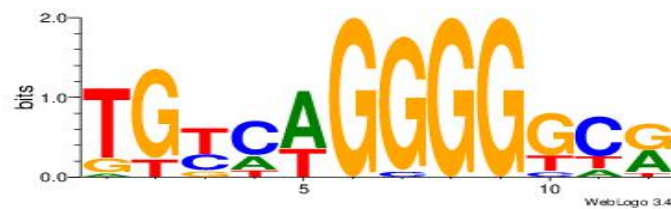
Dataset #: 2
 Motif ID: 35

Motif name:	INSM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0255256

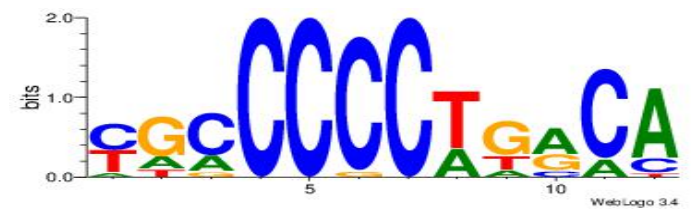
Alignment:

TGYCAGGGGGCR
 --KCAGAG----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



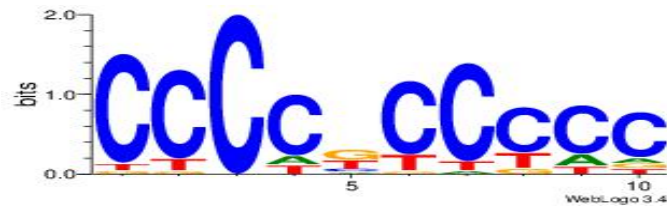
Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0349642

Alignment:

CCCCKCCCCC

CTCTGY----

Original motif Consensus sequence: CCCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0376108

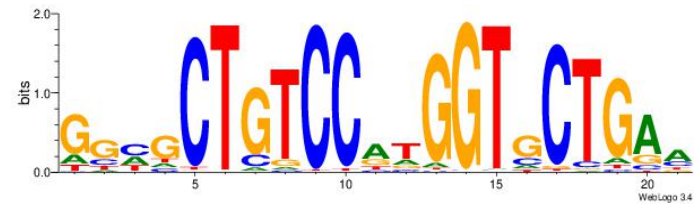
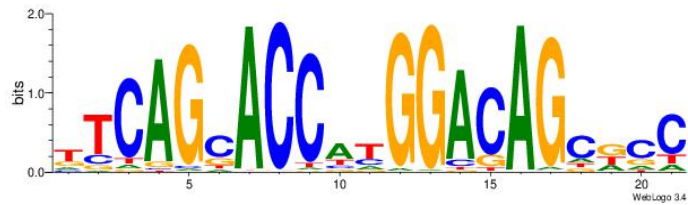
Alignment:

GGYGCTGTCCATGGTGCTGAA

--CTCTGY-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

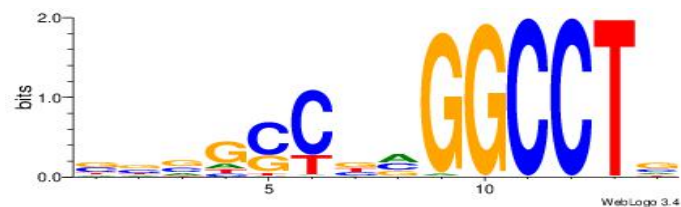
Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



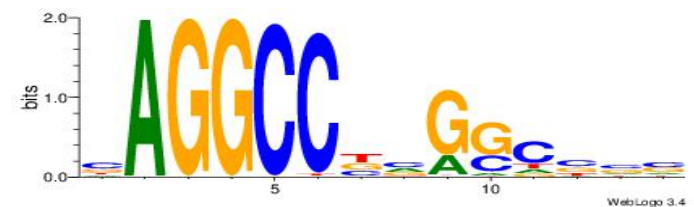
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0448449

Alignment:
 BBVGCCBVGGCCTV
 ---KCAGAG-----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



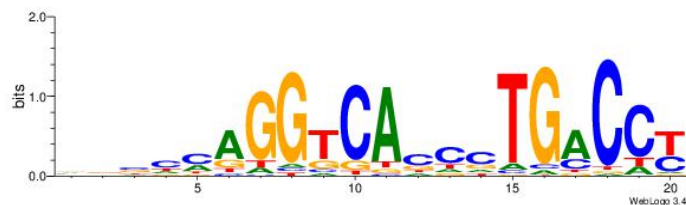
Dataset #: 2
 Motif ID: 29

Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0454269

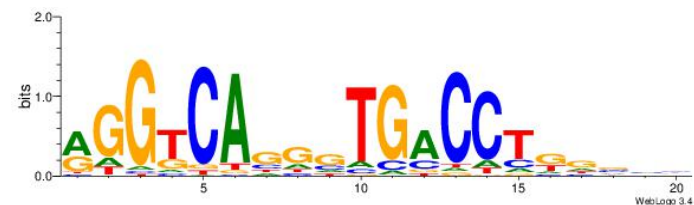
Alignment:

MGGTCAGGGTGACCTRDBHV
 ---KCAGAG-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 1 Motif ID: 5 Motif name: Motif 5

Original motif Consensus sequence: ATKTM



Reverse complement motif Consensus sequence: RARAT



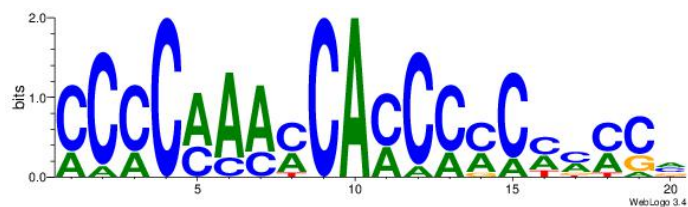
Best Matches for Top Significant Motif ID 5 (Highest to Lowest)

Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 5
 Similarity score: 0.0256083

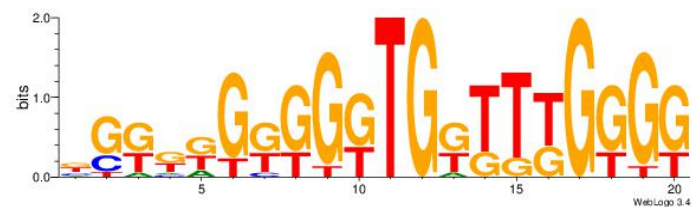
Alignment:

BGRRRGRGGRTGRTTYGGGG
 -----RARAT-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



Dataset #: 2
 Motif ID: 44
 Motif name: NR4A2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif

Direction: Backward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0276382

Alignment:
 AAGGTCAC
 RARAT---

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



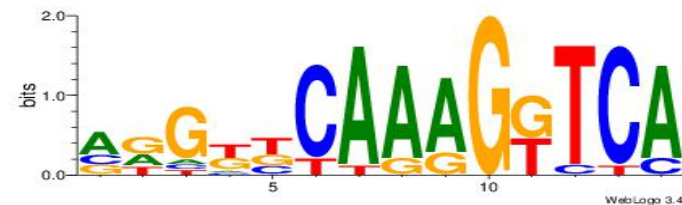
Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0279129

Alignment:
 AKGY YCAAAGRTCA
 -----RARAT--

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC



Dataset #: 2
Motif ID: 37
Motif name: MIZF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 5
Similarity score: 0.0292478

Alignment:

BAACGTCCGC

--ATKTM---

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV

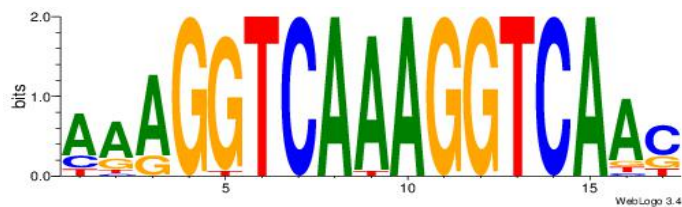


Dataset #: 2
 Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 5
 Similarity score: 0.0292478

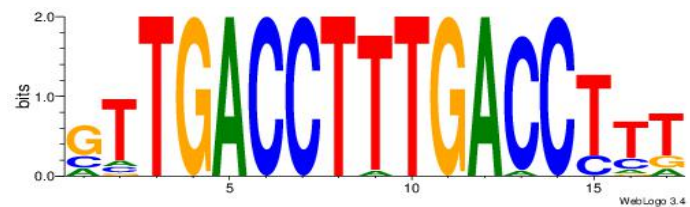
Alignment:

AAAGGTCAAAGGTCAAC
 -----ATKTM---

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

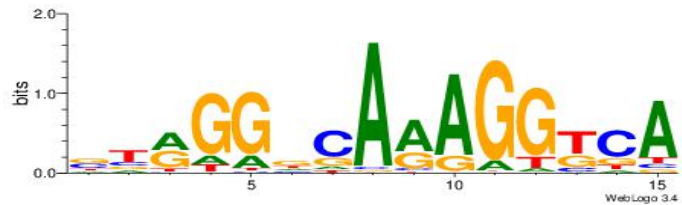


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

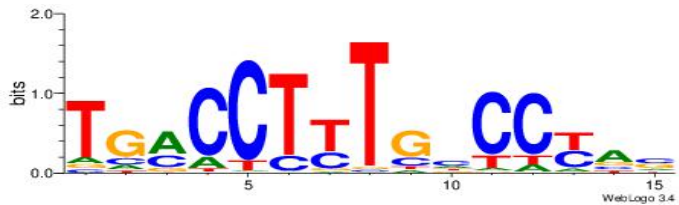
Number of overlap: 5
Similarity score: 0.0305369

Alignment:
TGRCCTKTGHCKAB
-----ATKTM-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB

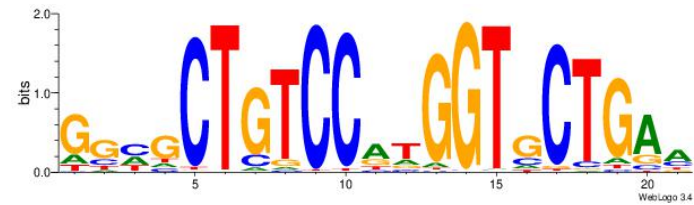
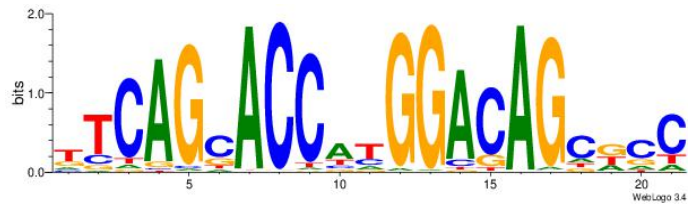


Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 5
Similarity score: 0.0315454

Alignment:
GGYGCTGTCCATGGTGCTGAA
-----ATKTM-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

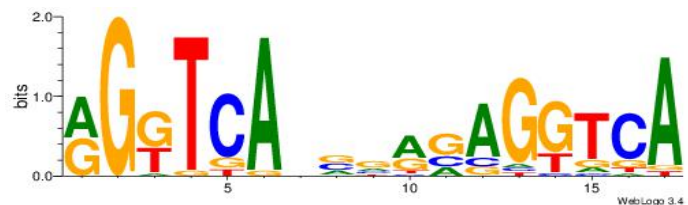
Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



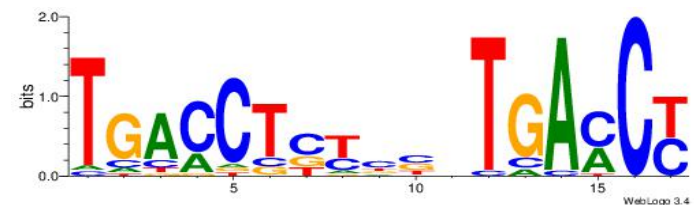
Dataset #: 2
 Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 13
 Number of overlap: 5
 Similarity score: 0.0335956

Alignment:
 RGKTCABVVRGAGGTCA
 ATKTM-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK



Dataset #: 2

Motif ID: 46
 Motif name: RORA_1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0336052

Alignment:
 AWVDAGGTCA
 ---RARAT--

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT



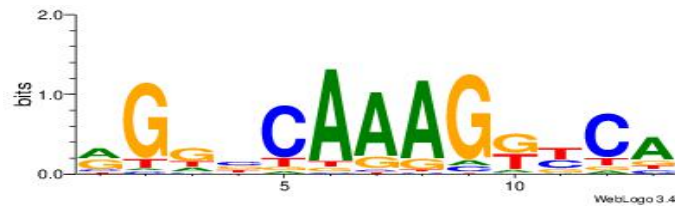
Dataset #: 2
 Motif ID: 34
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 5
 Similarity score: 0.0367105

Alignment:

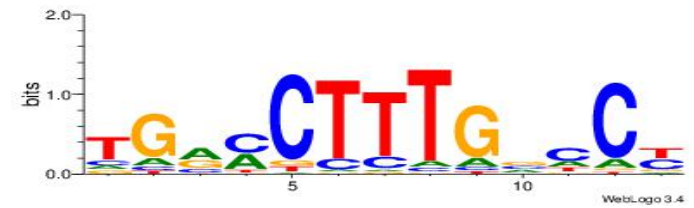
RGGBCAAAGKYCA

-----ATKTM-

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCCK



Dataset #: 1 Motif ID: 6 Motif name: Motif 6

Original motif Consensus sequence: CMGCRGC



Reverse complement motif Consensus sequence: GCKGCOYG



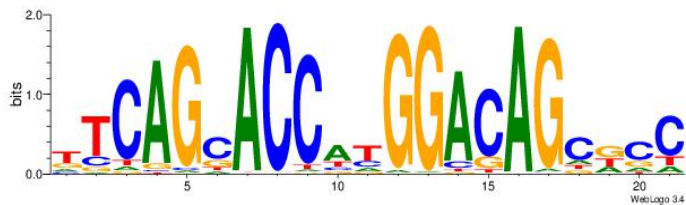
Best Matches for Top Significant Motif ID 6 (Highest to Lowest)

Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	13

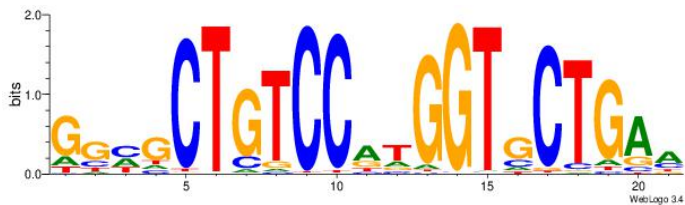
Number of overlap: 7
Similarity score: 0.0205607

Alignment:
TTCAGCACCATGGACAGCKCC
--CMGCRGC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2
Motif ID: 37
Motif name: MIZF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0322623

Alignment:
GCGGACGTTV
GCKGCTG---

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

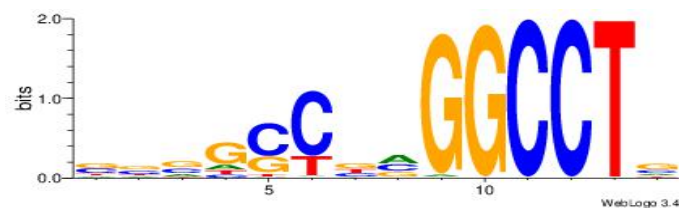


Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 7
 Similarity score: 0.038091

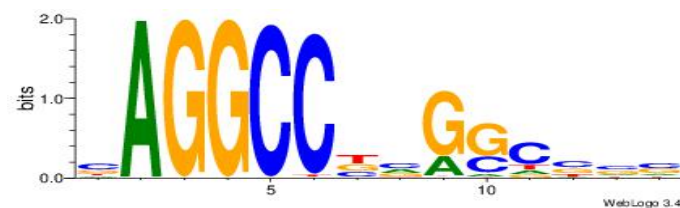
Alignment:

BBVGCCBVGGCCTV
 ----CMGCRGC---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



Dataset #: 2
 Motif ID: 15

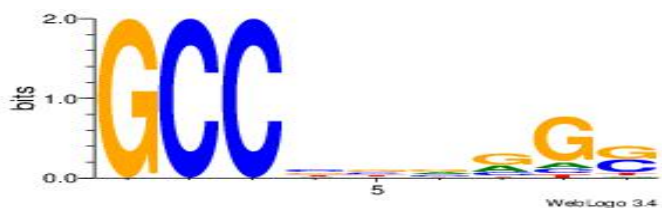
Motif name:	TFAP2A
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0.0393168

Alignment:

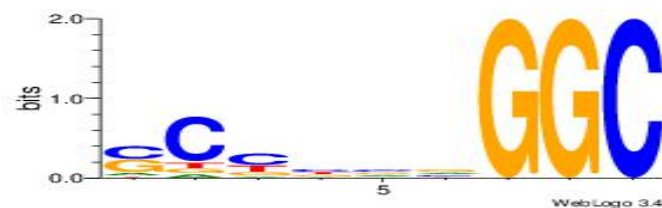
SCMVBBGGC

--CMGCRGC

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



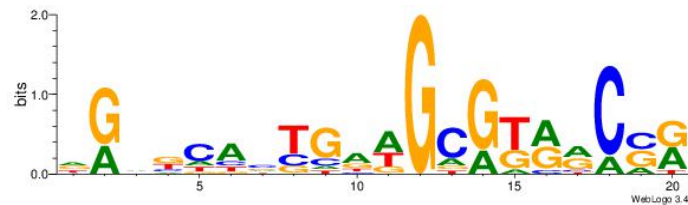
Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	7
Similarity score:	0.0448462

Alignment:

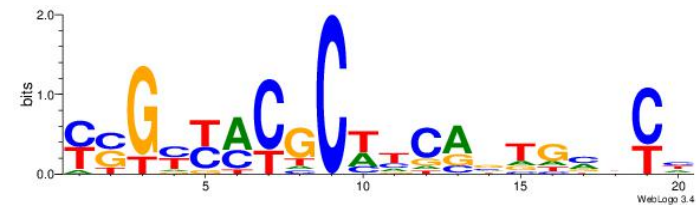
MSGKKRCGCWDCABTGGBCD

-----GCKGCGY-----

Original motif Consensus sequence: DGVBCABTGDWGCGRCSR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGGBCD



Dataset #:	2
Motif ID:	28
Motif name:	Egr1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.0453576

Alignment:

HGCGTGGGCGK

---GCKGCGY--

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YGCCCCACGCH



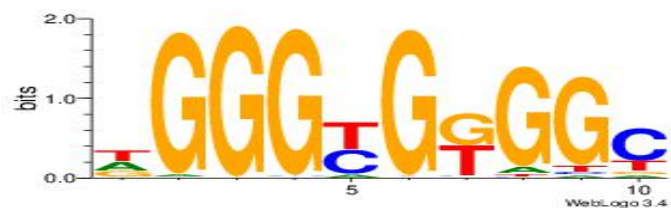
Dataset #: 2
 Motif ID: 36
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0476958

Alignment:

GCCYCMCCCD

-CMGCRGC--

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 2
 Motif ID: 16

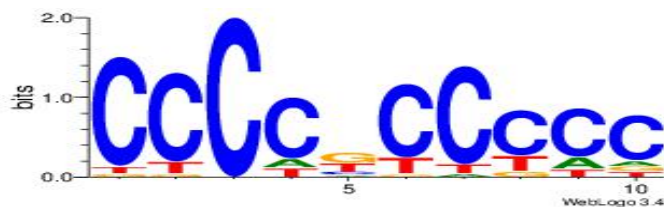
Motif name:	SP1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0490991

Alignment:

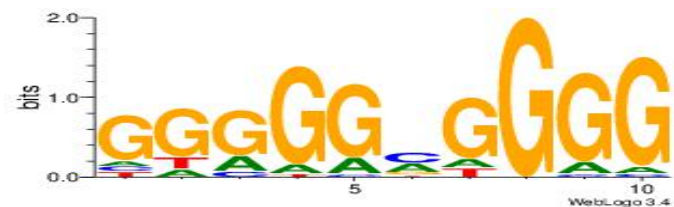
GGGGGYGGGG

GCKGCG---

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

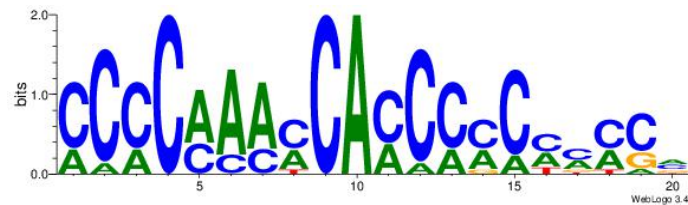


Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	7
Similarity score:	0.0498726

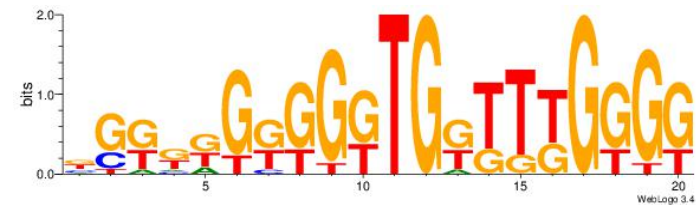
Alignment:

BGRRRGRGGRTGRTTYGGGG
-----GCKGCTY-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



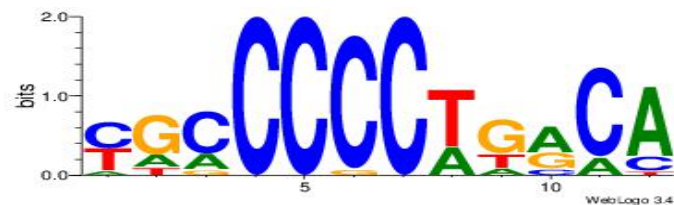
Dataset #:	2
Motif ID:	35
Motif name:	INSM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	7
Similarity score:	0.0511926

Alignment:

MGCCCCCTGMCA
---CMGCRGC---

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA



Dataset #: 1 Motif ID: 8 Motif name: Motif 8

Original motif Consensus sequence: CTGGGA



Reverse complement motif Consensus sequence: TCCCAG



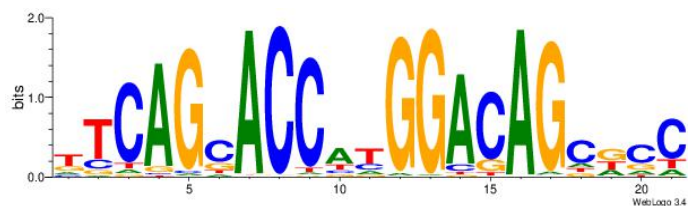
Best Matches for Top Significant Motif ID 8 (Highest to Lowest)

Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	6
Similarity score:	0.0392549

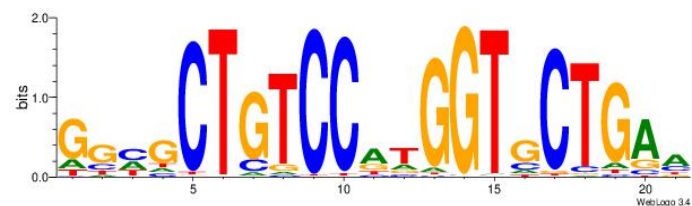
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
-----TCCCAG-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2
Motif ID: 23
Motif name: MZF1_1-4
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.0416319

Alignment:

TCCCCV

TCCCAG

Original motif Consensus sequence: BGGGGA



Reverse complement motif Consensus sequence: TCCCCV

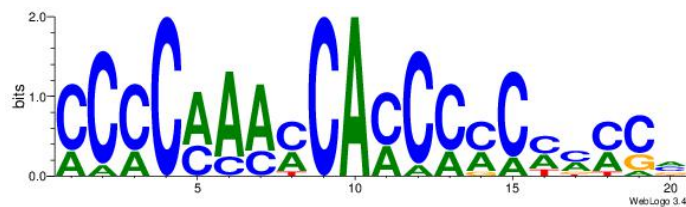


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0509122

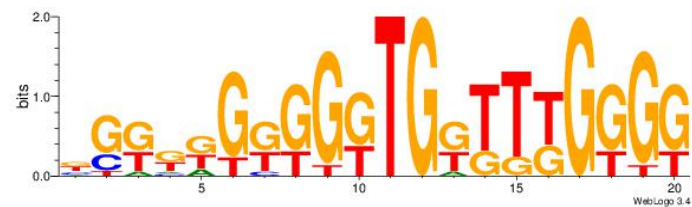
Alignment:

BGRRRGRGGRTGRTTYGGGG
 -----CTGGGA

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

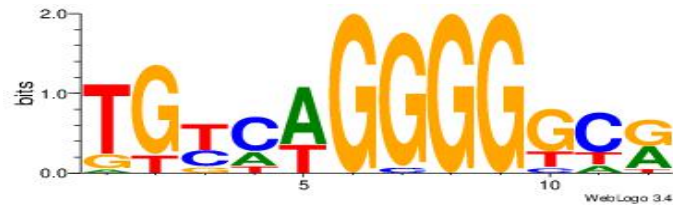


Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

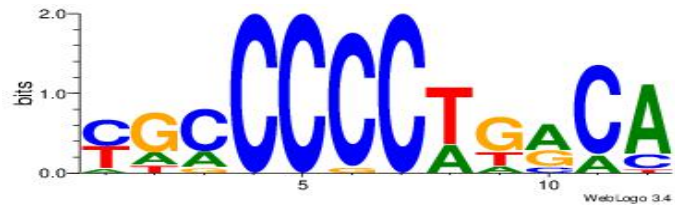
Number of overlap: 6
Similarity score: 0.0557857

Alignment:
TGYCAGGGGGCR
---CTGGGA---

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA

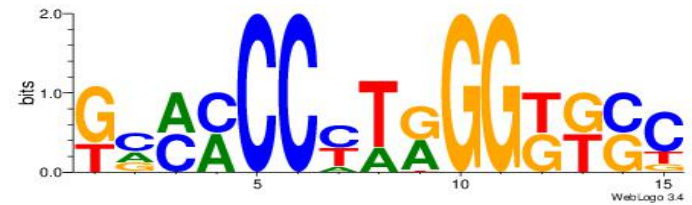
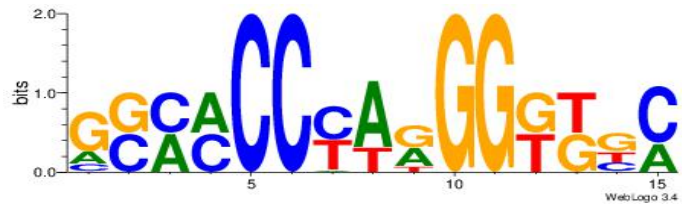


Dataset #: 2
Motif ID: 13
Motif name: Zfp423
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0624145

Alignment:
GYRYCCMTKGGYRSC
---TCCCAG-----

Original motif Consensus sequence: GSMCCYARGGKKKC

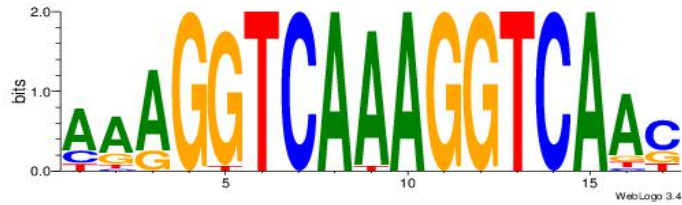
Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



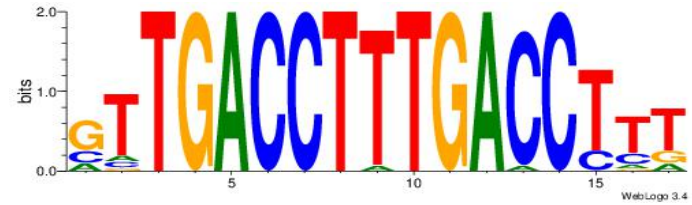
Dataset #: 2
 Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0650784

Alignment:
 AAAGGTCAAAGGTCAAC
 -----TCCCAG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

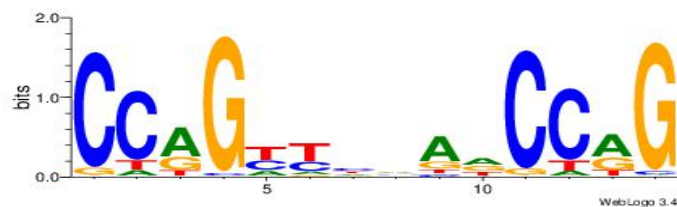


Dataset #: 2

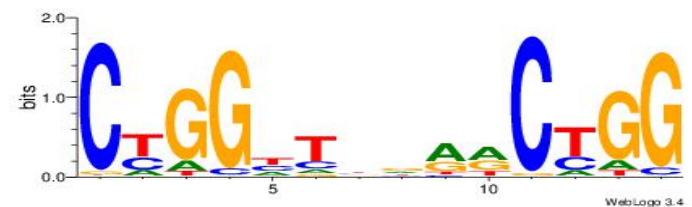
Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 6
 Similarity score: 0.0663804

Alignment:
 CKGGDTBDMMCTGG
 CTGGGA-----

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTGG



Dataset #: 2
 Motif ID: 28
 Motif name: Egr1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0678562

Alignment:

YCGCCCACGCH

--TCCCAG---

Original motif Consensus sequence: HCGTG GGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0714107

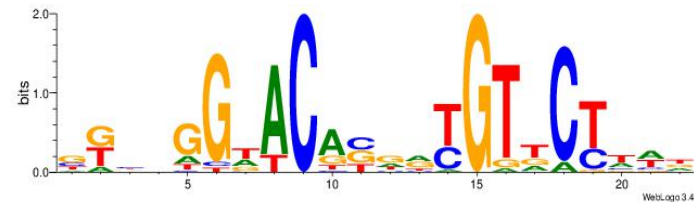
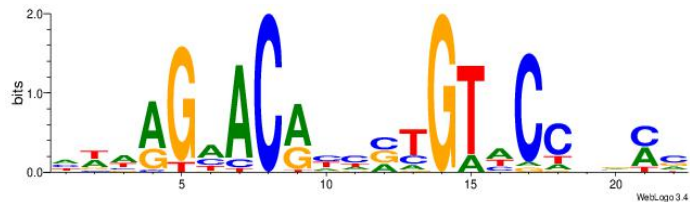
Alignment:

HWDAGHACRHHVTGTHCCHVMV

-----TCCCAG--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

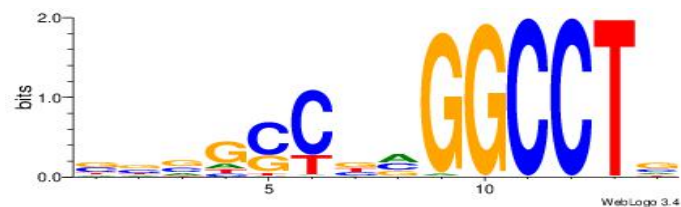
Reverse complement motif Consensus sequence:
VRVDGGHACAVDDKGTHCTDWH



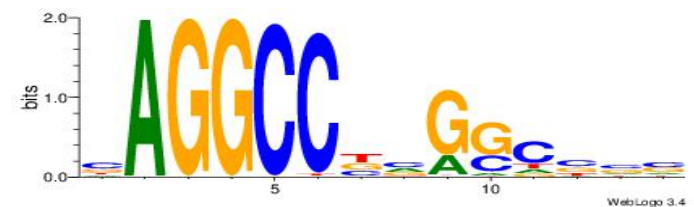
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0718041

Alignment:
 BBVGCCBVGGCCTV
 -----CTGGGA---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 1 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: AMACA



Reverse complement motif Consensus sequence: TGTRT



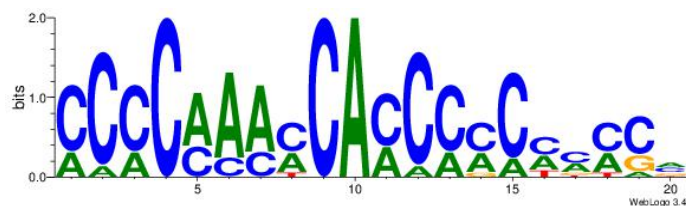
Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 5
 Similarity score: 0.0243918

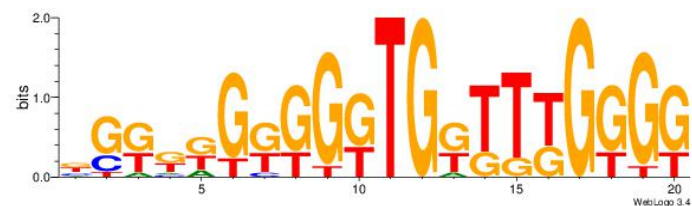
Alignment:

CCCCMAAMCAMECCMMMCV
 -----AMACA-----

Original motif Consensus sequence: CCCCMAAMCAMECCMMMCV



Reverse complement motif Consensus sequence: BGGRRGRGGRTGRTTYGGGG

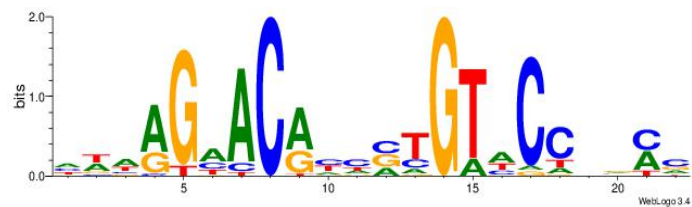


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 14
 Number of overlap: 5
 Similarity score: 0.0429089

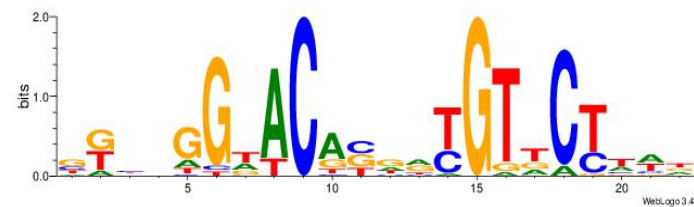
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 ----AMACA-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACA VDDKGTHCTDWH



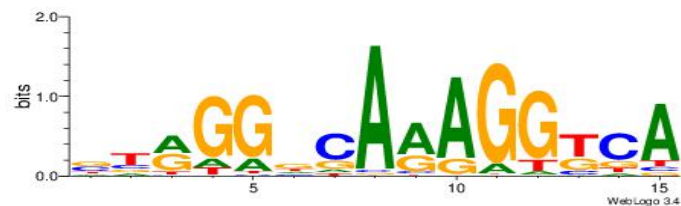
Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

Number of overlap: 5
Similarity score: 0.0595073

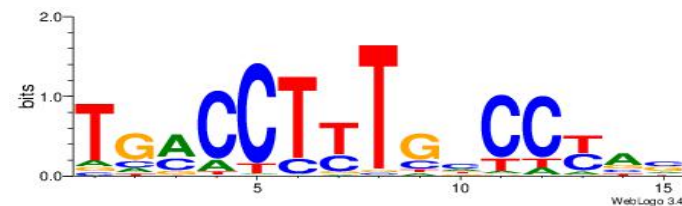
Alignment:

TGRCCTKTGHCKAB
-----TGTRT-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKK



Dataset #: 2
Motif ID: 26
Motif name: ArntAhr
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 5
Similarity score: 0.0600161

Alignment:

YGCGTG
TGTRT-

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

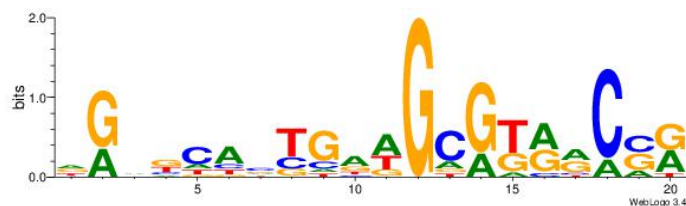


Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 5
 Similarity score: 0.0620995

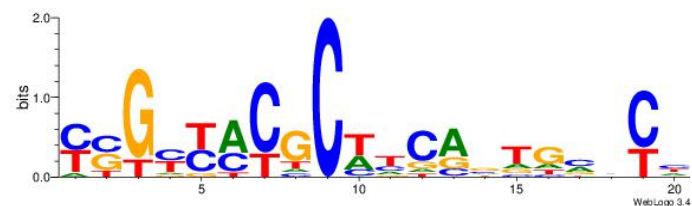
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----AMACA-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 2

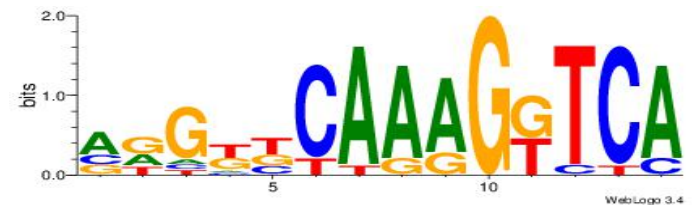
Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0650242

Alignment:
 AKGY YCAAAGRTCA
 -----AMACA---

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA



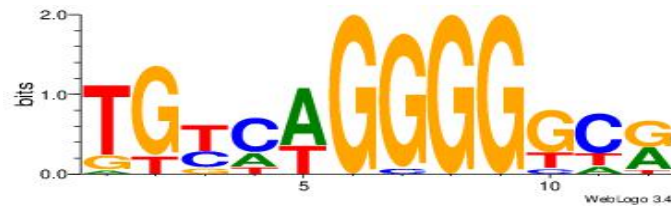
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 5
 Similarity score: 0.0670984

Alignment:

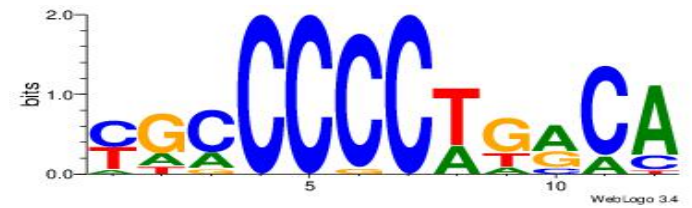
TGYCAGGGGGCR

TGTRT-----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



Dataset #:	2
Motif ID:	33
Motif name:	HIF1AARNT
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	5
Similarity score:	0.0700905

Alignment:

VCACGTBV

AMACA---

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV



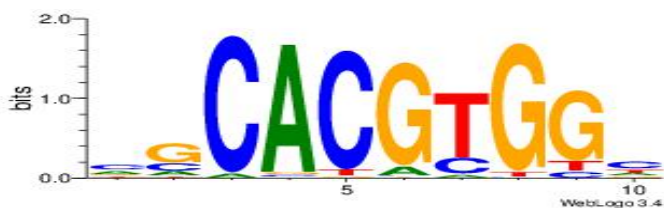
Dataset #: 2
 Motif ID: 38
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.0708148

Alignment:

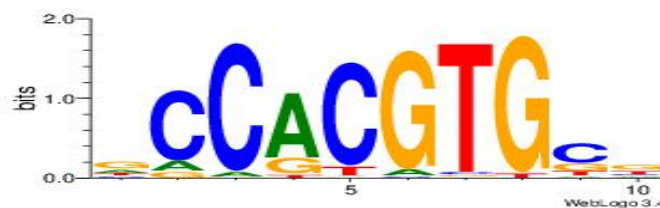
VGCACGTGGH

-AMACA----

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



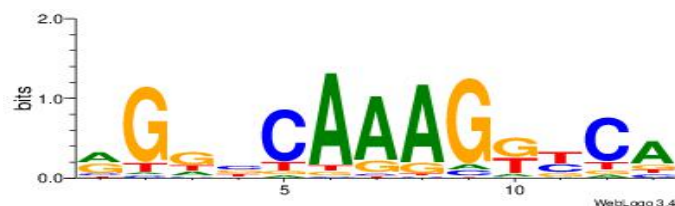
Dataset #: 2
 Motif ID: 34

Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.071574

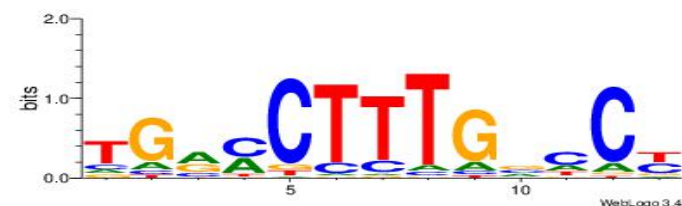
Alignment:

TGM YCTTTGBCCK
 -----TGTRT-----

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCCK



Dataset #: 1 Motif ID: 3 Motif name: Motif 3

Original motif Consensus sequence: AGSCWGG



Reverse complement motif Consensus sequence: CCWGSCT



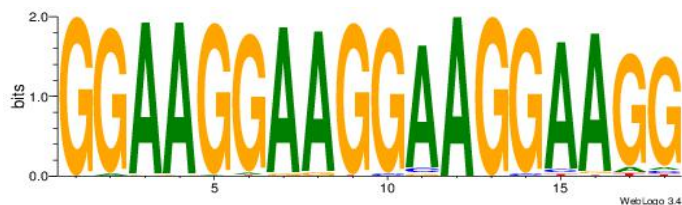
Best Matches for Top Significant Motif ID 3 (Highest to Lowest)

Dataset #: 2
 Motif ID: 32
 Motif name: EWSR1-FLI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 7
 Similarity score: 0.0395671

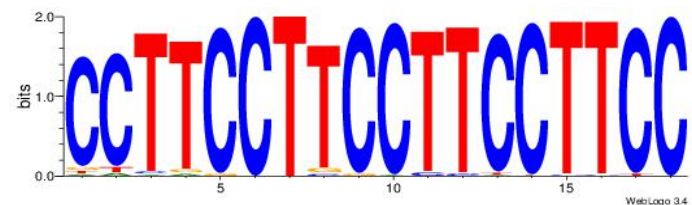
Alignment:

GGAAGGAAGGAAGGAAGG
 -----AGSCWGG-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

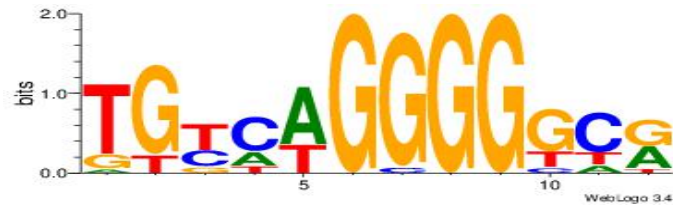


Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

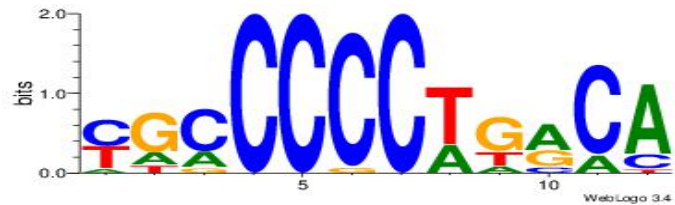
Number of overlap: 7
Similarity score: 0.0494688

Alignment:
MGCCCCCTGMCA
-----CCWGSCT

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA

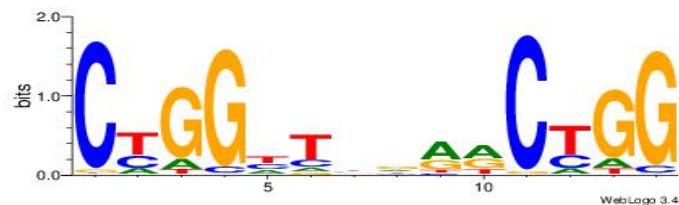
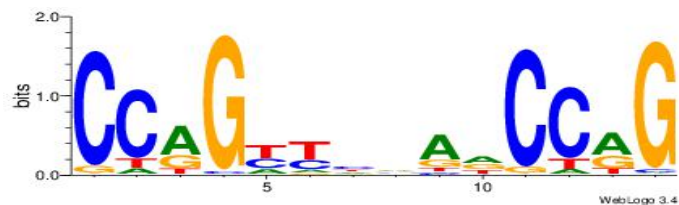


Dataset #: 2
Motif ID: 48
Motif name: Tcfcp2l1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0669354

Alignment:
CCAGYYHVADCCRG
CCWGSCT-----

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCTC

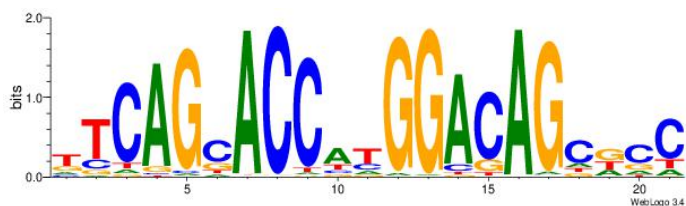


Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 7
 Similarity score: 0.0693747

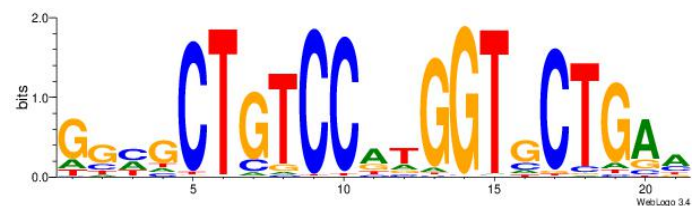
Alignment:

TTCAGCACCATGGACAGCKCC
 -----AGSCWGG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

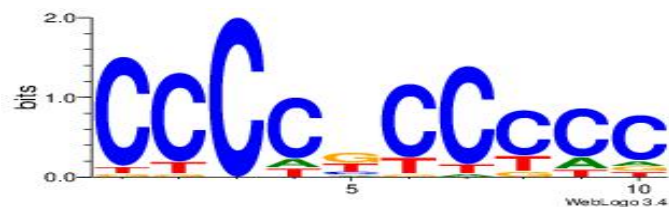


Dataset #: 2

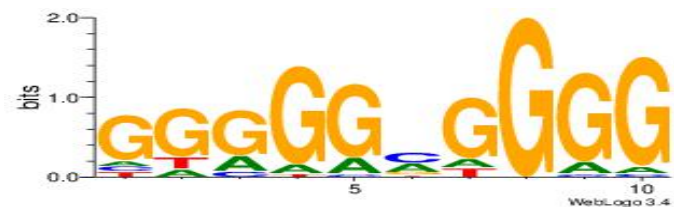
Motif ID: 16
 Motif name: SP1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0695377

Alignment:
 CCCCKCCCC
 -CCWGSCT--

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



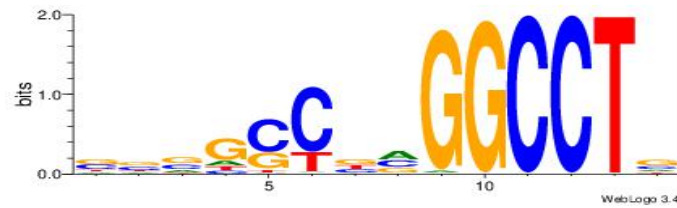
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0720685

Alignment:

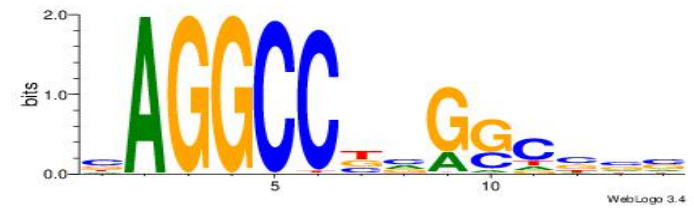
BBVGCCBVGGCCTV

-----CCWGSCT-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



Dataset #:	2
Motif ID:	29
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	13
Number of overlap:	7
Similarity score:	0.0771405

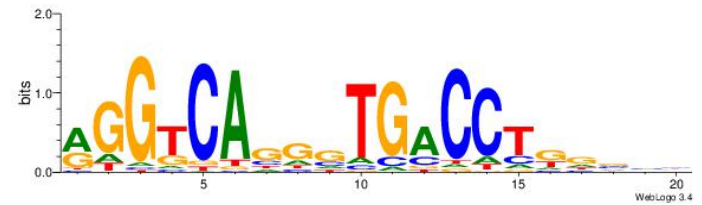
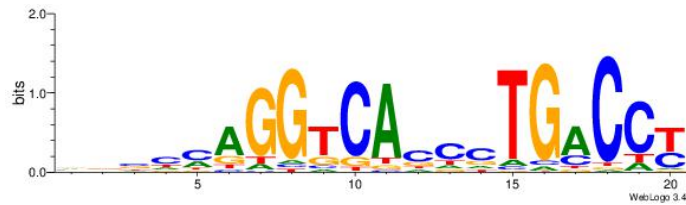
Alignment:

MGGTCAGGGTGACCTRDBHV

-----CCWGSCT-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV



Dataset #: 2
 Motif ID: 46
 Motif name: RORA_1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0772276

Alignment:
 TGACCTDVWT
 ---CCWGSCT

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT



Dataset #: 2
 Motif ID: 36

Motif name:	Klf4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0798994

Alignment:

```

GCCYCMCCCD
---CCWGSCT

```

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



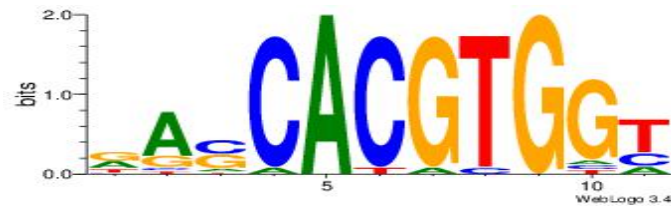
Dataset #:	2
Motif ID:	39
Motif name:	MYCMAX
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	7
Similarity score:	0.0839075

Alignment:

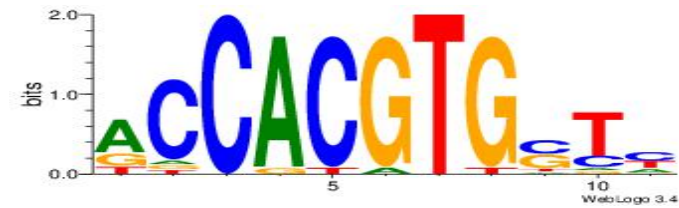
RASCACGTGGT

AGSCWGG----

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #: 1 Motif ID: 1 Motif name: Motif 1

Original motif Consensus sequence: RGGAAR



Reverse complement motif Consensus sequence: MTTCCK



Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

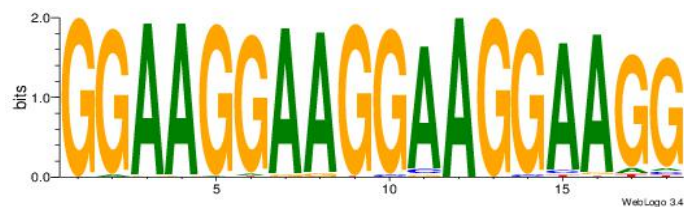
Dataset #:	2
Motif ID:	32
Motif name:	EWSR1-FLI1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	12

Number of overlap: 6
Similarity score: 0.0146511

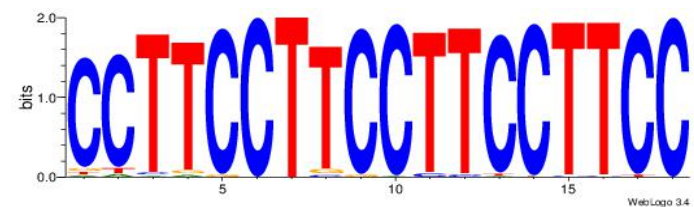
Alignment:

GGAAGGAAGGAAGGAAGG
-----RGGAAR-

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence:
CCTTCCTTCCTTCCTTCC



Dataset #: 2
Motif ID: 37
Motif name: MIZF
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0608243

Alignment:

BAACGTCCGC
---MTTCK-

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV



Dataset #: 2
 Motif ID: 41
 Motif name: MZF1_5-13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0753789

Alignment:

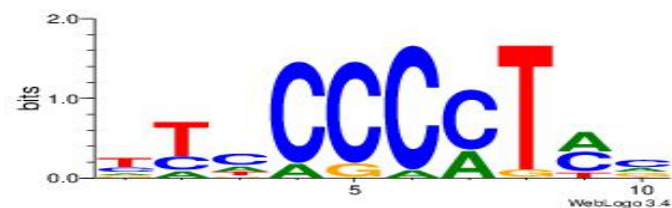
BKAGGGGDAD

----RGAAR

Original motif Consensus sequence: BKAGGGGDAD



Reverse complement motif Consensus sequence: BTHCCCTYB



Dataset #: 2
 Motif ID: 42

Motif name:	NFKB1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0757695

Alignment:

GGGGAAKCCCC

-RGGGAAR----

Original motif Consensus sequence: GGGGRTTCCCC



Reverse complement motif Consensus sequence: GGGGAAKCCCC



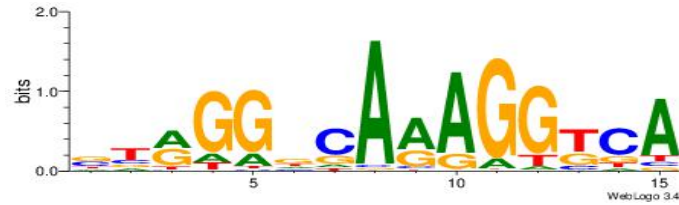
Dataset #:	2
Motif ID:	20
Motif name:	PPARGRXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.0800484

Alignment:

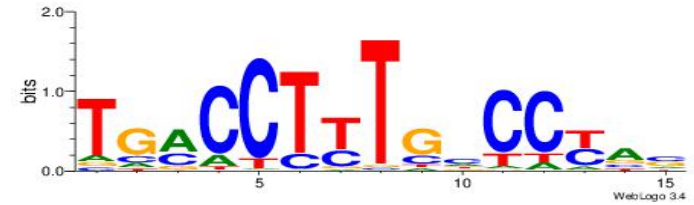
BTRGGDCARAGGKCA

---RGGAAR-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCCCK



Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.0829223

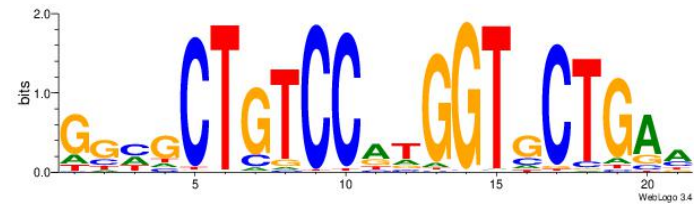
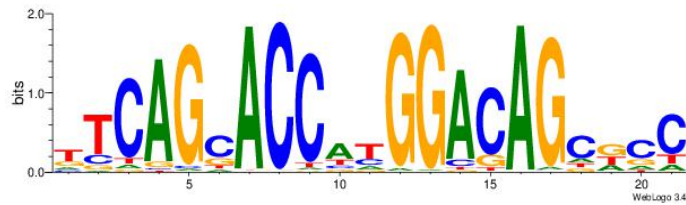
Alignment:

TTCAGCACCATGGACAGCKCC

-----RGGAAR-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA

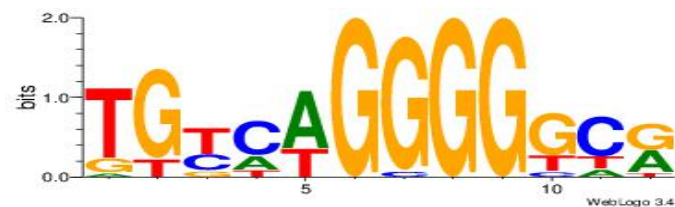


Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0832926

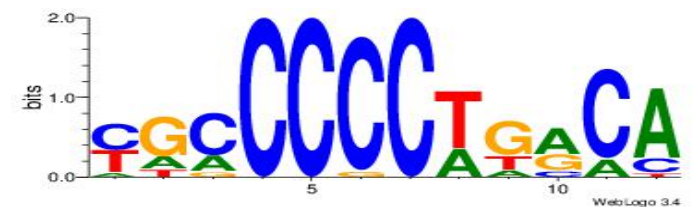
Alignment:

TGYCAGGGGGCR
 -----RGAAR

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCTGMCA



Dataset #: 2
 Motif ID: 18

Motif name:	RREB1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0835516

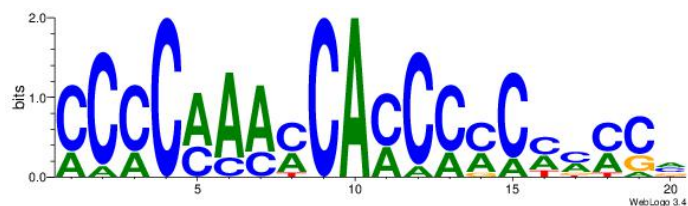
Alignment:

```

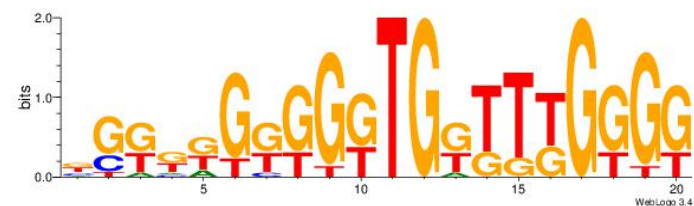
BGRRRGRGGRTGRTTYGGGG
----RGAAR-----

```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



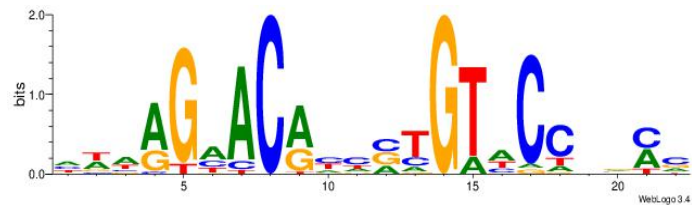
Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0836451

Alignment:

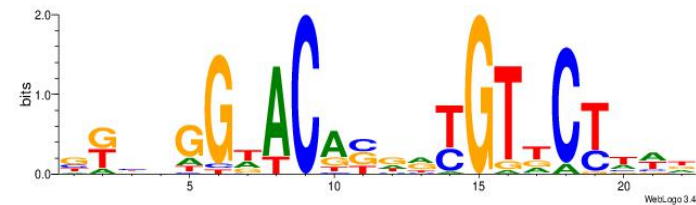
HWDAGHACRHHVTGTHCCHVMV

---RGGAAR-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



Dataset #:	2
Motif ID:	27
Motif name:	E2F1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0842331

Alignment:

GCGCSAAA

--RGGAAR

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

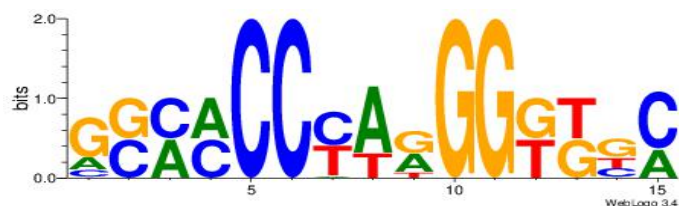


Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0850287

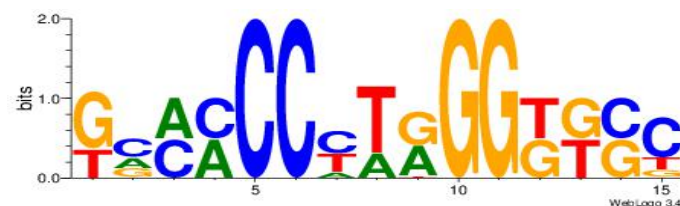
Alignment:

GYRYCCMTKGGYRSC
 -----RGAAR-

Original motif Consensus sequence: GSMMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



Dataset #: 1 **Motif ID: 7** **Motif name: Motif 7**

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG



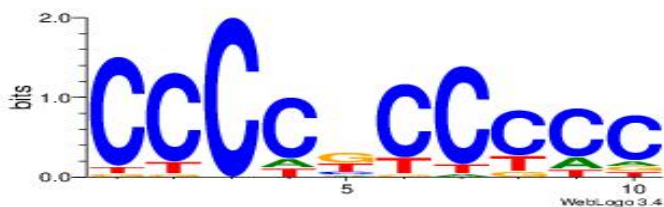
Best Matches for Top Significant Motif ID 7 (Highest to Lowest)

Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0423611

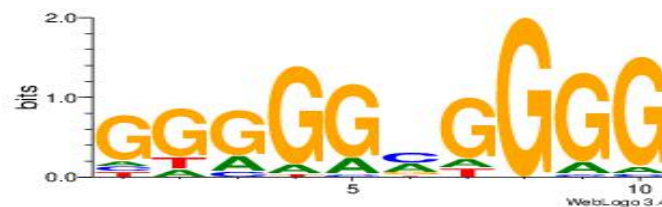
Alignment:

CCCCKCCCCC
-CCCRCCCC-

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



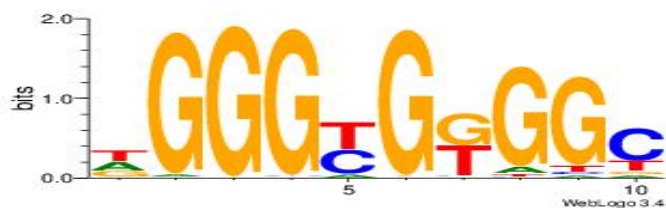
Dataset #: 2
 Motif ID: 36
 Motif name: Klf4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0461644

Alignment:

DGGGYGKGGC

GGGGMGGG--

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 2
 Motif ID: 28
 Motif name: Egr1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0650374

Alignment:
YCGCCACGCH
---CCCRCCCC

Original motif Consensus sequence: HCGTG GGGCGK



Reverse complement motif Consensus sequence: YCGCCACGCH

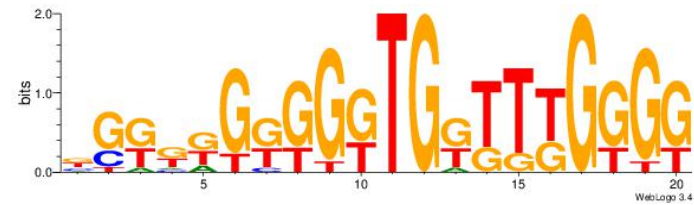
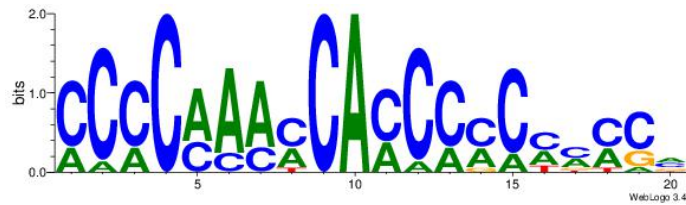


Dataset #: 2
Motif ID: 18
Motif name: RREB1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.076401

Alignment:
CCCCMAAMCAMCCMCMMMC
-CCCRCCCC-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC

Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG



Dataset #: 2
 Motif ID: 42
 Motif name: NFKB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0893429

Alignment:

GGGGA AKCCCC

GGGMGGG---

Original motif Consensus sequence: GGGGRTTCCCC



Reverse complement motif Consensus sequence: GGGGA AKCCCC



Dataset #: 2
 Motif ID: 35

Motif name:	INSM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0936832

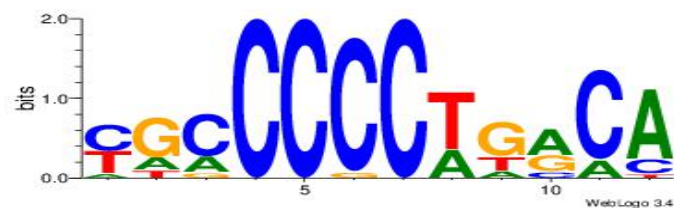
Alignment:

TGYCAGGGGGCR
GGGGMGGG----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



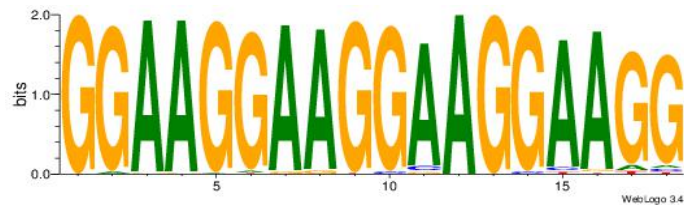
Dataset #:	2
Motif ID:	32
Motif name:	EWSR1-FLI1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.0950969

Alignment:

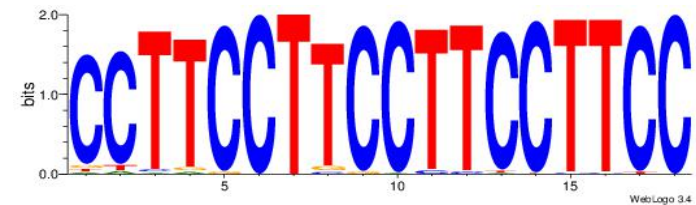
GGAAGGAAGGAAGGAAGG

-----GGGGMGG-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence:
CCTTCCTTCCTTCCTTCC



Dataset #:	2
Motif ID:	21
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0998932

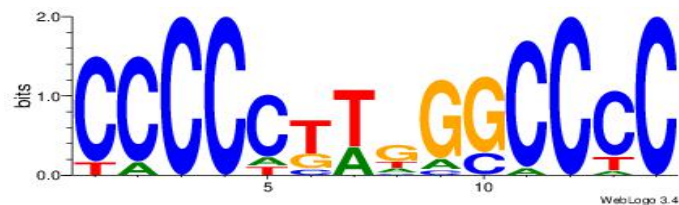
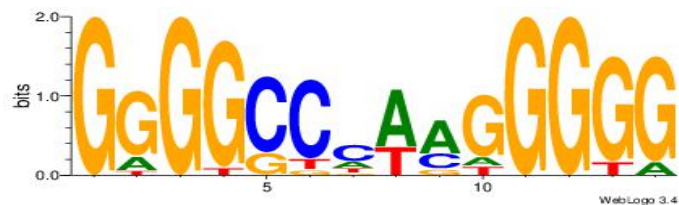
Alignment:

GGGGCCCAAGGGGG

GGGGMGG-----

Original motif Consensus sequence: GGGGCCCAAGGGGG

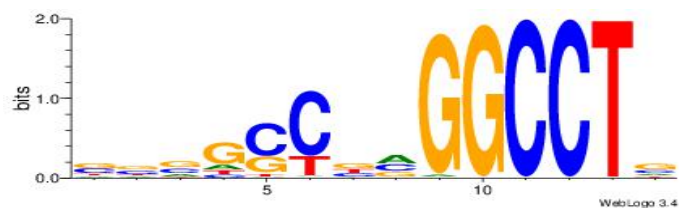
Reverse complement motif Consensus sequence: CCCCCTTGGGCC



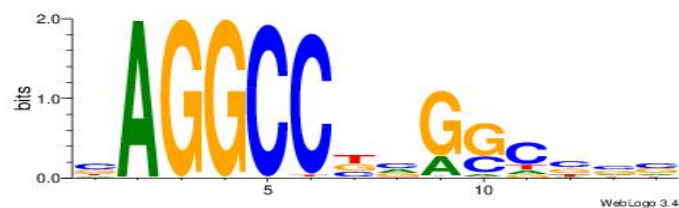
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.10221

Alignment:
 BBVGCCBVGGCCTV
 ----CCCRCCCC--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



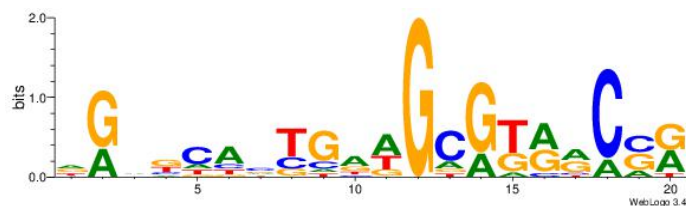
Dataset #: 2
 Motif ID: 45

Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.102497

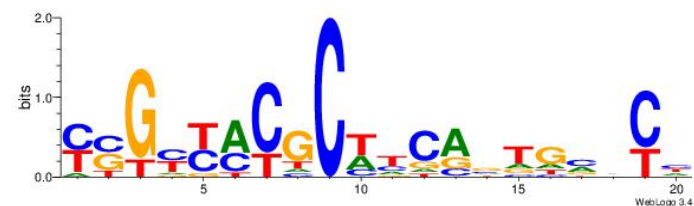
Alignment:

```
DGVBCABTGDWGCGRRCR
-----GGGGMGGG----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 2 Motif ID: 26 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



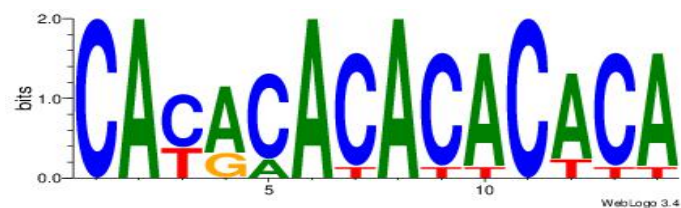
Best Matches for Top Significant Motif ID 26 (Highest to Lowest)

Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0308396

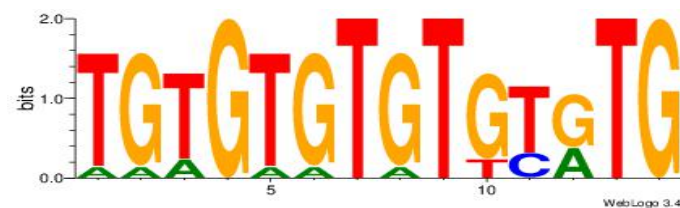
Alignment:

TGTGTGTGTGKTG
 -----YGCGTG--

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTG



Dataset #: 1
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif

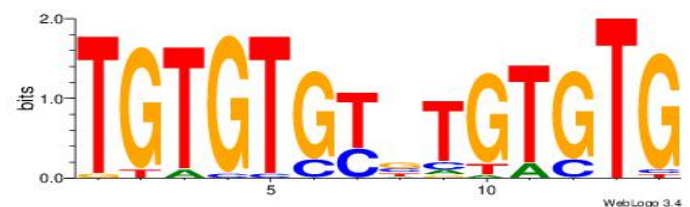
Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0350575

Alignment:
 CACACAVRCACACA
 -----CACGCM

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



Dataset #: 1
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0586538

Alignment:
 GGGGMGGG
 YGCGTG--

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG



Dataset #: 1
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0884818

Alignment:
CCWGSCT
-CACGCM

Original motif Consensus sequence: AGSCWGG



Reverse complement motif Consensus sequence: CCWGSCT



Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 5
 Similarity score: 0.563057

Alignment:

AMACA-
 CACGCM

Original motif Consensus sequence: AMACA



Reverse complement motif Consensus sequence: TGTRT



Dataset #: 1
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 5

Similarity score: 0.572774

Alignment:

-GCKGCTG

YGCCTG--

Original motif Consensus sequence: CMGCRGC



Reverse complement motif Consensus sequence: GCKGCTG



Dataset #: 1
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 5
Similarity score: 0.581904

Alignment:

-TCCCAG

CACGCM-

Original motif Consensus sequence: CTGGGA

Reverse complement motif Consensus sequence: TCCCAG



Dataset #: 1
 Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 4
 Similarity score: 1.06919

Alignment:
 --KCAGAG
 YGCGTG--

Original motif Consensus sequence: CTCTGY



Reverse complement motif Consensus sequence: KCAGAG



Dataset #: 2 Motif ID: 33 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



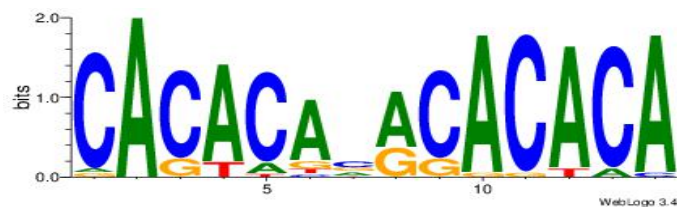
Best Matches for Top Significant Motif ID 33 (Highest to Lowest)

Dataset #: 1
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0745994

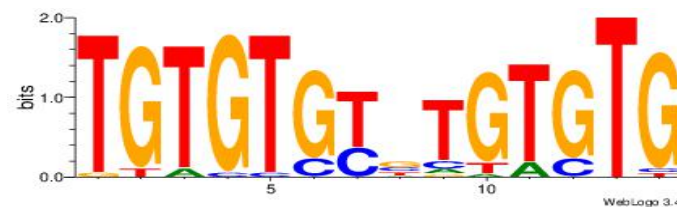
Alignment:

CACACAVRCACACA
 -----VCACGTBV-

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

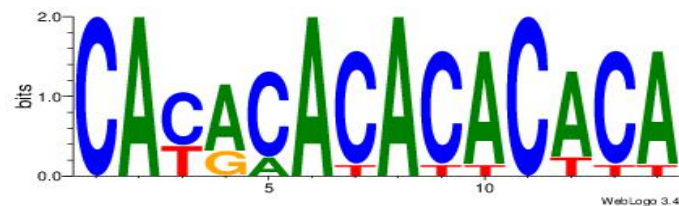


Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0850889

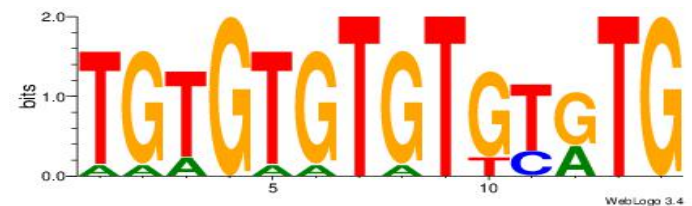
Alignment:

CAYACACACACACA
 ---VCACGTBV---

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKT



Dataset #: 1
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 7

Similarity score: 0.588622

Alignment:
CCCRCCCC-
-VCACGTBV

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG



Dataset #: 1
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 5
Similarity score: 1.55675

Alignment:
---AGSCWGG
VCACGTBV--

Original motif Consensus sequence: AGSCWGG

Reverse complement motif Consensus sequence: CCWGSCT



Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 5
 Similarity score: 1.57238

Alignment:
 TGTRT---
 VBACGTGV

Original motif Consensus sequence: AMACA



Reverse complement motif Consensus sequence: TGTRT



Results created by MOTIFSIM on 06-18-2018 23:13:48
Runtime: 761.535 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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