



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

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
Phylogenetic 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)

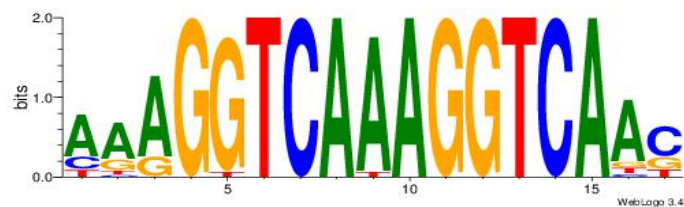
Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.012269

Alignment:

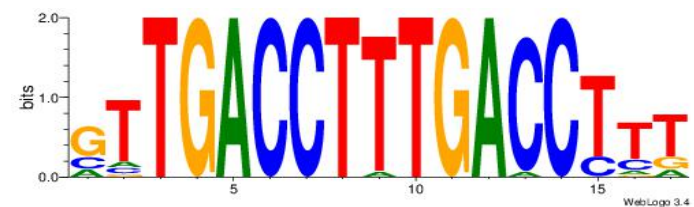
AAAGGTCAAAGGTCAAC

-----KCAGAG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

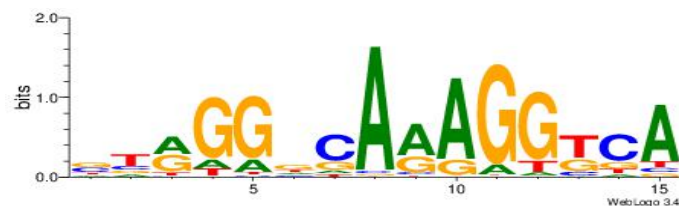


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0140102

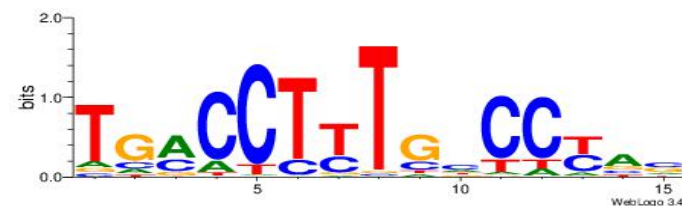
Alignment:

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

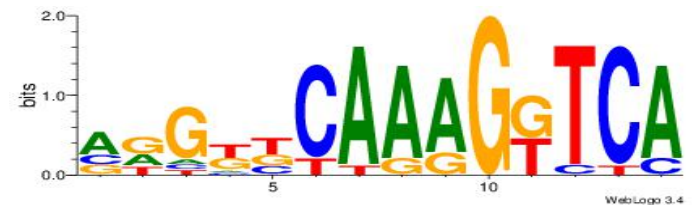
Number of overlap: 6
Similarity score: 0.0186793

Alignment:
AKGYICAAAGRTCA
----KCAGAG----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYICAAAGRTCA

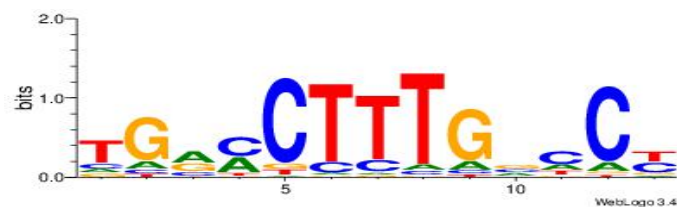
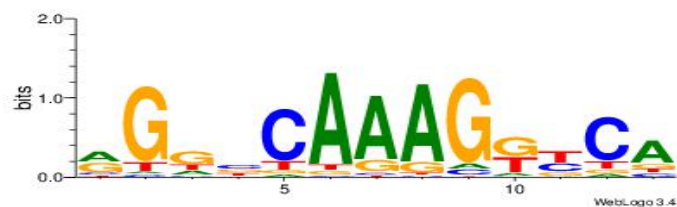


Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020602

Alignment:
RGGBCAAAGKYCA
---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA

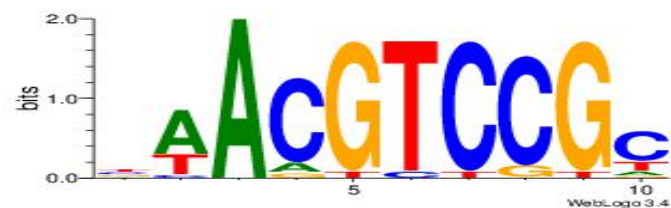
Reverse complement motif Consensus sequence: TGMTCCTTGBCCK



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: 1
 Number of overlap: 6
 Similarity score: 0.0221665

Alignment:
 BAACGTCCGC
 ----CTCTGY

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



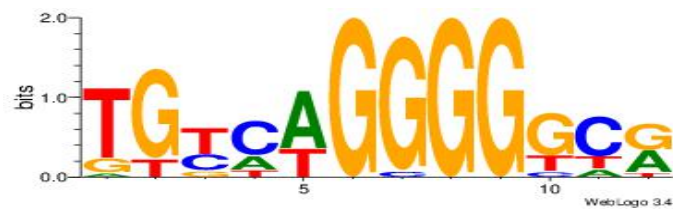
Dataset #: 2
 Motif ID: 35

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

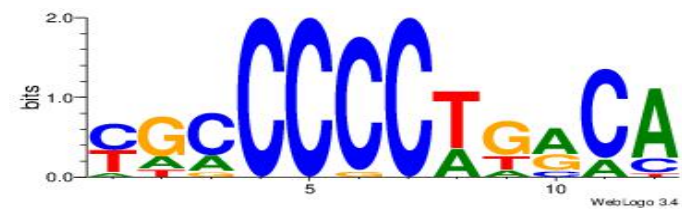
Alignment:

TGYCAGGGGGCR
 --KCAGAG----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



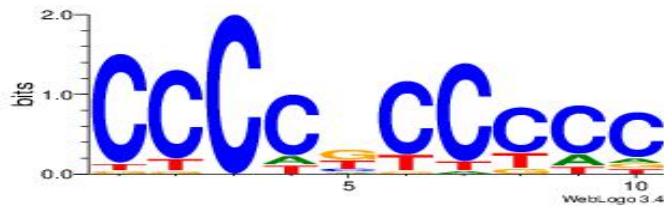
Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0349642

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

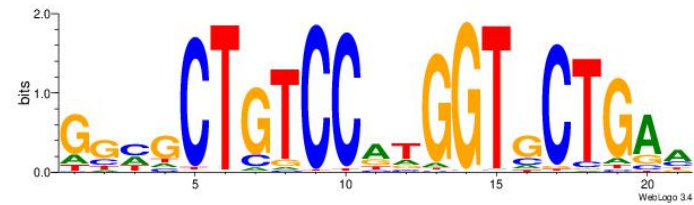
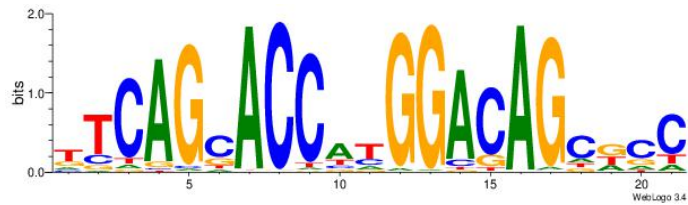
Alignment:

GGYGCTGTCCATGGTGCTGAA

--CTCTGY-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

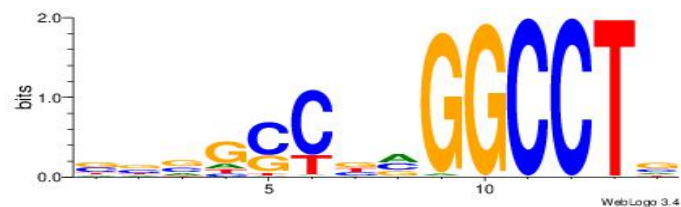
Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



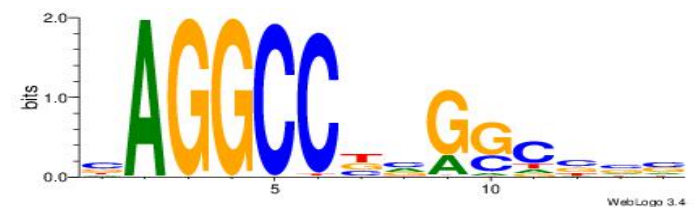
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0448449

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

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



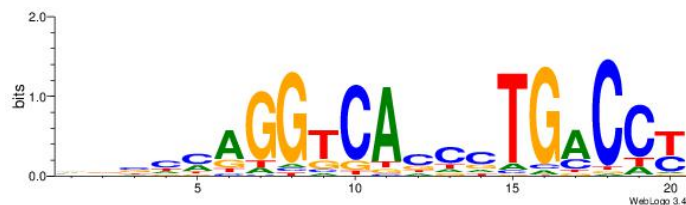
Dataset #: 2
 Motif ID: 29

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

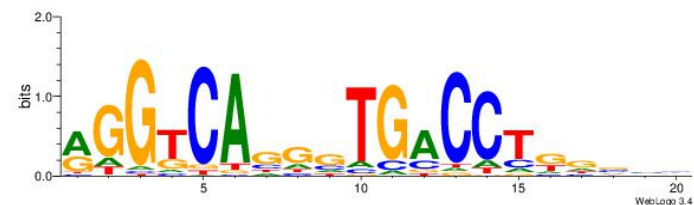
Alignment:

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



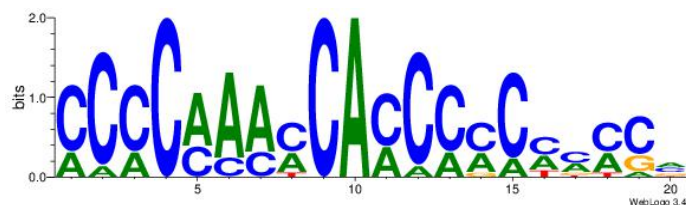
Best Matches for Top Significant Motif ID 5 (Highest to Lowest)

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

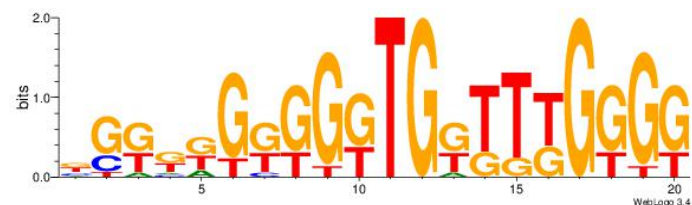
Alignment:

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



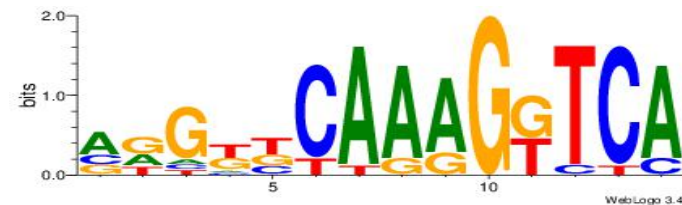
Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0279129

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

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA

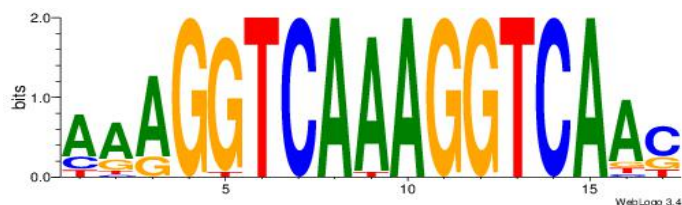


Dataset #: 2
 Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 5
 Similarity score: 0.0292478

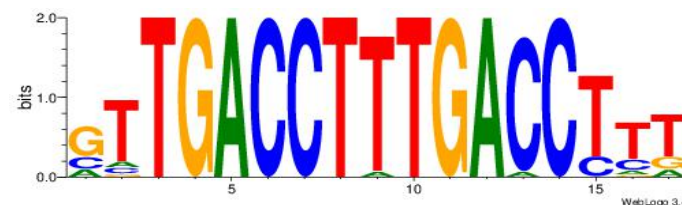
Alignment:

AAAGGTCAAAGGTCAAC
 -----ATKTM----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



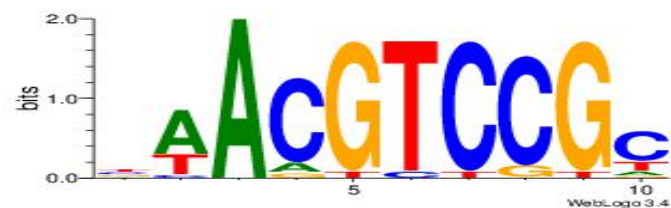
Dataset #: 2
 Motif ID: 37
 Motif name: MIZF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0292478

Alignment:

BAACGTCCGC

--ATKTM---

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT

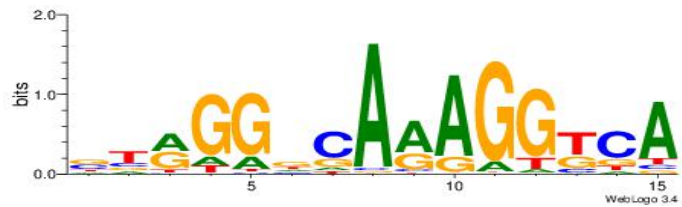


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 5

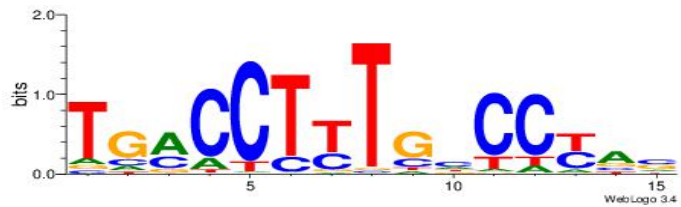
Similarity score: 0.0305369

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

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKK

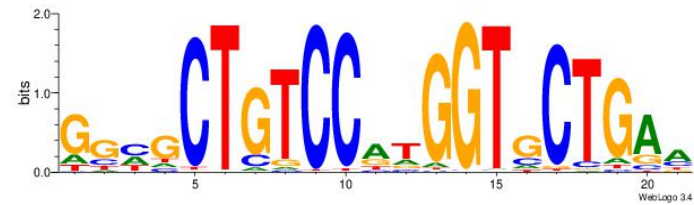
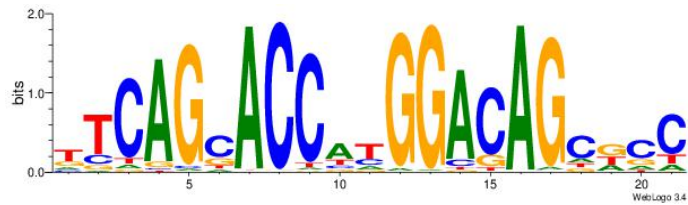


Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 13
Number of overlap: 5
Similarity score: 0.0315454

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

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

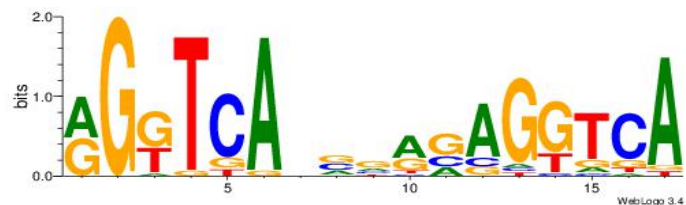
Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



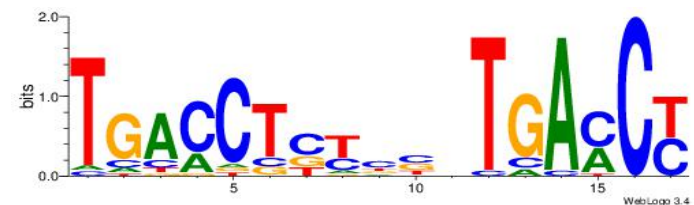
Dataset #: 2
 Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 5
 Similarity score: 0.0335956

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: Backward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0336052

Alignment:

AWVDAGGTCA

---RARAT--

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT



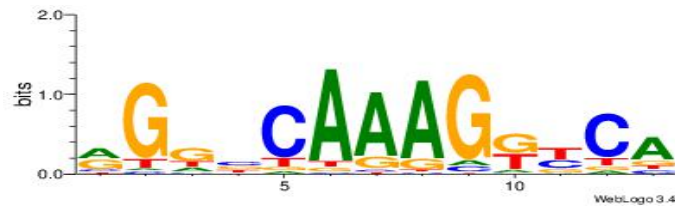
Dataset #: 2
 Motif ID: 34
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 5
 Similarity score: 0.0367105

Alignment:

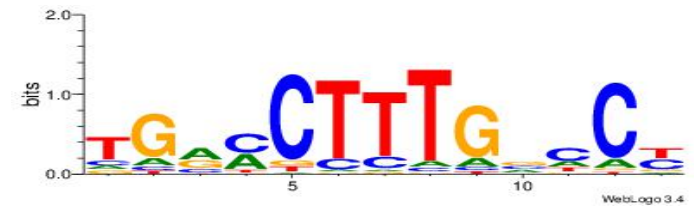
RGGBCAAAGKYCA

-----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



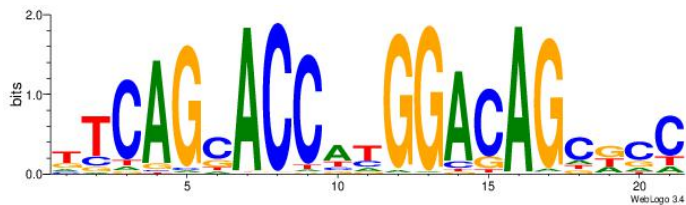
Best Matches for Top Significant Motif ID 6 (Highest to Lowest)

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

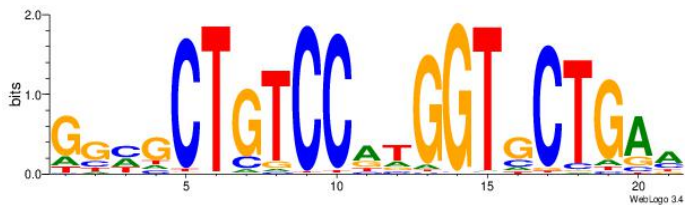
Number of overlap: 7
Similarity score: 0.0205607

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



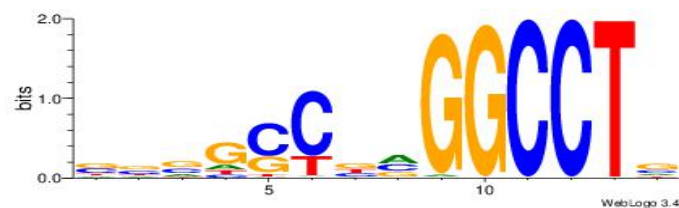
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 7
 Similarity score: 0.038091

Alignment:

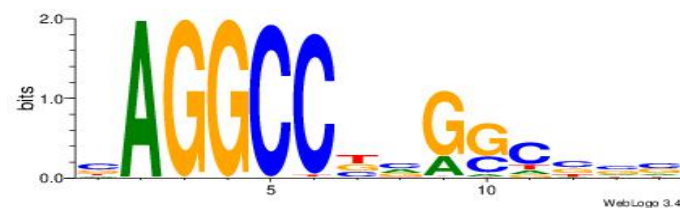
BBVGCCBVGGCCTV

----CMGCRGC---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 2
 Motif ID: 15

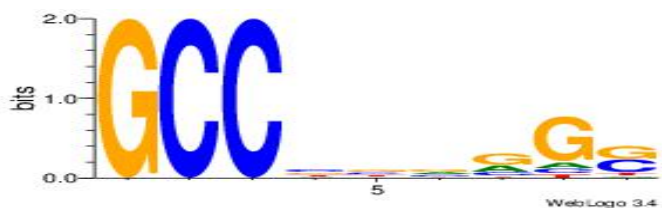
Motif name:	TFAP2A
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0393168

Alignment:

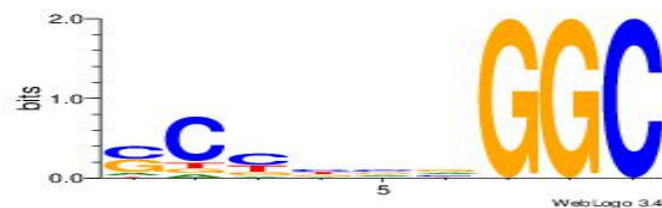
SCMVBBGGC

--CMGCRGC

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



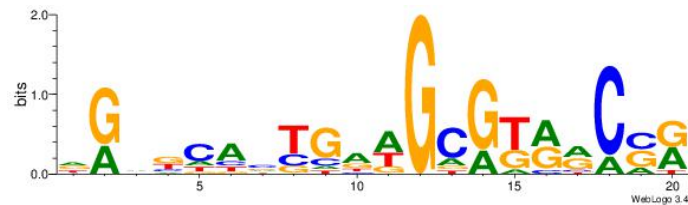
Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	7
Similarity score:	0.0448462

Alignment:

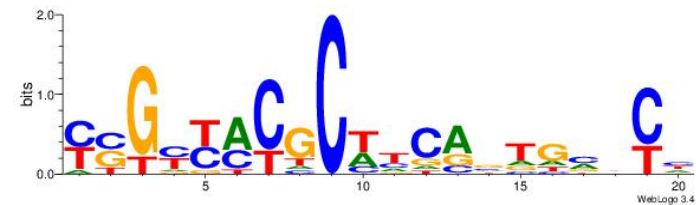
MSGKKRCGCWDCABTGBBCD

-----GCKGCGY-----

Original motif Consensus sequence: DGVBCABTGDWGCGRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



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



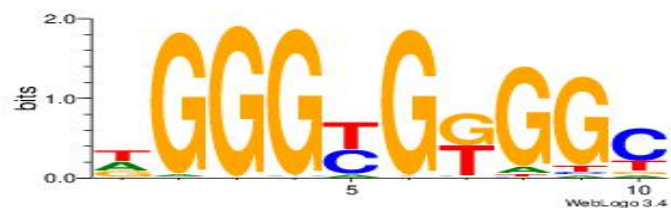
Dataset #: 2
 Motif ID: 36
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0476958

Alignment:

GCCYCMCCCD

-CMGCRGC--

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 2
 Motif ID: 16

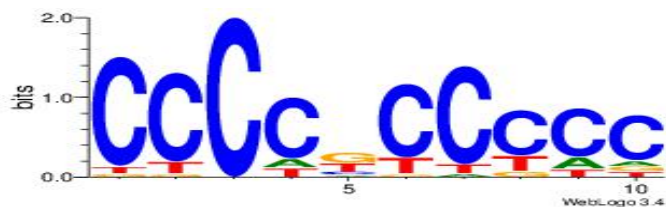
Motif name:	SP1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0490991

Alignment:

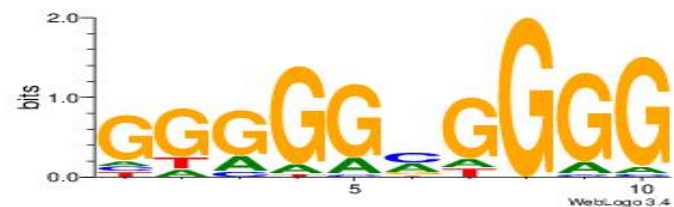
GGGGGYGGGG

GCKGCG---

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

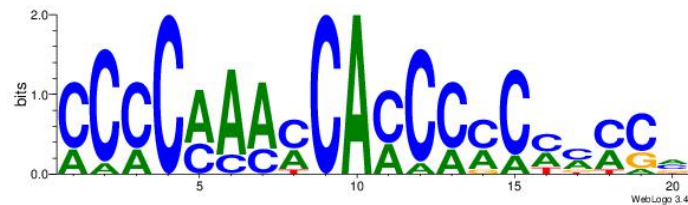


Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	7
Similarity score:	0.0498726

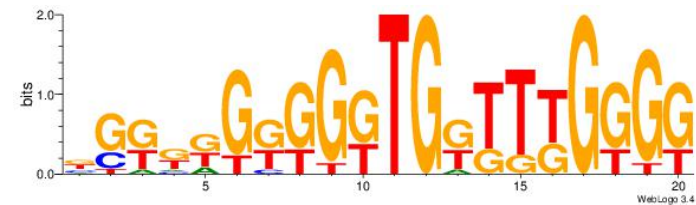
Alignment:

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

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG



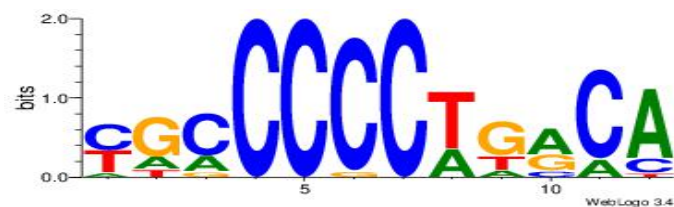
Dataset #:	2
Motif ID:	35
Motif name:	INSM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	7
Similarity score:	0.0511926

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



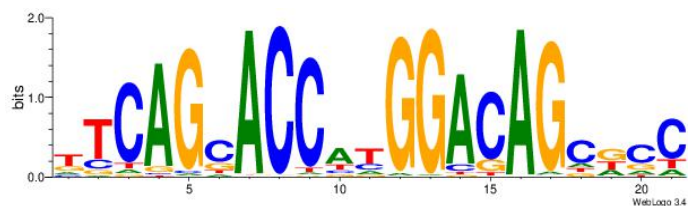
Best Matches for Top Significant Motif ID 8 (Highest to Lowest)

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

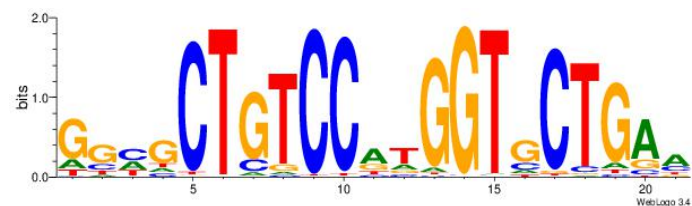
Alignment:

```
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

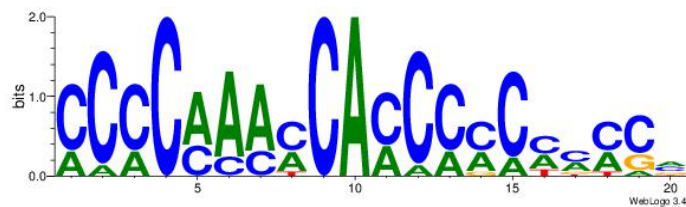


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0509122

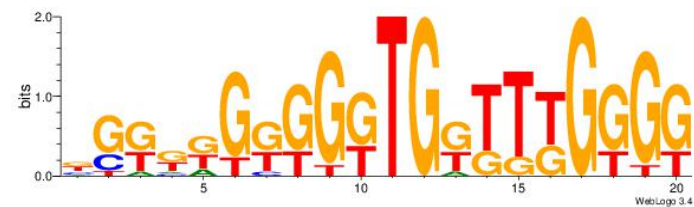
Alignment:

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: Backward
 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

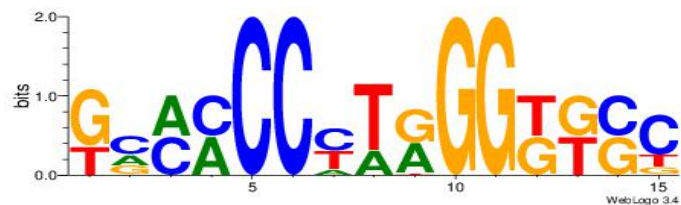
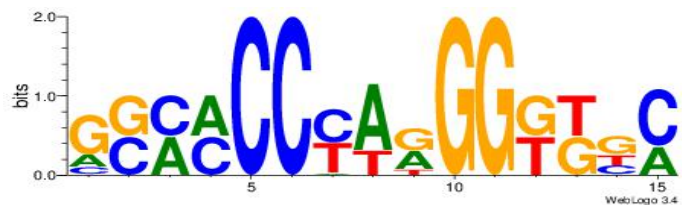


Dataset #: 2
Motif ID: 13
Motif name: Zfp423
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0624145

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

Original motif Consensus sequence: GSMCCYARGGKKKC

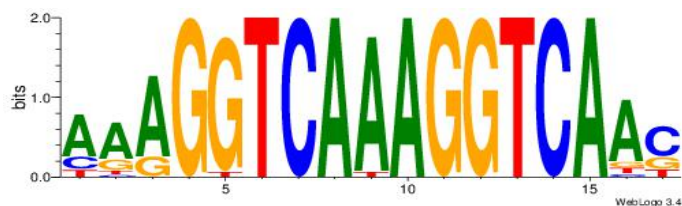
Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



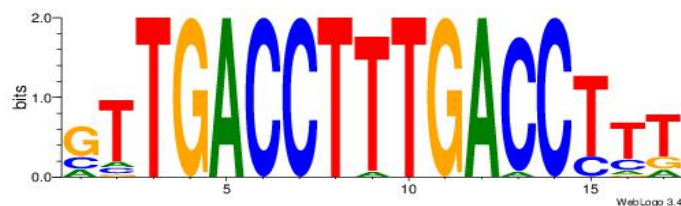
Dataset #: 2
 Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0650784

Alignment:
 GTTGACCTTTGACCTTT
 -----CTGGGA-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

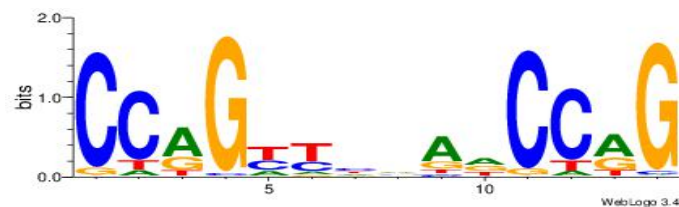


Dataset #: 2

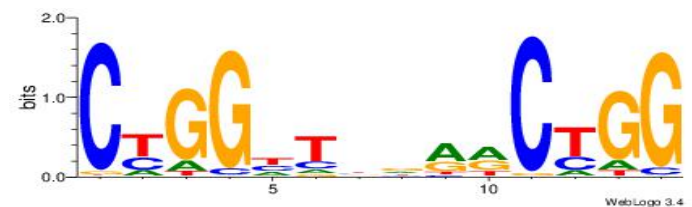
Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 6
 Similarity score: 0.0663804

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

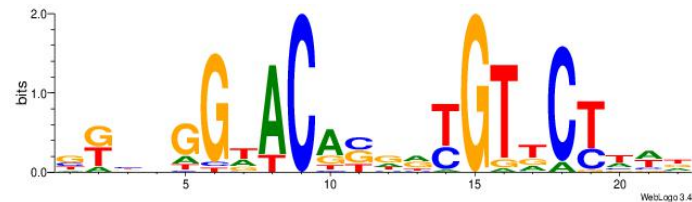
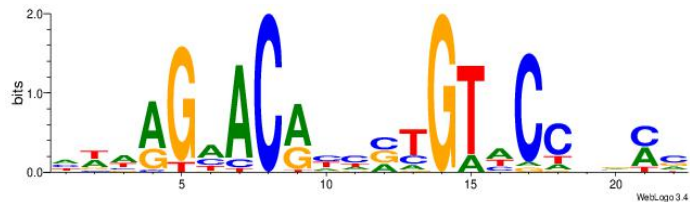
Alignment:

HWDAGHACRHHVTGTHCCHVMV

-----TCCCAG--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

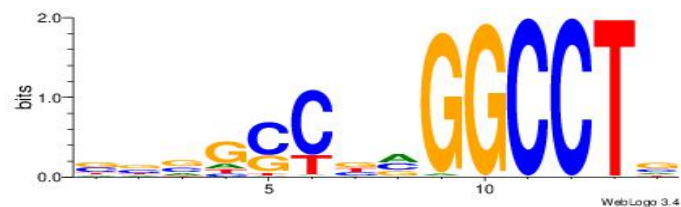
Reverse complement motif Consensus sequence:
VRVDGGHACAVDDKGTHCTDWH



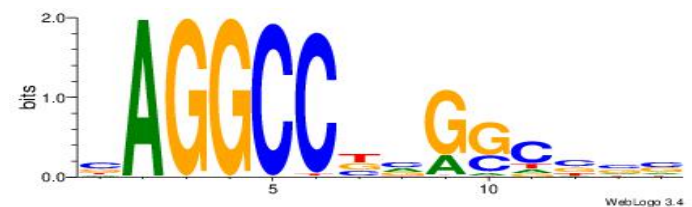
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0718041

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



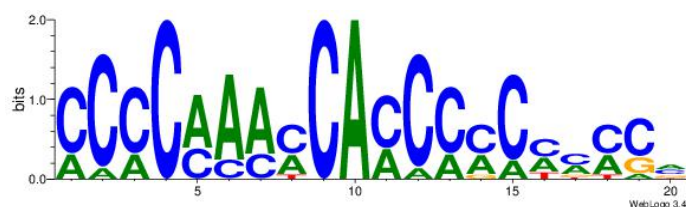
Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

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

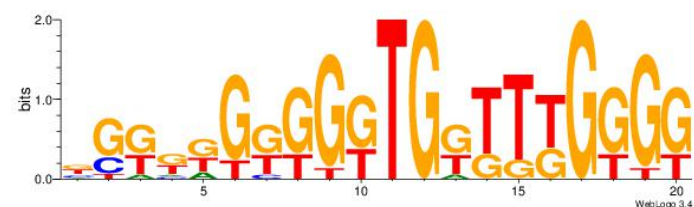
Alignment:

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

Original motif Consensus sequence: CCCCMAAMCAMECCMMMCV



Reverse complement motif Consensus sequence: BGGRRGRGGRTGRTTYGGGG

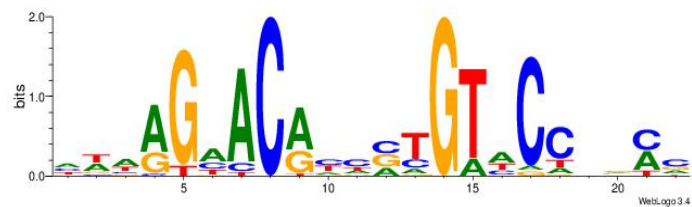


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.0429089

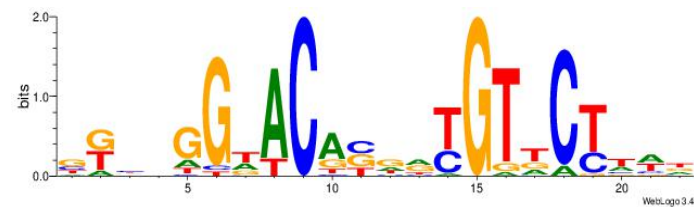
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 ----AMACA-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACA VDDKGTHCTDWH

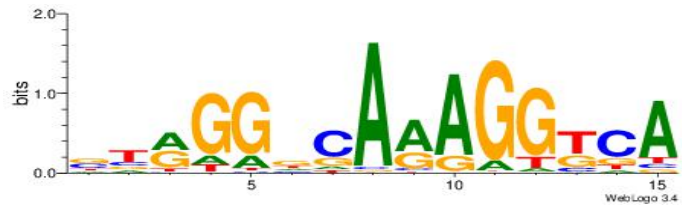


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

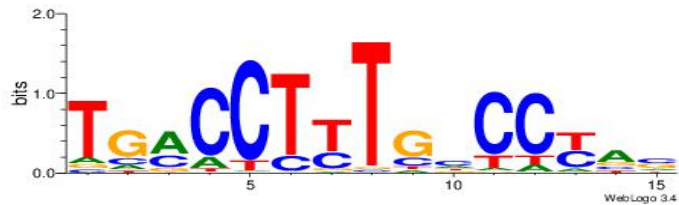
Number of overlap: 5
Similarity score: 0.0595073

Alignment:
TGRCCCTKTGHCCCKAB
-----TGTRT-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



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

Alignment:
YGCGTG
TGTRT-

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

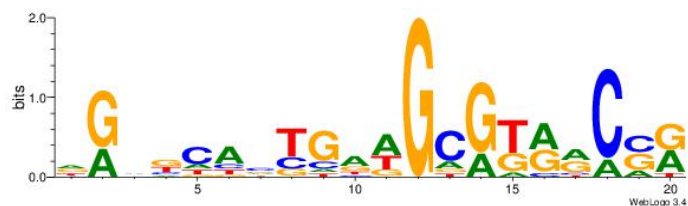


Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 5
 Similarity score: 0.0620995

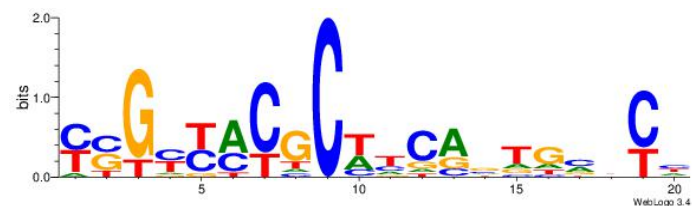
Alignment:

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

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 2

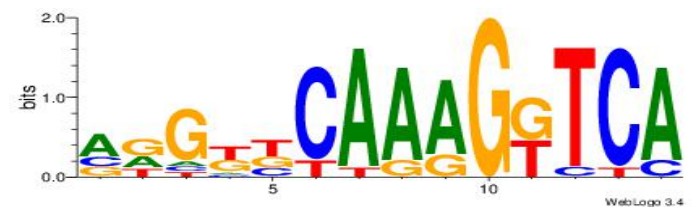
Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0650242

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

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA



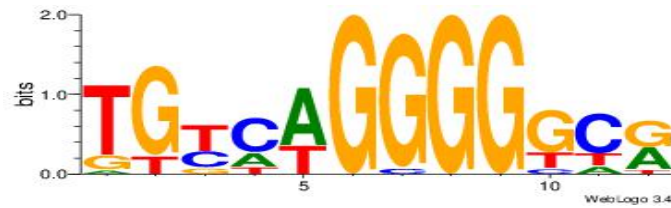
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 5
 Similarity score: 0.0670984

Alignment:

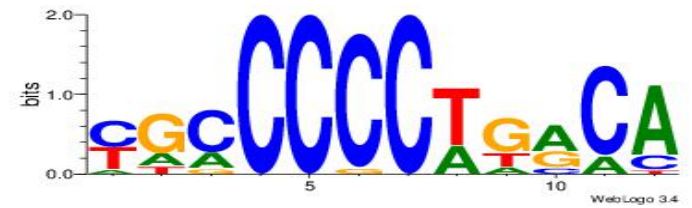
MGCCCCCTGMCA

-----AMACA

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:	Forward
Position number:	1
Number of overlap:	5
Similarity score:	0.0700905

Alignment:

VCACGTBV

AMACA---

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV



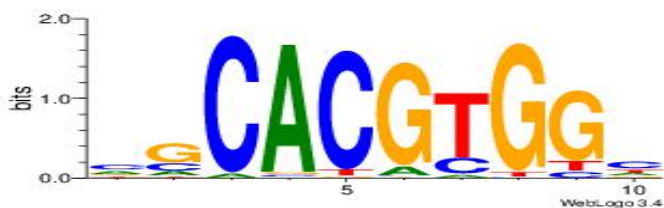
Dataset #: 2
 Motif ID: 38
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.0708148

Alignment:

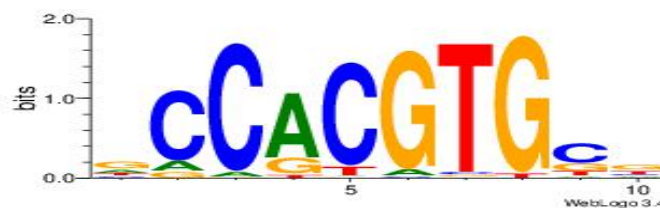
VGCACGTGGH

-AMACA----

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

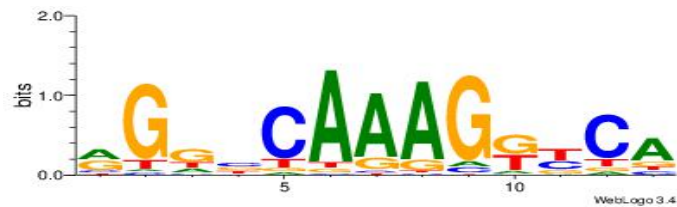


Dataset #: 2
 Motif ID: 34

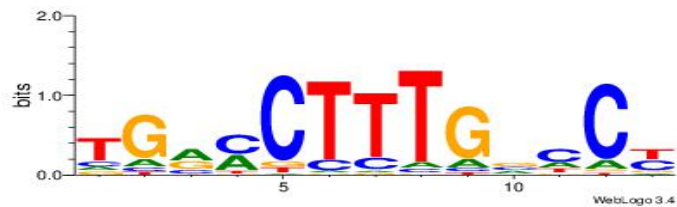
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 5
Similarity score: 0.071574

Alignment:
TGM YCTTTGB CCK
-----TGTRT----

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGB CCK



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

Original motif Consensus sequence: AGSCWGG



Reverse complement motif Consensus sequence: CCWGSCT



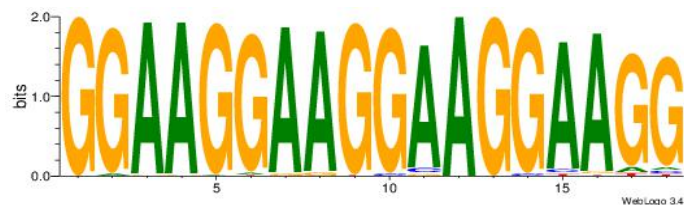
Best Matches for Top Significant Motif ID 3 (Highest to Lowest)

Dataset #: 2
 Motif ID: 32
 Motif name: EWSR1-FLI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 7
 Similarity score: 0.0395671

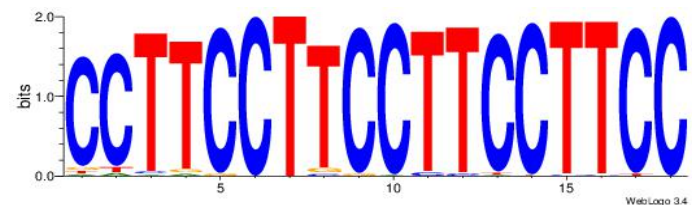
Alignment:

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

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

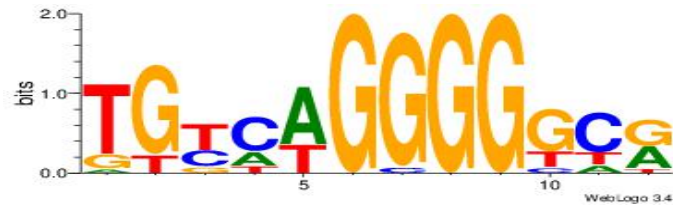


Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

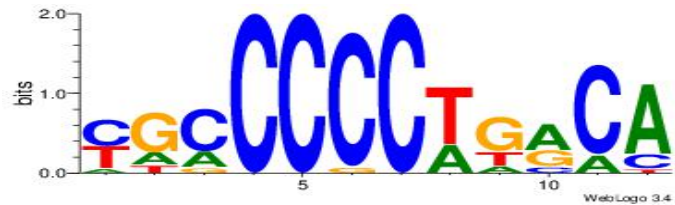
Number of overlap: 7
Similarity score: 0.0494688

Alignment:
MGCCCCCTGMCA
-----CCWGSCT

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA

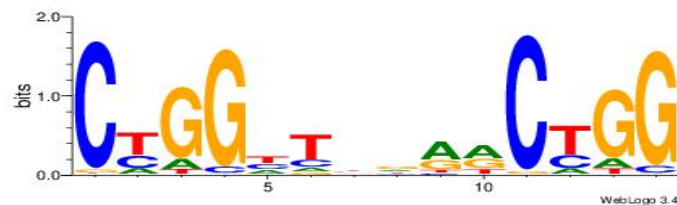
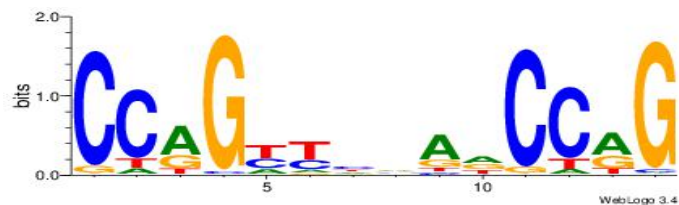


Dataset #: 2
Motif ID: 48
Motif name: Tcfcp2l1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0669354

Alignment:
CCAGYYHVADCCRG
CCWGSCT-----

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCTO

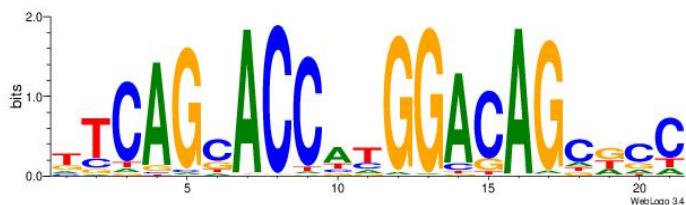


Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 7
 Similarity score: 0.0693747

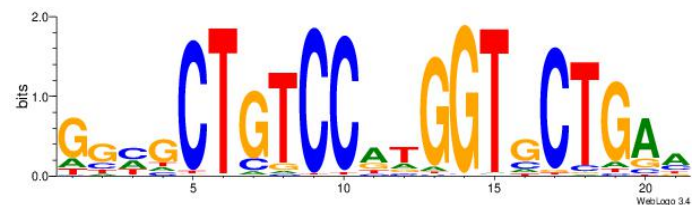
Alignment:

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

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2

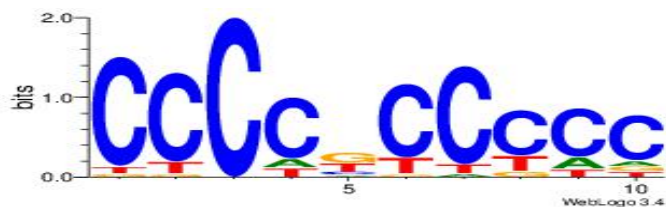
Motif ID: 16
 Motif name: SP1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0695377

Alignment:

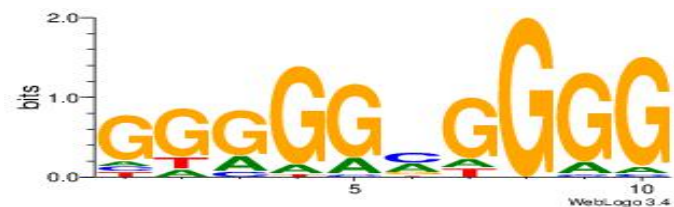
CCCCKCCCCC

-CCWGSCT--

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



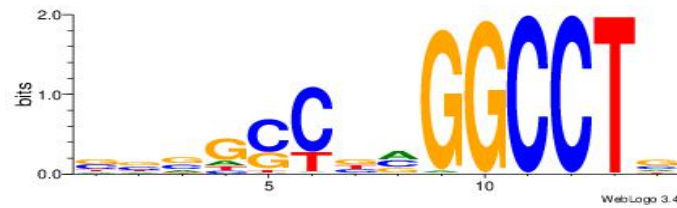
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0720685

Alignment:

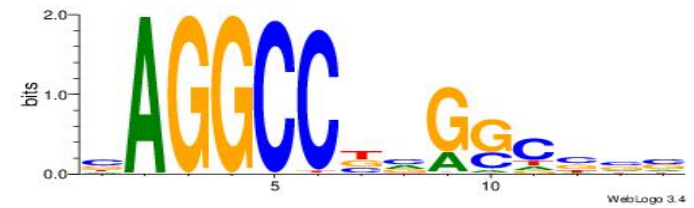
BBVGCCBVGGCCTV

-----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

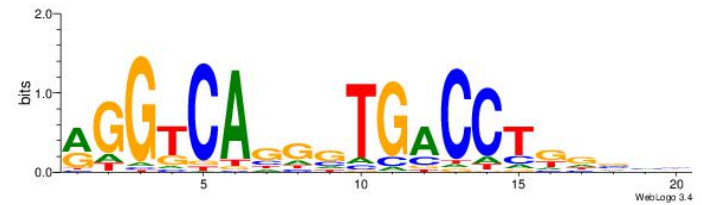
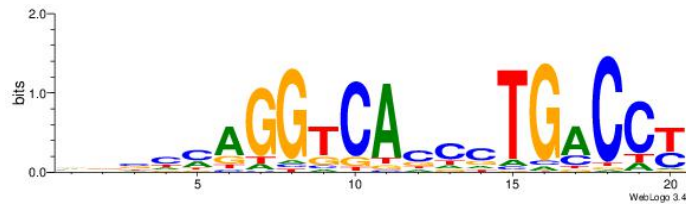
Alignment:

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: Forward
 Position number: 4
 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

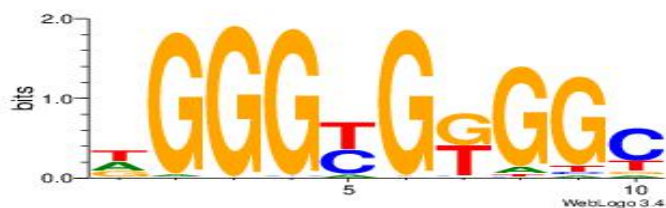
Motif name:	Klf4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0798994

Alignment:

GCCYCMCCCD

---CCWGSCT

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



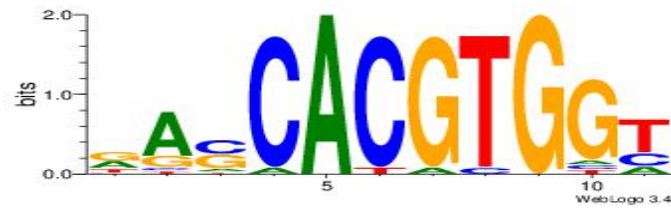
Dataset #:	2
Motif ID:	39
Motif name:	MYCMAX
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	7
Similarity score:	0.0839075

Alignment:

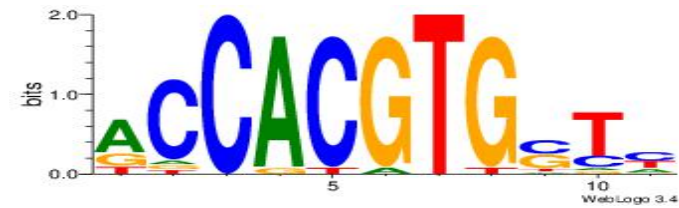
RASCACGTGGT

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: MTTCC



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

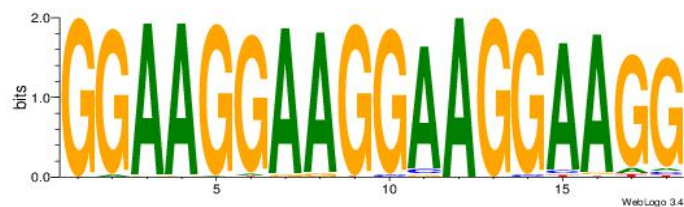
Dataset #:	2
Motif ID:	32
Motif name:	EWSR1-FLI1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	12

Number of overlap: 6
Similarity score: 0.0146511

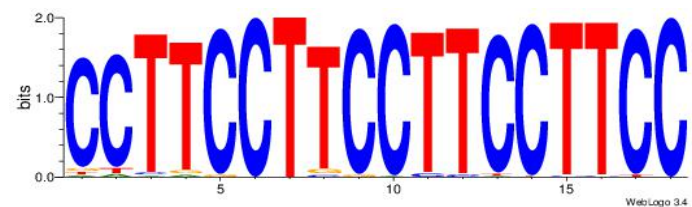
Alignment:

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
---MTTCCK-

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:

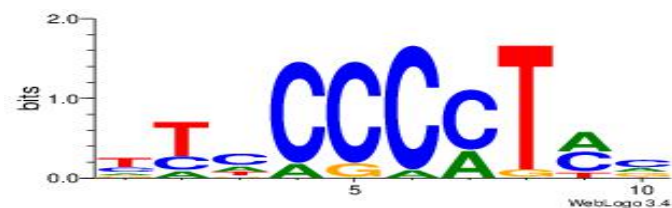
BKAGGGGDAD

----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

-RGAAR----

Original motif Consensus sequence: GGGGRTTCCCC



Reverse complement motif Consensus sequence: GGGGAACCCCC



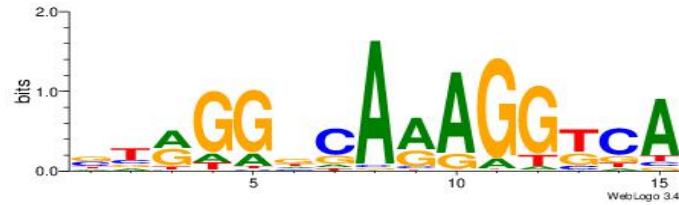
Dataset #:	2
Motif ID:	20
Motif name:	PPARGRXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.0800484

Alignment:

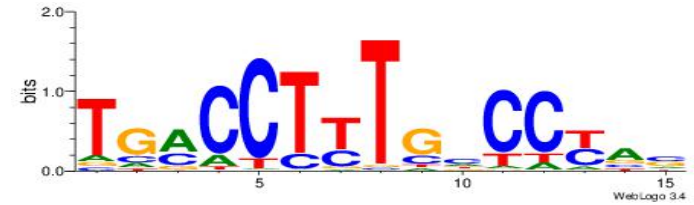
BTRGGDCARAGGKCA

---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

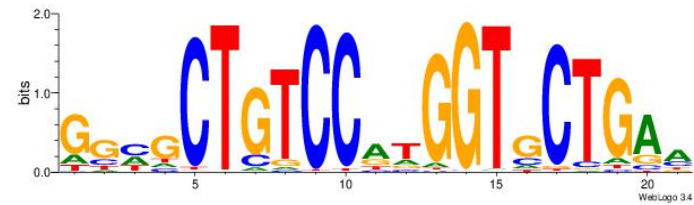
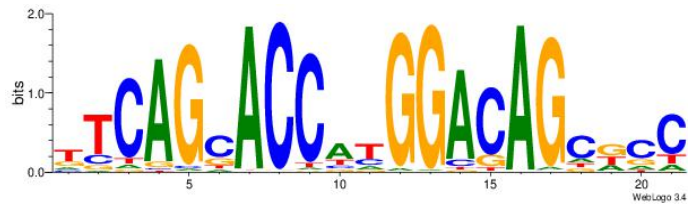
Alignment:

TTCAGCACCATGGACAGCKCC

-----RGGAAR-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



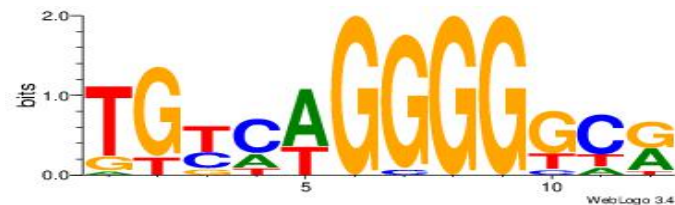
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0832926

Alignment:

TGYCAGGGGGCR

-----RGAAR

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



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

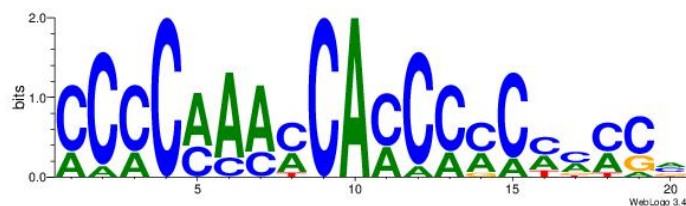
Alignment:

```

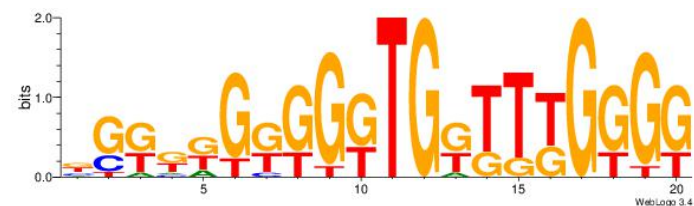
BGRRRGRGGRTGRTTYGGGG
----RGAAR-----

```

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



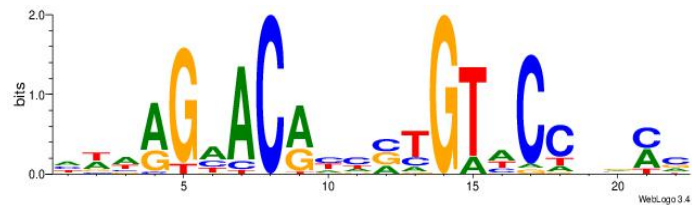
Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0836451

Alignment:

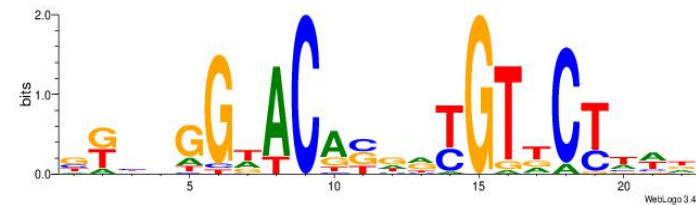
HWDAGHACRHHVTGTHCCHVMV

---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

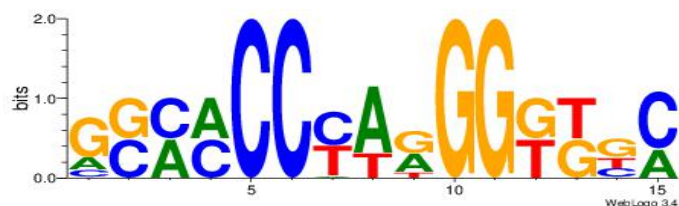
Reverse complement motif Consensus sequence: GCGCSAAA



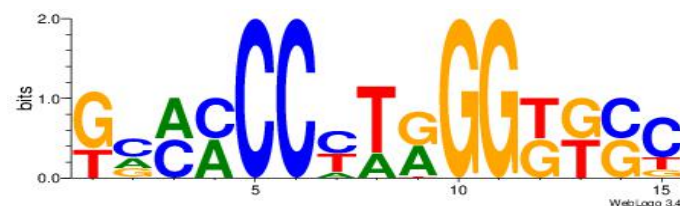
Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 6
 Similarity score: 0.0850287

Alignment:
 GYRYCCMTKGGYRSC
 -----RGGAAR-

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



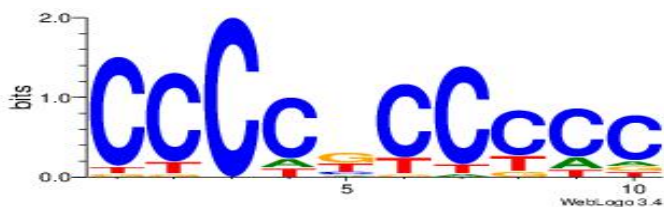
Best Matches for Top Significant Motif ID 7 (Highest to Lowest)

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

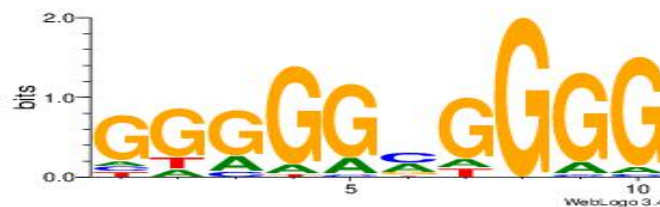
Alignment:

CCCCKCCCCC
-CCCRCCCC-

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



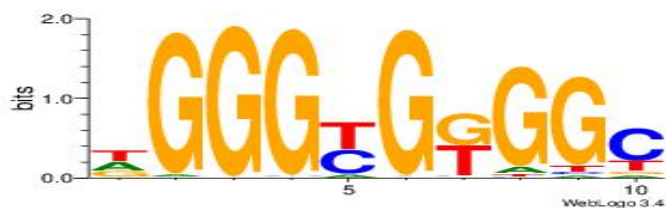
Dataset #: 2
 Motif ID: 36
 Motif name: Klf4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0461644

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: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0650374

Alignment:
YCGCCACGCH
---CCCRCCCC

Original motif Consensus sequence: HCGTG GGGCGK



Reverse complement motif Consensus sequence: YCGCCACGCH

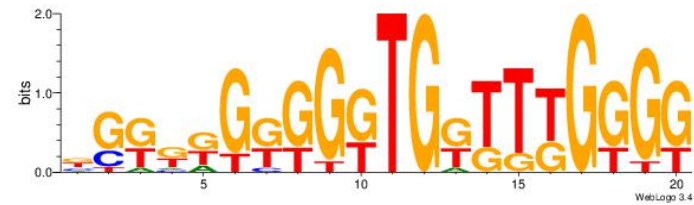


Dataset #: 2
Motif ID: 18
Motif name: RREB1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.076401

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:

GGGGAACCCC

GGGGMGGG---

Original motif Consensus sequence: GGGGRTTCCCC



Reverse complement motif Consensus sequence: GGGGAAKCCCC



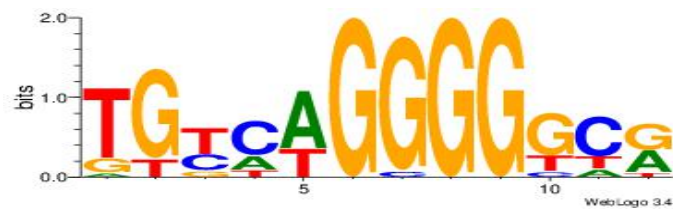
Dataset #: 2
Motif ID: 35

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

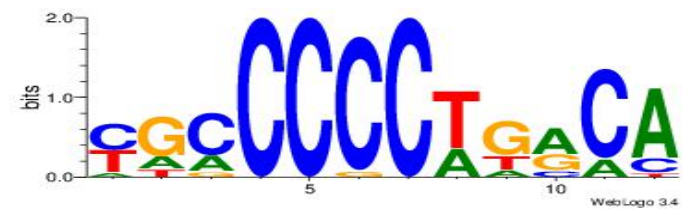
Alignment:

TGYCAGGGGGCR
GGGGMGGG----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



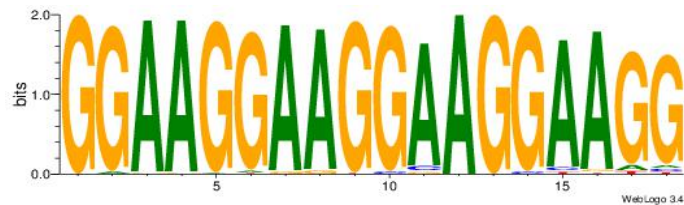
Dataset #:	2
Motif ID:	32
Motif name:	EWSR1-FLI1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.0950969

Alignment:

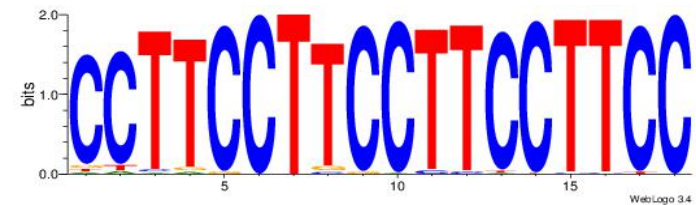
GGAAGGAAGGAAGGAAGG

-----GGGGMGGG-----

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

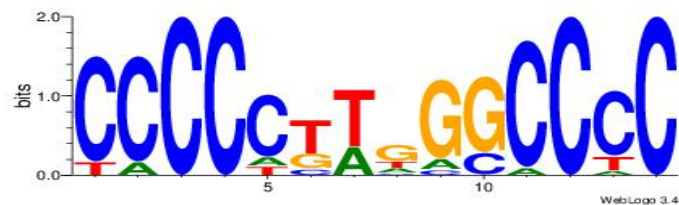
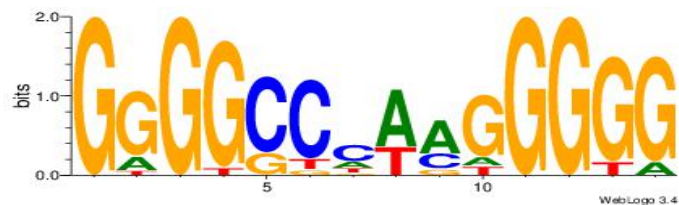
Alignment:

GGGGCCCAAGGGGG

GGGGMGGG-----

Original motif Consensus sequence: GGGGCCCAAGGGGG

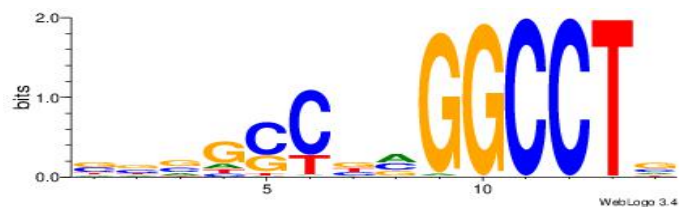
Reverse complement motif Consensus sequence: CCCCCTTGGGCC



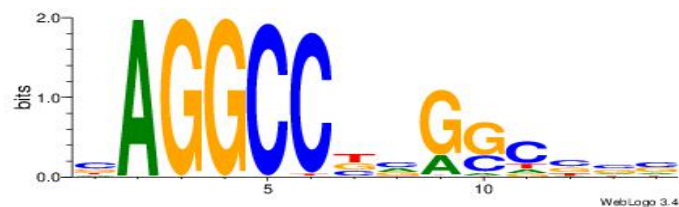
Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.10221

Alignment:
 BBVGCCBVGGCCTV
 ----CCCRCCCC--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



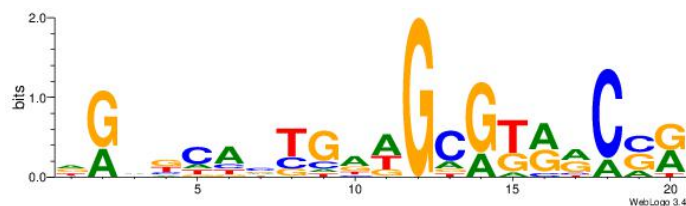
Dataset #: 2
 Motif ID: 45

Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.102497

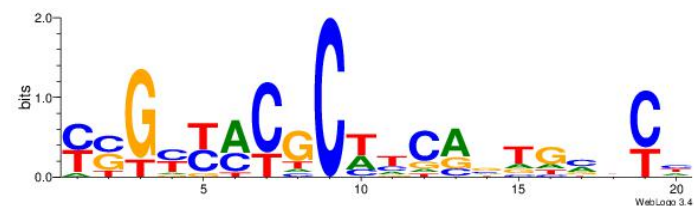
Alignment:

DGVBCABTGDWGCGRRCR
 -----GGGGMGGG-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD



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

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



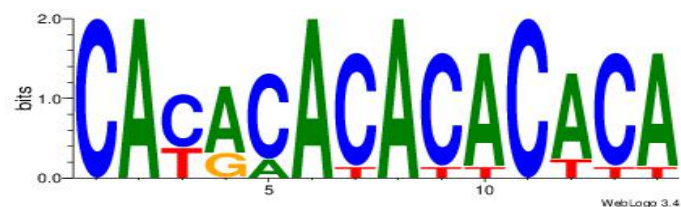
Best Matches for Top Significant Motif ID 26 (Highest to Lowest)

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

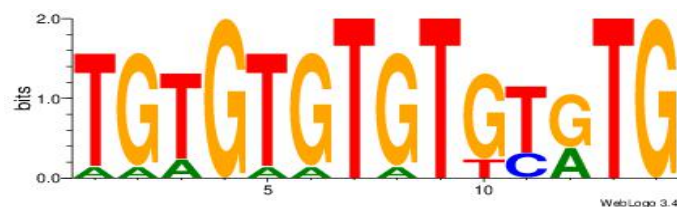
Alignment:

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

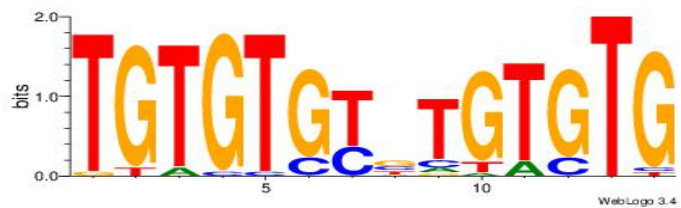
Direction: Forward
Position number: 9
Number of overlap: 6
Similarity score: 0.0350575

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: Forward
Position number: 1
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

YCGTG--

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: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 5
Similarity score: 0.581904

Alignment:

CTGGGA-

-YCGTG

Original motif Consensus sequence: CTGGGA

Reverse complement motif Consensus sequence: TCCAG



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:

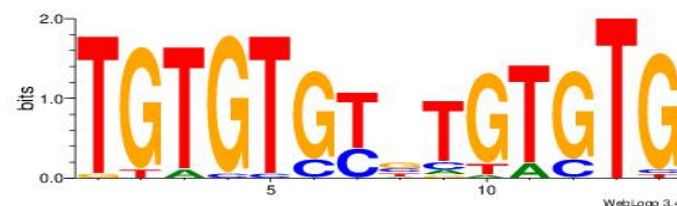
CACACAVRCACACA

-----VCACGTBV-

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

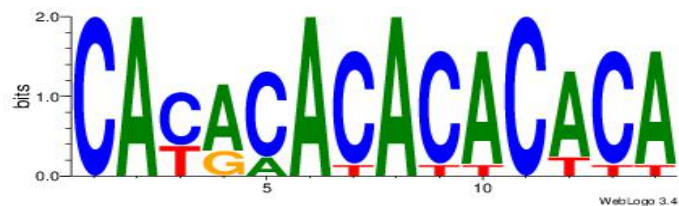


Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0850889

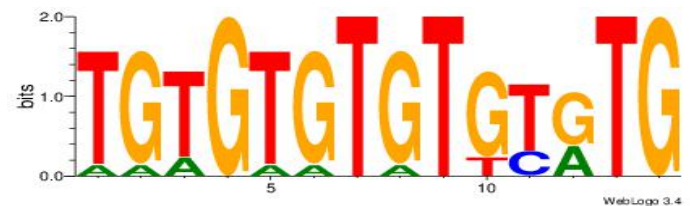
Alignment:

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:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	5
Similarity score:	1.55675

Alignment:

CCWGSCT---

--VBACGTGV

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



Significant Motifs - Global and Local Matching (Highest to Lowest)

Dataset #: 2 **Motif ID: 14** **Motif name: ZEB1**

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



Best Matches for Significant Motif ID 14 (Highest to Lowest)

Dataset #:	2
Motif ID:	46
Motif name:	RORA_1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	6
Similarity score:	0.0141289

Alignment:

TGACCTDVWT
-CACCTD---

Original motif Consensus sequence: AWVDAGGTCA

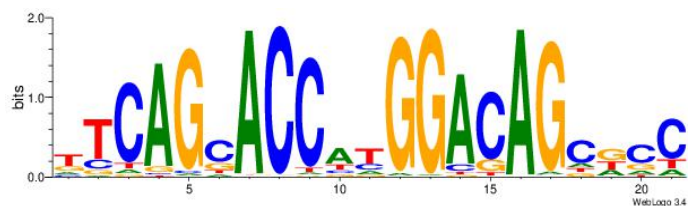
Reverse complement motif Consensus sequence: TGACCTDVWT



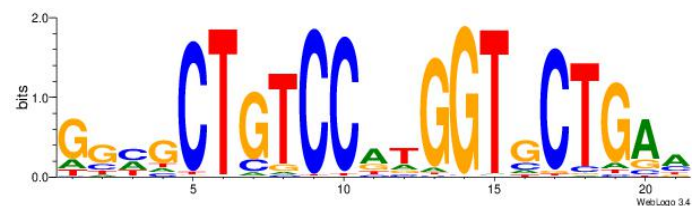
Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0143133

Alignment:
 GYGCTGTCCATGGTGCTGAA
 -----HAGGTG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2

Motif ID: 25
 Motif name: Arnt
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0207244

Alignment:
 CACGTG
 HAGGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 2
 Motif ID: 31
 Motif name: Esrrb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0207244

Alignment:

CACGTG

HAGGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
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:	0.0232753

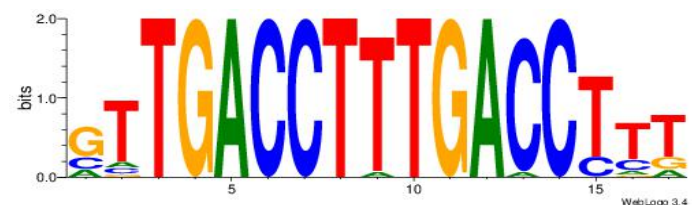
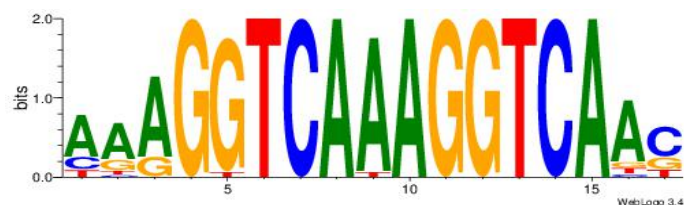
Alignment:

GTTGACCTTTGACCTTT

-----CACCTD-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Dataset #: 2
 Motif ID: 33
 Motif name: HIF1AARNT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0237889

Alignment:
 VBACGTGV
 -HAGGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



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:	4
Number of overlap:	6
Similarity score:	0.0262123

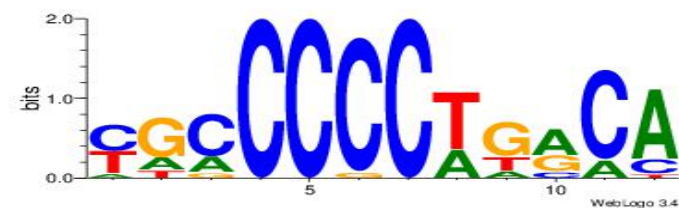
Alignment:

TGYCAGGGGGCR
 ---HAGGTG---

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



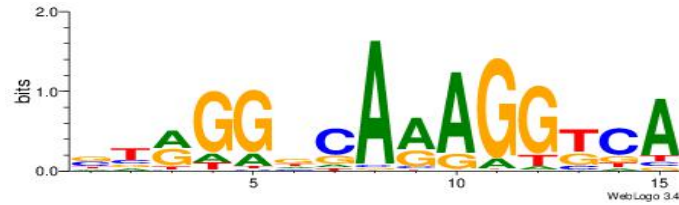
Dataset #:	2
Motif ID:	20
Motif name:	PPARGRXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	6
Similarity score:	0.0264837

Alignment:

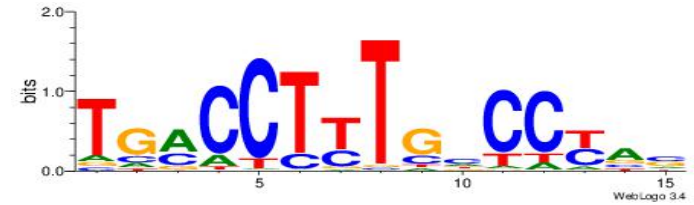
TGRCCTKTGHCKAB

-CACCTD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB



Dataset #:	2
Motif ID:	39
Motif name:	MYCMAX
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:	0.0269744

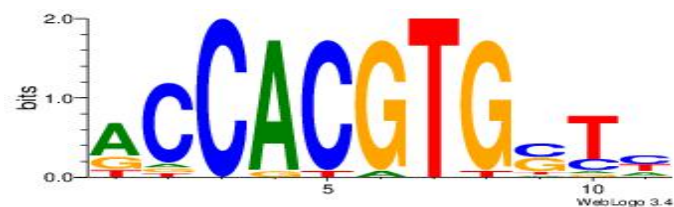
Alignment:

RASCACGTGGT

---HAGGTG--

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #: 2
 Motif ID: 44
 Motif name: NR4A2
 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: 0.0288897

Alignment:
 GTGACCTT
 --CACCTD

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



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

Original motif Consensus sequence: CTCTGY



Reverse complement motif Consensus sequence: KCAGAG



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

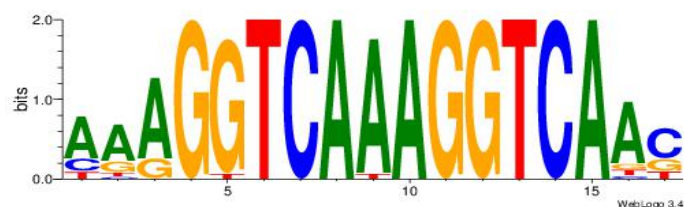
Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.012269

Alignment:

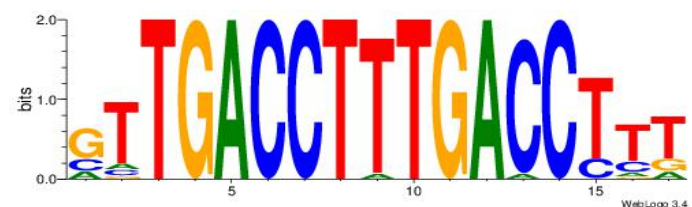
AAAGGTCAAAGGTCAAC

-----KCAGAG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTT

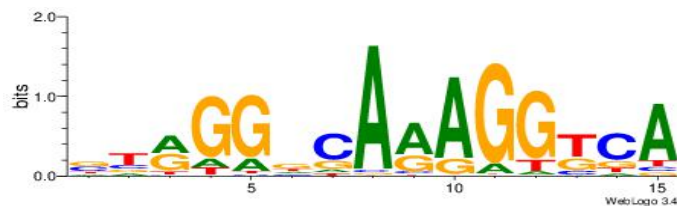


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0140102

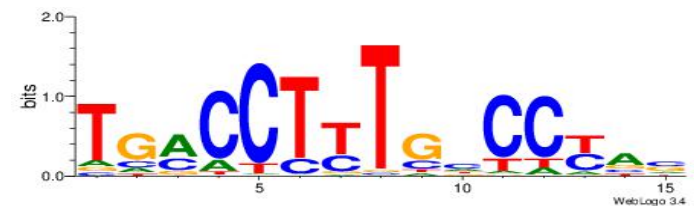
Alignment:

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

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKGHCCK



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

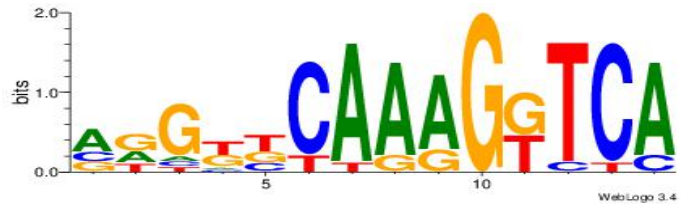
Similarity score: 0.0186793

Alignment:
AKGYCAAAGRTCA
----KCAGAG----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA

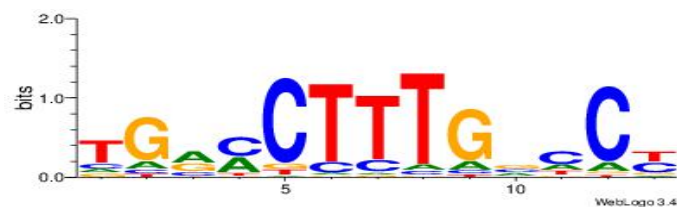
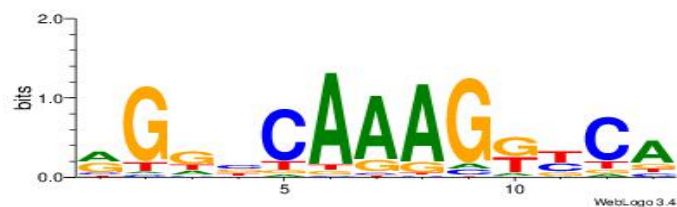


Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020602

Alignment:
RGGBCAAAGKYCA
---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



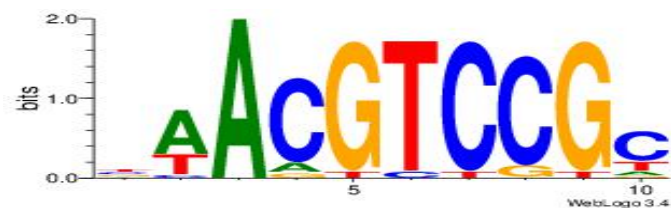
Dataset #: 2
 Motif ID: 37
 Motif name: MIZF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0221665

Alignment:

BAACGTCCGC

----CTCTGY

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



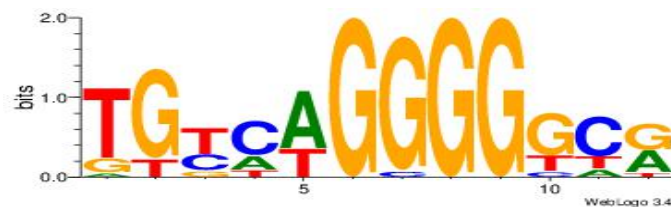
Dataset #: 2
 Motif ID: 35

Motif name:	INSM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0255256

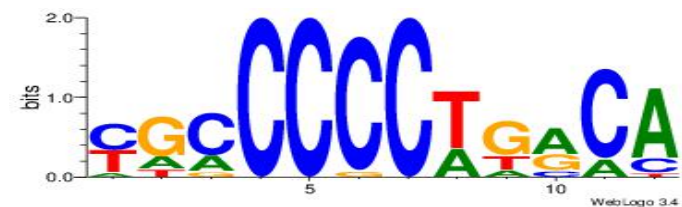
Alignment:

TGYCAGGGGGCR
 --KCAGAG----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



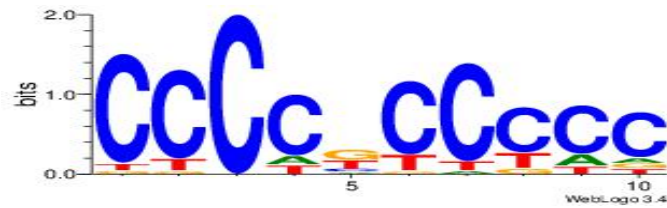
Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0349642

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

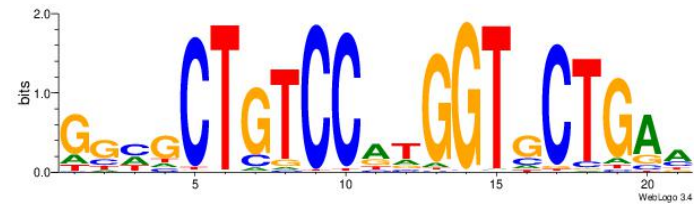
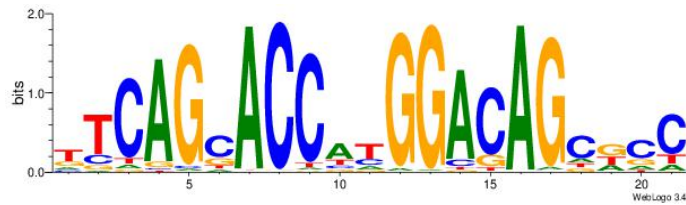
Alignment:

GGYGCTGTCCATGGTGCTGAA

--CTCTGY-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



Dataset #: 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: 1
 Number of overlap: 6
 Similarity score: 0.0446026

Alignment:

TCCCAG

KCAGAG

Original motif Consensus sequence: CTGGGA



Reverse complement motif Consensus sequence: TCCCAG

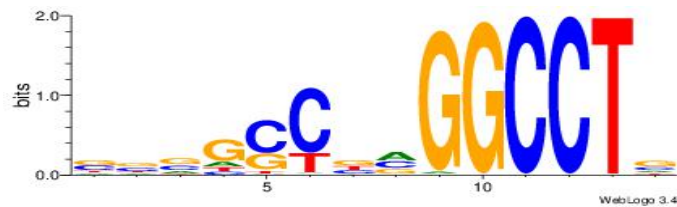


Dataset #: 2
 Motif ID: 12

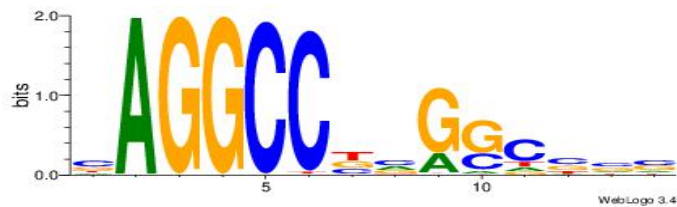
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 6
Similarity score: 0.0448449

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

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



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

Original motif Consensus sequence: ATKTM



Reverse complement motif Consensus sequence: RARAT



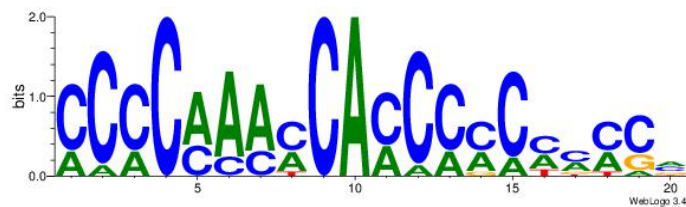
Best Matches for Significant Motif ID 5 (Highest to Lowest)

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

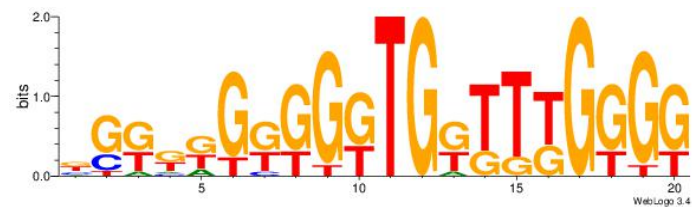
Alignment:

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

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

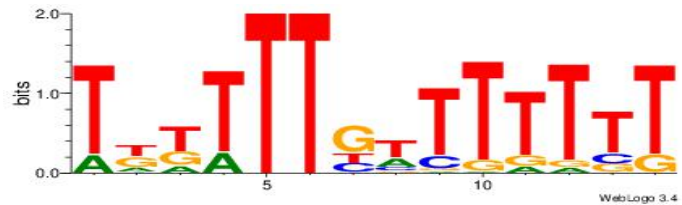


Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 5
Similarity score: 0.0260117

Alignment:
AAAAAAACAAARRA
-RARAT-----

Original motif Consensus sequence: TKKTTTGTTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR



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



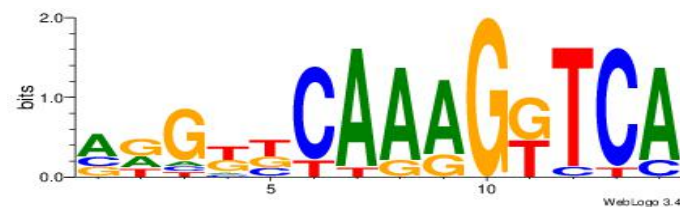
Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0279129

Alignment:
 AKGYCAAAGRTCA
 -----RARAT--

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



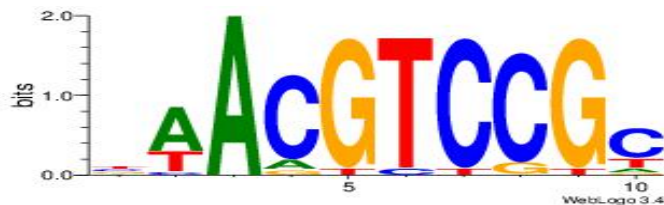
Dataset #: 2
 Motif ID: 37

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: GCGGACGTTT



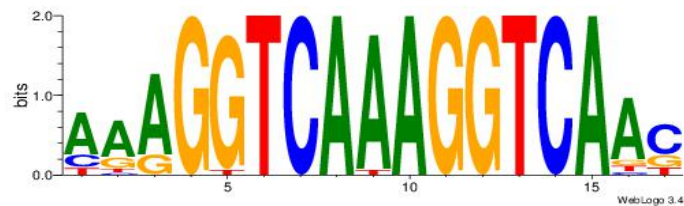
Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	10
Number of overlap:	5
Similarity score:	0.0292478

Alignment:

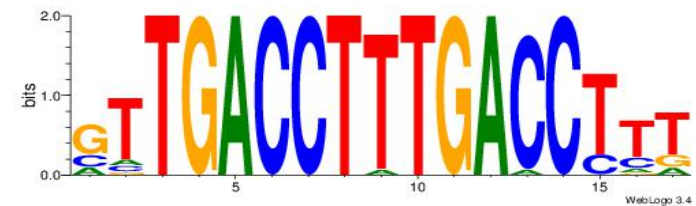
AAAGGTCAAAGGTCAAC

-----ATKTM----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Dataset #:	2
Motif ID:	20
Motif name:	PPARGRXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	5
Similarity score:	0.0305369

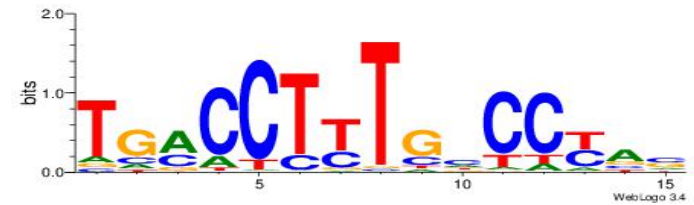
Alignment:

TGRCCTKTGHCKAB

-----ATKTM-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

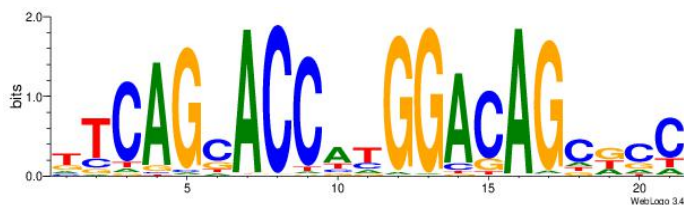
Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB



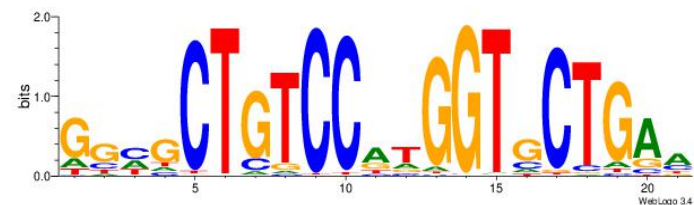
Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 13
 Number of overlap: 5
 Similarity score: 0.0315454

Alignment:
 GYGCTGTCCATGGTGCTGAA
 ----ATKTM-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GYGCTGTCCATGGTGCTGAA

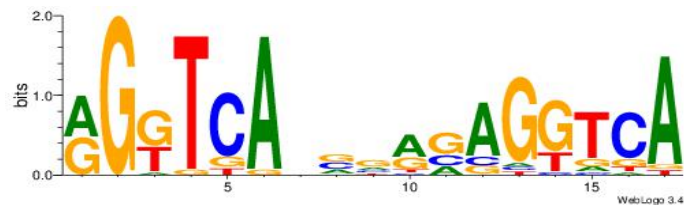


Dataset #: 2

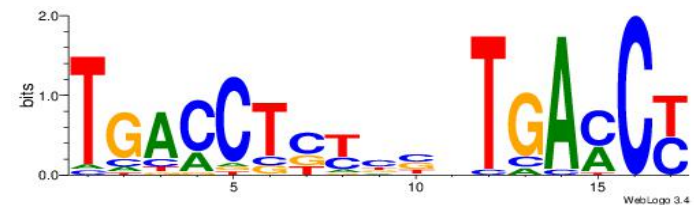
Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 5
 Similarity score: 0.0335956

Alignment:
 RGKTCABVVRGAGGTCA
 ATKTM-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBGTGAYCK



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: 26 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



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

Dataset #:	2
Motif ID:	28
Motif name:	Egr1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 1
 Number of overlap: 6
 Similarity score: 0

Alignment:

YCGCCCACGCH
 -----CACGCM

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



Dataset #: 2
 Motif ID: 33
 Motif name: HIF1AARNT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0112447

Alignment:

VBACGTGV
 -YGCGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

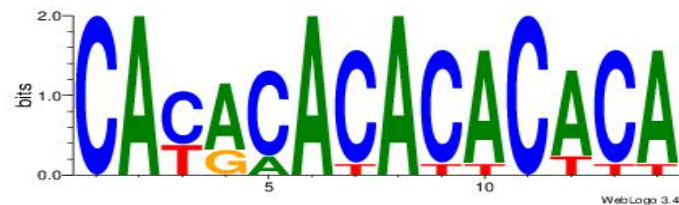


Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0308396

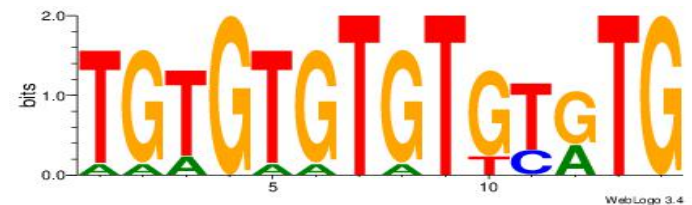
Alignment:

TGTGTGTGTTKTG
 -----YGCGTG--

Original motif Consensus sequence: CAYACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTTKTG



Dataset #: 2

Motif ID:	31
Motif name:	Esrrb
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:	0.0315972

Alignment:

CACGTG

YGCGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #:	2
Motif ID:	25
Motif name:	Arnt
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:	0.0315972

Alignment:

CACGTG

YGCGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #:	1
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0350575

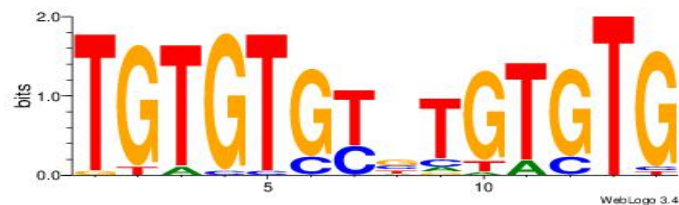
Alignment:

TGTGTGKVTGTGTG

YGCGTG-----

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGTG

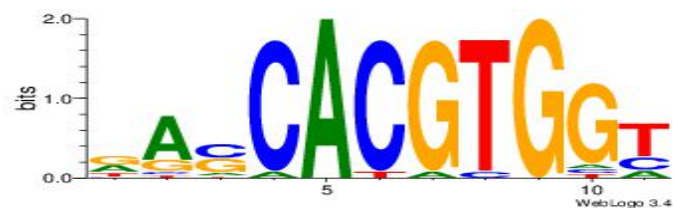


Dataset #: 2
 Motif ID: 39
 Motif name: MYCMAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0376488

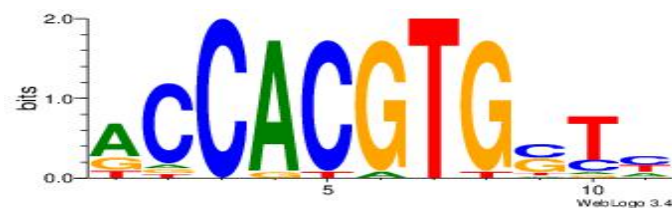
Alignment:

RASCACGTGGT
 ---YGCGTG--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #: 2
 Motif ID: 40

Motif name:	Mycn
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:	0.0377949

Alignment:

GCCACGTGSD

--YGCGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



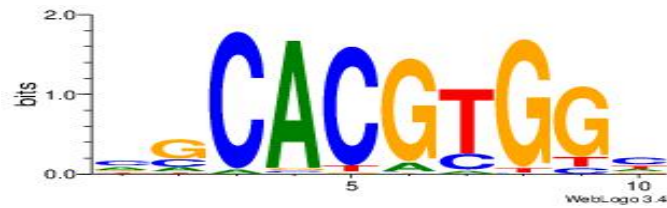
Dataset #:	2
Motif ID:	38
Motif name:	Myc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0399214

Alignment:

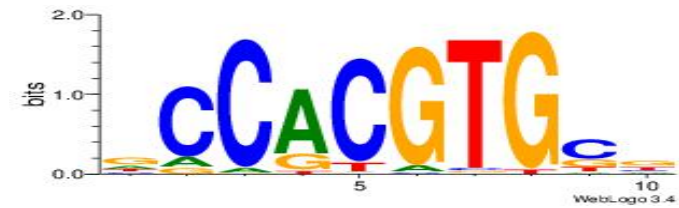
DCCACGTGCV

--YGCGTG--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



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:	7
Number of overlap:	6
Similarity score:	0.0433081

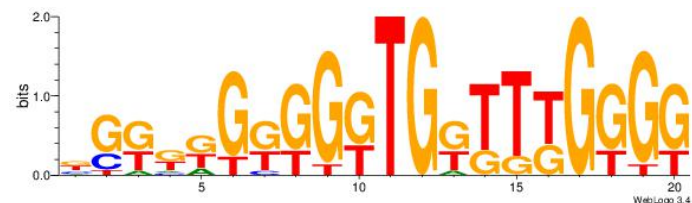
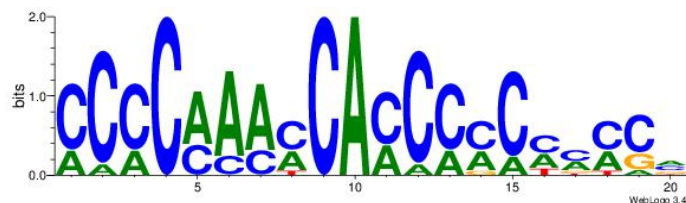
Alignment:

BGRRRGRGGRTGRTTYGGGG

-----YGCGTG-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC

Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG



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

Original motif Consensus sequence: CMGCRGC



Reverse complement motif Consensus sequence: GCKGCTG



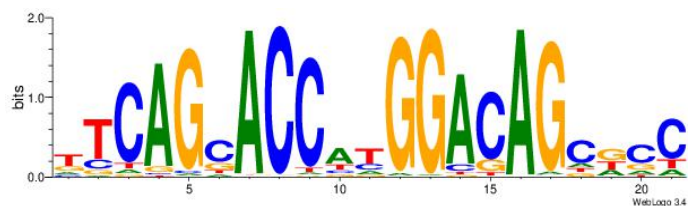
Best Matches for Significant Motif ID 6 (Highest to Lowest)

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

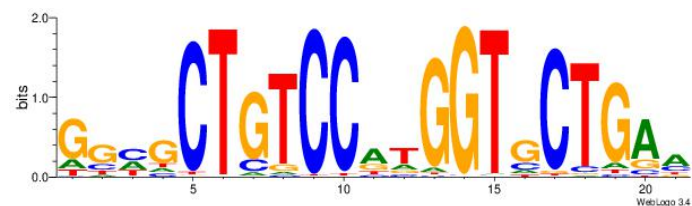
Alignment:

```
TTCAGCACCATGGACAGCKCC
--CMGCRGC-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



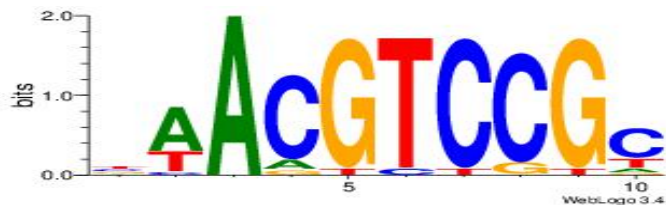
Dataset #: 2
Motif ID: 37
Motif name: MIZF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0322623

Alignment:

GCGGACGTTV

GCKGCGY---

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV

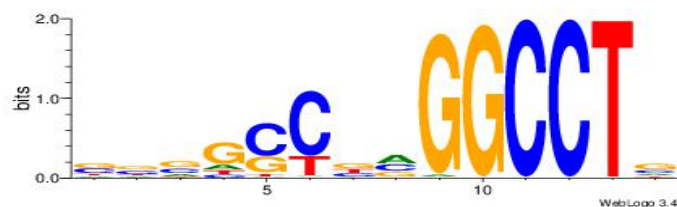


Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 7
 Similarity score: 0.038091

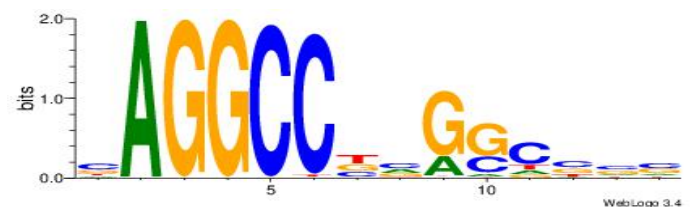
Alignment:

BBVGCCBVGGCCTV
 ----CMGCRGC----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

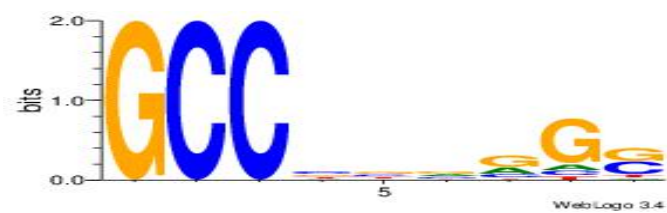


Dataset #: 2
 Motif ID: 15
 Motif name: TFAP2A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 7

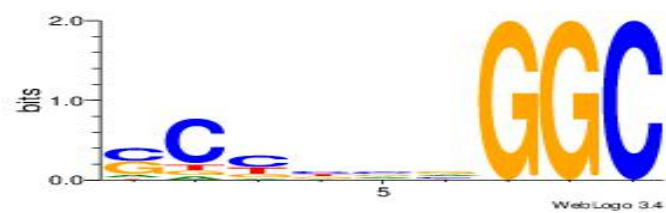
Similarity score: 0.0393168

Alignment:
SCMVBBGGC
--CMGCRGC

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



Dataset #: 1
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0443244

Alignment:
CCCRCCCC
-CMGCRGC

Original motif Consensus sequence: CCCRCCCC

Reverse complement motif Consensus sequence: GGGGMGGG

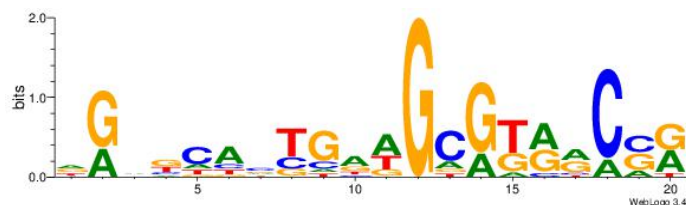


Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 7
 Similarity score: 0.0448462

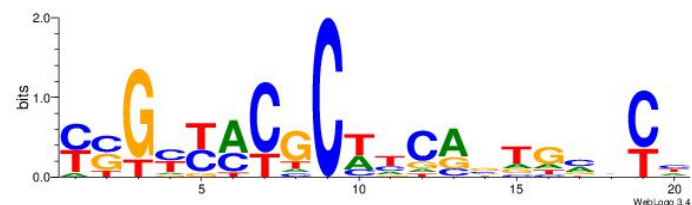
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----GCKGCGY-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



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



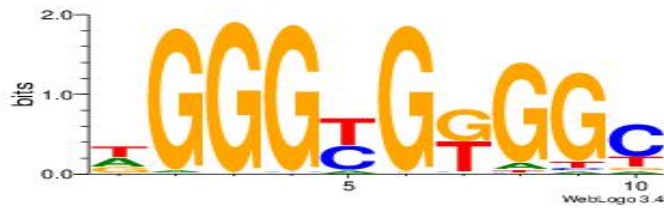
Dataset #: 2
 Motif ID: 36
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0476958

Alignment:

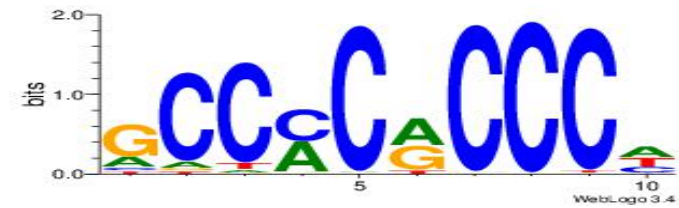
GCCYCMCCCD

-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

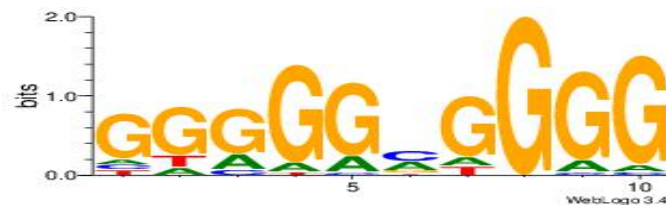
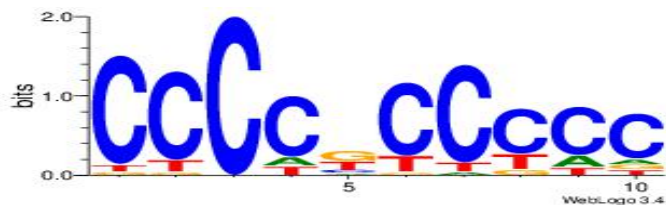
Alignment:

GGGGGYGGGG

GCKGCGY---

Original motif Consensus sequence: CCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG

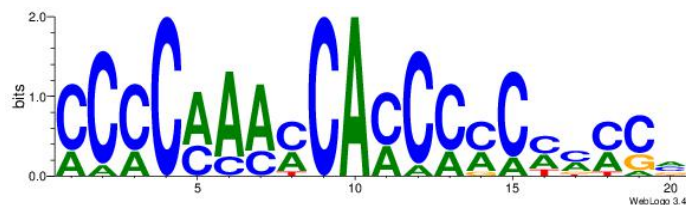


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 7
 Similarity score: 0.0498726

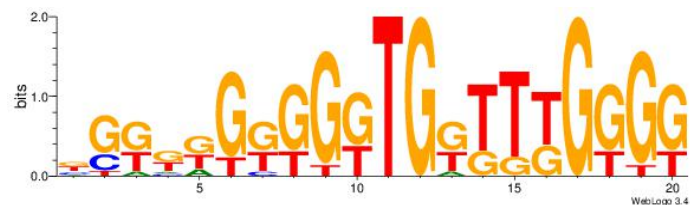
Alignment:

BGRRRGRGGRTGRTTYGGGG
 -----GCKGCG-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



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

Original motif Consensus sequence: AMACA



Reverse complement motif Consensus sequence: TGTRT



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

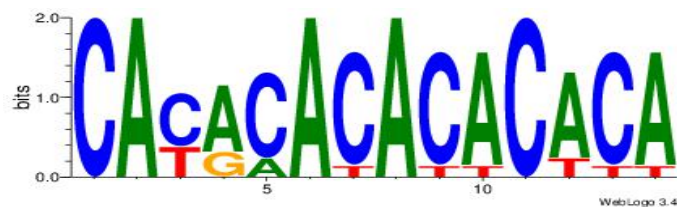
Dataset #:	1
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	5
Similarity score:	0

Alignment:

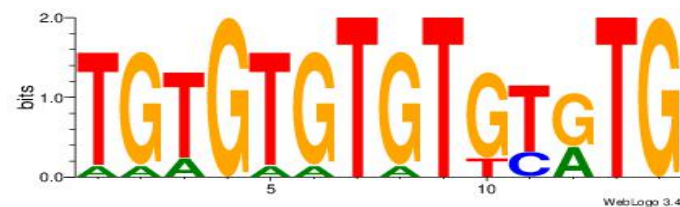
TGTGTGTGTGKTG

-----TGTRT-----

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTG



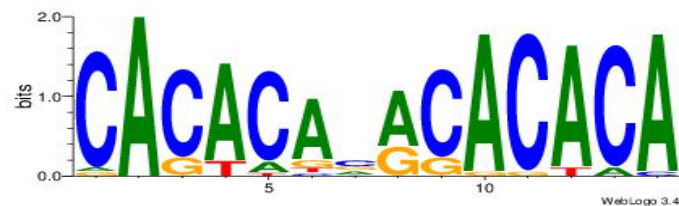
Dataset #: 1
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 5
 Similarity score: 0.0040753

Alignment:

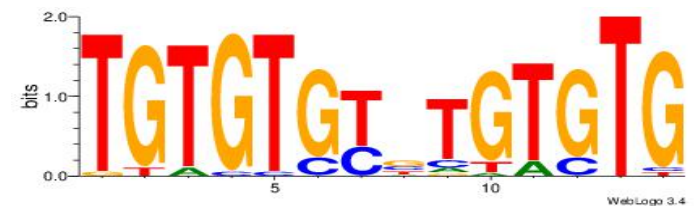
TGTGTGKVTGTGTG

TGTRT-----

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGTG

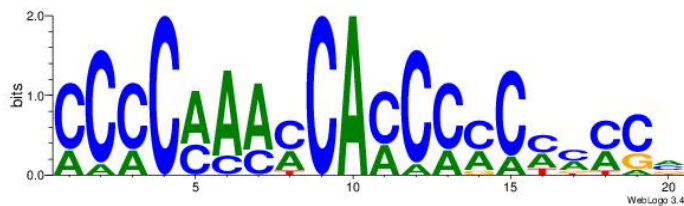


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 5

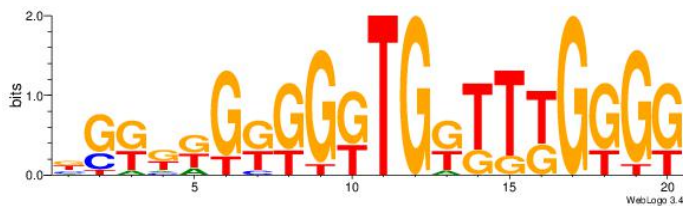
Similarity score: 0.0243918

Alignment:
CCCCMAAMCAMCCMCMMMC
-----AMACA-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

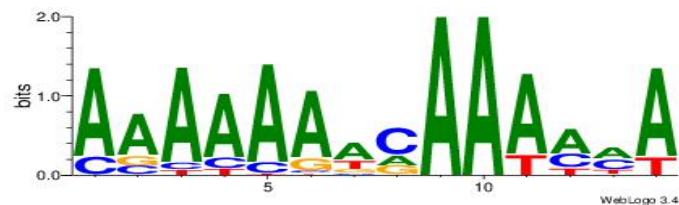


Dataset #: 1
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 5
Similarity score: 0.0394919

Alignment:
AAAAAAACAAARRA
-----AMACA-----

Original motif Consensus sequence: TKKTTTGTTTTTTT

Reverse complement motif Consensus sequence: AAAAAACAAARR

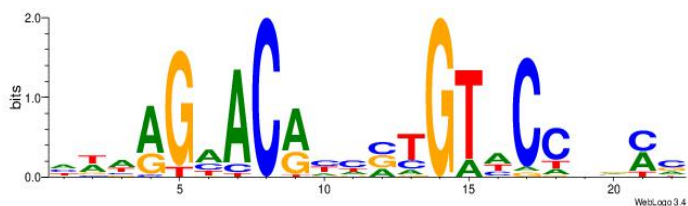


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.0429089

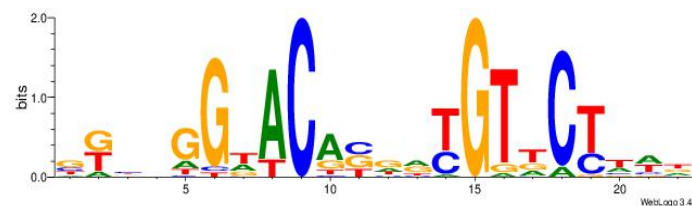
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 ----AMACA-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



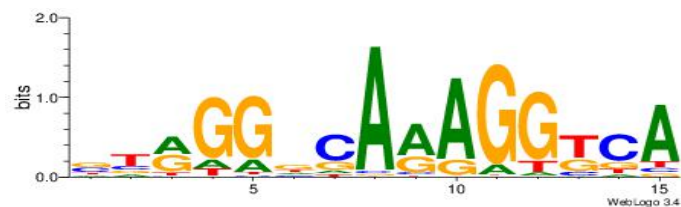
Dataset #: 2

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

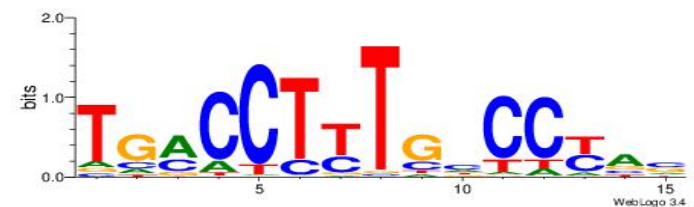
Alignment:

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

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKA



Dataset #: 2
 Motif ID: 26
 Motif name: ArntAhr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 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

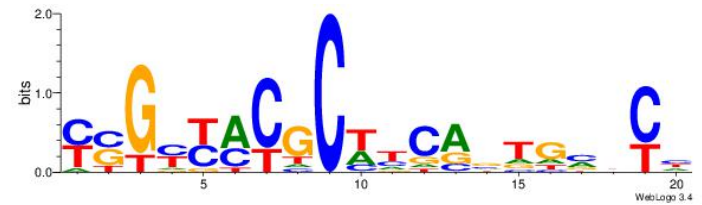
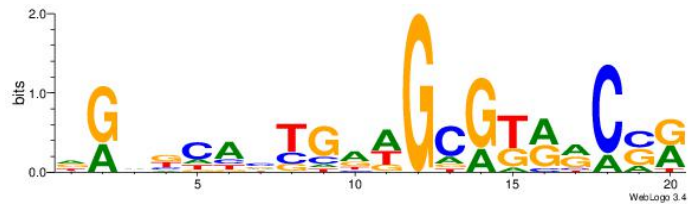
Alignment:

MSGKKRCGCWDCABTGGBCD

-----AMACA-----

Original motif Consensus sequence: DGVBCABTGDWGCGRCSR

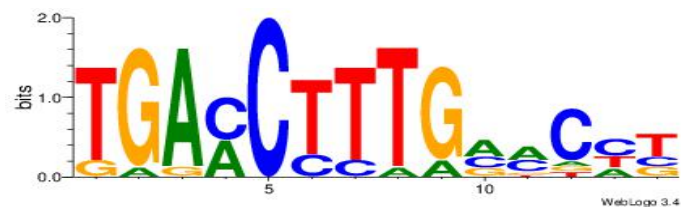
Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGGBCD



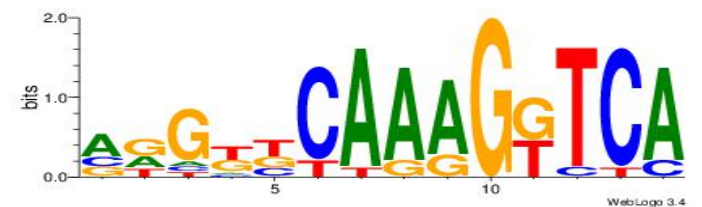
Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0650242

Alignment:
 AKGYCAAAGRTCA
 -----AMACA---

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA

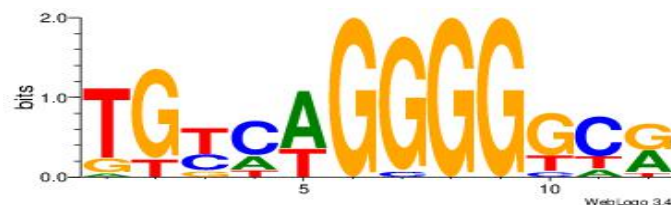


Dataset #: 2
 Motif ID: 35

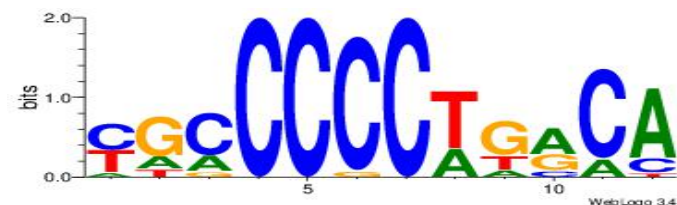
Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 5
 Similarity score: 0.0670984

Alignment:
 TGYCAGGGGGCR
 TGTRT-----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



Dataset #: 2 Motif ID: 23 Motif name: MZF1_1-4

Original motif Consensus sequence: BGGGGA



Reverse complement motif Consensus sequence: TCCCCV



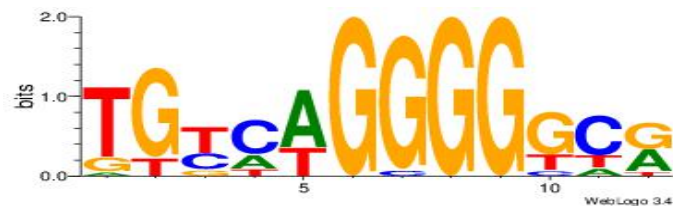
Best Matches for Significant Motif ID 23 (Highest to Lowest)

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: 5
 Number of overlap: 6
 Similarity score: 0.0276389

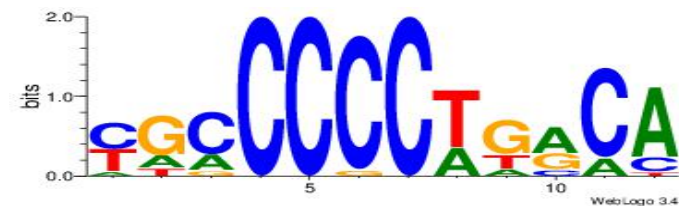
Alignment:

MGCCCCCTGMCA
 --TCCCCV-----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



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: 2
 Number of overlap: 6

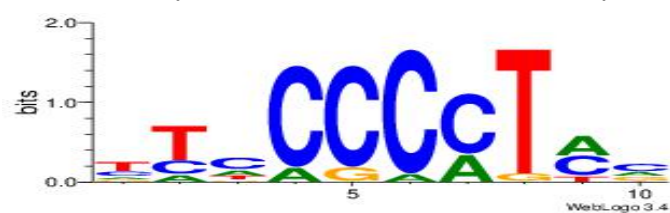
Similarity score: 0.0314583

Alignment:
BKAGGGGDAD
---BGGGGA-

Original motif Consensus sequence: BKAGGGGDAD



Reverse complement motif Consensus sequence: BTHCCCCTYB



Dataset #: 2
Motif ID: 36
Motif name: Klf4
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: 0.0406514

Alignment:
GCCYCMCCCD
TCCCCV----

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

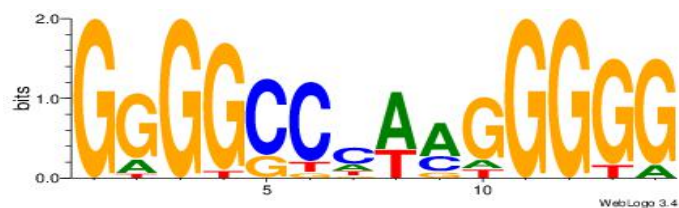


Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 6
 Similarity score: 0.0412963

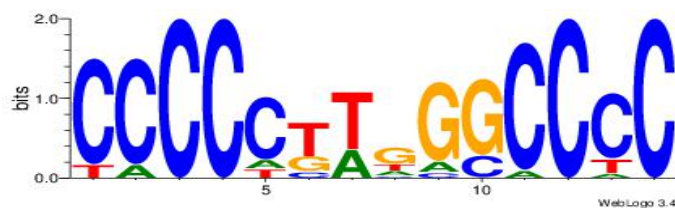
Alignment:

GGGGCCCAAGGGGG
 -----BGGGGA

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



Dataset #: 1
 Motif ID: 8

Motif name:	Motif 8
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:	0.0426517

Alignment:

TCCCAG

TCCCCV

Original motif Consensus sequence: CTGGGA



Reverse complement motif Consensus sequence: TCCCAG



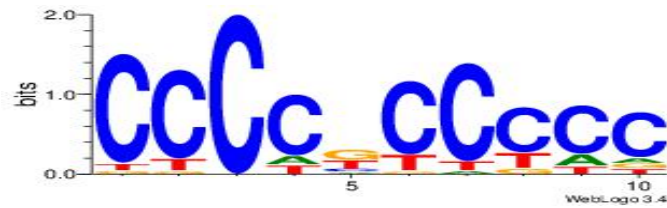
Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0464881

Alignment:

GGGGGYGGGG

----BGGGGA

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:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0493561

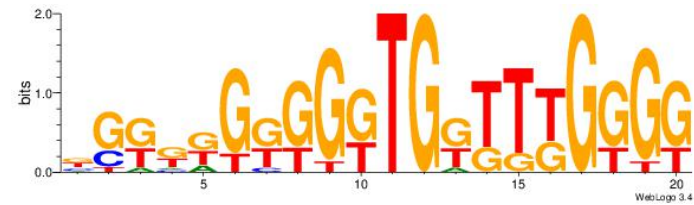
Alignment:

CCCCMAAMCAMCCMCMMMC

----TCCCCV-----

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:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0521759

Alignment:

GGGGRTCCCC

-----TCCCCV

Original motif Consensus sequence: GGGGRTTCCCC



Reverse complement motif Consensus sequence: GGGGAAKCCCC



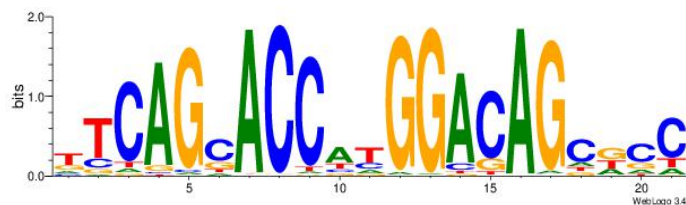
Dataset #: 2
Motif ID: 19

Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	11
Number of overlap:	6
Similarity score:	0.0581528

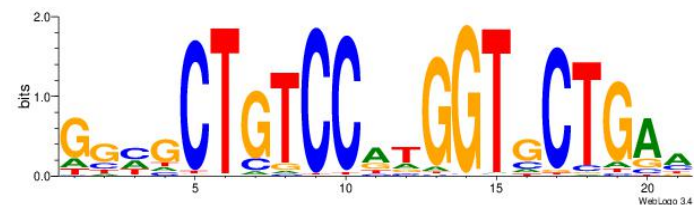
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
-----TCCCCV-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



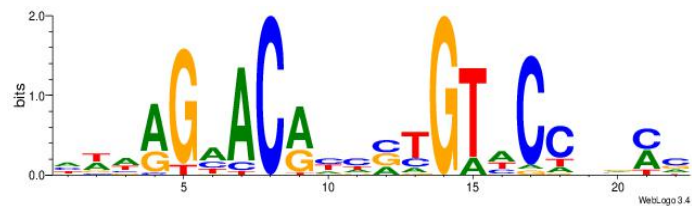
Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0585417

Alignment:

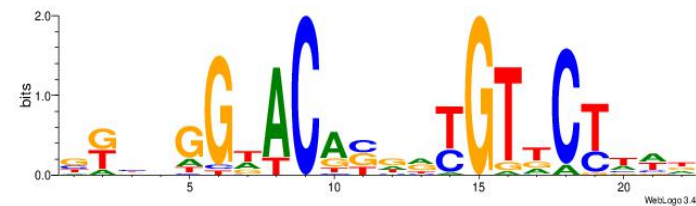
HWDAGHACRHHVTGTHCCHVMV

-----TCCCCV--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

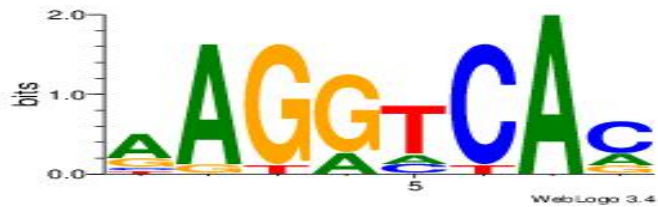


Reverse complement motif Consensus sequence: VRVDGGHACA VDDKGTHCTDWH



Dataset #: 2 Motif ID: 44 Motif name: NR4A2

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



Best Matches for Significant Motif ID 44 (Highest to Lowest)

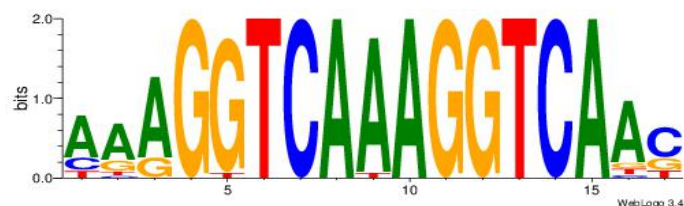
Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 2
 Number of overlap: 8
 Similarity score: 0.0167759

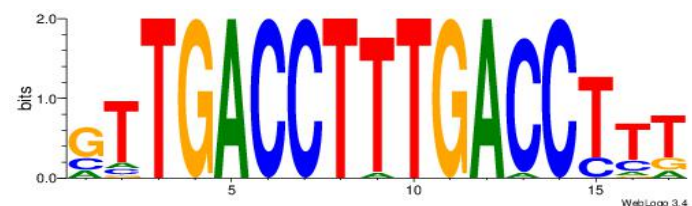
Alignment:

AAAGGTCAAAGGTCAAC
 -AAGGTCAC-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

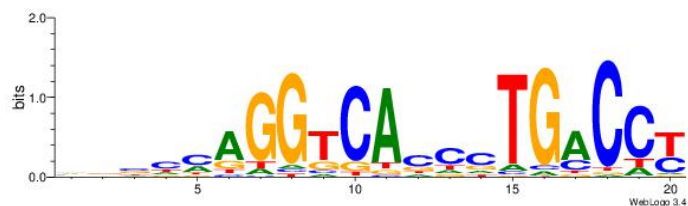


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0195235

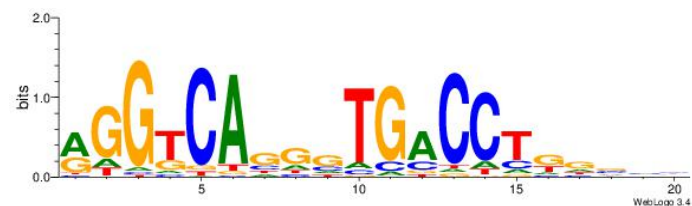
Alignment:

VDBHMAGGTCACCCTGACCY
 -----AAGGTCAC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

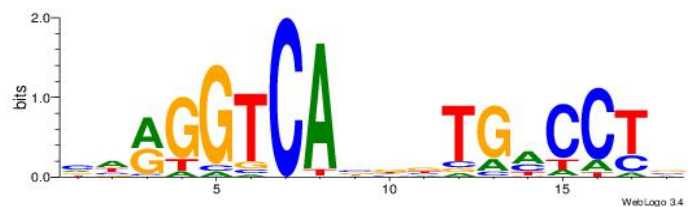


Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0198372

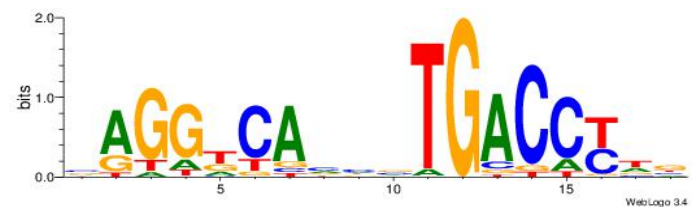
Alignment:

BAGGYCABHBTGACCKHV
-----GTGACCTT-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

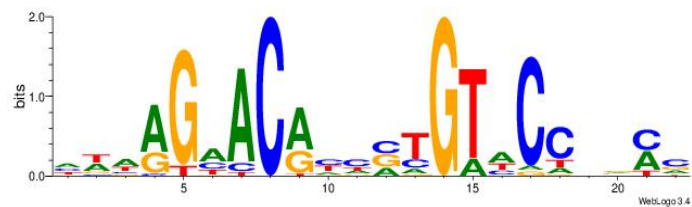


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 13
 Number of overlap: 8
 Similarity score: 0.0487608

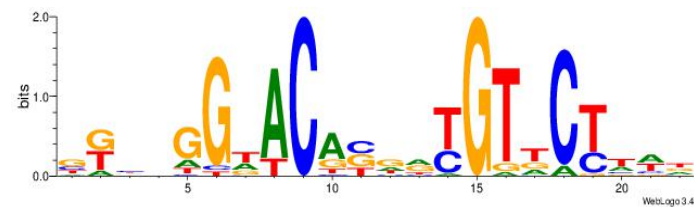
Alignment:

VRVDGGHACAVDDKGTHCTDWH
 -----GTGACCTT--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

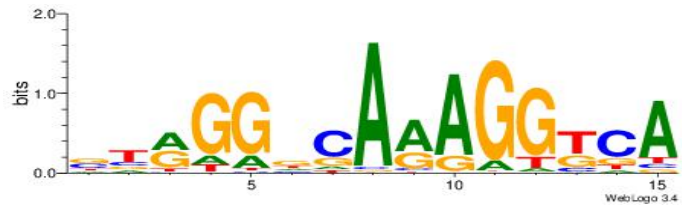


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7

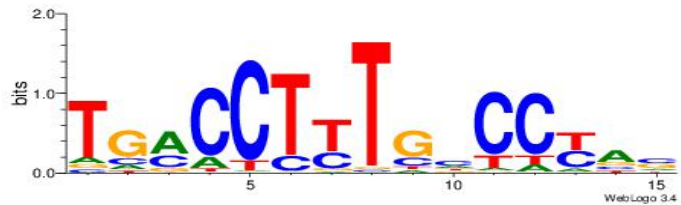
Number of overlap: 8
Similarity score: 0.0495607

Alignment:
BTRGGDCARAGGKCA
-AAGGTCAC-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCK

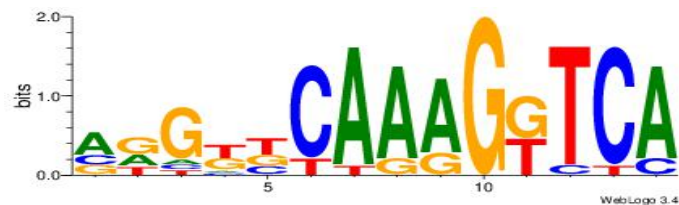


Dataset #: 2
Motif ID: 22
Motif name: NR2F1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.0564874

Alignment:
AKGY YCAAAGRTCA
-----AAGGTCAC

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGY YCAAAGRTC

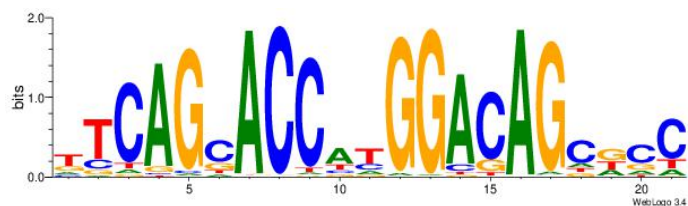


Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0594649

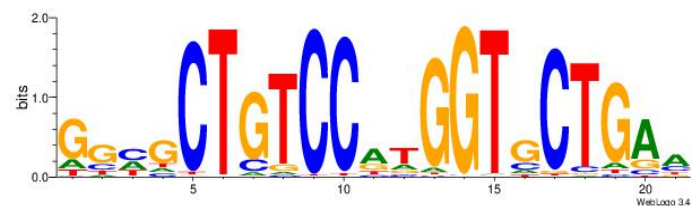
Alignment:

TTCAGCACCATGGACAGCKCC
 -----AAGGTCAC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



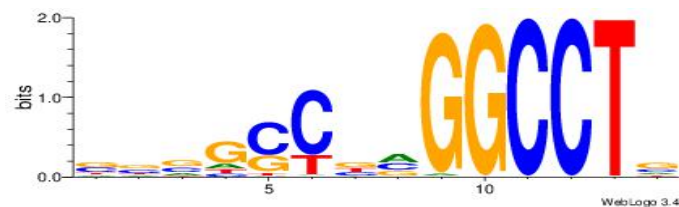
Dataset #: 2

Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0631514

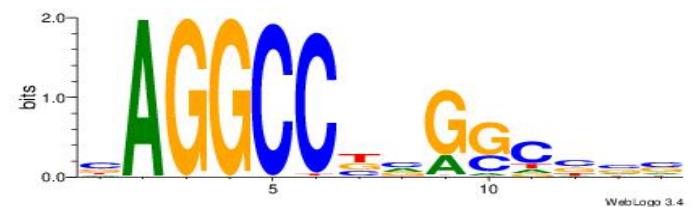
Alignment:

BBVGCCBVGGCCTV
 GTGACCTT-----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

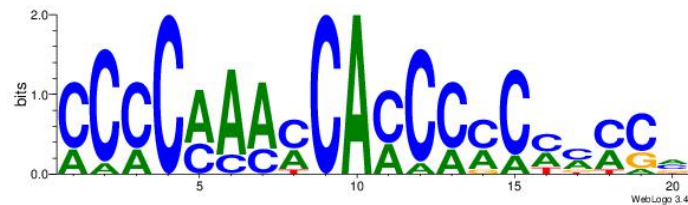


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0720656

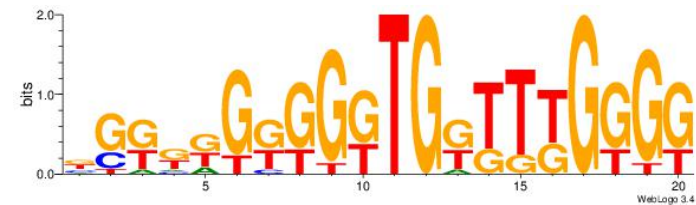
Alignment:

BGRRRGRGGRTGRTTYGGGG
 -----GTGACCTT----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence:
 BGRRRGRGGRTGRTTYGGGG



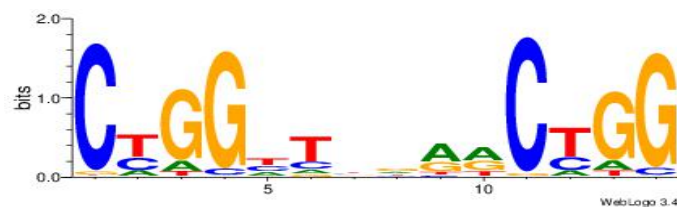
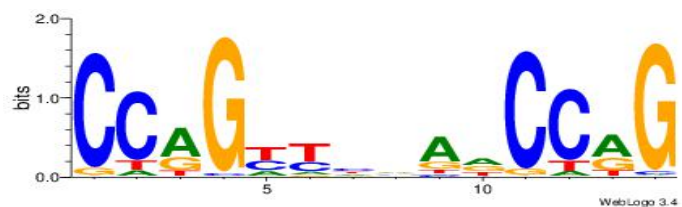
Dataset #:	2
Motif ID:	48
Motif name:	Tcfcp2l1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0740998

Alignment:

CKGGDTBDMCTGG
 -----GTGACCTT--

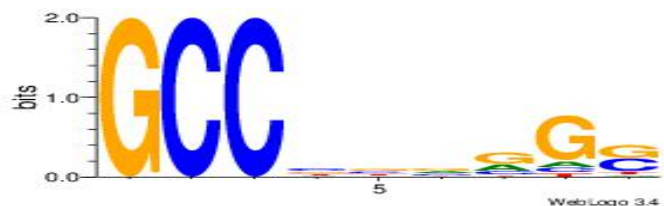
Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMCTGG

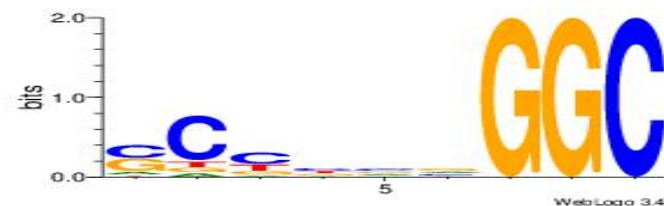


Dataset #: 2 **Motif ID: 15** **Motif name: TFAP2A**

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



Best Matches for Significant Motif ID 15 (Highest to Lowest)

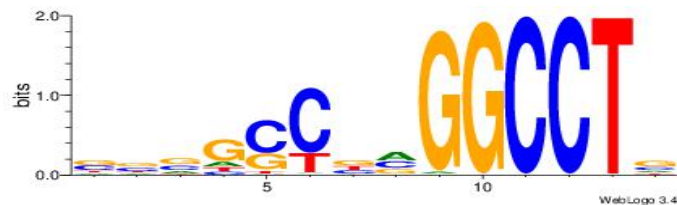
Dataset #:	2
Motif ID:	12
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.0131247

Alignment:

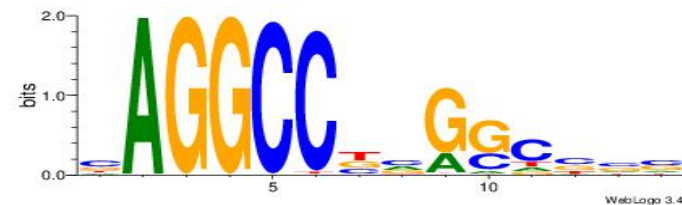
BBVGCCBVGGCTV

---SCMVBBGGC---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

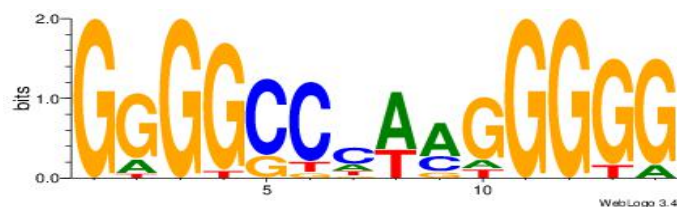


Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0414588

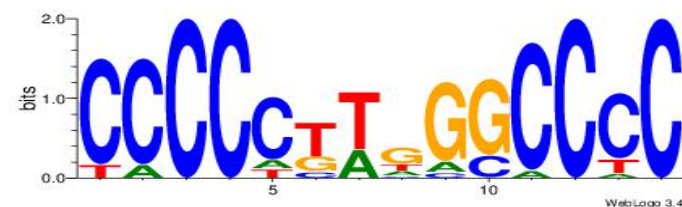
Alignment:

GGGGCCCAAGGGG
 ---GCCBBVRGS---

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

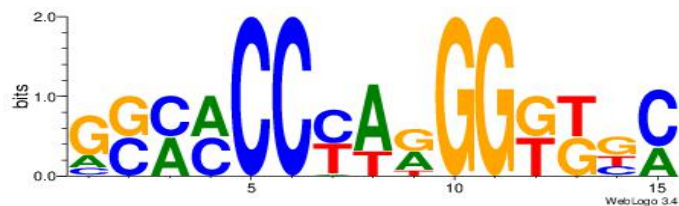


Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0438157

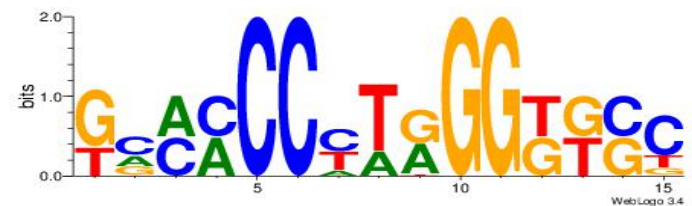
Alignment:

GYRYCCMTKGGYRSC
 ---SCMVBBGGC---

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

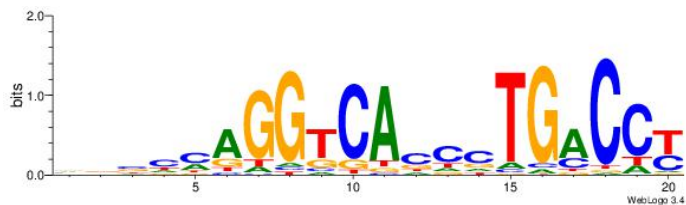


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 9

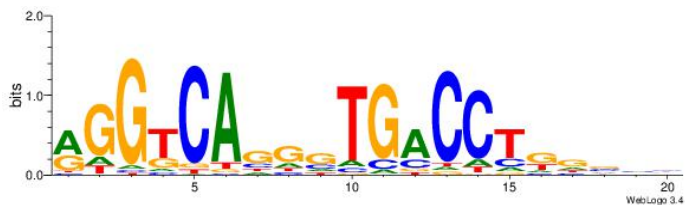
Similarity score: 0.0450672

Alignment:
MGGTCAGGGTGACCTRDBHV
-----GCCBBVRGS-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

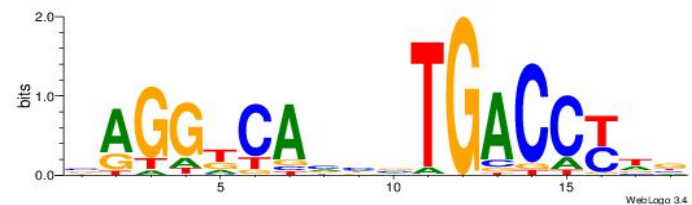
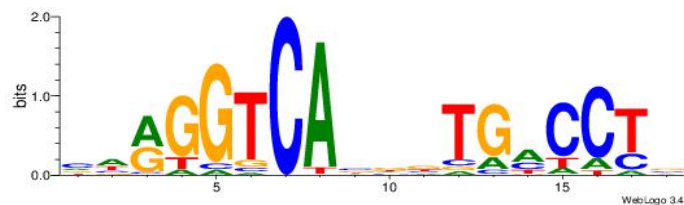


Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 9
Similarity score: 0.0531668

Alignment:
BAGGYCABHBTGACCKHV
-----SCMVBBGGC-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Dataset #: 2
 Motif ID: 40
 Motif name: Mycn
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0550803

Alignment:
 HSCACGTGGC
 -SCMVBBGGC

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



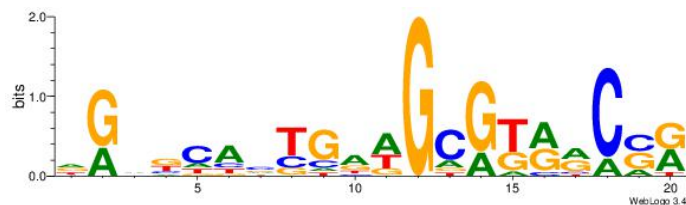
Dataset #: 2
 Motif ID: 45

Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	9
Similarity score:	0.0581255

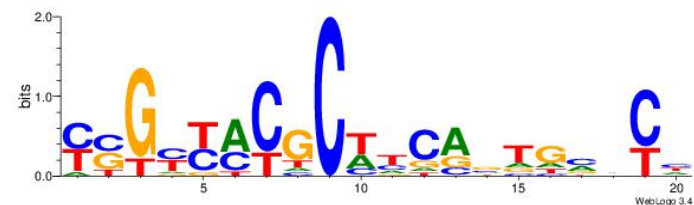
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----GCCBBVRGS-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



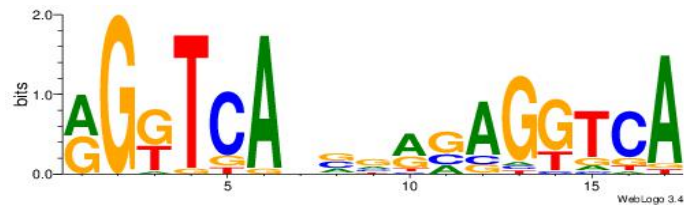
Dataset #:	2
Motif ID:	47
Motif name:	RXRRAR_DR5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	9
Similarity score:	0.0606062

Alignment:

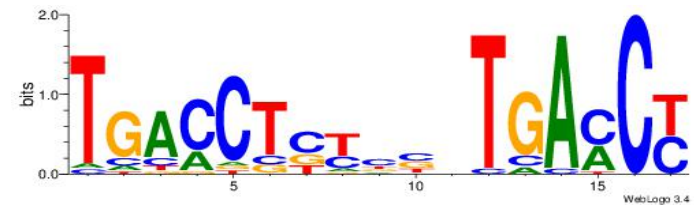
RGKTCABVVRGAGGTCA

--GCCBBVRGS-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence:
TGACCTCKVVB TGAYCK



Dataset #:	2
Motif ID:	38
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0.0613455

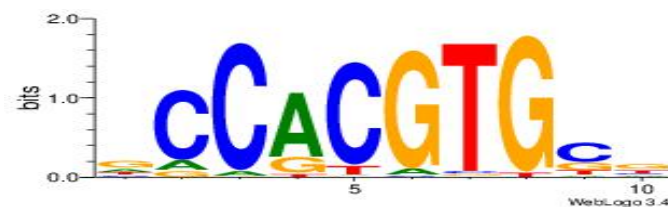
Alignment:

VGCACGTGGH

-SCMVBBGGC

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



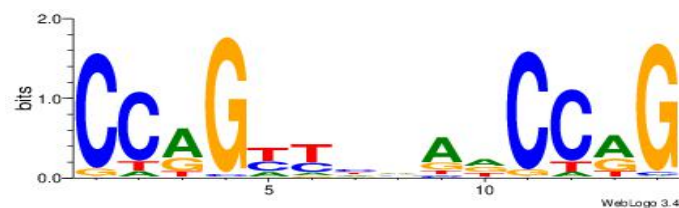
Dataset #: 2
 Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.0631412

Alignment:

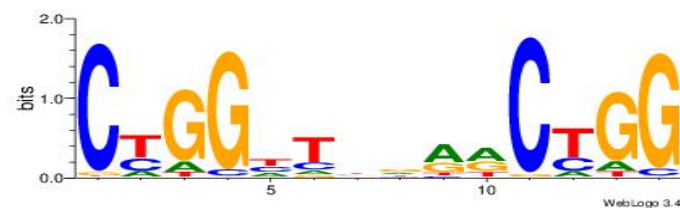
CCAGYYHVADCCRG

---GCCBBVRGS--

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTG



Dataset #: 2 Motif ID: 25 Motif name: Arnt

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Best Matches for Significant Motif ID 25 (Highest to Lowest)

Dataset #:	2
Motif ID:	31
Motif name:	Esrb
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

Alignment:

CACGTG

CACGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 2
 Motif ID: 39
 Motif name: MYCMAX
 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: 0.0143849

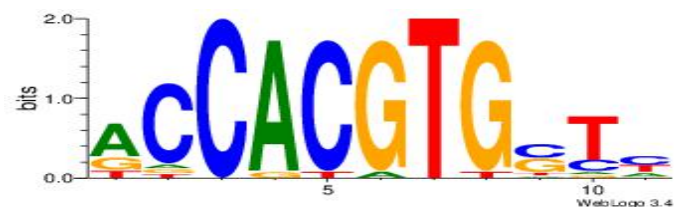
Alignment:

RASCACGTGGT
 ---CACGTG--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM

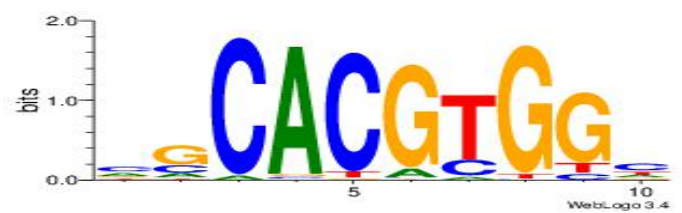


Dataset #: 2
 Motif ID: 38
 Motif name: Myc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6

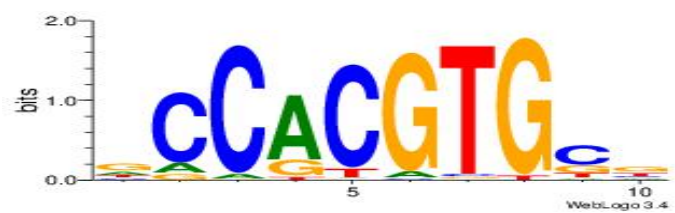
Similarity score: 0.0267529

Alignment:
DCCACGTGCV
--CACGTG--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

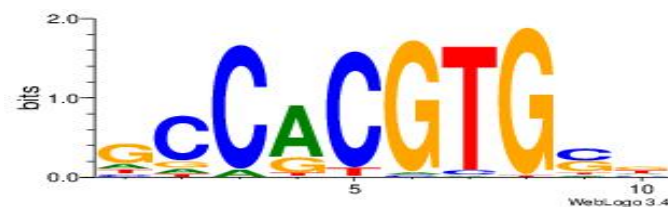


Dataset #: 2
Motif ID: 40
Motif name: Mycn
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0272641

Alignment:
HSCACGTGGC
--CACGTG--

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 2
 Motif ID: 33
 Motif name: HIF1AARNT
 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: 0.0347756

Alignment:
 VCACGTBV
 -CACGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Dataset #: 2
 Motif ID: 26

Motif name:	ArntAhr
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:	0.065625

Alignment:
YGCGTG
CACGTG

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Dataset #:	2
Motif ID:	14
Motif name:	ZEB1
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:	0.0689533

Alignment:

HAGGTG

CACGTG

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



Dataset #:	2
Motif ID:	28
Motif name:	Egr1
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:	0.0784722

Alignment:

HGCGTGGGCGK

CACGTG-----

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YGCCCCACGCH



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: 6
 Similarity score: 0.0854167

Alignment:

BAACGTCCGC

-CACGTG---

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



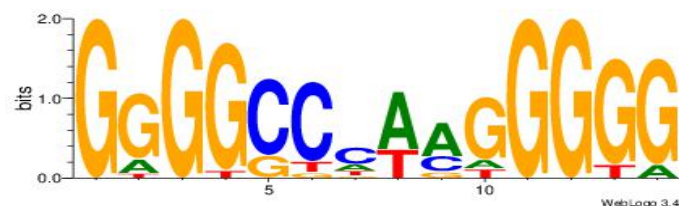
Dataset #: 2
 Motif ID: 21

Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.105093

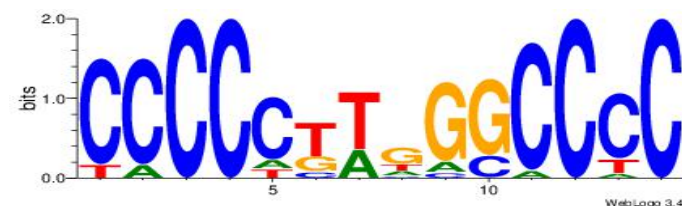
Alignment:

GGGGCCCAAGGGGG
 -----CACGTG--

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCTTGGCCCA



Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: RGGAAR Reverse complement motif Consensus sequence: MTTCCK



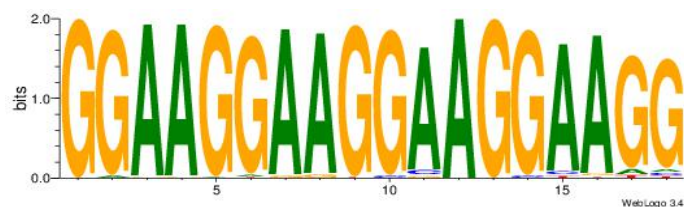
Best Matches for Motif ID 1 (Highest to Lowest)

Dataset #: 2
 Motif ID: 32
 Motif name: EWSR1-FLI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 12
 Number of overlap: 6
 Similarity score: 0.0146511

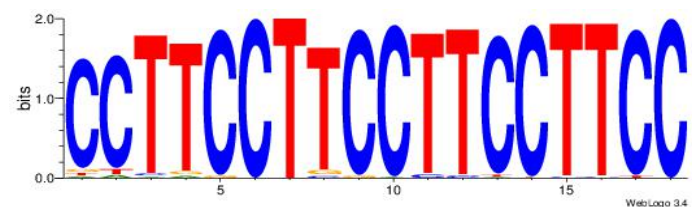
Alignment:

CCTTCCTTCCTTCCTTC
 -MTTCCK-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTC



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
 ---MTTCCK-

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



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

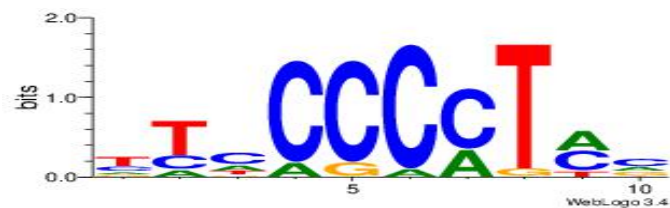
Similarity score: 0.0753789

Alignment:
BKAGGGGDAD
----RGGAAR

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: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0757695

Alignment:
GGGGA AKCCCC
-RGGAAR----

Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGA AKCCCC



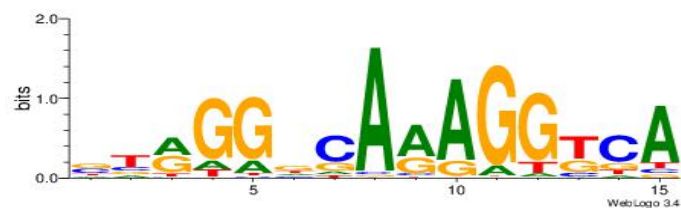
Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0800484

Alignment:

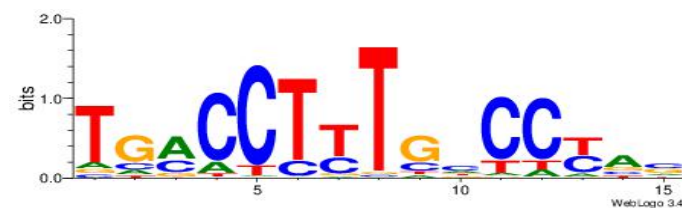
BTRGGDCARAGGKCA

---RGAAR-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



Dataset #: 1
 Motif ID: 7

Motif name:	Motif 7
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:	0.0827261

Alignment:
GGGGMGGG
-RGGAAR-

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG



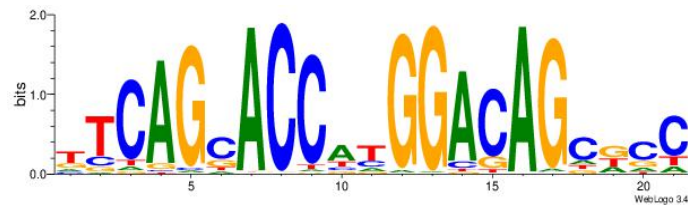
Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.0829223

Alignment:

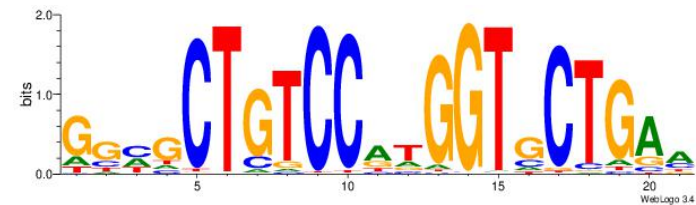
TTCAGCACCATGGACAGCKCC

-----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

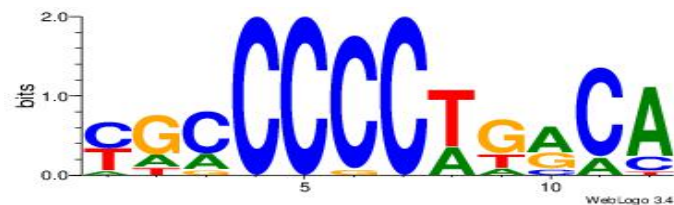
Alignment:

TGYCAGGGGGCR

-----RGGAAR

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

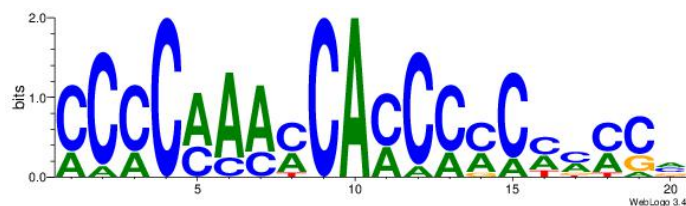


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0835516

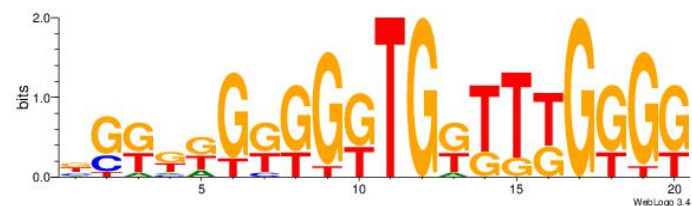
Alignment:

BGRRRGRGGRTGRTTYGGGG
 ----RGAAR-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



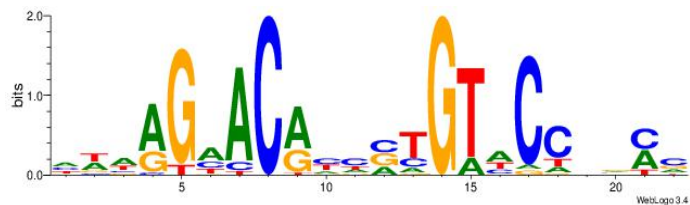
Dataset #: 2

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

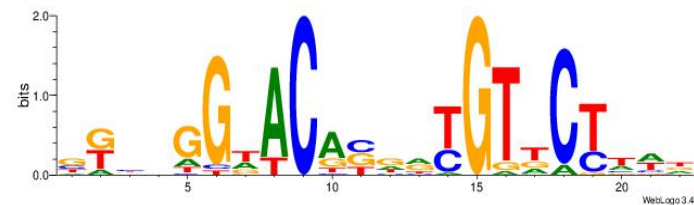
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 ---RGAAR-----

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

Original motif Consensus sequence: AMACA



Reverse complement motif Consensus sequence: TGTRT



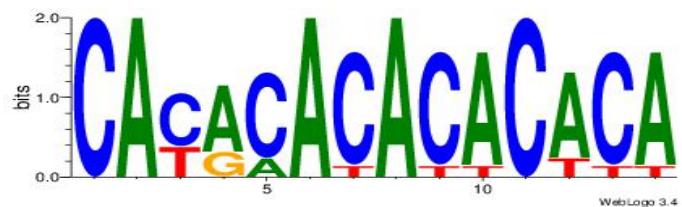
Best Matches for Motif ID 2 (Highest to Lowest)

Dataset #:	1
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

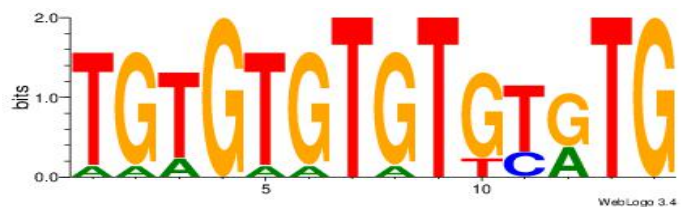
Position number: 5
Number of overlap: 5
Similarity score: 0

Alignment:
TGTGTGTGTGKTG
-----TGTRT-----

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTG

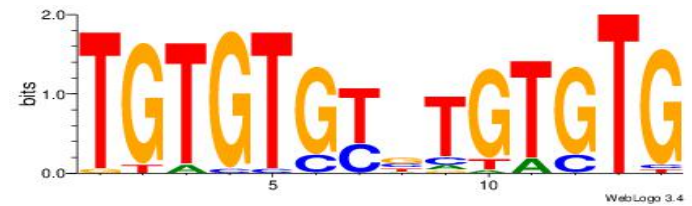


Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 10
Number of overlap: 5
Similarity score: 0.0040753

Alignment:
TGTGTGKVTGTGTG
TGTRT-----

Original motif Consensus sequence: CACACAVRCACACA

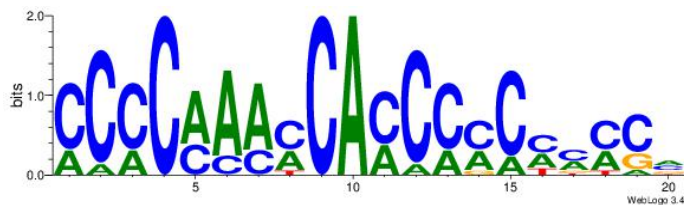
Reverse complement motif Consensus sequence: TGTGTGKVTGTGTG



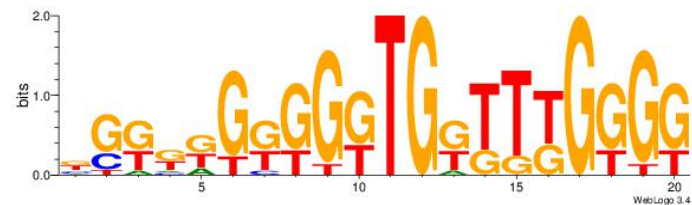
Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 5
 Similarity score: 0.0243918

Alignment:
 CCCCMAAMCAMCCMCMMMC
 -----AMACA-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGG

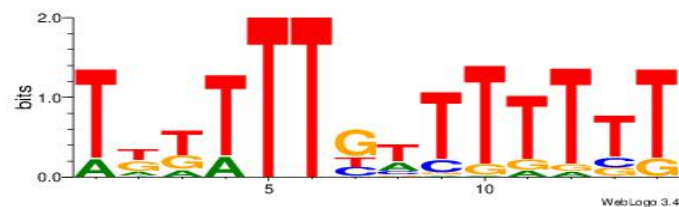


Dataset #: 1

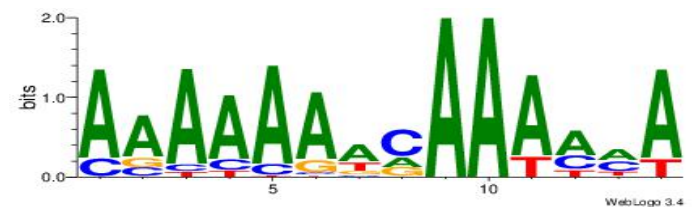
Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 5
 Similarity score: 0.0394919

Alignment:
 AAAAAACAAARRA
 ----AMACA-----

Original motif Consensus sequence: TKKTTTGTTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARRA



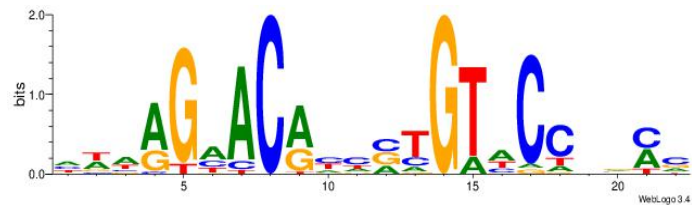
Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.0429089

Alignment:

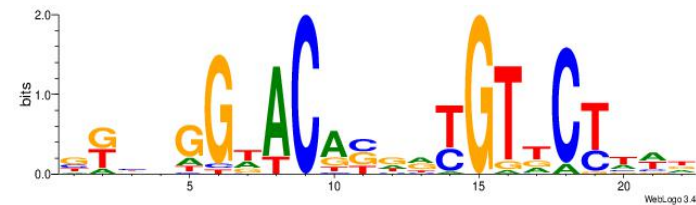
HWDAGHACRHHVTGTHCCHVMV

-----AMACA-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence:
VRVDGGHACAVDDKGTHCTDWH



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

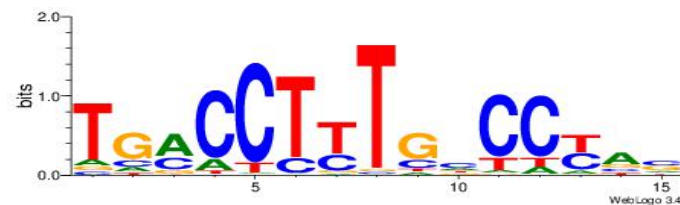
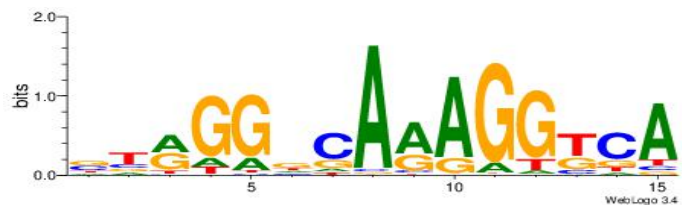
Alignment:

TGRCCTKTGHCKAB

-----TGTRT-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB



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

Alignment:

YGCGTG

TGTRT-

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



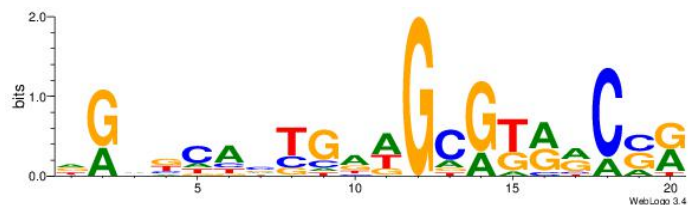
Dataset #: 2
 Motif ID: 45

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

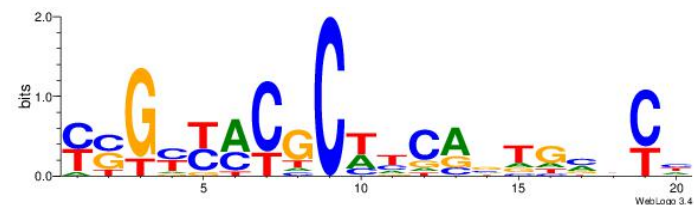
Alignment:

```
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:

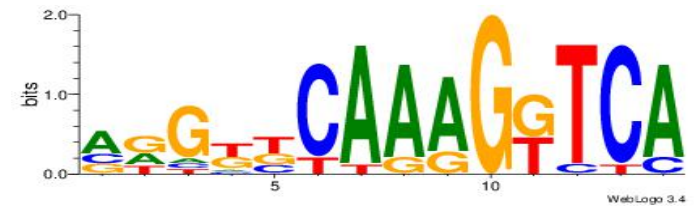
AKGY YCAAAGRTCA

-----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

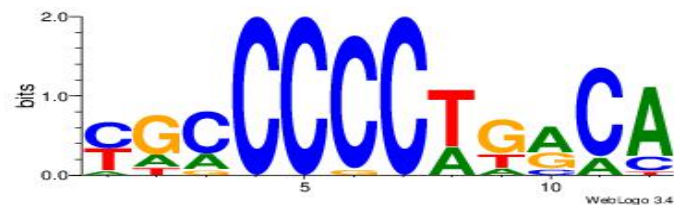
Alignment:

TGYCAGGGGGCR

TGTRT-----

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA



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

Original motif Consensus sequence: AGSCWGG



Reverse complement motif Consensus sequence: CCWGSCT



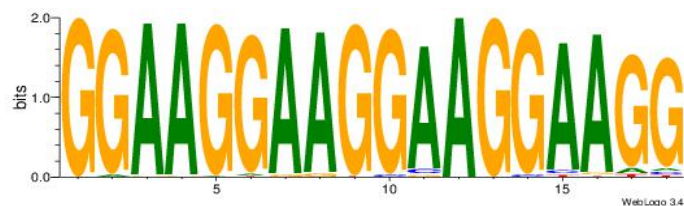
Best Matches for Motif ID 3 (Highest to Lowest)

Dataset #:	2
Motif ID:	32
Motif name:	EWSR1-FLI1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	7
Similarity score:	0.0395671

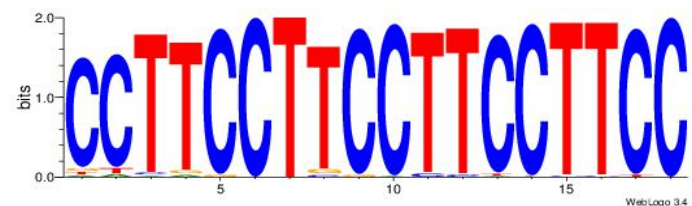
Alignment:

```
GGAAGGAAGGAAGGAAGG
-----AGSCWGG-----
```

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

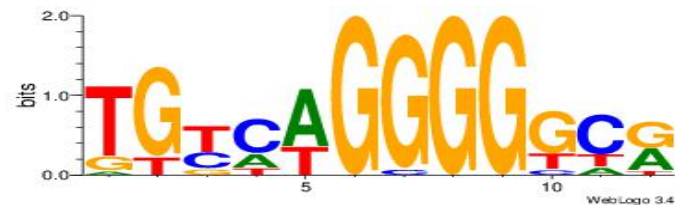


Dataset #: 2
Motif ID: 35
Motif name: INSM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 7
Similarity score: 0.0494688

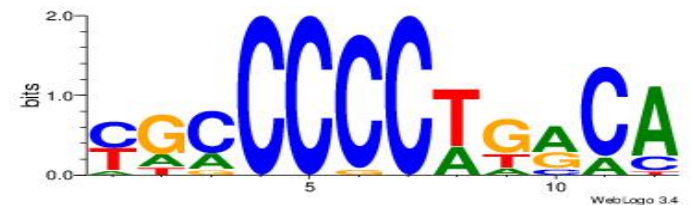
Alignment:

MGCCCCCTGMCA
-----CCWGSCT

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA

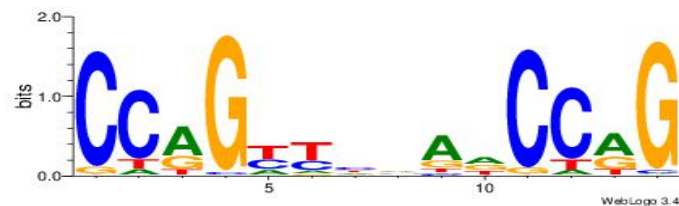


Dataset #: 2
 Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0669354

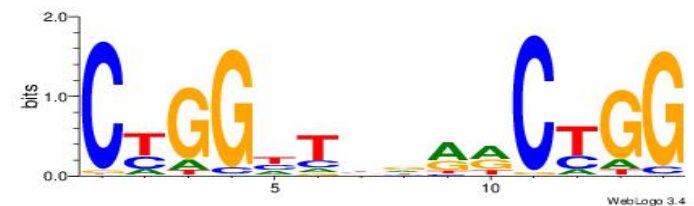
Alignment:

CCAGYYHVADCCRG
 CCWGSCT-----

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTG

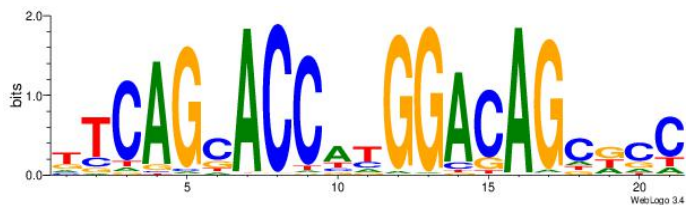


Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 7

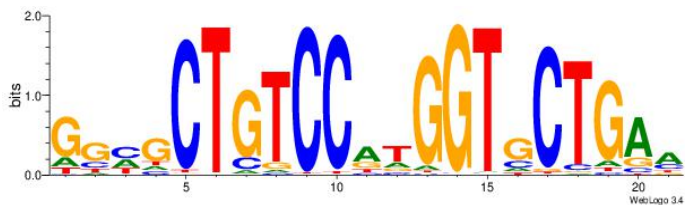
Similarity score: 0.0693747

Alignment:
TTCAGCACCATGGACAGCKCC
-----AGSCWGG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

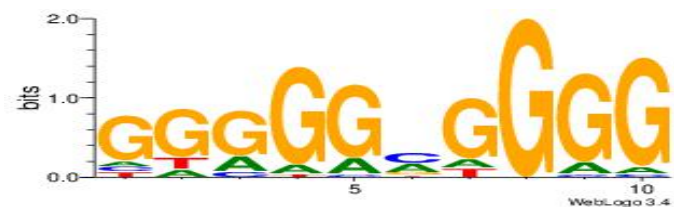
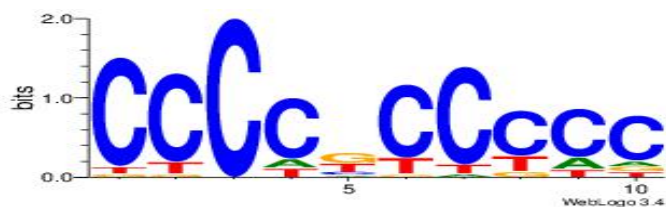


Dataset #: 2
Motif ID: 16
Motif name: SP1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 7
Similarity score: 0.0695377

Alignment:
CCCCKCCCCC
-CCWGSCT--

Original motif Consensus sequence: CCCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG

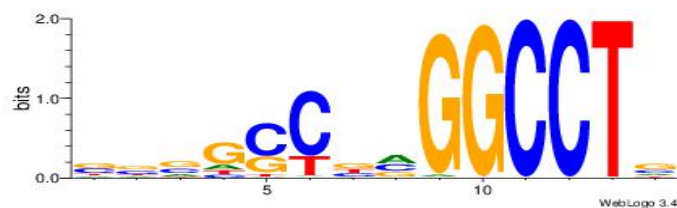


Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 7
 Similarity score: 0.0720685

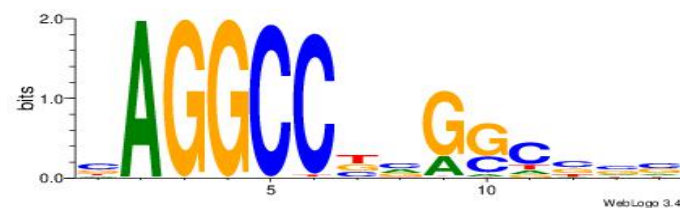
Alignment:

BBVGCCBVGGCCTV
 -----CCWGSCT-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



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:	1
Number of overlap:	7
Similarity score:	0.0742342

Alignment:
 CCCRCCCC
 CCWGSCT-

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG

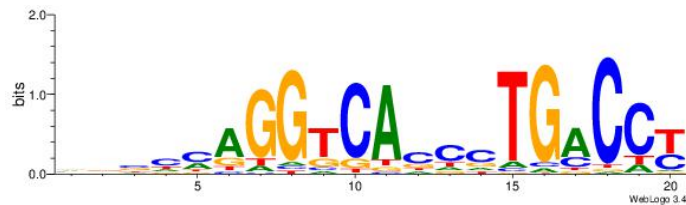


Dataset #:	2
Motif ID:	29
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	13
Number of overlap:	7
Similarity score:	0.0771405

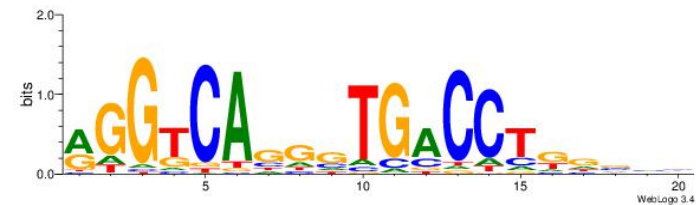
Alignment:

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



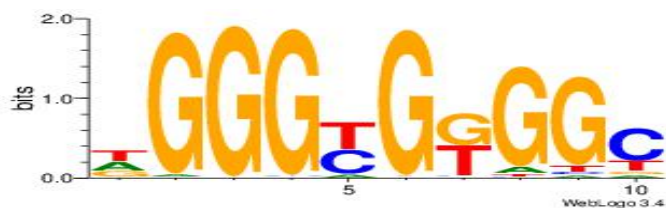
Dataset #: 2
 Motif ID: 36
 Motif name: Klf4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0798994

Alignment:

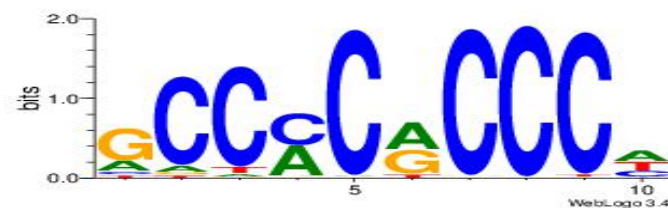
GCCYCMCCCD

---CCWGSCT

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



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

Original motif Consensus sequence: CTCTGY



Reverse complement motif Consensus sequence: KCAGAG



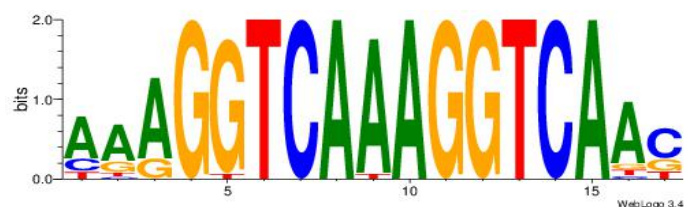
Best Matches for Motif ID 4 (Highest to Lowest)

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

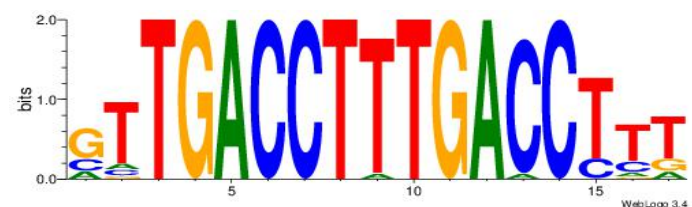
Alignment:

AAAGGTCAAAGGTCAAC
-----KCAGAG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

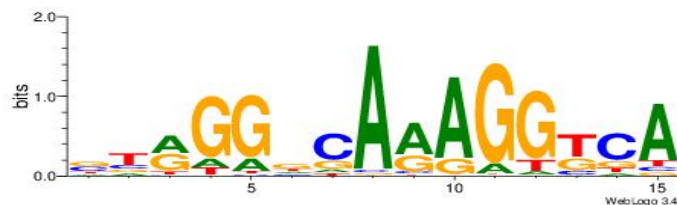


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0140102

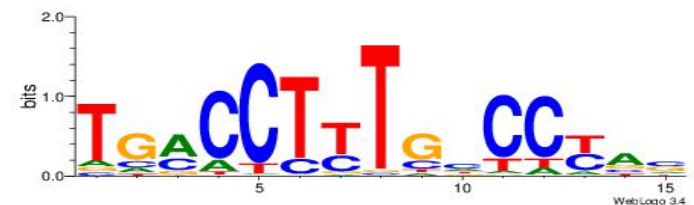
Alignment:

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

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKGHCCK



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

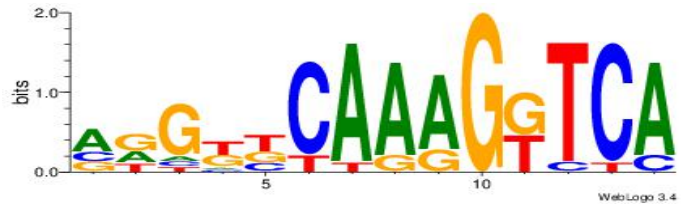
Similarity score: 0.0186793

Alignment:
AKGYCAAAGRTCA
----KCAGAG----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA

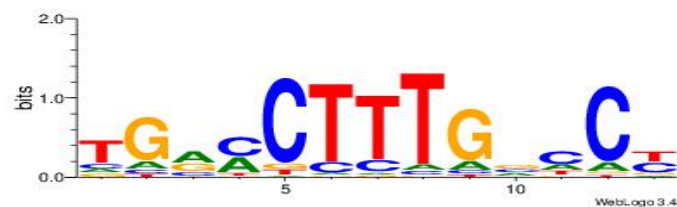
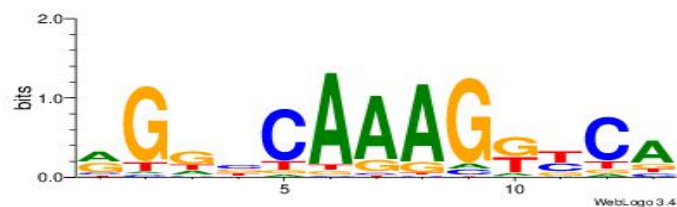


Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020602

Alignment:
RGGBCAAAGKYCA
---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



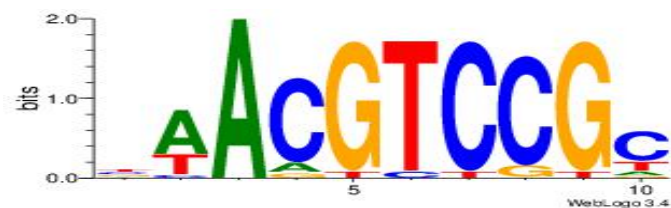
Dataset #: 2
 Motif ID: 37
 Motif name: MIZF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0221665

Alignment:

BAACGTCCGC

----CTCTGY

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



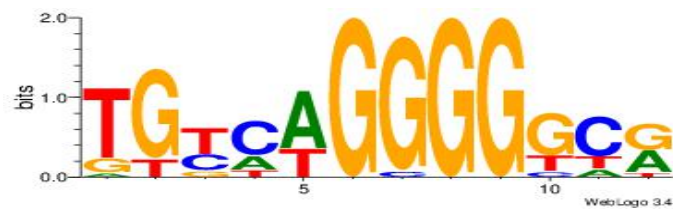
Dataset #: 2
 Motif ID: 35

Motif name:	INSM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0255256

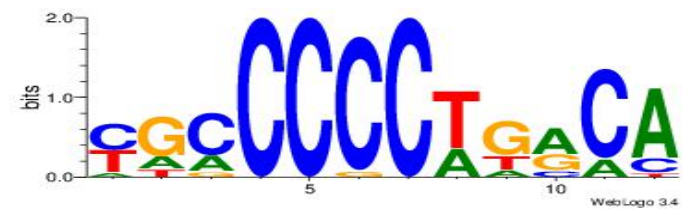
Alignment:

TGYCAGGGGGCR
 --KCAGAG----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



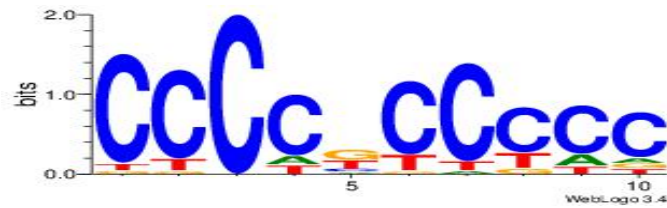
Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0349642

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

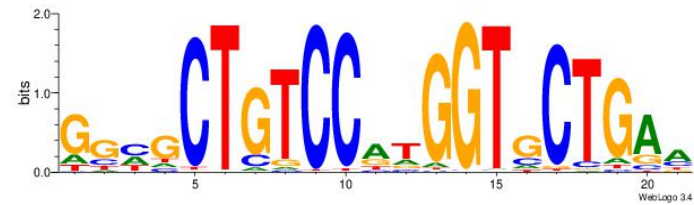
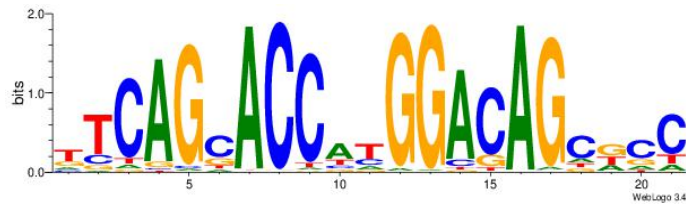
Alignment:

GGYGCTGTCCATGGTGCTGAA

--CTCTGY-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



Dataset #: 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: 1
 Number of overlap: 6
 Similarity score: 0.0446026

Alignment:

TCCCAG

KCAGAG

Original motif Consensus sequence: CTGGGA



Reverse complement motif Consensus sequence: TCCCAG

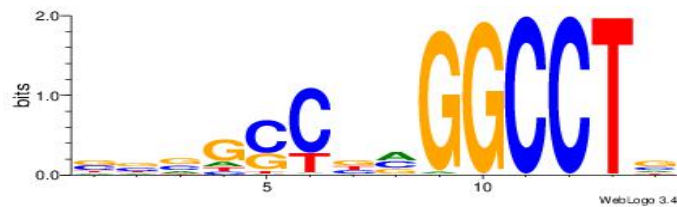


Dataset #: 2
 Motif ID: 12

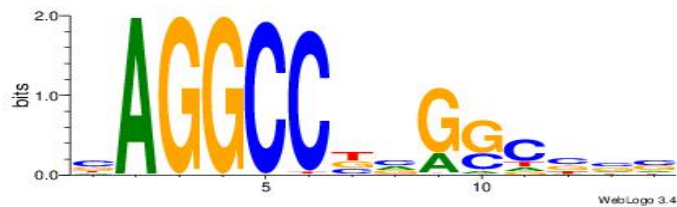
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 6
Similarity score: 0.0448449

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

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



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

Original motif Consensus sequence: ATKTM



Reverse complement motif Consensus sequence: RARAT



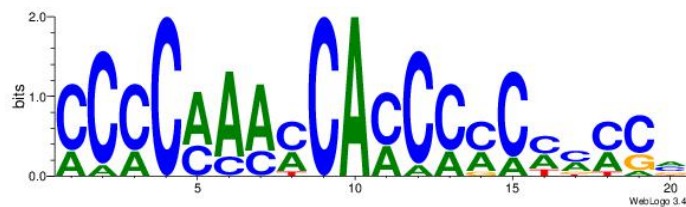
Best Matches for Motif ID 5 (Highest to Lowest)

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

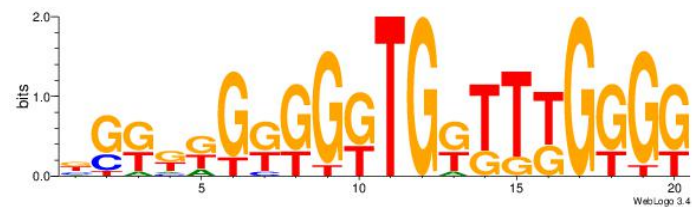
Alignment:

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

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

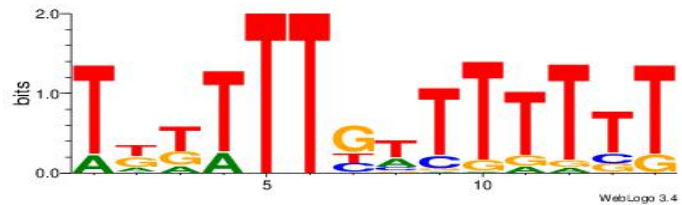


Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 5
Similarity score: 0.0260117

Alignment:
AAAAAAACAAARRA
-RARAT-----

Original motif Consensus sequence: TKKTTTGTTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR



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:
 AKGYCAAAGRTCA
 -----RARAT--

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



Dataset #: 2
 Motif ID: 37

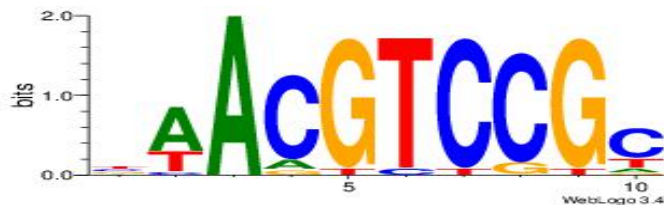
Motif name:	MIZF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	5
Similarity score:	0.0292478

Alignment:

BAACGTCCGC

--ATKTM---

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



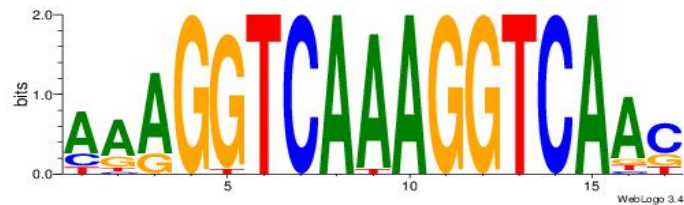
Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	10
Number of overlap:	5
Similarity score:	0.0292478

Alignment:

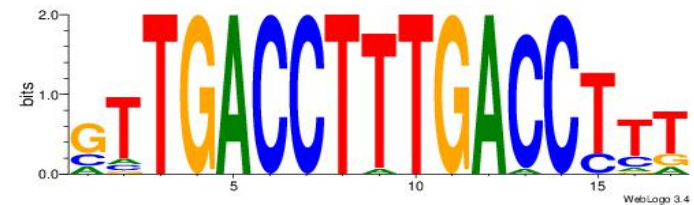
AAAGGTCAAAGGTCAAC

-----ATKTM----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Dataset #:	2
Motif ID:	20
Motif name:	PPARGRXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	5
Similarity score:	0.0305369

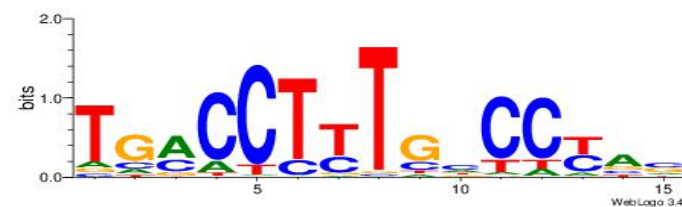
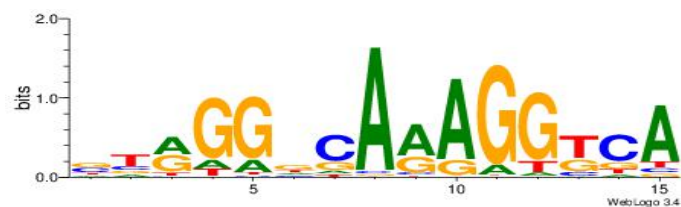
Alignment:

TGRCCTKTGHCKAB

-----ATKTM-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

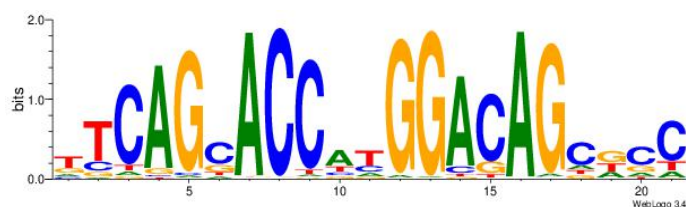
Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB



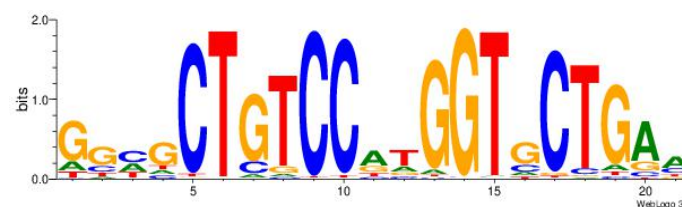
Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 13
 Number of overlap: 5
 Similarity score: 0.0315454

Alignment:
 GYGCTGTCCATGGTGCTGAA
 ----ATKTM-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

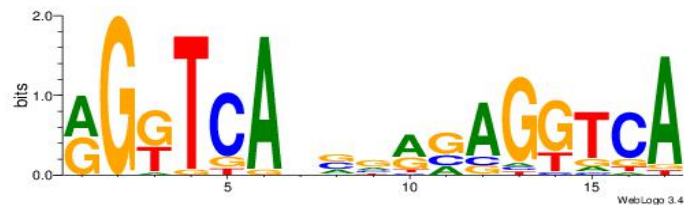


Dataset #: 2

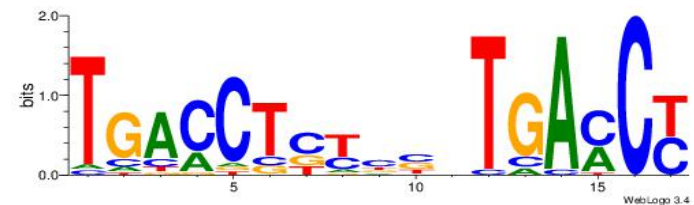
Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 5
 Similarity score: 0.0335956

Alignment:
 RGKTCABVVRGAGGTCA
 ATKTM-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBGTGAYCK



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

Original motif Consensus sequence: CMGCRGC



Reverse complement motif Consensus sequence: GCKGCOYG



Best Matches for Motif ID 6 (Highest to Lowest)

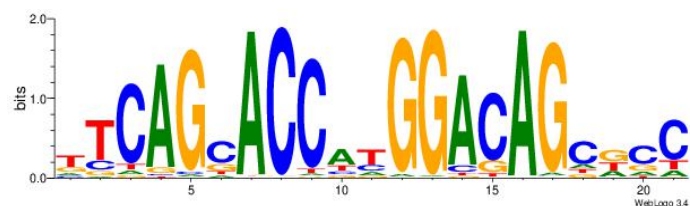
Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 13
Number of overlap: 7
Similarity score: 0.0205607

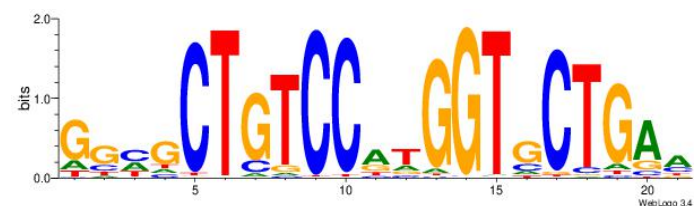
Alignment:

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: GCGGACGTTT

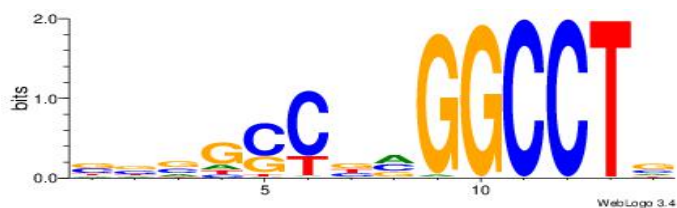


Dataset #: 2
Motif ID: 12
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 7
Similarity score: 0.038091

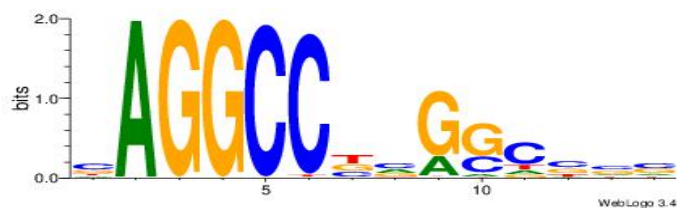
Alignment:

BBVGCCBVGGCCTV
-----CMGCRGC----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



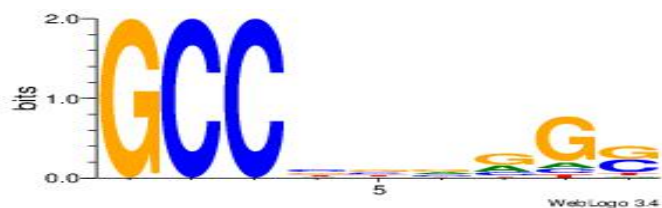
Dataset #: 2
 Motif ID: 15
 Motif name: TFAP2A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0393168

Alignment:

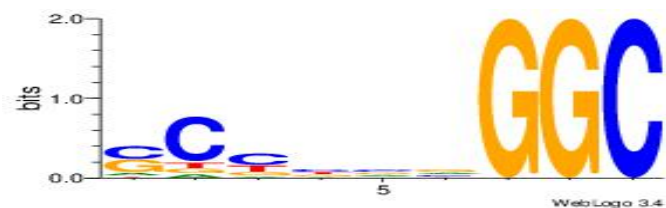
SCMVBBGGC

--CMGCRGC

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



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

Similarity score: 0.0443244

Alignment:
CCCRCCCC
-CMGCRGC

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG

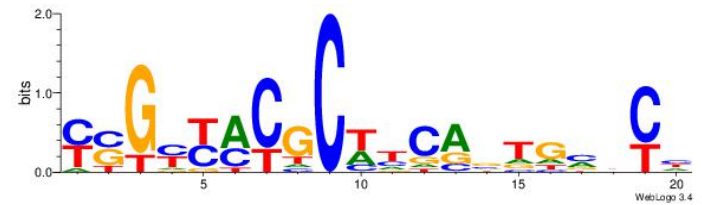
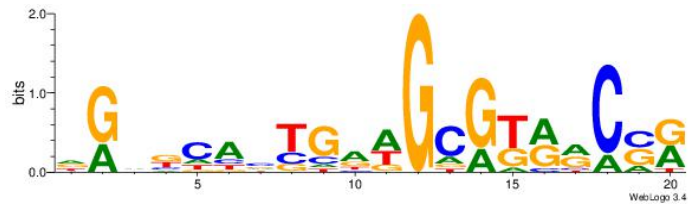


Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 7
Similarity score: 0.0448462

Alignment:
MSGKKRCGCWDCABTGBCD
-----GCKGCGY-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBCD



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:
 HCGTGGGCGK
 ---GCKGCGY--

Original motif Consensus sequence: HCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



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



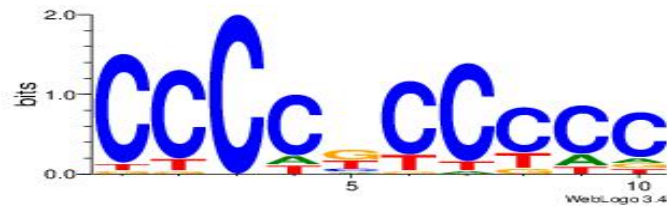
Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0490991

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

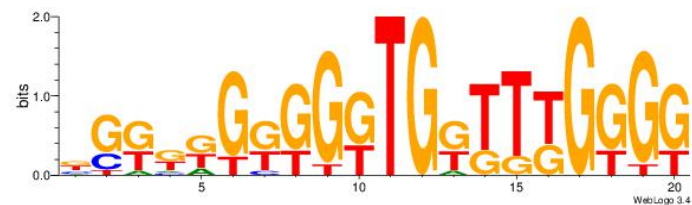
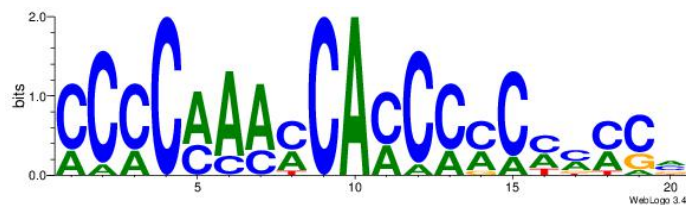
Alignment:

BGRRRGRGGRTGRTTYGGGG

-----GCKGCG-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC

Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG



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

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG



Best Matches for Motif ID 7 (Highest to Lowest)

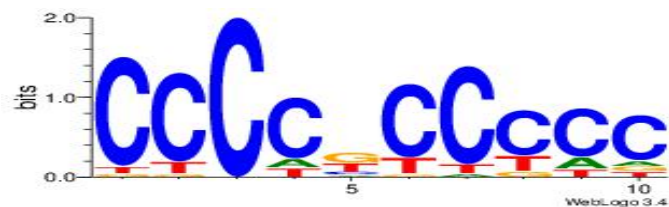
Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0423611

Alignment:

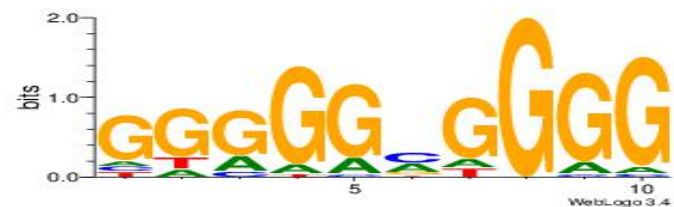
CCCCKCCCCC

-CCCRCCCC-

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



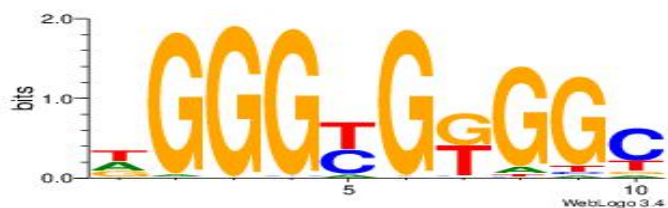
Dataset #: 2
Motif ID: 36
Motif name: Klf4
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0461644

Alignment:

DGGGYGKGGC

GGGGMGG--

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

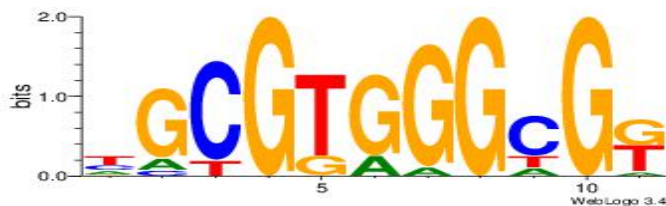


Dataset #: 2
 Motif ID: 28
 Motif name: Egr1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0650374

Alignment:

YCGCCCACGCH
 ---CCCRCCCC

Original motif Consensus sequence: HCGTG GGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH

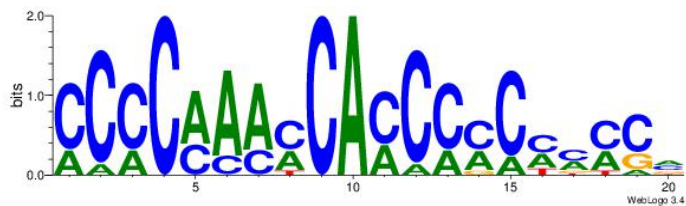


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8

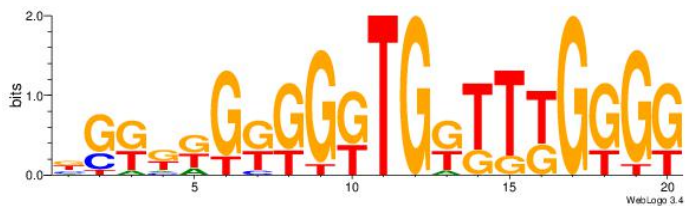
Similarity score: 0.076401

Alignment:
CCCCMAAMCAMCCMCMMMCV
-----CCCRCCCC-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV



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:
GGGGAACCCCC
GGGGMGGG---

Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGAACCCCC



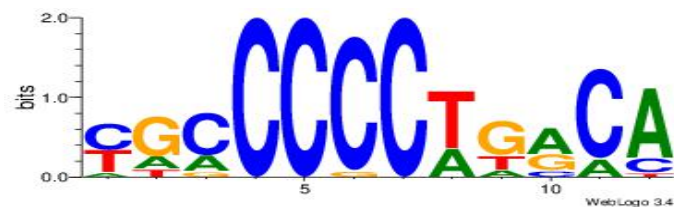
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0936832

Alignment:
 TGYCAGGGGGCR
 GGGGMGGG----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



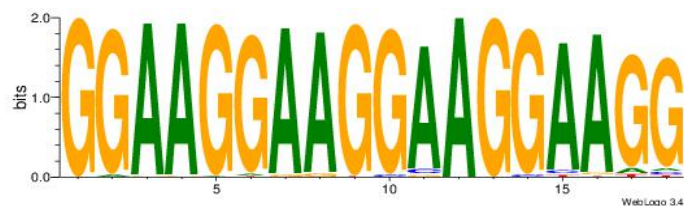
Dataset #: 2
 Motif ID: 32

Motif name:	EWSR1-FLI1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	8
Similarity score:	0.0950969

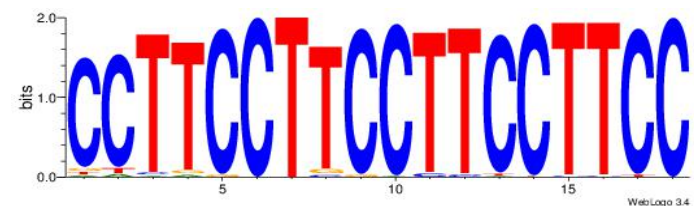
Alignment:

```
GGAAGGAAGGAAGGAAGG
-----GGGGMGGG-----
```

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC



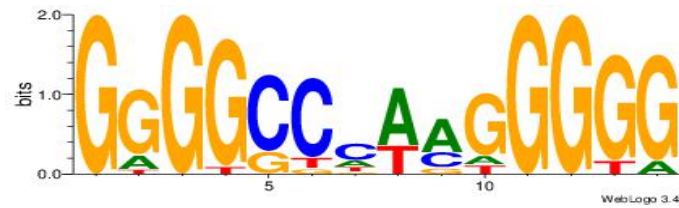
Dataset #:	2
Motif ID:	21
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0998932

Alignment:

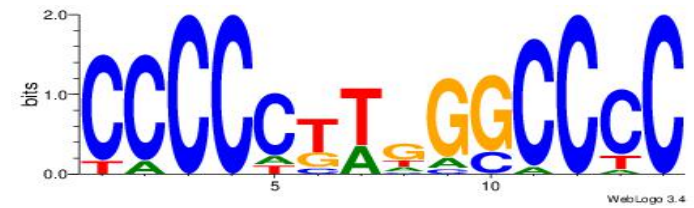
GGGGCCCAAGGGG

GGGGMGG-----

Original motif Consensus sequence: GGGGCCCAAGGGG



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

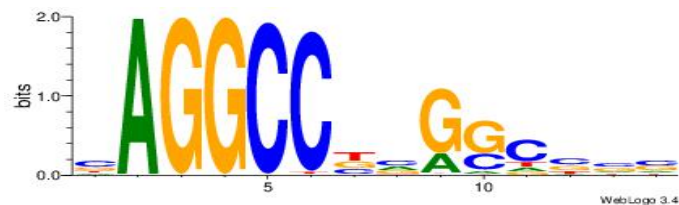
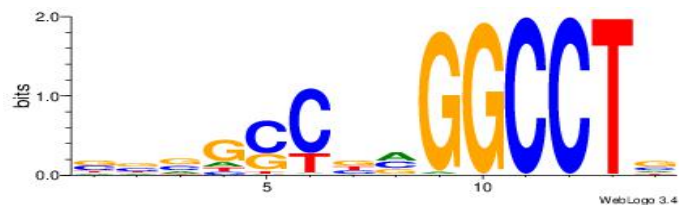
Alignment:

BBVGCCBVGGCCTV

-----CCCRCCCC--

Original motif Consensus sequence: BBVGCCBVGGCCTV

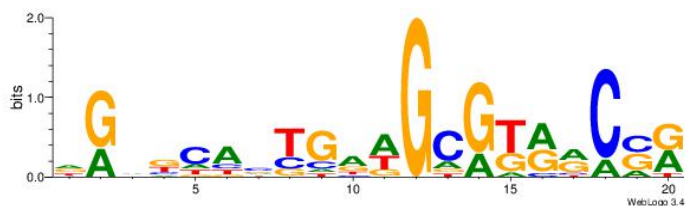
Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



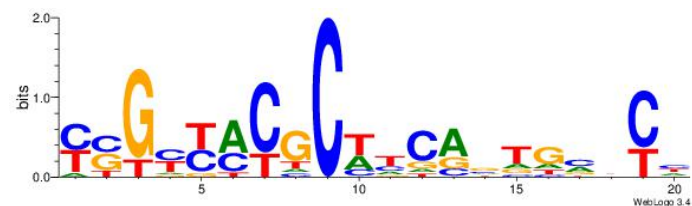
Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.102497

Alignment:
 DGVCABTGDWGCGRRCR
 -----GGGGMGG-----

Original motif Consensus sequence: DGVCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD



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

Original motif Consensus sequence: CTGGGA



Reverse complement motif Consensus sequence: TCCCAG



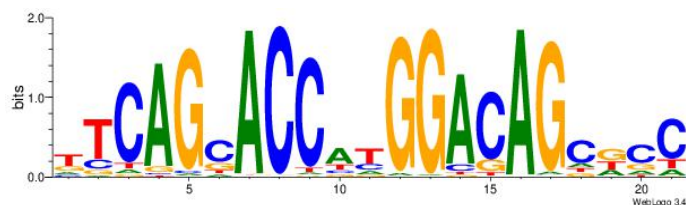
Best Matches for Motif ID 8 (Highest to Lowest)

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

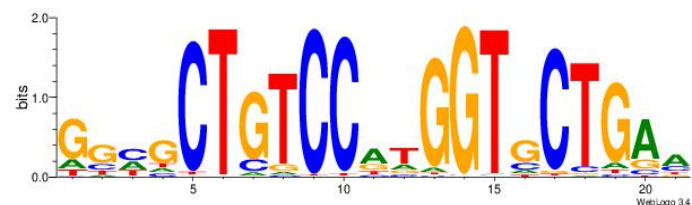
Alignment:

```
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

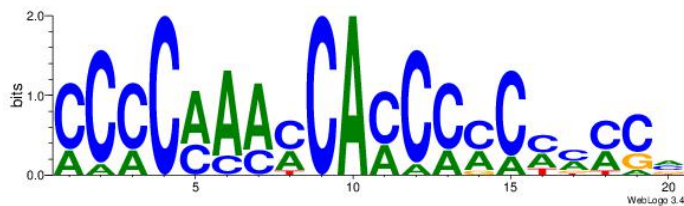


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6

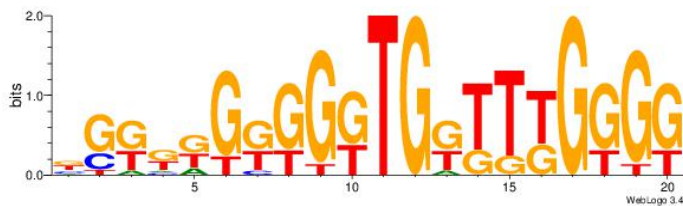
Similarity score: 0.0509122

Alignment:
BGRRRGRGGRTGRTTYGGGG
-----CTGGGA

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

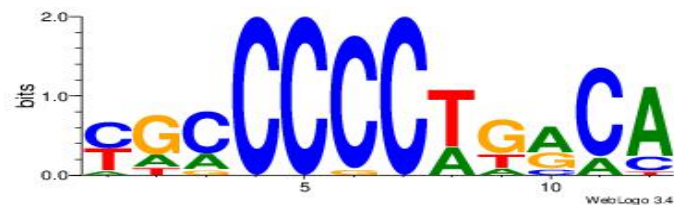


Dataset #: 2
Motif ID: 35
Motif name: INSM1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0557857

Alignment:
TGYCAGGGGGCR
---CTGGGA---

Original motif Consensus sequence: TGYCAGGGGGCR

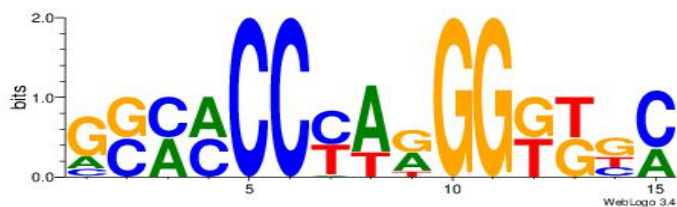
Reverse complement motif Consensus sequence: MGCCCCCTGMCA



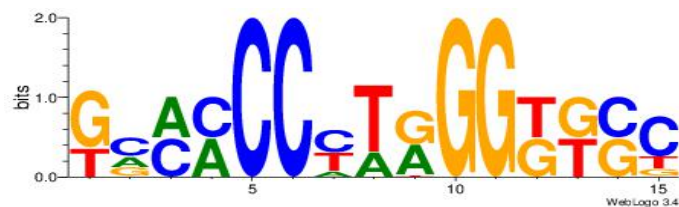
Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0624145

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

Original motif Consensus sequence: GSMGCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



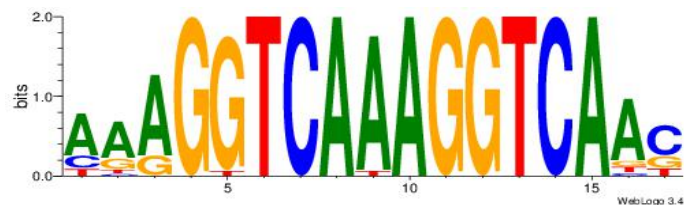
Dataset #: 2
 Motif ID: 43

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

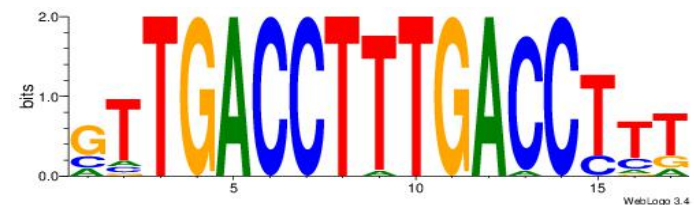
Alignment:

```
AAAGGTCAAAGGTCAAC
-----TCCCAG-----
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

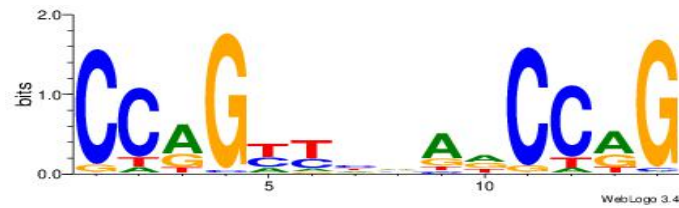


Dataset #:	2
Motif ID:	48
Motif name:	Tcfcp2l1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0663804

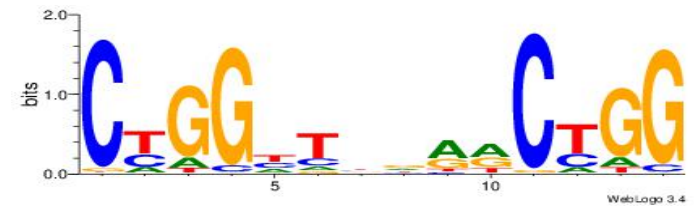
Alignment:

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: HCGTGCGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

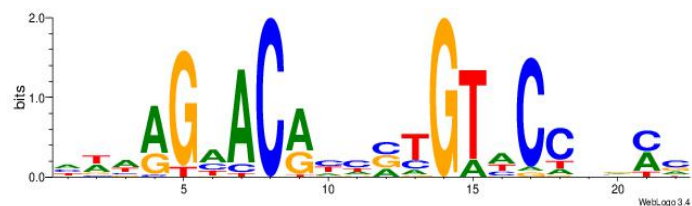


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0714107

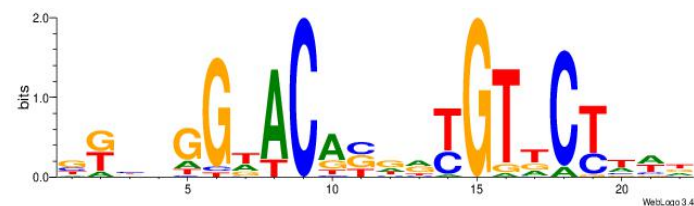
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 -----TCCCAG--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

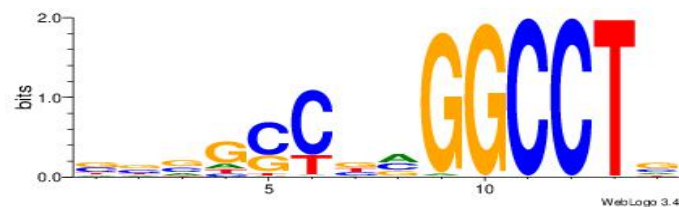


Dataset #: 2

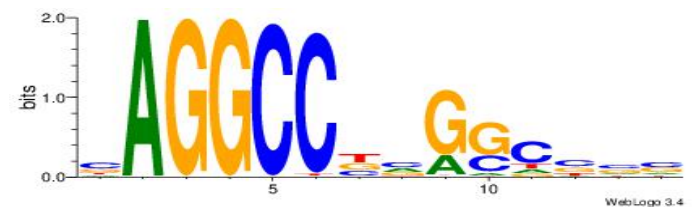
Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0718041

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

Original motif Consensus sequence: BBVGCCBVGGCCTV

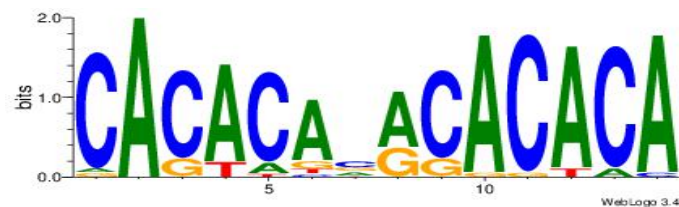


Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

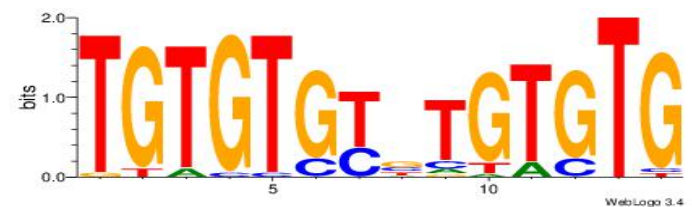


Dataset #: 1 Motif ID: 9 Motif name: Motif 9

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



Best Matches for Motif ID 9 (Highest to Lowest)

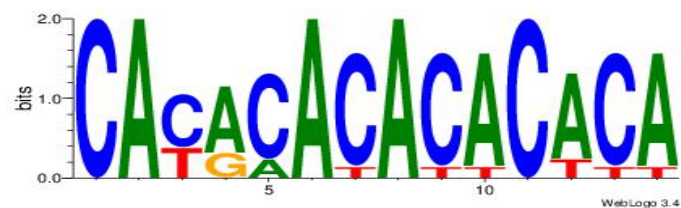
Dataset #: 1
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0170175

Alignment:

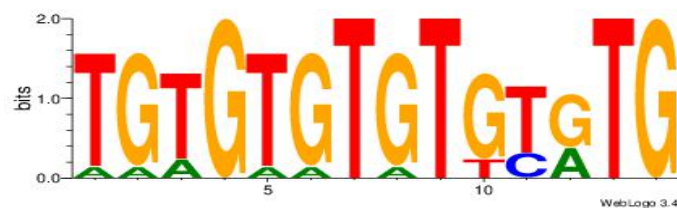
CAYACACACACACA

CACACAVRCACACA

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKT



Dataset #: 2
Motif ID: 18
Motif name: RREB1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

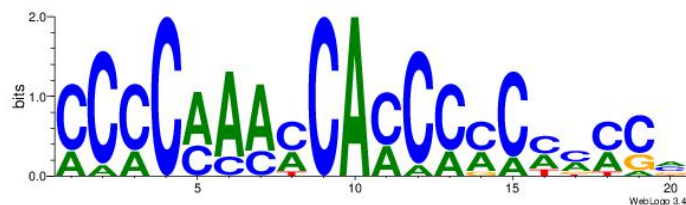
Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0868786

Alignment:

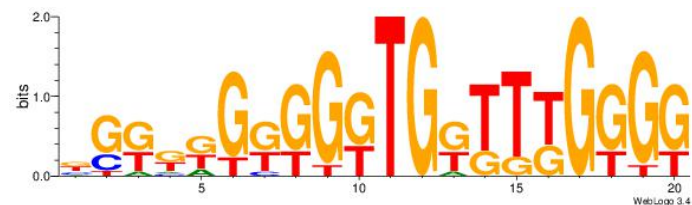
CCCCMAAMCAMCCMCMMMCV

----CACACAVRCACACA--

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



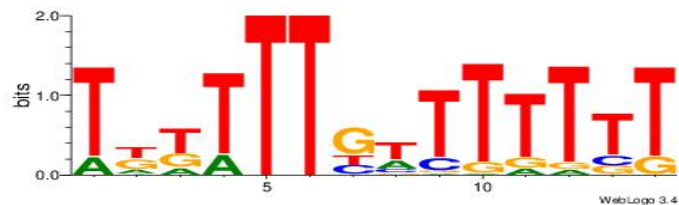
Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.578949

Alignment:

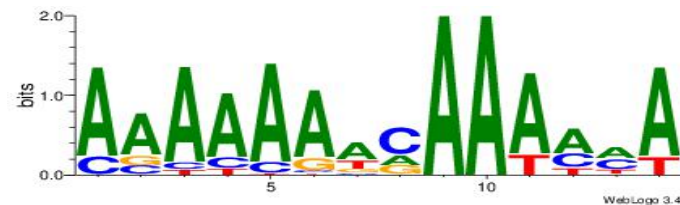
TKKTTTGT TTTT TTTT-

-TGTGTGKVTGTGTG

Original motif Consensus sequence: TKKTTTGT TTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR

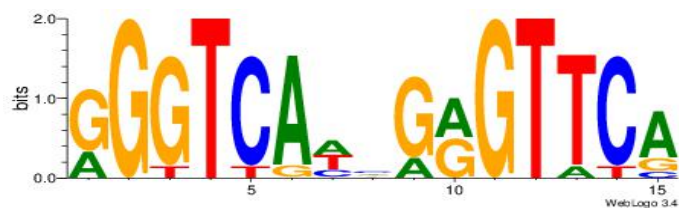


Dataset #: 2
 Motif ID: 17
 Motif name: RXRAVDR
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.593978

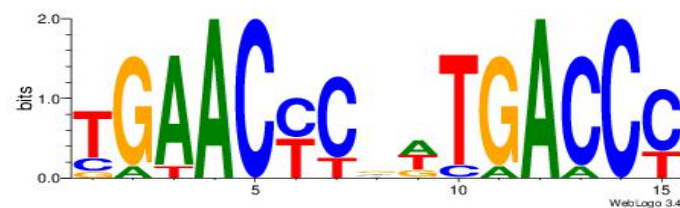
Alignment:

TGAACKBWTGACCC-
 --CACACAVRCACACA

Original motif Consensus sequence: GGGTCAWBGRGTTCA



Reverse complement motif Consensus sequence: TGAACKBWTGAC



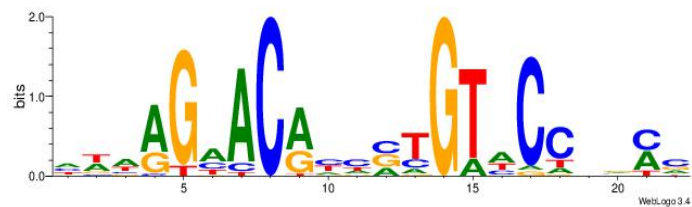
Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 12
 Similarity score: 1.09291

Alignment:

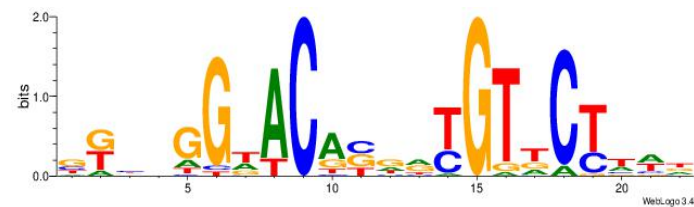
```

--VRVDGGHACAVDDKGTHCTDWH
CACACAVRCACACA-----
  
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



Dataset #: 2
 Motif ID: 28
 Motif name: Egr1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 11
 Similarity score: 1.57424

Alignment:
 HCGTG GGGCGK---
 TGTGTGKVTGTGTG

Original motif Consensus sequence: HCGTG GGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH

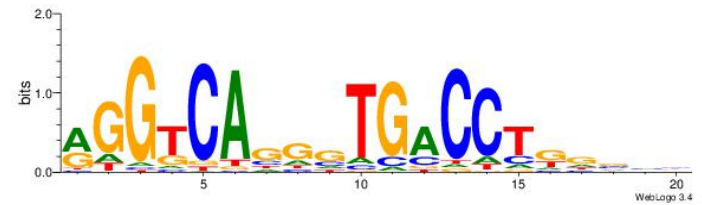
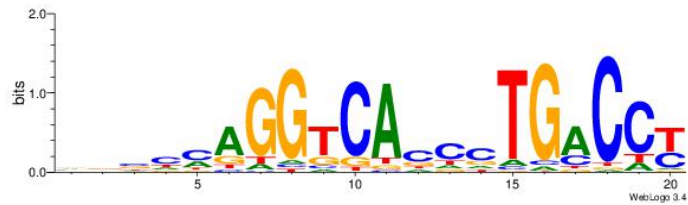


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 11
 Similarity score: 1.58704

Alignment:
 VDBHMAGGTCACCCTGACCY---
 -----CACACAVRCACACA

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
 MGGTCAGGGTGACCTRDBHV

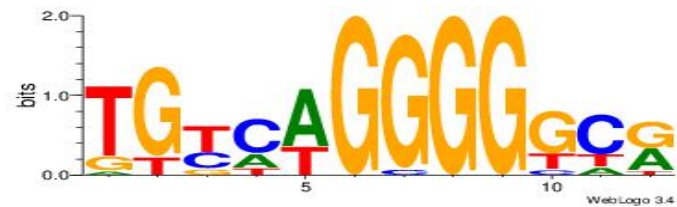


Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 2.08086

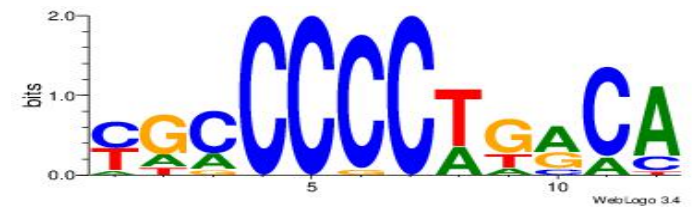
Alignment:

----TGYCAGGGGGCR
 TGTGTGKVTGTGTG--

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



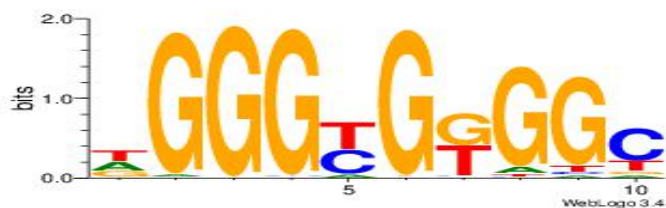
Dataset #: 2
 Motif ID: 36

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:	10
Similarity score:	2.0884

Alignment:

```
DGGGYGKGGC-----
TGTGTGKVTGTGTG
```

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

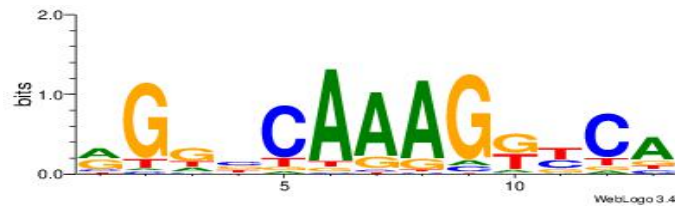


Dataset #:	2
Motif ID:	34
Motif name:	HNF4A
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	2.09226

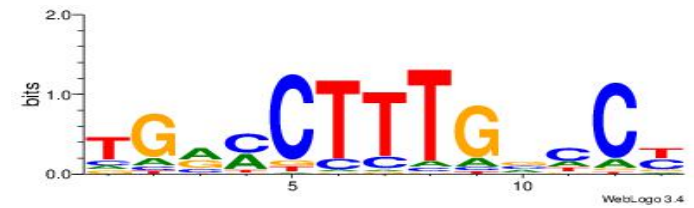
Alignment:

TGMYCTTTGBCK-----
---TGTGTGKVTGTGTG

Original motif Consensus sequence: RGGBCAAAGKYCA

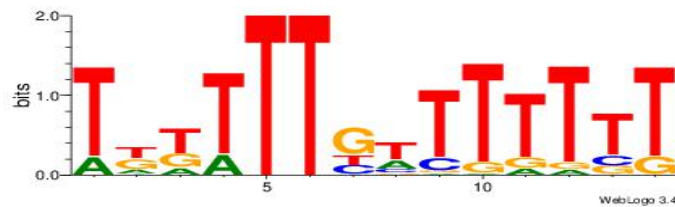


Reverse complement motif Consensus sequence: TGMYCTTTGBCK



Dataset #: 1 Motif ID: 10 Motif name: Motif 10

Original motif Consensus sequence: TKKTTTGTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR



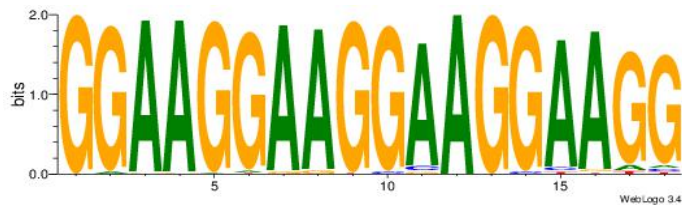
Best Matches for Motif ID 10 (Highest to Lowest)

Dataset #:	2
Motif ID:	32
Motif name:	EWSR1-FLI1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

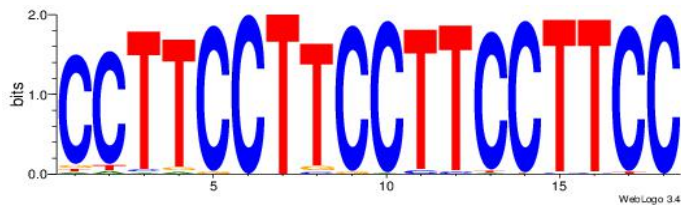
Number of overlap: 14
Similarity score: 0.0424269

Alignment:
GGAAGGAAGGAAGGAAGG
--AAAAAAACAAARRA--

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

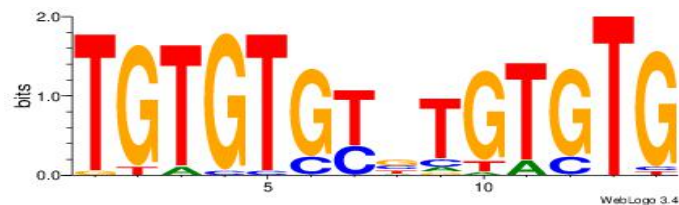


Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.529035

Alignment:
-CACACAVRCACACA
AAAAAAACAAARRA-

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: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.531594

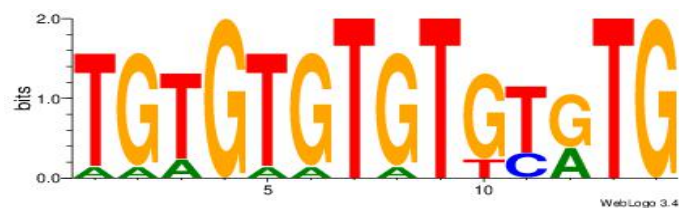
Alignment:

-TGTGTGTGTGKTG
 TKKTTTGT TTTT TTT-

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTG



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:	5
Number of overlap:	13
Similarity score:	0.535643

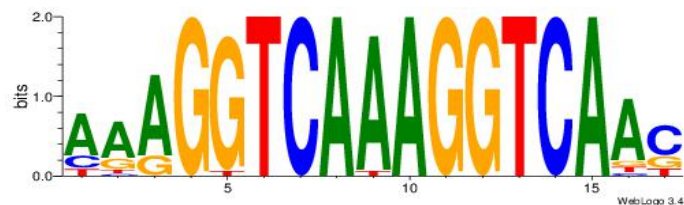
Alignment:

```

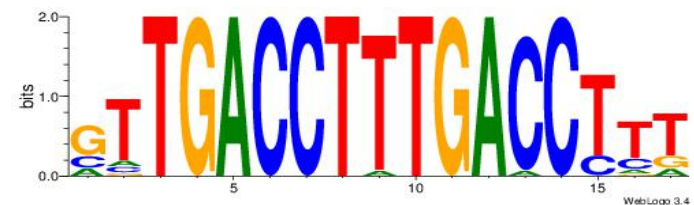
-AAAGGTCAAAGGTCAAC
AAAAAAACAAARRA-----

```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

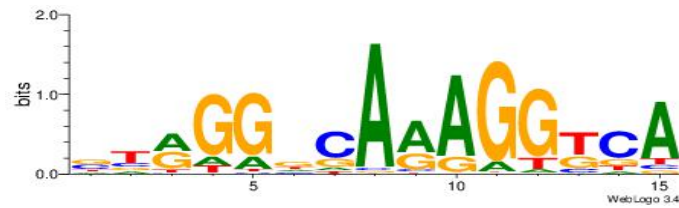


Dataset #:	2
Motif ID:	20
Motif name:	PPARGRXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	13
Similarity score:	0.543043

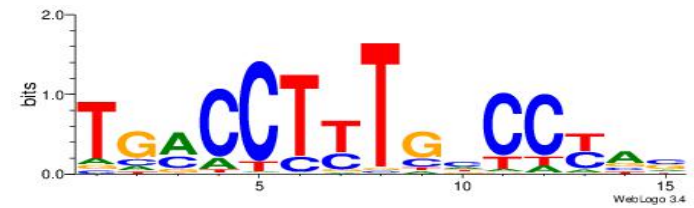
Alignment:

-BTRGGDCARAGGKCA
 AAAAAACAAARRA--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKGHCCK



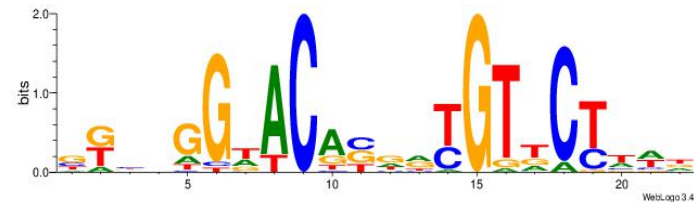
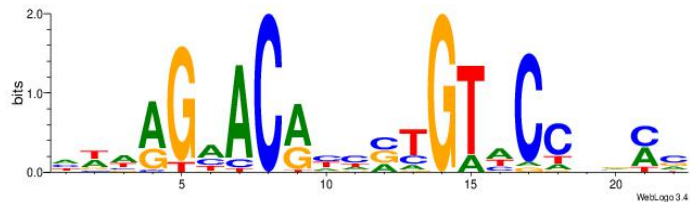
Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	10
Number of overlap:	13
Similarity score:	0.544053

Alignment:

VRVDGGHACAVDDKGTHTDWH-
 -----TKKTTTGTTTTTTT

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence:
 VRVDGGHACAVDDKGTHTDWH

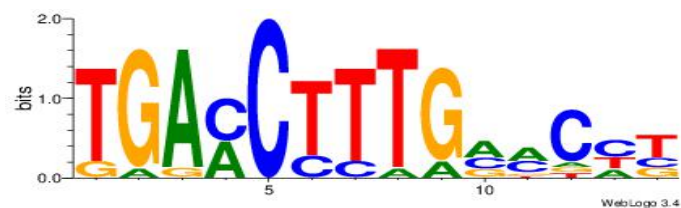


Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 1.04059

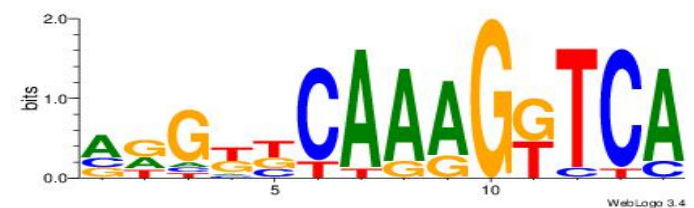
Alignment:

--AKGY YCAAAGRTCA
 AAAAAA CAAARRA--

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA



Dataset #: 2
 Motif ID: 34

Motif name:	HNH4A
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	1.53429

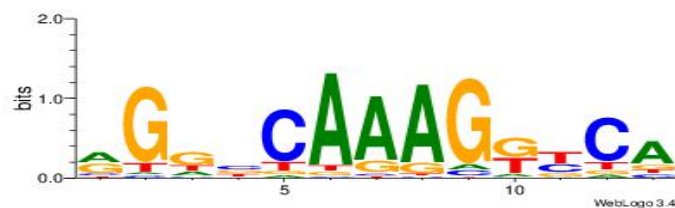
Alignment:

```

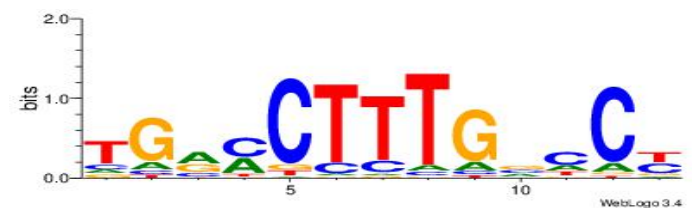
---RGGBCAAAGKYCA
AAAAAACAAARRA--

```

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

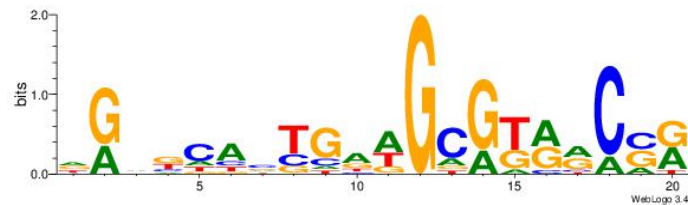


Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	11
Similarity score:	1.54022

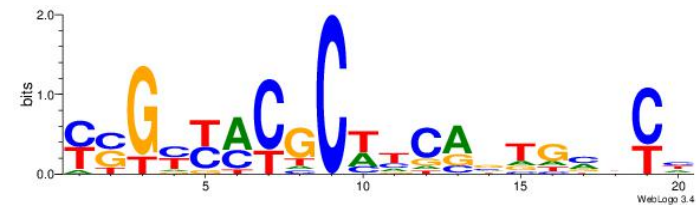
Alignment:

---DGVBCABTGDWGCGRRCR
AAAAAAACAAARRA-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



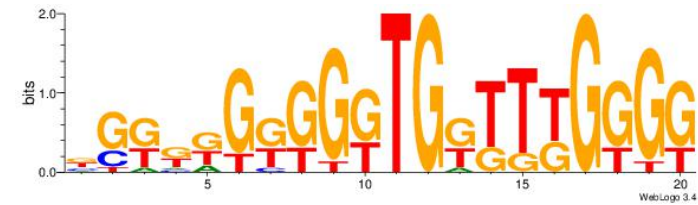
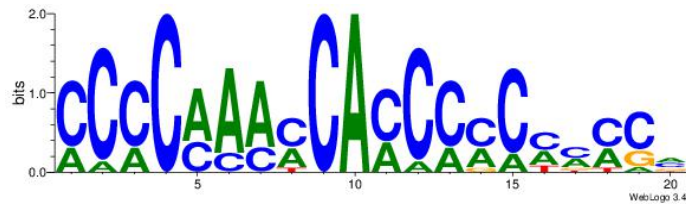
Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	11
Number of overlap:	10
Similarity score:	2.0484

Alignment:

----CCCCMAAMCAMCCMCMCMCV
AAAAAAACAAARRA-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMCMCV

Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG

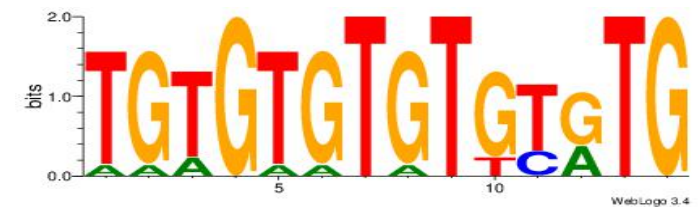


Dataset #: 1 Motif ID: 11 Motif name: Motif 11

Original motif Consensus sequence: CAYACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKT



Best Matches for Motif ID 11 (Highest to Lowest)

Dataset #:	1
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0170175

Alignment:

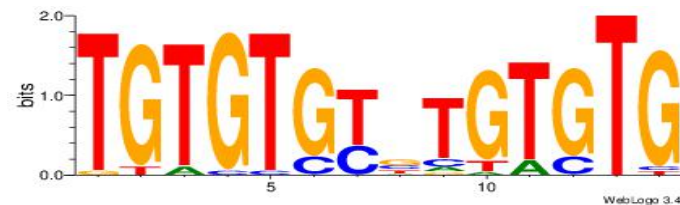
CACACAVRCACACA

CAYACACACACACA

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

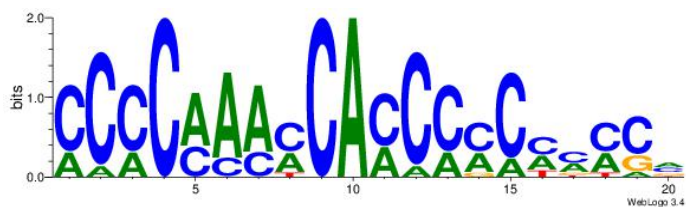


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0837439

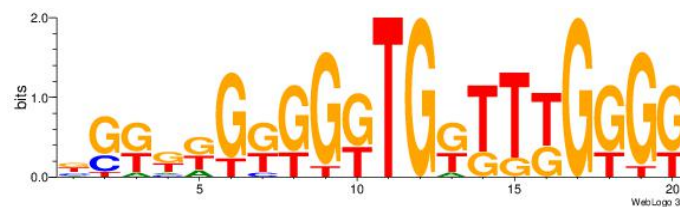
Alignment:

CCCCMAAMCAMCCMCMMMC
 ----CAYACACACACACA--

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

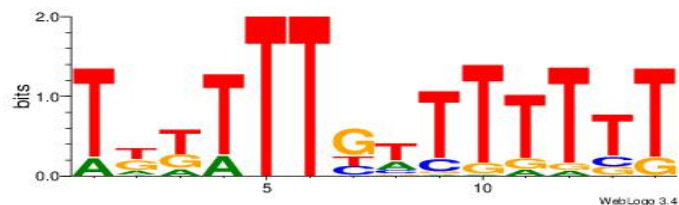


Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.581509

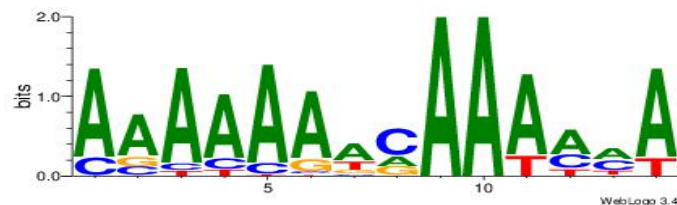
Alignment:

AAAAAACAAARRA-
 -CAYACACACACACA

Original motif Consensus sequence: TKKTTTGTTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR

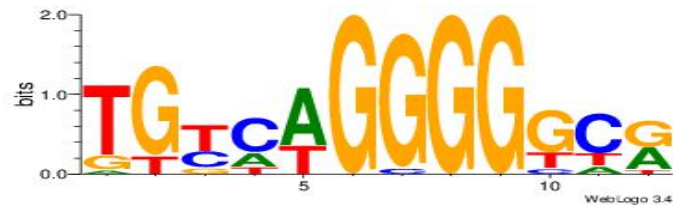


Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12

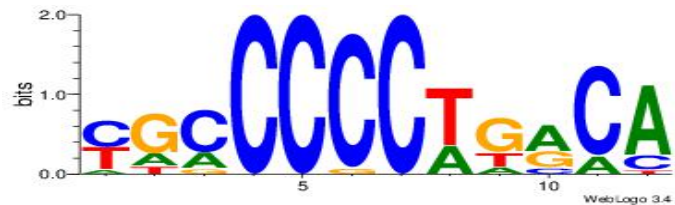
Similarity score: 1.09362

Alignment:
--TGYCAGGGGGCR
TGTGTGTGTGKTG

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCTGMCA



Dataset #: 2
Motif ID: 28
Motif name: Egr1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 1.56977

Alignment:
HCGTGGGCGK---
TGTGTGTGTGKTG

Original motif Consensus sequence: HCGTGGGCGK

Reverse complement motif Consensus sequence: YGCCCCACGCH

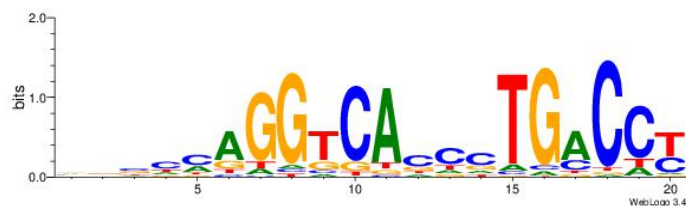


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 11
 Similarity score: 1.59795

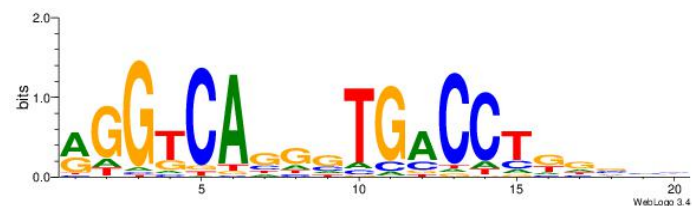
Alignment:

VDBHMAGGTCACCCTGACCY---
 -----CAYACACACACACA

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



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: 10
 Similarity score: 2.08683

Alignment:

DGGGYGKGGC----
 TGTGTGTGTGKTG

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

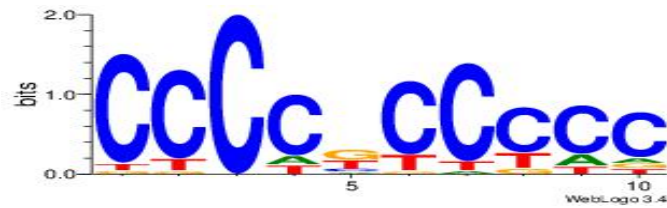


Dataset #: 2
 Motif ID: 16
 Motif name: SP1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 2.59204

Alignment:

-----GGGGGYGGGG
TGTGTGTGTGKTG-

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	3.09205

Alignment:

-----CCCRCCCC
CAYACACACACA

Original motif Consensus sequence: CCCRCCCC

Reverse complement motif Consensus sequence: GGGGMGGG



Dataset #: 2
 Motif ID: 33
 Motif name: HIF1AARNT
 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: 3.58699

Alignment:

-----VBACGTGV
 TGTGTGTGTGKTG-

Original motif Consensus sequence: VBACGTGV

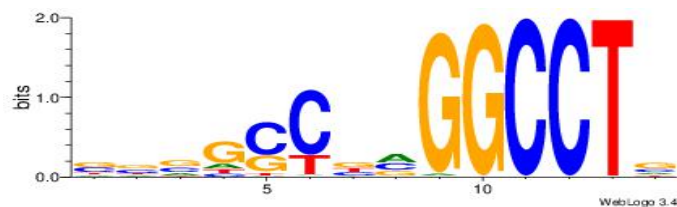


Reverse complement motif Consensus sequence: VCACGTBV

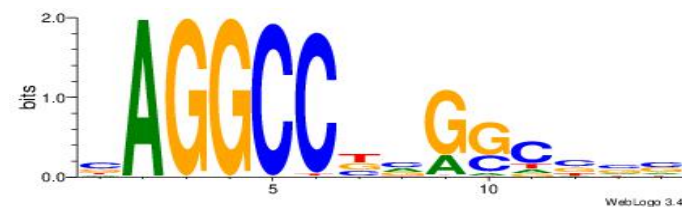


Dataset #: 2 Motif ID: 12 Motif name: Zfx

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



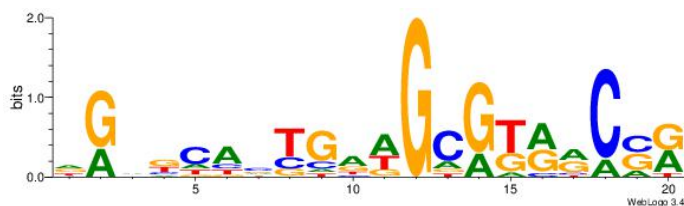
Best Matches for Motif ID 12 (Highest to Lowest)

Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	14
Similarity score:	0.0611182

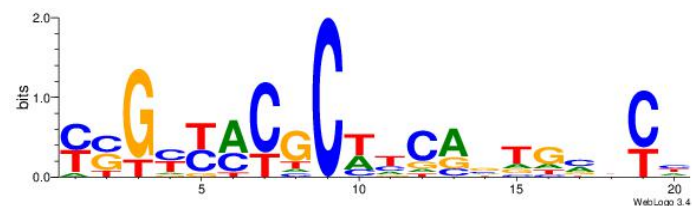
Alignment:

```
DGVBCABTGDWGCGRRCR
--BBVGCCBVGGCCTV----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCA BTGBBCD

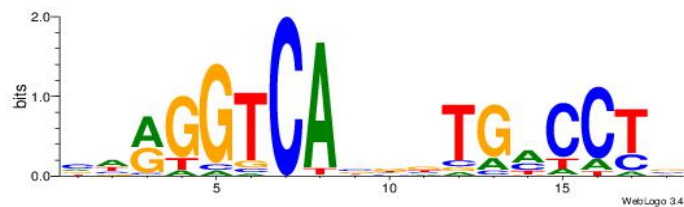


Dataset #: 2
 Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0635714

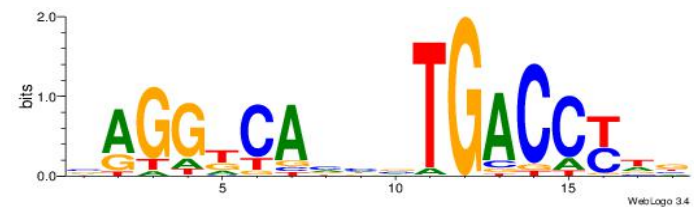
Alignment:

BAGGYCABHBTGACCKHV
 ---BBVGCCBVGGCCTV-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

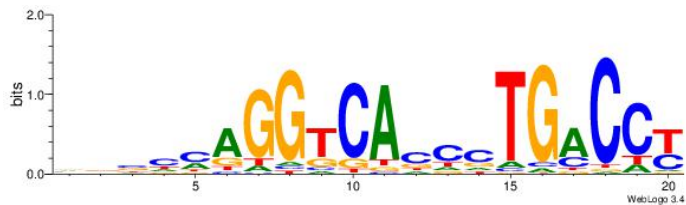


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5

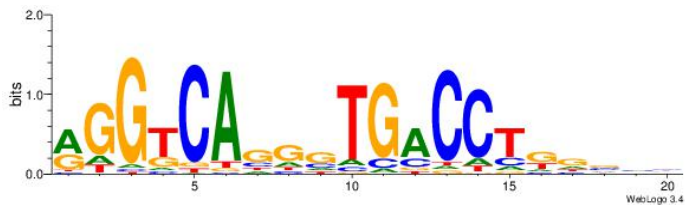
Number of overlap: 14
Similarity score: 0.0722733

Alignment:
MGGTCAGGGTGACCTRDBHV
--BBVGCCBVGGCCTV----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

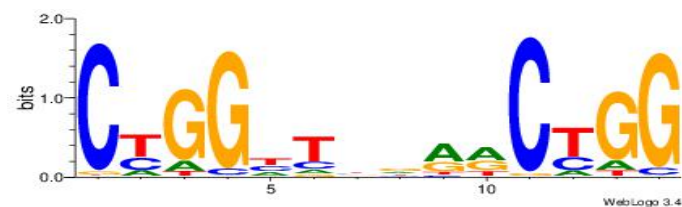
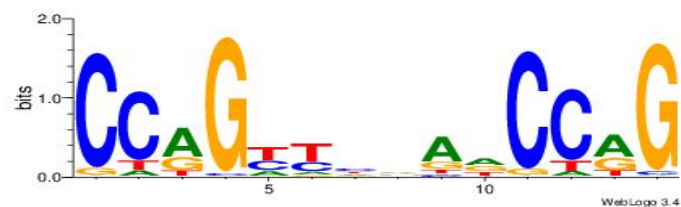


Dataset #: 2
Motif ID: 48
Motif name: Tcfcp2l1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0732898

Alignment:
CCAGYYHVADCCRG
BBVGCCBVGGCCTV

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCTG

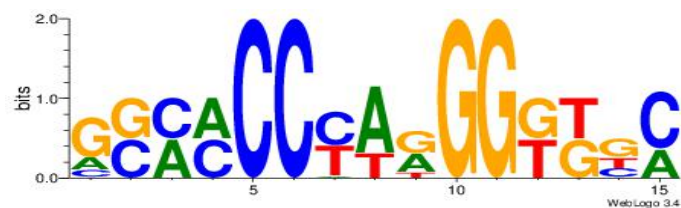


Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0747812

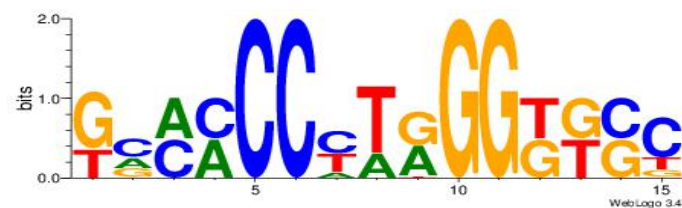
Alignment:

GYRYCCMTKGGYRSC
 -VAGGCCBBGGCVBB

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



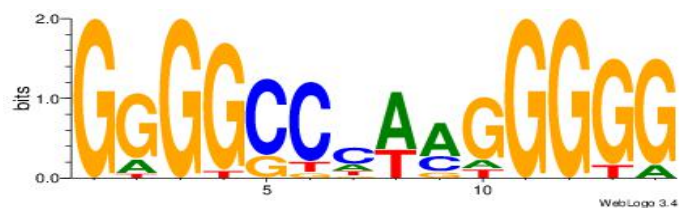
Dataset #: 2
 Motif ID: 21

Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0796879

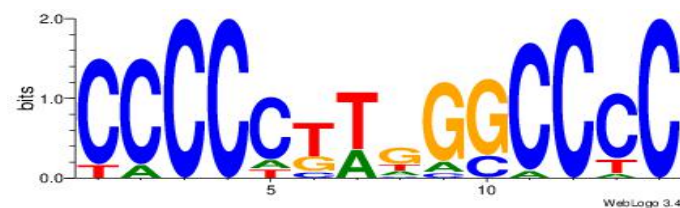
Alignment:

```
CCCCCTTGGGCCCC
BBVGCCBVGCCCTV
```

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC



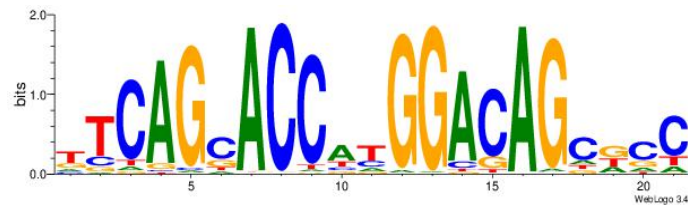
Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.0812253

Alignment:

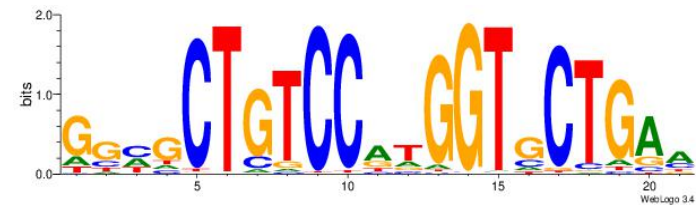
GGYGCTGTCCATGGTGCTGAA

----VAGGCCBBGGCVBB---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



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:	4
Number of overlap:	14
Similarity score:	0.0832838

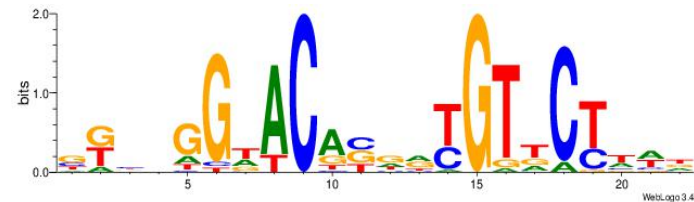
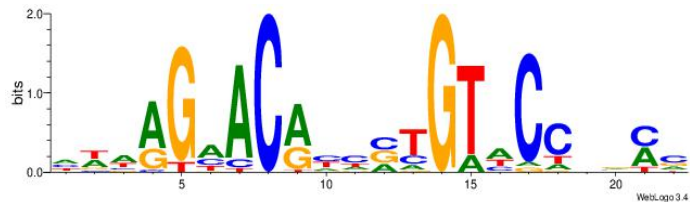
Alignment:

HWDAGHACRHHVTGTHCCHVMV

-----VAGGCCBBGGCVBB---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence:
VRVDGGHACAVDDKGTHCTDWH



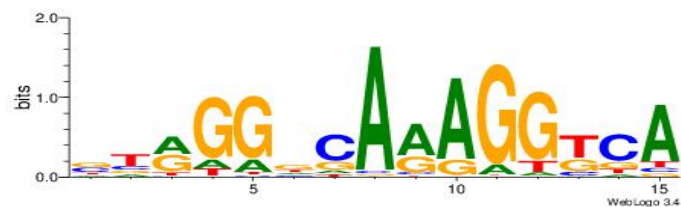
Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0836605

Alignment:

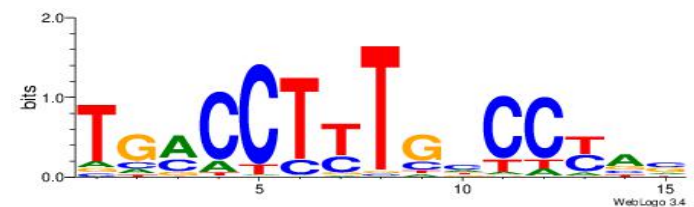
TGRCCTKTGHCCCKAB

BBVGCCBVGGCCTV-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



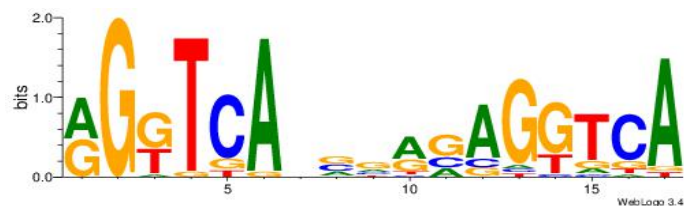
Dataset #: 2
 Motif ID: 47

Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.570818

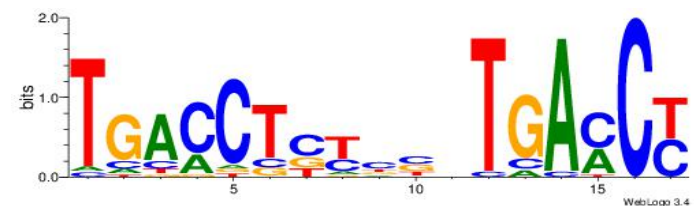
Alignment:

TGACCTCKVVB TGAYCK-
 ----BBVGCCBVGGCCTV

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

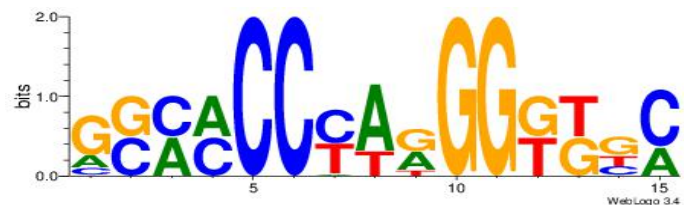


Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

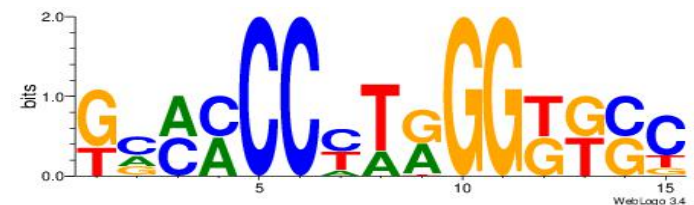


Dataset #: 2 Motif ID: 13 Motif name: Zfp423

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



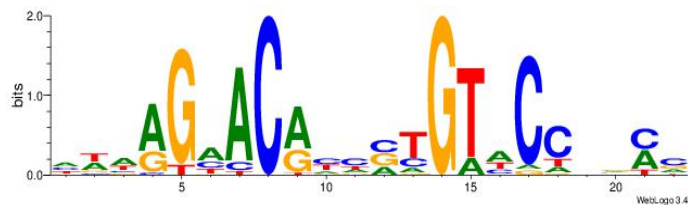
Best Matches for Motif ID 13 (Highest to Lowest)

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: 5
Number of overlap: 15
Similarity score: 0.0400042

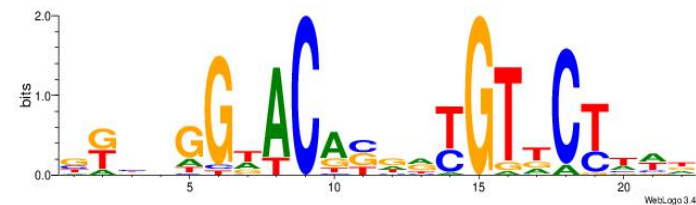
Alignment:

HWDAGHACRHHVTGTHCCHVMV
---GSMCCYARGGKKKC----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

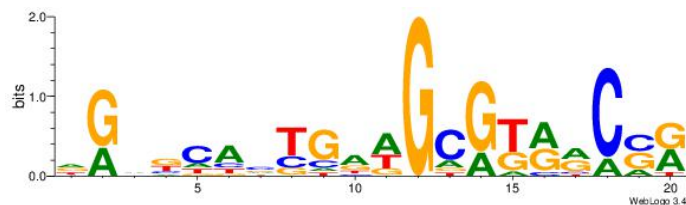


Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

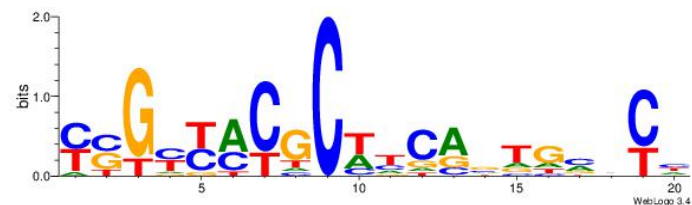
Direction: Forward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0400673

Alignment:
 DGVBCABTGDWGCGRRCR
 --GSMCCYARGGKKKC---

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



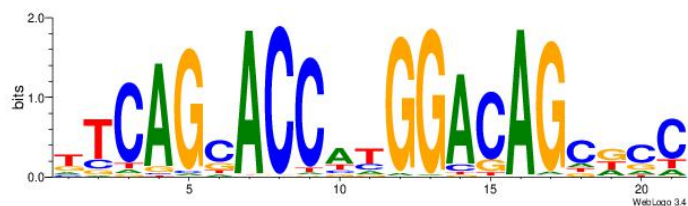
Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD



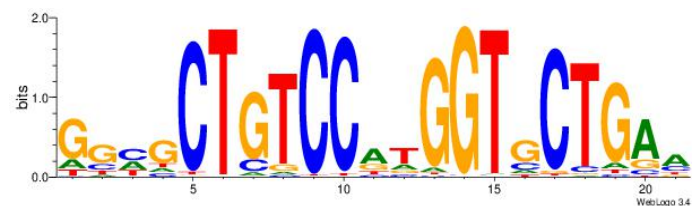
Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.0410001

Alignment:
 TTCAGCACCATGGACAGCKCC
 ---GYRYCCMTKGGYRSC---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2
Motif ID: 17
Motif name: RXRAVDR
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0465067

Alignment:

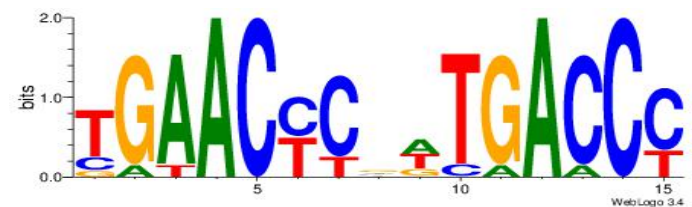
GGGTCAWBGRGTTCA

GYRYCCMTKGGYRSC

Original motif Consensus sequence: GGGTCAWBGRGTTCA



Reverse complement motif Consensus sequence: TGAACKCBWTGAC

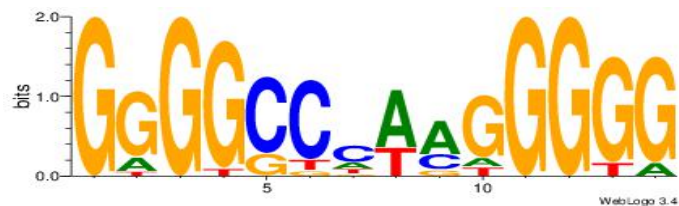


Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.527928

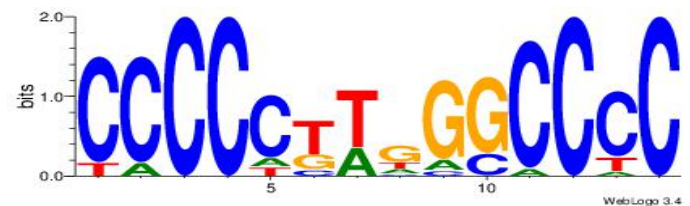
Alignment:

GGGGCCCAAGGGG-
 GSMMCCYARGGKKKC

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

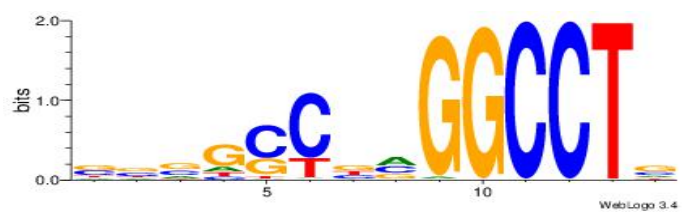


Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14

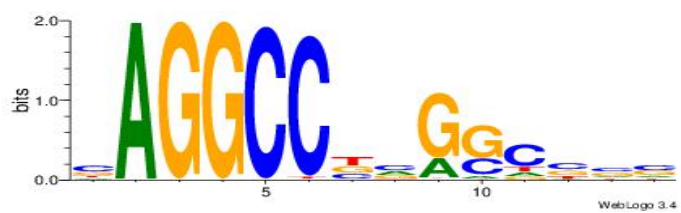
Similarity score: 0.53991

Alignment:
-VAGGCCBBGGCVBB
GYRYCCMTKGGYRSC

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

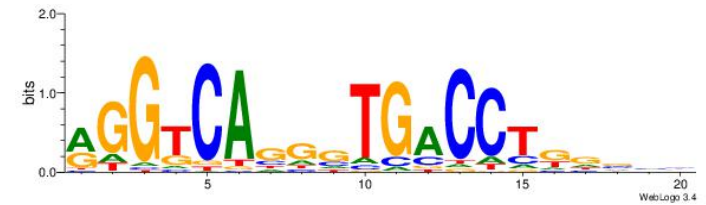


Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 13
Similarity score: 1.03254

Alignment:
--VDBHMAGGTCACCCTGACCY
GYRYCCMTKGGYRSC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

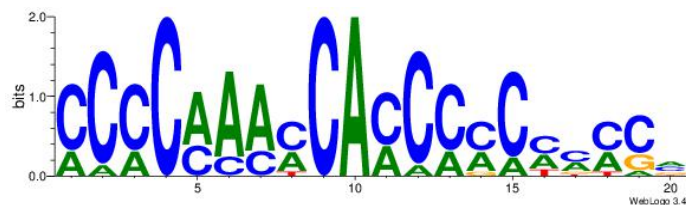


Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	13
Similarity score:	1.04952

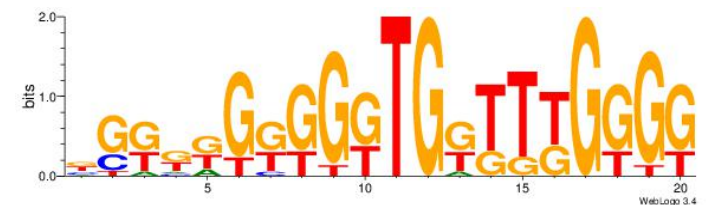
Alignment:

BGRRRGRGGRTGRTTYGGGG--
-----GYRYCCMTKGGYRSC

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG



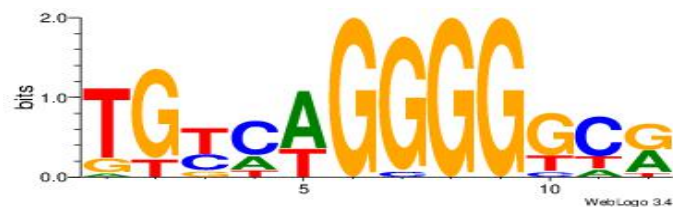
Dataset #: 2

Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.54193

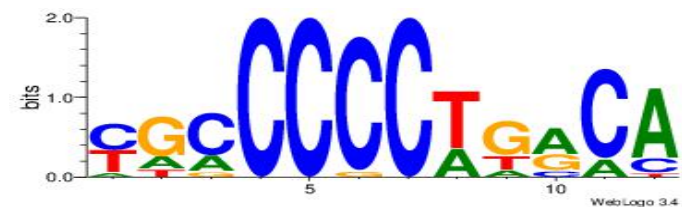
Alignment:

---TGYCAGGGGGCR
 GSMCCYARGGKKKC

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA

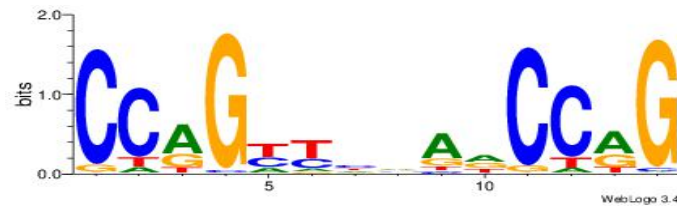


Dataset #: 2
 Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 2.04218

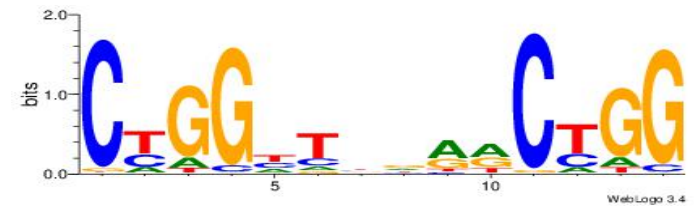
Alignment:

```
CKGGDTBDMCTGG----  
---GYRYCCMTKGGYRSC
```

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMCTGG



Dataset #: 2 Motif ID: 14 Motif name: ZEB1

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



Best Matches for Motif ID 14 (Highest to Lowest)

Dataset #:	2
Motif ID:	46
Motif name:	RORA_1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4

Number of overlap: 6
 Similarity score: 0.0141289

Alignment:
 TGACCTDVWT
 -CACCTD---

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT

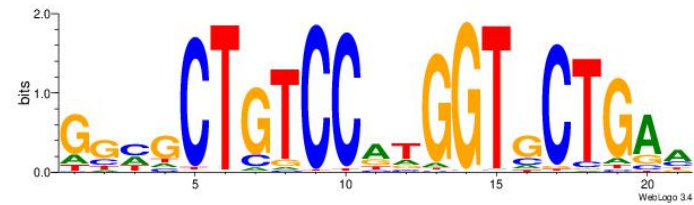
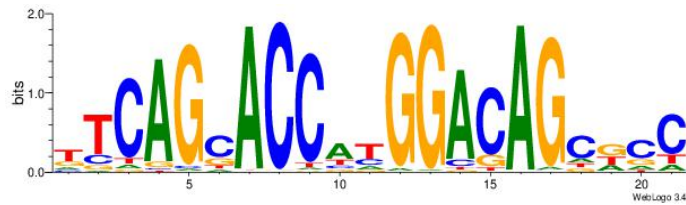


Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0143133

Alignment:
 GYGCTGTCCATGGTGCTGAA
 -----HAGGTG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
 GYGCTGTCCATGGTGCTGAA



Dataset #: 2
 Motif ID: 25
 Motif name: Arnt
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0207244

Alignment:

CACGTG

HAGGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 2
 Motif ID: 31

Motif name:	Esrrb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0207244

Alignment:

CACGTG

HAGGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



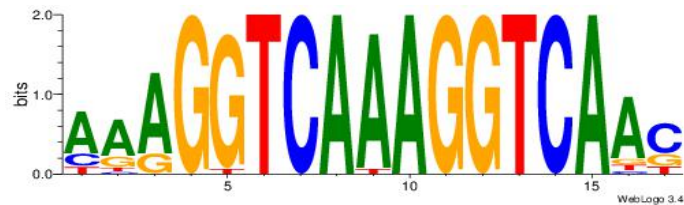
Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0232753

Alignment:

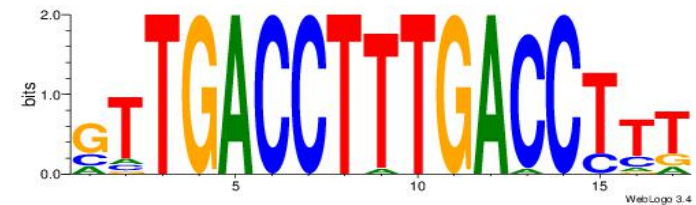
GTGACCTTTGACCTTT

-----CACCTD-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Dataset #:	2
Motif ID:	33
Motif name:	HIF1AARNT
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0237889

Alignment:

VBACGTGV

-HAGGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV



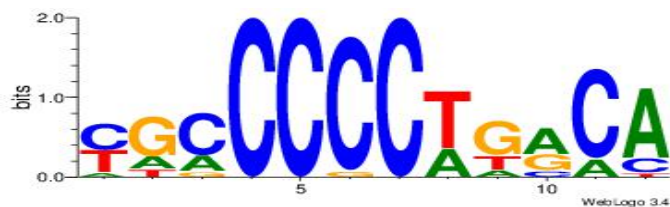
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0262123

Alignment:
 TGYCAGGGGGCR
 ---HAGGTG---

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



Dataset #: 2
 Motif ID: 20

Motif name:	PPARGRXRA
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:	0.0264837

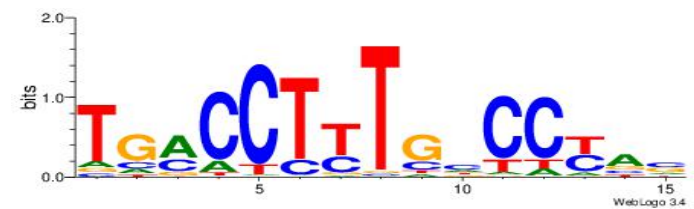
Alignment:

TGRCCTKTGHCKAB
 -CACCTD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKA



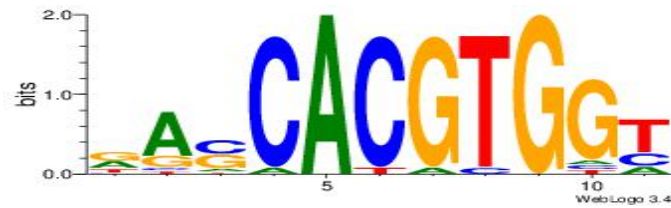
Dataset #:	2
Motif ID:	39
Motif name:	MYCMAX
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0269744

Alignment:

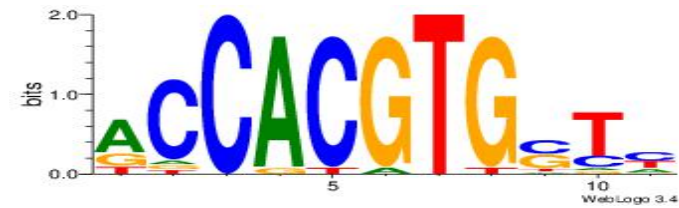
RASCACGTGGT

---HAGGTG--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #:	2
Motif ID:	44
Motif name:	NR4A2
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:	0.0288897

Alignment:

GTGACCTT

--CACCTD

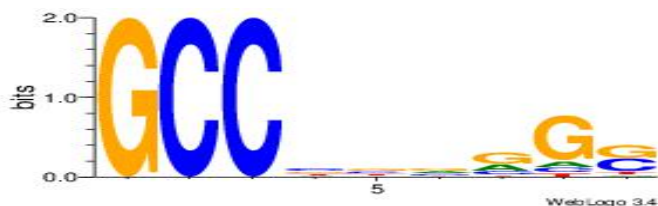
Original motif Consensus sequence: AAGGTCAC

Reverse complement motif Consensus sequence: GTGACCTT

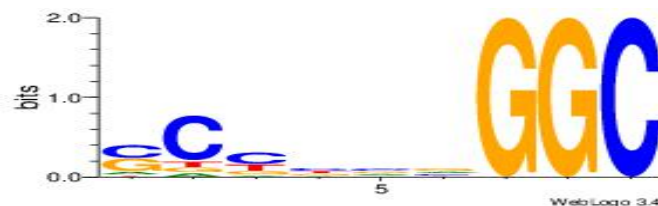


Dataset #: 2 Motif ID: 15 Motif name: TFAP2A

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



Best Matches for Motif ID 15 (Highest to Lowest)

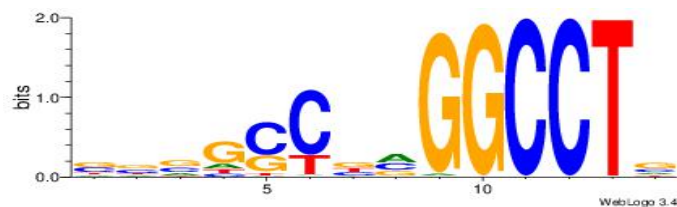
Dataset #:	2
Motif ID:	12
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.0131247

Alignment:

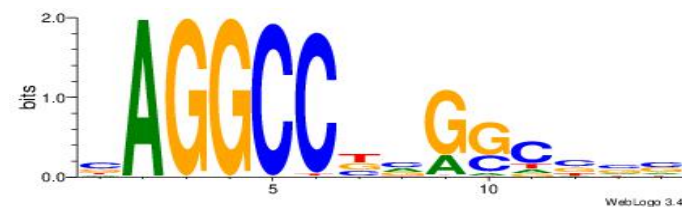
BBVGCCBVGGCTV

---SCMVBBGGC--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

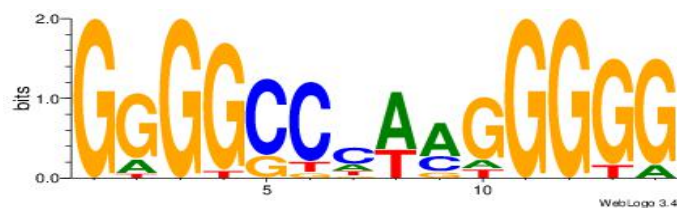


Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0414588

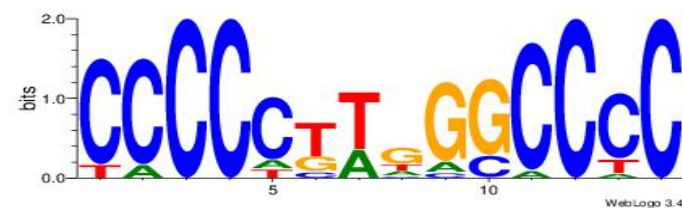
Alignment:

GGGGCCCAAGGGG
 ---GCCBBVRGS---

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

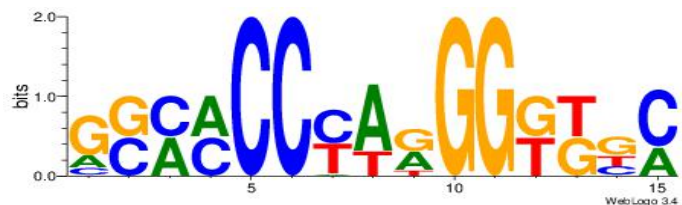


Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0438157

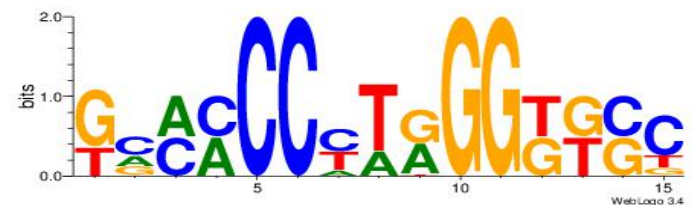
Alignment:

GYRYCCMTKGGYRSC
 ---SCMVBBGGC---

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



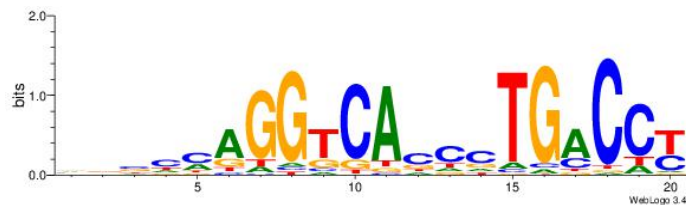
Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 9

Similarity score: 0.0450672

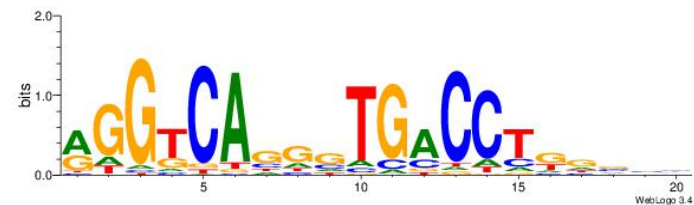
Alignment:

MGGTCAGGGTGACCTRDBHV
-----GCCBBVRGS-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV



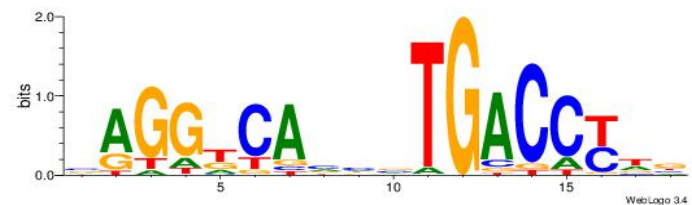
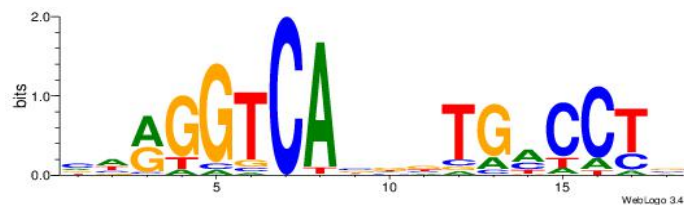
Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 9
Similarity score: 0.0531668

Alignment:

BAGGYCABHBTGACCKHV
-----SCMVBBGGC-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV



Dataset #: 2
 Motif ID: 40
 Motif name: Mycn
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0550803

Alignment:

HSCACGTGGC

–SCMVBBGGC

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



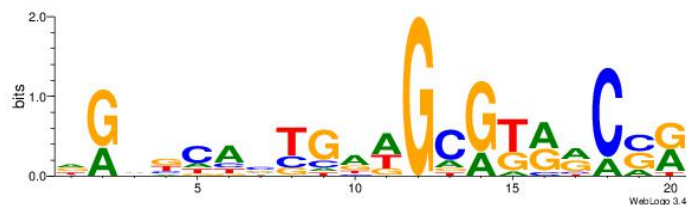
Dataset #: 2
 Motif ID: 45

Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	9
Similarity score:	0.0581255

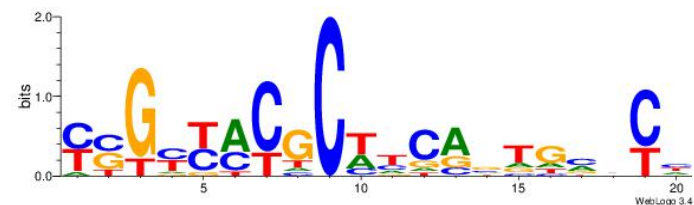
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----GCCBBVRGS-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



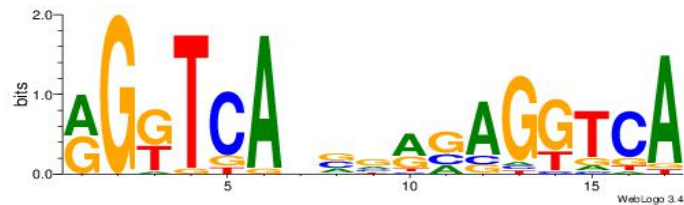
Dataset #:	2
Motif ID:	47
Motif name:	RXRRAR_DR5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	9
Similarity score:	0.0606062

Alignment:

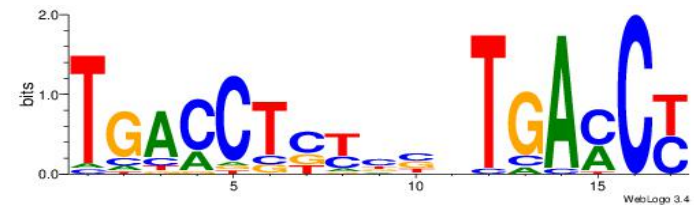
RGKTCABVVRGAGGTCA

--GCCBBVRGS-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBGTGAYCK



Dataset #:	2
Motif ID:	38
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0.0613455

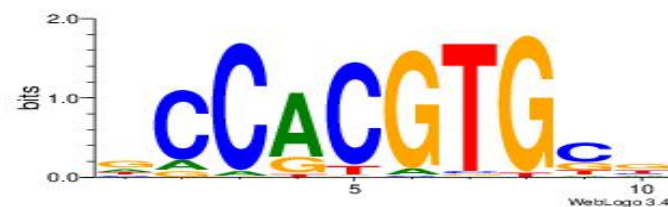
Alignment:

VGCACGTGGH

-SCMVBBGGC

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



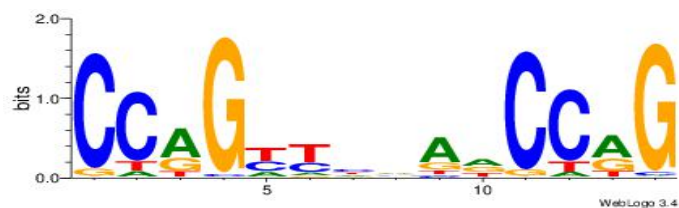
Dataset #: 2
 Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.0631412

Alignment:

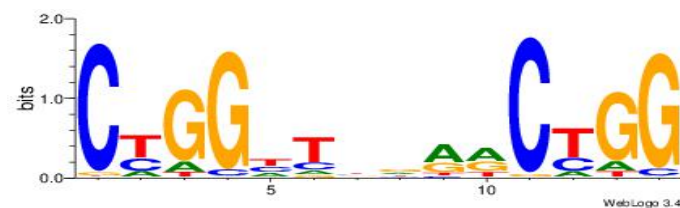
CCAGYYHVADCCRG

---GCCBBVRGS--

Original motif Consensus sequence: CCAGYYHVADCCRG

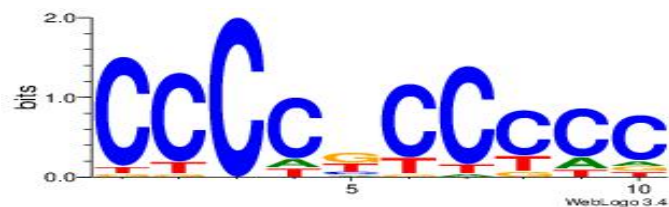


Reverse complement motif Consensus sequence: CKGGDTBDMMCTG

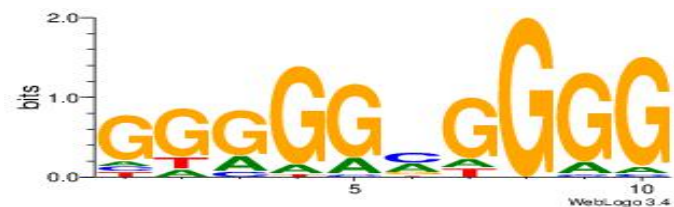


Dataset #: 2 Motif ID: 16 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



Best Matches for Motif ID 16 (Highest to Lowest)

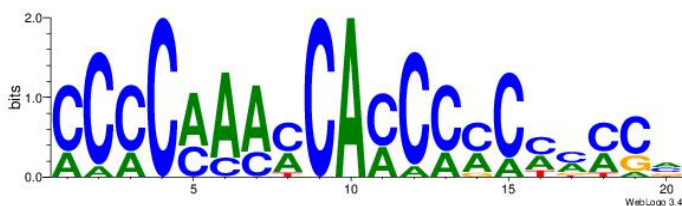
Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0646465

Alignment:

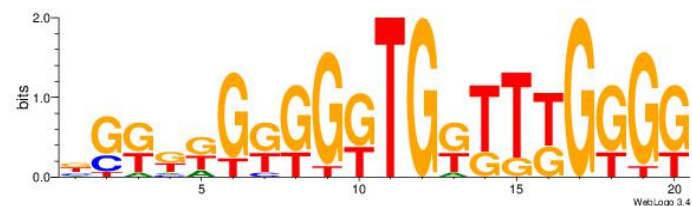
BGRRRGRGGRTGRTTYGGGG

-GGGGGYGGGG-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

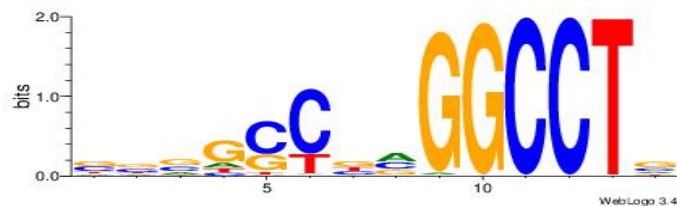


Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0664832

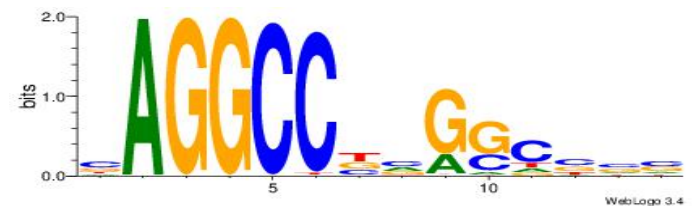
Alignment:

BBVGCCBVGGCCTV
 ----GGGGGYGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10

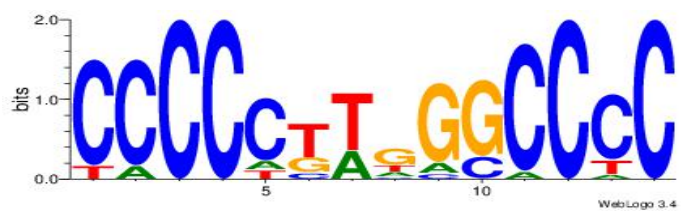
Similarity score: 0.0725

Alignment:
CCCCCTGGGCCCC
-CCCCKCCCCC---

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTGGGCCC

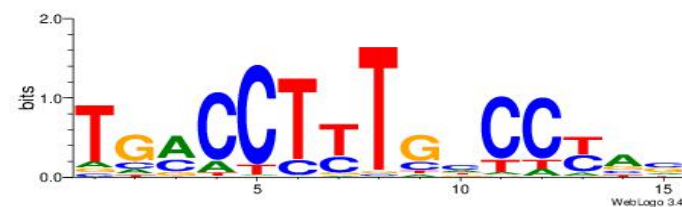
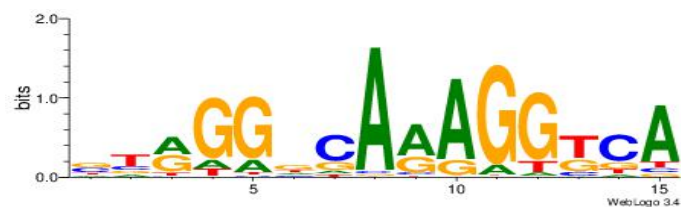


Dataset #: 2
Motif ID: 20
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0731995

Alignment:
TGRCCTKTGHCKAB
--CCCCKCCCCC---

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCK



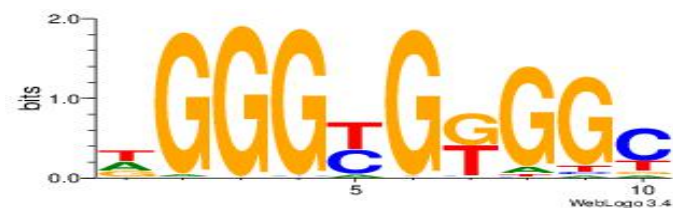
Dataset #: 2
 Motif ID: 36
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0761191

Alignment:

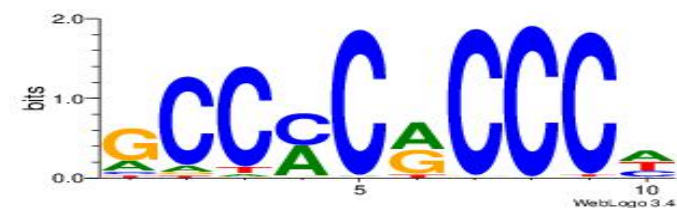
GCCYCMCCCD

CCCCKCCCCC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 2
 Motif ID: 28

Motif name:	Egr1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0798413

Alignment:

HGCGTGGGCGK
GGGGYGGGG-

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH



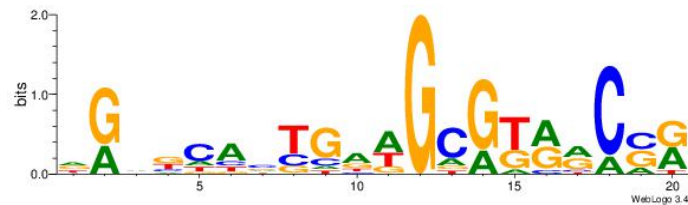
Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	10
Similarity score:	0.0846627

Alignment:

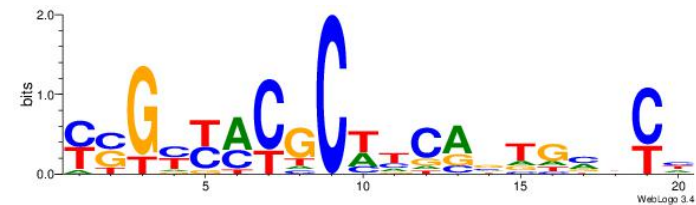
DGVBCABTGDWGCGRRCR

-----GGGGGYGGGG---

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBB



Dataset #:	2
Motif ID:	41
Motif name:	MZF1_5-13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0884127

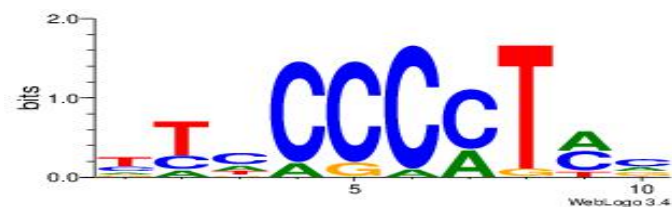
Alignment:

BKAGGGGDAD

GGGGGYGGGG

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB



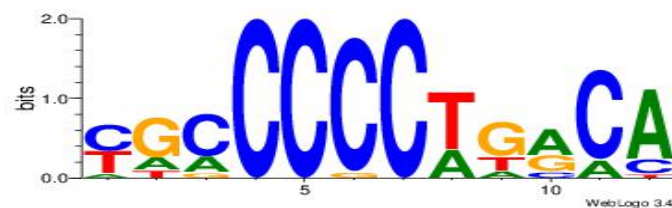
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.089127

Alignment:
 TGYCAGGGGGCR
 GGGGYGGGG--

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCTGMCA



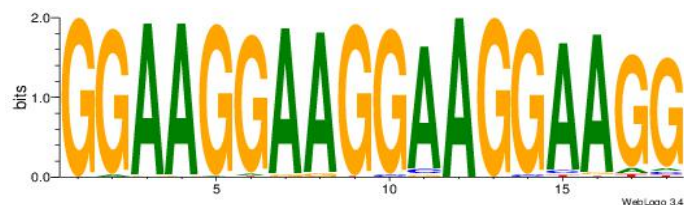
Dataset #: 2
 Motif ID: 32

Motif name: EWSR1-FLI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0893651

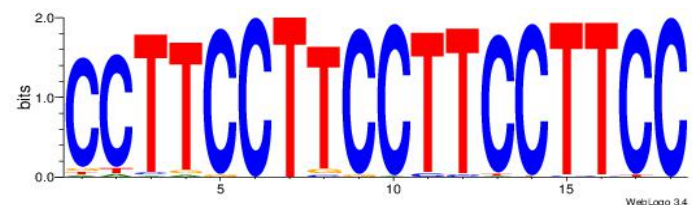
Alignment:

CCTTCCTTCCTTCCTTCC
 ---CCCCKCCCCC-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

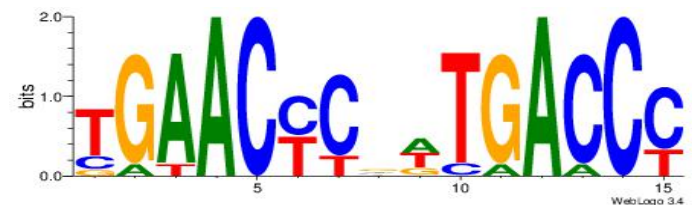


Dataset #: 2 Motif ID: 17 Motif name: RXRAVDR

Original motif Consensus sequence: GGGTCAWBGRGTTCA



Reverse complement motif Consensus sequence: TGAACKCBWTGAC



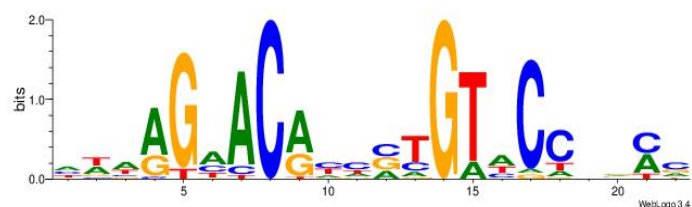
Best Matches for Motif ID 17 (Highest to Lowest)

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: 5
Number of overlap: 15
Similarity score: 0.0566667

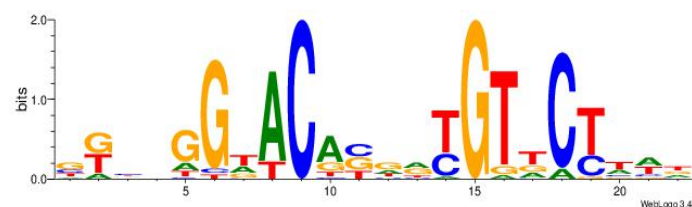
Alignment:

HWDAGHACRHHVTGTHCCHVMV
---TGAACKCBWTGACCC----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACA VDDKGTHCTDWH



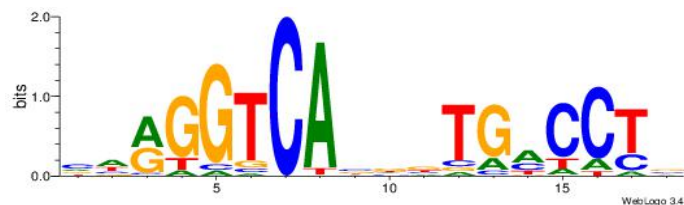
Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0617507

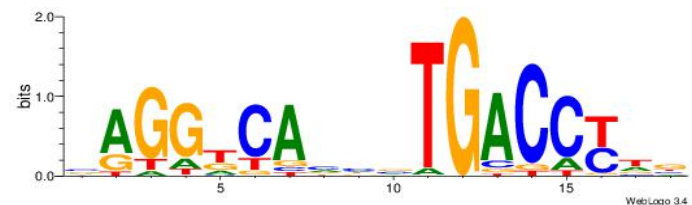
Alignment:

VHRGGTCABDBTGMCTB
 --GGGTCAWBGRGTTCA--

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

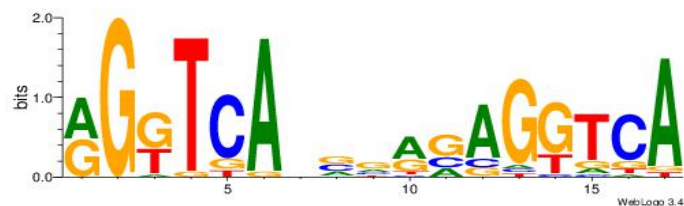


Dataset #: 2
 Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.062029

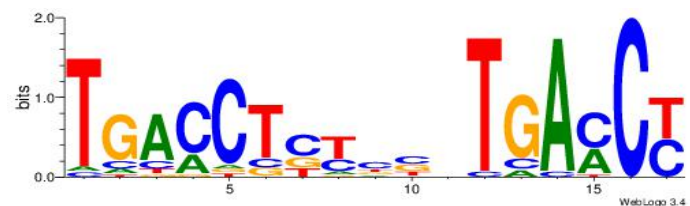
Alignment:

RGKTCABVVRGAGGTCA
 GGGTCAWBGRGTTCA--

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

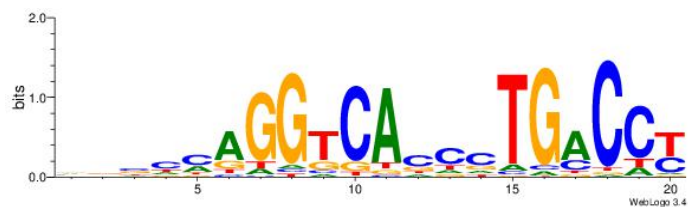


Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15
Similarity score: 0.0714525

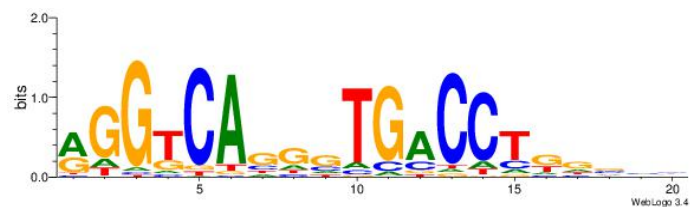
Alignment:

VDBHMAGGTCACCCTGACCY
-----TGAACKCBWTGACCC

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

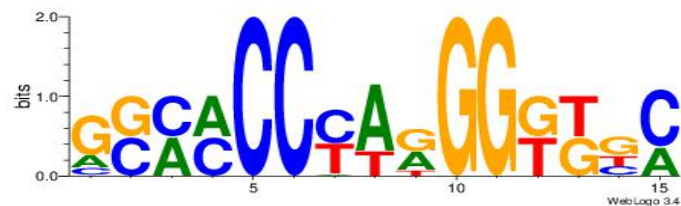


Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0849495

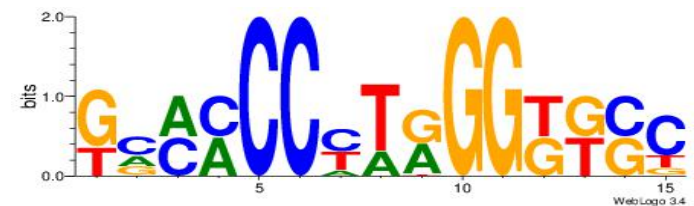
Alignment:

GSMCCYARGGKKKC
 TGAACKCBWTGACCC

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

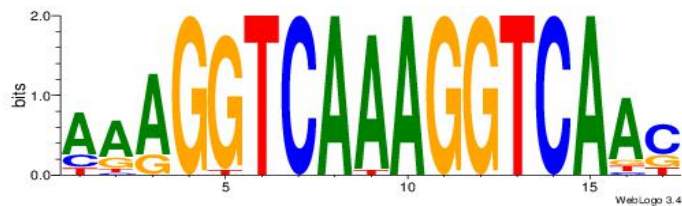


Dataset #: 2
 Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15

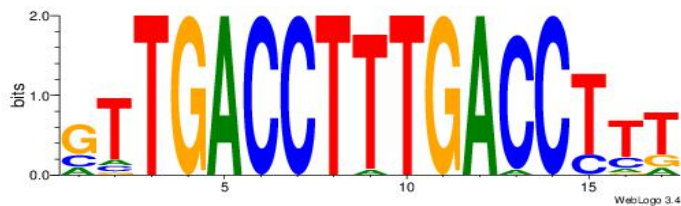
Similarity score: 0.0866667

Alignment:
AAAGGTCAAAGGTCAAC
--GGGTCAWBGRGTTCA

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

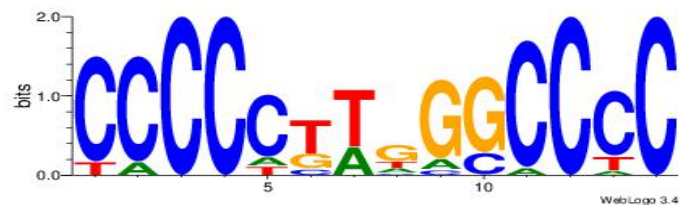
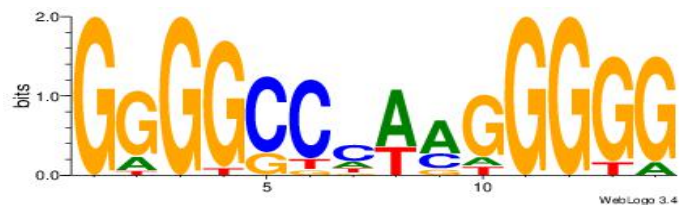


Dataset #: 2
Motif ID: 21
Motif name: PLAG1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 1.06201

Alignment:
GGGGCCCAAGGGG--
-GGGTCAWBGRGTTCA

Original motif Consensus sequence: GGGGCCCAAGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCC

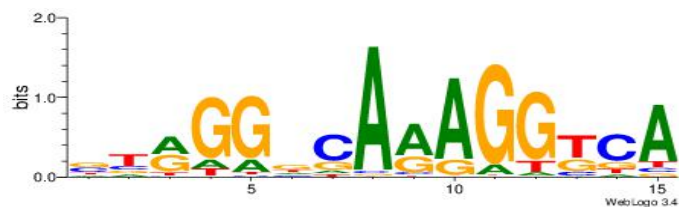


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 1.07837

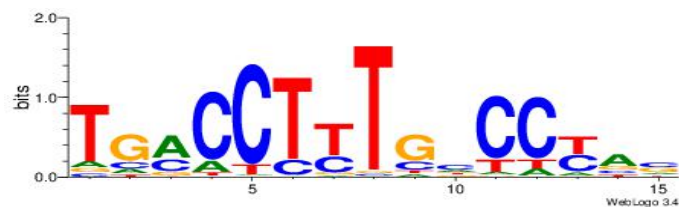
Alignment:

BTRGGDCARAGGKCA--
 --GGGTCAWBGRGTTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



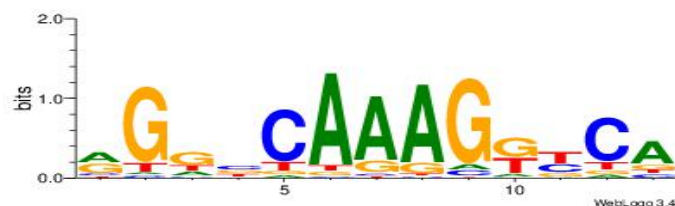
Dataset #: 2
 Motif ID: 34

Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 1.0801

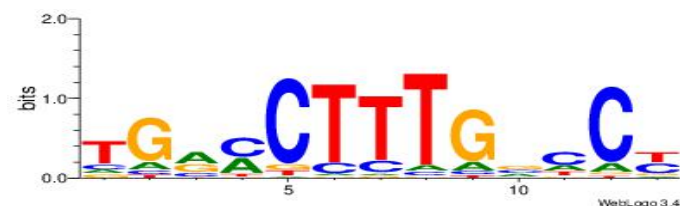
Alignment:

RGGBCAAAGKYCA--
 GGGTCAWBGRGTTCA

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 1.08482

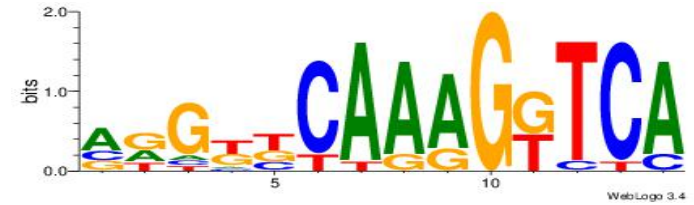
Alignment:

AKGY YCAAAGRTCA--
-GGGTC A WBGRGTTCA

Original motif Consensus sequence: TGAMCTTTGMMCYT

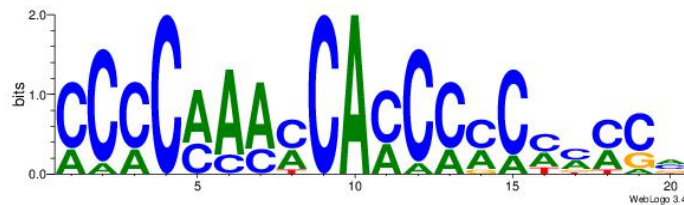


Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA

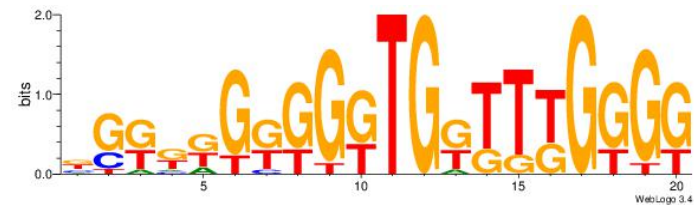


Dataset #: 2 Motif ID: 18 Motif name: RREB1

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGGRRGRGGRTGRTTYGGGG



Best Matches for Motif ID 18 (Highest to Lowest)

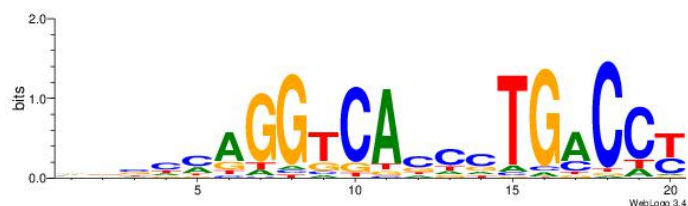
Dataset #:	2
Motif ID:	29
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 2
Number of overlap: 19
Similarity score: 0.0874679

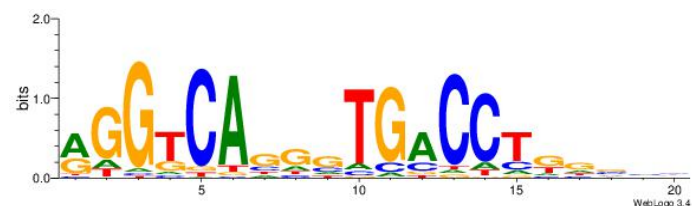
Alignment:

-MGGTCAGGGTGACCTRDBHV
BGRRRGRGGRTGRTTYGGGG-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

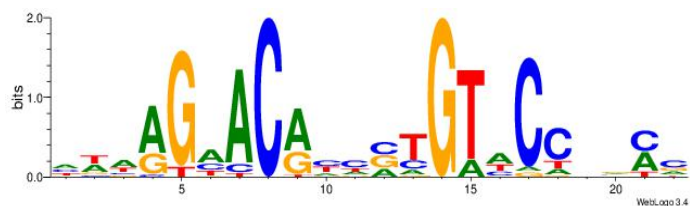


Dataset #: 2
Motif ID: 24
Motif name: Ar
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 19
Similarity score: 0.0927532

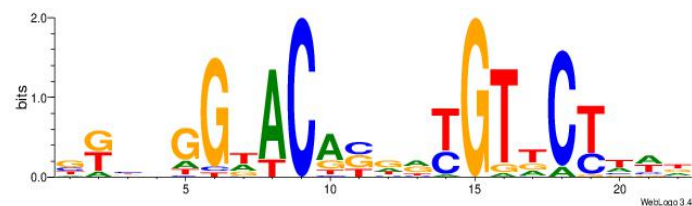
Alignment:

-HWDAGHACRHHVTGTHCCHVMV
CCCCMAAMCAMCCMCMVMCV---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

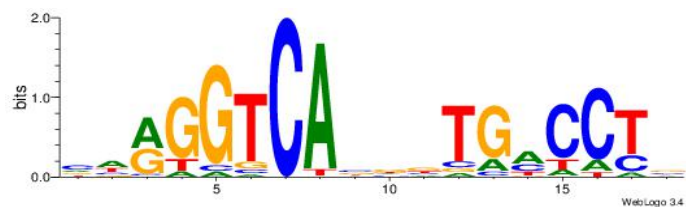


Dataset #: 2
 Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.593122

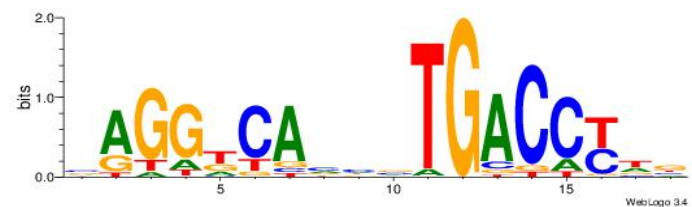
Alignment:

BAGGYCABHBTGACCKHV--
 BGRRRGRGGRTGRTTYGGGG

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

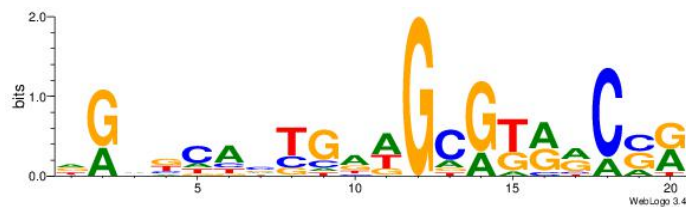


Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 1.09431

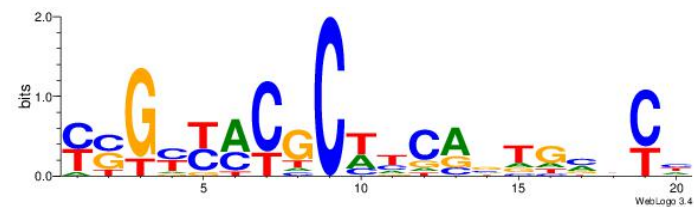
Alignment:

---DGVBCABTGDWGCGRRCR
 BGRRRGRGGRTGRTTYGGG---

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD



Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 14
Similarity score: 2.5804

Alignment:
CCCCCTTGGGCCCC-----
CCCCMAAMCAMCCMCMMMC

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

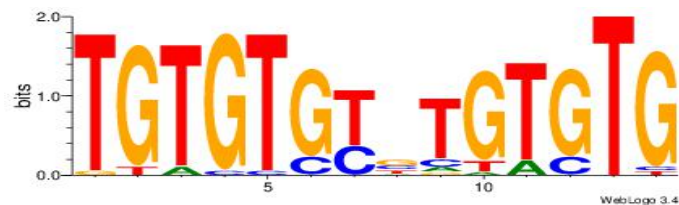


Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 2.58596

Alignment:
-----CACACAVRCACACA
CCCCMAAMCAMCCMCMMMC

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

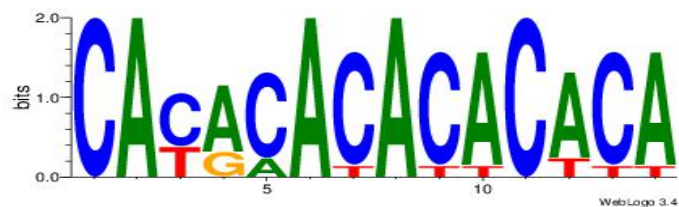


Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 2.59077

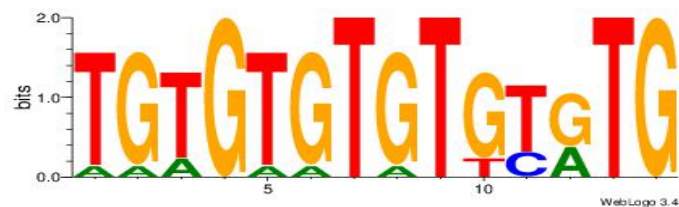
Alignment:

-----CAYACACACACACA
 CCCCMAAMCAMCCMCMCMCV

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGTGTGT



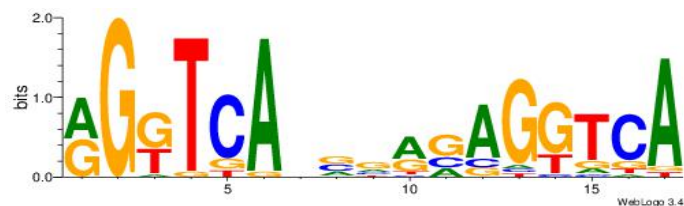
Dataset #: 2
 Motif ID: 47

Motif name:	RXRRAR_DR5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	13
Similarity score:	3.07964

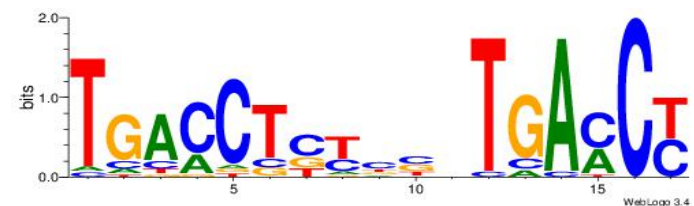
Alignment:

```
RGKTCABVVRGAGGTCA-----
----BGRRRGRGGRTGRTTYGGGG
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

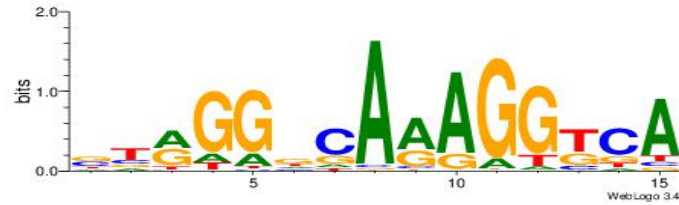


Dataset #:	2
Motif ID:	20
Motif name:	PPARGRXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	13
Similarity score:	3.08033

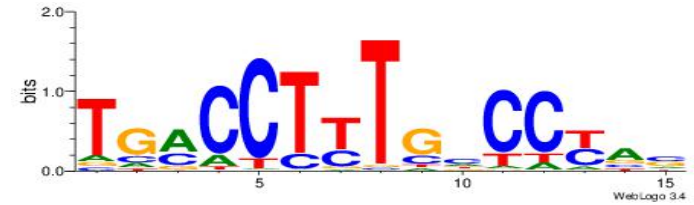
Alignment:

BTRGGDCARAGGKCA-----
 --BGRRRRGRGGRTGRTTYGGGG

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



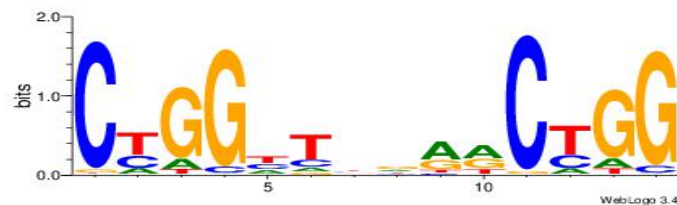
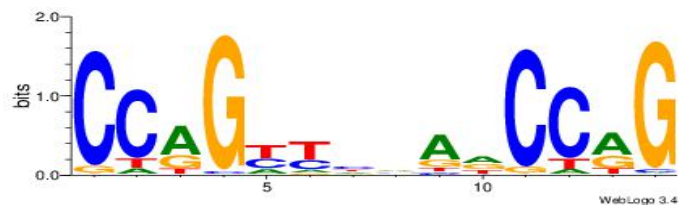
Dataset #:	2
Motif ID:	48
Motif name:	Tcfcp2l1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	3.08771

Alignment:

-----CCAGYYHVADCCRG
 CCCCMAAMCAMECCMMCMCV-

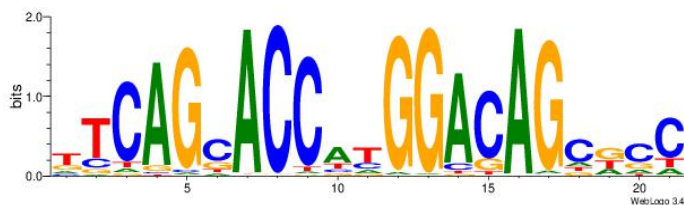
Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCTO

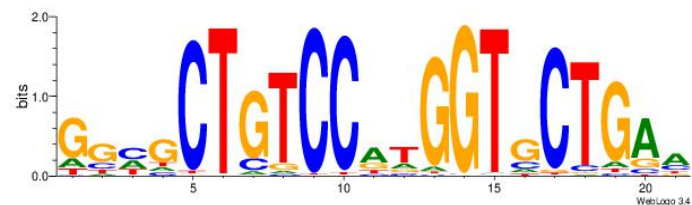


Dataset #: 2 Motif ID: 19 Motif name: REST

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



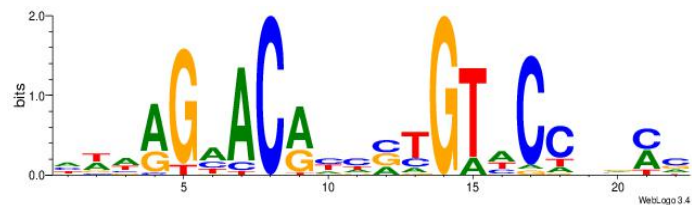
Best Matches for Motif ID 19 (Highest to Lowest)

Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	0.0685835

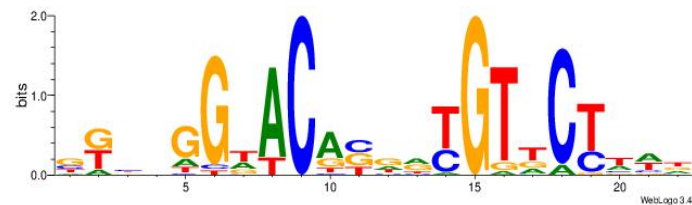
Alignment:

VRVDGGHACAVDDKGTHTDWH
 -GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence:
 VRVDGGHACAVDDKGTHTDWH



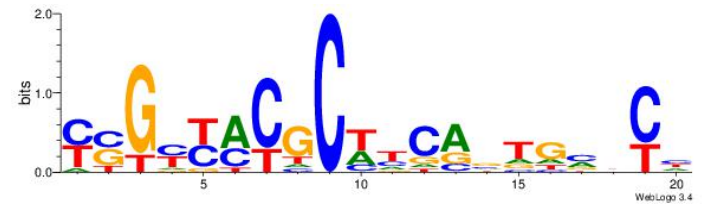
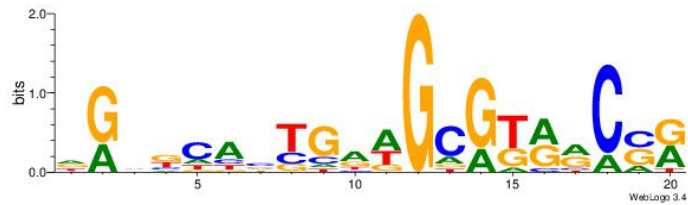
Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	18
Similarity score:	1.577

Alignment:

MSGKKRCGCWDCABTGBB CD---
 --GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif Consensus sequence:
 MSGKKRCGCWDCABTGBB CD



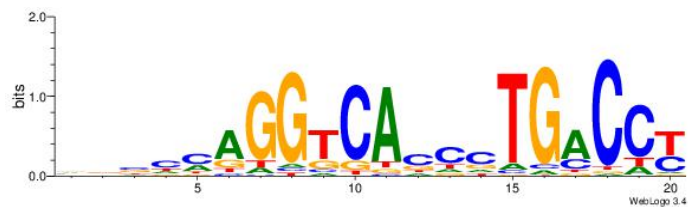
Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 2.56863

Alignment:

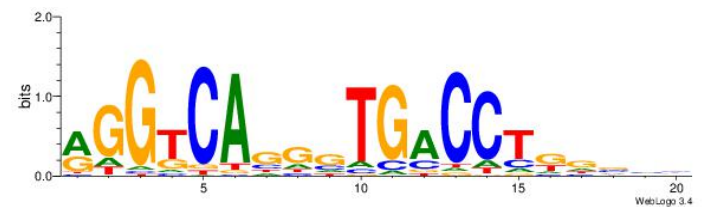
```

-----VDBHMAGGTCACCCTGACCY
TTCAGCACCATGGACAGCKCC-----
  
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



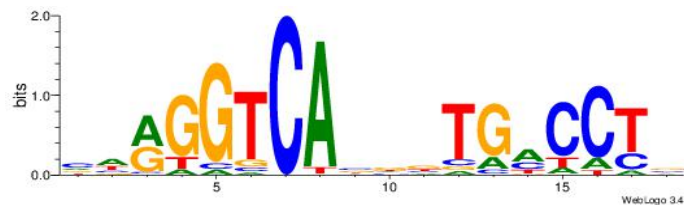
Dataset #: 2

Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 13
 Similarity score: 4.05754

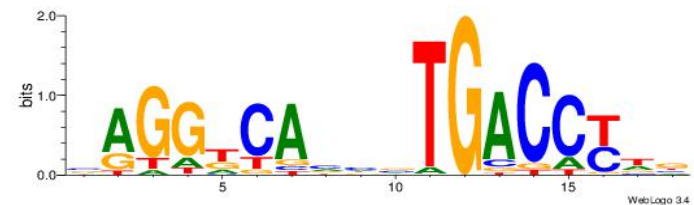
Alignment:

BAGGYCABHBTGACCKHV-----
 -----GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

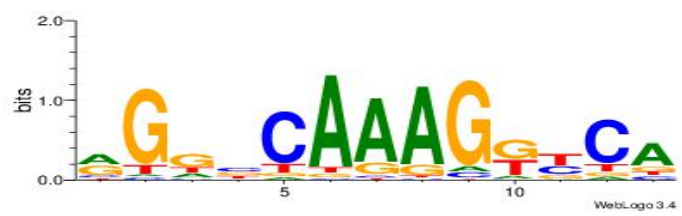


Dataset #: 2
 Motif ID: 34
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13

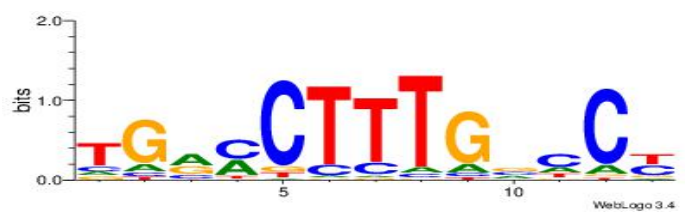
Similarity score: 4.06973

Alignment:
TGM YCTTTGBCK-----
GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCK

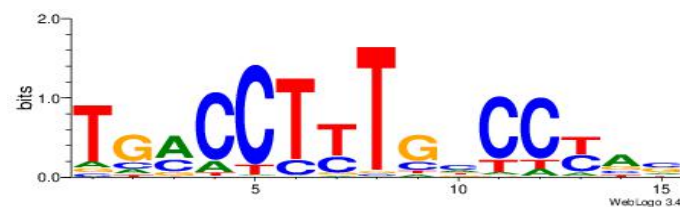
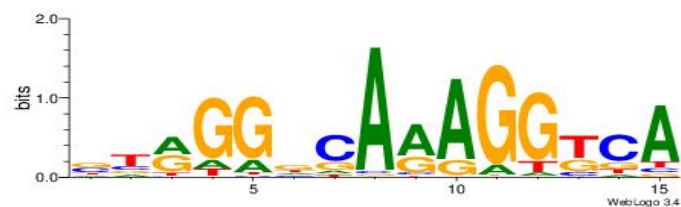


Dataset #: 2
Motif ID: 20
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 4.07172

Alignment:
-----BTRGGDCARAGGKCA
TTCAGCACCATGGACAGCKCC--

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCC TKTGHCK

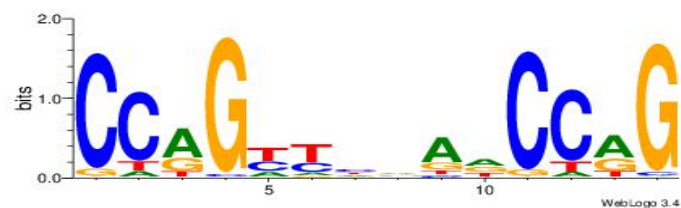


Dataset #: 2
 Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 4.57098

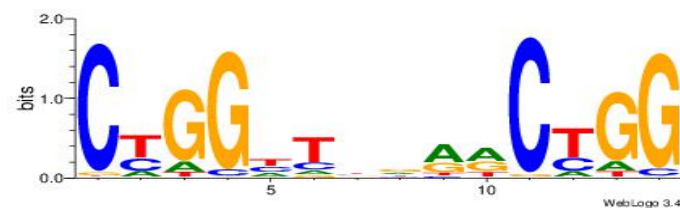
Alignment:

CCAGYYHVADCCRG-----
 --GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTC



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:	3
Number of overlap:	12
Similarity score:	4.57482

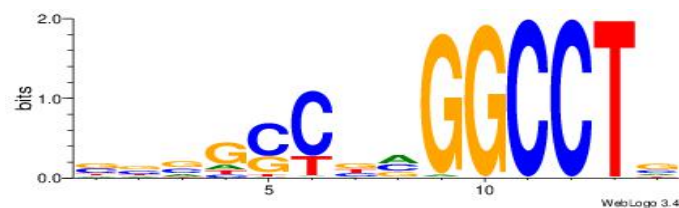
Alignment:

```

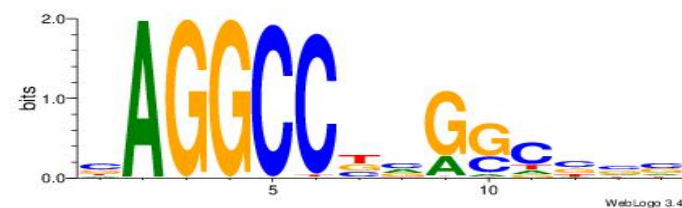
-----BBVGCCBVGGCCTV
GGYGCTGTCCATGGTGCTGAA--

```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

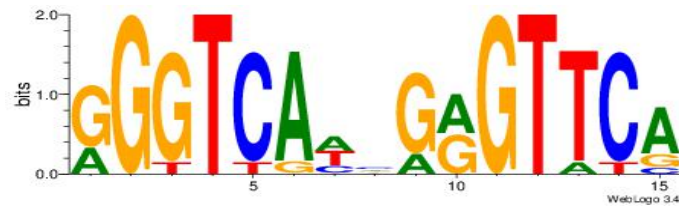


Dataset #:	2
Motif ID:	17
Motif name:	RXRAVDR
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	11
Similarity score:	5.05758

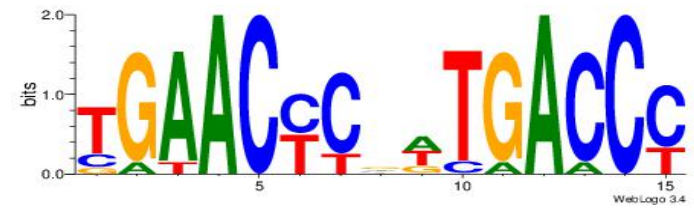
Alignment:

TGAACKCBWTGACCC-----
----GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: GGGTCAWBGRGTTCA



Reverse complement motif Consensus sequence: TGAACKCBWTGAC



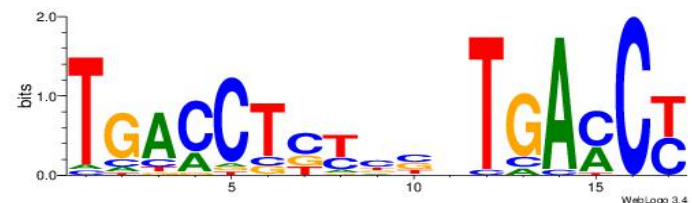
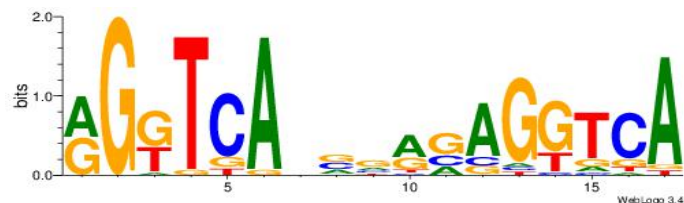
Dataset #:	2
Motif ID:	47
Motif name:	RXRRAR_DR5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	11
Similarity score:	5.05947

Alignment:

TGACCTCKVVB TGAYCK-----
-----GGYGCTGTCCATGGTGCTGAA

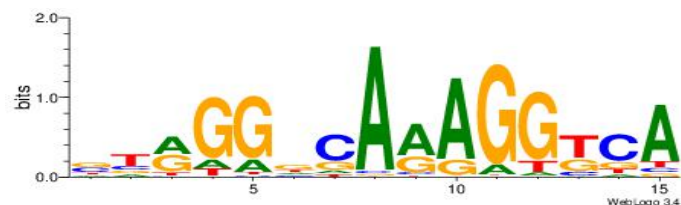
Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence:
TGACCTCKVVB TGAYCK

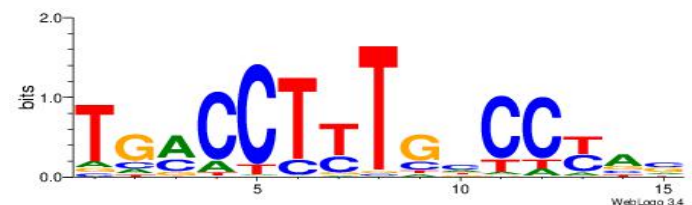


Dataset #: 2 Motif ID: 20 Motif name: PPARGRXRA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

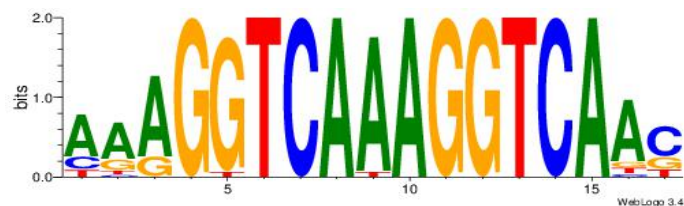


Best Matches for Motif ID 20 (Highest to Lowest)

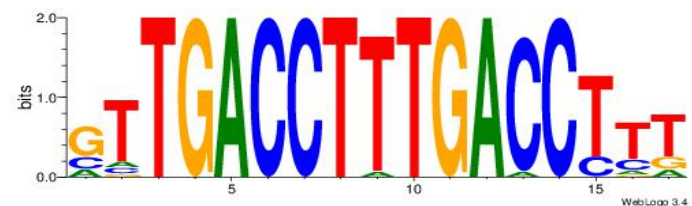
Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	15
Similarity score:	0.0442974

Alignment:
AAAGGTCAAAGGTCAAC
BTRGGDCARAGGKCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

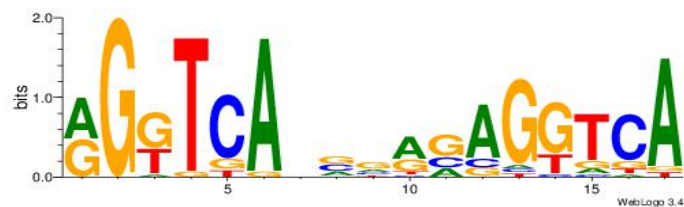


Dataset #: 2
 Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0500583

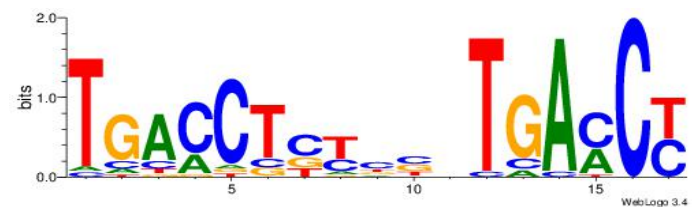
Alignment:

RGKTCABVVRGAGGTCA
 --BTRGGDCARAGGKCA

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

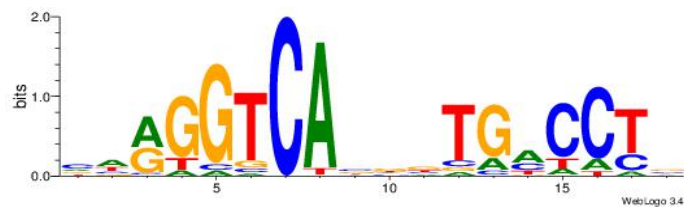


Dataset #: 2
 Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.0602408

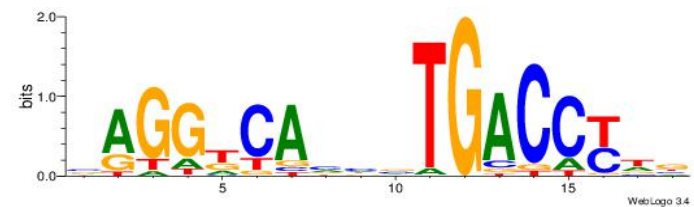
Alignment:

VHRGGTCABDBTGMCTB
 BTRGGDCARAGGKCA---

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



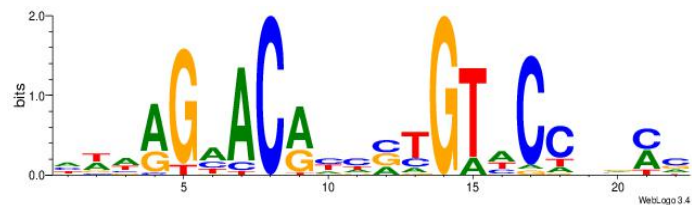
Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8

Number of overlap: 15
Similarity score: 0.0714981

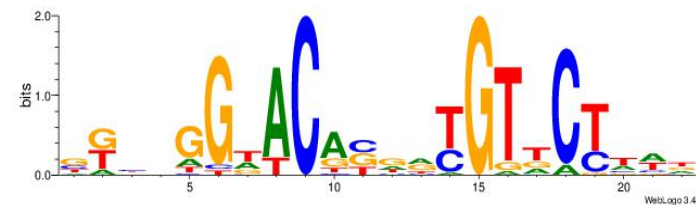
Alignment:

HWDAGHACRHHVTGTHCCHVMV
-----TGRCCTKTGHCKAB

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

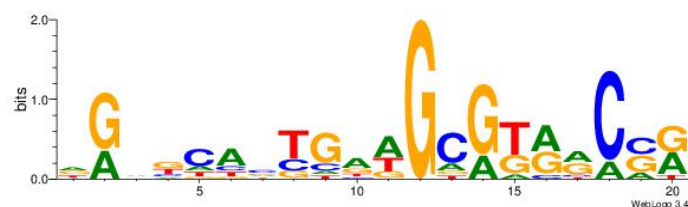


Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 15
Similarity score: 0.0720255

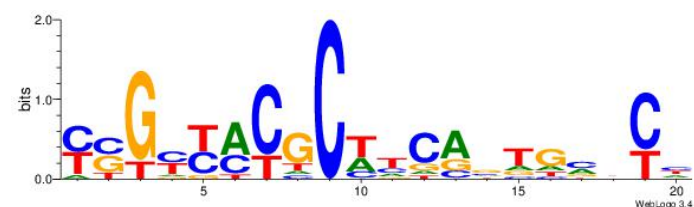
Alignment:

MSGKKRCGCWDCABTGBCD
---TGRCCTKTGHCKAB--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBBCD

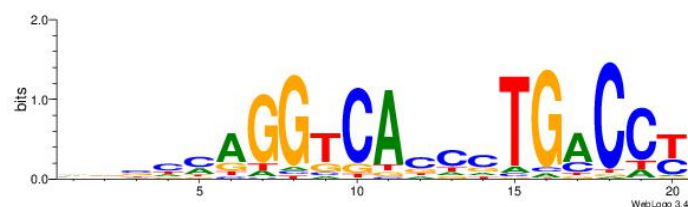


Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 15
Similarity score: 0.0723092

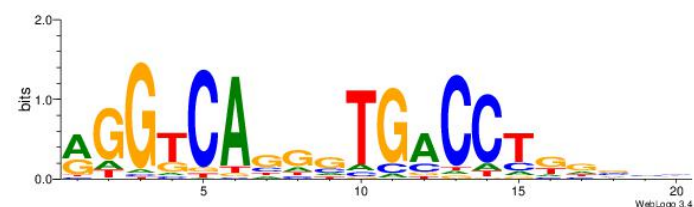
Alignment:

VDBHMAGGTCACCCTGACCY
---BTRGGDCARAGGKCA--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDHVB

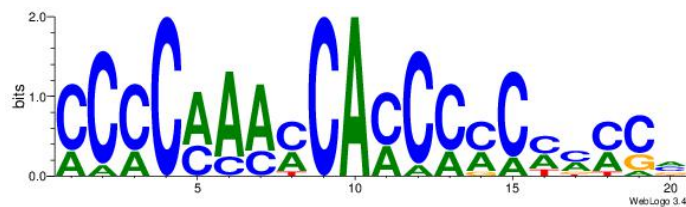


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0755648

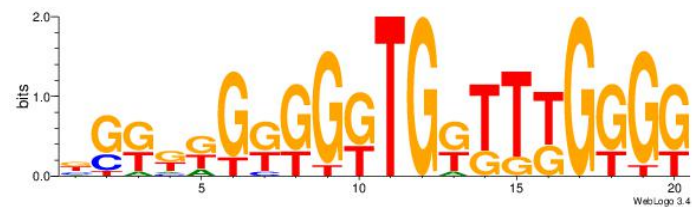
Alignment:

CCCCMAAMCAMCCMCMMMC
 -TGRCCCTKTGHCCCKAB----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

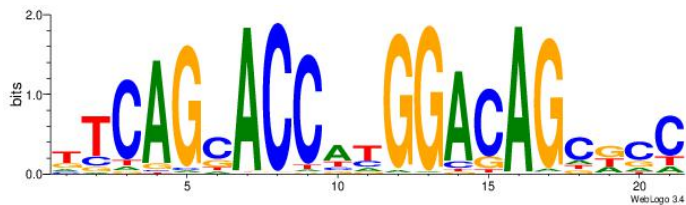


Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

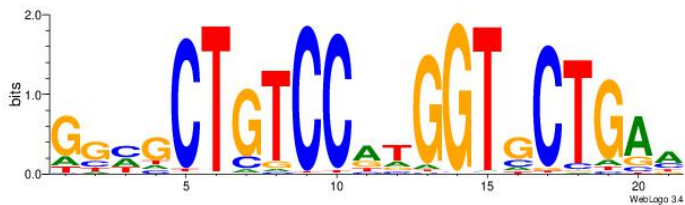
Number of overlap: 15
Similarity score: 0.0796159

Alignment:
TTCAGCACCATGGACAGCKCC
-BTRGGDCARAGGKCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

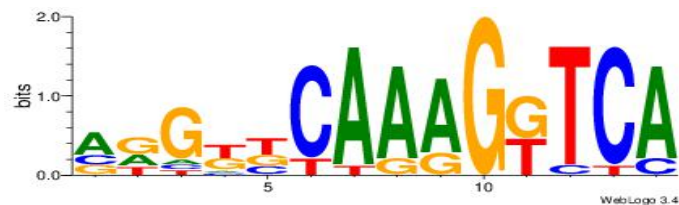


Dataset #: 2
Motif ID: 22
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.536521

Alignment:
TGAMCTTTGMMCYT-
TGRCCCTKGHCCKAB

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYCAAAGRTC

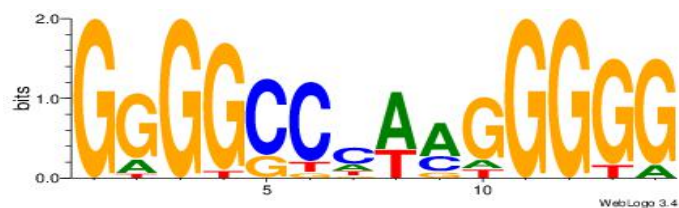


Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.575248

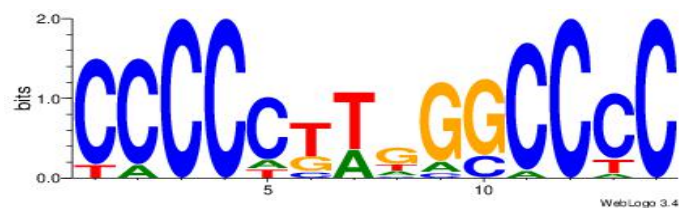
Alignment:

-GGGGCCCAAGGGGG
 BTRGGDCARAGGKCA

Original motif Consensus sequence: GGGGCCCAAGGGGG

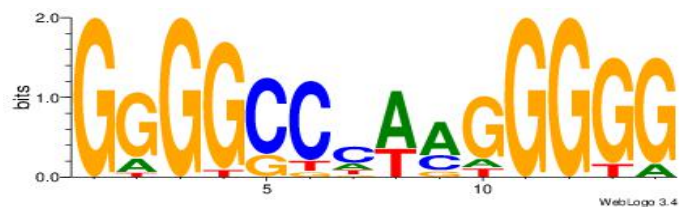


Reverse complement motif Consensus sequence: CCCCCTTGGGCC

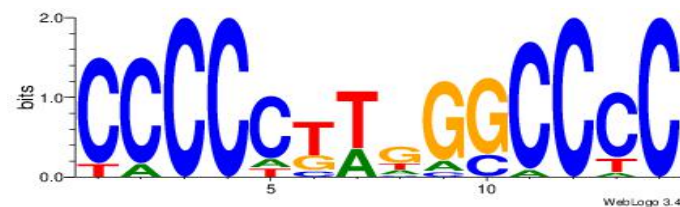


Dataset #: 2 Motif ID: 21 Motif name: PLAG1

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



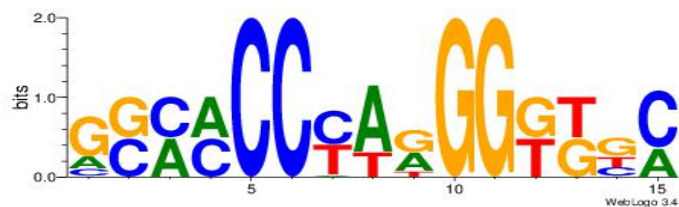
Best Matches for Motif ID 21 (Highest to Lowest)

Dataset #:	2
Motif ID:	13
Motif name:	Zfp423
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0944264

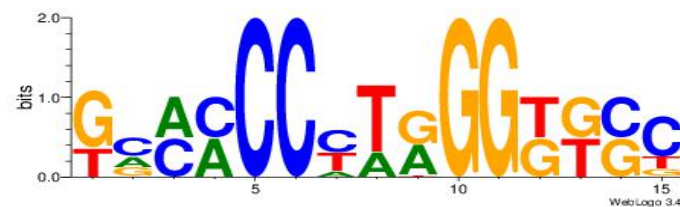
Alignment:

```
GSMCCYARGGKKKC
GGGGCCCAAGGGG-
```

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

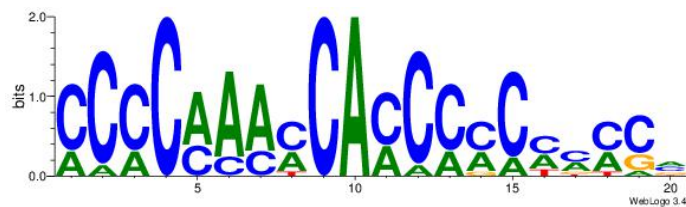


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.102814

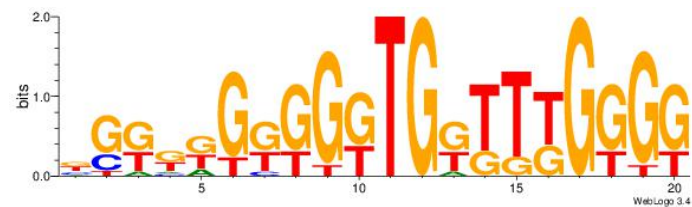
Alignment:

BGRRRGRGGRTGRTTYGGGG
 GGGGCCCAAGGGG-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

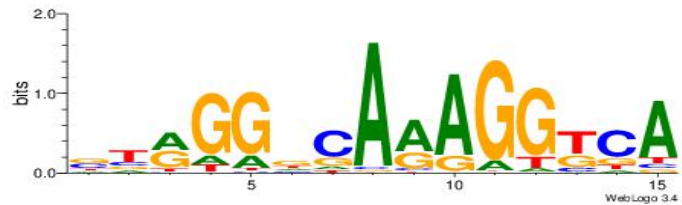


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

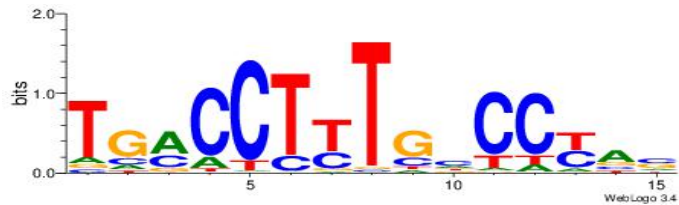
Number of overlap: 14
Similarity score: 0.107206

Alignment:
BTRGGDCARAGGKCA
-GGGGCCCAAGGGGG

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

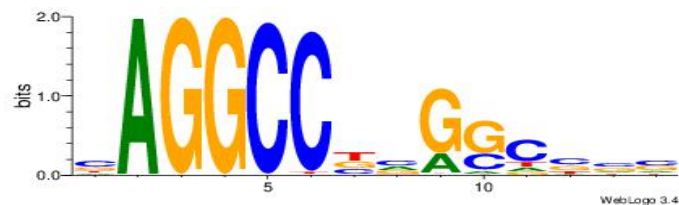
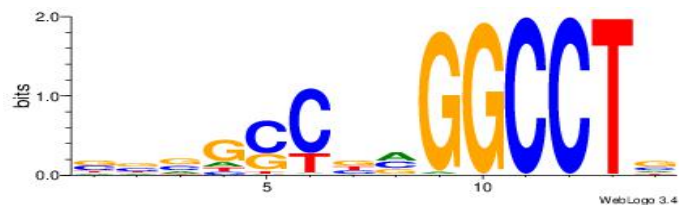


Dataset #: 2
Motif ID: 12
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.111315

Alignment:
VAGGCCBBGGCVBB
GGGGCCCAAGGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

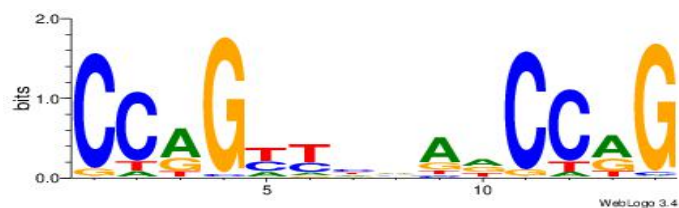


Dataset #: 2
 Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.115151

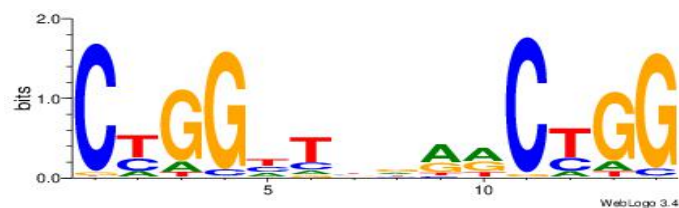
Alignment:

CCAGYYHVADCCRG
 CCCCTTGGGCCCC

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTC



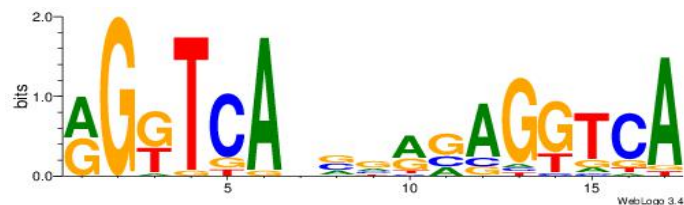
Dataset #: 2
 Motif ID: 47

Motif name:	RXRRAR_DR5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.116287

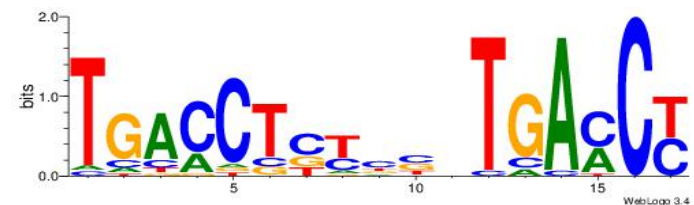
Alignment:

```
RGKTCABVVRGAGGTCA
GGGGCCCAAGGGG---
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

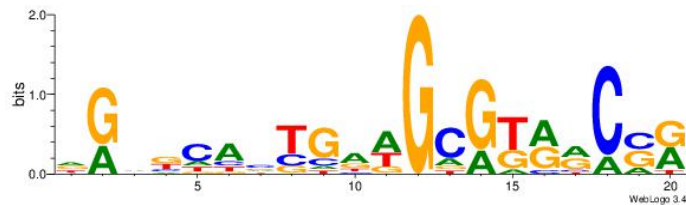


Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.117063

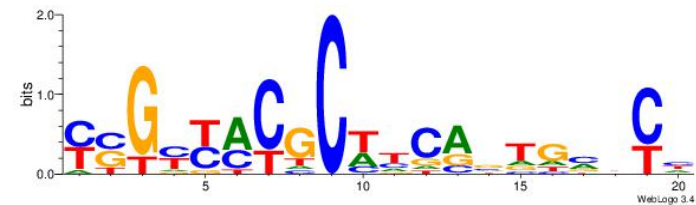
Alignment:

DGVBCABTGDWGCGRRCR
GGGGCCCAAGGGG-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



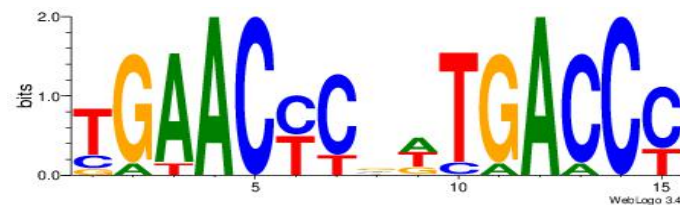
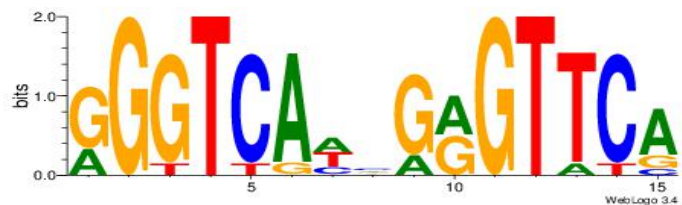
Dataset #:	2
Motif ID:	17
Motif name:	RXRAVDR
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	13
Similarity score:	0.590064

Alignment:

-GGGTCAWBGRGTTCA
GGGGCCCAAGGGG--

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC

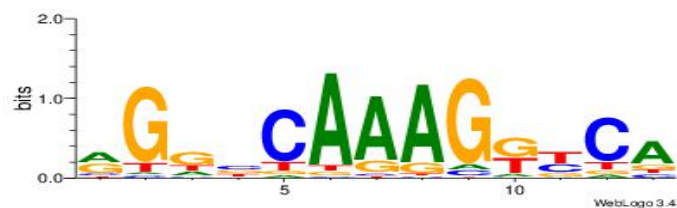


Dataset #: 2
 Motif ID: 34
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.603385

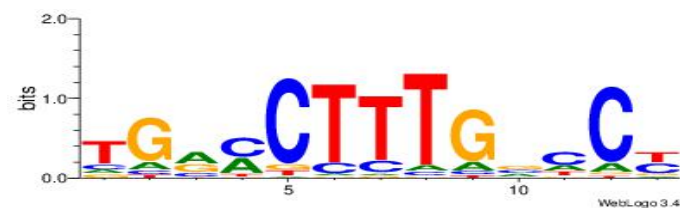
Alignment:

-RGGBCAAAGKYCA
 GGGGCCCAAGGGG

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



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: 2
Number of overlap: 13
Similarity score: 0.613207

Alignment:
-AKGY YCAAAGRTCA
GGGGCCCAAGGGG-

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA

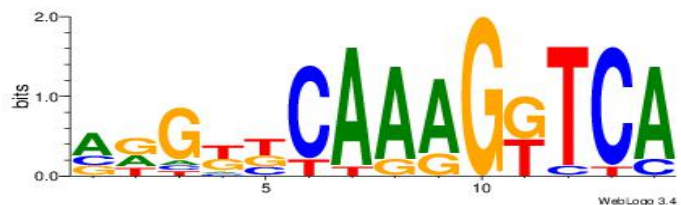


Dataset #: 2 Motif ID: 22 Motif name: NR2F1

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA



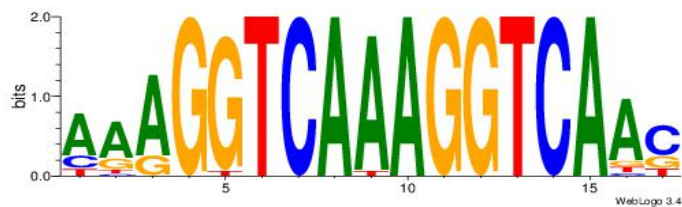
Best Matches for Motif ID 22 (Highest to Lowest)

Dataset #: 2
 Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0174588

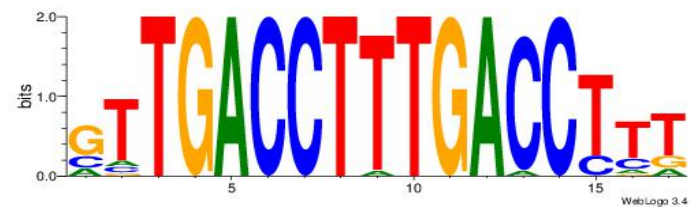
Alignment:

GTTGACCTTTGACCTTT
 --TGAMCTTTGMMCYT-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

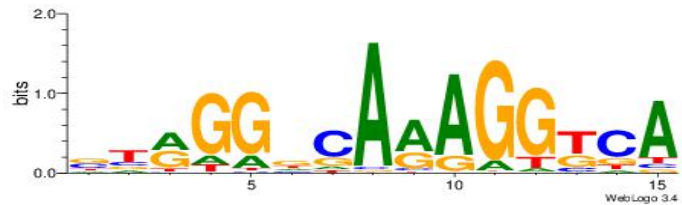


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

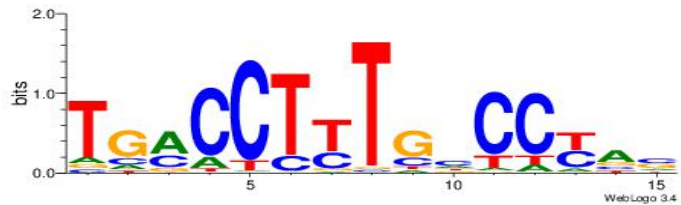
Number of overlap: 14
Similarity score: 0.0278283

Alignment:
BTRGGDCARAGGKCA
AKGY YCAAAGRTCA-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCK

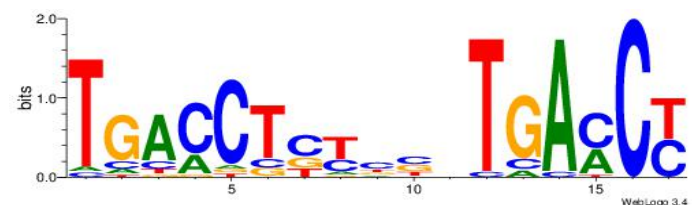
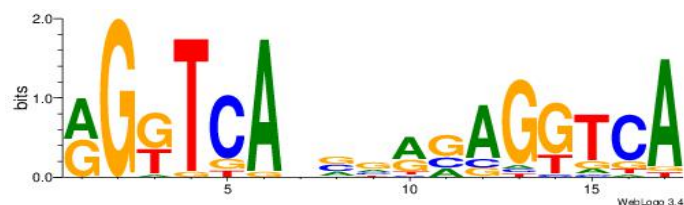


Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0625328

Alignment:
RGKTCABVVRGAGGTCA
---AKGY YCAAAGRTCA

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence:
TGACCTCKVVB TGAYCK

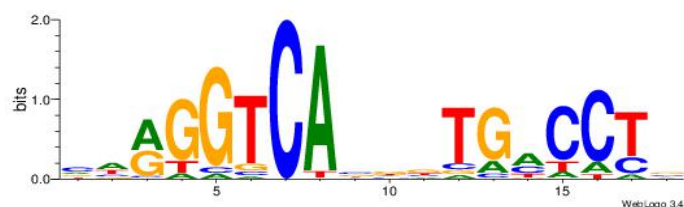


Dataset #: 2
 Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0710475

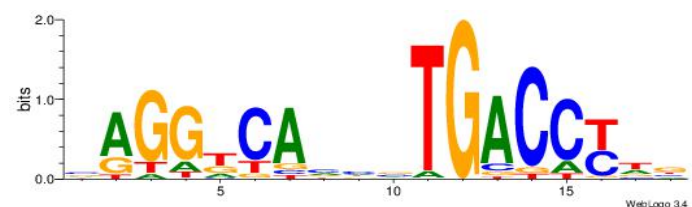
Alignment:

BAGGYCABHBTGACCKHV
 ---TGAMCTTTGMMCYT-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Dataset #: 2

Motif ID:	19
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	14
Similarity score:	0.071796

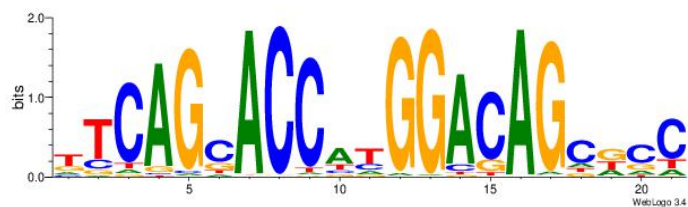
Alignment:

```

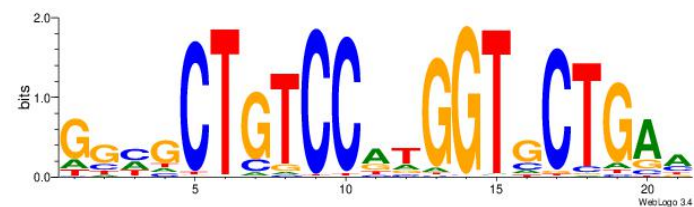
GGYGCTGTCCATGGTGCTGAA
--TGAMCTTTGMMCYT-----

```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

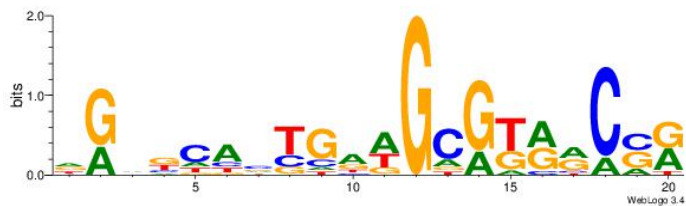


Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	14

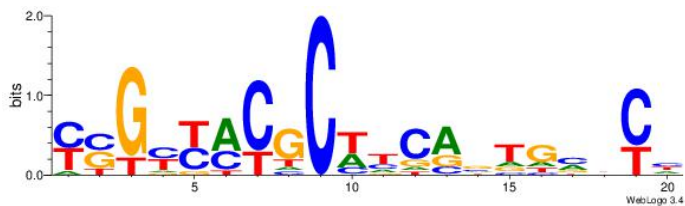
Similarity score: 0.0741987

Alignment:
MSGKKRCGCWDCABTGGBCD
----TGAMCTTTGMMCYT--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD

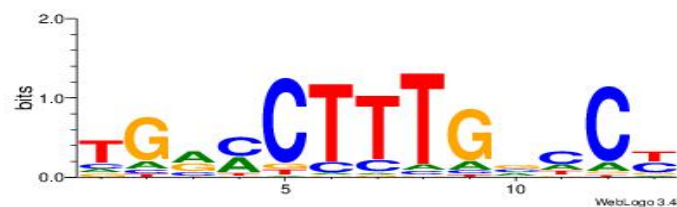
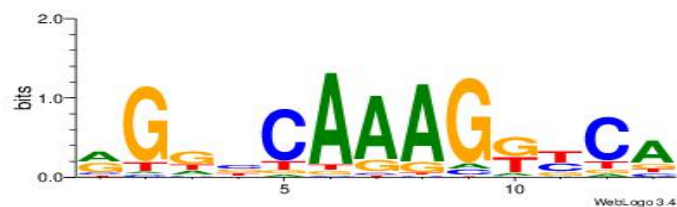


Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.514048

Alignment:
-RGGBCAAAGKYCA
AKGY YCAAAGRTCA

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGM YCTTTGBCCK

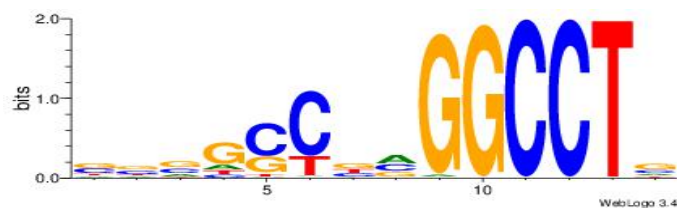


Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.568042

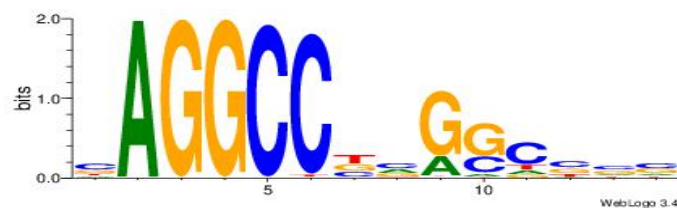
Alignment:

BBVGCCBVGGCCTV-
 -AKGY YCAAAGRTCA

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



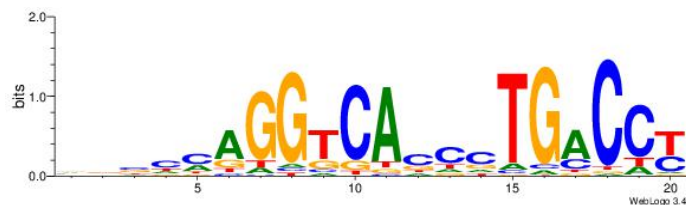
Dataset #: 2
 Motif ID: 29

Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.569869

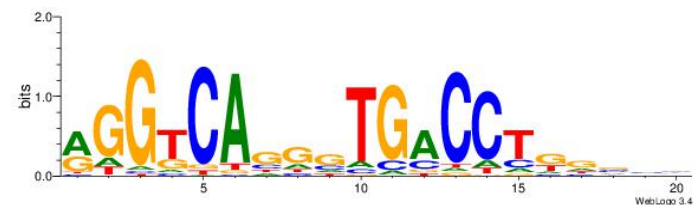
Alignment:

VDBHMAGGTCACCCTGACCY-
 -----TGAMCTTTGMMCYT

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



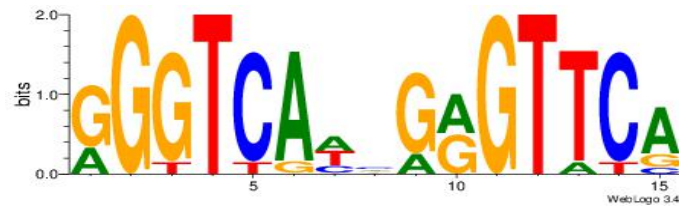
Dataset #: 2
 Motif ID: 17
 Motif name: RXRAVDR
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.572226

Alignment:

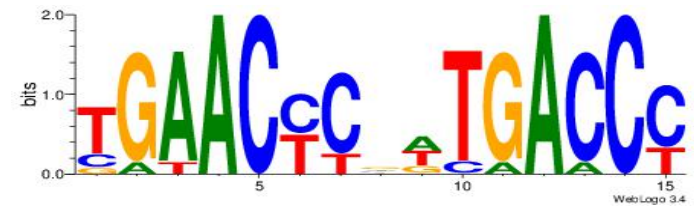
-TGAACKBWTGACCC

TGAMCTTTGMMCYT--

Original motif Consensus sequence: GGGTCAWBGRGTTCA



Reverse complement motif Consensus sequence: TGAACKBWTGACCC



Dataset #: 2 Motif ID: 23 Motif name: MZF1_1-4

Original motif Consensus sequence: BGGGGA



Reverse complement motif Consensus sequence: TCCCCV



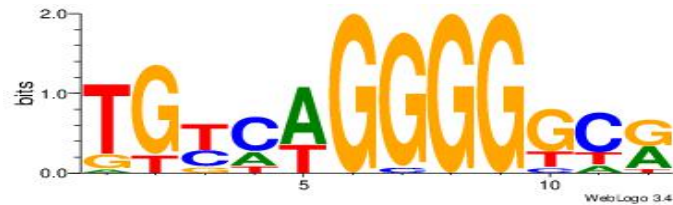
Best Matches for Motif ID 23 (Highest to Lowest)

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:	5

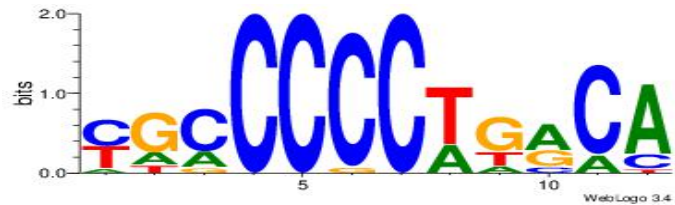
Number of overlap: 6
Similarity score: 0.0276389

Alignment:
MGCCCCCTGMCA
--TCCCCV----

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



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: 2
Number of overlap: 6
Similarity score: 0.0314583

Alignment:
BKAGGGGDAD
---BGGGGA-

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB



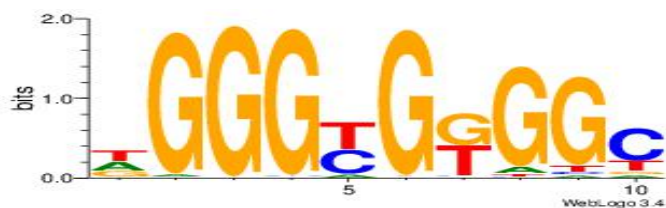
Dataset #: 2
 Motif ID: 36
 Motif name: Klf4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0406514

Alignment:

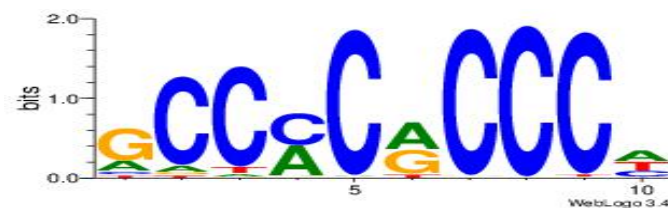
GCCYCMCCCD

TCCCV----

Original motif Consensus sequence: DGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



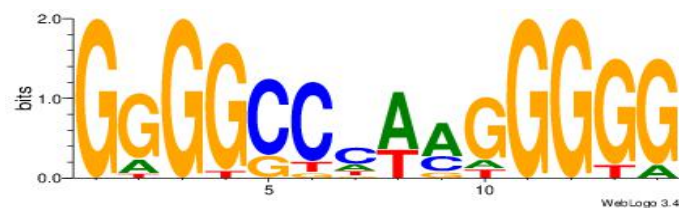
Dataset #: 2
 Motif ID: 21

Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	6
Similarity score:	0.0412963

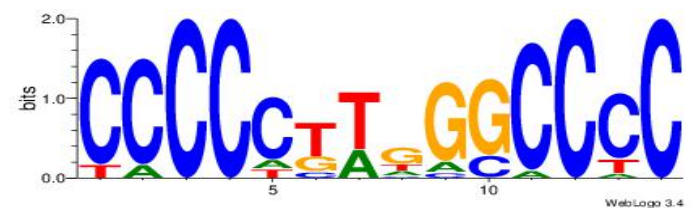
Alignment:

```
GGGGCCCAAGGGGG
-----BGGGGA
```

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
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:	0.0426517

Alignment:

TCCCAG

TCCCV

Original motif Consensus sequence: CTGGGA



Reverse complement motif Consensus sequence: TCCCAG



Dataset #:	2
Motif ID:	16
Motif name:	SP1
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:	0.0464881

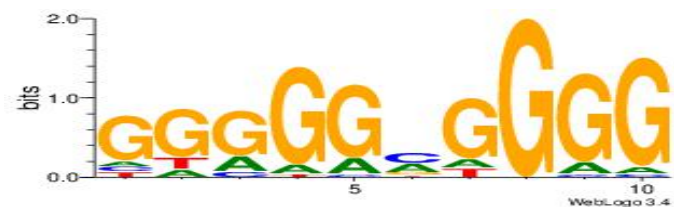
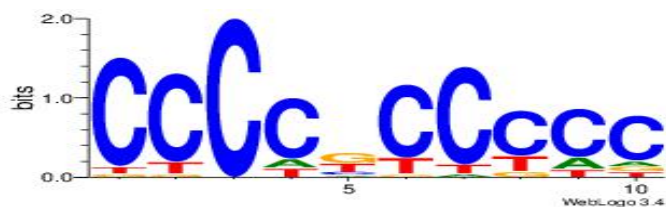
Alignment:

GGGGYGGGG

----BGGGA

Original motif Consensus sequence: CCCCKCCCC

Reverse complement motif Consensus sequence: GGGGYGGGG

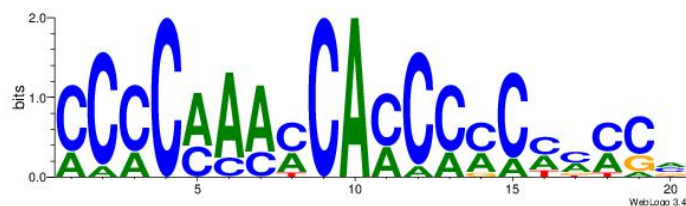


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0493561

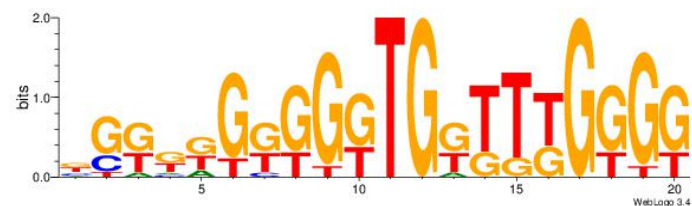
Alignment:

CCCCMAAMCAMCCMCMMMC
 ----TCCCCV-----

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: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0521759

Alignment:

GGGGRTTCCCC
 -----TCCCCV

Original motif Consensus sequence: GGGGRTTCCCC



Reverse complement motif Consensus sequence: GGGGAATCCCC



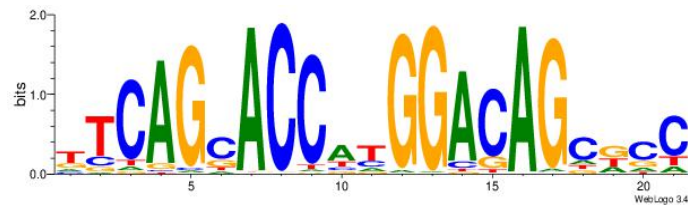
Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 6
 Similarity score: 0.0581528

Alignment:

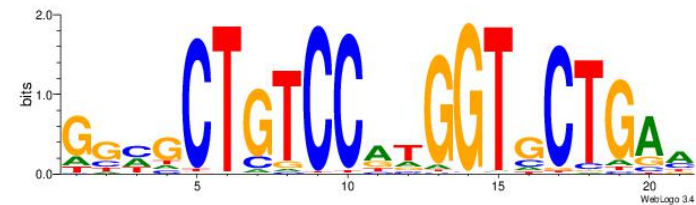
GGYGCTGTCCATGGTGCTGAA

-----TCCCCV-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



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:	0.0585417

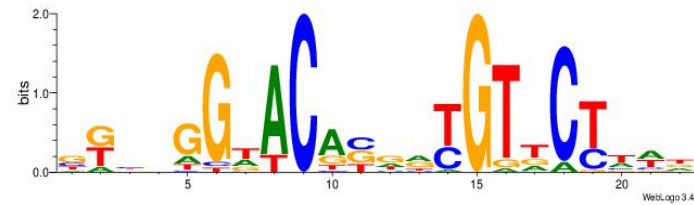
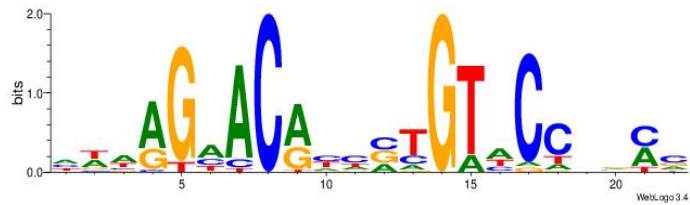
Alignment:

HWDAGHACRHHVTGTHCCHVMV

-----TCCCCV--

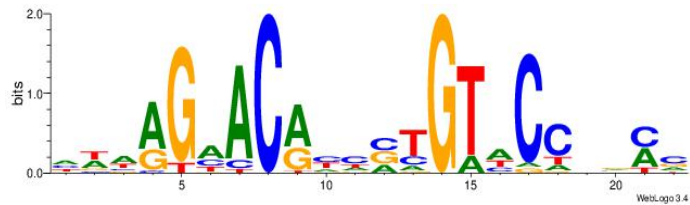
Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence:
VRVDGGHACAVDDKGTHCTDWH

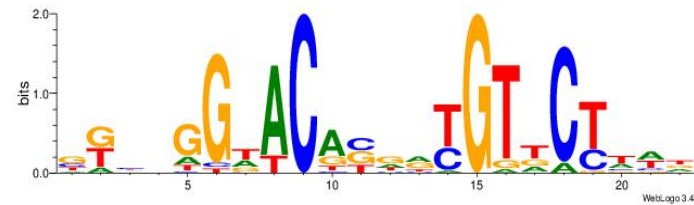


Dataset #: 2 **Motif ID: 24** **Motif name: Ar**

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



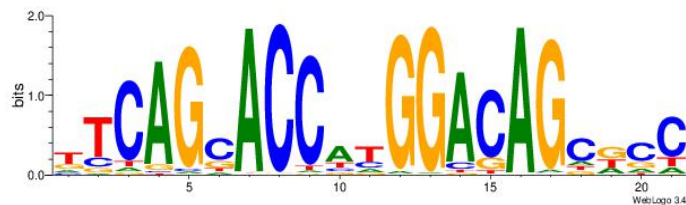
Best Matches for Motif ID 24 (Highest to Lowest)

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:	1
Number of overlap:	21
Similarity score:	0.0696331

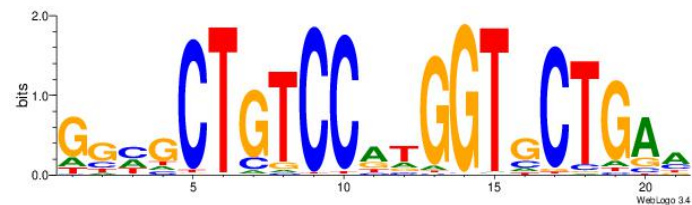
Alignment:

-GGYGCTGTCCATGGTGCTGAA
VRVDGGHACAVDDKGTHTDWH

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



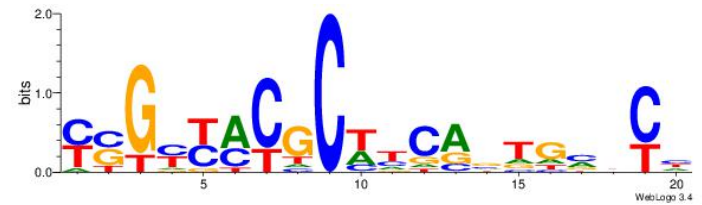
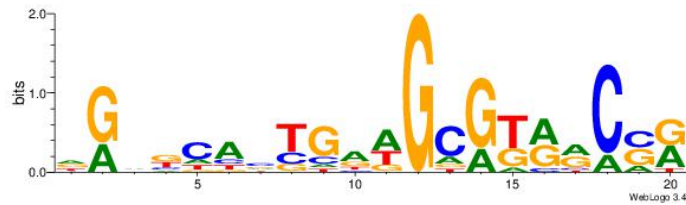
Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.564914

Alignment:

--MSGKKRCGCWDCABTGBBCD
VRVDGGHACAVDDKGTHTDWH

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

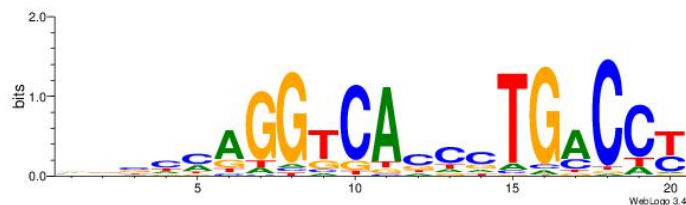


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 1.05195

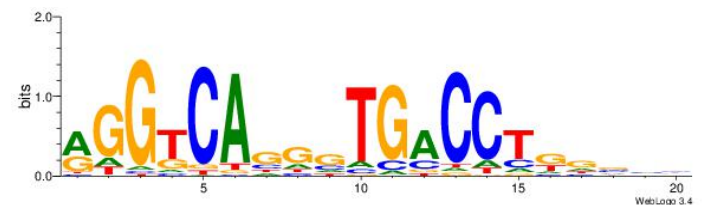
Alignment:

VDBHMAGGTCACCCTGACCY---
 -VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

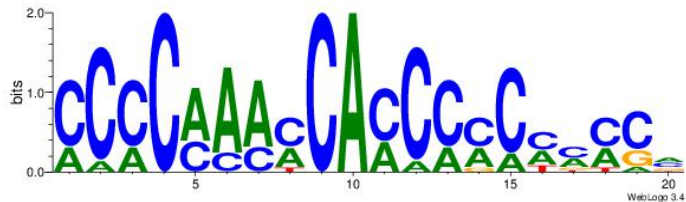


Dataset #: 2

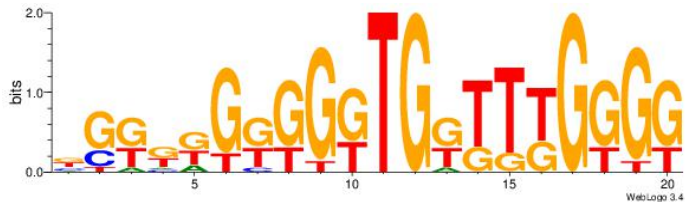
Motif ID: 18
Motif name: RREB1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 1.07661

Alignment:
CCCCMAAMCAMCCMCMMMCV---
-HWDAGHACRHHVTGTHCCHVMV

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

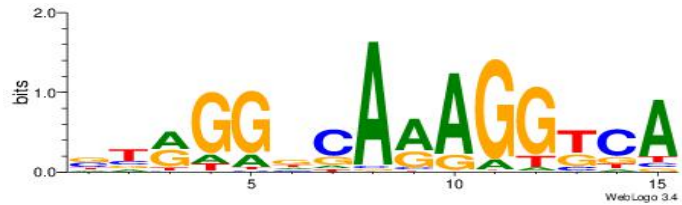


Dataset #: 2
Motif ID: 20
Motif name: PPARGRXRA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15

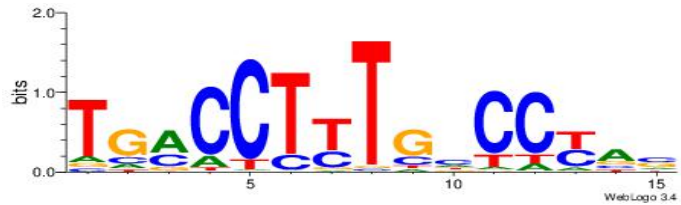
Similarity score: 3.0649

Alignment:
-----BTRGGDCARAGGKCA
VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKGHCCK

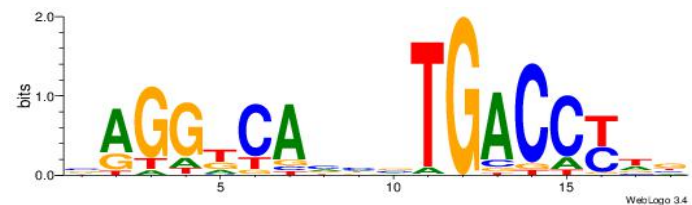
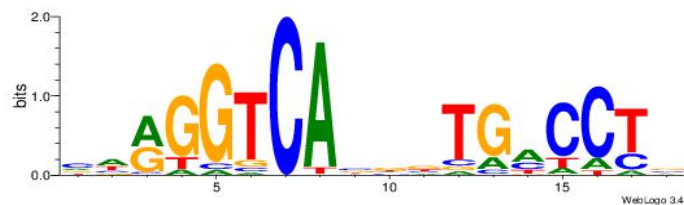


Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 3.57597

Alignment:
-----VHRGGTCABDBTGMCTB
VRVDGGHACAVDDKGTHCTDWH----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

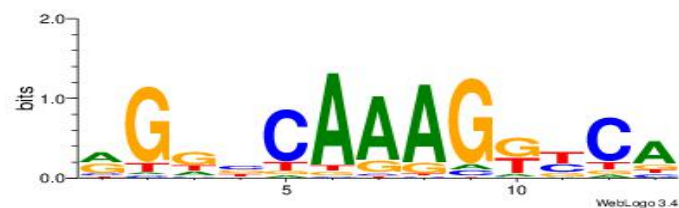


Dataset #: 2
 Motif ID: 34
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 4.07506

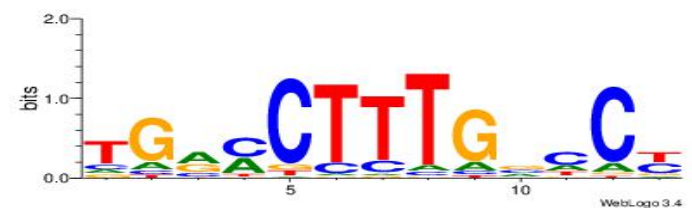
Alignment:

-----TGM YCTTTGB CCK
 HWDAGHACRHHVTGTHCCHVMV

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGB CCK



Dataset #: 1
 Motif ID: 10

Motif name:	Motif 10
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	4.07511

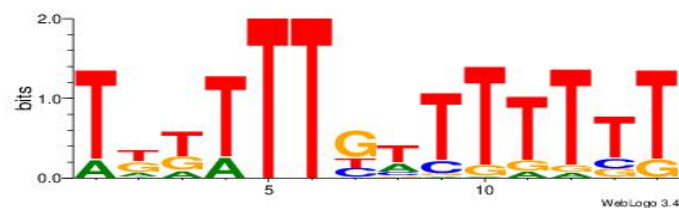
Alignment:

```

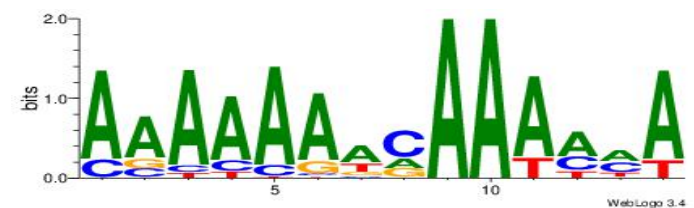
-----AAAAAACAAARRA
HWDAGHACRHHVTGTHCCHVMV-

```

Original motif Consensus sequence: TKKTTTGT TTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR

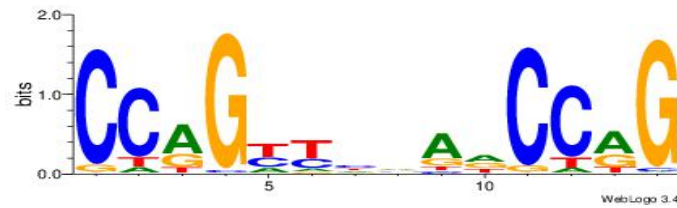


Dataset #:	2
Motif ID:	48
Motif name:	Tcfcp2l1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	4.0791

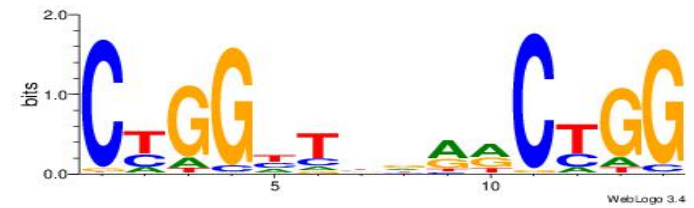
Alignment:

CKGGDTBDMMCTGG-----
-VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTG



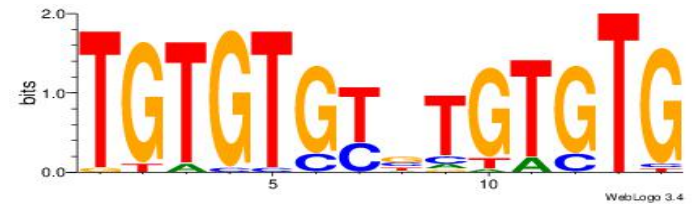
Dataset #:	1
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	4.57405

Alignment:

TGTGTGKVTGTGTG-----
--HWDAGHACRHHVTGTHCCHVMV

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGTG



Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #:	2
Motif ID:	31
Motif name:	Esrrb
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

CACGTG

CACGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 2
Motif ID: 39
Motif name: MYCMAX
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: 0.0143849

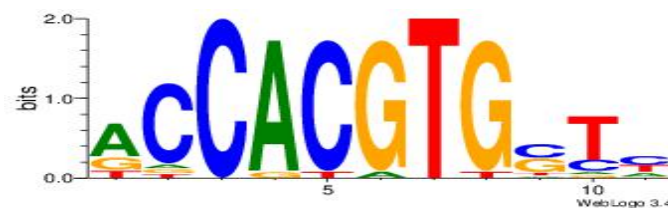
Alignment:

RASCACGTGGT
---CACGTG---

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



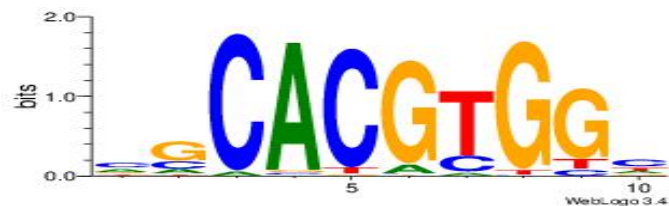
Dataset #: 2
 Motif ID: 38
 Motif name: Myc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0267529

Alignment:

DCCACGTGCV

--CACGTG--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

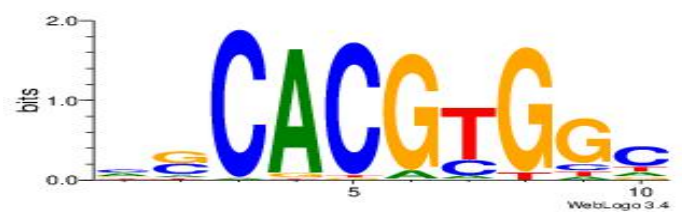


Dataset #: 2
 Motif ID: 40
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6

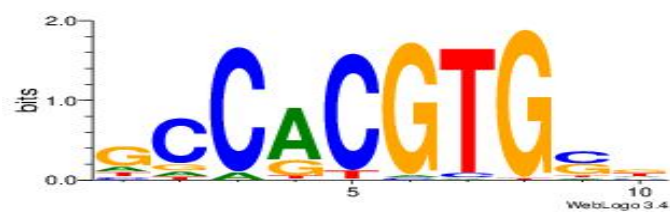
Similarity score: 0.0272641

Alignment:
HSCACGTGGC
--CACGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 2
Motif ID: 33
Motif name: HIF1AARNT
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: 0.0347756

Alignment:
VCACGTBV
-CACGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV



Dataset #: 2
 Motif ID: 26
 Motif name: ArntAhr
 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: 0.065625

Alignment:

YGCGTG

CACGTG

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Dataset #: 2
 Motif ID: 14

Motif name:	ZEB1
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:	0.0689533

Alignment:
HAGGTG
CACGTG

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



Dataset #:	2
Motif ID:	28
Motif name:	Egr1
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:	0.0784722

Alignment:

HGCGTGGGCGK
CACGTG-----

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



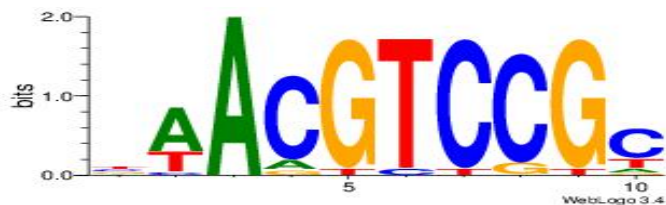
Dataset #:	2
Motif ID:	37
Motif name:	MIZF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	6
Similarity score:	0.0854167

Alignment:

BAACGTCCGC
-CACGTG----

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

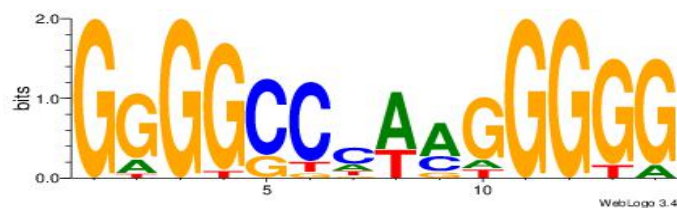


Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.105093

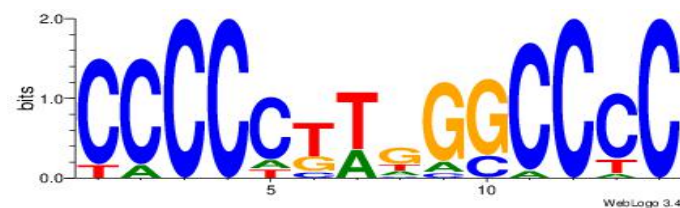
Alignment:

GGGGCCCAAGGGGG
 -----CACGTG--

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



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

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Best Matches for Motif ID 26 (Highest to Lowest)

Dataset #:	2
Motif ID:	28
Motif name:	Egr1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

```
YCGCCCACGCH
-----CACGCM
```

Original motif Consensus sequence: HGC GTGGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



Dataset #: 2
 Motif ID: 33
 Motif name: HIF1AARNT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0112447

Alignment:
 VBACGTGV
 -YGCGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV

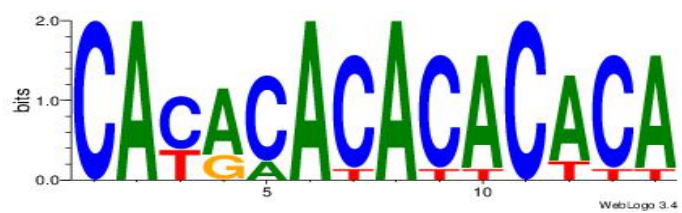


Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 6

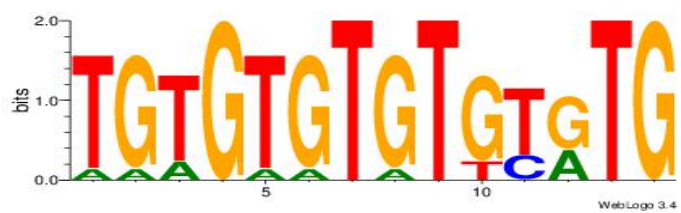
Similarity score: 0.0308396

Alignment:
TGTGTGTGTGKTG
-----YGCGTG--

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTG



Dataset #: 2
Motif ID: 31
Motif name: Esrrb
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: 0.0315972

Alignment:
CACGTG
YGCGTG

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG



Dataset #: 2
 Motif ID: 25
 Motif name: Arnt
 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: 0.0315972

Alignment:

CACGTG

YGCGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 1
 Motif ID: 9

Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0350575

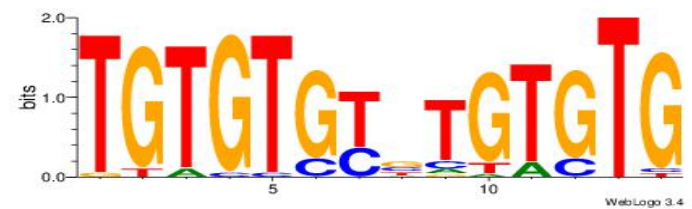
Alignment:

```
TGTGTGKVTGTGTG
YGCGTG-----
```

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGTG



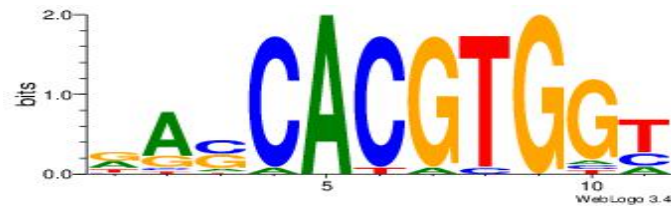
Dataset #:	2
Motif ID:	39
Motif name:	MYCMAX
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0376488

Alignment:

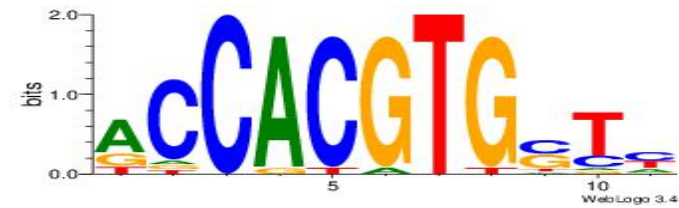
RASCACGTGGT

---YGCGTG--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #:	2
Motif ID:	40
Motif name:	Mycn
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:	0.0377949

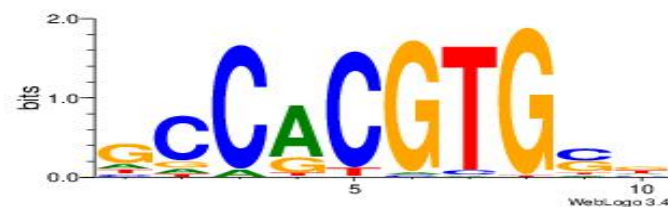
Alignment:

GCCACGTGSD

--YGCGTG--

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 2
 Motif ID: 38
 Motif name: Myc
 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: 0.0399214

Alignment:

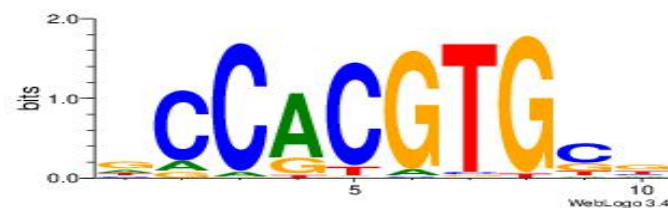
DCCACGTGCV

--YGCGTG--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



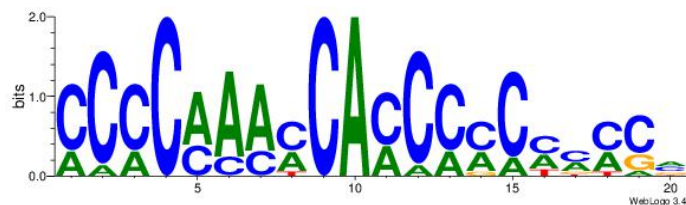
Dataset #: 2
 Motif ID: 18

Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0433081

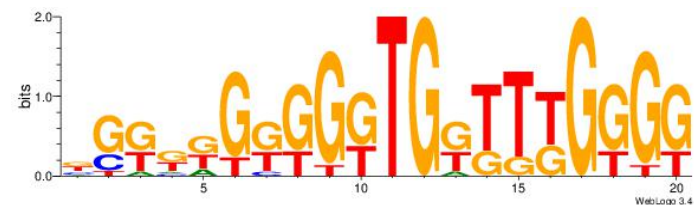
Alignment:

BGRRRGRGGRTGRTTYGGGG
 -----YCGTG-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



Dataset #: 2 Motif ID: 27 Motif name: E2F1

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGCSAAA



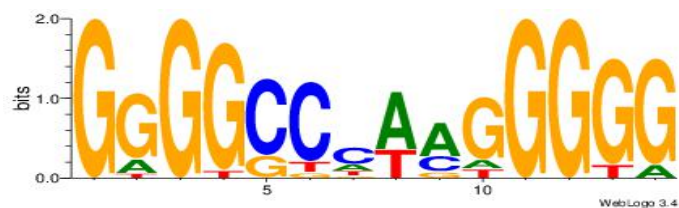
Best Matches for Motif ID 27 (Highest to Lowest)

Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0255644

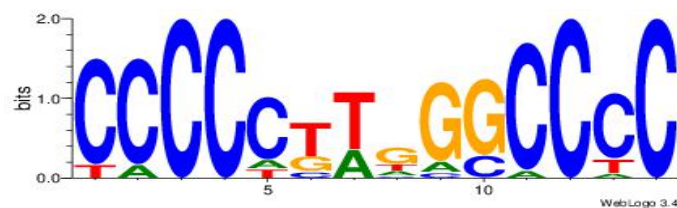
Alignment:

CCCCCTTGGGCCCC
 -TTTSGCGC-----

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC



Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement

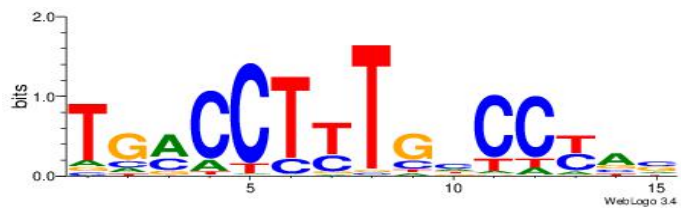
Direction: Backward
Position number: 6
Number of overlap: 8
Similarity score: 0.0280436

Alignment:
TGRCCTKTGHCKAB
--TTTSGCGC-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



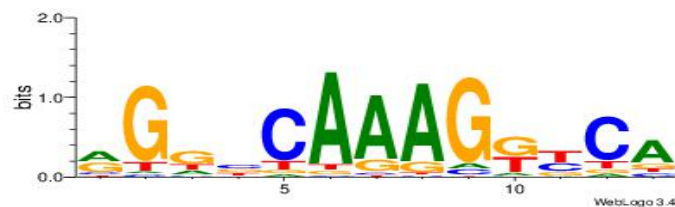
Reverse complement motif Consensus sequence: TGRCCTKTGHCKA



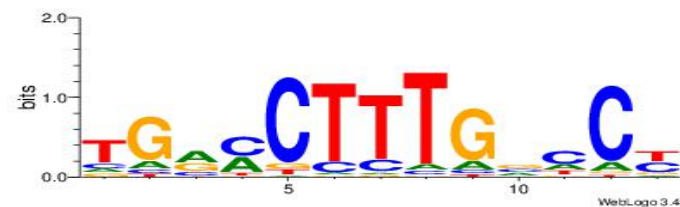
Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0283733

Alignment:
RGGBCAAAGKYCA
GCGCSAAA-----

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

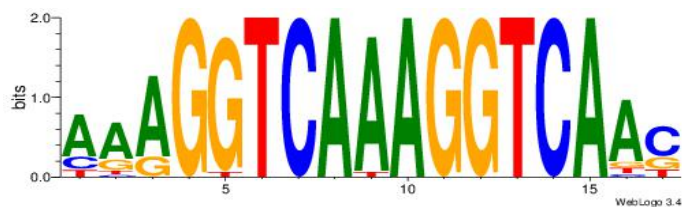


Dataset #: 2
 Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0298005

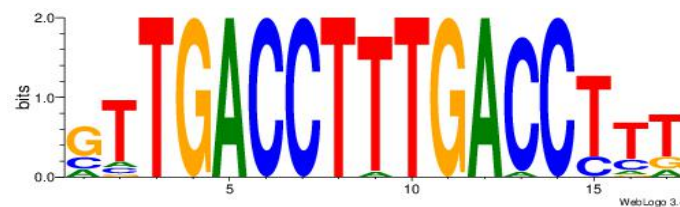
Alignment:

AAAGGTCAAAGGTCAAC
 --GCGCSAAA-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 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: 0.0369159

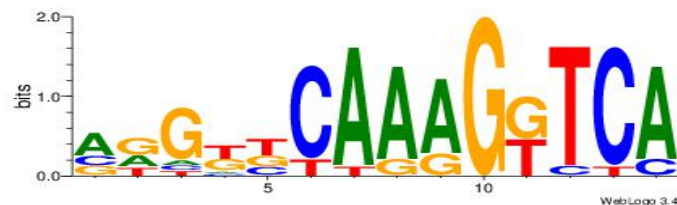
Alignment:

TGAMCTTTGMMCYT
 -----TTTSGCGC-

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

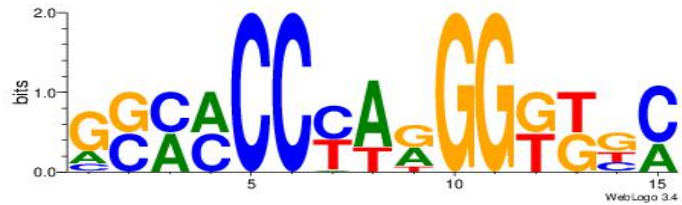


Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8

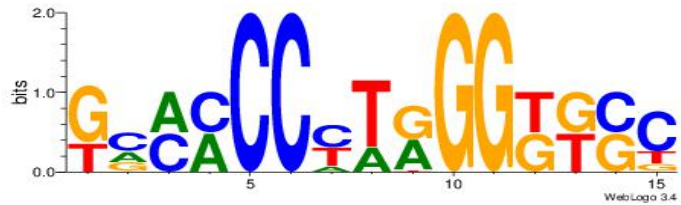
Similarity score: 0.0423573

Alignment:
GSMCCYARGGKKKC
-----GCGCSAAA--

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



Dataset #: 2
Motif ID: 28
Motif name: Egr1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0470922

Alignment:
YCGCCCACGCH
GCGCSAAA---

Original motif Consensus sequence: HCGTG G GCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

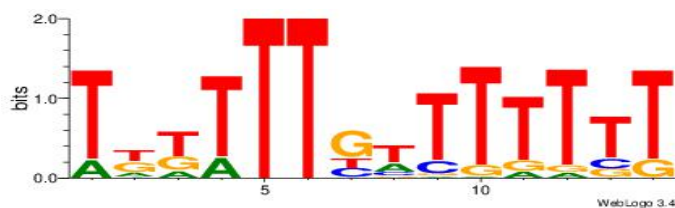


Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0486459

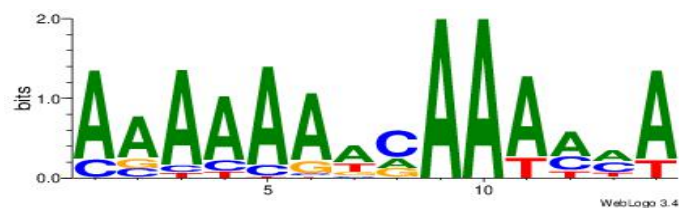
Alignment:

TKKTTTGTTTTTTT
 ---TTTSGCGC---

Original motif Consensus sequence: TKKTTTGTTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR



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:	13
Number of overlap:	8
Similarity score:	0.0497437

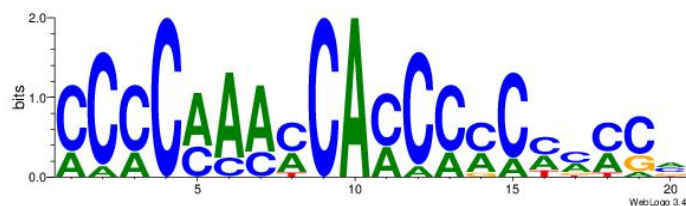
Alignment:

```

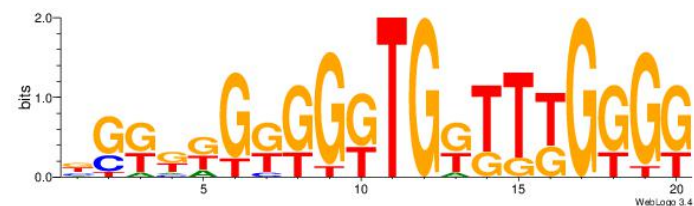
BGRRRGRGGRTGRTTYGGGG
TTTSGCGC-----

```

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
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:	1.03392

Alignment:

--MTTCCK

TTTSGCGC

Original motif Consensus sequence: RGGAAAR



Reverse complement motif Consensus sequence: MTTCCK



Dataset #: 2 Motif ID: 28 Motif name: Egr1

Original motif Consensus sequence: HCGTGCGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



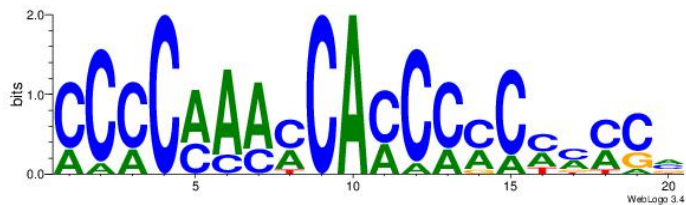
Best Matches for Motif ID 28 (Highest to Lowest)

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:	3

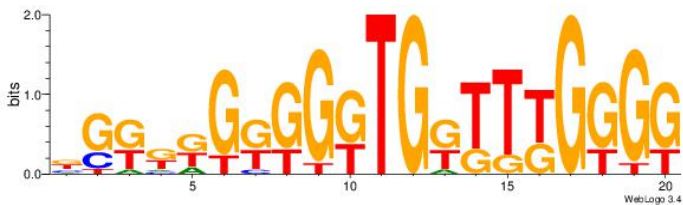
Number of overlap: 11
Similarity score: 0.0550907

Alignment:
BGRRRGRGGRTGRTTYGGGG
-----HCGTGGGCGK--

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG

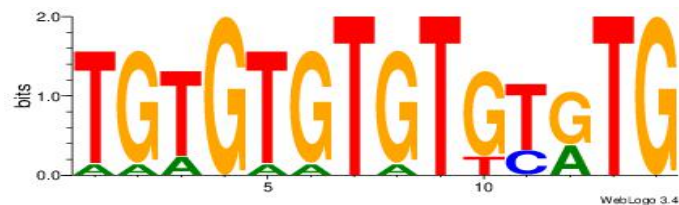
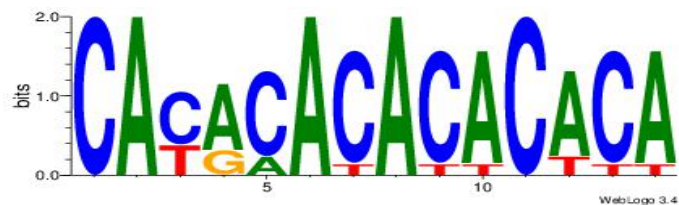


Dataset #: 1
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.062391

Alignment:
CAYACACACACACA
YCGCCACGCH---

Original motif Consensus sequence: CAYACACACACACA

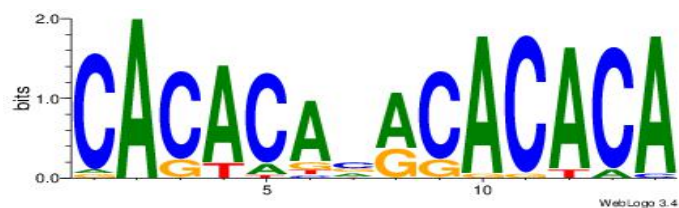
Reverse complement motif Consensus sequence: TGTGTGTGTGKT



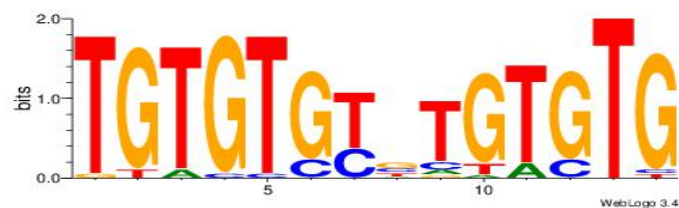
Dataset #: 1
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0668604

Alignment:
 CACACAVRCACACA
 YGCCCCACGCH---

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



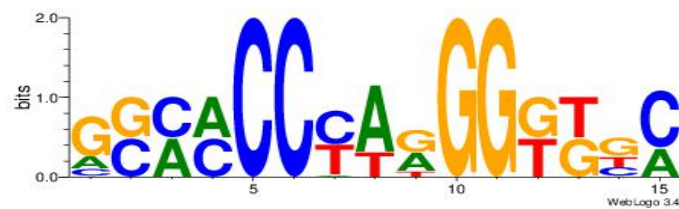
Dataset #: 2
 Motif ID: 13

Motif name:	Zfp423
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0673496

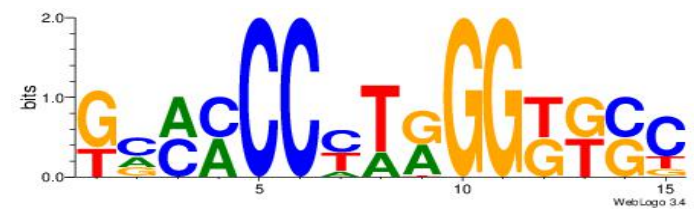
Alignment:

```
GSMCCYARGGKKKC
---YCGCCACGCH-
```

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



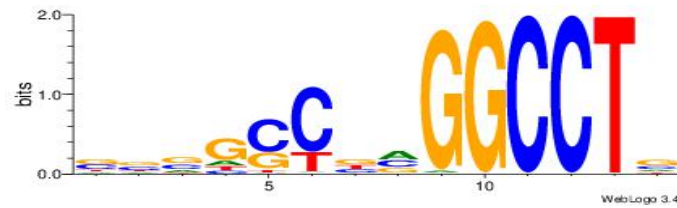
Dataset #:	2
Motif ID:	12
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0764878

Alignment:

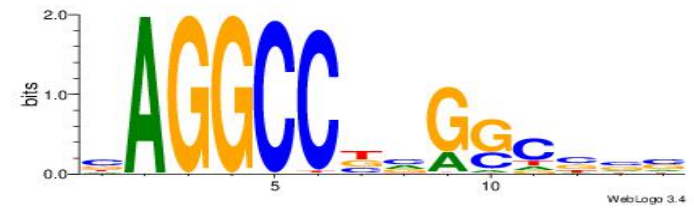
BBVGCCBVGGCCTV

--HGCGTGGGCGK--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	11
Similarity score:	0.0765783

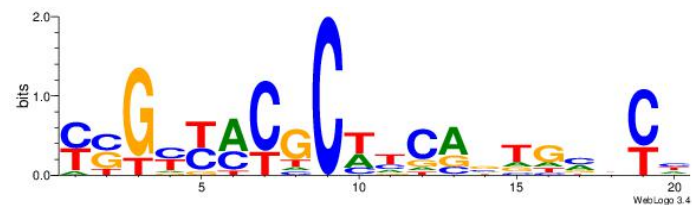
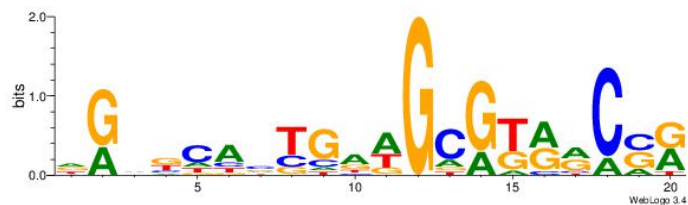
Alignment:

DGVBCABTGDWGCGRRCR

----HGCGTGGGCGK-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif Consensus sequence:
MSGKKRCGCWDCA BTGBBCD



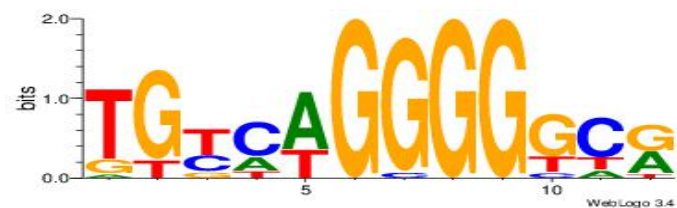
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0830177

Alignment:

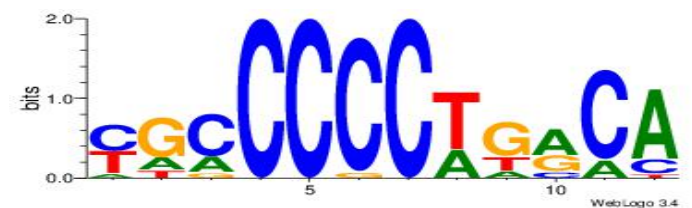
TGYCAGGGGGCR

HGCGTGGGCGK-

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



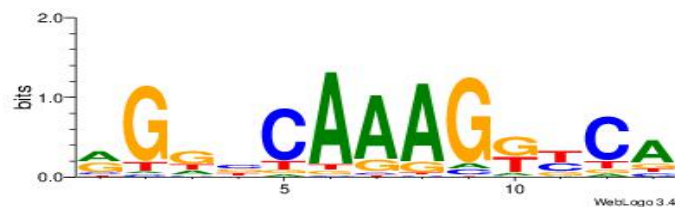
Dataset #: 2
 Motif ID: 34

Motif name:	HNF4A
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0857144

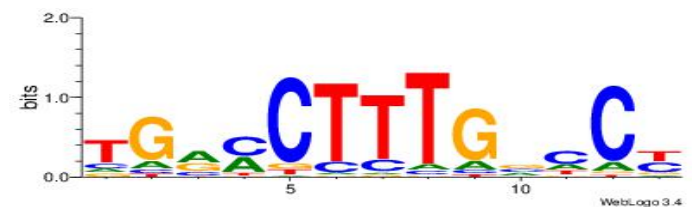
Alignment:

```
TGMYCTTTGBCCK
--HGCGTGGGCGK
```

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

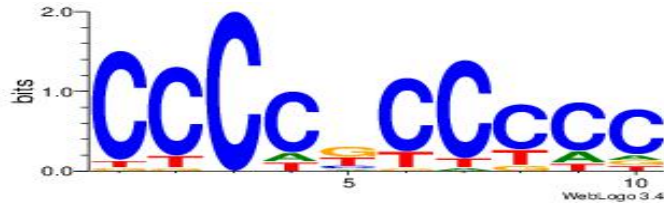


Dataset #:	2
Motif ID:	16
Motif name:	SP1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.572401

Alignment:

CCCCKCCCCC-
YCGCCCACGCH

Original motif Consensus sequence: CCCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



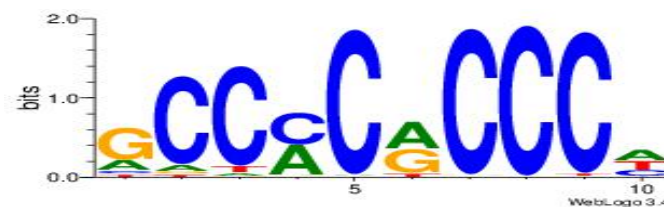
Dataset #:	2
Motif ID:	36
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.580823

Alignment:

DGGGYGKGGC-
HCGTGGGCGK

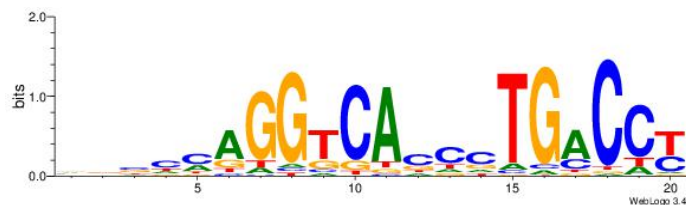
Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

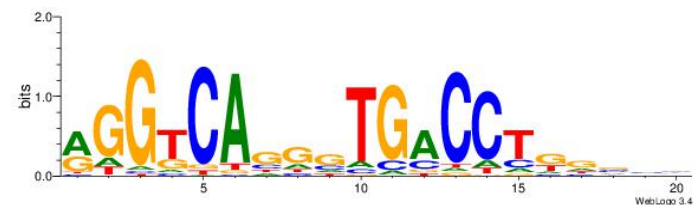


Dataset #: 2 Motif ID: 29 Motif name: ESR1

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



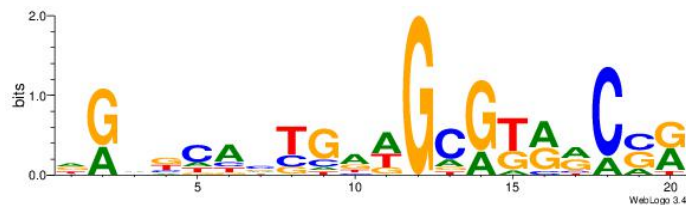
Best Matches for Motif ID 29 (Highest to Lowest)

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:	1
Number of overlap:	20
Similarity score:	0.0624908

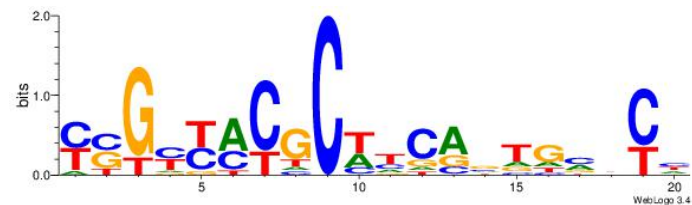
Alignment:

MSGKKRCGCWDCABTGBBCD
MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

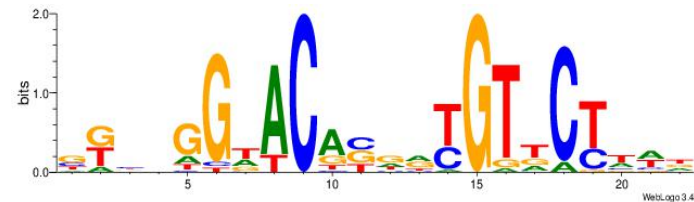
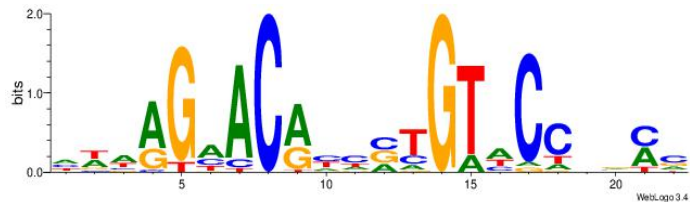


Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	19
Similarity score:	0.556363

Alignment:
-HWDAGHACRHHVTGTHCCHVMV
MGGTCAGGGTGACCTRDBHV---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

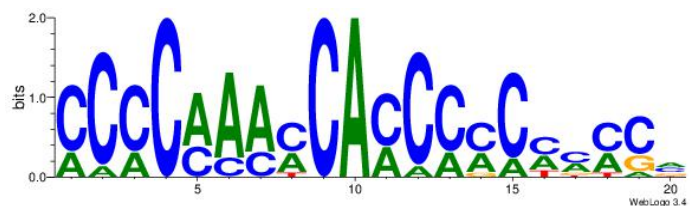


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.575732

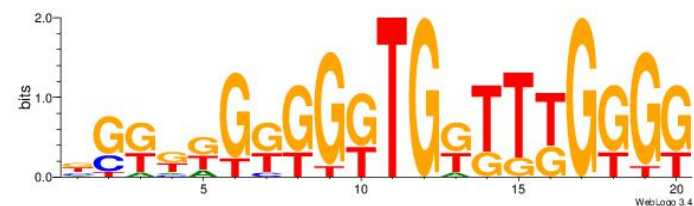
Alignment:

BGRRRGRGGRTGRTTYGGGG-
 -MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



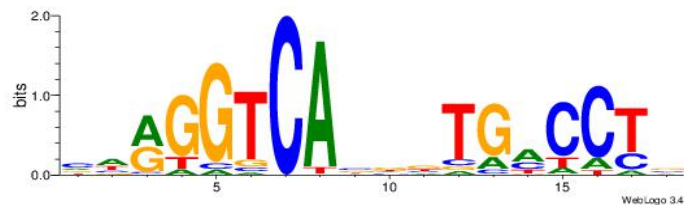
Dataset #: 2

Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 1.50287

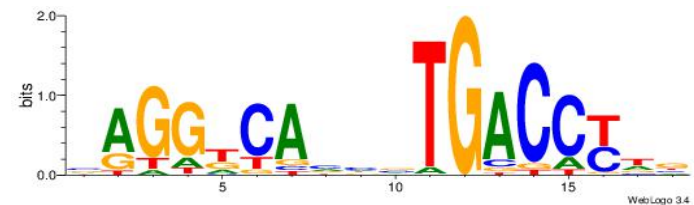
Alignment:

---VHRGGTCABDBTGMCCCTB
 VDBHMAAGGTCACCCTGACCY-

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

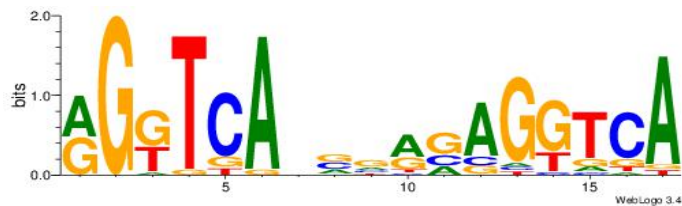


Dataset #: 2
 Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17

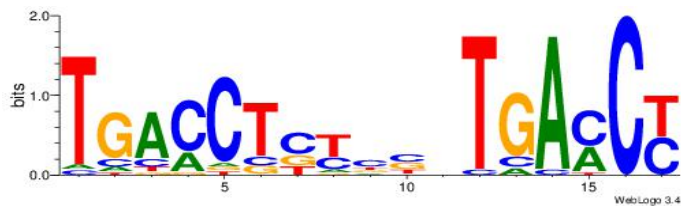
Similarity score: 1.55839

Alignment:
---TGACCTCKVVB TGAYCK
VDBHMAGGTCACCCTGACC Y

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

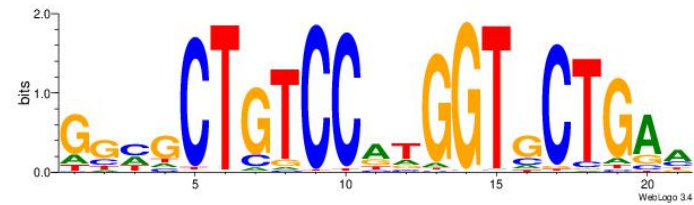
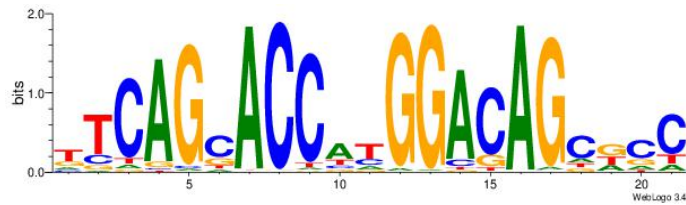


Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 16
Similarity score: 2.07409

Alignment:
TTCAGCACCATGGACAGCKCC----
-----VDBHMAGGTCACCCTGACC Y

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GYGCTGTCCATGGTGCTGAA



Dataset #: 2
 Motif ID: 17
 Motif name: RXRAVDR
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 2.56536

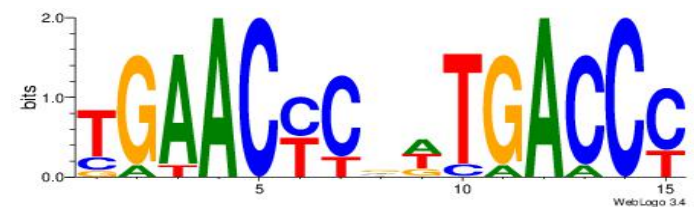
Alignment:

-----GGGTCAWBGRGTTCA
 MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: GGGTCAWBGRGTTCA



Reverse complement motif Consensus sequence: TGAACKCBWTGAC



Dataset #: 2
 Motif ID: 20

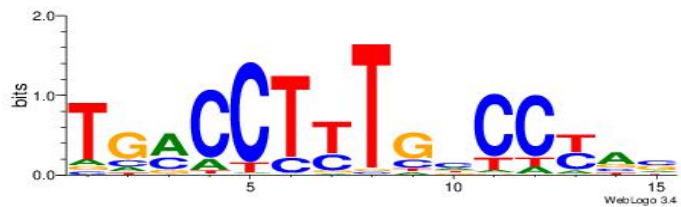
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 3.07055

Alignment:
-----TGRCCTKTGHCKAB
VDBHMAGGTCACCCTGACCY-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKK

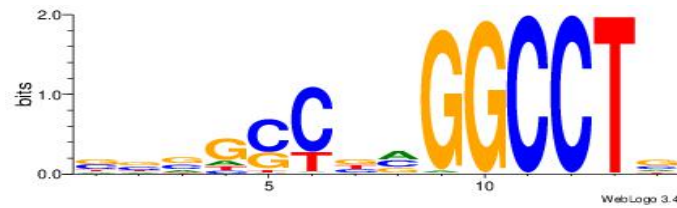


Dataset #: 2
Motif ID: 12
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 3.56429

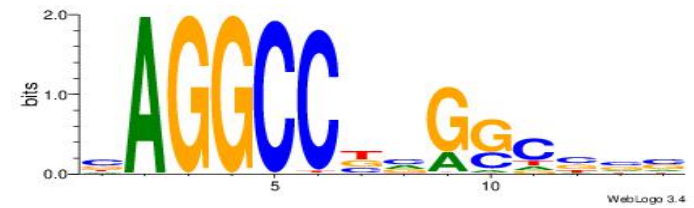
Alignment:

VAGGCCBBGGCVBB-----
-MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



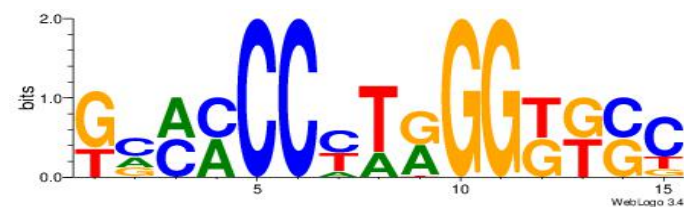
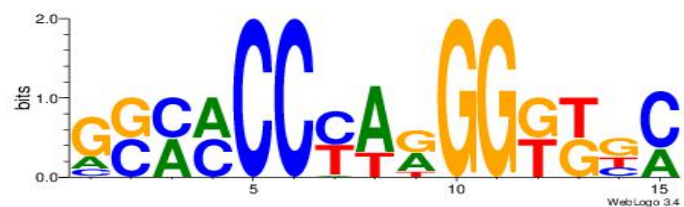
Dataset #:	2
Motif ID:	13
Motif name:	Zfp423
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	13
Similarity score:	3.56489

Alignment:

GSMMCCYARGGKKKC-----
--MGGTCAGGGTGACCTRDBHV

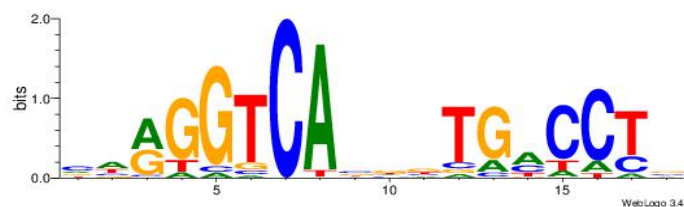
Original motif Consensus sequence: GSMMCCYARGGKKKC

Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

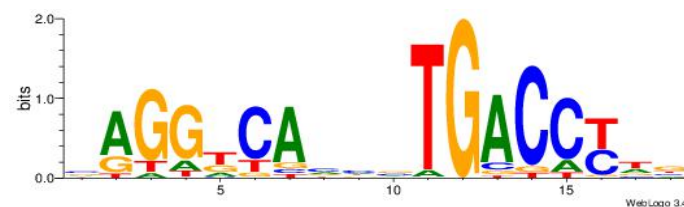


Dataset #: 2 Motif ID: 30 Motif name: ESR2

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



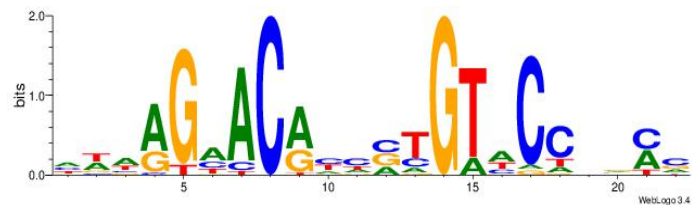
Best Matches for Motif ID 30 (Highest to Lowest)

Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	18
Similarity score:	0.0488603

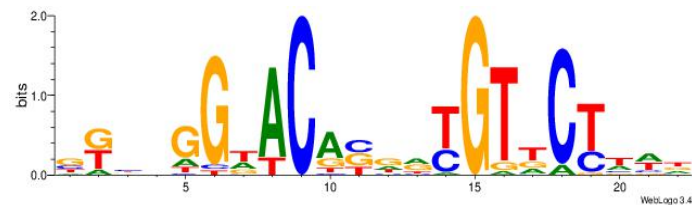
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 --BAGGYCABHBTGACCKHV--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

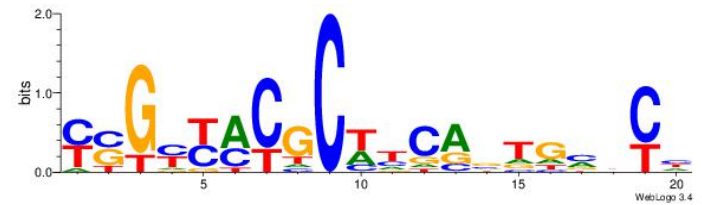
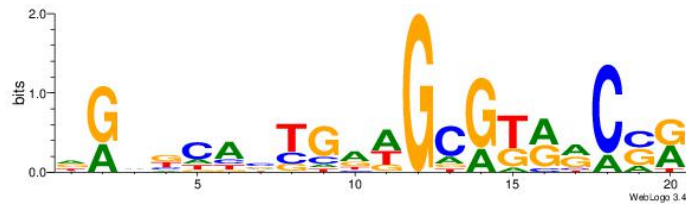


Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	18
Similarity score:	0.0851144

Alignment:
 MSGKKRCGCWDCABTGGBCD
 BAGGYCABHBTGACCKHV--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD

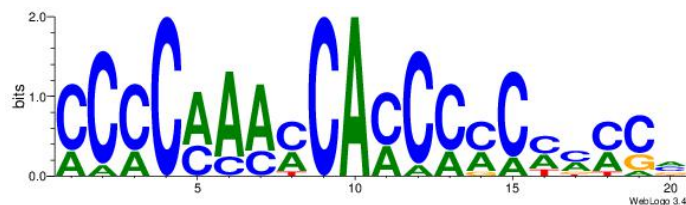


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0903249

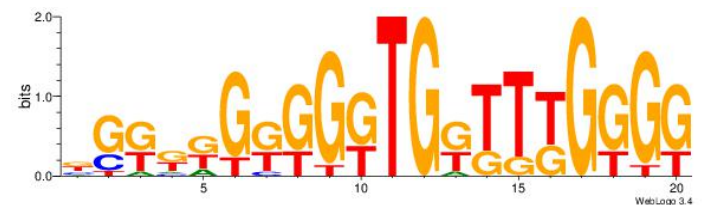
Alignment:

BGRRRGRGGRTGRTTYGGGG
 BAGGYCABHBTGACCKHV--

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



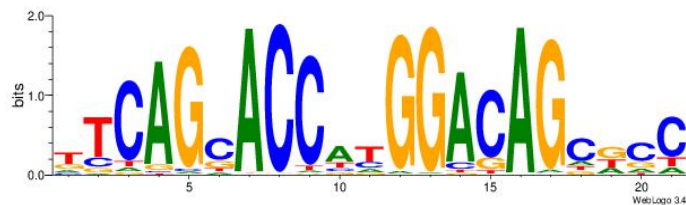
Dataset #: 2

Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0916961

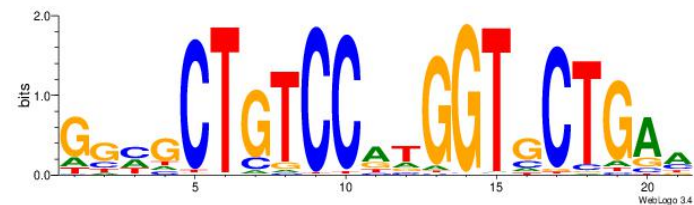
Alignment:

GYGCTGTCCATGGTGCTGAA
 -VHRGGTCABDBTGMCTB--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GYGCTGTCCATGGTGCTGAA

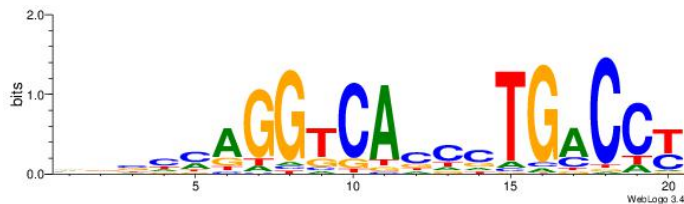


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17

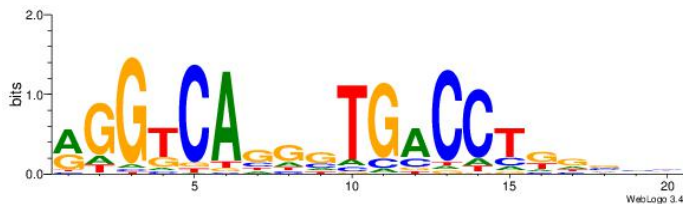
Similarity score: 0.511812

Alignment:
VDBHMAGGTCACCCTGACCY-
---VHRGGTCABDBTGMCTB

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

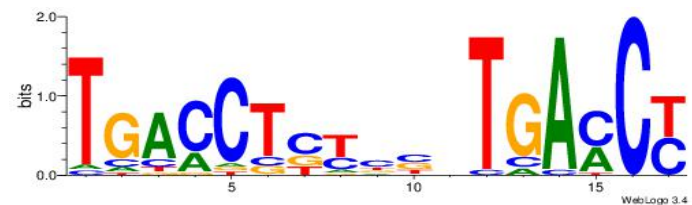
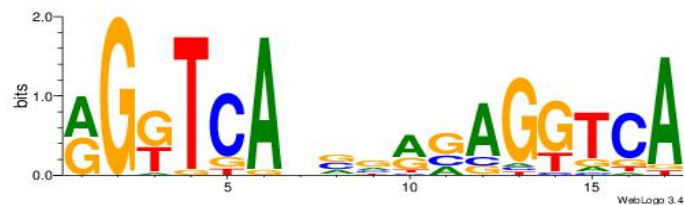


Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.570972

Alignment:
-RGKTCABVVRGAGGTCA
BAGGYCABHBTGACCKHV

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

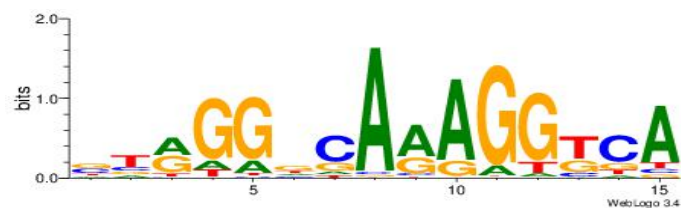


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 1.56699

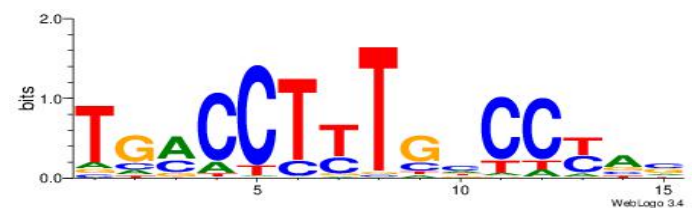
Alignment:

BTRGGDCARAGGKCA---
 VHRGGTCABDBTGMCTB

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



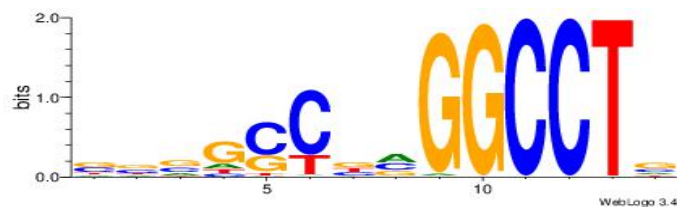
Dataset #: 2
 Motif ID: 12

Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	2.07891

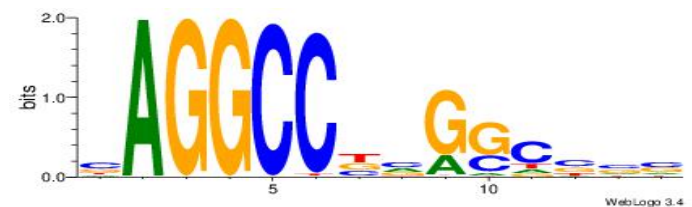
Alignment:

VAGGCCBBGGCVBB-----
BAGGYCABHBTGACCKHV

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Dataset #:	2
Motif ID:	22
Motif name:	NR2F1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	2.08921

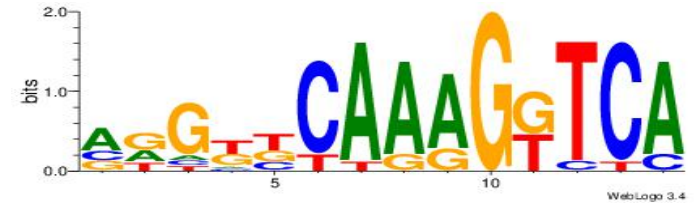
Alignment:

----TGAMCTTTGMMCYT
VHRGGTCABDBTGMCTB

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC



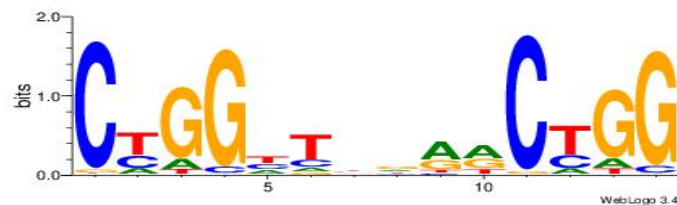
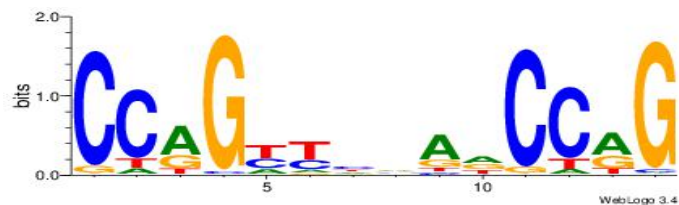
Dataset #:	2
Motif ID:	48
Motif name:	Tcfcp2l1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	2.09109

Alignment:

----CCAGYYHVADCCRG
BAGGYCABHBTGACCKHV

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCT



Dataset #: 2 Motif ID: 31 Motif name: Esrrb

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Best Matches for Motif ID 31 (Highest to Lowest)

Dataset #:	2
Motif ID:	25
Motif name:	Arnt
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

Alignment:

CACGTG

CACGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



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: 3
Number of overlap: 6
Similarity score: 0.0143849

Alignment:

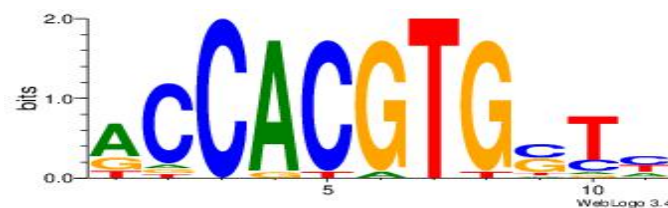
RASCACGTGGT

---CACGTG---

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM

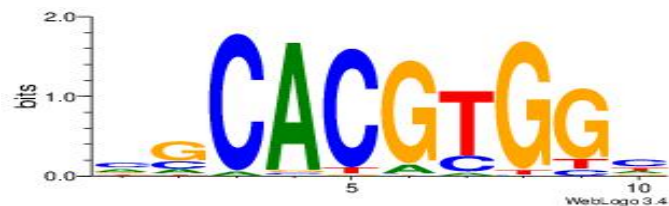


Dataset #: 2
 Motif ID: 38
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0267529

Alignment:

VGCACGTGGH
 --CACGTG--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

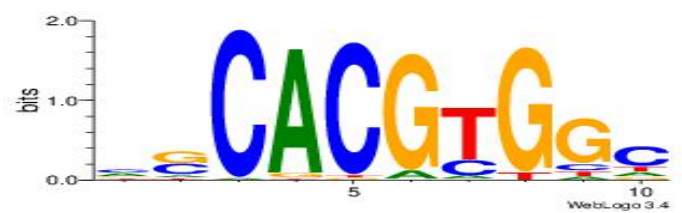


Dataset #: 2
 Motif ID: 40
 Motif name: Mycn
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6

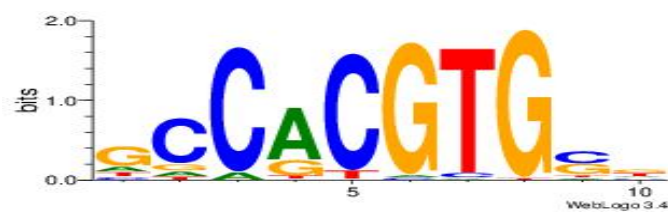
Similarity score: 0.0272641

Alignment:
GCCACGTGSD
--CACGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 2
Motif ID: 33
Motif name: HIF1AARNT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 6
Similarity score: 0.0347756

Alignment:
VBACGTGV
-CACGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV



Dataset #: 2
 Motif ID: 26
 Motif name: ArntAhr
 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: 0.065625

Alignment:

YGCGTG

CACGTG

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Dataset #: 2
 Motif ID: 14

Motif name:	ZEB1
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:	0.0689533

Alignment:
HAGGTG
CACGTG

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



Dataset #:	2
Motif ID:	28
Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0784722

Alignment:

HGCGTGGGCGK

CACGTG-----

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



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:	6
Similarity score:	0.0854167

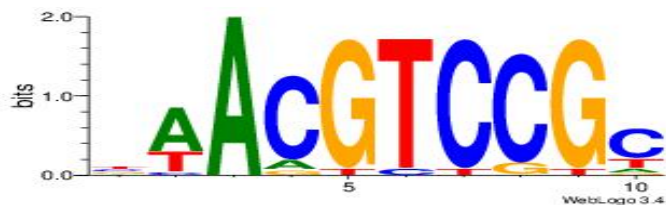
Alignment:

BAACGTCCGC

-CACGTG----

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV



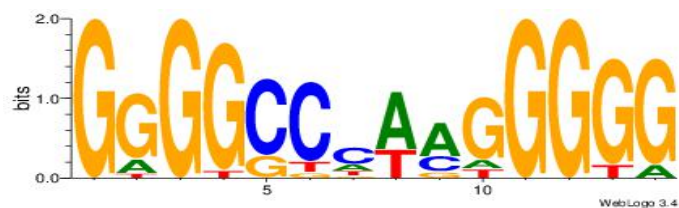
Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.105093

Alignment:

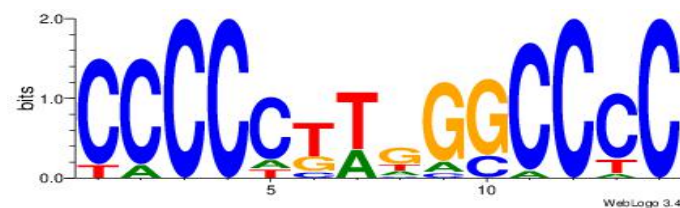
GGGGCCCAAGGGGG

-----CACGTG--

Original motif Consensus sequence: GGGGCCCAAGGGGG

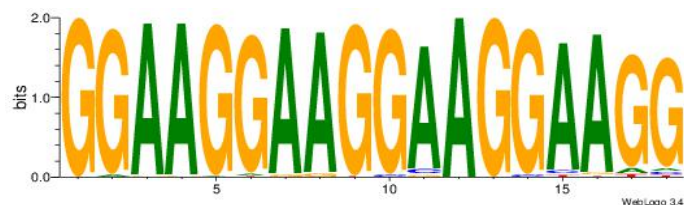


Reverse complement motif Consensus sequence: CCCCCTTGGGCC

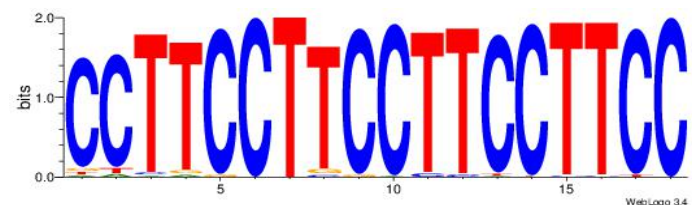


Dataset #: 2 Motif ID: 32 Motif name: EWSR1-FLI1

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC



Best Matches for Motif ID 32 (Highest to Lowest)

Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	12
Similarity score:	1.09472

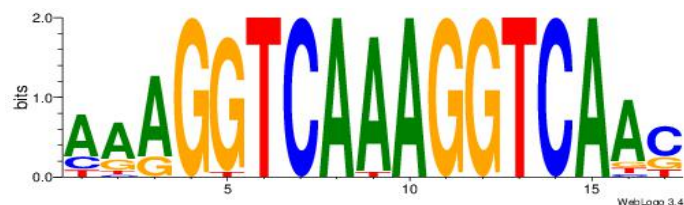
Alignment:

```

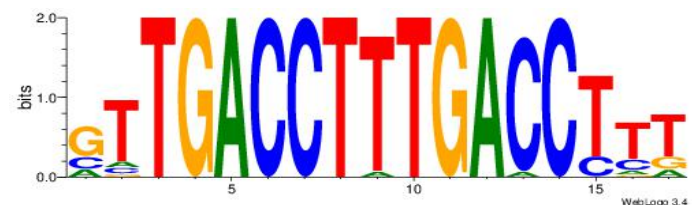
-----AAAGGTCAAAGGTCAAC
GGAAGGAAGGAAGGAAGG-----

```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

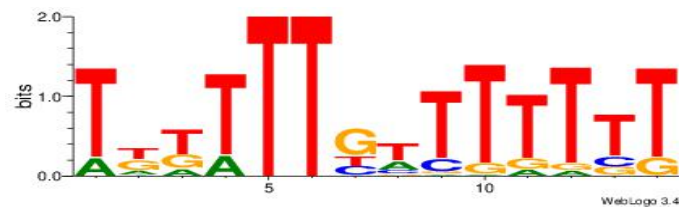


Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 1.1007

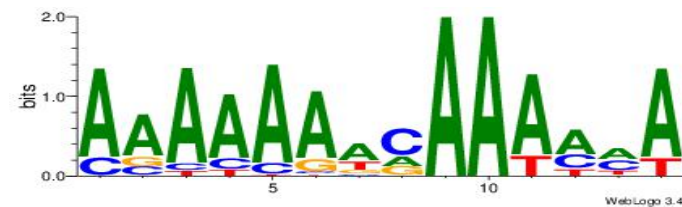
Alignment:

-----TKKTTTGTTTTTTT
 CCTTCCTTCCTTCCTTCC--

Original motif Consensus sequence: TKKTTTGTTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR

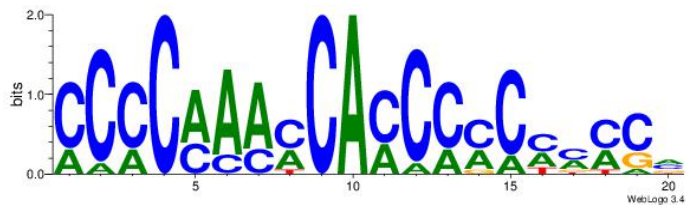


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11

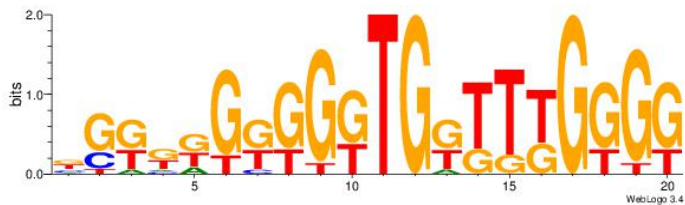
Number of overlap: 10
Similarity score: 2.09833

Alignment:
-----CCCCMAAMCAMCCMCMMMCV
CCTTCCTTCCTTCCTTCC-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV



Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG

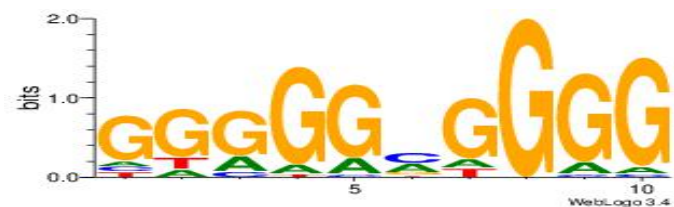
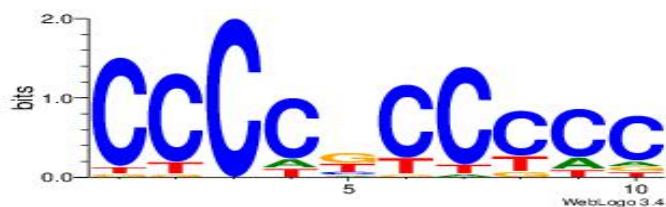


Dataset #: 2
Motif ID: 16
Motif name: SP1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 2.58264

Alignment:
GGGGGYGGGG-----
-GGAAGGAAGGAAGGAAGG

Original motif Consensus sequence: CCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG



Dataset #: 2
 Motif ID: 37
 Motif name: MIZF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 3.0896

Alignment:

-----BAACGTCCGC
 CCTTCCTTCCTTCCTTCC--

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



Dataset #: 1
 Motif ID: 7

Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	3.09107

Alignment:

```

-----CCCRCCCC
CCTTCCTTCCTTCCTTC

```

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG

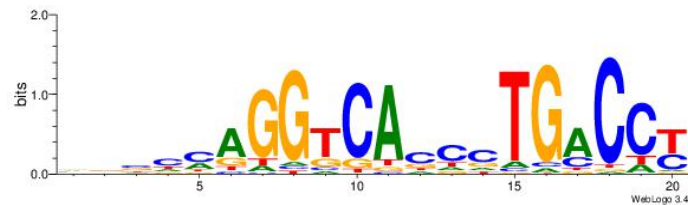


Dataset #:	2
Motif ID:	29
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	13
Number of overlap:	8
Similarity score:	3.09836

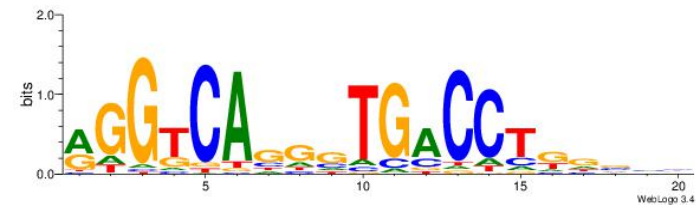
Alignment:

MGGTCAGGGTGACCTRDBHV-----
 -----GGAAGGAAGGAAGGAAGG

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence:
 MGGTCAGGGTGACCTRDBHV



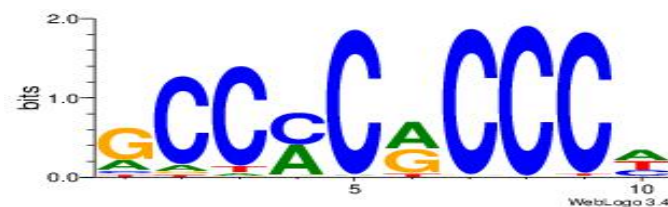
Dataset #:	2
Motif ID:	36
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	3.10206

Alignment:

-----DGGGYGKGGC
 GGAAGGAAGGAAGGAAGG--

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 3.55161

Alignment:

-----AGSCWGG
 GGAAGGAAGGAAGGAAGG

Original motif Consensus sequence: AGSCWGG



Reverse complement motif Consensus sequence: CCWGSCT



Dataset #: 2
 Motif ID: 46

Motif name: RORA_1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 7
 Similarity score: 3.58428

Alignment:

TGACCTDVWT-----
 ---CCTTCCTTCCTTCCTTCC

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT



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

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Best Matches for Motif ID 33 (Highest to Lowest)

Dataset #: 2
 Motif ID: 40
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0228069

Alignment:

GCCACGTGSD

-VBACGTGV-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



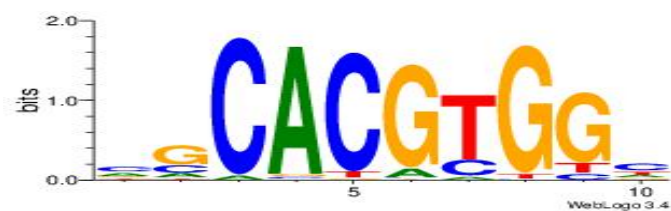
Dataset #: 2
 Motif ID: 38
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8

Similarity score: 0.0249459

Alignment:

DCCACGTGCV
-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



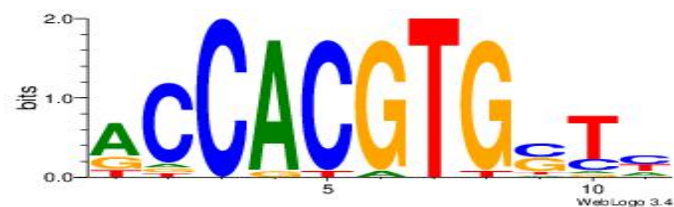
Dataset #: 2
Motif ID: 39
Motif name: MYCMAX
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0254922

Alignment:

ACCACGTGSTM
-VCACGTBV--

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM



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: 3
 Number of overlap: 8
 Similarity score: 0.0482171

Alignment:

GCGGACGTTV

--VCACGTBV

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



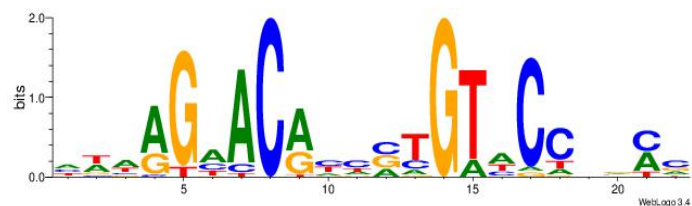
Dataset #: 2
 Motif ID: 24

Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	11
Number of overlap:	8
Similarity score:	0.0533654

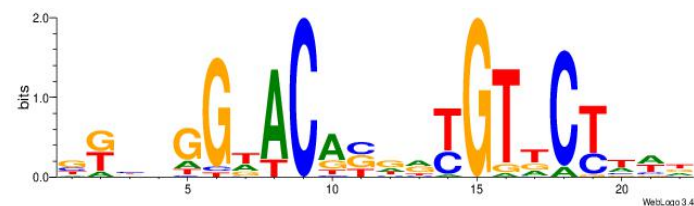
Alignment:

```
VRVDGGHACAVDDKGTHTCDWH
----VBACGTGV-----
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHTCDWH



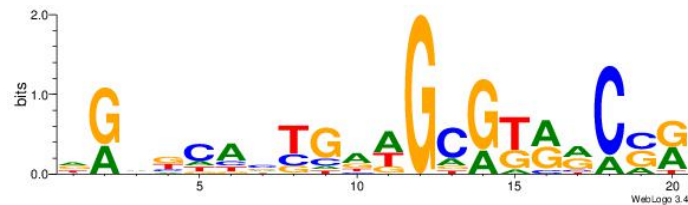
Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	8
Similarity score:	0.0661859

Alignment:

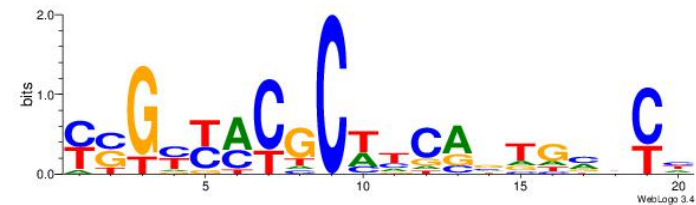
MSGKKRCGCWDCABTGGBCD

-----VCACGTBV-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGGBCD



Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	8
Number of overlap:	8
Similarity score:	0.0666776

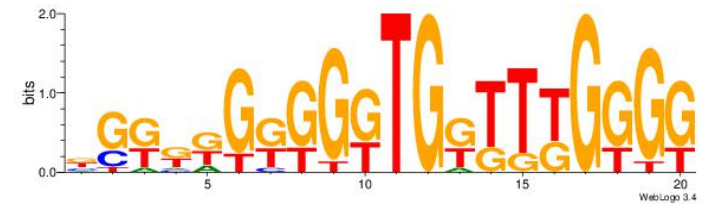
Alignment:

CCCCMAAMCAMCCMCMMMC

-----VCACGTBV-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC

Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGG



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:	3
Number of overlap:	8
Similarity score:	0.0703926

Alignment:

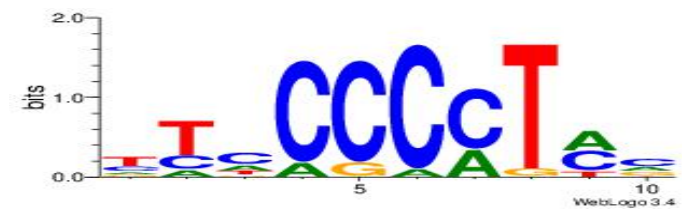
BKAGGGGDAD

VBACGTGV--

Original motif Consensus sequence: BKAGGGGDAD



Reverse complement motif Consensus sequence: BTHCCCCTYB



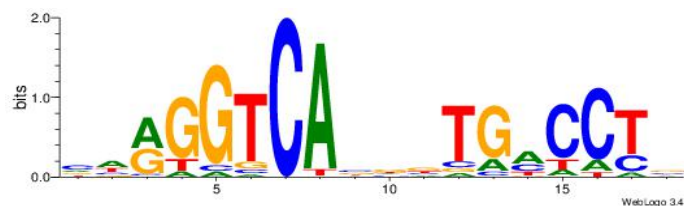
Dataset #: 2
Motif ID: 30

Motif name:	ESR2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	8
Similarity score:	0.0716055

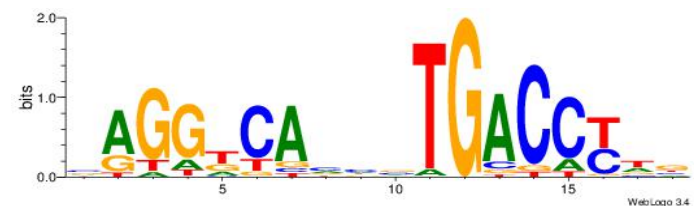
Alignment:

BAGGYCABHBTGACCKHV
 -----VBACGTGV-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



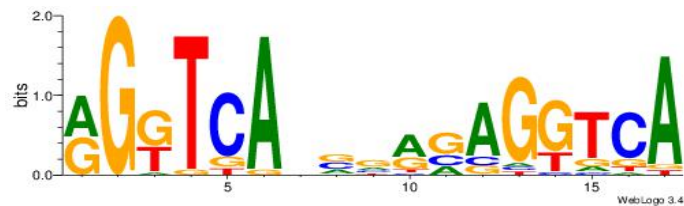
Dataset #:	2
Motif ID:	47
Motif name:	RXRRAR_DR5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0726789

Alignment:

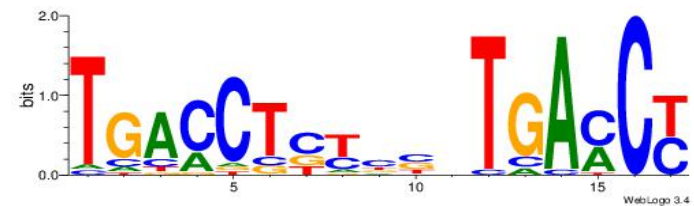
TGACCTCKVVBTGAYCK

-----VBACGTGV----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

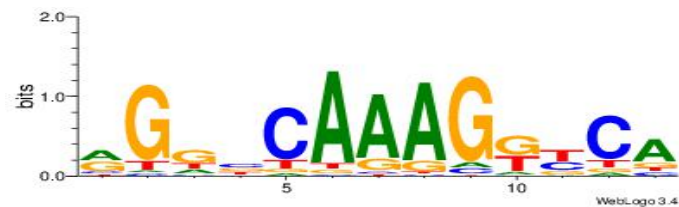


Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

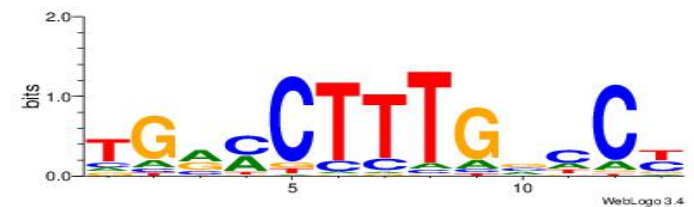


Dataset #: 2 Motif ID: 34 Motif name: HNF4A

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCK



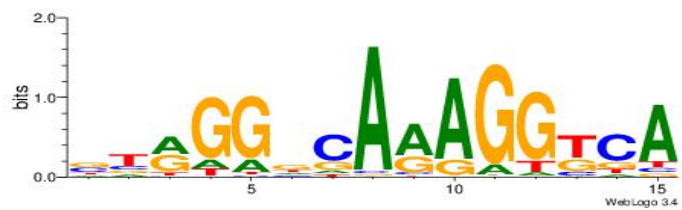
Best Matches for Motif ID 34 (Highest to Lowest)

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

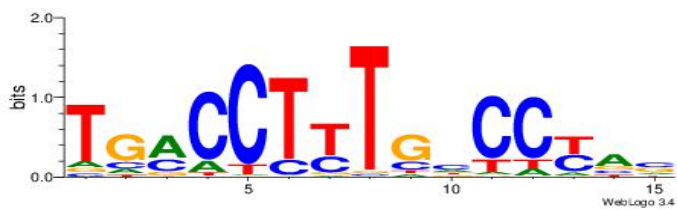
Position number: 3
Number of overlap: 13
Similarity score: 0

Alignment:
TGRCCTKTGHCKAB
TGMYYCTTTGBCK--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKA

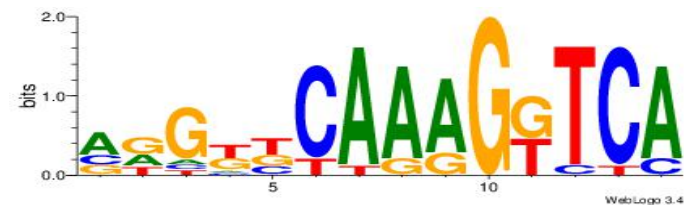


Dataset #: 2
Motif ID: 22
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0227413

Alignment:
TGAMCTTTGMMCYT
-TGMYYCTTTGBCK

Original motif Consensus sequence: TGAMCTTTGMMCYT

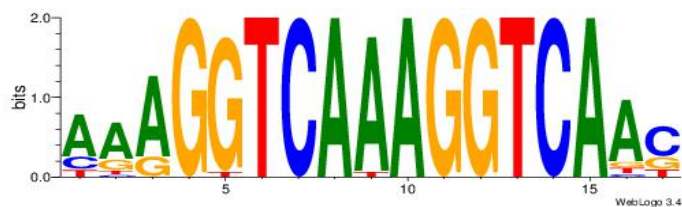
Reverse complement motif Consensus sequence: AKGYCAAAGRTC



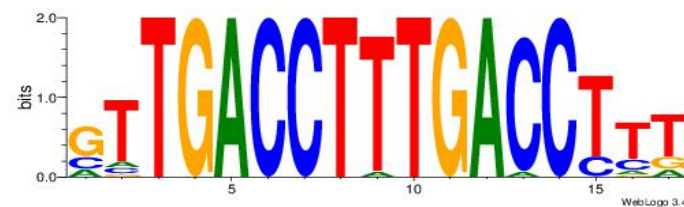
Dataset #: 2
 Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0423023

Alignment:
 AAAGGTCAAAGGTCAAC
 --RGGBCAAAGKYCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



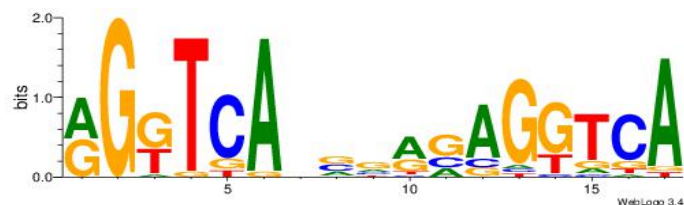
Dataset #: 2

Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.048852

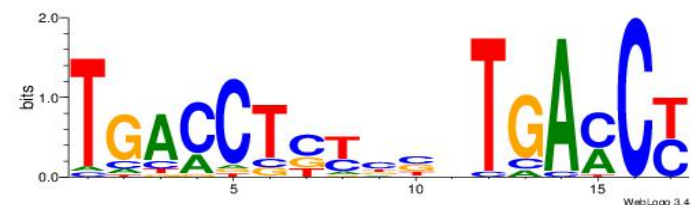
Alignment:

TGACCTCKVVB TGAYCK
 TGM YCTTTGB CCK----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

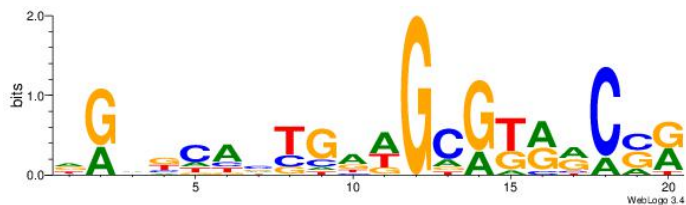


Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 13

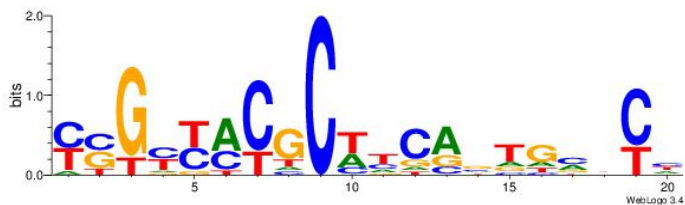
Similarity score: 0.063924

Alignment:
MSGKKRCGCWDCABTGGBCD
-----RGGBCAAAGKYCA

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGGBCD

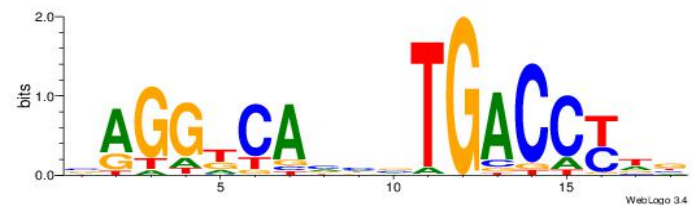
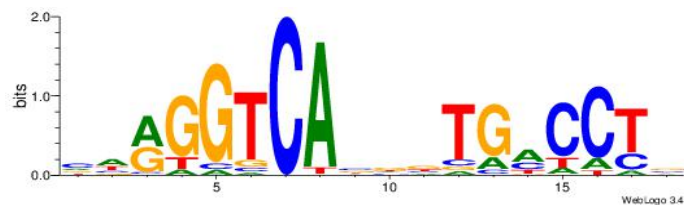


Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0671615

Alignment:
VHRGGTCABDBTGMCTB
--RGGBCAAAGKYCA--

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

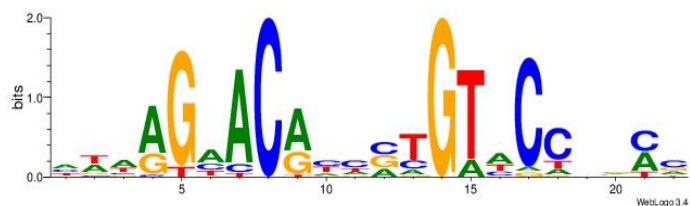


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.067775

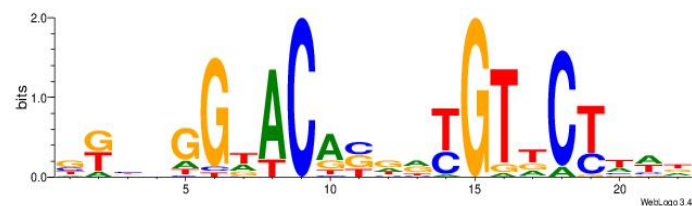
Alignment:

VRVDGGHACAVDDKGTHTDWH
 -----TGM YCTTTGB CCK---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHTDWH



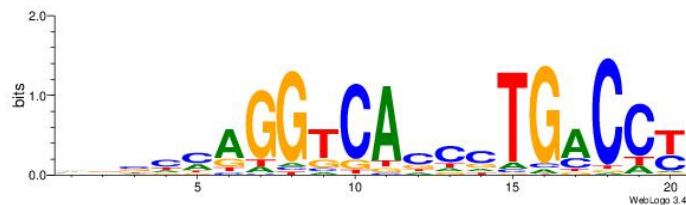
Dataset #: 2

Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0711137

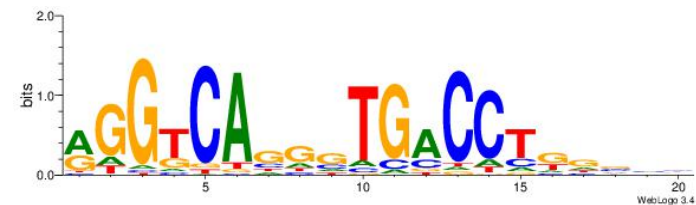
Alignment:

VDBHMAGGTCACCCTGACCY
 TGM YCTTTGBCK-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13

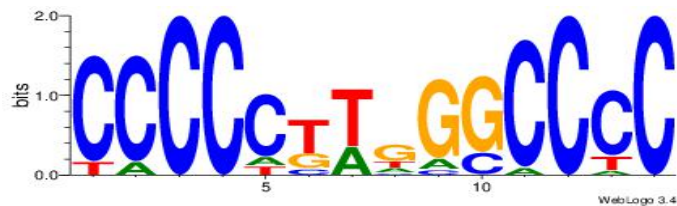
Similarity score: 0.0714266

Alignment:
GGGGCCCAAGGGG
-RGGBCAAAGKYCA

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

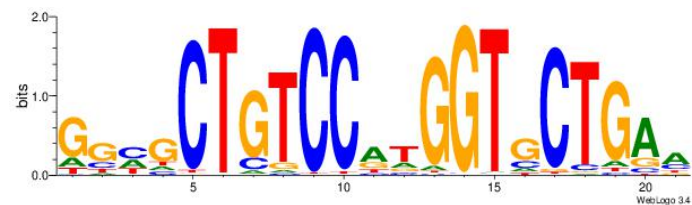
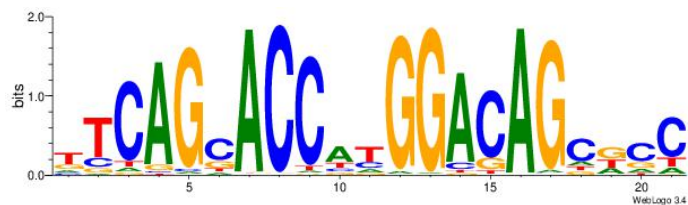


Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 13
Similarity score: 0.0741922

Alignment:
GGYGCTGTCCATGGTGCTGAA
-----TGM YCTTTGBCK---

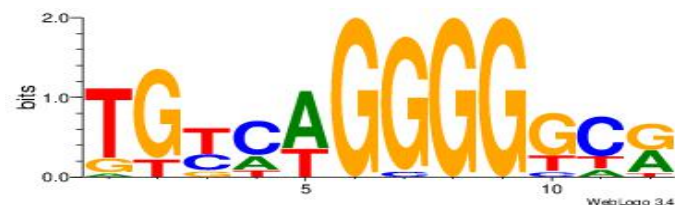
Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



Dataset #: 2 Motif ID: 35 Motif name: INSM1

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCTGMCA

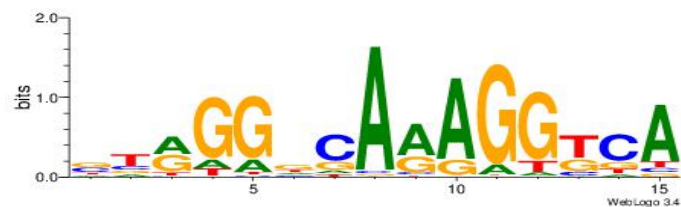


Best Matches for Motif ID 35 (Highest to Lowest)

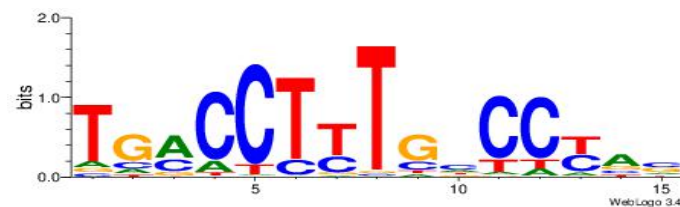
Dataset #:	2
Motif ID:	20
Motif name:	PPARGRXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	12
Similarity score:	0.0472454

Alignment:
 BTRGGDCARAGGKCA
 ---TGYCAGGGGGCR

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

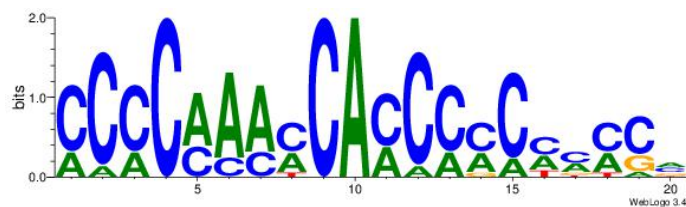


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0499162

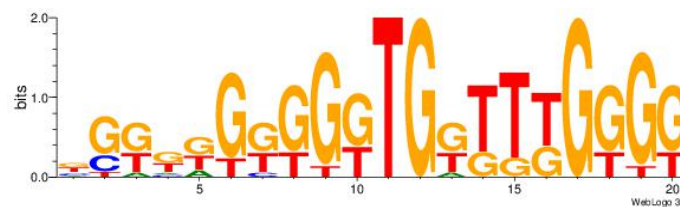
Alignment:

BGRRRGRGGRTGRTTYGGGG
 -----TGYCAGGGGGCR

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

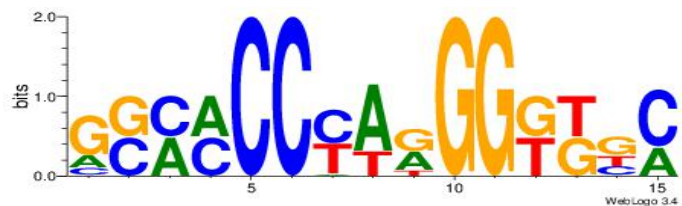


Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0538619

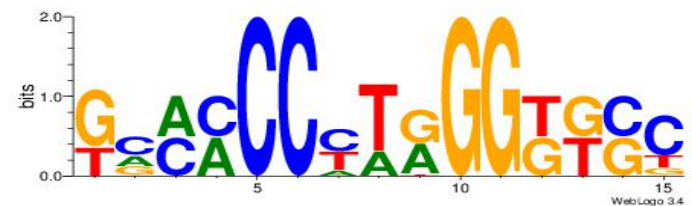
Alignment:

GYRYCCMTKGGYRSC
 -MGCCCCCTGMCA--

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



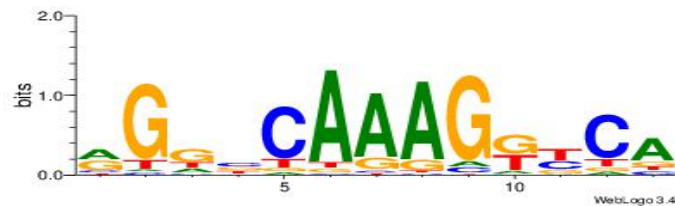
Dataset #: 2
 Motif ID: 34
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12

Similarity score: 0.0551858

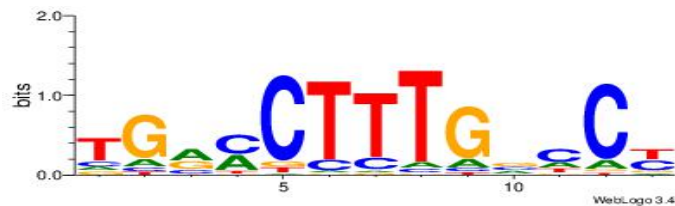
Alignment:

RGGBCAAAGKYCA
-TGYCAGGGGGCR

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYYCTTTGBCCK



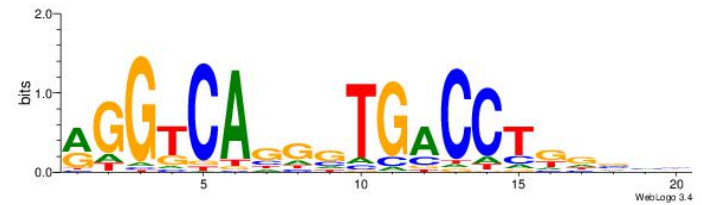
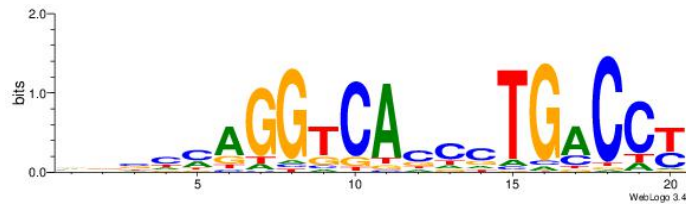
Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0630846

Alignment:

VDBHMAGGTCACCCTGACCY
-TGYCAGGGGGCR-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

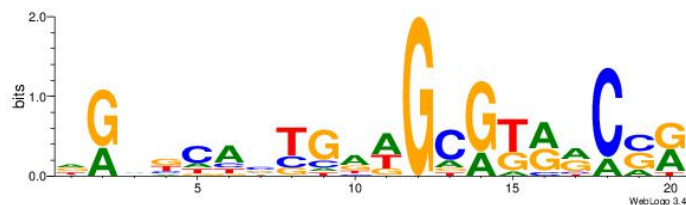


Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0679087

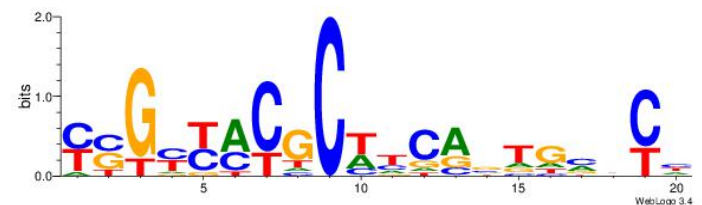
Alignment:

DGVBCABTGDWGCGRRCR
 -----TGYCAGGGGGCR----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD



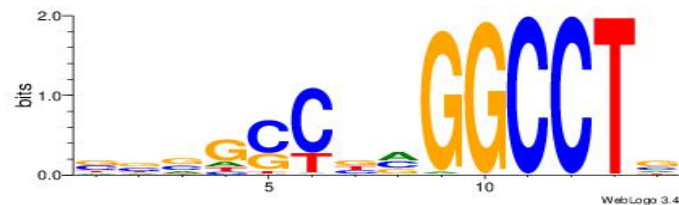
Dataset #: 2

Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.069037

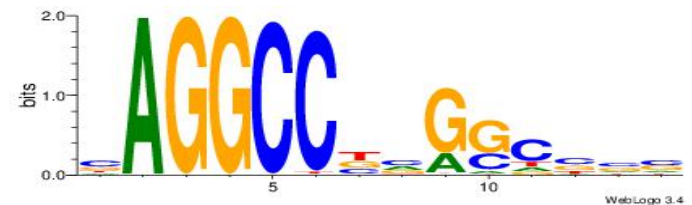
Alignment:

VAGGCCBBGGCVBB
 -MGCCCCCTGMCA-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



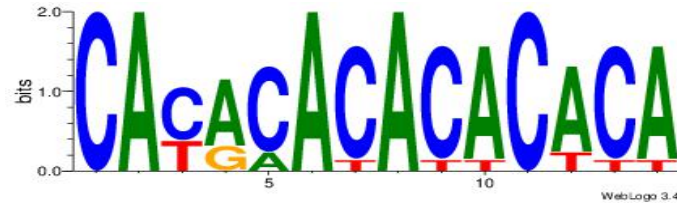
Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0692502

Alignment:

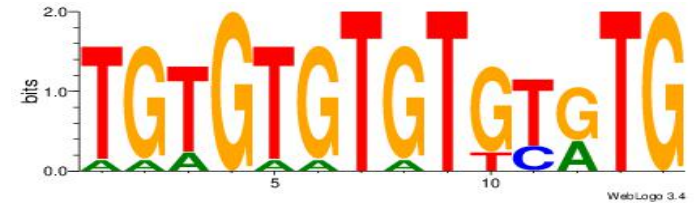
CAYACACACACA

--MGCCCCCTGMCA

Original motif Consensus sequence: CAYACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKT



Dataset #:	2
Motif ID:	43
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0696795

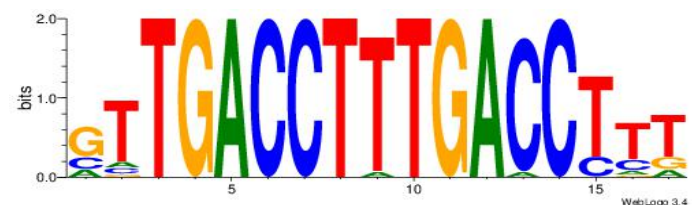
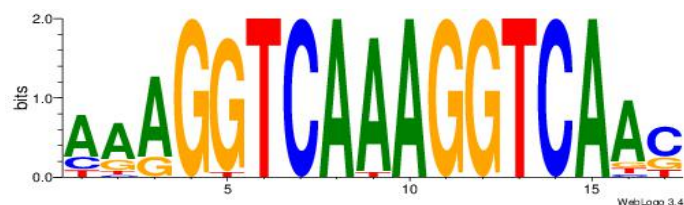
Alignment:

AAAGGTCAAAGGTCAAC

---TGYCAGGGGGCR--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0705128

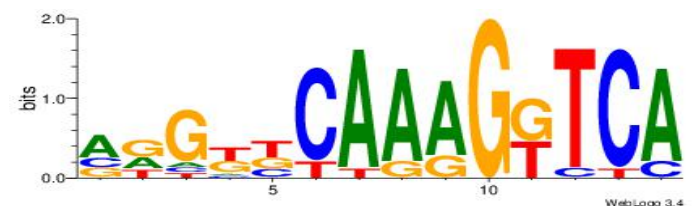
Alignment:

TGAMCTTTGMMCYT
 --MGCCCCCTGMCA

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

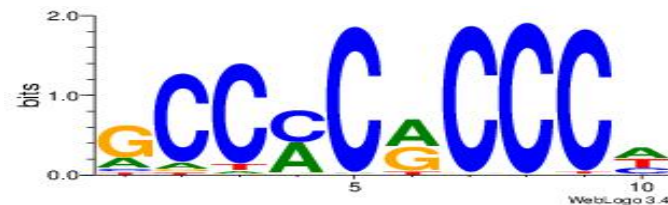


Dataset #: 2 Motif ID: 36 Motif name: Klf4

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Best Matches for Motif ID 36 (Highest to Lowest)

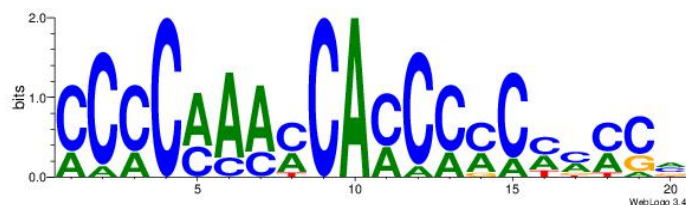
Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.065355

Alignment:

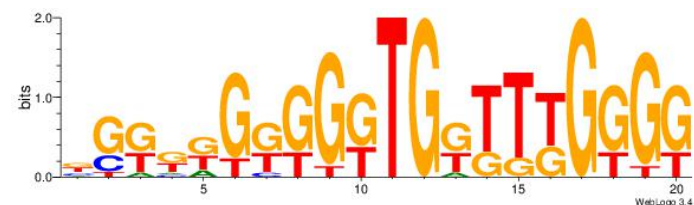
```

BGRRRGRGGRTGRTTYGGGG
-----DGGGYGKGGC
  
```

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

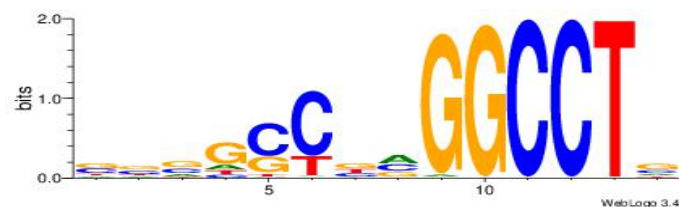


Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0734166

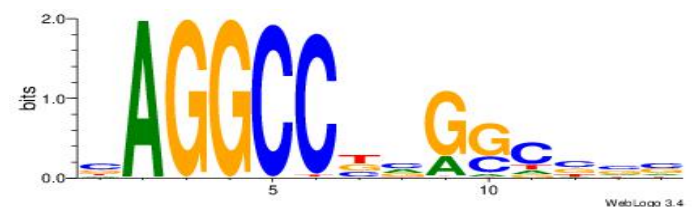
Alignment:

BBVGCCBVGGCCTV
 -GCCYCMCCCD---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



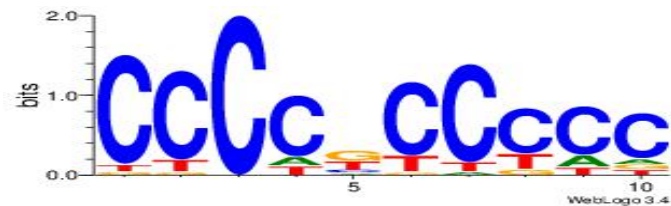
Dataset #: 2
 Motif ID: 16
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0773711

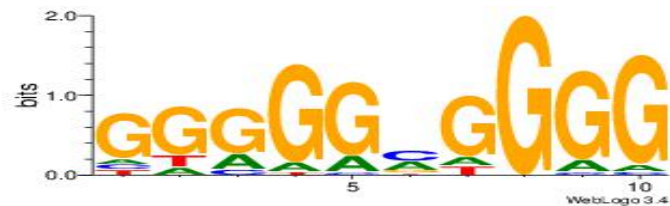
Alignment:

GGGGGYGGGG
DGGGYGKGGC

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



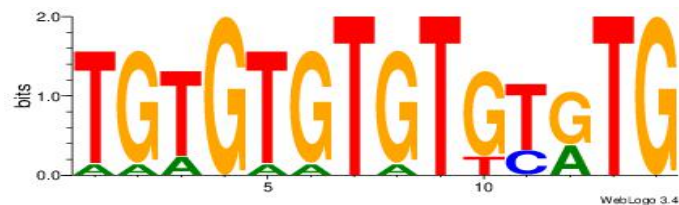
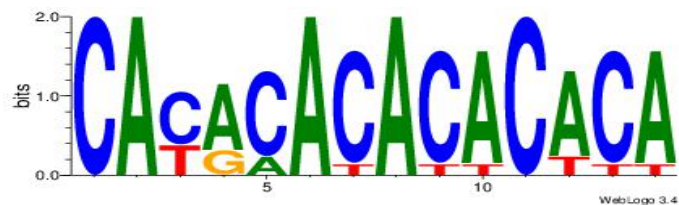
Dataset #: 1
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0781179

Alignment:

CAYACACACACACA
--GCCYCMCCCD--

Original motif Consensus sequence: CAYACACACACACA

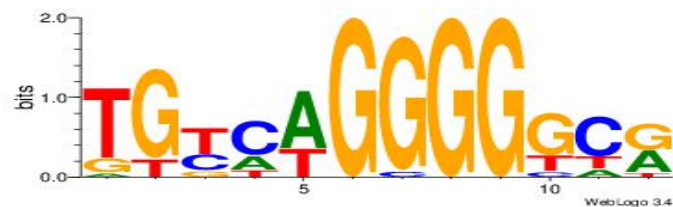
Reverse complement motif Consensus sequence: TGTGTGTGTGKT



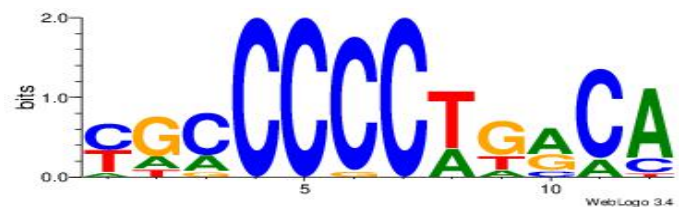
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0785684

Alignment:
 MGCCCCCTGMCA
 --GCCYCMCCCD

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



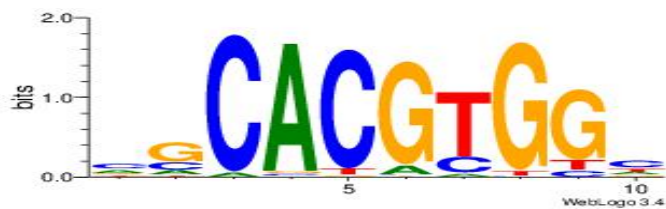
Dataset #: 2
 Motif ID: 38

Motif name:	Myc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0797423

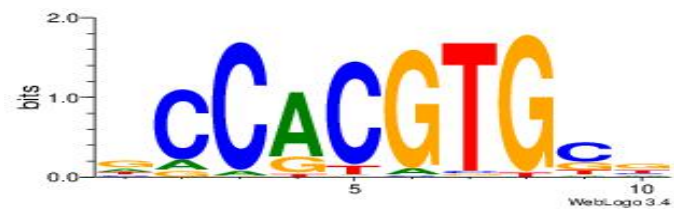
Alignment:

VGCACGTGGH
DGGGYGKGGC

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



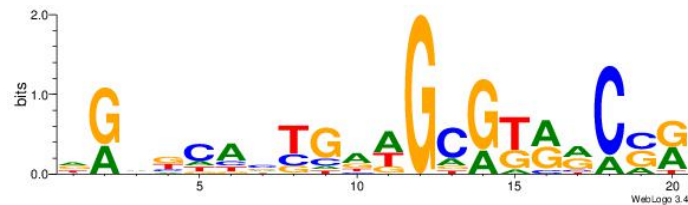
Dataset #:	2
Motif ID:	45
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.0806175

Alignment:

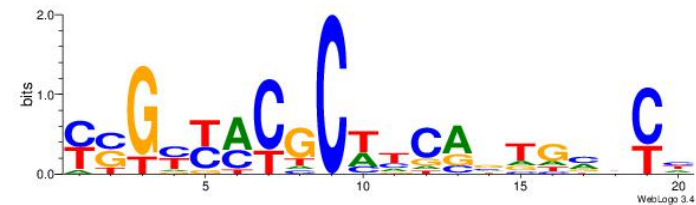
DGVBCABTGDWGCGRRCR

-----DGGGYGKGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBCD



Dataset #:	2
Motif ID:	40
Motif name:	Mycn
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.080695

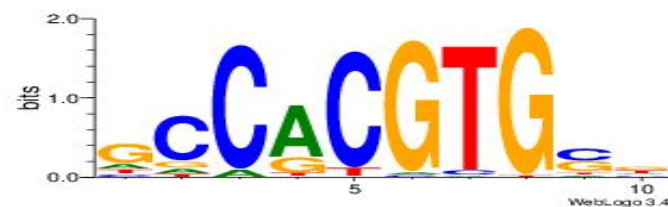
Alignment:

HSCACGTGGC

DGGGYGKGGC

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

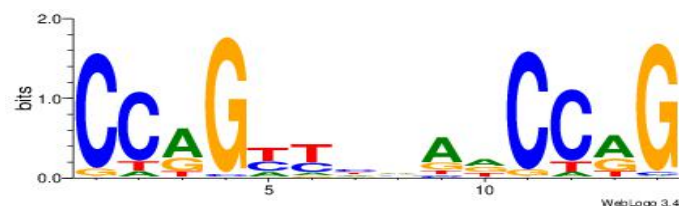


Dataset #: 2
 Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0807235

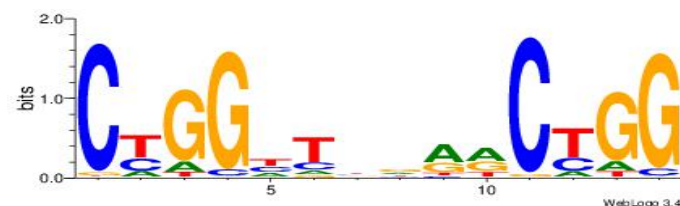
Alignment:

CCAGYYHVADCCRG
 ---GCCYCMCCCD-

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTC



Dataset #: 2
 Motif ID: 28

Motif name: Egr1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.089515

Alignment:

HCGTG GGGCGK
 DGGGYGKGGC-

Original motif Consensus sequence: HCGTG GGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH



Dataset #: 2 Motif ID: 37 Motif name: MIZF

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



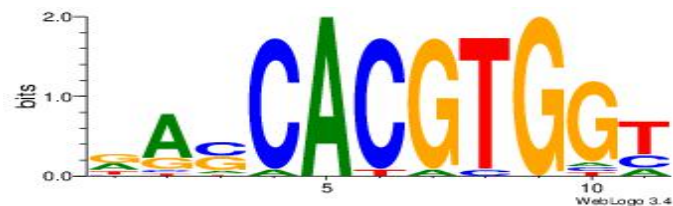
Best Matches for Motif ID 37 (Highest to Lowest)

Dataset #: 2
 Motif ID: 39
 Motif name: MYCMAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0390724

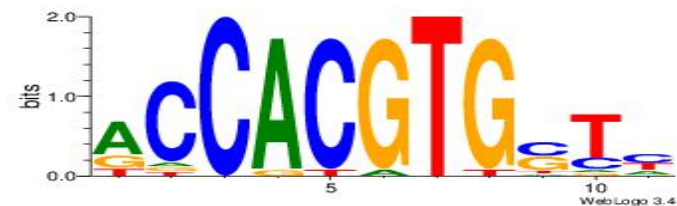
Alignment:

ACCACGTGSTM
 -BAACGTCCGC

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



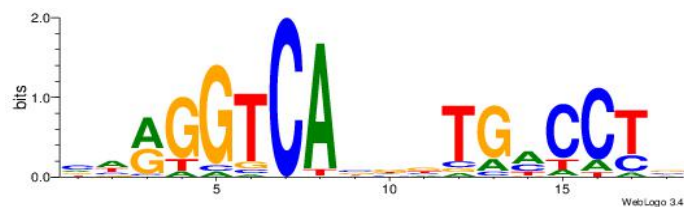
Dataset #: 2
 Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0399477

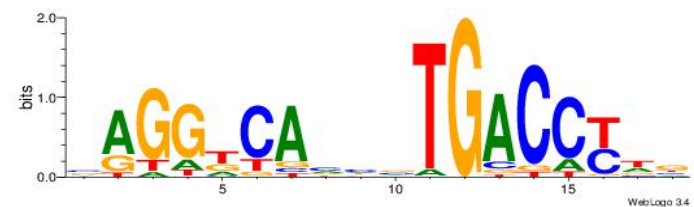
Alignment:

BAGGYCABHBTGACCKHV
-----GCGGACGTTV

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV



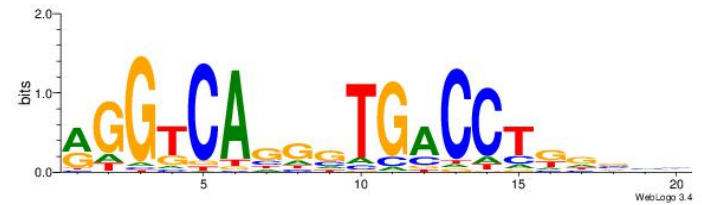
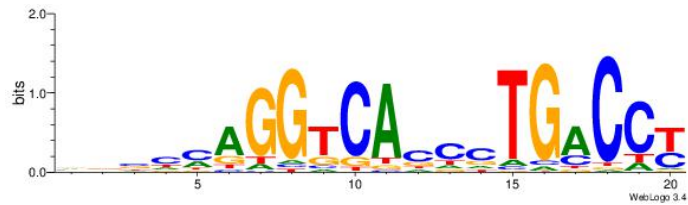
Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 10
Similarity score: 0.0408267

Alignment:

VDBHMAGGTCACCCTGACCY
---BAACGTCCGC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

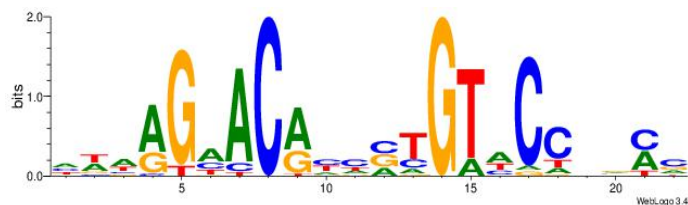


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0432688

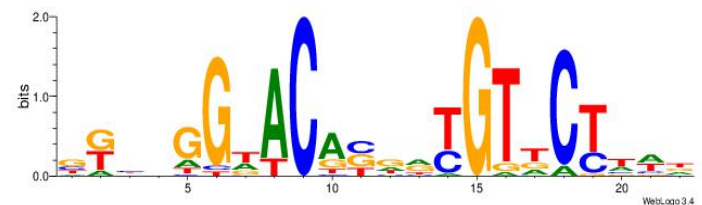
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 -----BAACGTCCGC---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



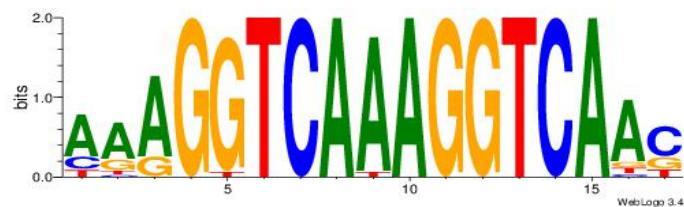
Dataset #: 2

Motif ID: 43
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0439771

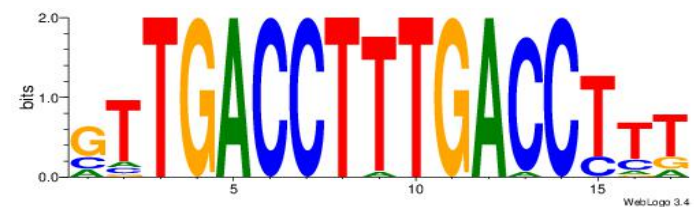
Alignment:

AAAGGTCAAAGGTCAAC
 -----BAACGTCCGC

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

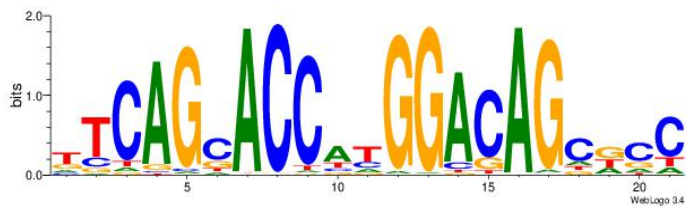


Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10

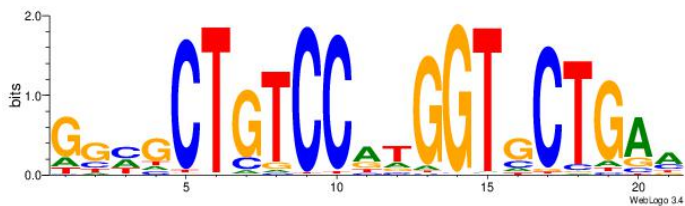
Similarity score: 0.0501848

Alignment:
GGYGCTGTCCATGGTGCTGAA
-----BAACGTCCGC--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA

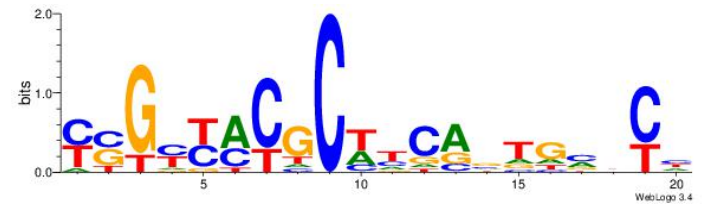
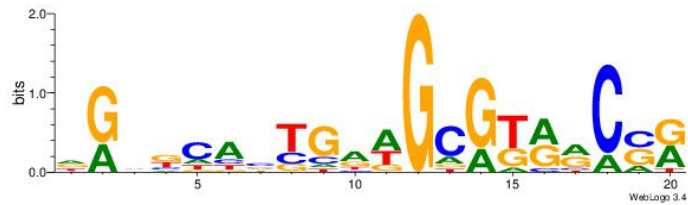


Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 10
Number of overlap: 10
Similarity score: 0.0576438

Alignment:
MSGKKRCGCWDCABTGBBCD
-GCGGACGTTV-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



Dataset #: 2
 Motif ID: 38
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.535015

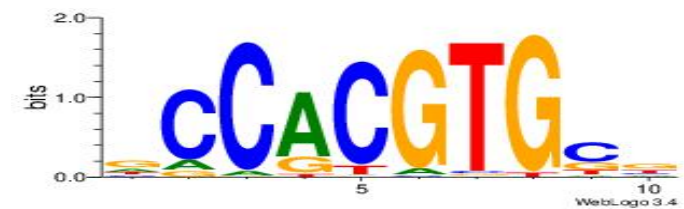
Alignment:

DCCACGTGCV-
 -BAACGTCCGC

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 2
 Motif ID: 28

Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.537968

Alignment:
 -HCGTG GCGK
 BAACGTCCGC--

Original motif Consensus sequence: HCGTG GCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH

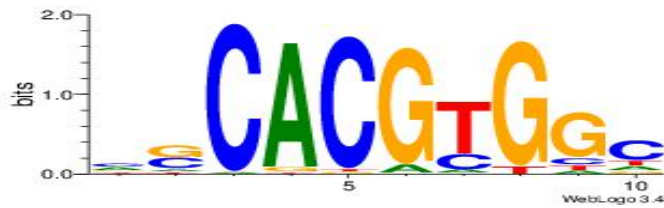


Dataset #:	2
Motif ID:	40
Motif name:	Mycn
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0.540549

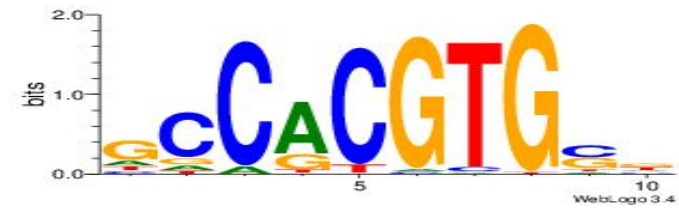
Alignment:

GCCACGTGSD-
-BAACGTCCGC

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

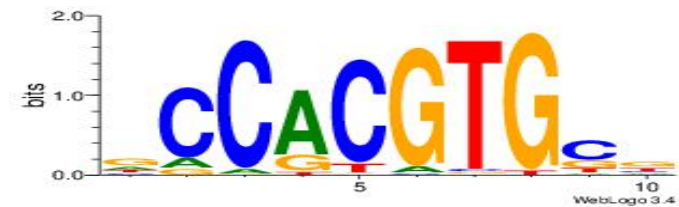


Dataset #: 2 Motif ID: 38 Motif name: Myc

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #:	2
Motif ID:	40
Motif name:	Mycn
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

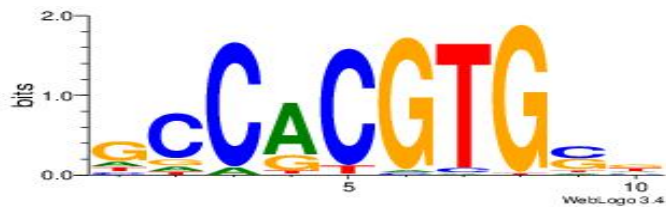
Number of overlap: 10
Similarity score: 0

Alignment:
GCCACGTGSD
DCCACGTGCV

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

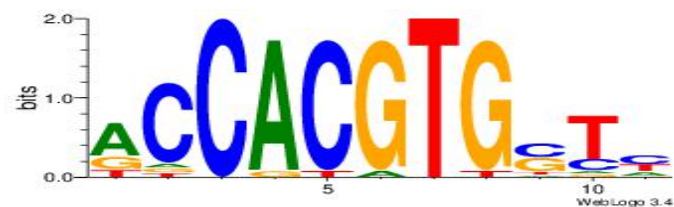


Dataset #: 2
Motif ID: 39
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0209359

Alignment:
RASCACGTGGT
-VGCACGTGGH

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM



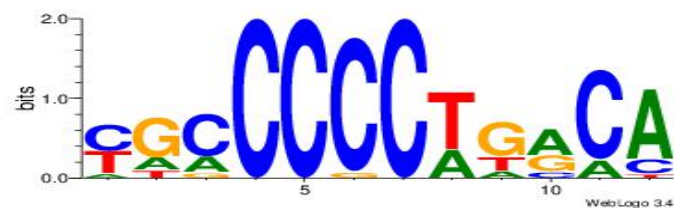
Dataset #: 2
 Motif ID: 35
 Motif name: INSM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0844808

Alignment:
 MGCCCCCTGMCA
 -DCCACGTGCV-

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



Dataset #: 2
 Motif ID: 36

Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0883745

Alignment:

DGGGYGKGGC
VGCACGTGGH

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



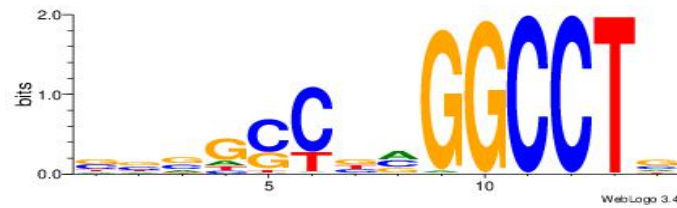
Dataset #:	2
Motif ID:	12
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.0925451

Alignment:

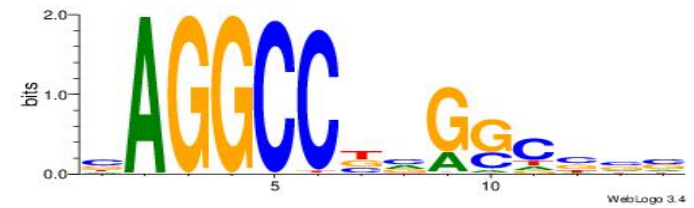
VAGGCCBBGGCVBB

---DCCACGTGCV-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Dataset #:	2
Motif ID:	21
Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.0930375

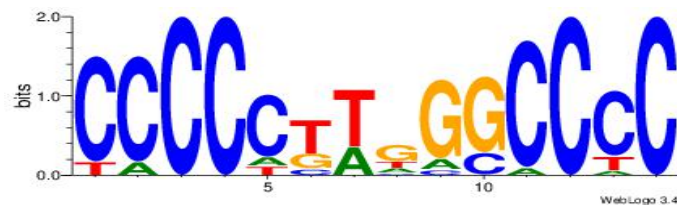
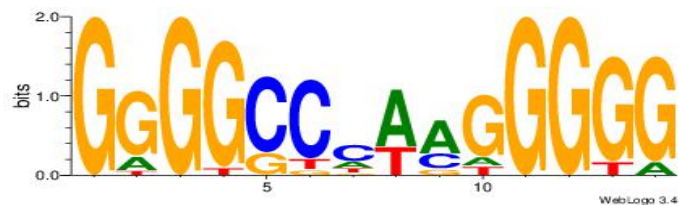
Alignment:

CCCCCTTGGGCCCC

----VGCACGTGGH

Original motif Consensus sequence: GGGGCCCAAGGGGG

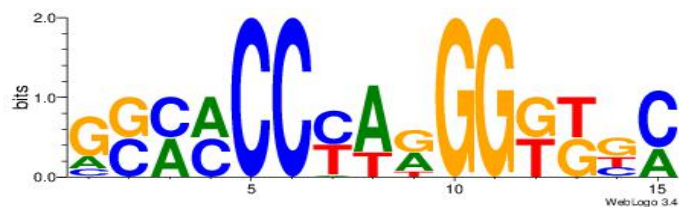
Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC



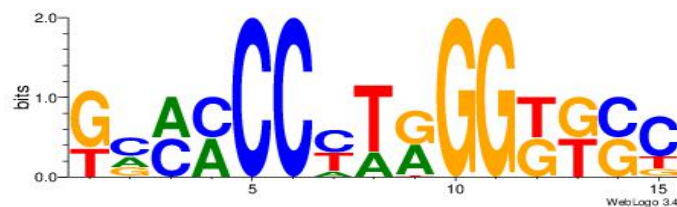
Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0930519

Alignment:
 GYRYCCMTKGGYRSC
 ---DCCACGTGCV--

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



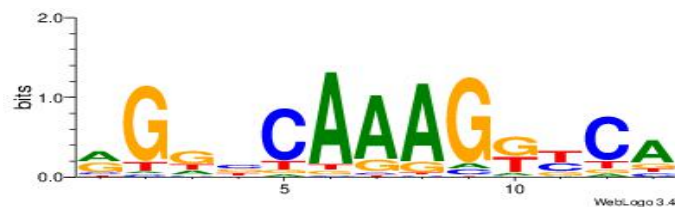
Dataset #: 2
 Motif ID: 34

Motif name:	HNF4A
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0934488

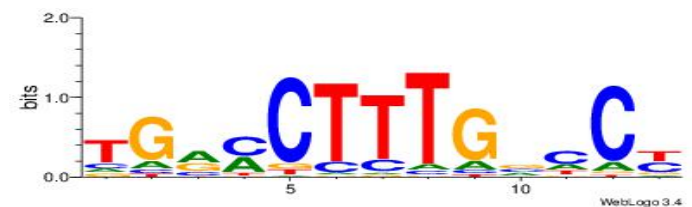
Alignment:

```
TGMYCTTTGBCK
---VGCACGTGGH
```

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCK

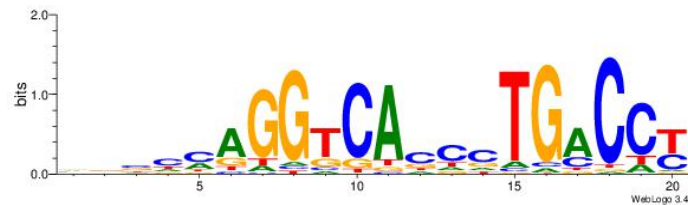


Dataset #:	2
Motif ID:	29
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.0940438

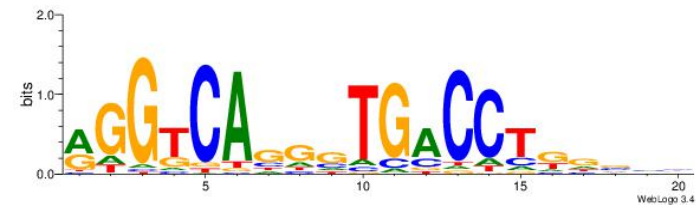
Alignment:

MGGTCAGGGTGACCTRDBHV
-----DCCACGTGCV--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV



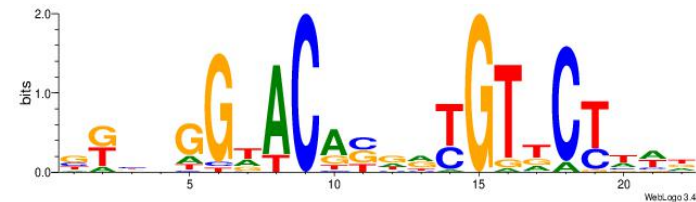
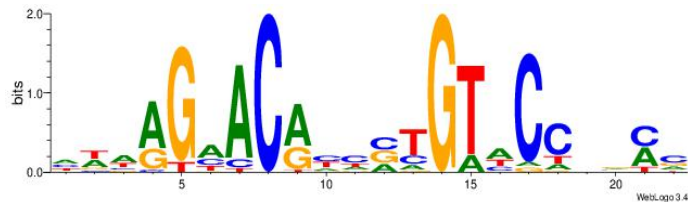
Dataset #:	2
Motif ID:	24
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	10
Similarity score:	0.0966137

Alignment:

HWDAGHACRHHVTGTHCCHVMV
-----DCCACGTGCV-----

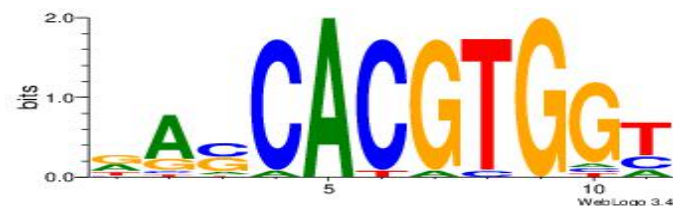
Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence:
VRVDGGHACAVDDKGTHCTDWH

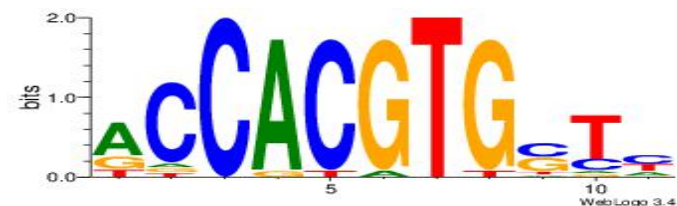


Dataset #: 2 Motif ID: 39 Motif name: MYCMAX

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



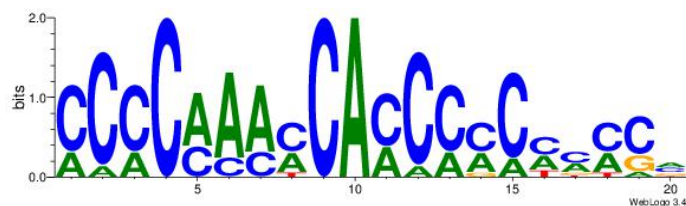
Best Matches for Motif ID 39 (Highest to Lowest)

Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0862644

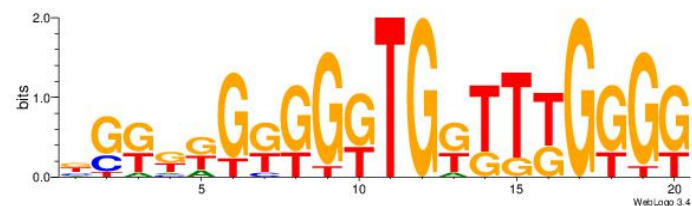
Alignment:

```
CCCCMAAMCAMCCMCMCMCV
---ACCACGTGSTM-----
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

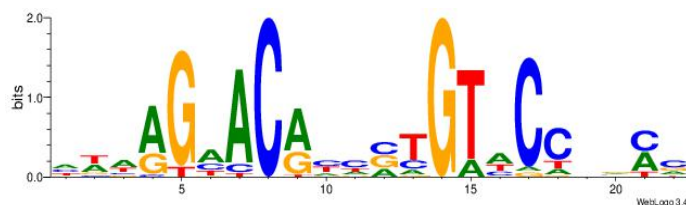


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.0877525

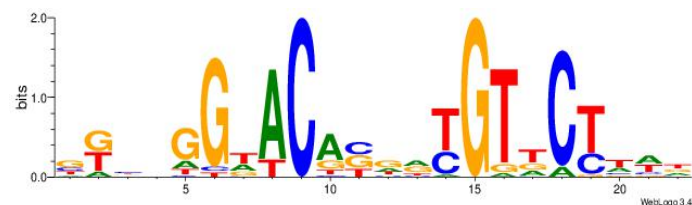
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 --RASCACGTGGT-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

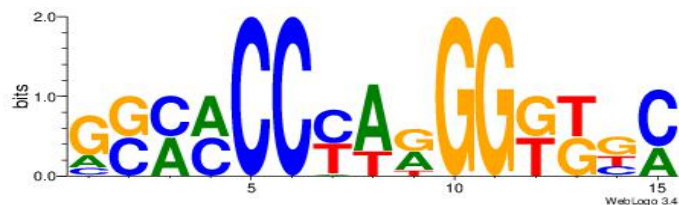


Dataset #: 2
 Motif ID: 13
 Motif name: Zfp423
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0933483

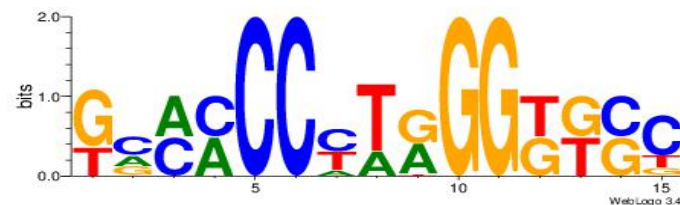
Alignment:

GSMGCCYARGGKKKC
 -ACCACGTGSTM---

Original motif Consensus sequence: GSMGCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

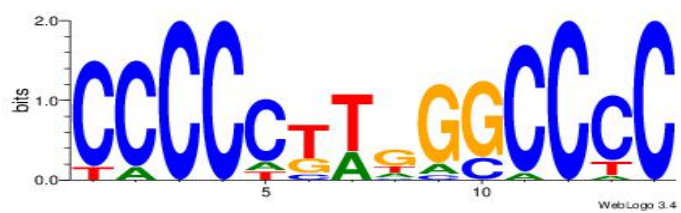
Similarity score: 0.10358

Alignment:
CCCCCTTGGGCCCC
ACCACGTGSTM---

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

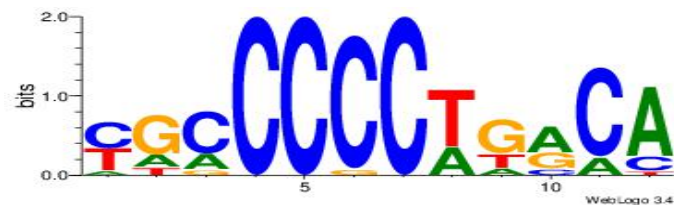


Dataset #: 2
Motif ID: 35
Motif name: INSM1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.104527

Alignment:
TGYCAGGGGGCR
RASCACGTGGT-

Original motif Consensus sequence: TGYCAGGGGGCR

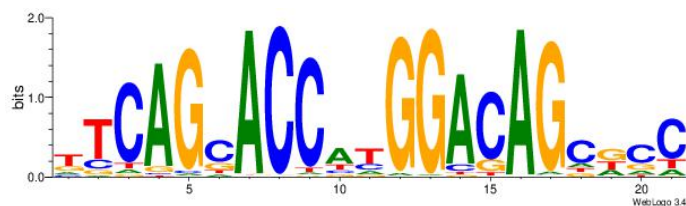
Reverse complement motif Consensus sequence: MGCCCCTGMCA



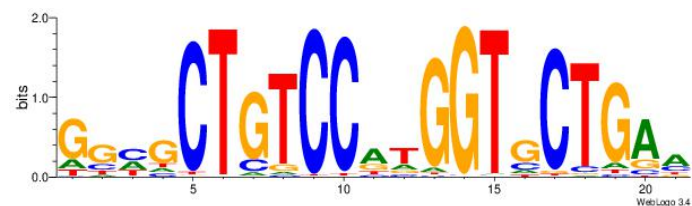
Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.105174

Alignment:
 GYGCTGTCCATGGTGCTGAA
 -----ACCACGTGSTM--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



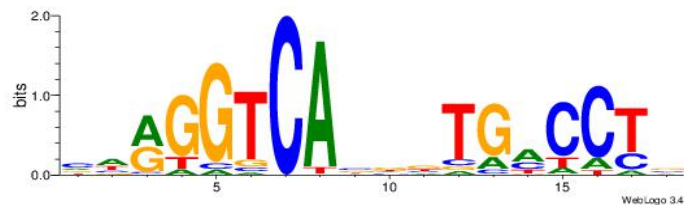
Dataset #: 2

Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.105681

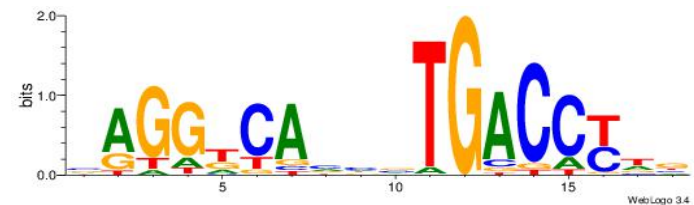
Alignment:

VHRGGTCABDBTGMCCCTB
 ---RASCACGTGGT----

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



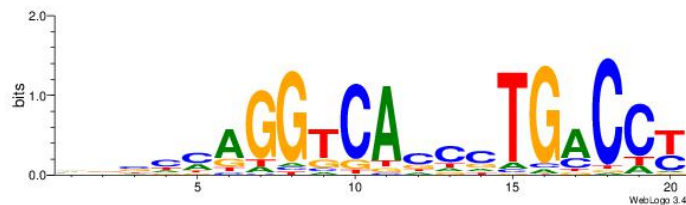
Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.107782

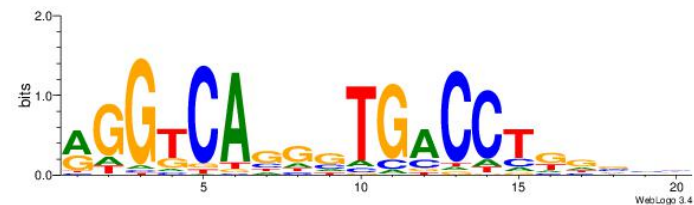
Alignment:

MGGTCAGGGTGACCTRDBHV
-----ACCACGTGSTM-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



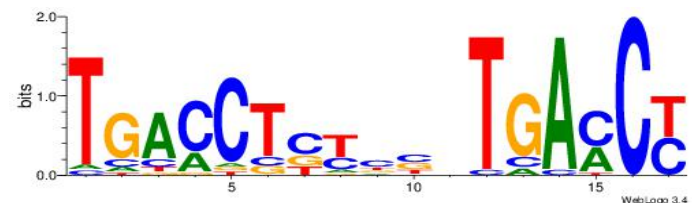
Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.108615

Alignment:

TGACCTCKVVB TGAYCK
--ACCACGTGSTM----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK



Alignment:

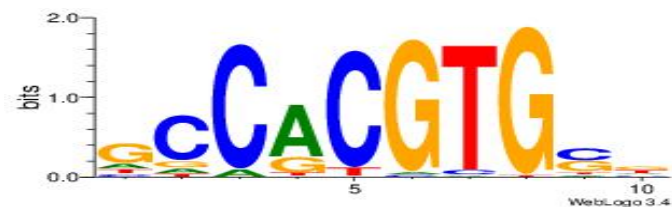
```
BBVGCCBVGGCCTV
RASCACGTGGT---
```

[illegible]

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Best Matches for Motif ID 40 (Highest to Lowest)

Dataset #:	2
Motif ID:	38
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0

Alignment:

DCCACGTGCV

GCCACGTGSD

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

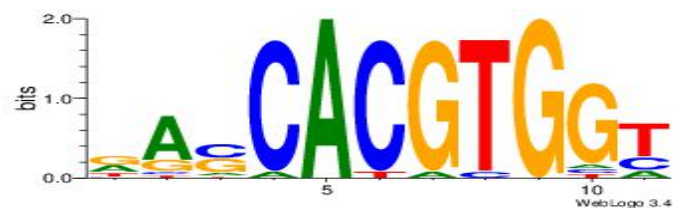


Dataset #: 2
 Motif ID: 39
 Motif name: MYCMAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0200467

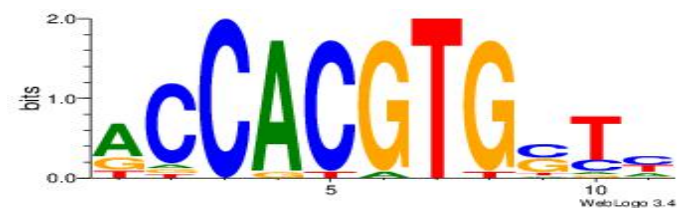
Alignment:

RASCACGTGGT
 -HSCACGTGGC

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



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: 2
 Number of overlap: 10

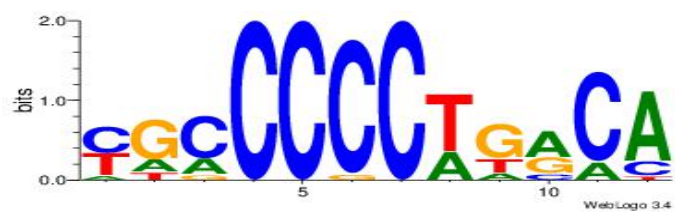
Similarity score: 0.0834824

Alignment:
MGCCCCCTGMCA
-GCCACGTGSD-

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA

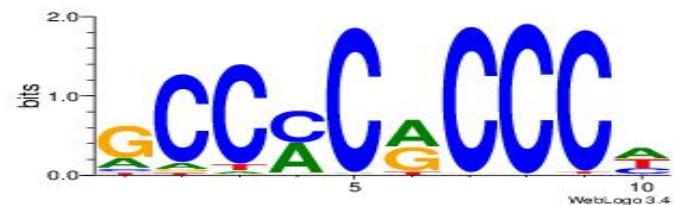


Dataset #: 2
Motif ID: 36
Motif name: Klf4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0893272

Alignment:
DGGGYGKGGC
HSCACGTGGC

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

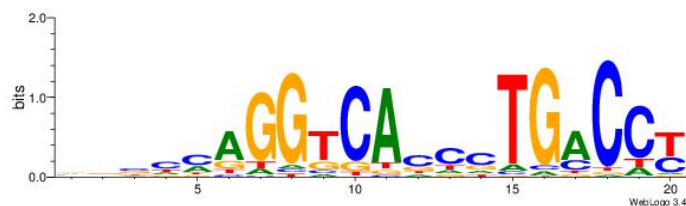


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.089863

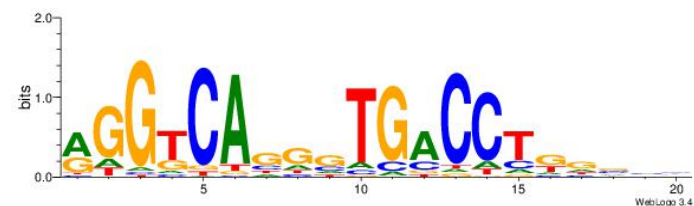
Alignment:

MGGTCAGGGTGACCTRDBHV
 -----GCCACGTGSD--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



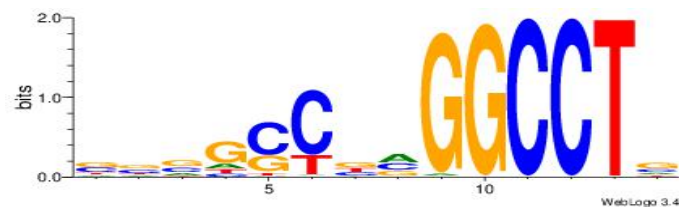
Dataset #: 2

Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0899944

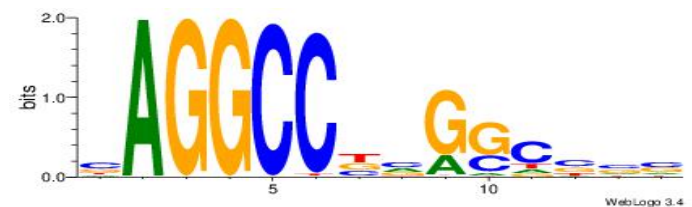
Alignment:

VAGGCCBBGGCVBB
 ---GCCACGTGSD-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

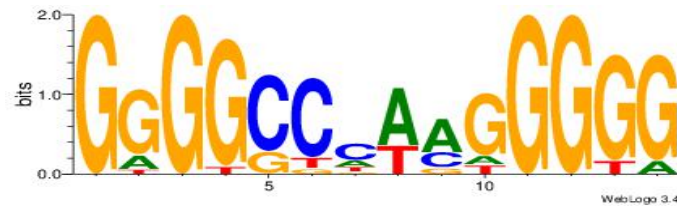


Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0921439

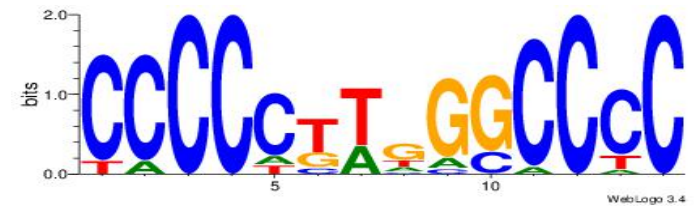
Alignment:

CCCCCTTGGGCCCC
----HSCACGTGGC

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



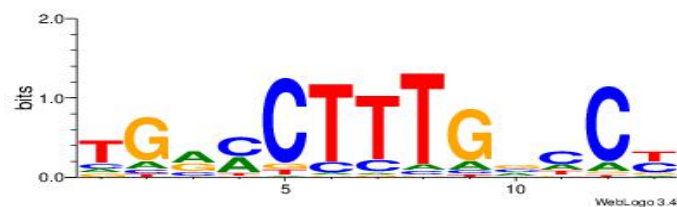
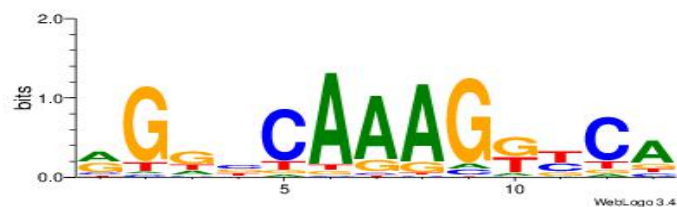
Dataset #:	2
Motif ID:	34
Motif name:	HNF4A
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0947124

Alignment:

TGMYCTTTGBCK
-GCCACGTGSD--

Original motif Consensus sequence: RGGBCAAAGKYCA

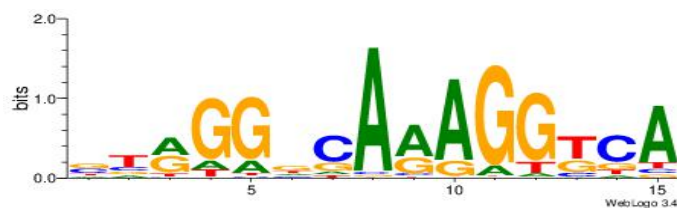
Reverse complement motif Consensus sequence: TGMYCTTTGBCK



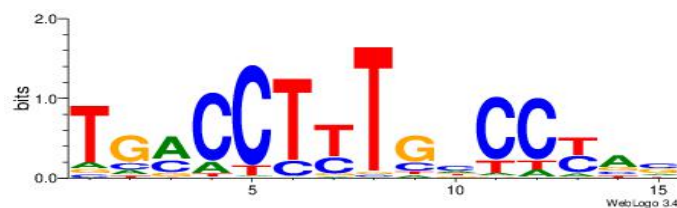
Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0954444

Alignment:
 TGRCCCTKTGHCCCKAB
 -GCCACGTGSD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



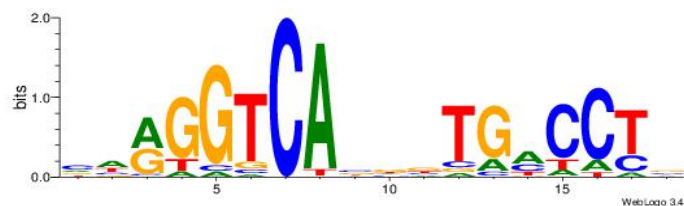
Dataset #: 2
 Motif ID: 30

Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0964708

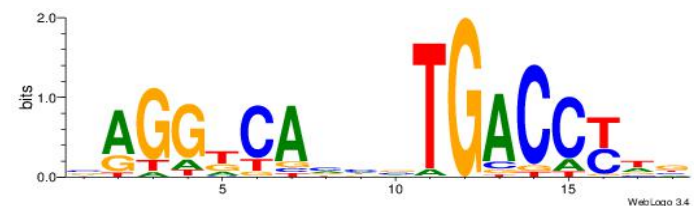
Alignment:

VHRGGTCABDBTGMCTB
 ----HSCACGTGGC----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Dataset #: 2 Motif ID: 41 Motif name: MZF1_5-13

Original motif Consensus sequence: BKAGGGGDAD



Reverse complement motif Consensus sequence: BTHCCCTYB



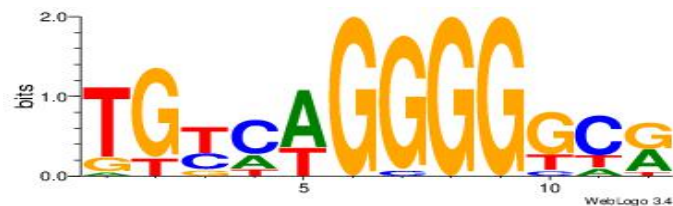
Best Matches for Motif ID 41 (Highest to Lowest)

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: 3
Number of overlap: 10
Similarity score: 0.0360532

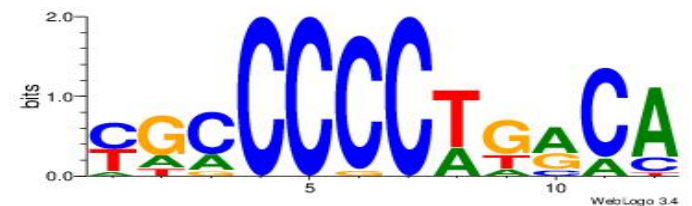
Alignment:

TGYCAGGGGGCR
--BKAGGGGDAD

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA

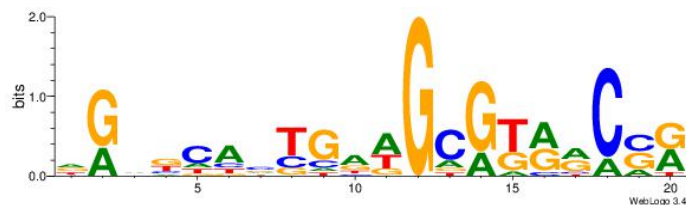


Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

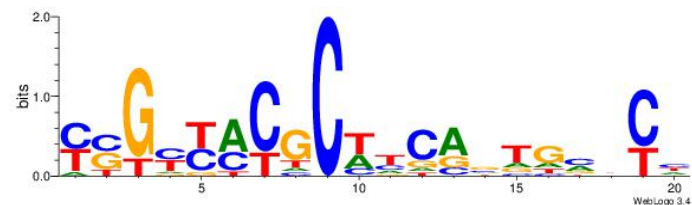
Direction: Forward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.0428241

Alignment:
 DGVCABTGDWGCGRRCR
 -----BKAGGGGDAD----

Original motif Consensus sequence: DGVCABTGDWGCGRRCR



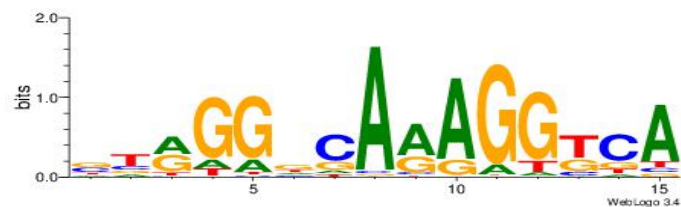
Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD



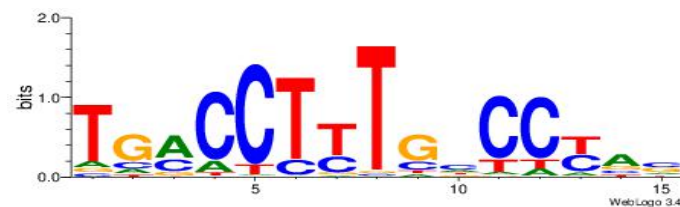
Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0470779

Alignment:
 BTRGGDCARAGGKCA
 BKAGGGGDAD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

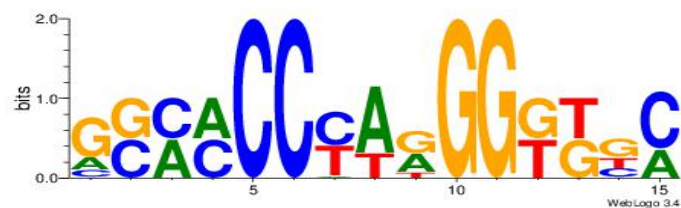


Dataset #: 2
Motif ID: 13
Motif name: Zfp423
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.0524832

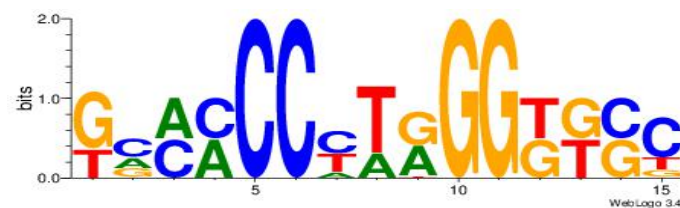
Alignment:

GSMCCYARGGKKKC
-----BKAGGGGDAD

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

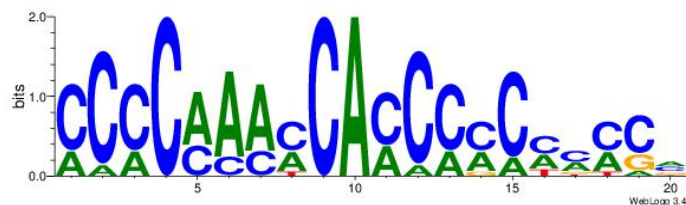


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0548506

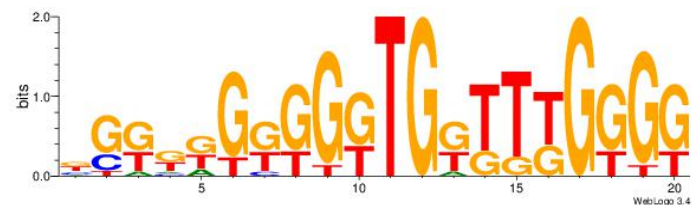
Alignment:

CCCCMAAMCAMCCMCMMMC
 -BTHCCCCTYB-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

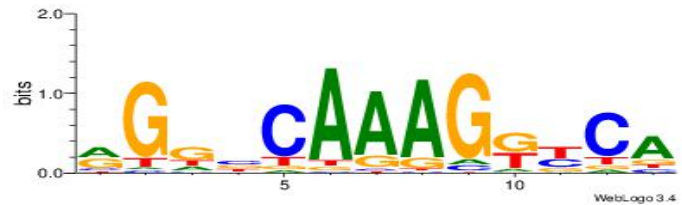


Dataset #: 2
 Motif ID: 34
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

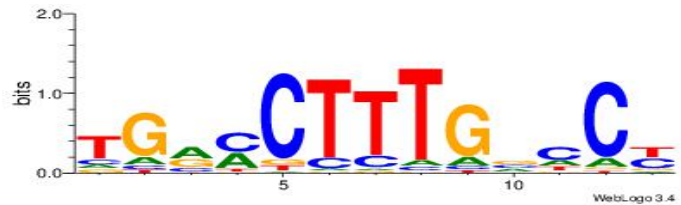
Number of overlap: 10
Similarity score: 0.0568244

Alignment:
TGM YCTTTGB CCK
BTHCC C TYB---

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGB CCK



Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0581547

Alignment:
TGACCTCKVVB TGAYCK
BTHCC C TYB-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

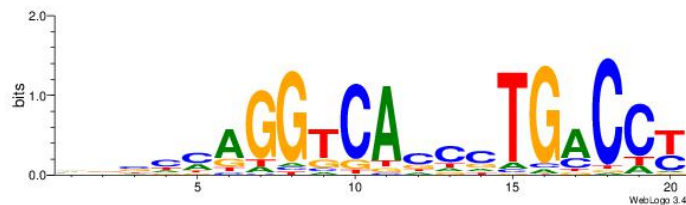
Reverse complement motif Consensus sequence:
TGACCTCKVVB TGAYCK

Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.0642057

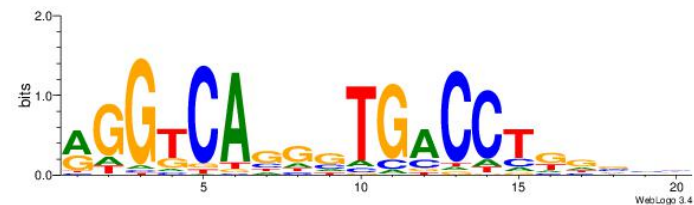
Alignment:

VDBHMAGGTCACCCTGACCY
 --BKAGGGGDAD-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

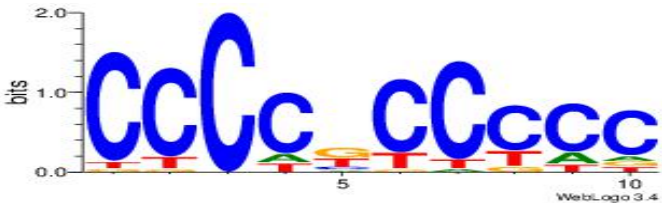


Dataset #: 2
 Motif ID: 16
 Motif name: SP1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0692824

Alignment:
CCCCKCCCCC
BTHCCCTYB

Original motif Consensus sequence: CCCC



Reverse complement motif Consensus sequence: GGGG



Dataset #: 2 Motif ID: 42 Motif name: NFKB1

Original motif Consensus sequence: GGGGRTTCCC



Reverse complement motif Consensus sequence: GGGGAATCCC



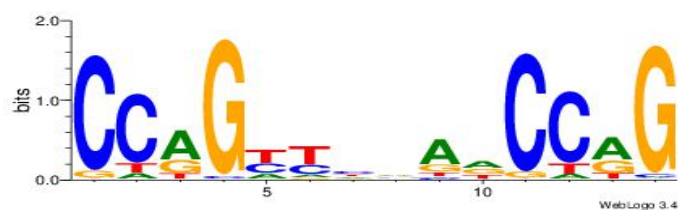
Best Matches for Motif ID 42 (Highest to Lowest)

Dataset #:	2
Motif ID:	48
Motif name:	Tcfcp2l1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward

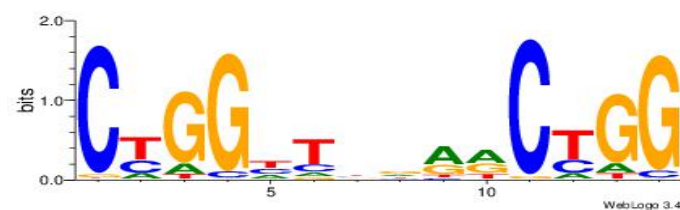
Position number: 4
 Number of overlap: 11
 Similarity score: 0.103405

Alignment:
 CKGGDTBDMMCTGG
 GGGGRTTCCCC---

Original motif Consensus sequence: CCAGYYHVADCCRG



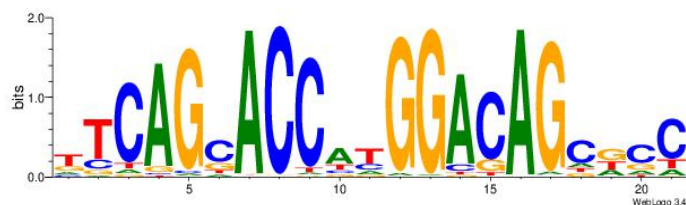
Reverse complement motif Consensus sequence: CKGGDTBDMMCTGG



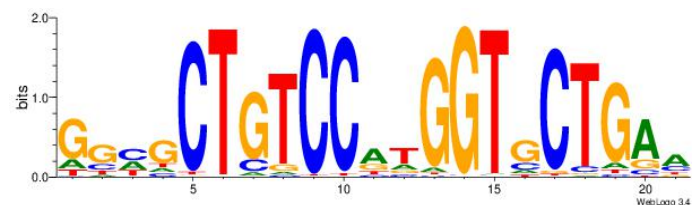
Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.112926

Alignment:
 TTCAGCACCATGGACAGCKCC
 GGGGAACKCCCC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

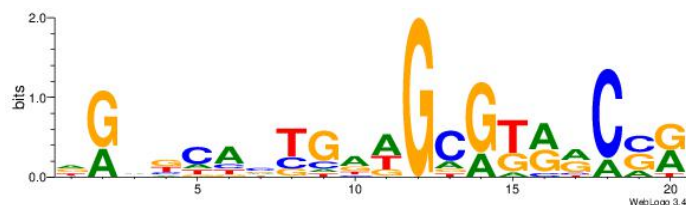


Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 9
Number of overlap: 11
Similarity score: 0.116162

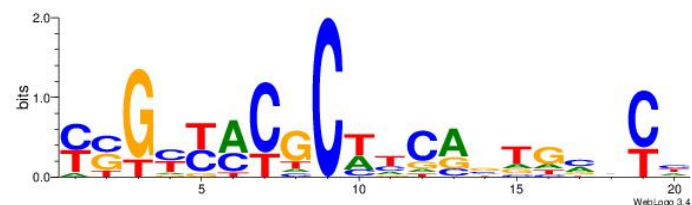
Alignment:

MSGKKRCGCWDCABTGGBCD
-GGGGAAKCCCC-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD

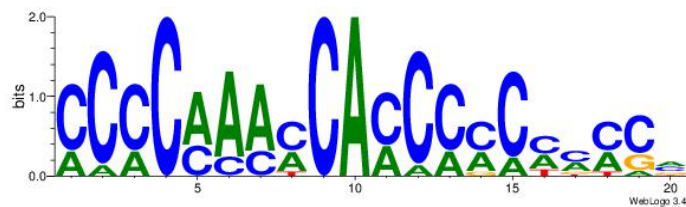


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.117826

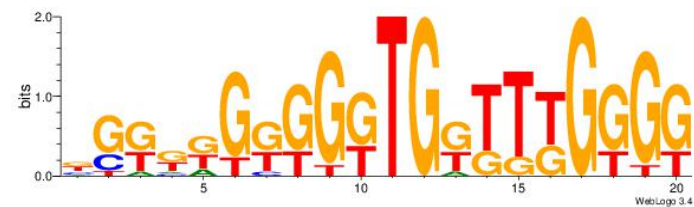
Alignment:

CCCCMAAMCAMCCMCMMMC
 -----GGGGAACCCCC-----

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



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: 1

Number of overlap: 10
 Similarity score: 0.616368

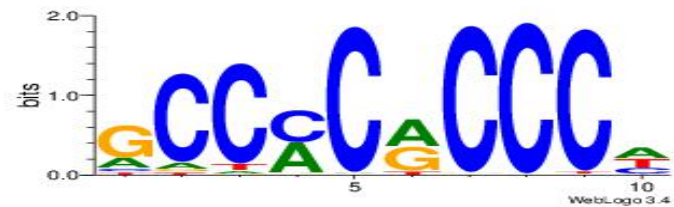
Alignment:

GCCYCMCCCD-
 GGGGRTTCCCC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



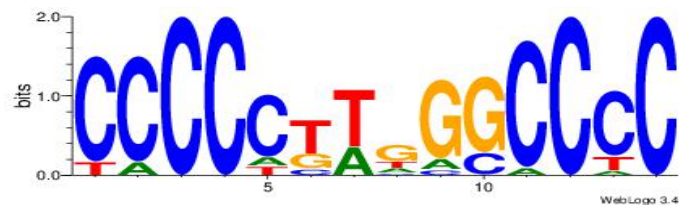
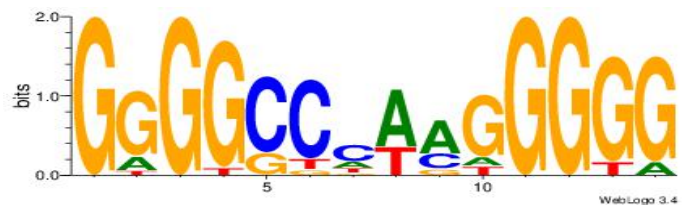
Dataset #: 2
 Motif ID: 21
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 9
 Similarity score: 1.11497

Alignment:

--GGGGCCCAAGGGGG
 GGGGRTTCCCC-----

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCC



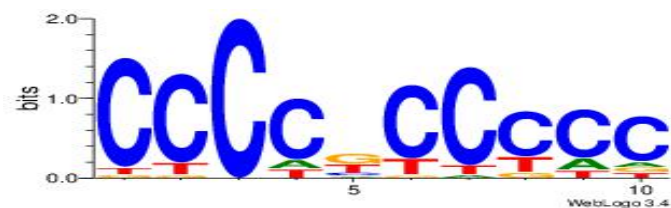
Dataset #: 2
 Motif ID: 16
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 1.11585

Alignment:

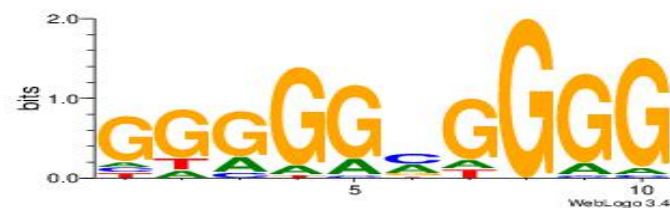
--GGGGGYGGGG

GGGRTTCCCC-

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



Dataset #: 1
 Motif ID: 7

Motif name:	Motif 7
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:	1.59629

Alignment:

```
GGGGMGGG---
GGGGAACCCC
```

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG

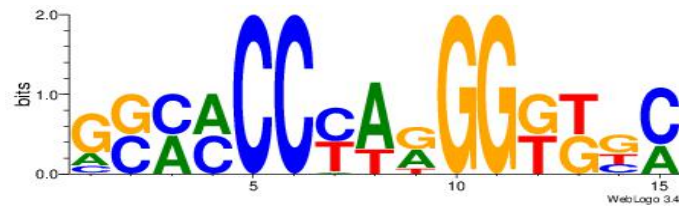


Dataset #:	2
Motif ID:	13
Motif name:	Zfp423
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	8
Similarity score:	1.59848

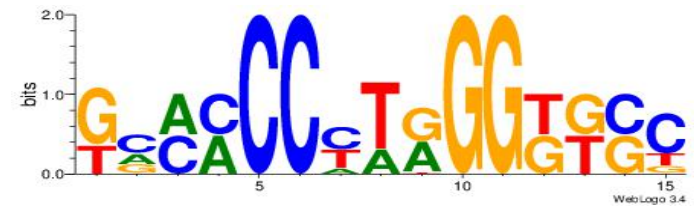
Alignment:

GSMCCYARGGKKKC---
 -----GGGGRTTCCCC

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



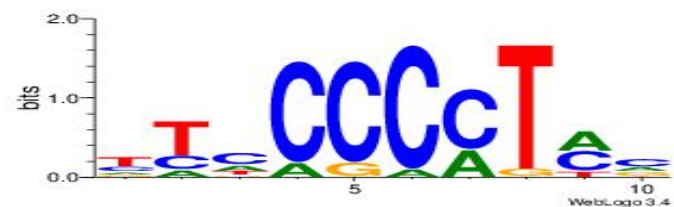
Dataset #:	2
Motif ID:	41
Motif name:	MZF1_5-13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	1.61306

Alignment:

---BKAGGGGDAD
 GGGGAACKCCC--

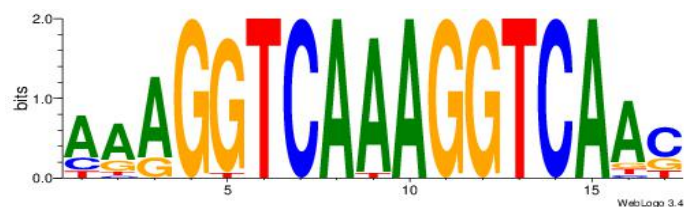
Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

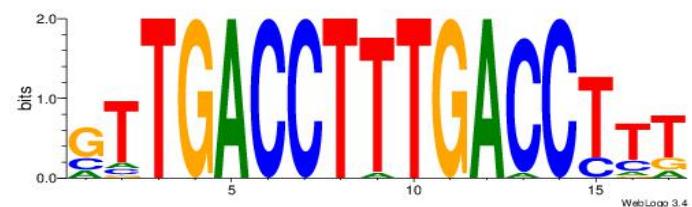


Dataset #: 2 Motif ID: 43 Motif name: NR1H2RXRA

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



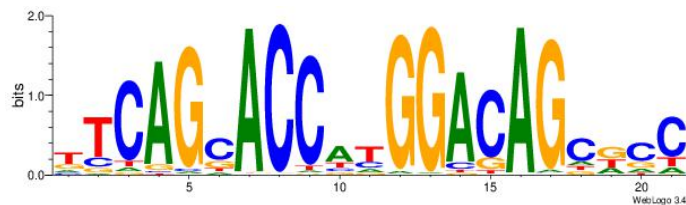
Best Matches for Motif ID 43 (Highest to Lowest)

Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	17
Similarity score:	0.0911991

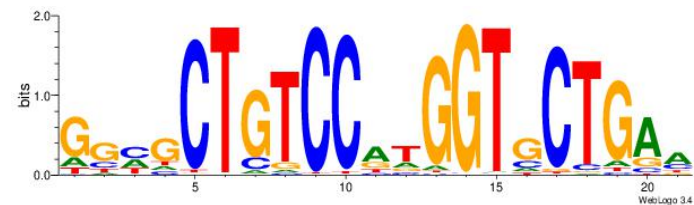
Alignment:

GGYGCTGTCCATGGTGCTGAA
 ---GTTGACCTTTGACCTTT-

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

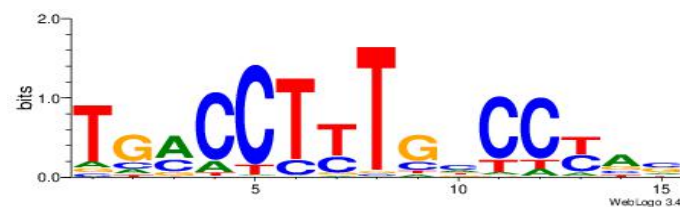
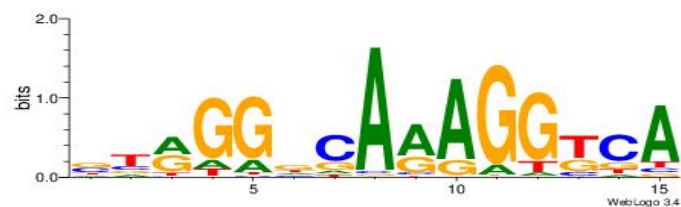


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 1.05945

Alignment:
 BTRGGDCARAGGKCA--
 AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



Dataset #: 2
 Motif ID: 17
 Motif name: RXRAVDR
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 1.09792

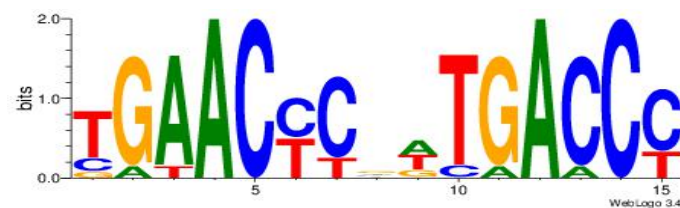
Alignment:

--GGGTCAWBGRGTTCA
 AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: GGGTCAWBGRGTTCA



Reverse complement motif Consensus sequence: TGAACKCBWTGAC



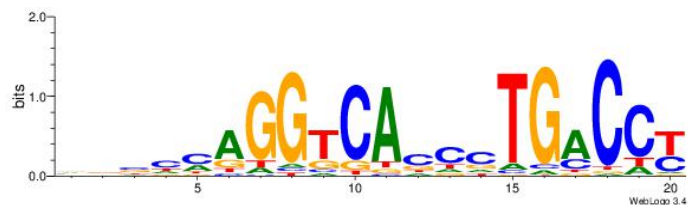
Dataset #: 2
 Motif ID: 29

Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 13
 Similarity score: 2.08514

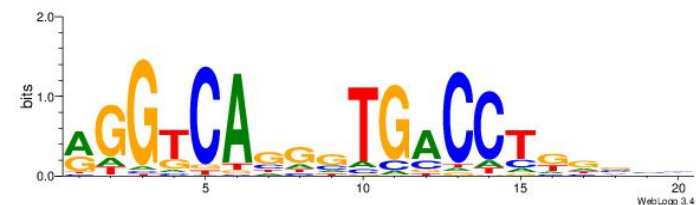
Alignment:

-----VDBHMAGGTCACCCTGACCY
 AAAGGTCAAAGGTCAAC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDDBHV

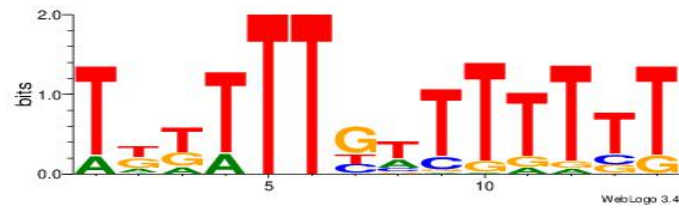


Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 2.08845

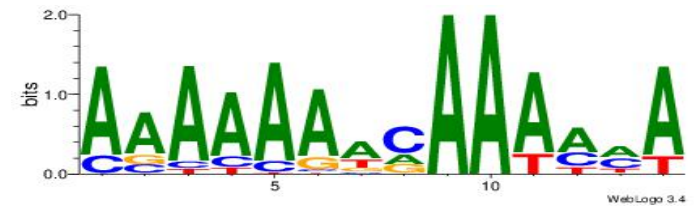
Alignment:

TKKTTTGTTTTTTT-----
 -GTTGACCTTTGACCTTT

Original motif Consensus sequence: TKKTTTGTTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR



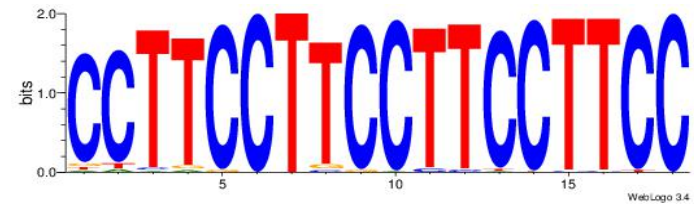
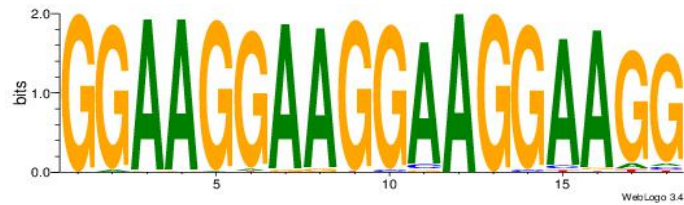
Dataset #:	2
Motif ID:	32
Motif name:	EWSR1-FLI1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	12
Similarity score:	2.59335

Alignment:

GGAAGGAAGGAAGGAAGG-----
 -----AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG

Reverse complement motif Consensus sequence:
 CCTTCCTTCCTTCCTTCC

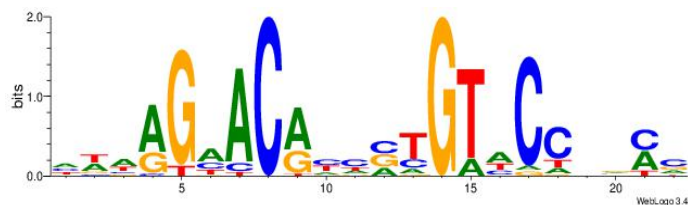


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 11
 Similarity score: 3.09595

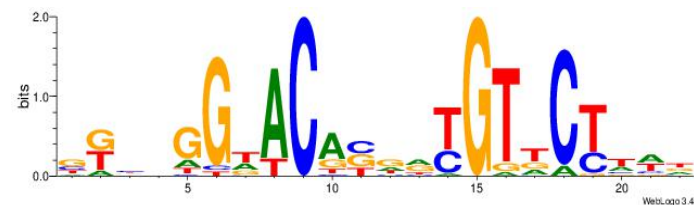
Alignment:

VRVDGGHACAVDDKGTHCTDWH-----
 -----GTTGACCTTTGACCTTT

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



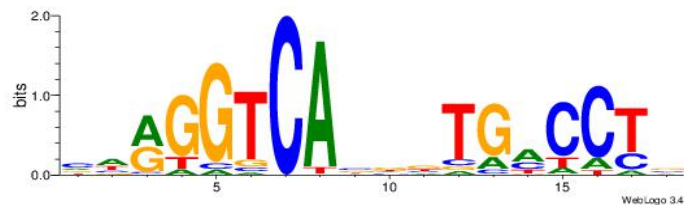
Dataset #: 2

Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 10
 Similarity score: 3.56221

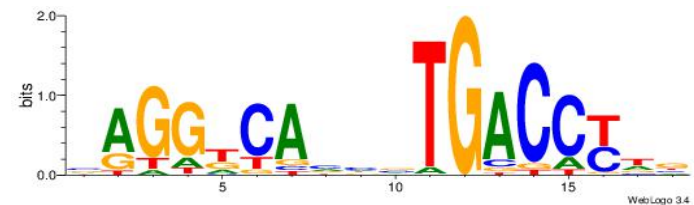
Alignment:

BAGGYCABHBTGACCKHV-----
 -----GTTGACCTTTGACCTTT

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

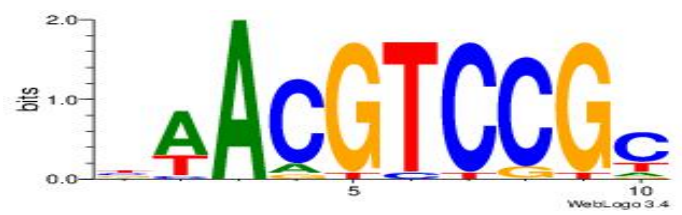


Dataset #: 2
 Motif ID: 37
 Motif name: MIZF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10

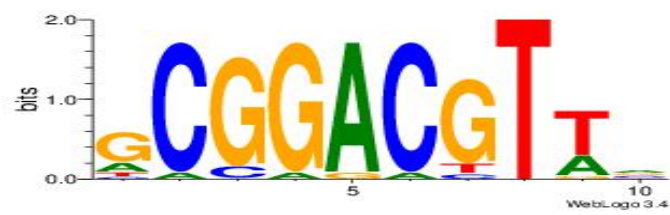
Similarity score: 3.5855

Alignment:
-----BAACGTCCGC
AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT

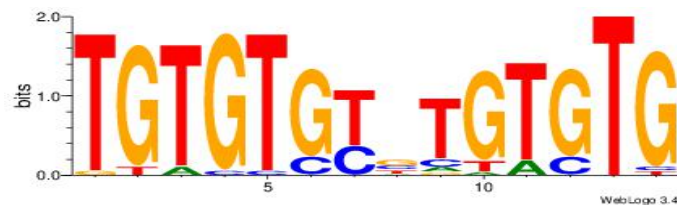


Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 3.59839

Alignment:
CACACAVRCACACA-----
----AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



Dataset #: 2 Motif ID: 44 Motif name: NR4A2

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



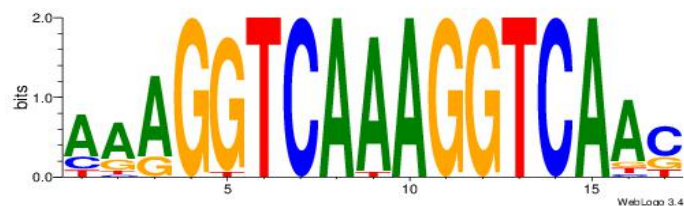
Best Matches for Motif ID 44 (Highest to Lowest)

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:	2
Number of overlap:	8
Similarity score:	0.0167759

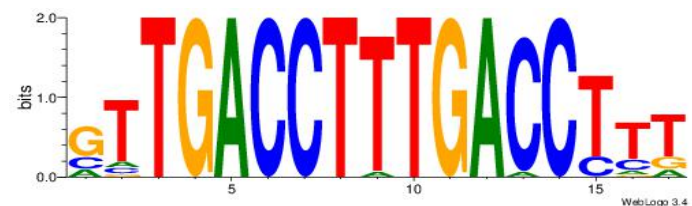
Alignment:

```
AAAGGTCAAAGGTCAAC
-AAGGTCAC-----
```


Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

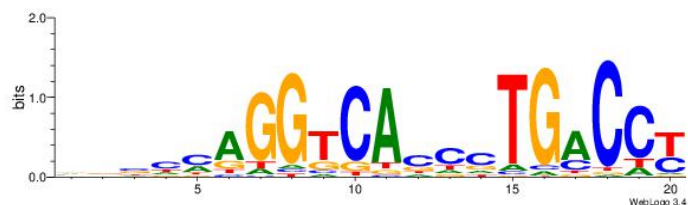


Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0195235

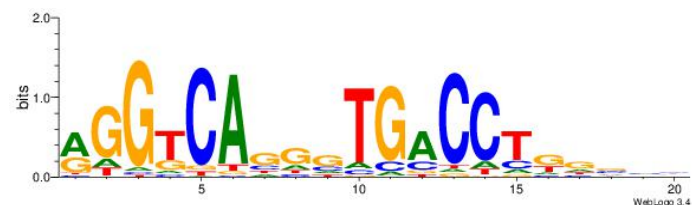
Alignment:

VDBHMAGGTCACCCTGACCY
-----AAGGTCAC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

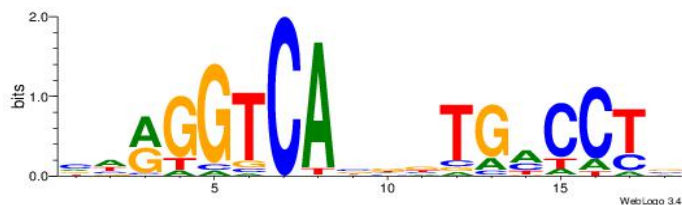


Dataset #: 2
 Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0198372

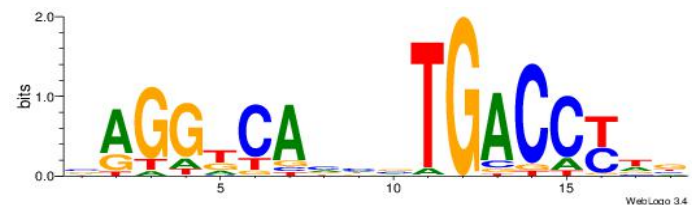
Alignment:

BAGGYCABHBTGACCKHV
 -----GTGACCTT-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

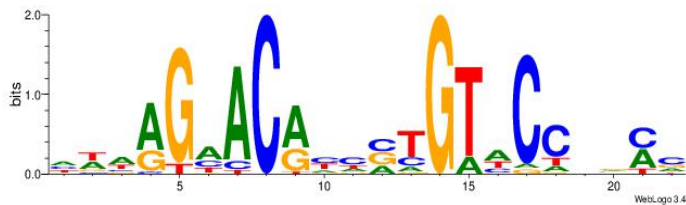


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 13

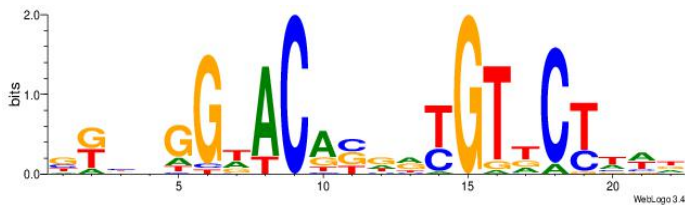
Number of overlap: 8
Similarity score: 0.0487608

Alignment:
VRVDGGHACAVDDKGTHCTDWH
-----GTGACCTT--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

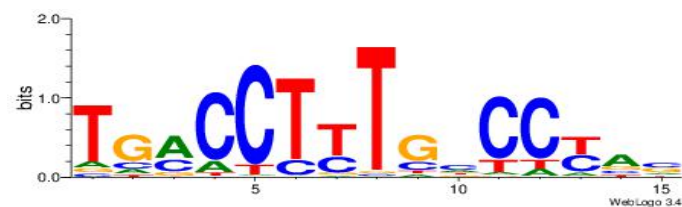
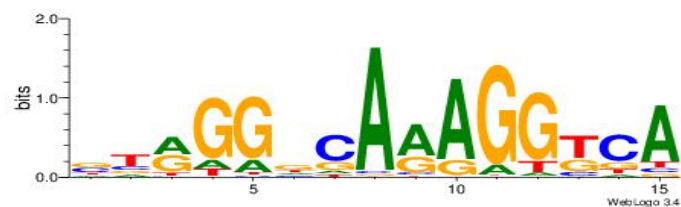


Dataset #: 2
Motif ID: 20
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.0495607

Alignment:
BTRGGDCARAGGKCA
-AAGGTCAC-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

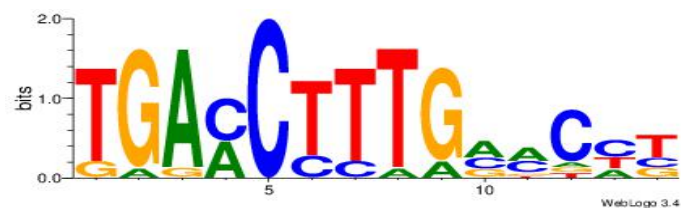
Reverse complement motif Consensus sequence: TGRCCCTKGHCCK



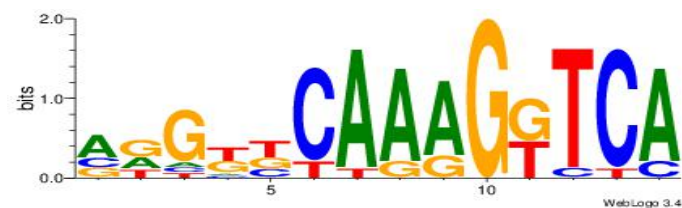
Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0564874

Alignment:
 AKGYCAAAGRTCA
 -----AAGGTCAC

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



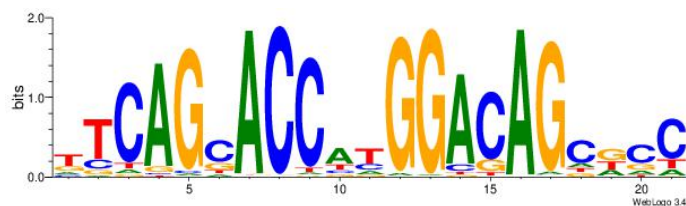
Dataset #: 2
 Motif ID: 19

Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.0594649

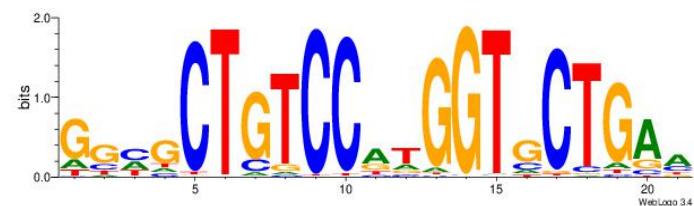
Alignment:

```
TTCAGCACCATGGACAGCKCC
-----AAGGTCAC-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

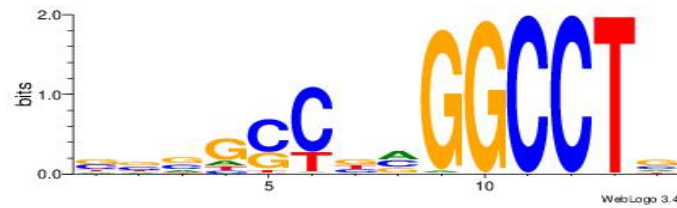


Dataset #:	2
Motif ID:	12
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0631514

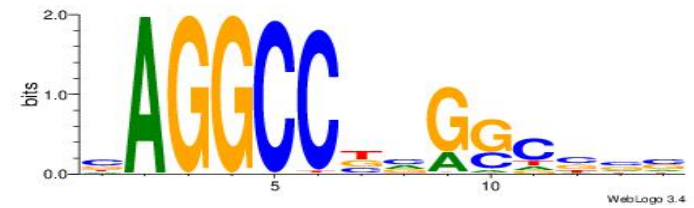
Alignment:

BBVGCCBVGGCCTV
GTGACCTT-----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



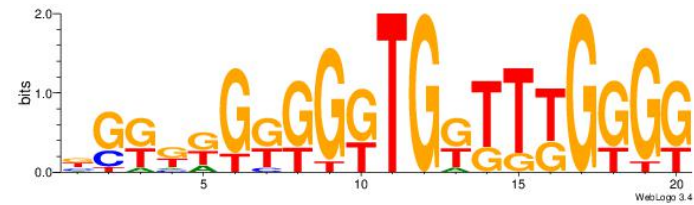
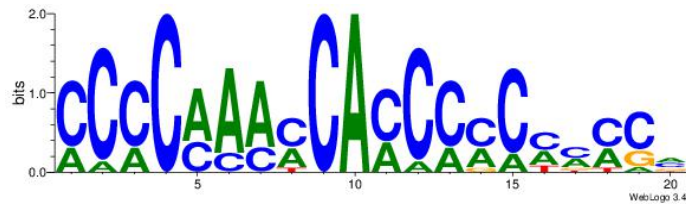
Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0720656

Alignment:

BGRRRGRGGRTGRTTYGGGG
-----GTGACCTT---

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC

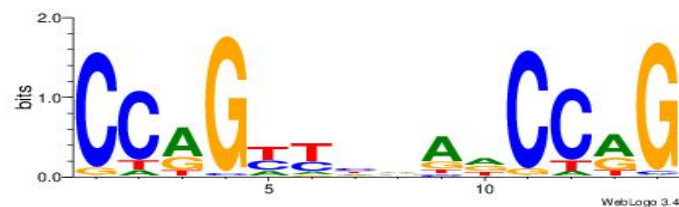
Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG



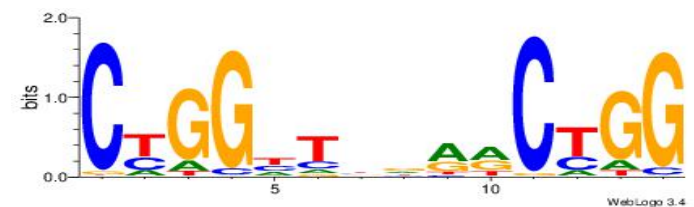
Dataset #: 2
 Motif ID: 48
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0740998

Alignment:
 CKGGDTBDMCTGG
 -----GTGACCTT-

Original motif Consensus sequence: CCAGYYHVADCCRG

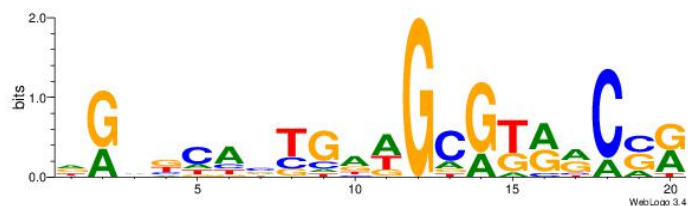


Reverse complement motif Consensus sequence: CKGGDTBDMCTGG

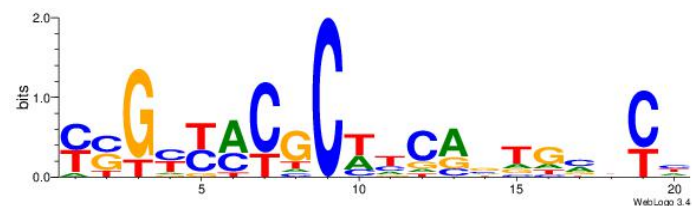


Dataset #: 2 Motif ID: 45 Motif name: Pax5

Original motif Consensus sequence: DGVBCABTGDWGCGRRCRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBBCD



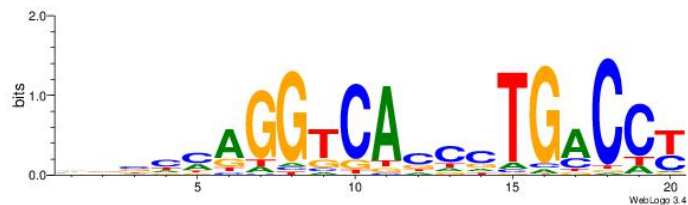
Best Matches for Motif ID 45 (Highest to Lowest)

Dataset #:	2
Motif ID:	29
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0382347

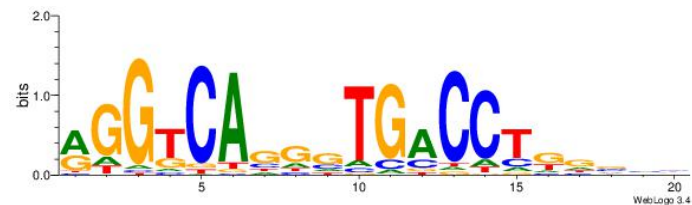
Alignment:

MGGTCAGGGTGACCTRDBHV
MSGKKRCGCWDCABTGBBBCD

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

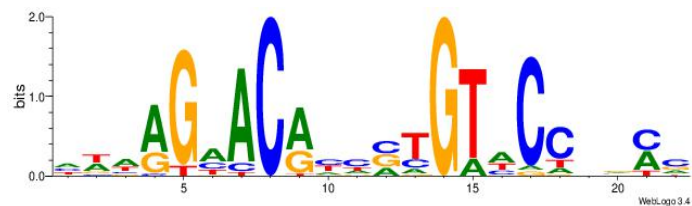


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0450685

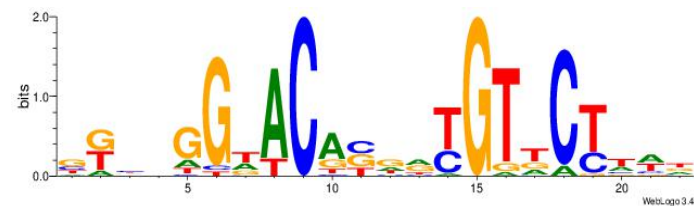
Alignment:

VRVDGGHACAVDDKGTHTDWH
 --MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHTDWH



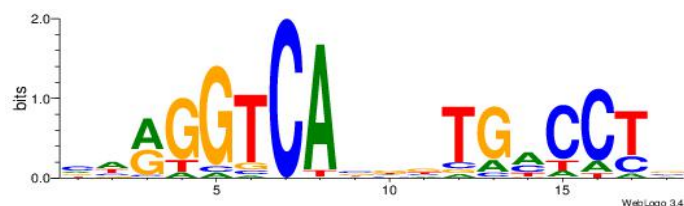
Dataset #: 2
 Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 1
Number of overlap: 18
Similarity score: 1.05192

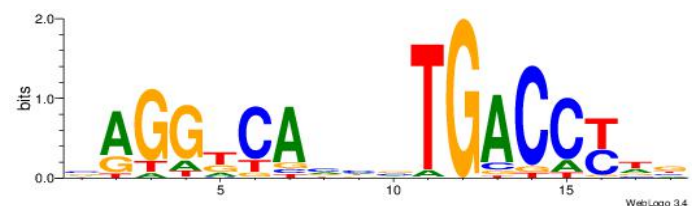
Alignment:

BAGGYCABHBTGACCKHV--
MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

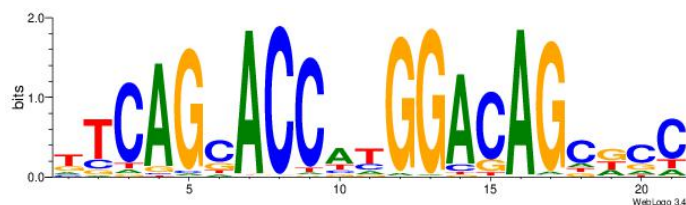


Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 18
Similarity score: 1.0582

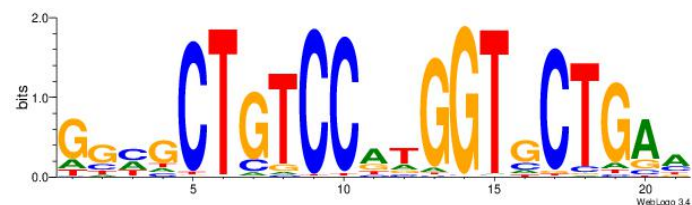
Alignment:

--GGYGCTGTCCATGGTGCTGAA
MSGKKRCGCWDCABTGBBCD---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGTCTGAA

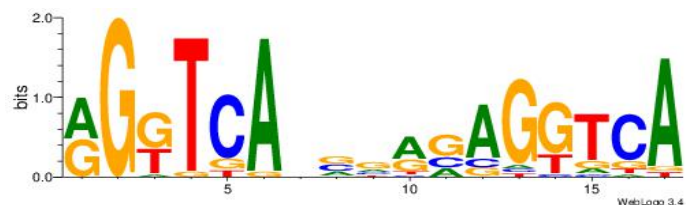


Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 1.53818

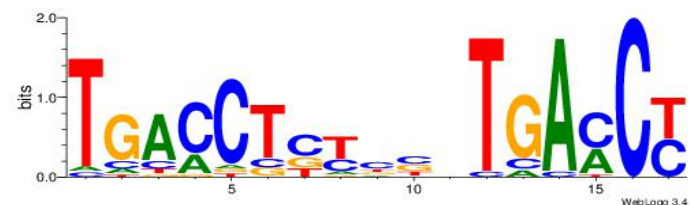
Alignment:

---TGACCTCKVVB TGAYCK
MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

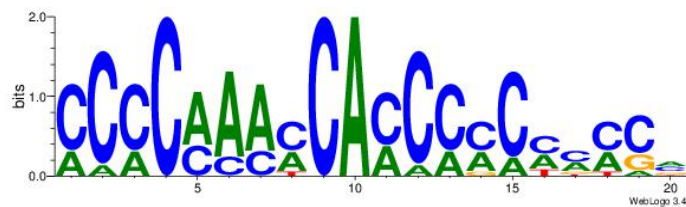


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 1.55831

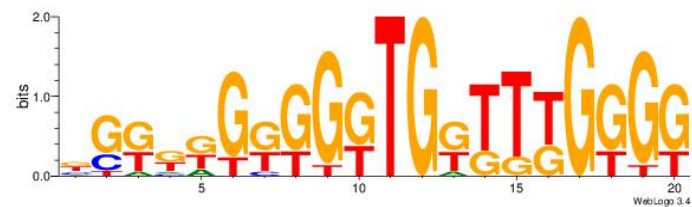
Alignment:

CCCCMAAMCAMCCMCMMMCVC---
 ---MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCVC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

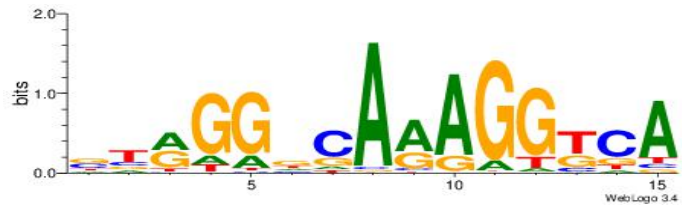


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

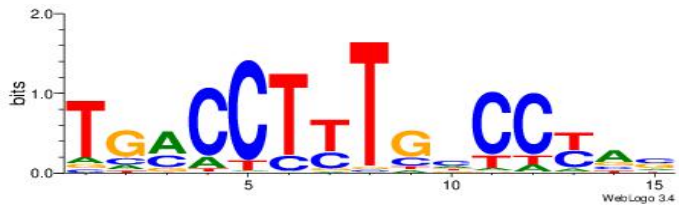
Number of overlap: 15
Similarity score: 2.55126

Alignment:
-----TGRCCCTKTGHCCCKAB
DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

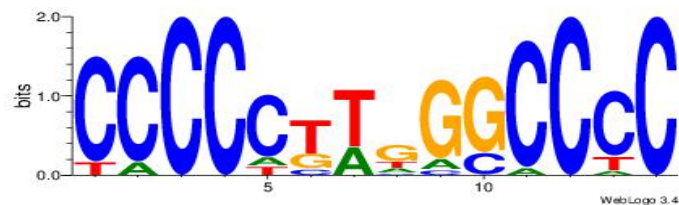
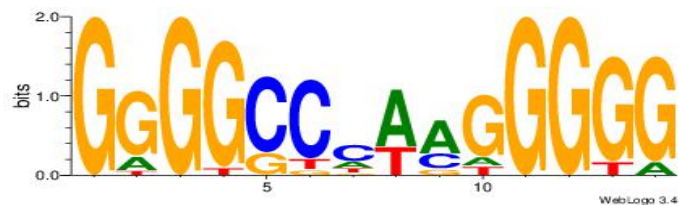


Dataset #: 2
Motif ID: 21
Motif name: PLAG1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 3.05866

Alignment:
GGGGCCCAAGGGG-----
DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: GGGGCCCAAGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCC



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: 1
 Number of overlap: 14
 Similarity score: 3.05897

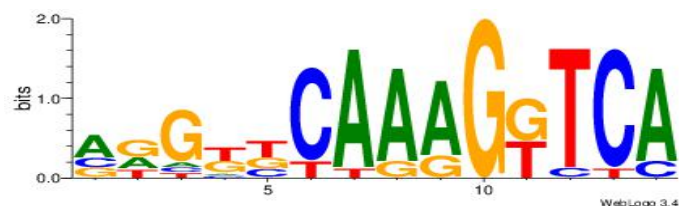
Alignment:

-----AKGYCAAAGRTCA
 MSGKKRCGCWDCABTGBCD

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



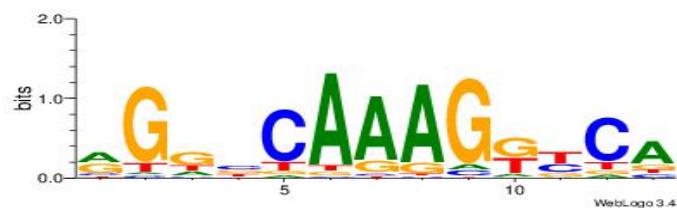
Dataset #: 2
 Motif ID: 34

Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 3.53748

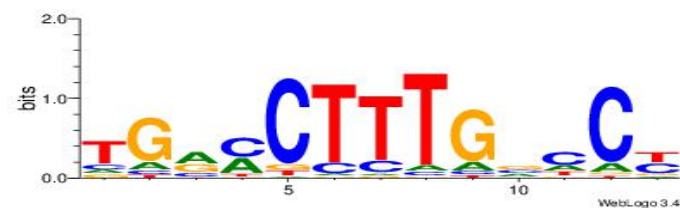
Alignment:

-----TGM YCTTTGBCCK
 DGVBCABTGDWGCGRRC SR

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCCK



Dataset #: 2 Motif ID: 46 Motif name: RORA_1

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT



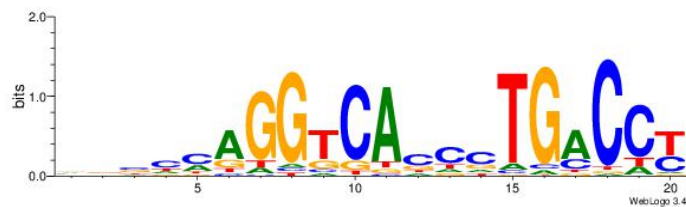
Best Matches for Motif ID 46 (Highest to Lowest)

Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0417851

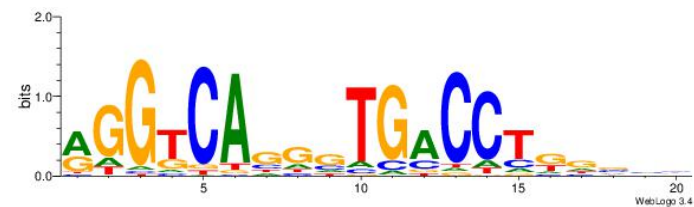
Alignment:

MGGTCAGGGTGACCTRDBHV
 -----TGACCTDVWT-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 2
 Motif ID: 17
 Motif name: RXRAVDR
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

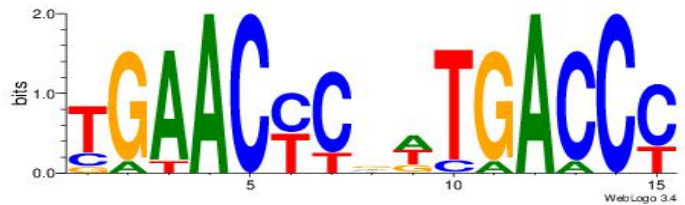
Number of overlap: 10
Similarity score: 0.05325

Alignment:
GGGTCAWBGRGTTCA
-----AWVDAGGTCA

Original motif Consensus sequence: GGGTCAWBGRGTTCA



Reverse complement motif Consensus sequence: TGAACKCBWTGAC

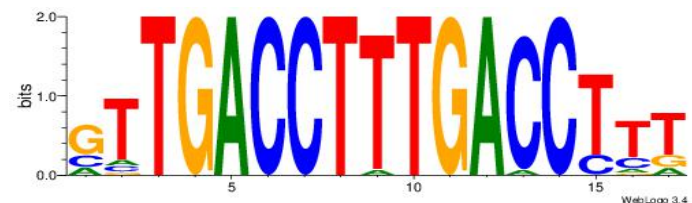
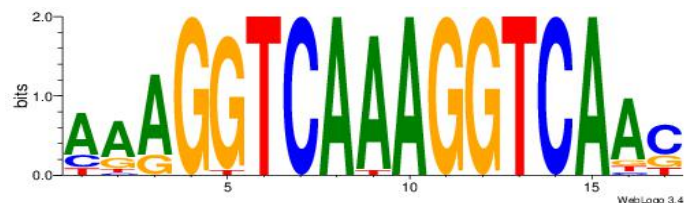


Dataset #: 2
Motif ID: 43
Motif name: NR1H2RXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.05425

Alignment:
AAAGGTCAAAGGTCAAC
-----AWVDAGGTCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

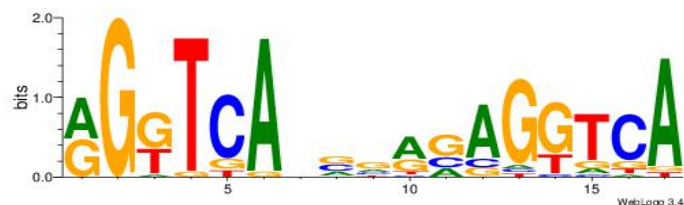
Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



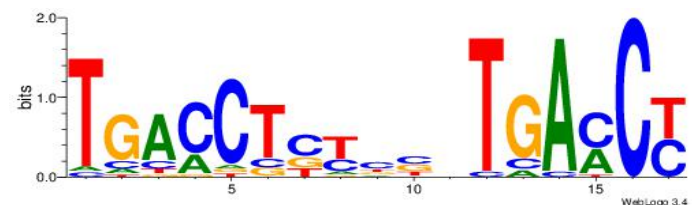
Dataset #: 2
 Motif ID: 47
 Motif name: RXRRAR_DR5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0600761

Alignment:
 TGACCTCKVVB TGAYCK
 TGACCTDVWT-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK



Dataset #: 2

Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0654808

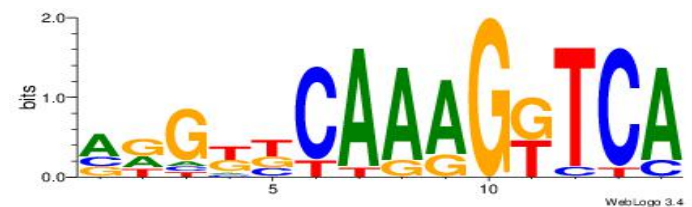
Alignment:

TGAMCTTTGMMCYT
 ----TGACCTDVWT

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC



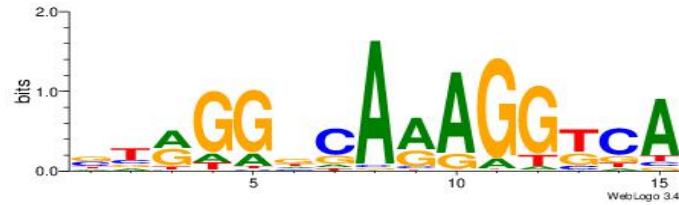
Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.06668

Alignment:

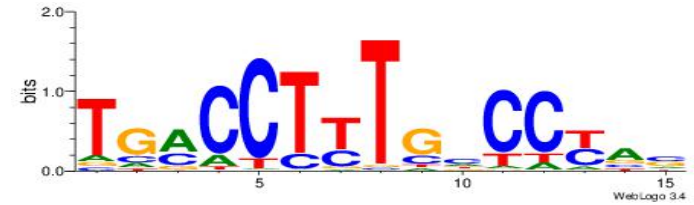
BTRGGDCARAGGKCA

-----AWVDAGGTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



Dataset #:	2
Motif ID:	19
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	10
Similarity score:	0.0755608

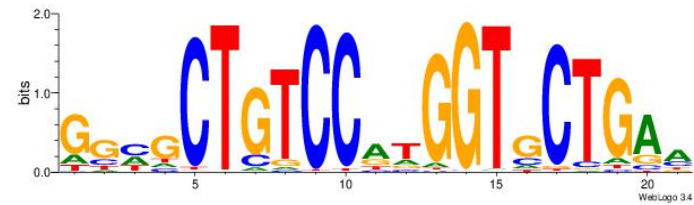
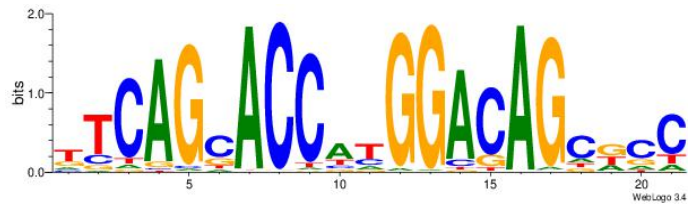
Alignment:

TTCAGCACCATGGACAGCKCC

-----AWVDAGGTCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA

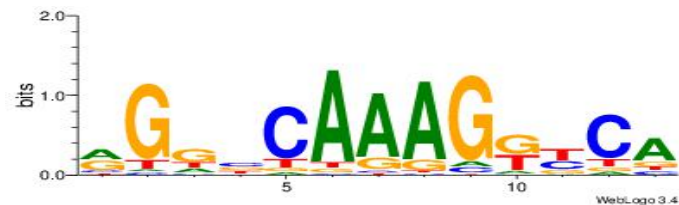


Dataset #: 2
 Motif ID: 34
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0803396

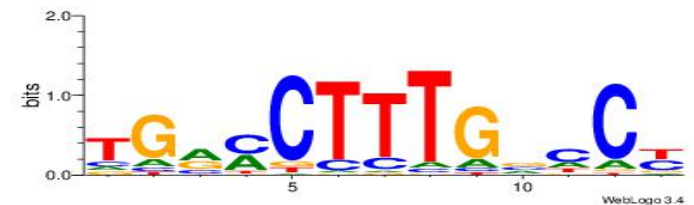
Alignment:

RGGBCAAAGKYCA
 ---AWVDAGGTCA

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCCK



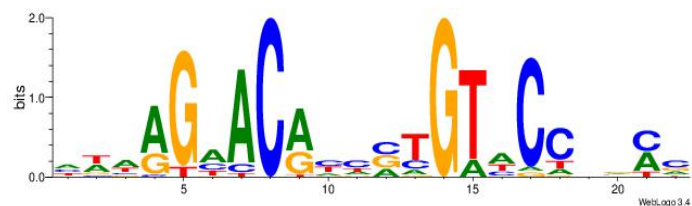
Dataset #: 2
 Motif ID: 24

Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	13
Number of overlap:	10
Similarity score:	0.0814167

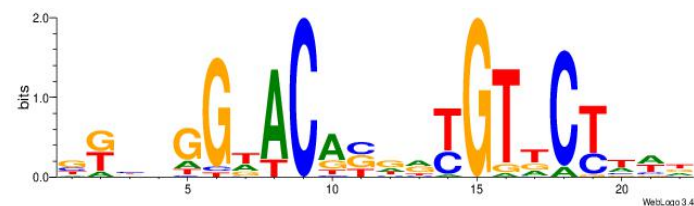
Alignment:

```
VRVDGGHACAVDDKGTCTDWH
-----AWVDAGGTCA
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTCTDWH



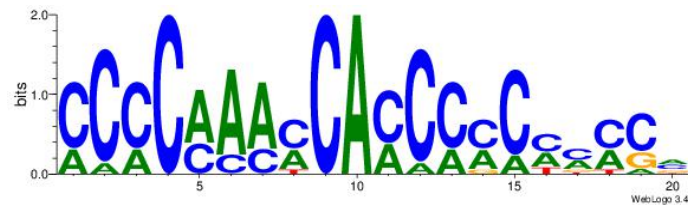
Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0901591

Alignment:

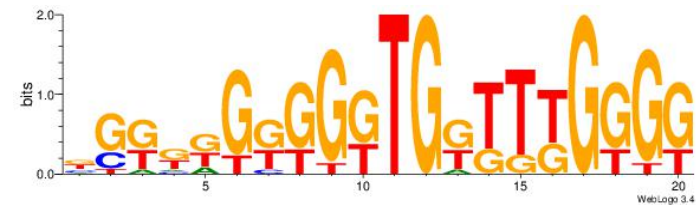
CCCCMAAMCAMECCMMCMCV

---TGACCTDVWT-----

Original motif Consensus sequence: CCCCMAAMCAMECCMMCMCV

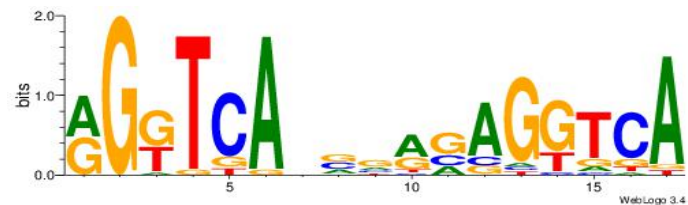


Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

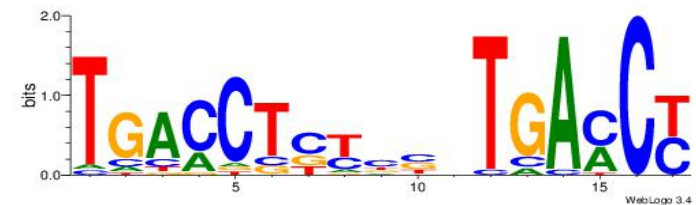


Dataset #: 2 Motif ID: 47 Motif name: RXRRAR_DR5

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBGTGAYCK



Best Matches for Motif ID 47 (Highest to Lowest)

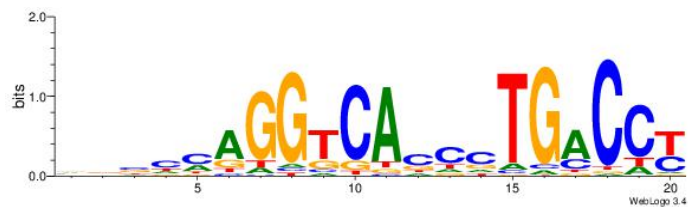
Dataset #:	2
Motif ID:	29
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.0554256

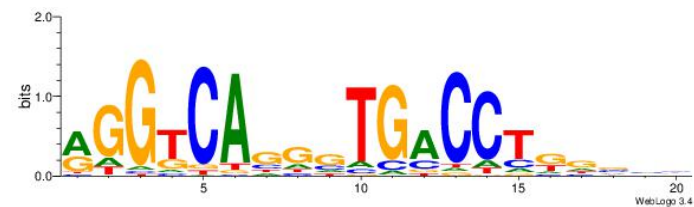
Alignment:

MGGTCAGGGTGACCTRDBHV
---RGKTCABVVRGAGGTCA

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

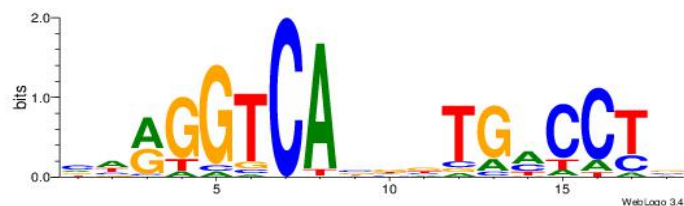


Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.0590677

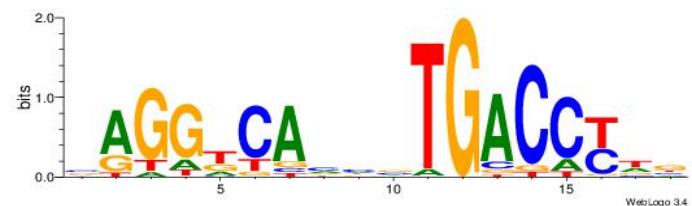
Alignment:

VHRGGTCABDBTGMCCCTB
-TGACCTCKVVB TGAYCK

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

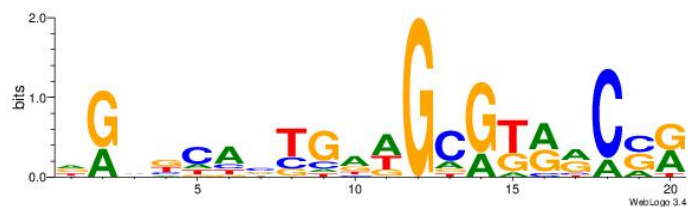


Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.0594693

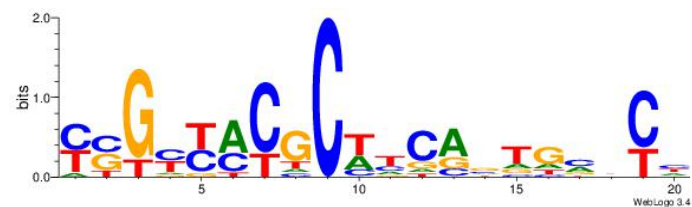
Alignment:

MSGKKRCGCWDCABTGGBCD
 ---TGACCTCKVVBGTGAYCK

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD

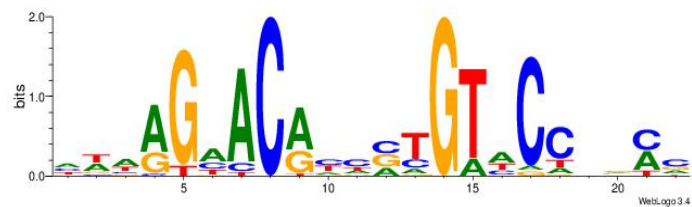


Dataset #: 2
 Motif ID: 24
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0751876

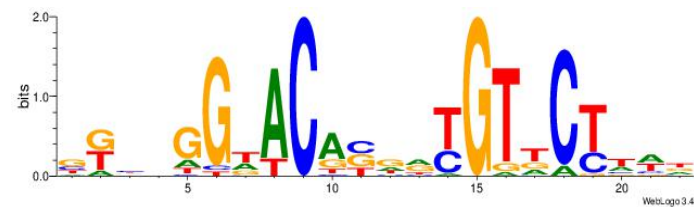
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 ----TGACCTCKVVB TGAYCK-

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACA VDDKGTHCTDWH

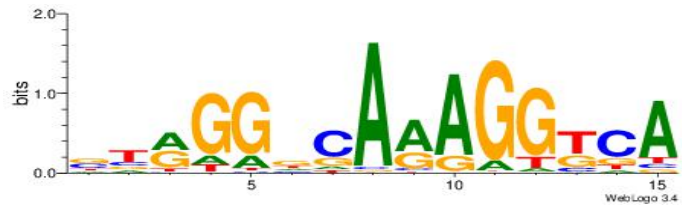


Dataset #: 2
 Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

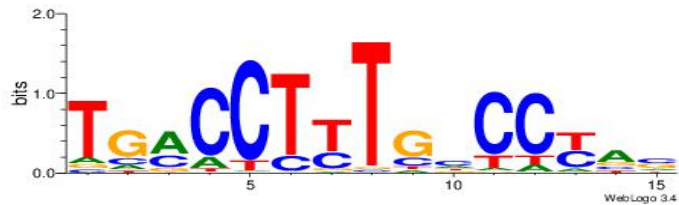
Number of overlap: 15
Similarity score: 1.0449

Alignment:
--BTRGGDCARAGGKCA
RGKTCABVVRGAGGTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCK

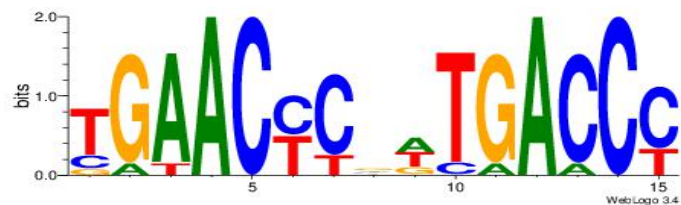
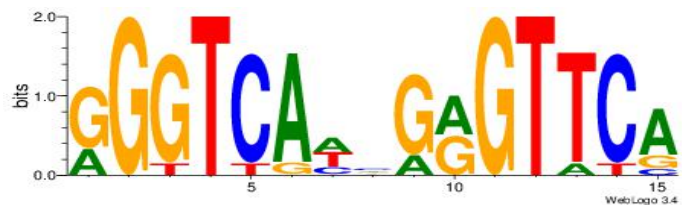


Dataset #: 2
Motif ID: 17
Motif name: RXRAVDR
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 1.05297

Alignment:
GGGTCAWBGRGTTCA--
RGKTCABVVRGAGGTCA

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC



Dataset #: 2
 Motif ID: 22
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 1.56607

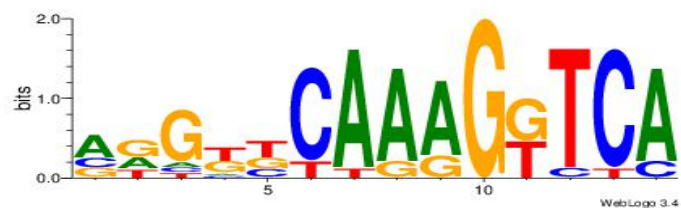
Alignment:

---TGAMCTTTGMMCYT
 TGACCTCKVVB TGAYCK

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC



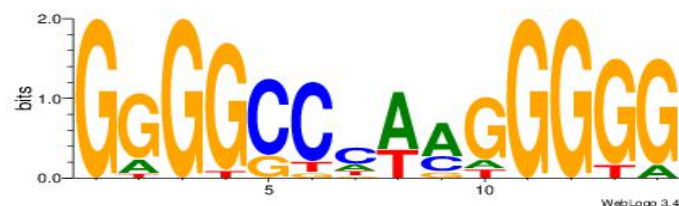
Dataset #: 2
 Motif ID: 21

Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	1.57917

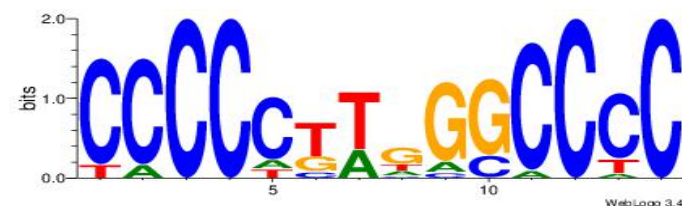
Alignment:

```
GGGGCCCAAGGGG---
RGKTCABVVRGAGGTCA
```

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

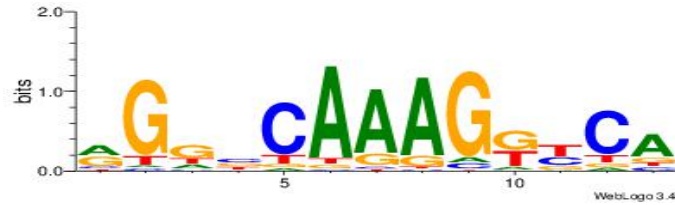


Dataset #:	2
Motif ID:	34
Motif name:	HNF4A
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	2.0437

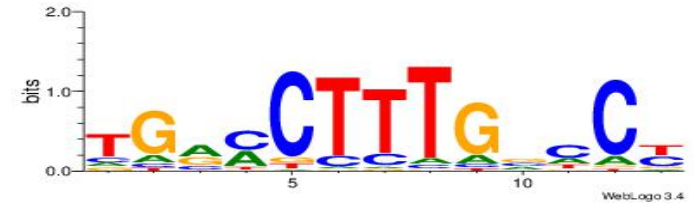
Alignment:

TGMYCTTTGBCK-----
TGACCTCKVVB TGAYCK

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCK



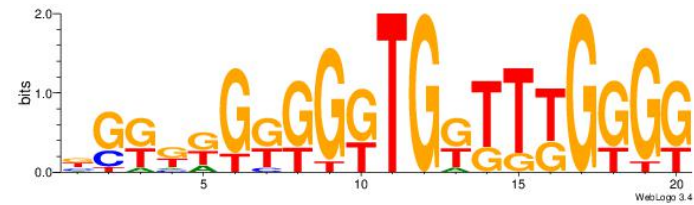
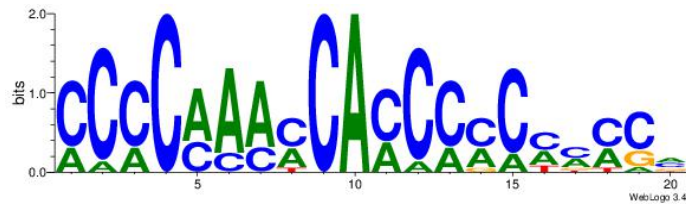
Dataset #:	2
Motif ID:	18
Motif name:	RREB1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	8
Number of overlap:	13
Similarity score:	2.06494

Alignment:

----CCCCMAAMCAMCCMCMMMC
TGACCTCKVVB TGAYCK-----

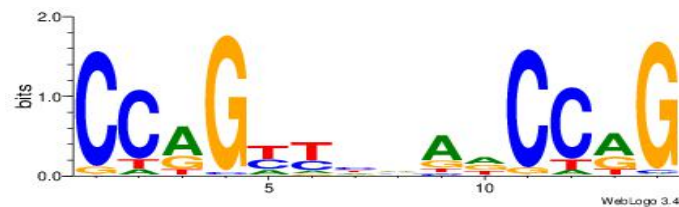
Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC

Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG

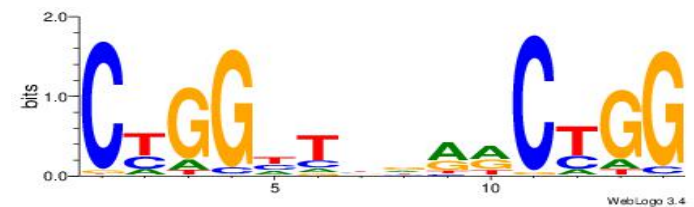


Dataset #: 2 Motif ID: 48 Motif name: Tcfcp2l1

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTG



Best Matches for Motif ID 48 (Highest to Lowest)

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:	3
Number of overlap:	14
Similarity score:	0.0679942

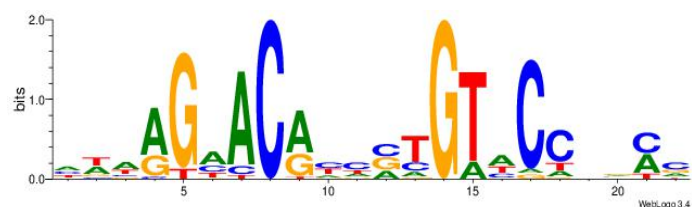
Alignment:

```

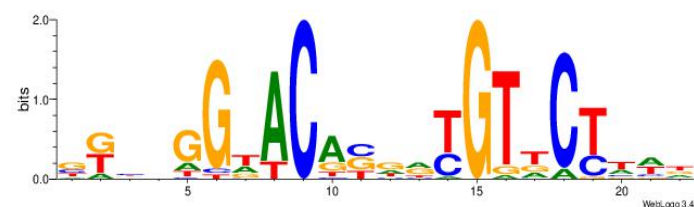
HWDAGHACRHHVTGTHCCHVMV
-----CCAGYYHVADCCRG--

```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

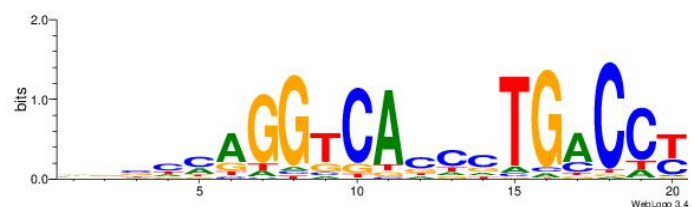


Dataset #: 2
 Motif ID: 29
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0713928

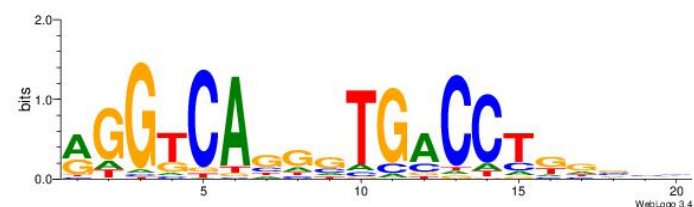
Alignment:

MGGTCAGGGTGACCTRDBHV
 ---CCAGYYHVADCCRG---

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

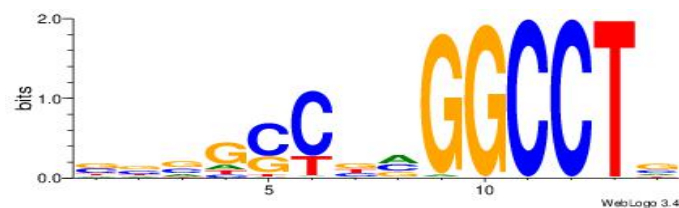


Dataset #: 2
 Motif ID: 12
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0714852

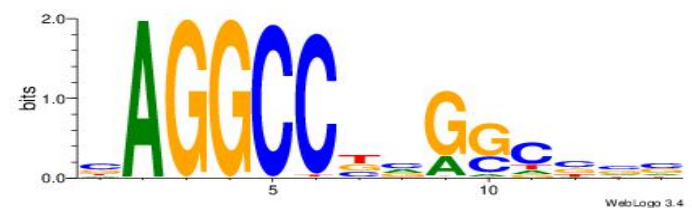
Alignment:

BBVGCCBVGGCCTV
 CCAGYYHVADCCRG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

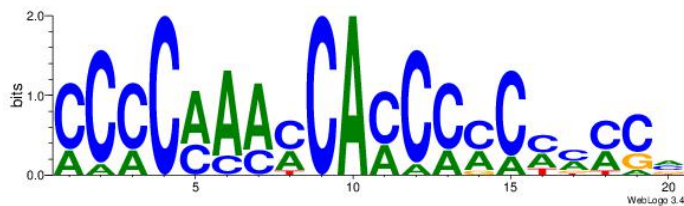


Dataset #: 2
 Motif ID: 18
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14

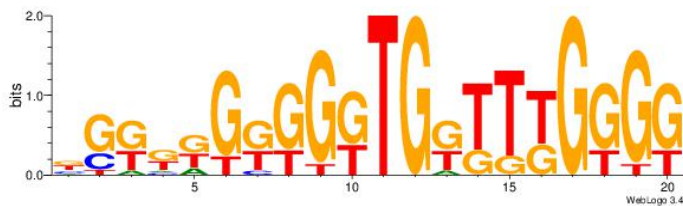
Similarity score: 0.0777364

Alignment:
BGRRRGRGGRTGRTTYGGGG
-----CKGGDTBDMMCTGG--

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

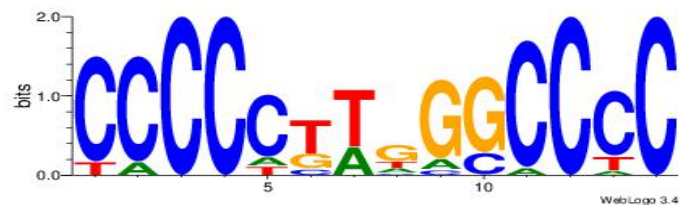
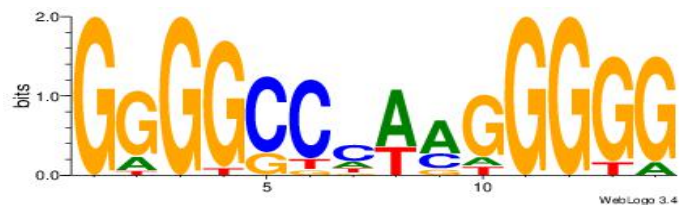


Dataset #: 2
Motif ID: 21
Motif name: PLAG1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0817193

Alignment:
GGGGCCCAAGGGGG
CKGGDTBDMMCTGG

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCC

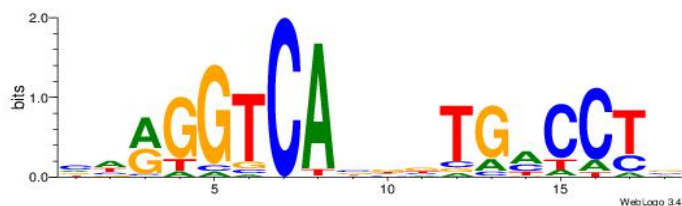


Dataset #: 2
 Motif ID: 30
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0828703

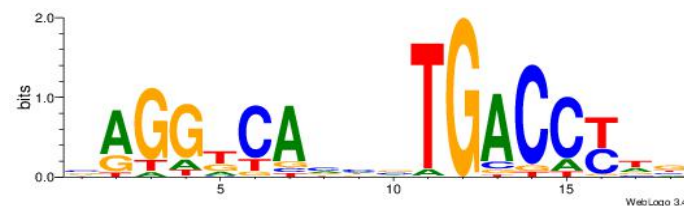
Alignment:

VHRGGTCABDBTGMCTB
 ----CKGGDTBDMCTGG

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



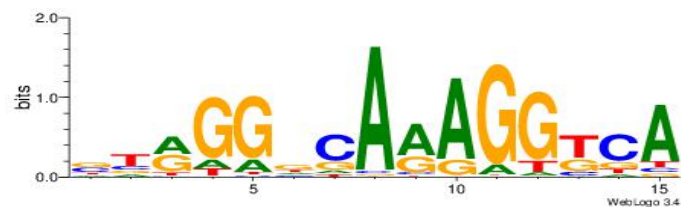
Dataset #: 2

Motif ID: 20
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0829929

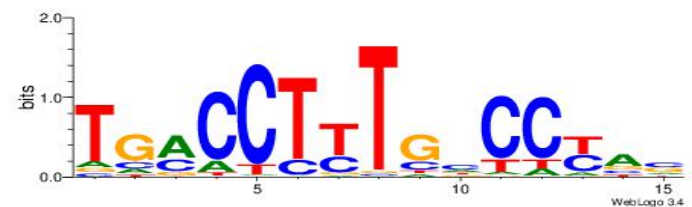
Alignment:

TGRCCTKTGHCKAB
 -CKGGDTBDMCTGG

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKA

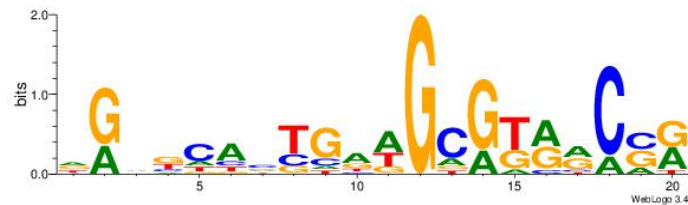


Dataset #: 2
 Motif ID: 45
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.575635

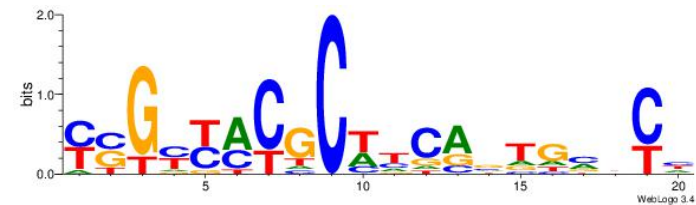
Alignment:

DGVBCABTGDWGCGRRCR-
-----CKGGDTBDMCTGG

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



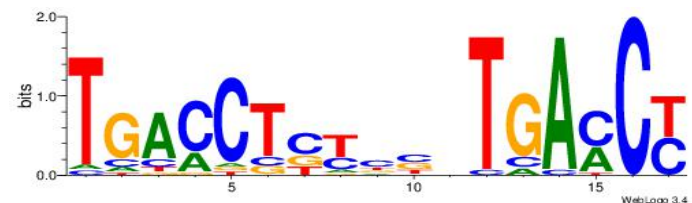
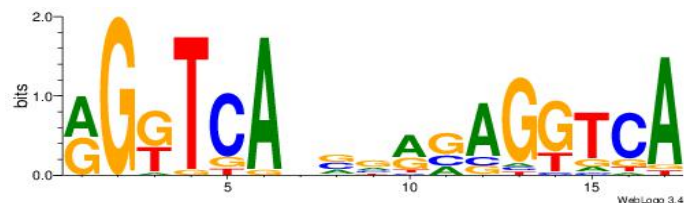
Dataset #:	2
Motif ID:	47
Motif name:	RXRRAR_DR5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	13
Similarity score:	0.578477

Alignment:

RGKTCABVVRGAGGTCA-
----CKGGDTBDMCTGG

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence:
TGACCTCKVVBGTGAYCK



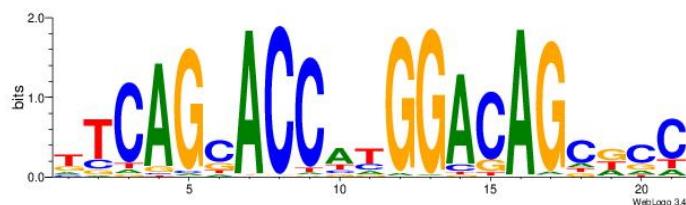
Dataset #: 2
 Motif ID: 19
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 12
 Similarity score: 1.07716

Alignment:

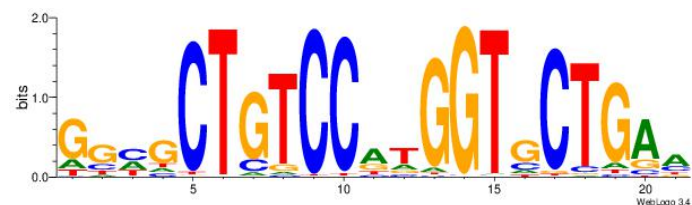
```

--TTCAGCACCATGGACAGCKCC
CKGGDTBDMCTGG-----
  
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Results created by MOTIFSIM on 11-20-2016 13:44:02
Runtime: 673.485 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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