



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

Number of files:	5
Number of top significant motifs:	10
Number of best matches:	10
Similarity cutoff $\geq$	0.75
Matching motif database:	UniProbe Mus Musculus
Motif tree:	Yes
Combined similar motifs:	Yes
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
DREME_DM230.txt	1	1
MEME_DM230.txt	20	2
PScanChIP_DM230.txt	14	3
RSAT_peak-motifs_DM230.txt	10	4
W-ChIPMotifs_DM230.txt	11	5

RESULTS

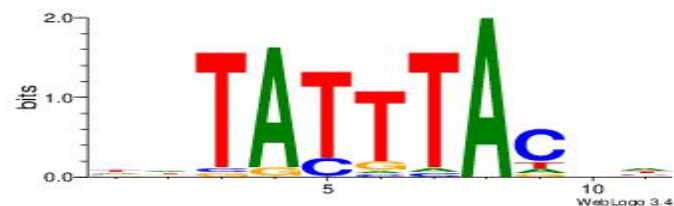
Top 10 Significant Motifs - Global Matching (Highest to Lowest)

Dataset #: 4 **Motif ID: 45** **Motif name: wbgTAAATAww**

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



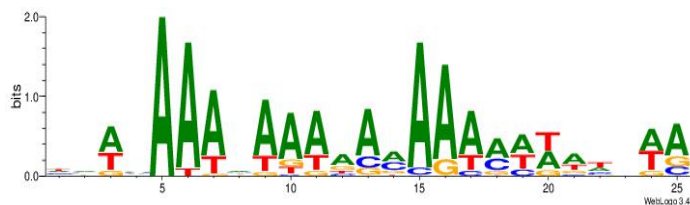
Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	15
Number of overlap:	11
Similarity score:	0.0192768

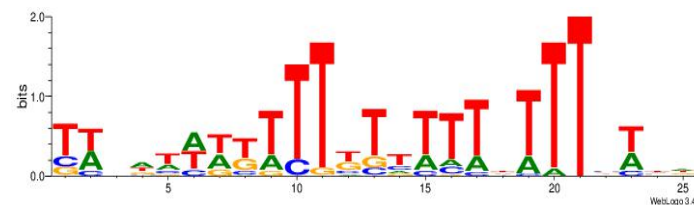
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
-----DHTATTTACBD
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTTHTTTVWBH



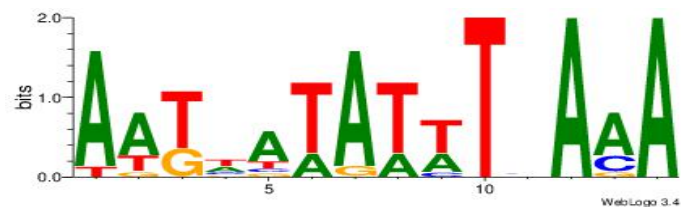
Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0250541

Alignment:

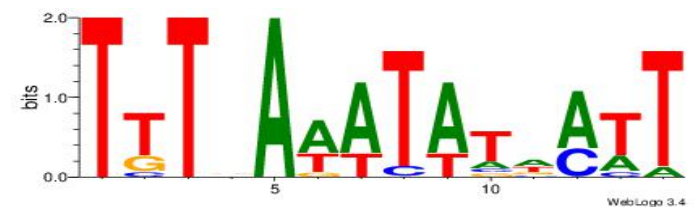
AATHATATWTHAAA

DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.027895

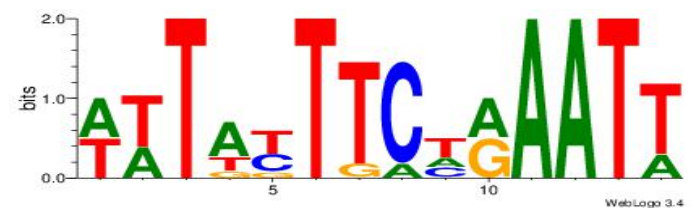
Alignment:

AATTYDGAARTAWW
 ---DBGTAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

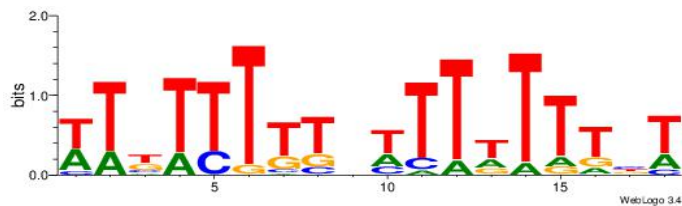


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

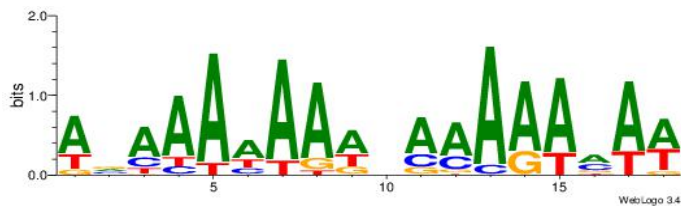
Similarity score: 0.0283217

Alignment:
ABAAAAAAWHAAAAARAW
DBGTAATAHD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW

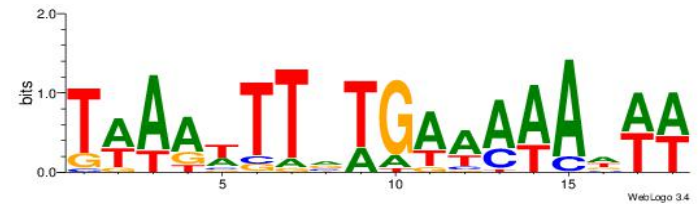
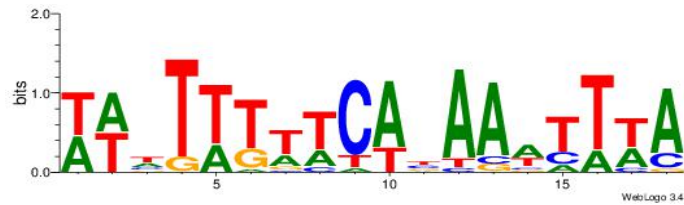


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0308097

Alignment:
TWAAWTTVTGAAAAHWW
-----DBGTAATAHD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TWAAWTTVTGAAAAHWW

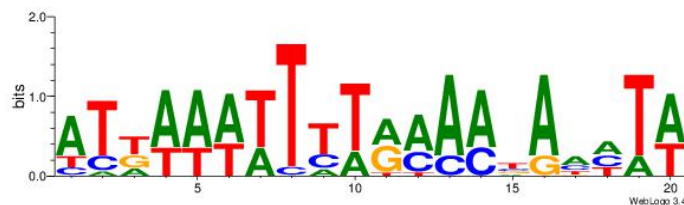


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0333874

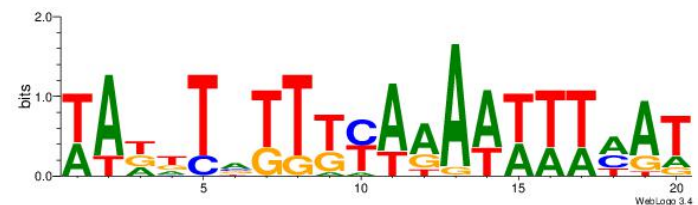
Alignment:

ATKAAWTTTTRMAABAHHTW
 -----DBGTAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2

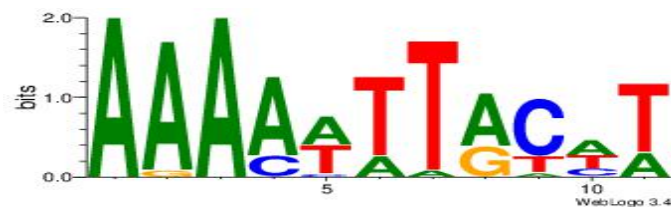
Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0361187

Alignment:

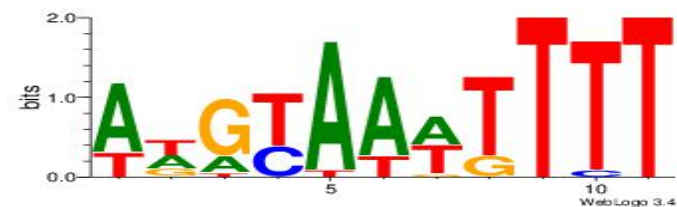
AAAWTTTCWT

DHTATTTACBD

Original motif Consensus sequence: AAAAWTTTCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



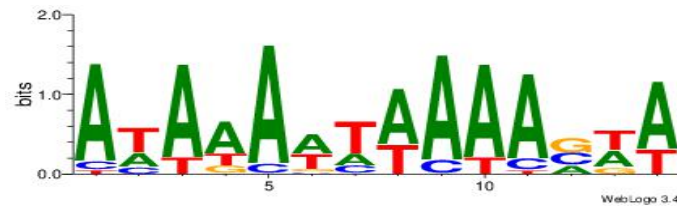
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0410381

Alignment:

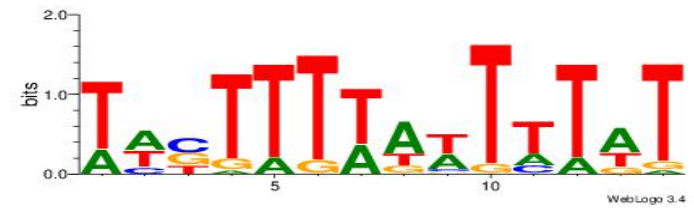
AWAAAWTWAAASWA

--DHTATTTACBD--

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV



Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0477814

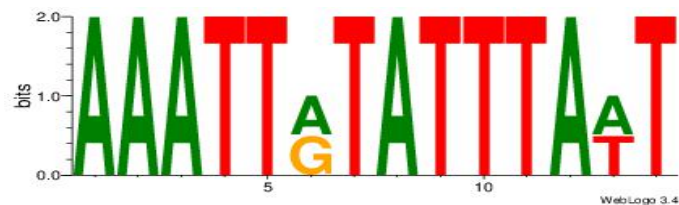
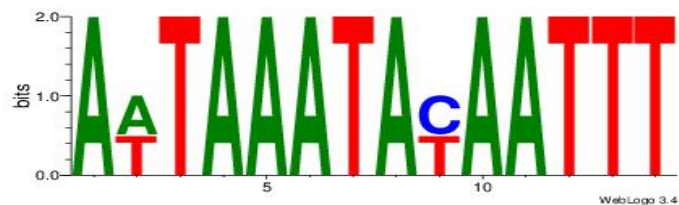
Alignment:

AWTAAATAYAATTT

---DHTATTTACBD

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW

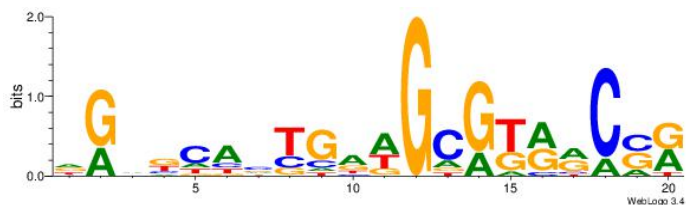


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0512987

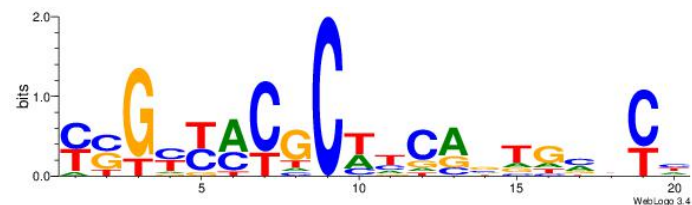
Alignment:

DGVBCABTGDWGCGRRCR
 DBGTAATAHD-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

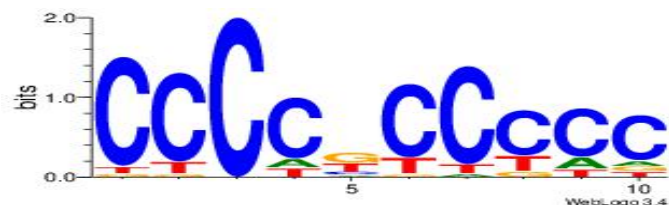


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

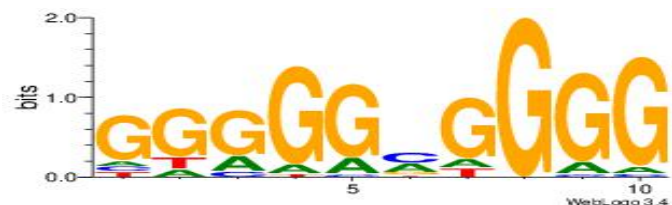


Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



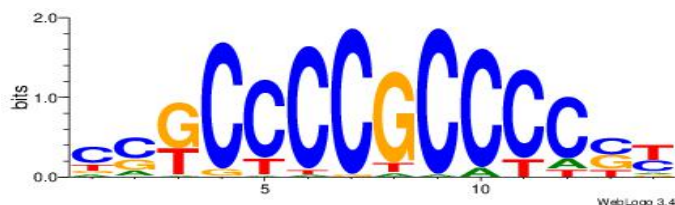
Best Matches for Top Significant Motif ID 24 (Highest to Lowest)

Dataset #:	2
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:	2
Number of overlap:	10
Similarity score:	0.00451594

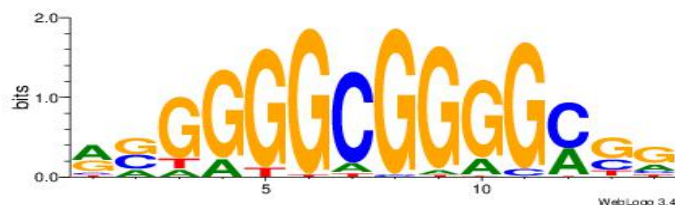
Alignment:

```
CSKCCCCGCCCSY
---CCCCKCCCCC-
```

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

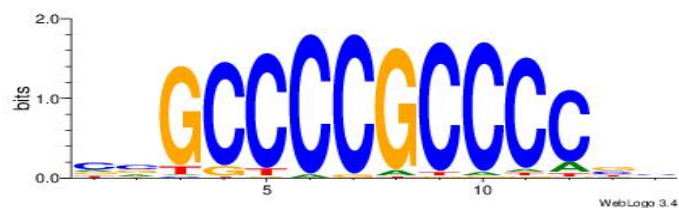


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.00965796

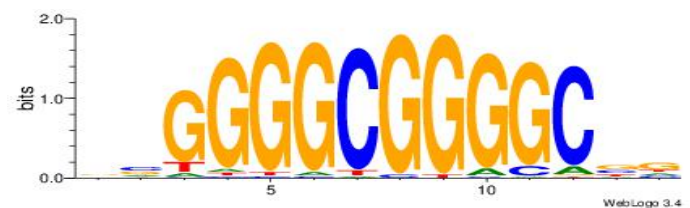
Alignment:

BBGGGGCGGGGCVD
 -GGGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

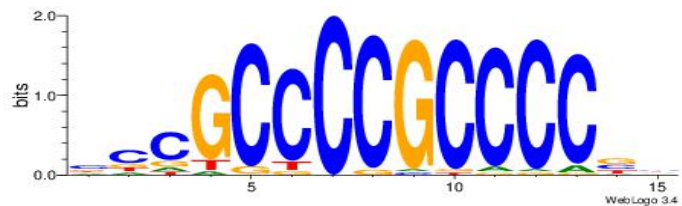


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 10

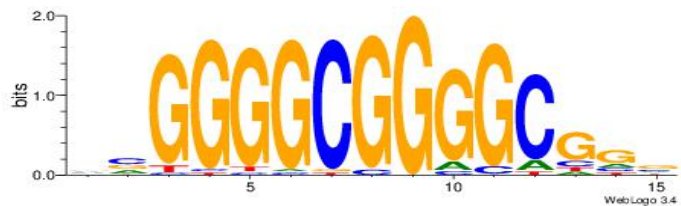
Similarity score: 0.0127292

Alignment:
BBGGGGCGGGGCGGB
-GGGGGYGGGG----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

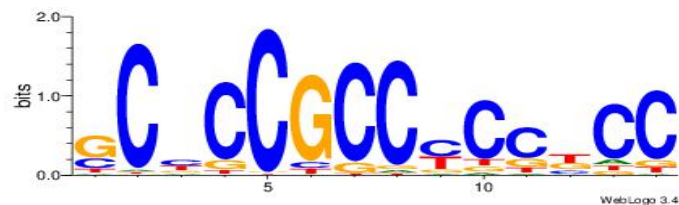
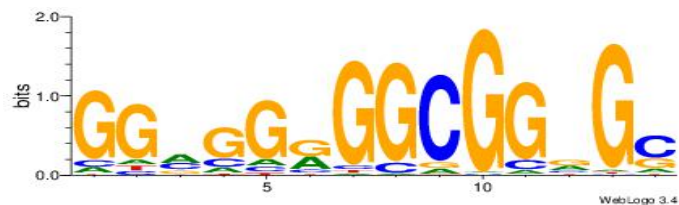


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0174405

Alignment:
GGMGGRGGCGGVGC
---GGGGGYGGGG-

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY

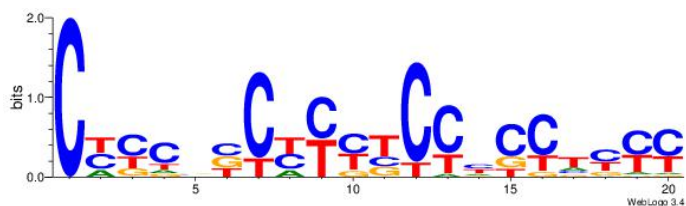


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0301548

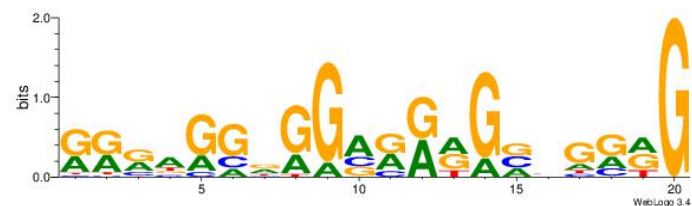
Alignment:

CYYCBBCYYYTCCHCCTYYY
 -----CCCCKCCCC-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



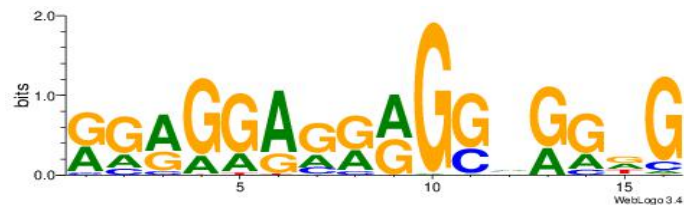
Dataset #: 5

Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0329167

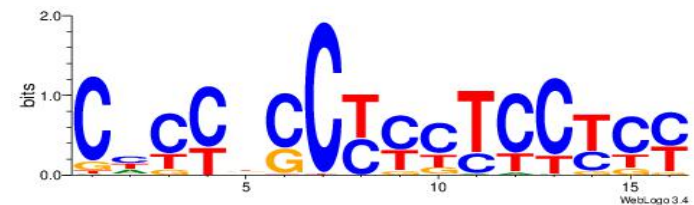
Alignment:

RGRGGAGRRGGHGGDG
 -----GGGGGYGGGG

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

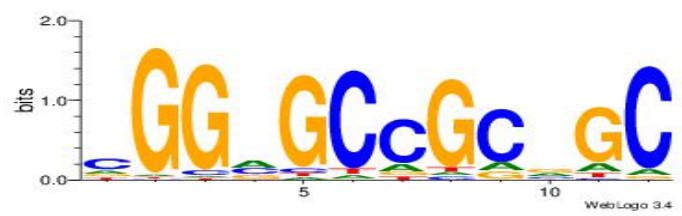


Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10

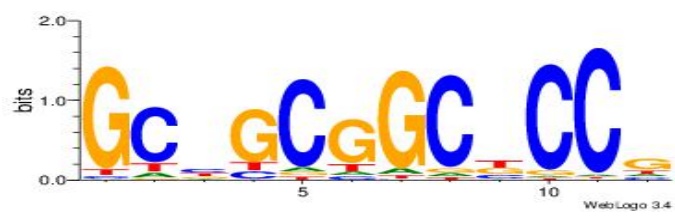
Similarity score: 0.0557738

Alignment:
GCVGCGGCBCCG
-CCCCKCCCCC-

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

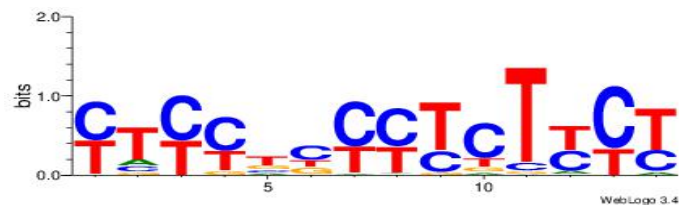
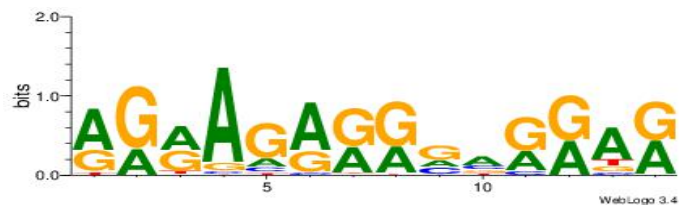


Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0648214

Alignment:
MTMMTCMMTCTKCK
----CCCCKCCCCC

Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



Dataset #: 5
 Motif ID: 48
 Motif name: TFW3
 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: 0.0762976

Alignment:

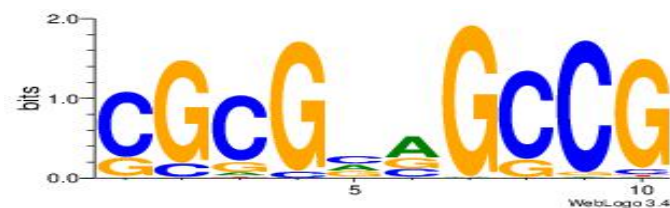
CGGCYBCGCG

CCCCKCCCCC

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



Dataset #: 4
 Motif ID: 40

Motif name: kcACCTGCAGc
 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: 0.0841987

Alignment:

GBTGCAGGTGB
 GGGGGYGGGG-

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 3 Motif ID: 32 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



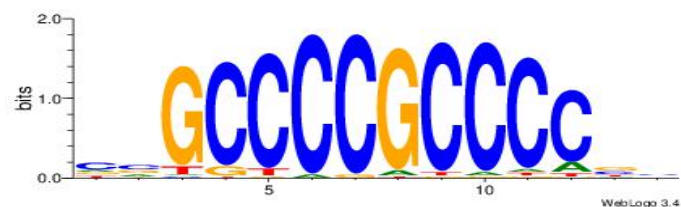
Best Matches for Top Significant Motif ID 32 (Highest to Lowest)

Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 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: 0.0396403

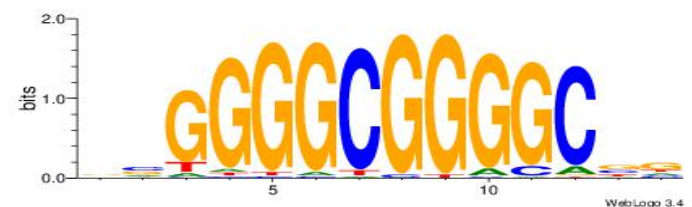
Alignment:

HVGCCCCGCCCCBB
 ----CACGCM----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 1
 Motif ID: 1
 Motif name: Motif 1
 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: 0.040625

Alignment:
GCCCCGCC
--CACGCM

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCCGCC

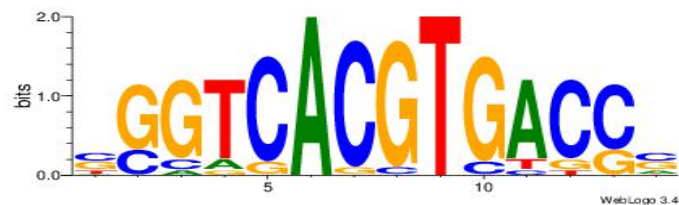
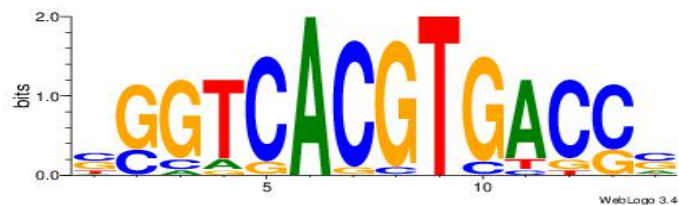


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0412037

Alignment:
SGGTCACGTGACCS
----YGCGTG----

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACCS

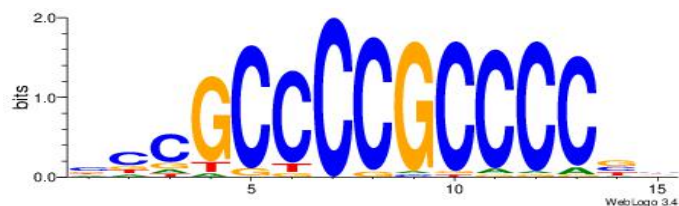


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0425089

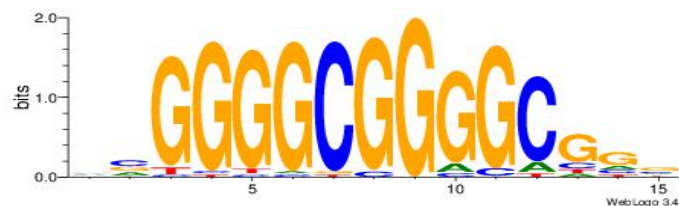
Alignment:

BCCGCCCCGCCCCBB
 -----CACGCM-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

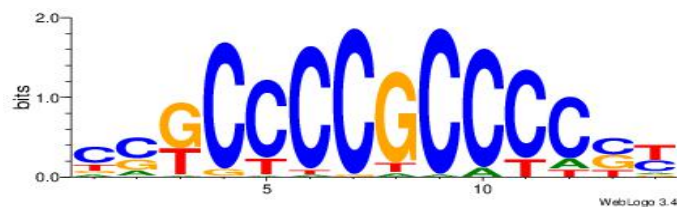


Dataset #: 2

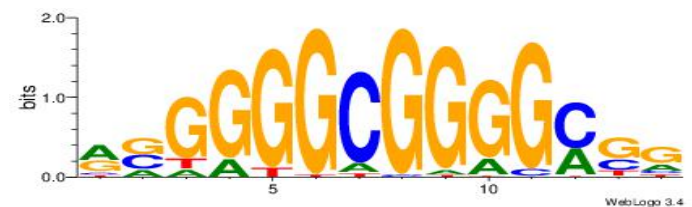
Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0465867

Alignment:
 MSGGGGCGGGYSG
 ----YGCGTG----

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 5
 Motif ID: 47
 Motif name: TFW2
 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: 0.0469722

Alignment:
SCGCGCGG
-YGCGTG-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS

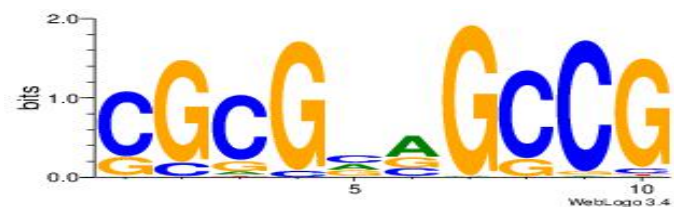
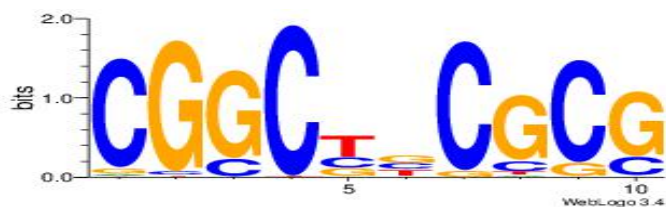


Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0586806

Alignment:
CGCGBMGCCG
CACGCM----

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG



Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 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: 0.0637286

Alignment:

BCACCTGCABC

-YGCGTG----

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



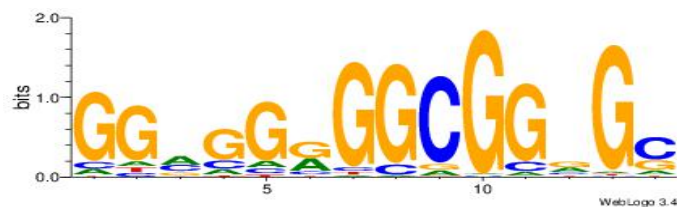
Dataset #: 5
 Motif ID: 50

Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.066121

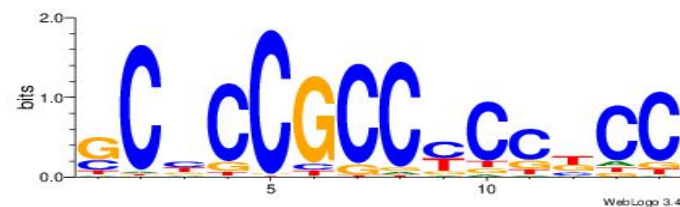
Alignment:

GCVCCGCCMCCYCC
 --CACGCM-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 5
 Motif ID: 46
 Motif name: TFW1
 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: 0.0756826

Alignment:

CGCGAC

CACGCM

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



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

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCCGCC



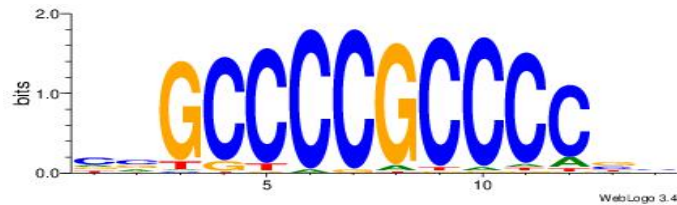
Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5

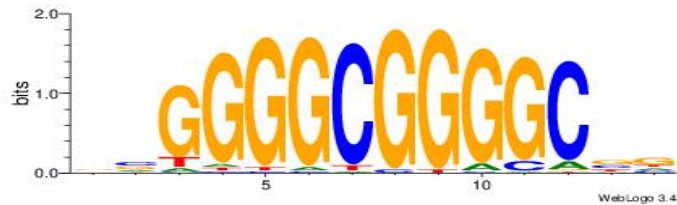
Number of overlap: 8
Similarity score: 0

Alignment:
BBGGGGCGGGGCVD
----GGCGGGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

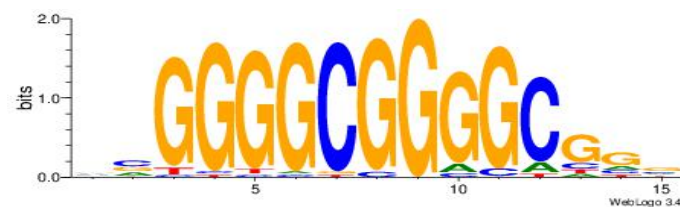
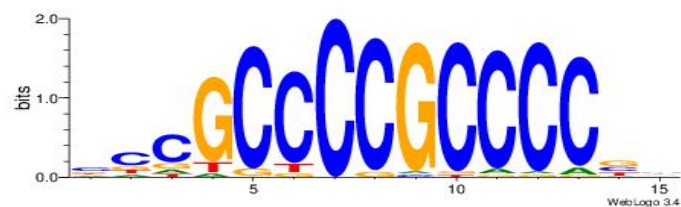


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.00250079

Alignment:
BCCGCCCCGCCCCBB
---GCCCGGCC----

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGB



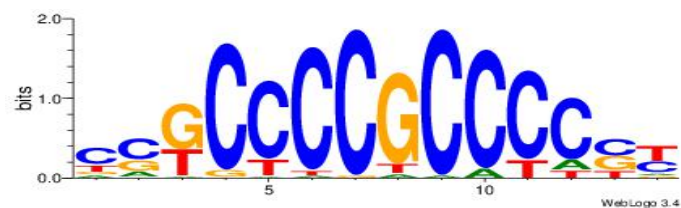
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0149958

Alignment:

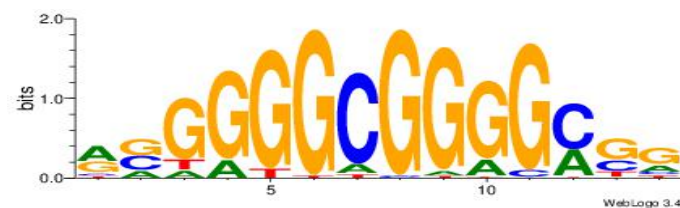
MSGGGGCGGGYSG

----GGCGGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY



Dataset #: 5
 Motif ID: 50

Motif name:	TFF11
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:	0.0348969

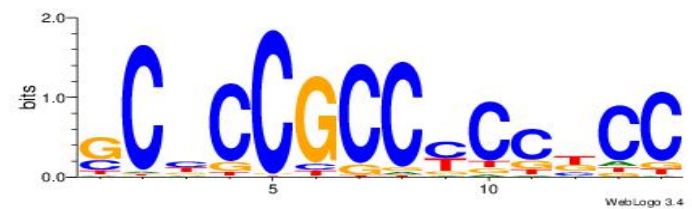
Alignment:

```
GGMGGRGGCGGVGC
-----GGCGGGGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



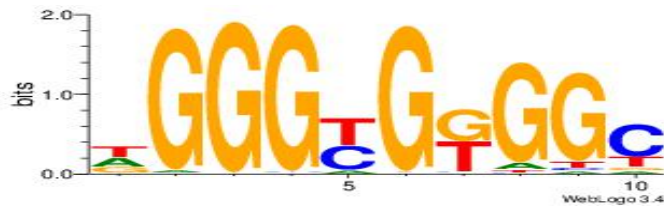
Dataset #:	3
Motif ID:	27
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0349983

Alignment:

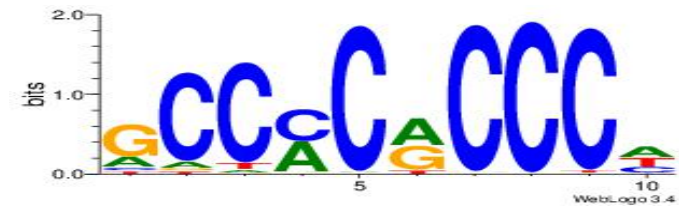
DGGGYGKGGC

--GGCGGGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #:	3
Motif ID:	22
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:	8
Similarity score:	0.0708224

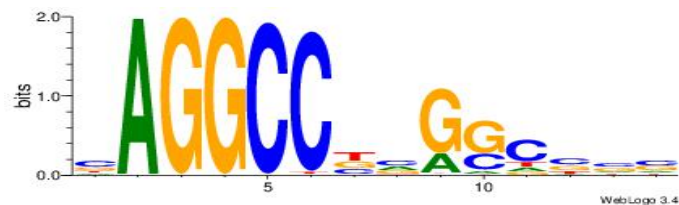
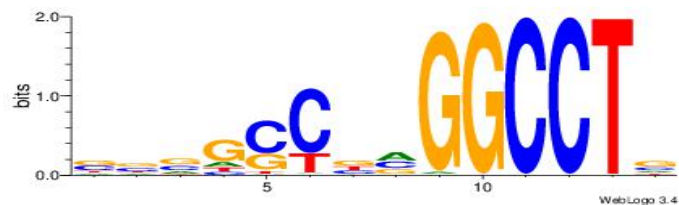
Alignment:

VAGGCCBBGGCVBB

---GCCCGCC---

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Dataset #: 5
 Motif ID: 48
 Motif name: TFW3
 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: 0.071681

Alignment:

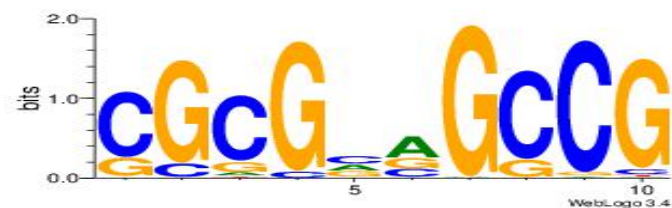
CGCGBMGCCG

-GCCCCGCC-

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

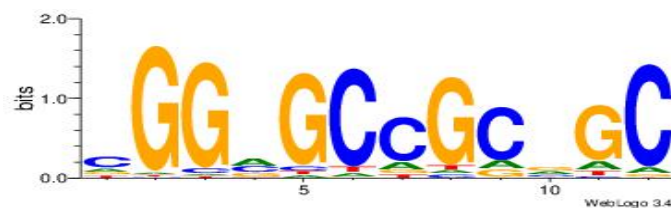


Dataset #: 5
 Motif ID: 49

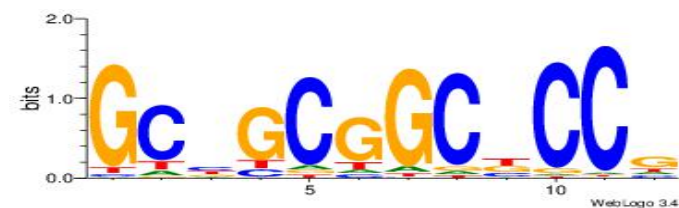
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0803996

Alignment:
CGGVGCCGCVGC
--GCCCCGCC--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



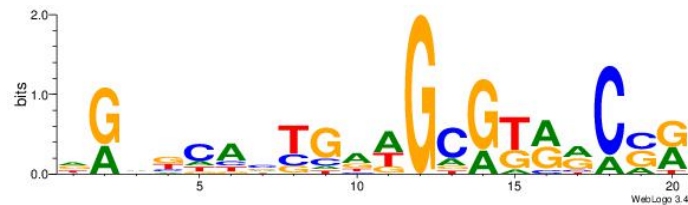
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0853847

Alignment:

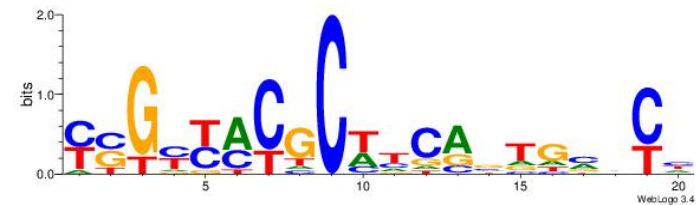
DGVBCABTGDWGCGRRCR

-----GGCGGGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



Dataset #:	3
Motif ID:	23
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:	8
Similarity score:	0.0878731

Alignment:

YCGCCCACGCH

---GCCCCGCC

Original motif Consensus sequence: HGCGTGGGCGK

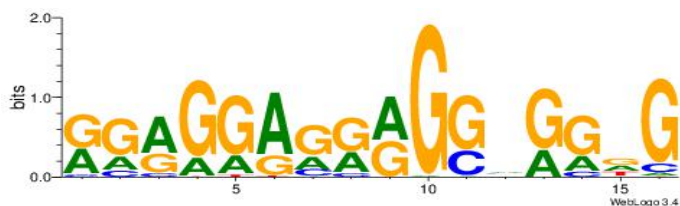
Reverse complement motif Consensus sequence: YCGCCCACGCH



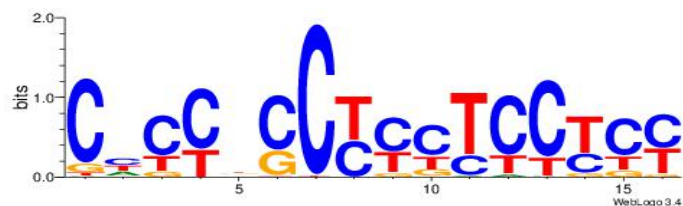
Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0928252

Alignment:
 CHCCBCKMCTCCKCM
 --GCCCCGCC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



Dataset #: 5 Motif ID: 46 Motif name: TFW1

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



Best Matches for Top Significant Motif ID 46 (Highest to Lowest)

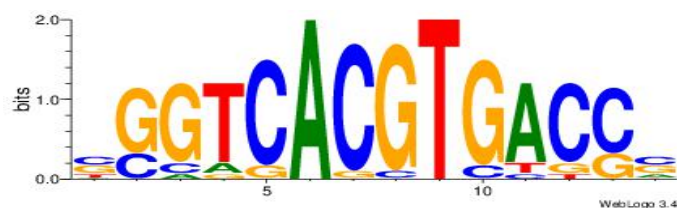
Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACCS
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0375102

Alignment:

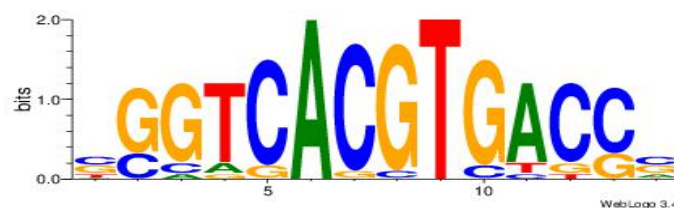
SGGTCACGTGACCS

--GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 3
 Motif ID: 33
 Motif name: Mycn
 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: 0.0537993

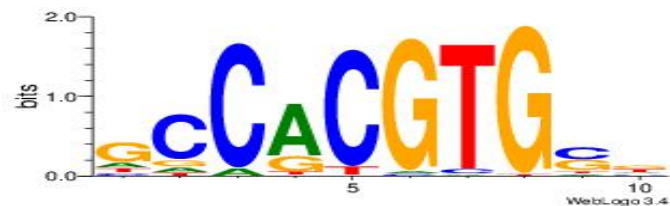
Alignment:

GCCACGTGSD
 ----GTCGCG

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

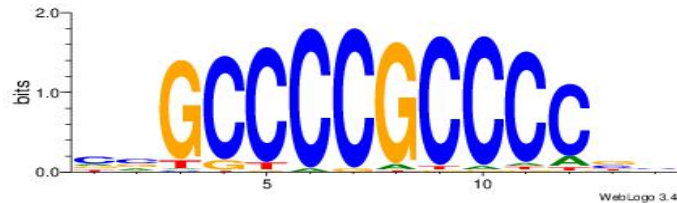


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6

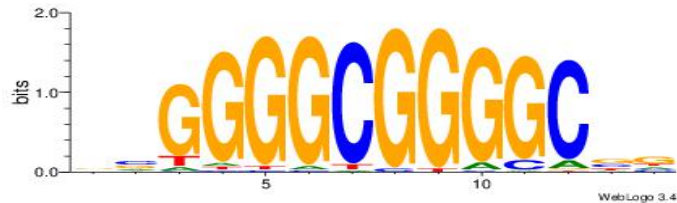
Similarity score: 0.0539

Alignment:
HVGCCCGCCCCBB
--GTCGCG-----

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC



Dataset #: 1
Motif ID: 1
Motif name: Motif 1
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: 0.0554263

Alignment:
GCCCGGCC
--GTCGCG

Original motif Consensus sequence: GCCCGGCC

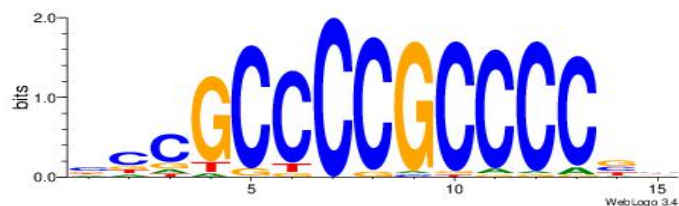
Reverse complement motif Consensus sequence: GCCCGGCC



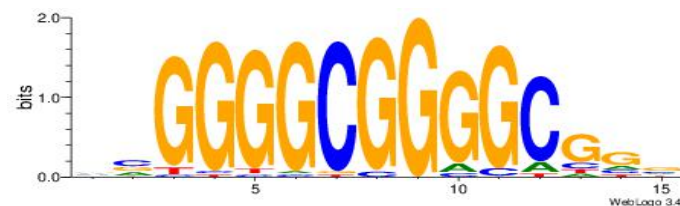
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0558733

Alignment:
 BBGGGGCGGGGCGGB
 -----GTCGCG--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

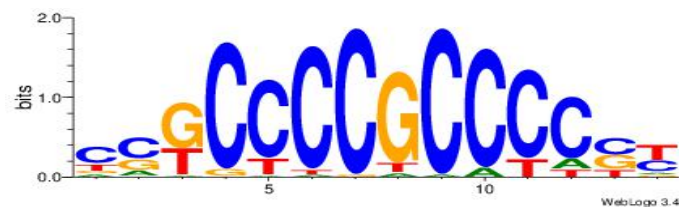


Dataset #: 2

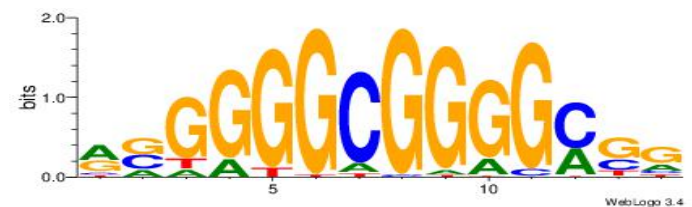
Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0644512

Alignment:
 CSKCCCCGCCCSY
 --CGCGAC-----

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

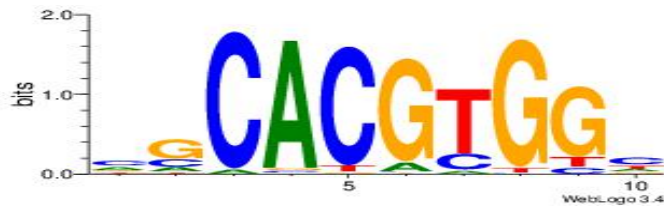


Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0664905

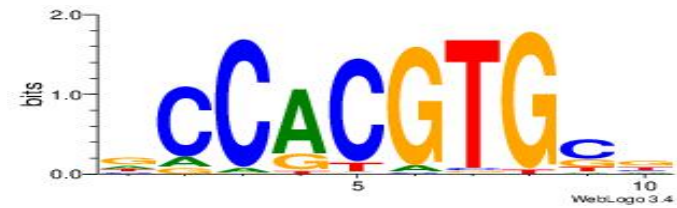
Alignment:

DCCACGTGCV
----GTCGCG

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #:	3
Motif ID:	28
Motif name:	E2F1
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:	0.0698654

Alignment:

GCGCSAAA
-CGCGAC-

Original motif Consensus sequence: TTTSGCGC

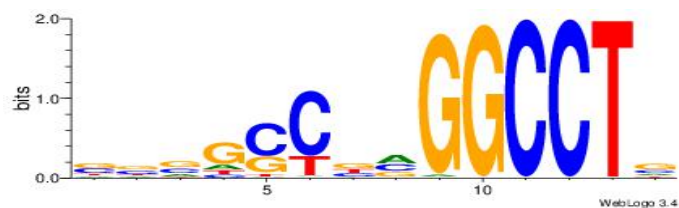
Reverse complement motif Consensus sequence: GCGCSAAA



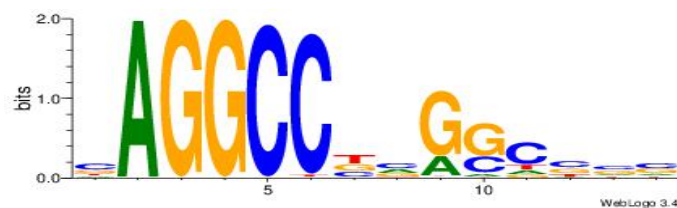
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.069909

Alignment:
 BBVGCCBVGGCCTV
 ---GTCGCG-----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



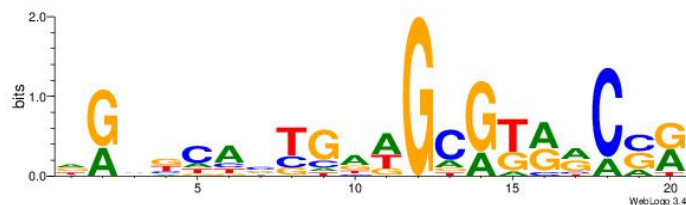
Dataset #: 3
 Motif ID: 31

Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.072456

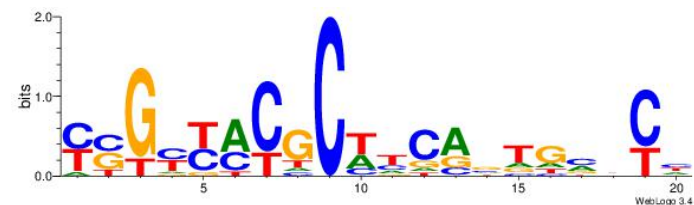
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----CGCGAC-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

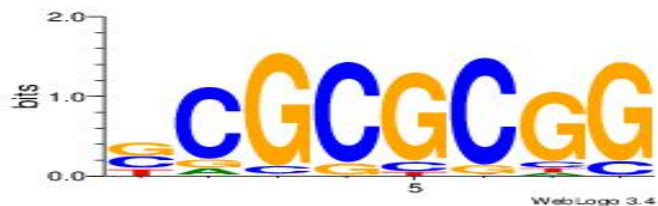


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 5 Motif ID: 47 Motif name: TFW2

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



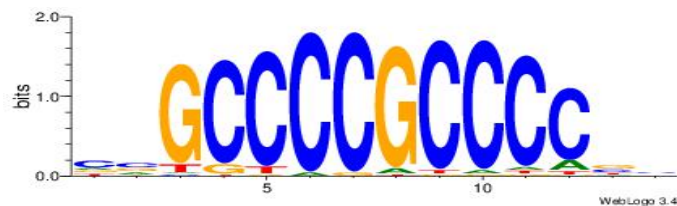
Best Matches for Top Significant Motif ID 47 (Highest to Lowest)

Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0456233

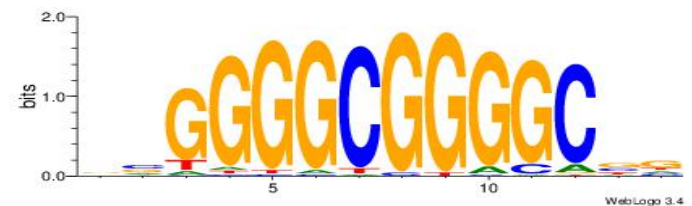
Alignment:

HVGCCCCGCCCCBB
 -CCGCGCGS-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

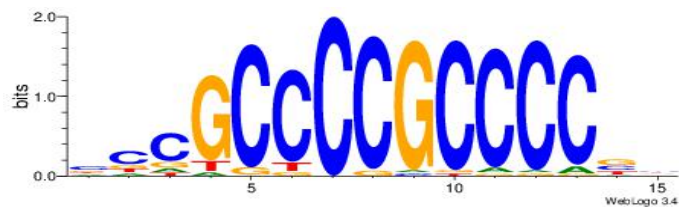


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement

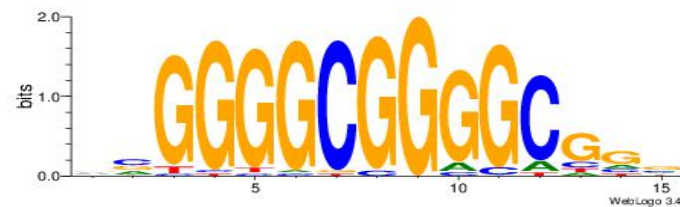
Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

Alignment:
 BBGGGGCGGGGCGGB
 -----SCGCGCGG--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



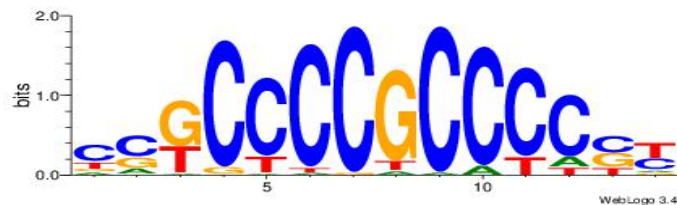
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



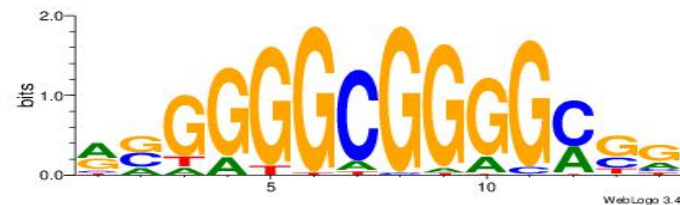
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0504058

Alignment:
 CSKCCCCGCCCCSY
 -CCGCGCGS-----

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 3
Motif ID: 33
Motif name: Mycn
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: 0.0527532

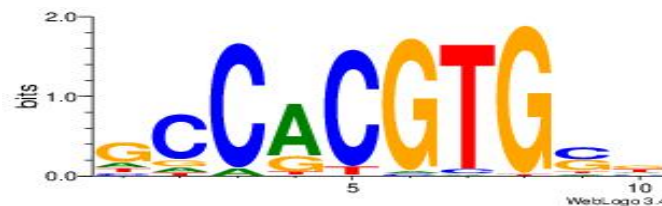
Alignment:

HSCACGTGGC
-SCGCGCGG-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 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: 0.0574543

Alignment:

VGCACGTGGH

–SCGCGCGG–

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 3
 Motif ID: 25
 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: 8

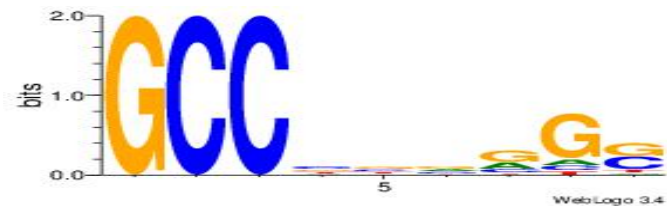
Similarity score: 0.0678925

Alignment:

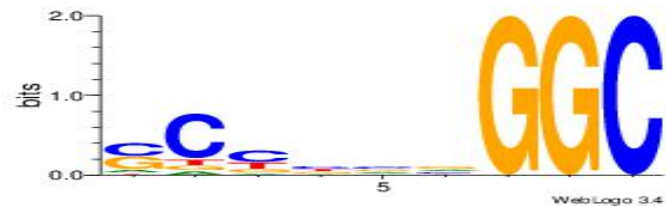
SCMVBBGGC

-SCGCGCGG

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



Dataset #: 3
Motif ID: 24
Motif name: SP1
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: 0.07018

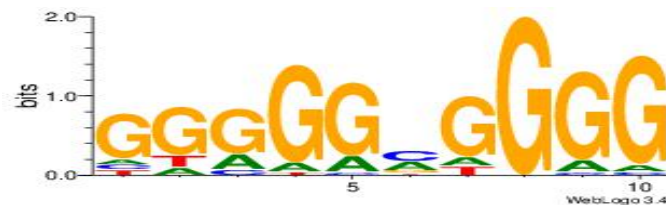
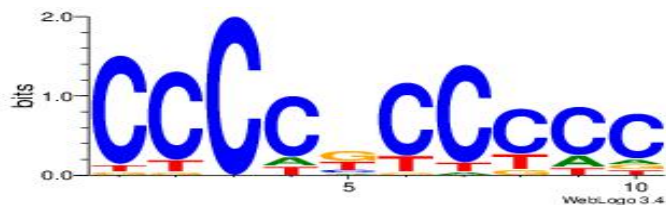
Alignment:

CCCCKCCCCC

--CCGCGCGS

Original motif Consensus sequence: CCCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG



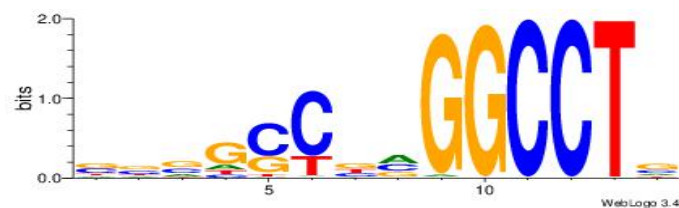
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0710499

Alignment:

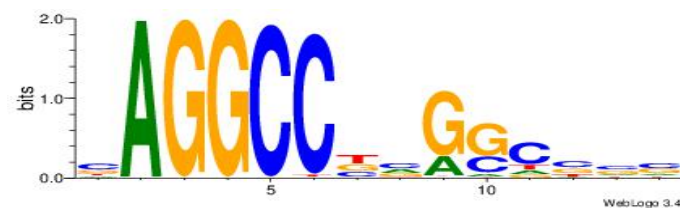
BBVGCCBVGGCCTV

--SCGCGCGG----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



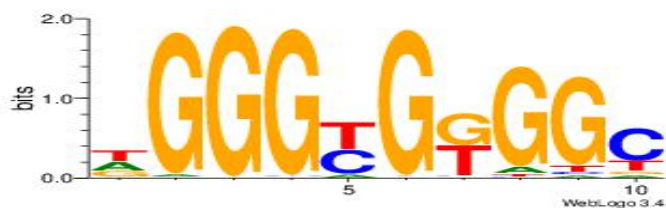
Dataset #: 3
 Motif ID: 27

Motif name:	Klf4
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:	0.0768965

Alignment:

DGGGYGKGGC
 -SCGCGCGG-

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



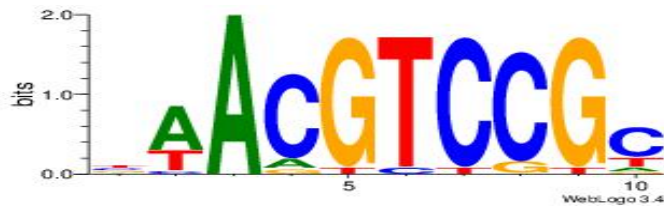
Dataset #:	3
Motif ID:	26
Motif name:	MIZF
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0837414

Alignment:

GCGGACGTTV

--SCGCGCGG

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



Dataset #: 3 Motif ID: 29 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Best Matches for Top Significant Motif ID 29 (Highest to Lowest)

Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAGc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

Number of overlap: 8
Similarity score: 0.0295473

Alignment:
GBTGCAGGTGB
---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

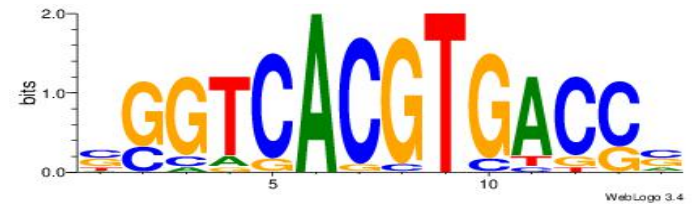
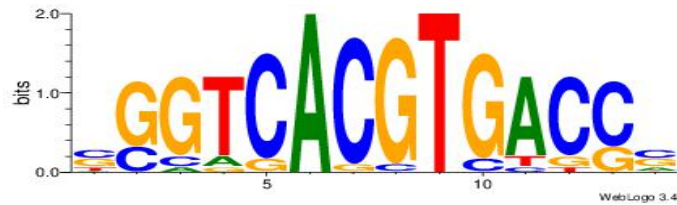


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACs
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0314837

Alignment:
SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 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: 0.0640024

Alignment:
 DHACATTCTGH
 VCACGTBV---

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 5
 Motif ID: 47

Motif name:	TFW2
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:	0.0660185

Alignment:
CCGCGCGS
VBACGTGV

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.067219

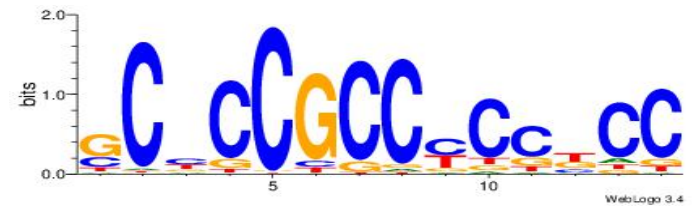
Alignment:

GCVCCGCCMCCYCC
 -----VCACGTBV

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



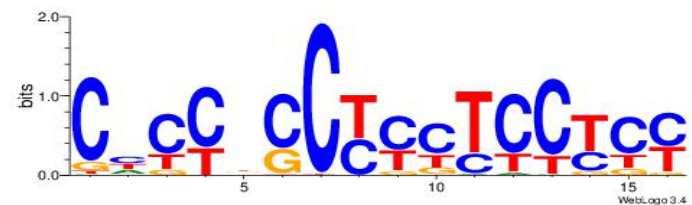
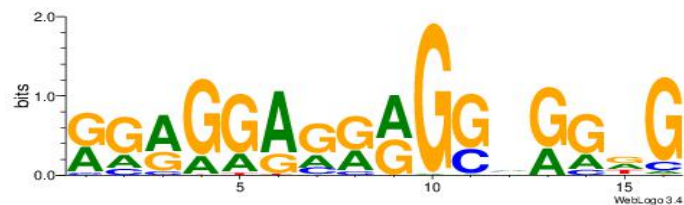
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0698117

Alignment:

RGRGGAGRRGGHGGDG
 ---VBACGTGV-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

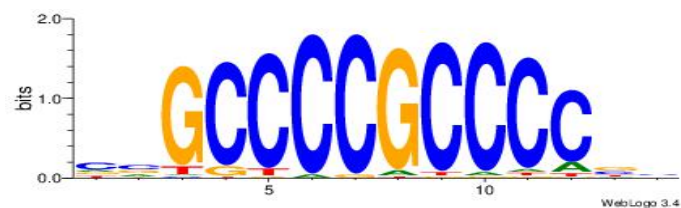
Reverse complement motif Consensus sequence:
 CHCCBCKMCTCCKCM



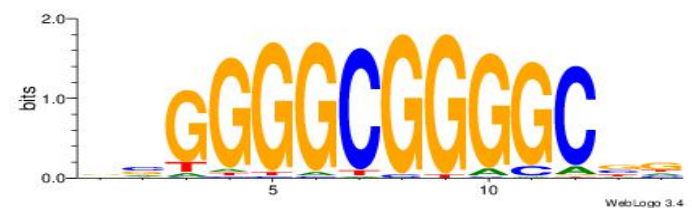
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0711168

Alignment:
 BBGGGGCGGGGCVD
 ---VBACGTGV---

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 4
 Motif ID: 38

Motif name:	cccGCCCCGCCCCsb
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:	0.0735453

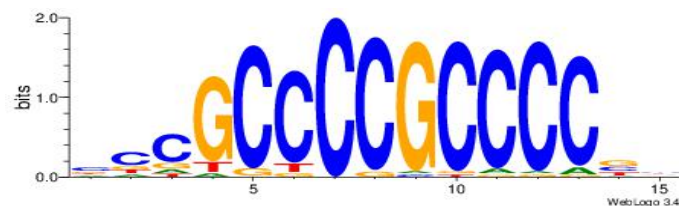
Alignment:

```

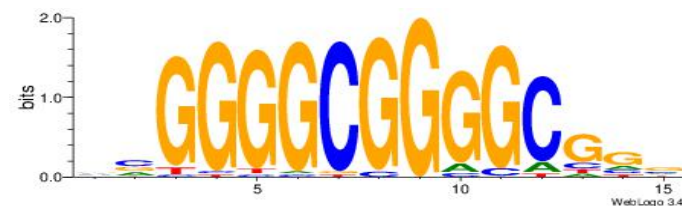
BBGGGGCGGGGCGGB
---VBACGTGV-----

```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

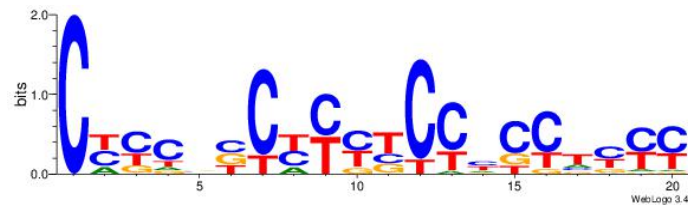


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	12
Number of overlap:	8
Similarity score:	0.0757612

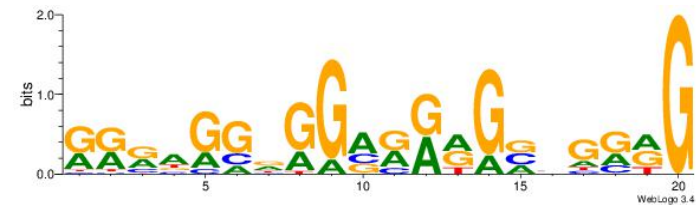
Alignment:

KKKAGGDGGAKKMGBBGKMG
-VBACGTGV-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



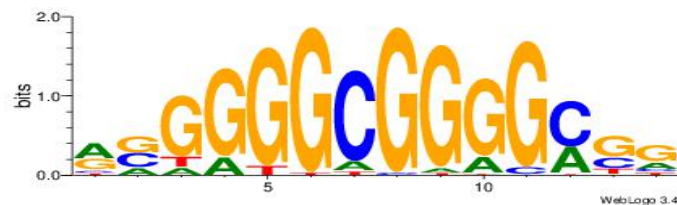
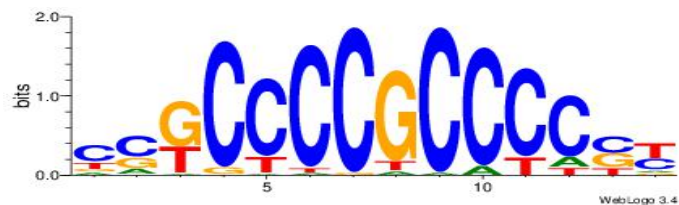
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0775335

Alignment:

CSKCCCCGCCCSY
---VCACGTBV---

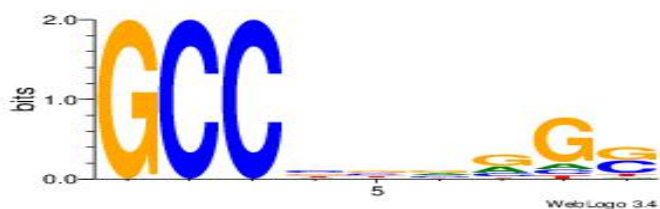
Original motif Consensus sequence: CSKCCCCGCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY

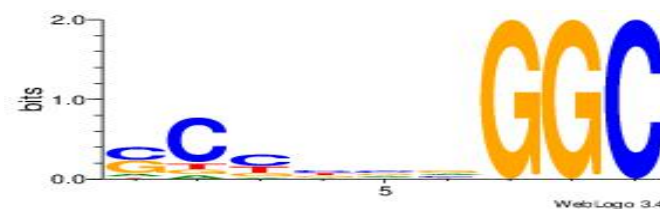


Dataset #: 3 **Motif ID: 25** **Motif name: TFAP2A**

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



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

Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.0415732

Alignment:

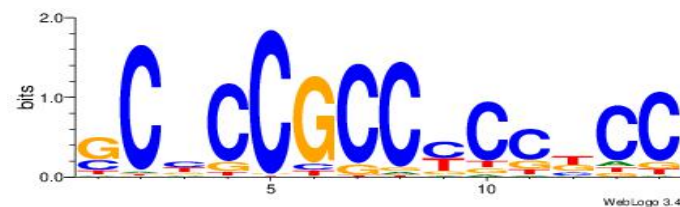
GGMGGRGGCGGVGC

SCMVBBGGC-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

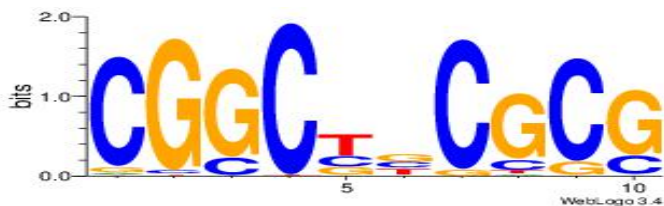


Dataset #: 5
Motif ID: 48
Motif name: TFW3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 9
Similarity score: 0.0552877

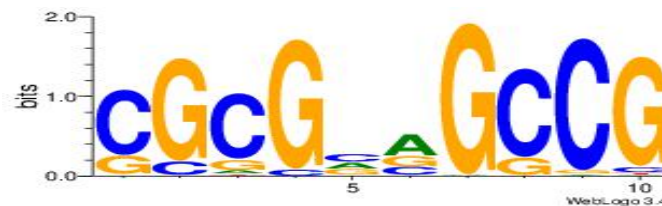
Alignment:

CGGCYBCGCG
-GCCBBVRGS

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

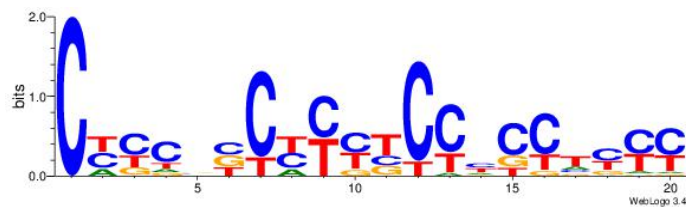


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 9
 Similarity score: 0.0630429

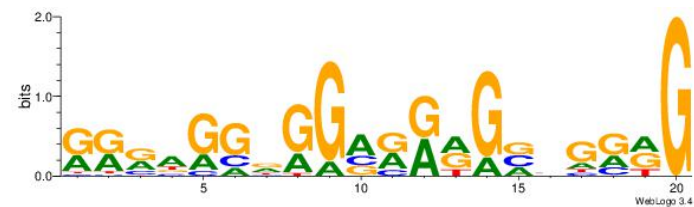
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -SCMVBBGGC-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

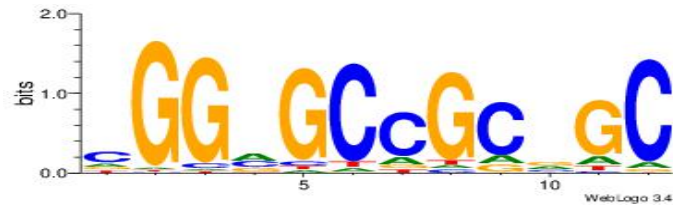


Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

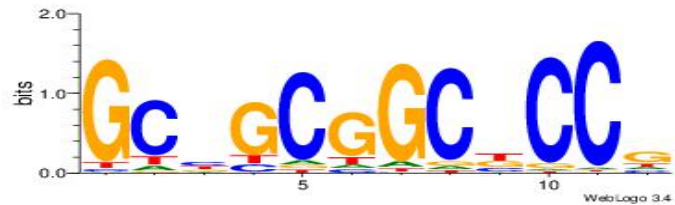
Number of overlap: 9
Similarity score: 0.0669772

Alignment:
GCVGCGGCBCCG
SCMVBBGGC---

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

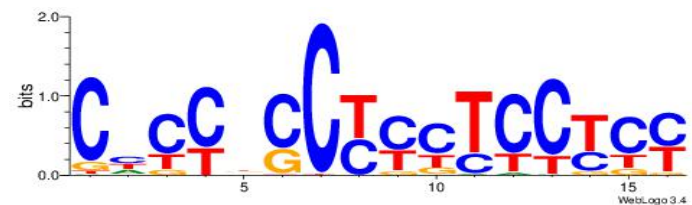
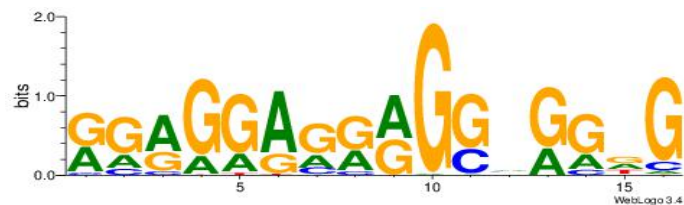


Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 9
Similarity score: 0.069755

Alignment:
CHCCBCKMCTCCKCM
SCMVBBGGC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM



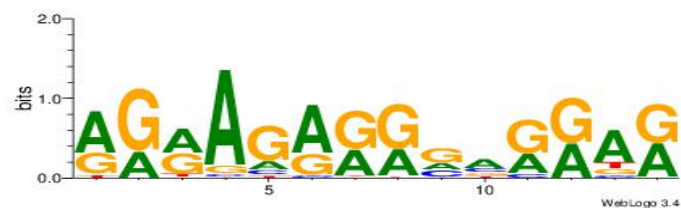
Dataset #: 2
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0715961

Alignment:

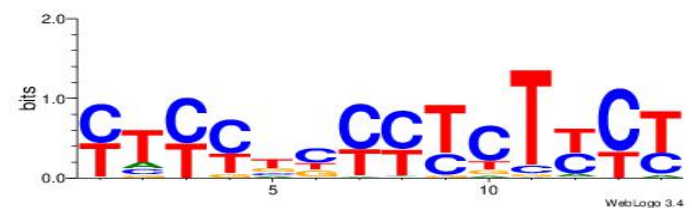
MTMMTCMMTCTKCK

----SCMVBBGGC--

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



Dataset #: 4
 Motif ID: 38

Motif name:	cccGCCCCGCCCCsb
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:	0.0719489

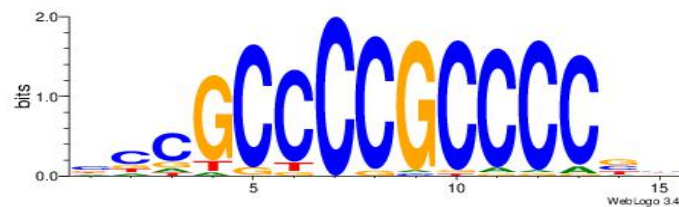
Alignment:

```

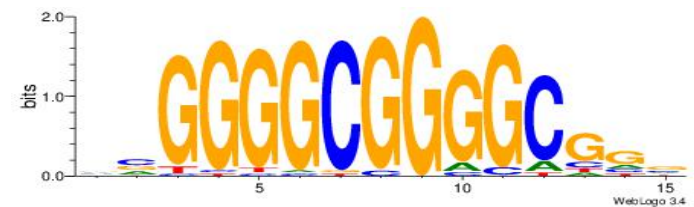
BBGGGGCGGGGCGGB
-----GCCBBVRGS-

```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



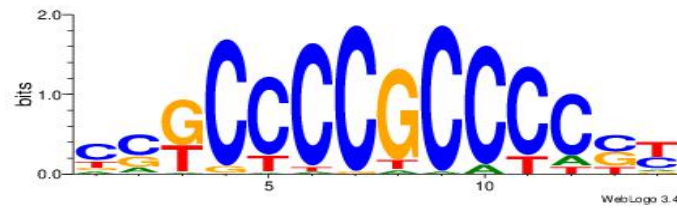
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0781606

Alignment:

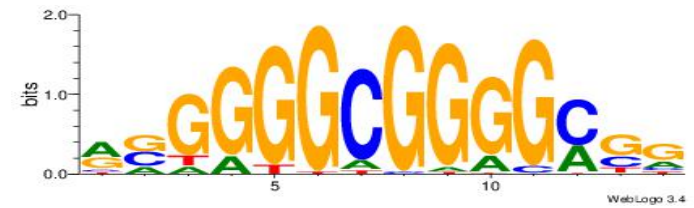
CSKCCCCGCCCCSY

-----SCMVBBGGC

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0800026

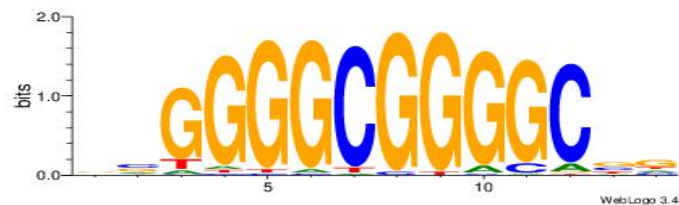
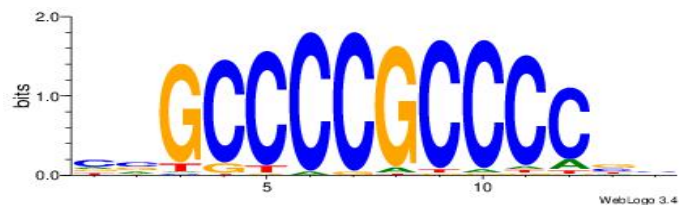
Alignment:

BBGGGGCGGGGCVD

-----GCCBBVRGS

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0857416

Alignment:

BCACCTGCABC

--GCCBBVRGS

Original motif Consensus sequence: BCACCTGCABC

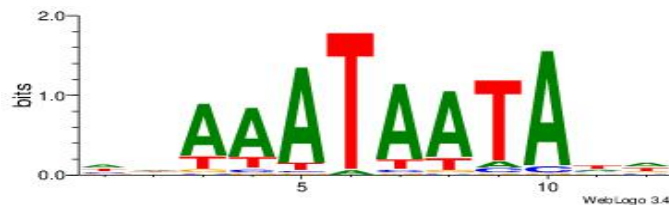


Reverse complement motif Consensus sequence: GBTGCAGGTGB

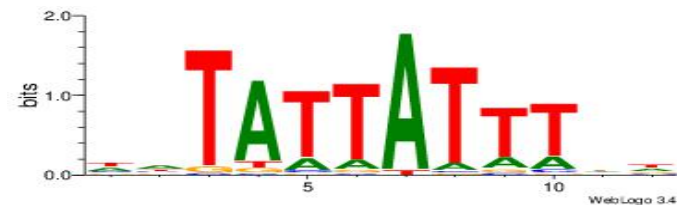


Dataset #: 4 Motif ID: 41 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTDDH



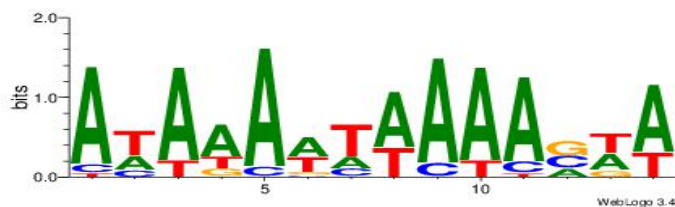
Best Matches for Top Significant Motif ID 41 (Highest to Lowest)

Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
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:	0.0536028

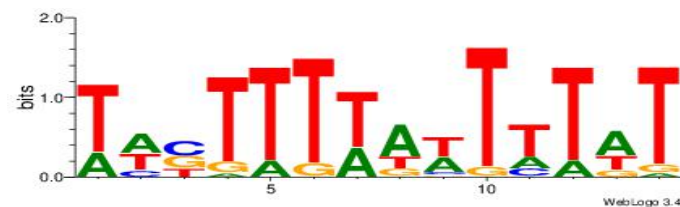
Alignment:

AWAAAWTWAAASWA
 -HDAAATAATADD-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV

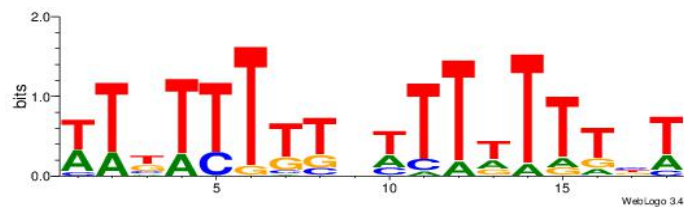


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0565705

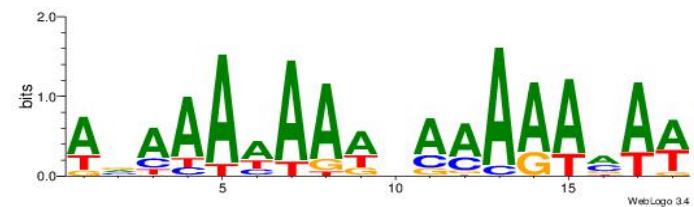
Alignment:

WTKTTTTTHWTTTTTBT
 -----DDTATTATTTDH

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

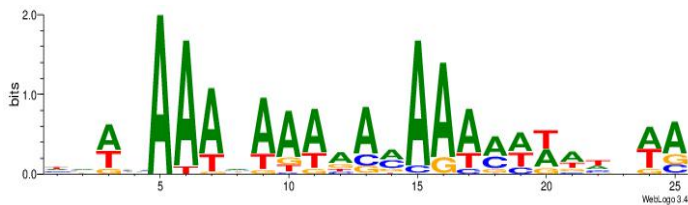


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

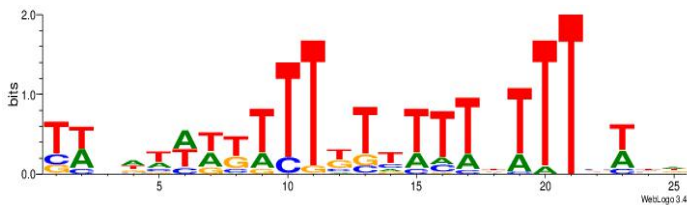
Number of overlap: 12
Similarity score: 0.0575935

Alignment:
HDWVAAAHA AAAA MAAAMWWWHBWA
--HDAAATAATADD-----

Original motif Consensus sequence:
HDWVAAAHA AAAA MAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH

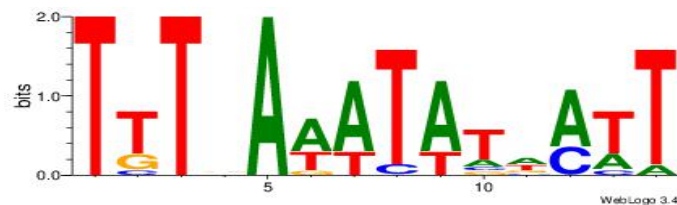
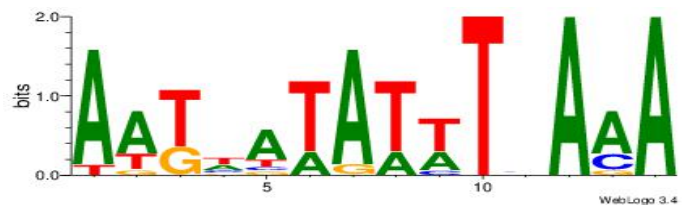


Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0591821

Alignment:
AATHATATWTHAAA
--DDTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT

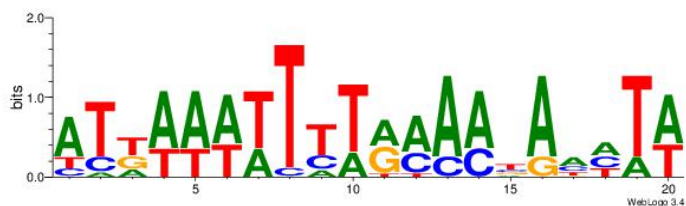


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0712963

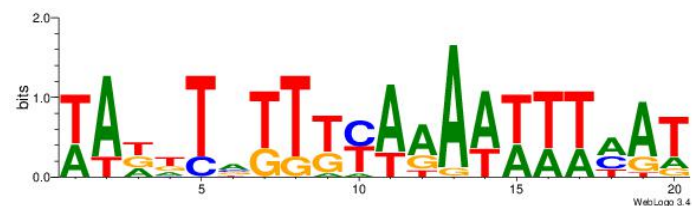
Alignment:

WAHHTVTTYKAAAATTRAT
 -----HDAAATAATADD

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

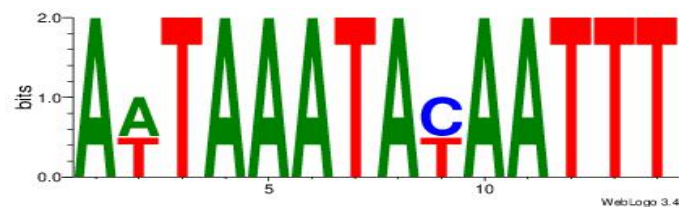


Dataset #: 2

Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0715278

Alignment:
 AAATTKTATTTAWT
 -DDTATTATTTDH-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

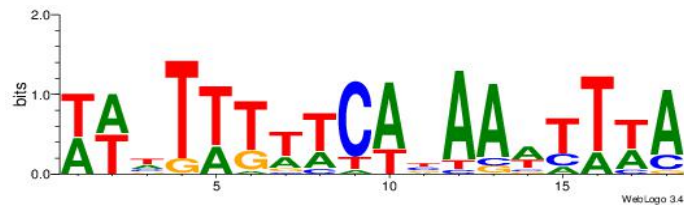


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0733516

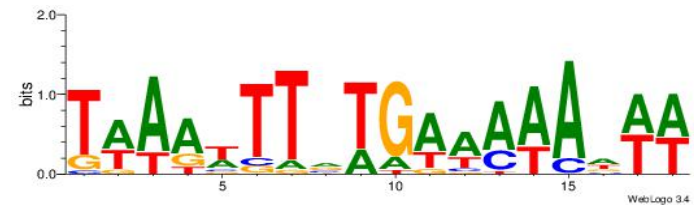
Alignment:

WWHTTTTTCABAAWTTWA
-----DDTATTATTTDH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
TAAWTTVTGAAAAHWW



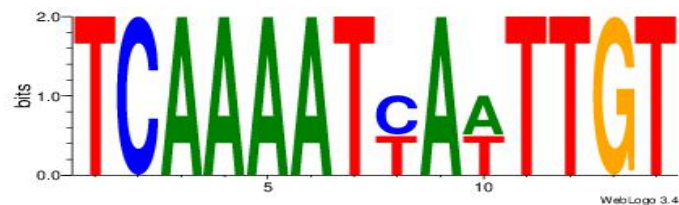
Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0912037

Alignment:

TCAAAATKAWTTGT
--DDTATTATTTDH

Original motif Consensus sequence: ACAAWTRATTTTGA

Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 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: 0.0924576

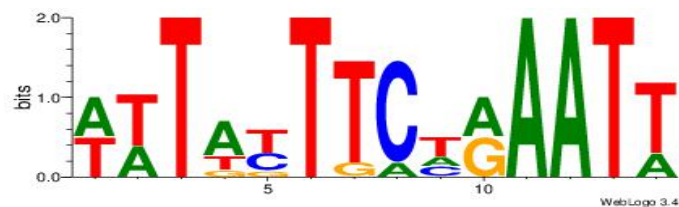
Alignment:

WWTAKTTCDKAATT
 DDTATTATTTDH--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAATT



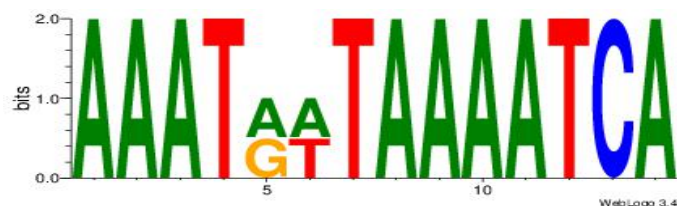
Dataset #: 2
 Motif ID: 8

Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0989198

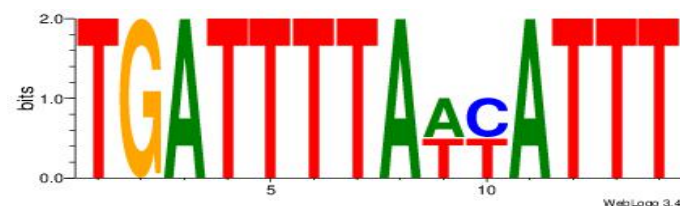
Alignment:

```
TGATTTTAWKATTT
-DDTATTATTDDH-
```

Original motif Consensus sequence: AAATRWTAATCA

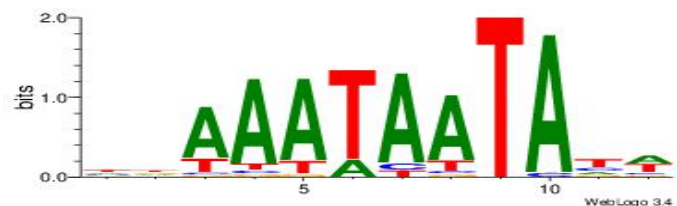


Reverse complement motif Consensus sequence: TGATTTTAWKATTT

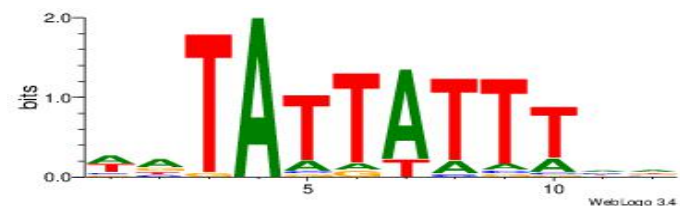


Dataset #: 4 Motif ID: 37 Motif name: tkAAATAATAtw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



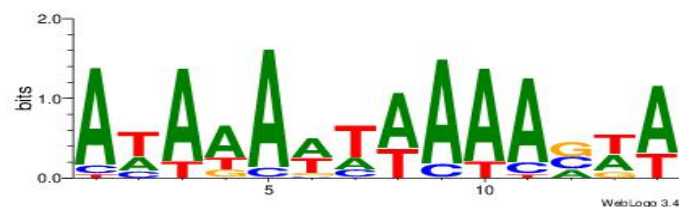
Best Matches for Top Significant Motif ID 37 (Highest to Lowest)

Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 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: 0.0522317

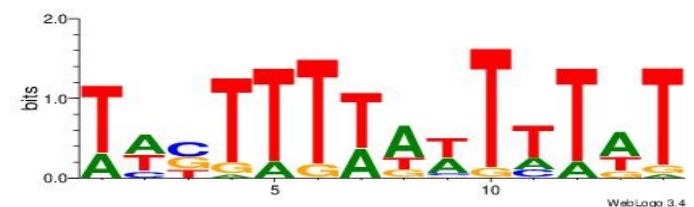
Alignment:

TWSTTTWAWTTTWT
 -WHTATTATTTDH-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

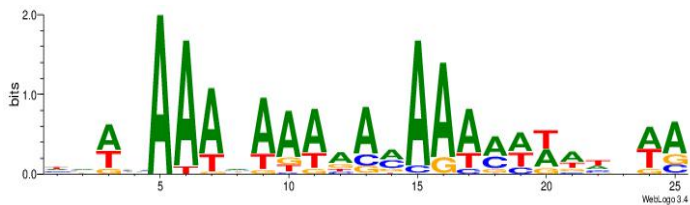


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 12

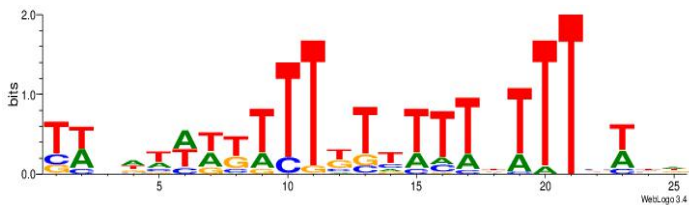
Similarity score: 0.0590505

Alignment:
TWVHWWYTTTYTTTTTHTTTVWBH
-----WHTATTATTTDH--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
TWVHWWYTTTYTTTTTHTTTVWBH

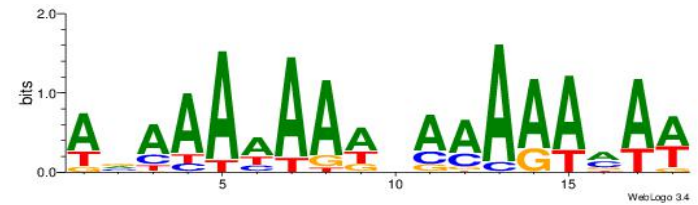
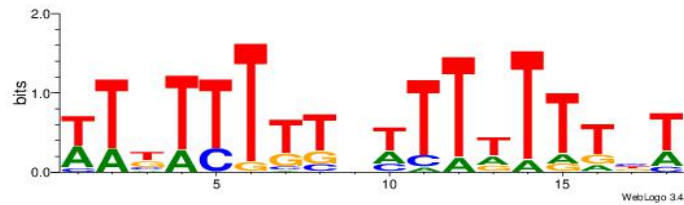


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0637702

Alignment:
ABAAAAAWhAAAAARAW
HDAAATAATAHW-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

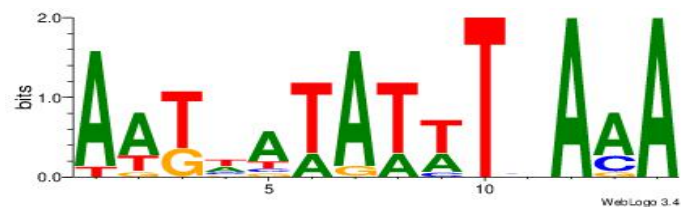
Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW



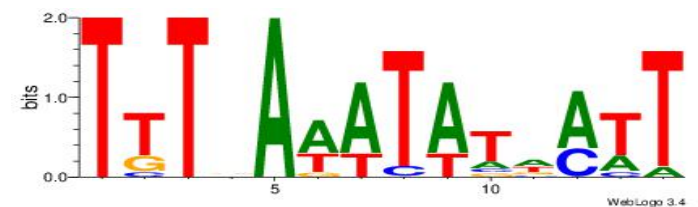
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0641975

Alignment:
 AATHATATWTHAAA
 --WHTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



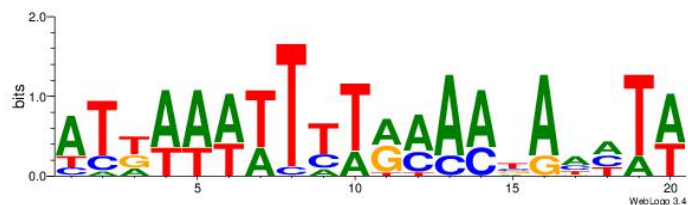
Dataset #: 5
 Motif ID: 55

Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 12
 Similarity score: 0.0704475

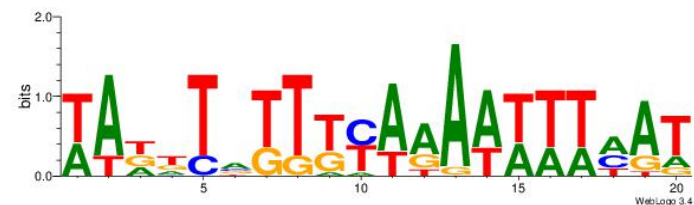
Alignment:

WAHHTVTTYKAAAATTRAT
 -----HDAAATAATAHW

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

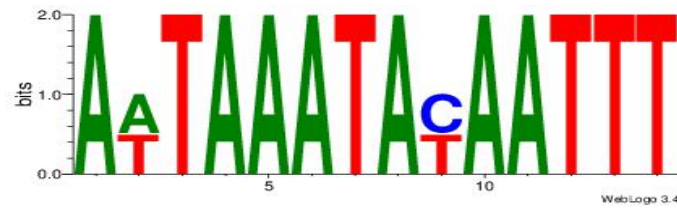


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0704475

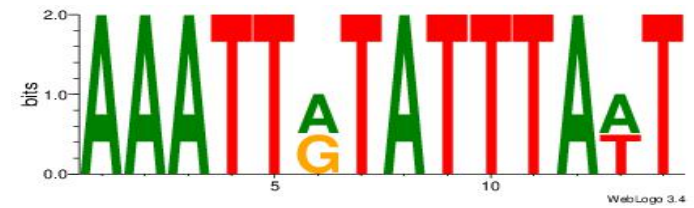
Alignment:

AAATTKTATTTAWT
-WHTATTATTTDH-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



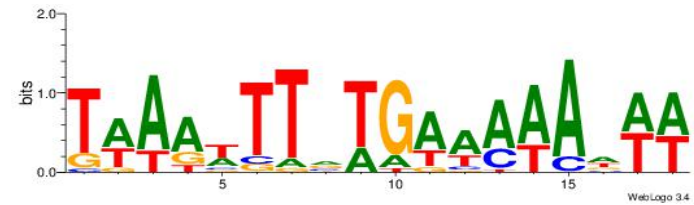
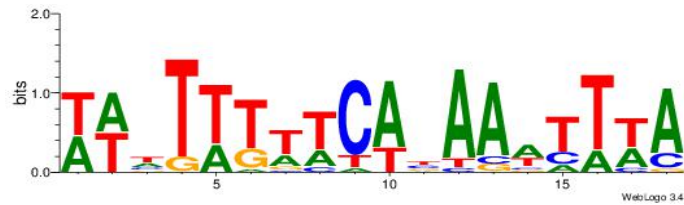
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0763819

Alignment:

WWHTTTTTCABAAWTTWA
-----WHTATTATTTDH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

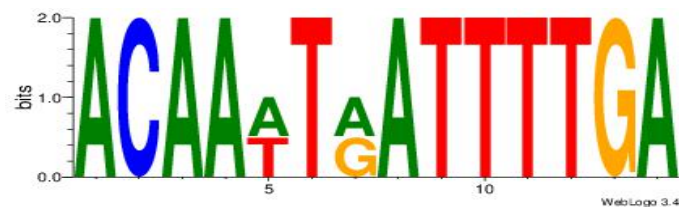
Reverse complement motif Consensus sequence:
TAAWTTVTGAAAAHWW



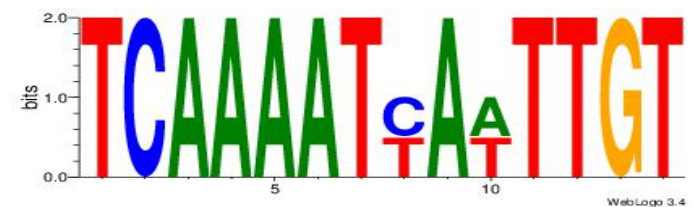
Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0864198

Alignment:
 TCAAAATKAWTTGT
 --WHTATTATTTDH

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTGT



Dataset #: 2
 Motif ID: 6

Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.09076

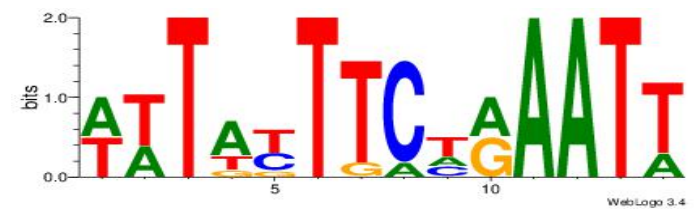
Alignment:

WWTAKTTCDKAATT
WHTATTATTTDH--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAATT



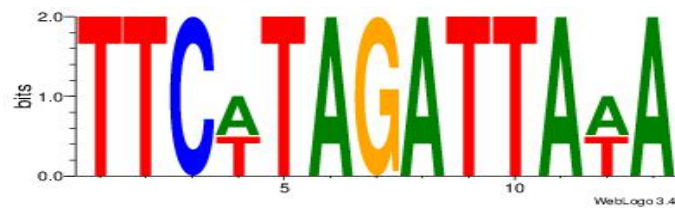
Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.096142

Alignment:

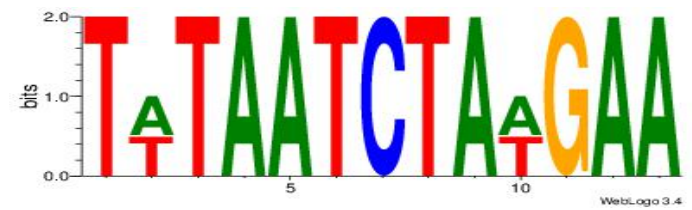
TWTAATCTAWGAA

WHTATTATTTDH-

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAATCTAWGAA



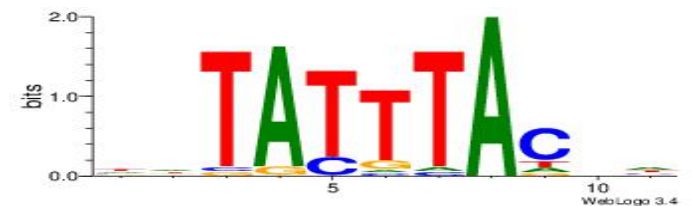
Significant Motifs - Global and Local Matching (Highest to Lowest)

Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Best Matches for Significant Motif ID 45 (Highest to Lowest)

Dataset #: 4

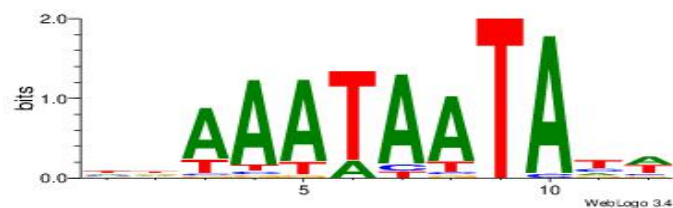
Motif ID: 37

Motif name: tkAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0162338

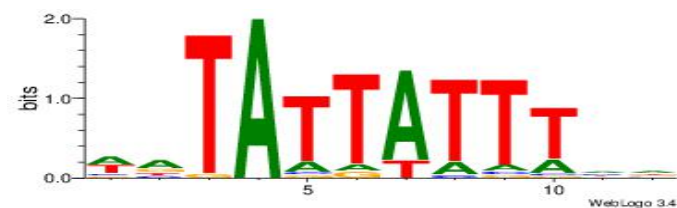
Alignment:

HDAAATAATAHW
 -DBGTAATAAHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH

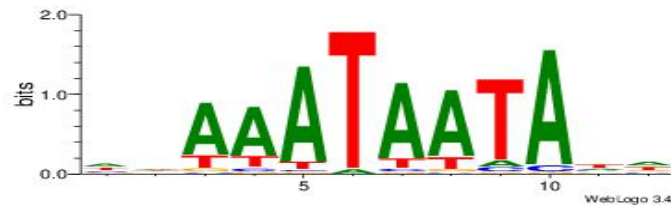


Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0164863

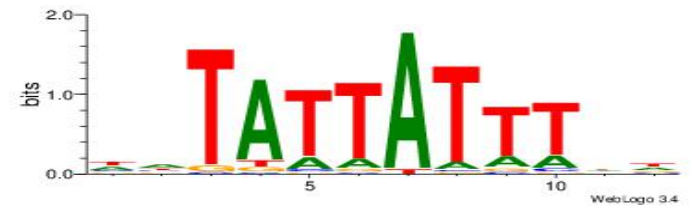
Alignment:

DDTATTATTTDH
DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



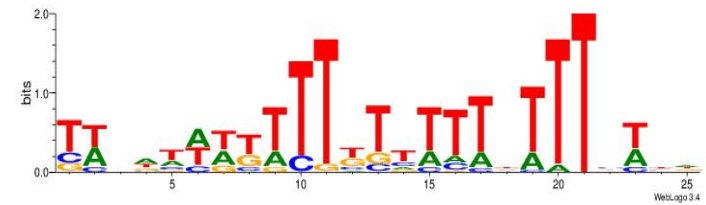
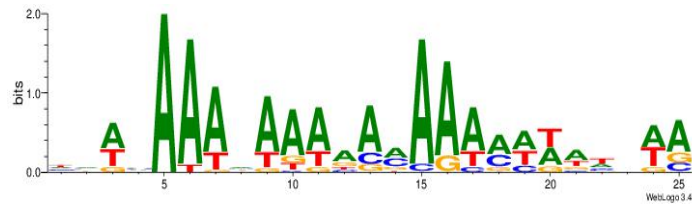
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	15
Number of overlap:	11
Similarity score:	0.0192768

Alignment:

TWVHWWYTTTYTTTTHTTTVWBH
-----DHTATTTACBD

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBWA

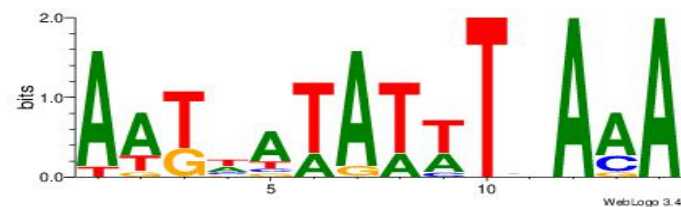
Reverse complement motif Consensus sequence:
TWVHWWYTTTYTTTTHTTTVWBH



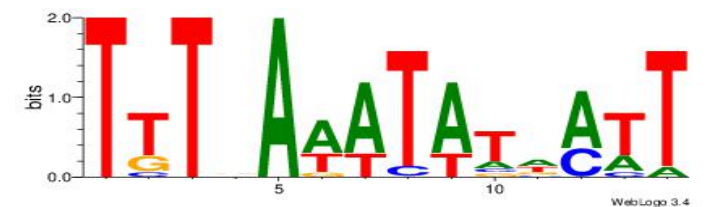
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0250541

Alignment:
 AATHATATWTHAAA
 DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



Dataset #: 2
 Motif ID: 6

Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.027895

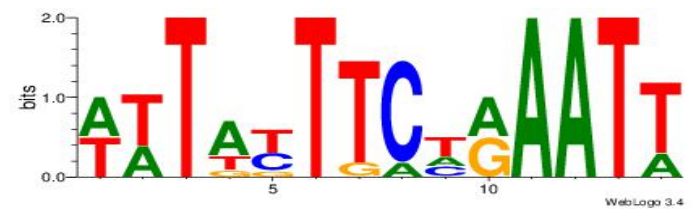
Alignment:

```
AATTYDGAARTAWW
---DBGTAAATAHD
```

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



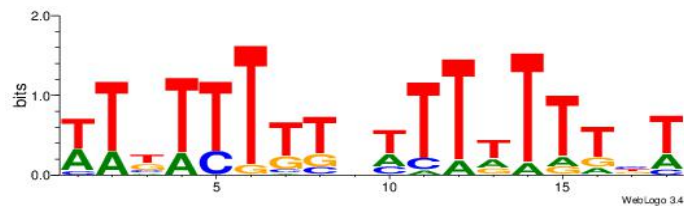
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0283217

Alignment:

ABAAAAAWhAAAAARAW

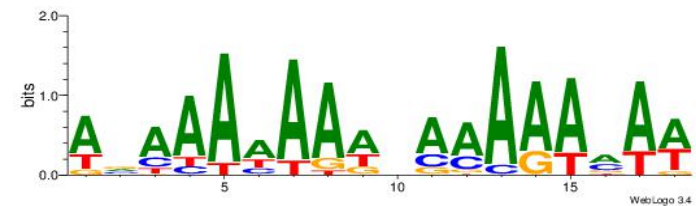
DBGTAAATAHD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif
ABAAAAAWhAAAAARAW

Consensus sequence:



Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0308097

Alignment:

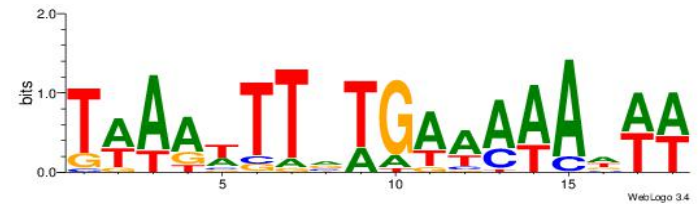
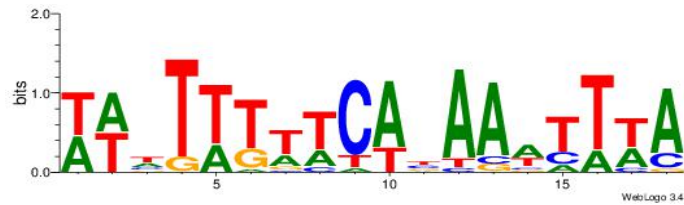
TWAAWTTVTGAAAAHWW

-----DBGTAAATAHD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif
TWAAWTTVTGAAAAHWW

Consensus sequence:

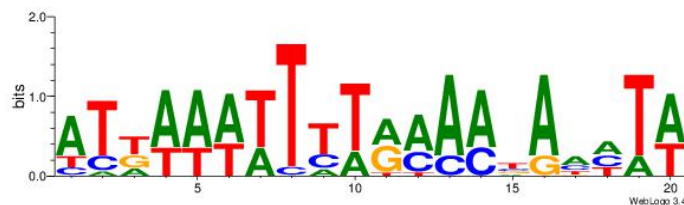


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0333874

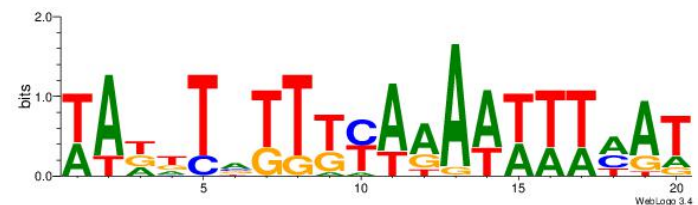
Alignment:

ATKAAWTTTTRMAABAHHTW
 -----DBGTAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2

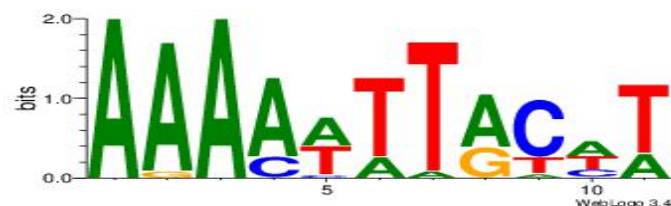
Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0361187

Alignment:

AAAWTTTCWT

DHTATTTACBD

Original motif Consensus sequence: AAAAWTTTCWT



Reverse complement motif Consensus sequence: AWGKAAWTTT



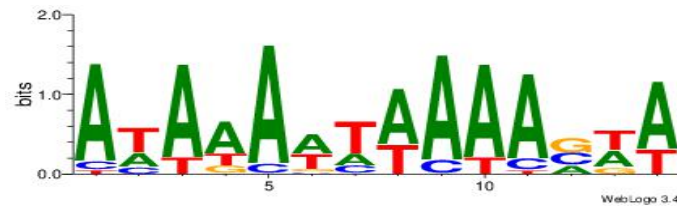
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0410381

Alignment:

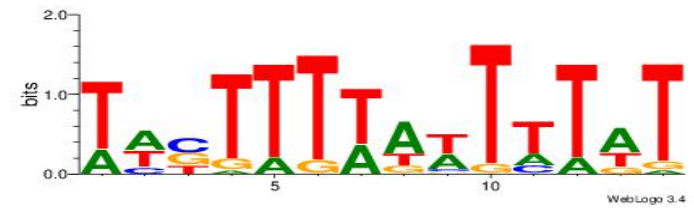
AWAAAWTWAAASWA

--DHTATTTACBD--

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTT



Dataset #: 4 Motif ID: 44 Motif name: dhACATTCTkh

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



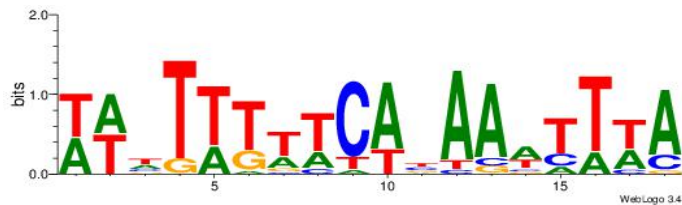
Best Matches for Significant Motif ID 44 (Highest to Lowest)

Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8

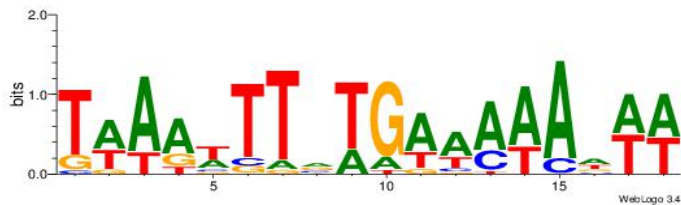
Number of overlap: 11
Similarity score: 0.0217516

Alignment:
TWAAWTTVTGAAAAHWW
DHACATTCTGH-----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 4
Motif ID: 40
Motif name: kcACCTGCAGc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0238442

Alignment:
BCACCTGCABC
DHACATTCTGH

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



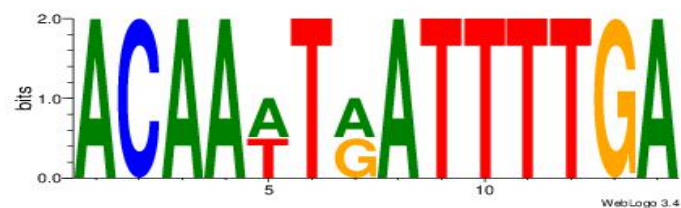
Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0258838

Alignment:

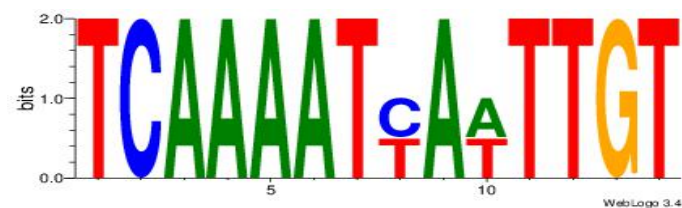
TCAAAATKAWTTGT

HCAGAATGTHD---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

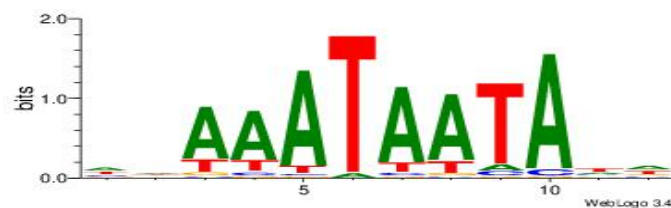


Dataset #: 4
 Motif ID: 41

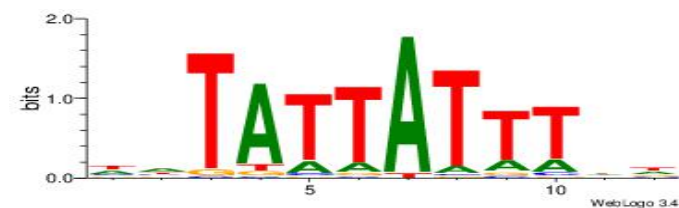
Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0292508

Alignment:
 DDTATTATTTDH
 -HCAGAAATGTHD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

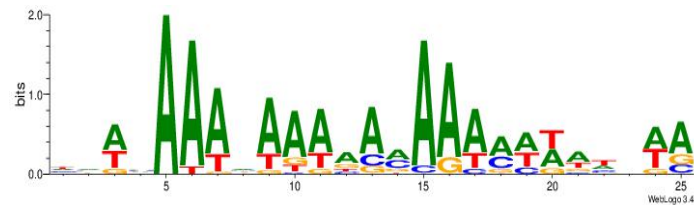


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0307858

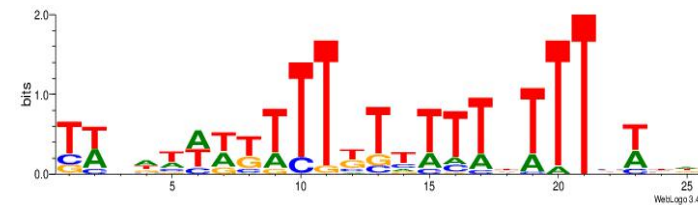
Alignment:

TWVHWWYTTTYYTTTTHTTTVWBH
----DHACATTCTGH-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
TWVHWWYTTTYYTTTTHTTTVWBH



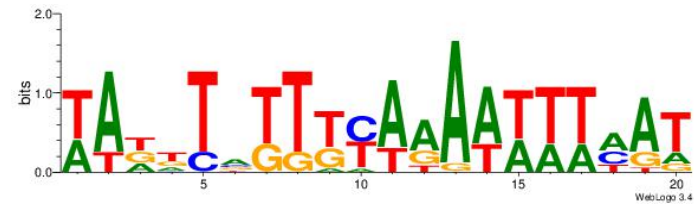
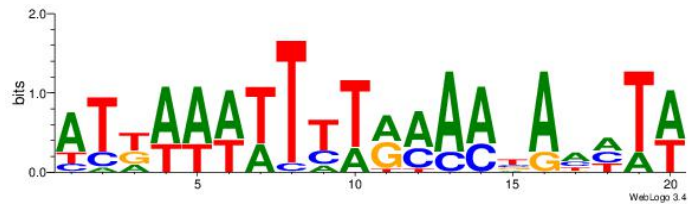
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	11
Similarity score:	0.0357323

Alignment:

ATKAAWTTTTRMAABAHHTW
-DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

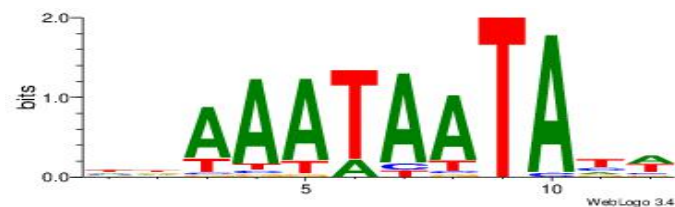
Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT



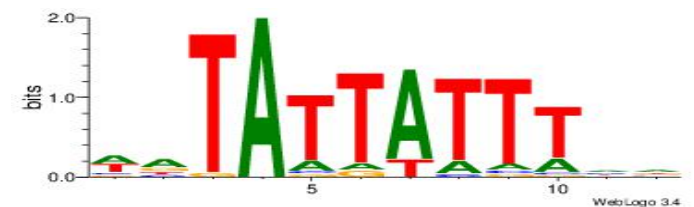
Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0364899

Alignment:
 WHTATTATTDDH
 -HCAGAAATGTHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH



Dataset #: 2
 Motif ID: 6

Motif name:	Motif 6
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:	0.0400884

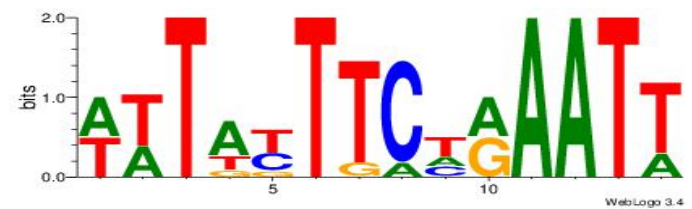
Alignment:

```
AATTYDGAARTAWW
HCAGAAATGTHD---
```

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #:	4
Motif ID:	39
Motif name:	kCAGCCAATmr
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:	0.0412582

Alignment:

MBATTGGCTGH

DHACATTCTGH

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



Dataset #:	3
Motif ID:	35
Motif name:	GABPA
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:	0.0418896

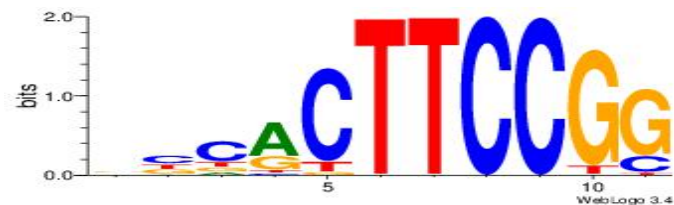
Alignment:

CCGGAAGTGVV

HCAGAATGTHD

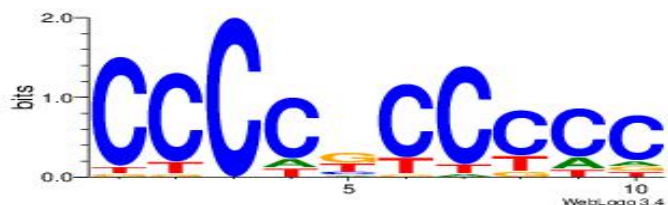
Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTCCGG



Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



Best Matches for Significant Motif ID 24 (Highest to Lowest)

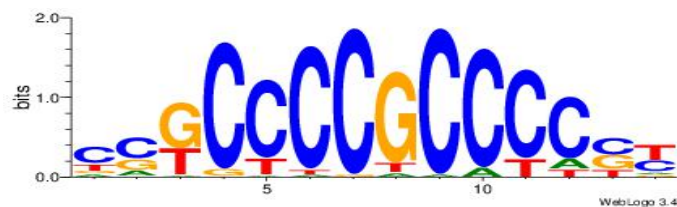
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.00451594

Alignment:

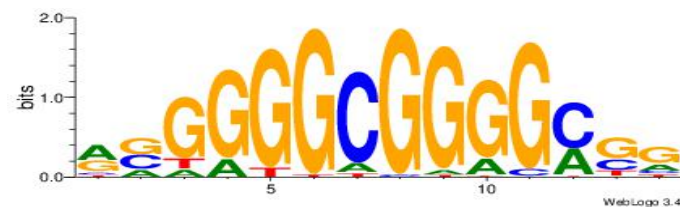
MSGGGGCGGGYSG

-GGGGGYGGGG---

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

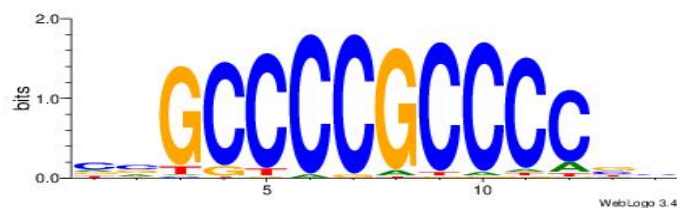


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.00965796

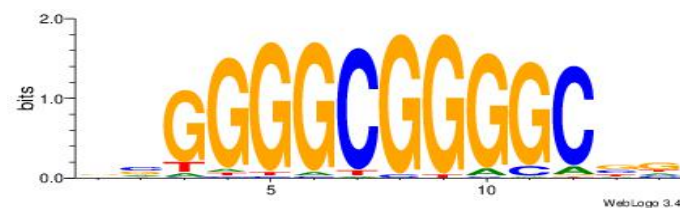
Alignment:

BBGGGGCGGGGCVD
 -GGGGGYGGGG----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

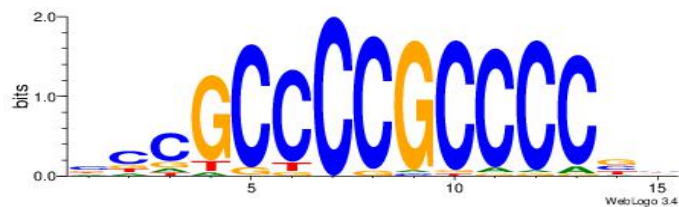


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0127292

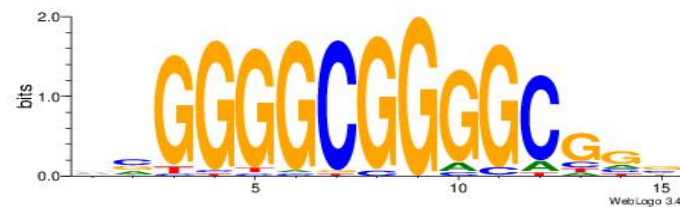
Alignment:

BCCGCCCCGCCCCBB
 ----CCCCKCCCC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

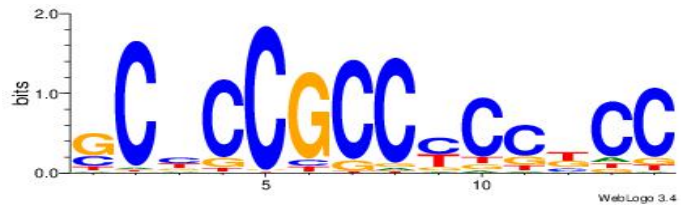
Number of overlap: 10
Similarity score: 0.0174405

Alignment:
GGMGGRGGCGGVGC
---GGGGYGGG---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCY

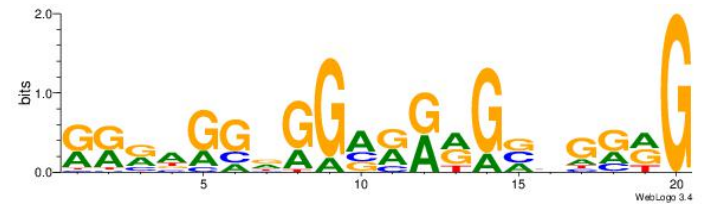


Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 10
Similarity score: 0.0301548

Alignment:
CYYCBBCYYYTCCHCCTYYY
-----CCCCKCCCC-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



Alignment:

```
RGRGGAGRRGGHGGDG
-----GGGGGYGGGG
```

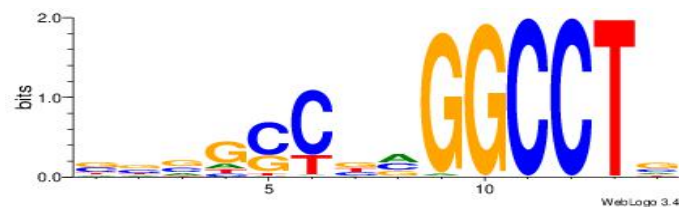
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Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0540825

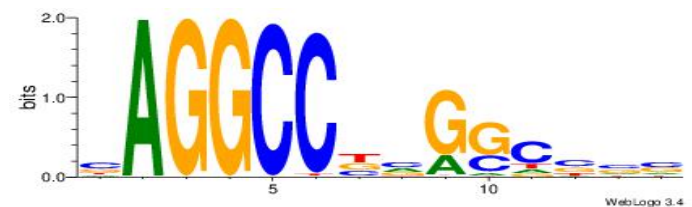
Alignment:

BBVGCCBVGGCCTV
 ----GGGGGYGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

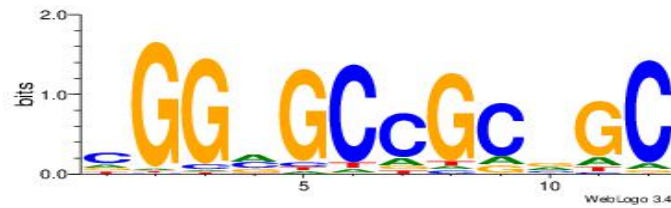


Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0557738

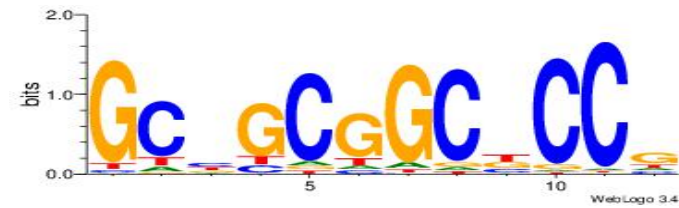
Alignment:

GCVGCGGCBCCG
-CCCCKCCCC-

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



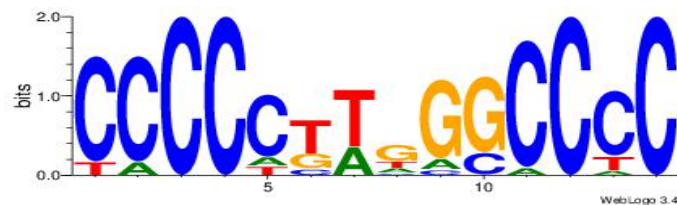
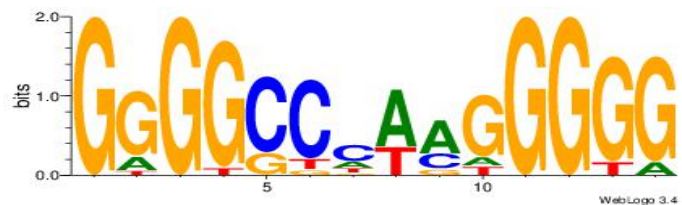
Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.0600992

Alignment:

CCCCCTTGGGCCCC
-CCCCKCCCC---

Original motif Consensus sequence: GGGGCCCAAGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCC



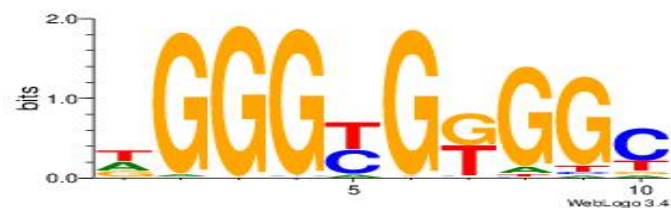
Dataset #: 3
 Motif ID: 27
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0637183

Alignment:

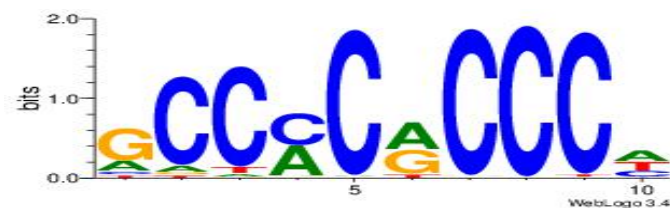
GCCYCMCCCD

CCCCKCCCCC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 3 **Motif ID: 32** **Motif name: ArntAhr**

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Best Matches for Significant Motif ID 32 (Highest to Lowest)

Dataset #: 3
 Motif ID: 23
 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 #: 3
 Motif ID: 29
 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: 0.0112447

Alignment:
 VBACGTGV
 -YGCGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV

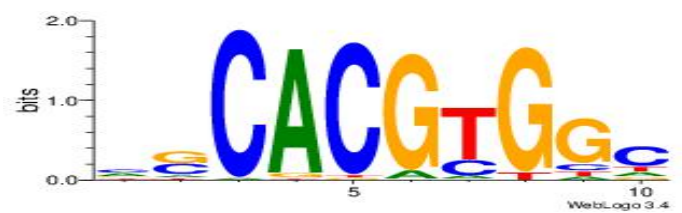


Dataset #: 3
 Motif ID: 33
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6

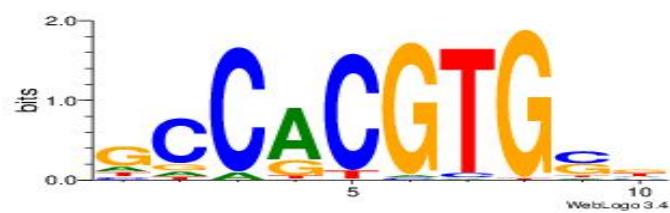
Similarity score: 0.0377949

Alignment:
GCCACGTGSD
--YGCGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

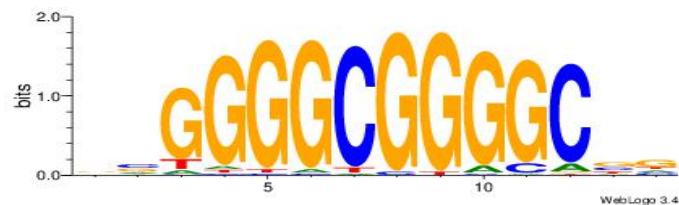
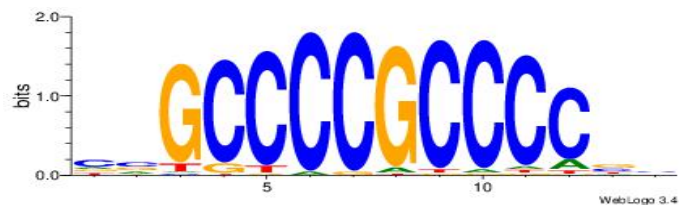


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0396403

Alignment:
HVGCCCCGCCCCBB
-----CACGCM-----

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 3
 Motif ID: 34
 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:

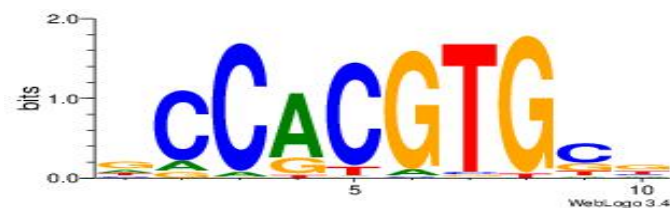
DCCACGTGCV

--YGCGTG--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 1
 Motif ID: 1

Motif name:	Motif 1
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:	0.040625

Alignment:
GCCCCGCC
--CACGCM

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCCGCC



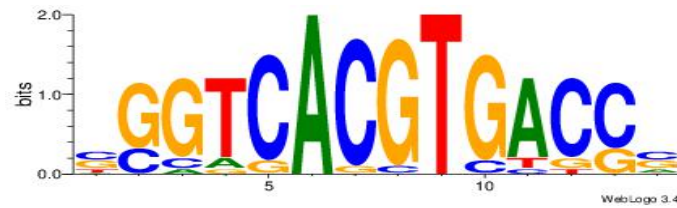
Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSS
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0412037

Alignment:

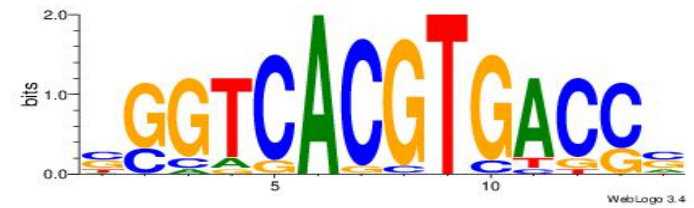
SGGTCACGTGACCS

-----YGCGTG-----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
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:	0.0425089

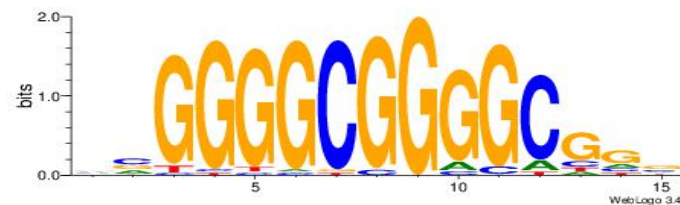
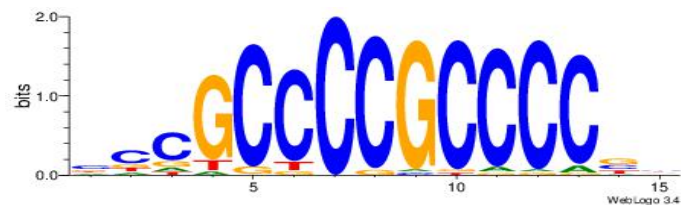
Alignment:

BCCGCCCCGCCCCBB

-----CACGCM-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB

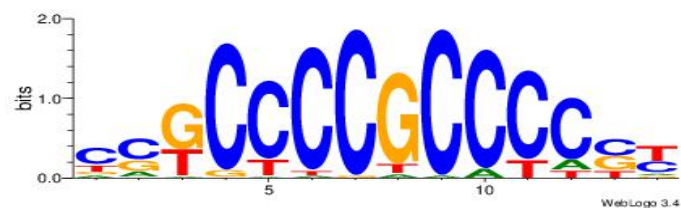
Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



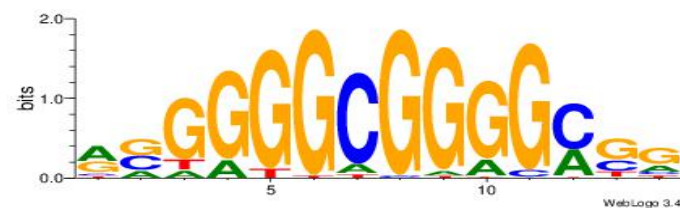
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0465867

Alignment:
 MSGGGGCGGGYSG
 ----YGCGTG----

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY

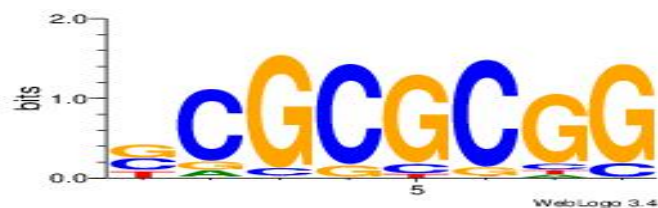


Dataset #: 5
 Motif ID: 47

Motif name: TFW2
 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: 0.0469722

Alignment:
 SCGCGCGG
 -YGCGTG-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



Dataset #: 4 Motif ID: 40 Motif name: kcACCTGCAGc

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Best Matches for Significant Motif ID 40 (Highest to Lowest)

Dataset #: 4
 Motif ID: 43
 Motif name: wsTACwGTAsw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0215284

Alignment:

DBTACWGTAVH

BCACCTGCABC

Original motif Consensus sequence: HVTACWG TABD



Reverse complement motif Consensus sequence: DBTACWGTAVH

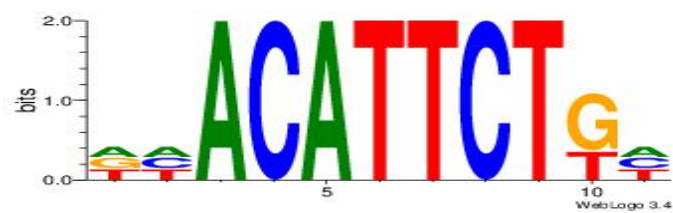


Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0254134

Alignment:
DHACATTCTGH
BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

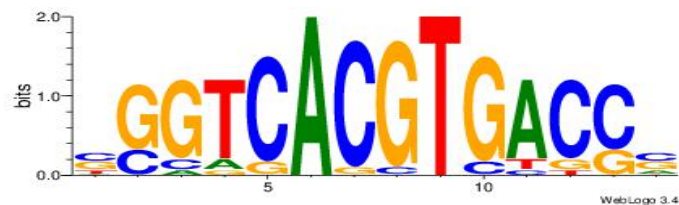
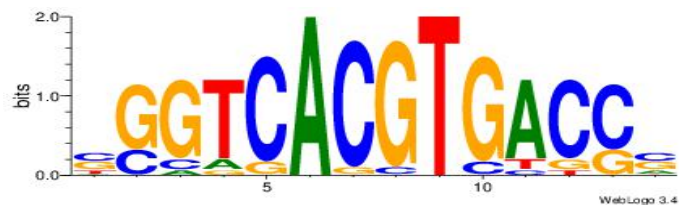


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACCS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.031338

Alignment:
SGGTCACGTGACCS
---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACCS



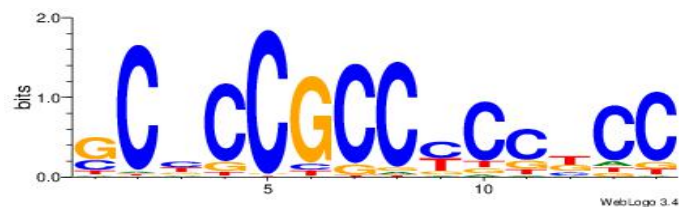
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.034471

Alignment:
 GCVCCGCCMCCYCC
 BCACCTGCABC---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



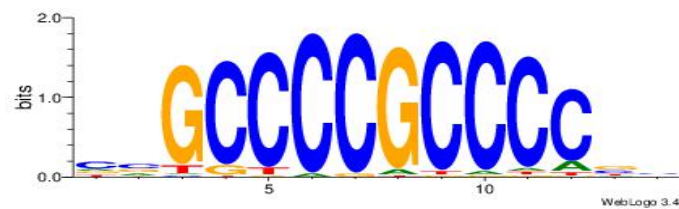
Dataset #: 4
 Motif ID: 36

Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0402518

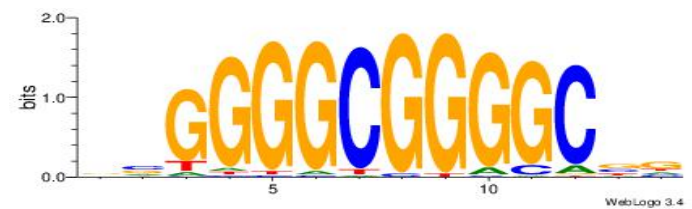
Alignment:

HVGCCCCGCCCCBB
 -BCACCTGCABC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



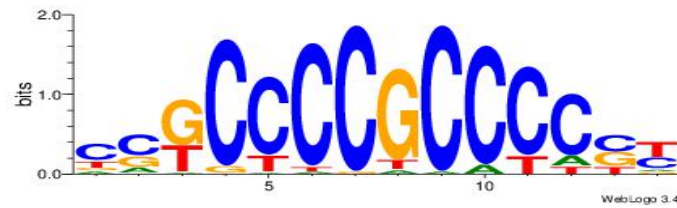
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0411257

Alignment:

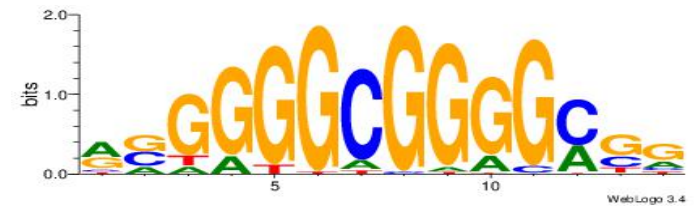
CSKCCCCGCCCCSY

-BCACCTGCABC--

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	11
Similarity score:	0.0420218

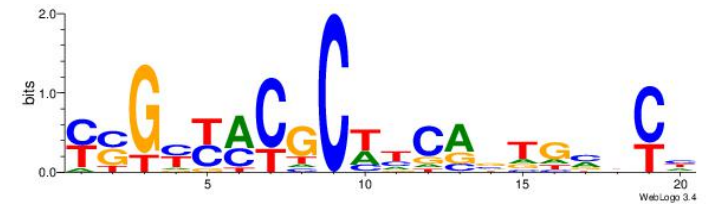
Alignment:

DGVBCABTGDWCGKRRCSR

----GBTGCAGGTGB-----

Original motif Consensus sequence: DGVBCABTGDWCGKRRCSR

Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBCD



Alignment:

```
CCGGAAGTG VV
GBTGCAGGTGB
```

bits

WebLogo 3.4

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Motif name:	kCAGCCAATmr
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:	0.0439586

Alignment:

DCAGCCAATVR
 GBTGCAGGTGB

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



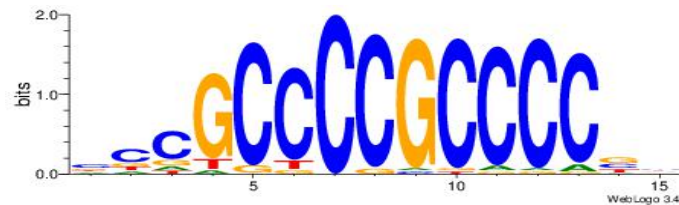
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0461444

Alignment:

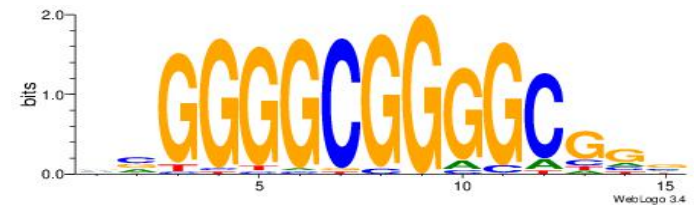
BCCGCCCCGCCCCBB

--BCACCTGCABC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Dataset #: 4 Motif ID: 43 Motif name: wsTACwGTAsw

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



Best Matches for Significant Motif ID 43 (Highest to Lowest)

Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAGc
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: 0.0199592

Alignment:
 GBTGCAGGTGB
 HVTACWG TABD

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

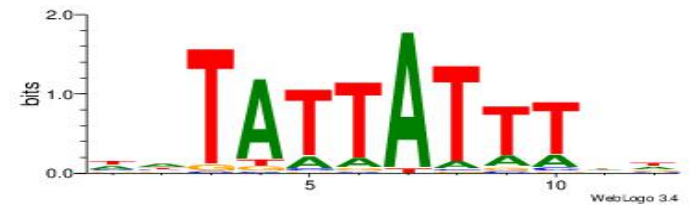
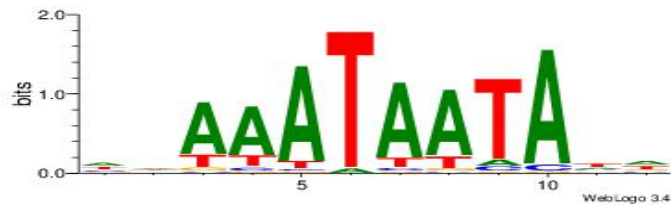


Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0309343

Alignment:
 DDTATTATTTDH
 -HVTACWG TABD

Original motif Consensus sequence: HDAAATAATADD

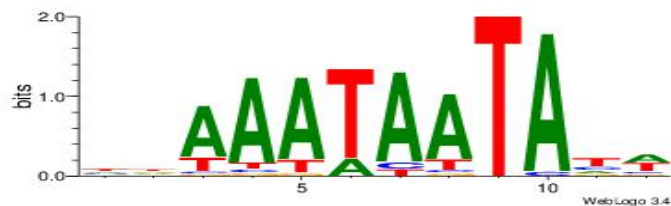
Reverse complement motif Consensus sequence: DDTATTATTTDH



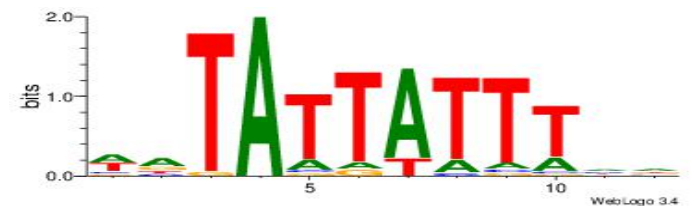
Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0337121

Alignment:
 WHTATTATTTDH
 -HVTACWG TABD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #: 2

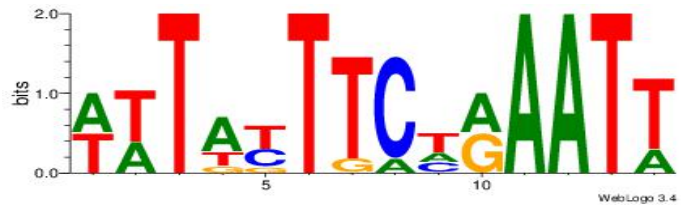
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0353535

Alignment:
AATTYDGAARTAWW
HVTACWG TABD---

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT



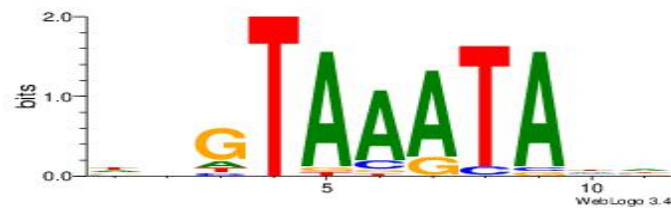
Dataset #: 4
Motif ID: 45
Motif name: wbgTAAATAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.037518

Alignment:

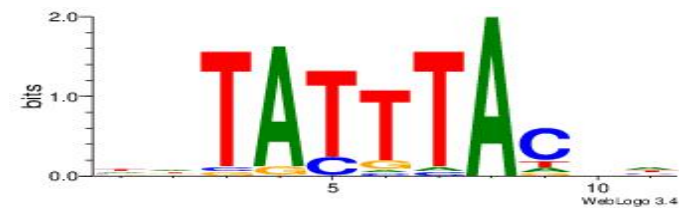
DBGTAAATAHD

DBTACWGTAVH

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #:	2
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:	4
Number of overlap:	11
Similarity score:	0.0397727

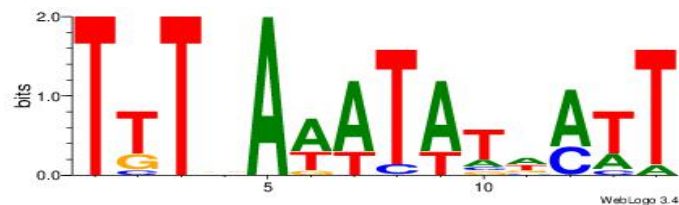
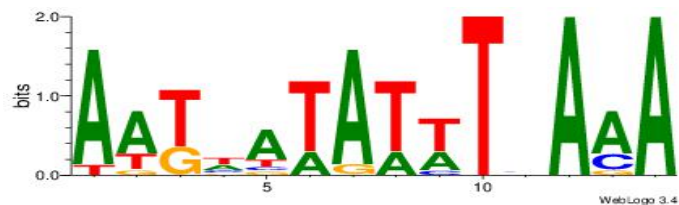
Alignment:

TTTDAWATATHATT

DBTACWGTAVH---

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHATT

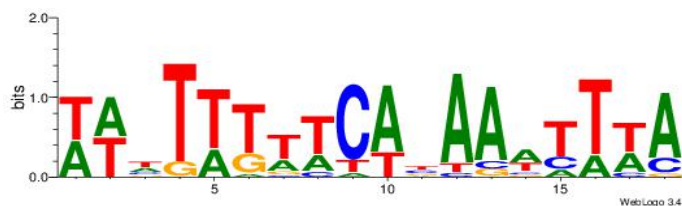


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0413797

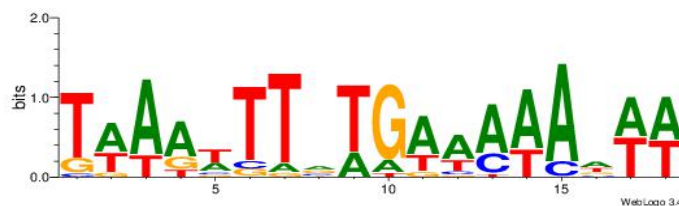
Alignment:

TWAAWTTVTGAAAAHWW
 ---HVTACWGATABD----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



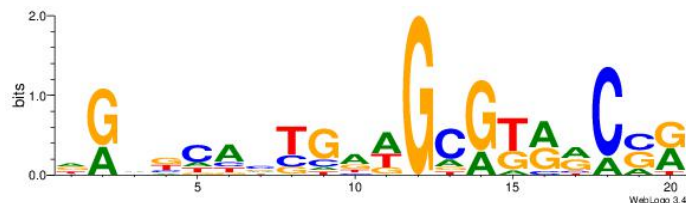
Dataset #: 3

Motif ID: 31
 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: 11
 Similarity score: 0.042298

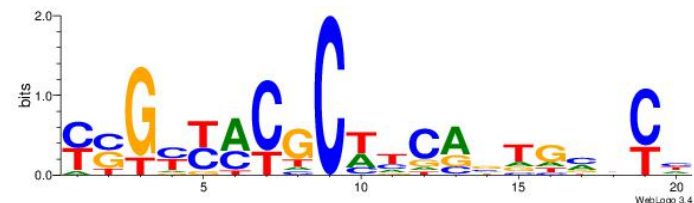
Alignment:

DGVBCABTGDWGCGRRCR
 -----HVTACWGTTABD-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD

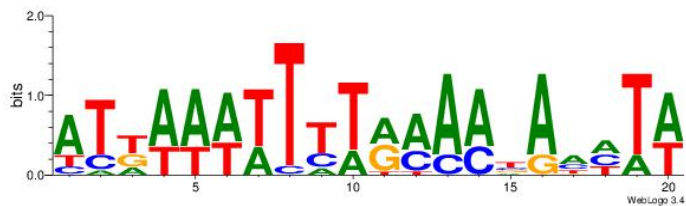


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11

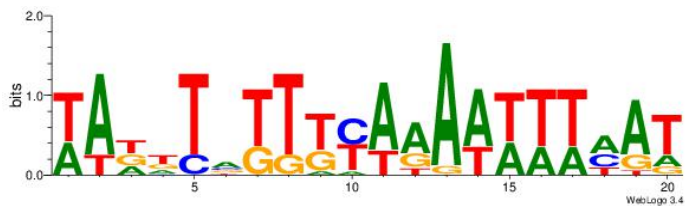
Similarity score: 0.0445707

Alignment:
ATKAAWTTTTRMAABAHHTW
-----DBTACWGTAVH--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

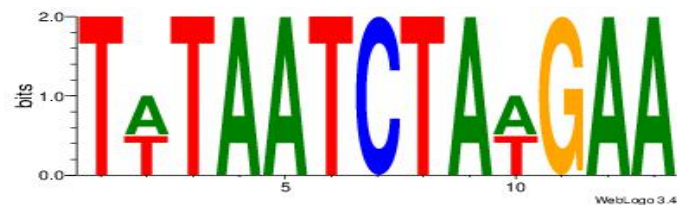


Dataset #: 2
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0460859

Alignment:
TTCWTAGATTAWA
DBTACWGTAVH--

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAACTAWGAA



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

Original motif Consensus sequence: ATAAAA



Reverse complement motif Consensus sequence: TTTTAT



Best Matches for Significant Motif ID 21 (Highest to Lowest)

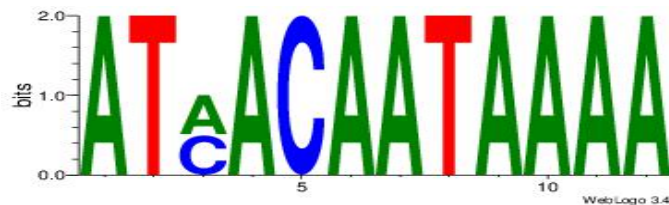
Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0

Alignment:

TTTTATTGTYAT

TTTTAT-----

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

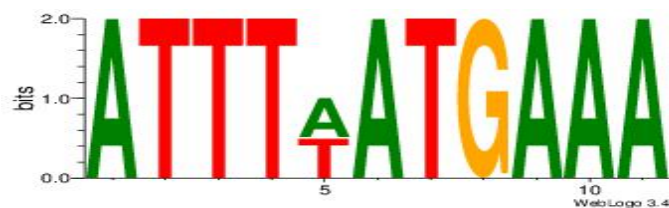


Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0208333

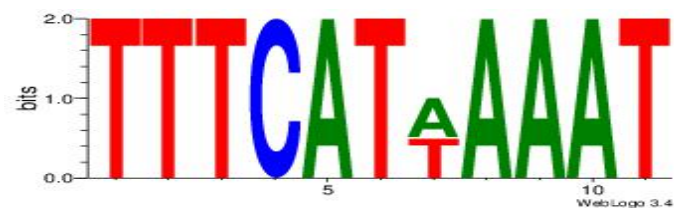
Alignment:

TTTCATWAAAT
-ATAAAA-----

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

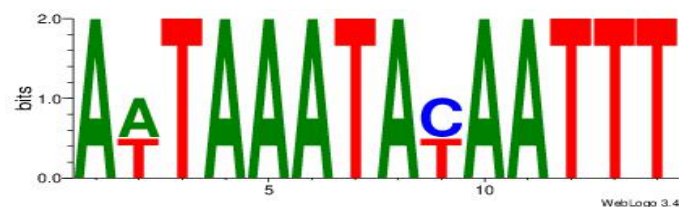


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0208333

Alignment:

AAATTKTATTTAWT
 ---TTTAT-----

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

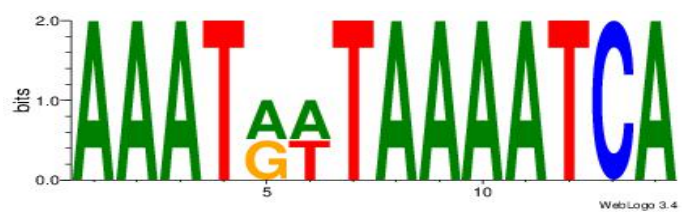


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 6

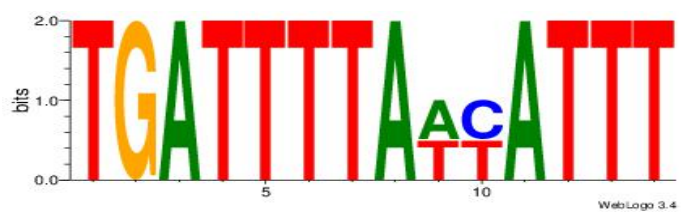
Similarity score: 0.0208333

Alignment:
TGATTTTAWKATTT
---TTTTAT-----

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT

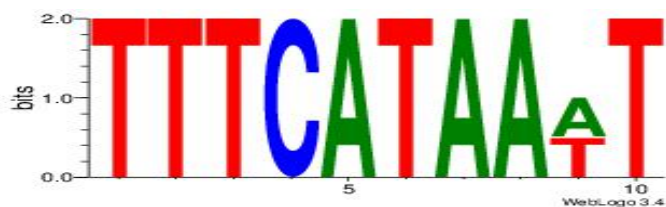


Dataset #: 2
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0416667

Alignment:
TTTCATAAWT
----TTTTAT

Original motif Consensus sequence: TTTCATAAWT

Reverse complement motif Consensus sequence: AWTATGAAA



Dataset #: 2
 Motif ID: 14
 Motif name: Motif 14
 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: 0.0625

Alignment:
 AWAAATAA
 ATAAAA--

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTWT



Dataset #: 2
 Motif ID: 20

Motif name:	Motif 20
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:	0.0625

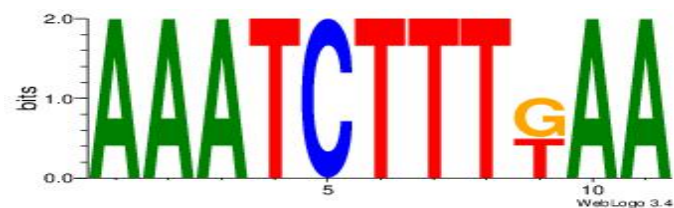
Alignment:

```
TTMAAAGATTT
ATAAAA-----
```

Original motif Consensus sequence: TTMAAAGATTT



Reverse complement motif Consensus sequence: AAATCTTTYAA



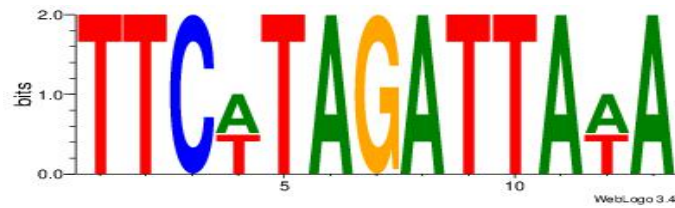
Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	6
Similarity score:	0.0625

Alignment:

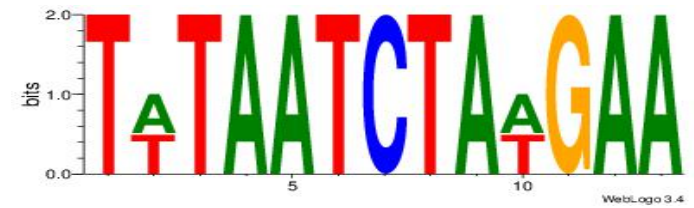
TTCWTAGATTAWA

-----ATAAAA

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTATGAA



Dataset #: 4

Motif ID: 41

Motif name: wwAAATAATAtw

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: 0.0632716

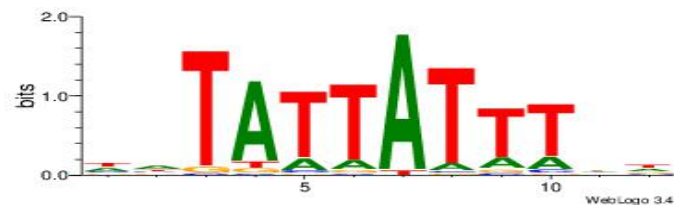
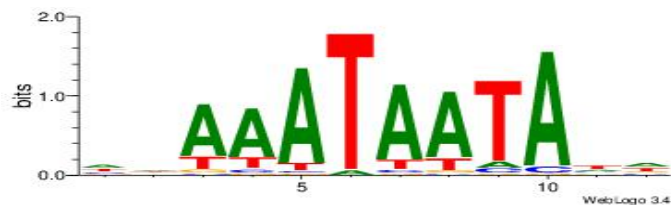
Alignment:

DDTATTATTDDH

--TTTTAT----

Original motif Consensus sequence: HDAAATAATADD

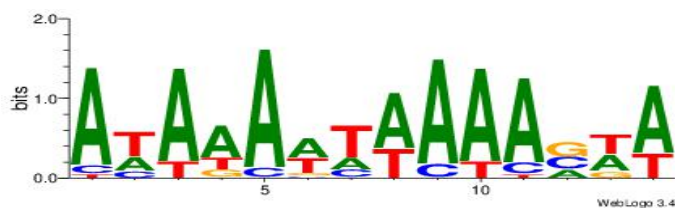
Reverse complement motif Consensus sequence: DDTATTATTDDH



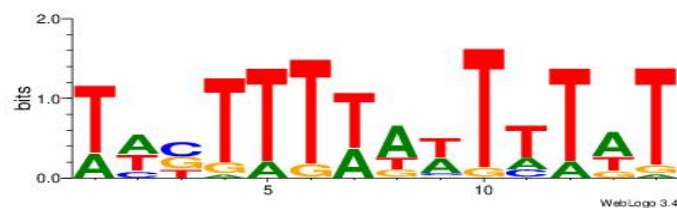
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0689103

Alignment:
 TWSTTTWAWTTTWT
 ---TTTAT-----

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT



Dataset #: 3 Motif ID: 29 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Best Matches for Significant Motif ID 29 (Highest to Lowest)

Dataset #:	3
Motif ID:	33
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:	8
Similarity score:	0.0123101

Alignment:

GCCACGTGSD

-VBACGTGV-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

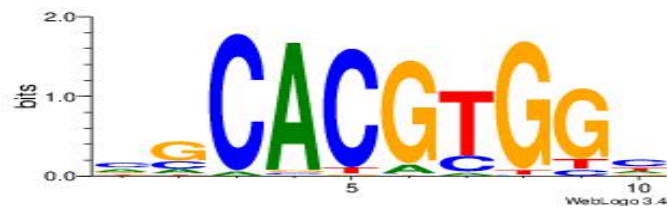


Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0144491

Alignment:

DCCACGTGCV
 -VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

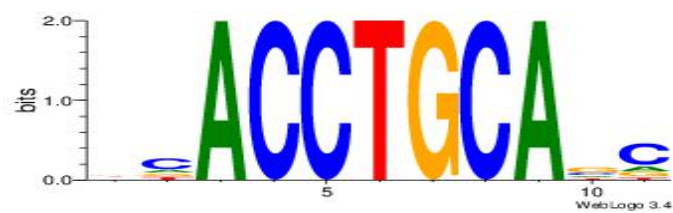


Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAgc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0295473

Alignment:
GBTGCAGGTGB
---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

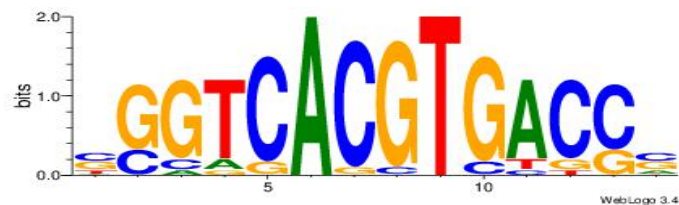
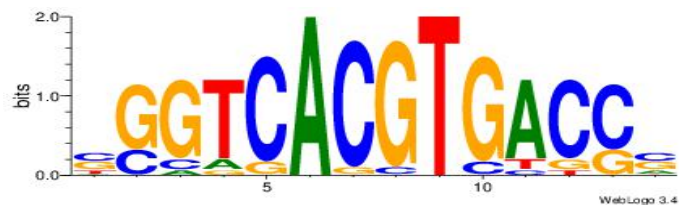


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACs
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0314837

Alignment:
SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS

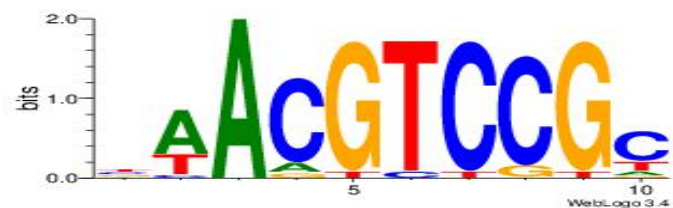
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 3
 Motif ID: 26
 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: 0.0377204

Alignment:
 GCGGACGTTV
 --VCACGTBV

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



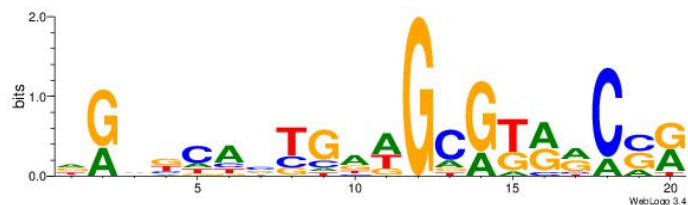
Dataset #: 3
 Motif ID: 31

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:	0.0556891

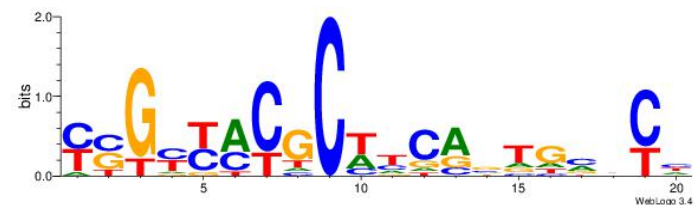
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----VCACGTBV-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #:	4
Motif ID:	44
Motif name:	dhACATTCTkh
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0640024

Alignment:

DHACATTCTGH

VCACGTBV---

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #:	3
Motif ID:	35
Motif name:	GABPA
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:	0.0648153

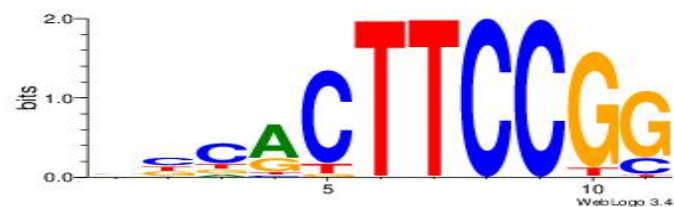
Alignment:

CCGGAAGTGVV

--VCACGTBV-

Original motif Consensus sequence: CCGGAAGTGVV

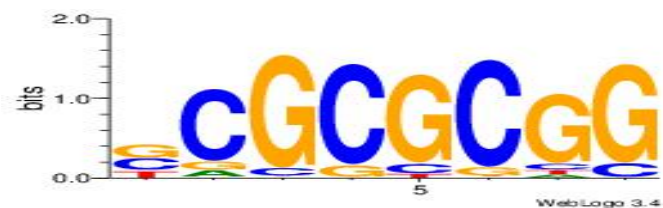
Reverse complement motif Consensus sequence: VVCACTCCGG



Dataset #: 5
 Motif ID: 47
 Motif name: TFW2
 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: 0.0660185

Alignment:
 CCGCGCGS
 VBACGTGV

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



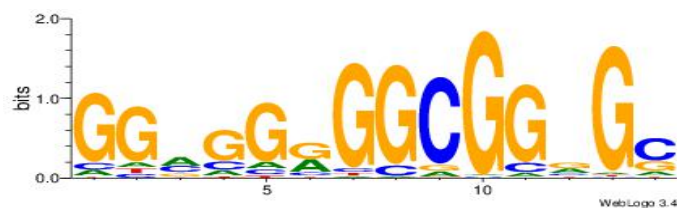
Dataset #: 5
 Motif ID: 50

Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.067219

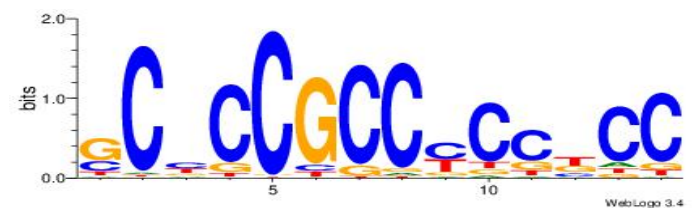
Alignment:

GCVCCGCCMCCYCC
 -----VCACGTBV

Original motif Consensus sequence: GGMGGRGGCGGVGC

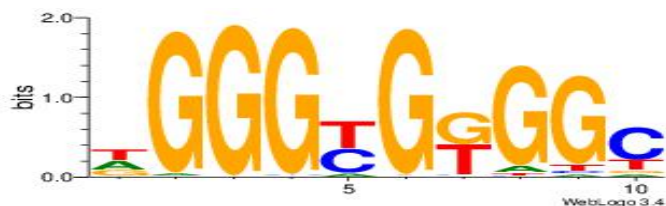


Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

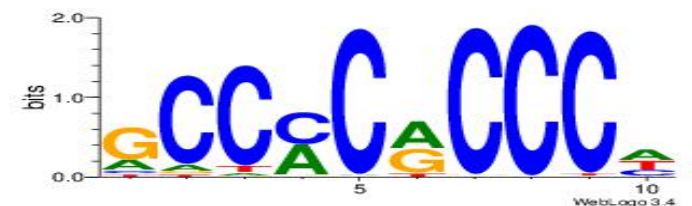


Dataset #: 3 Motif ID: 27 Motif name: Klf4

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



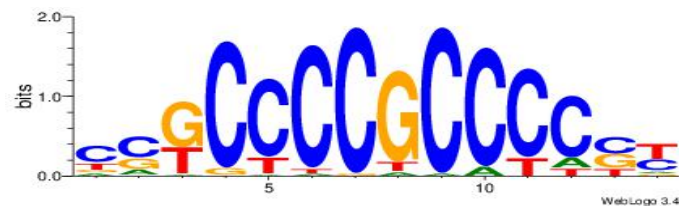
Best Matches for Significant Motif ID 27 (Highest to Lowest)

Dataset #: 2
 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: 3
 Number of overlap: 10
 Similarity score: 0.0152457

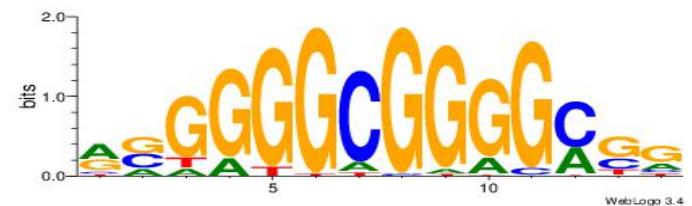
Alignment:

CSKCCCCGCCCSY
 --GCCYCMCCCD--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

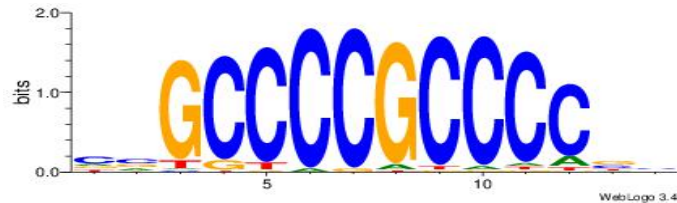


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCSY
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10

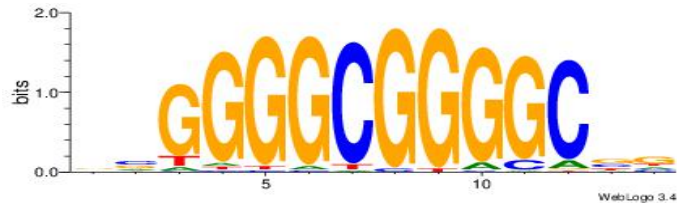
Similarity score: 0.0160185

Alignment:
BBGGGGCGGGGCVD
--DGGGYGKGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

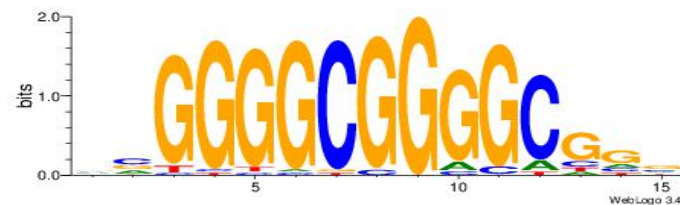
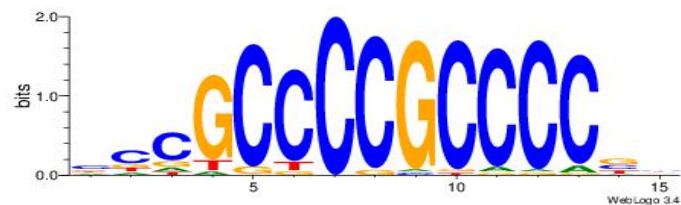


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0194893

Alignment:
BBGGGGCGGGGCGGB
--DGGGYGKGGC---

Original motif Consensus sequence: BCCGCCCCGCCCCBB

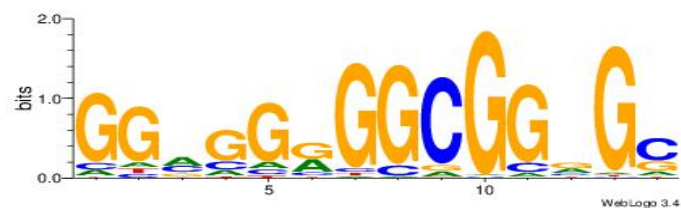
Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



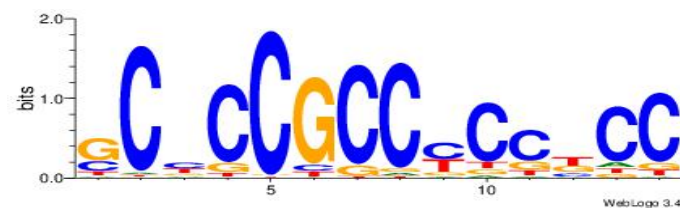
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0402906

Alignment:
 GGMGGRGGCGGVGC
 ----DGGGYGKGGC

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 5
 Motif ID: 54

Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0556427

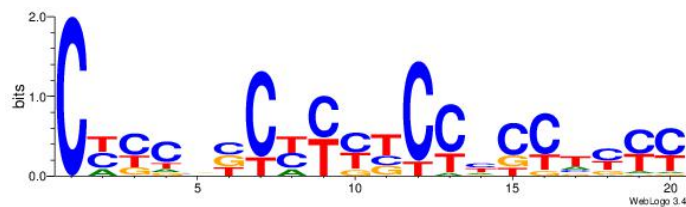
Alignment:

```

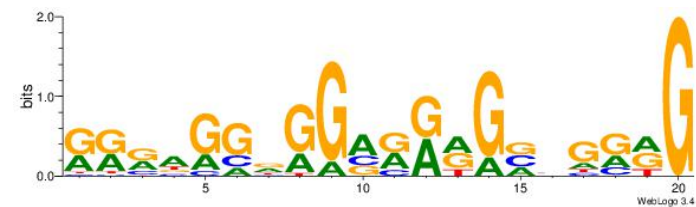
CYYCBBCYYYTCCHCCTYYY
----GCCYCMCCCD-----

```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

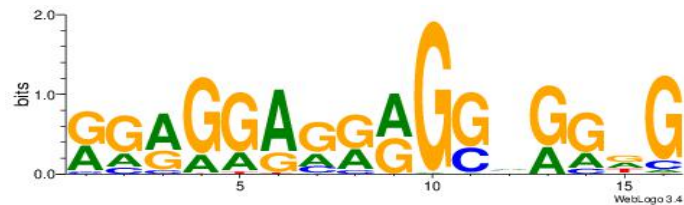


Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0606033

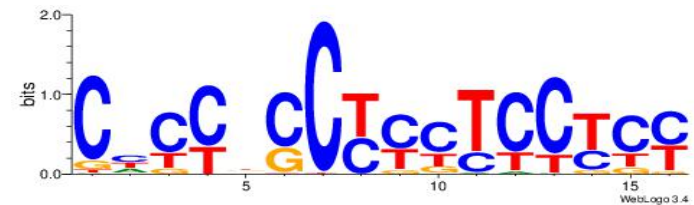
Alignment:

CHCCBCKMCTCCKCM
 ----GCCYCMCCCD--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence:
 CHCCBCKMCTCCKCM



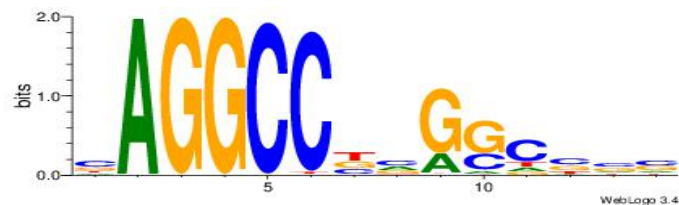
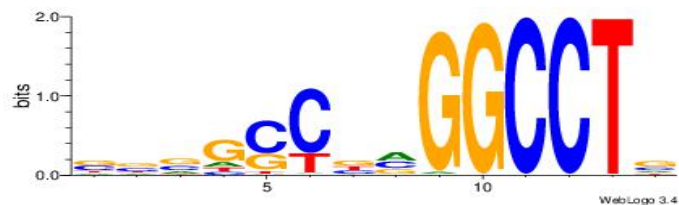
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.0623591

Alignment:

BBVGCCBVGGCCTV
 -GCCYCMCCCD---

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



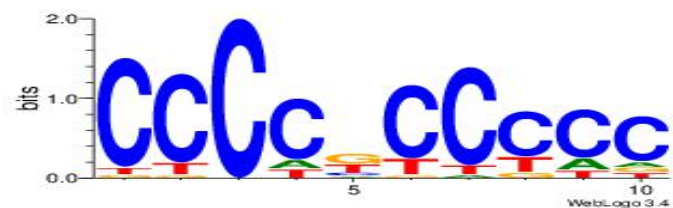
Dataset #: 3
 Motif ID: 24
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0663136

Alignment:

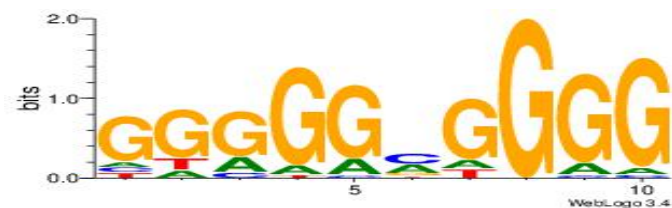
GGGGYGGGG

DGGYGKGGC

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



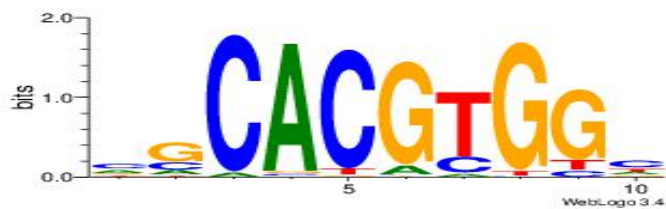
Dataset #: 3
 Motif ID: 34

Motif name:	Myc
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:	0.0686848

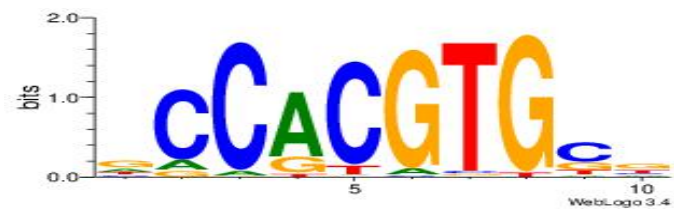
Alignment:

VGCACGTGGH
DGGGYGKGGC

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



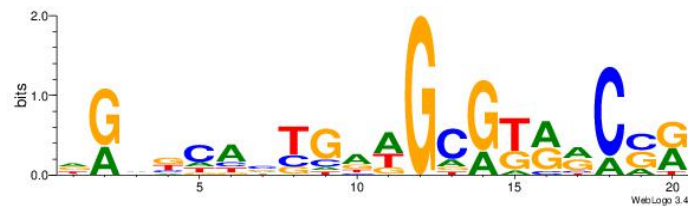
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.06956

Alignment:

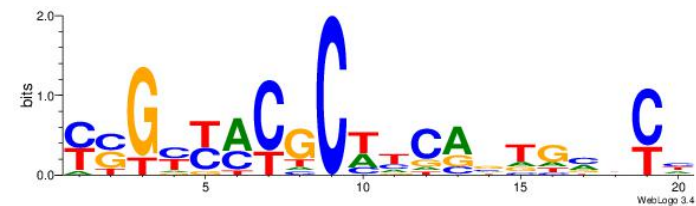
DGVBCABTGDWGCGRRCR

-----DGGGYGKGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

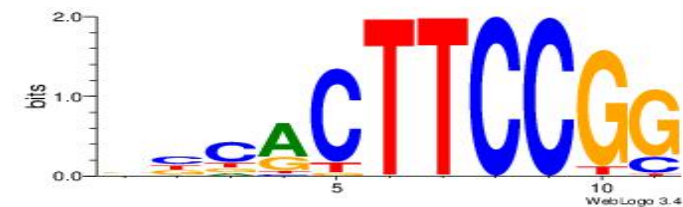


Dataset #: 3 Motif ID: 35 Motif name: GABPA

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCGG



Best Matches for Significant Motif ID 35 (Highest to Lowest)

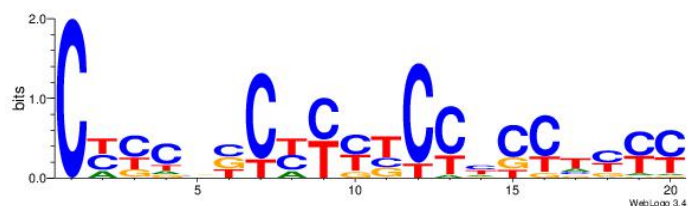
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 5
 Number of overlap: 11
 Similarity score: 0.0360984

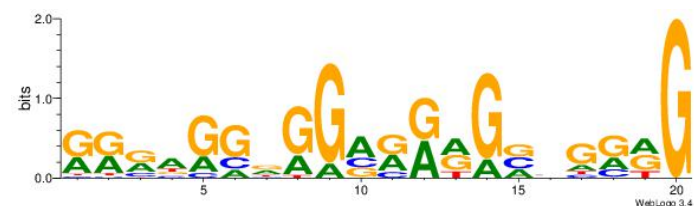
Alignment:

CYYCBBCYYYTCCHCCTYYY
 ----VVCACTTCCGG-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

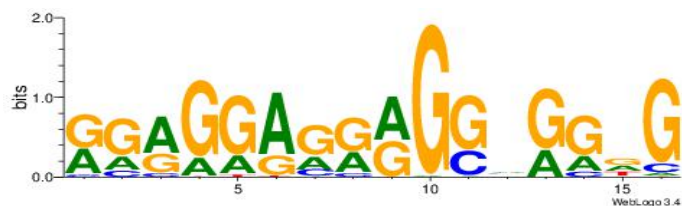


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0445566

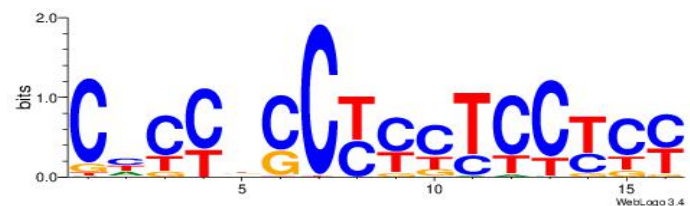
Alignment:

RGRGGAGRRGGHGGDG
 -CCGGAAGTGVV-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

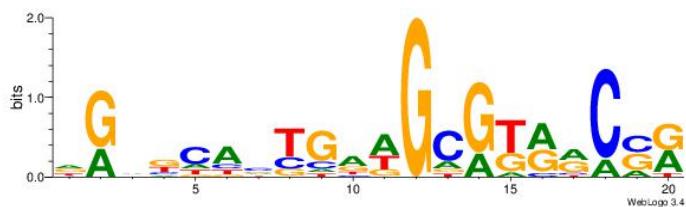


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0446257

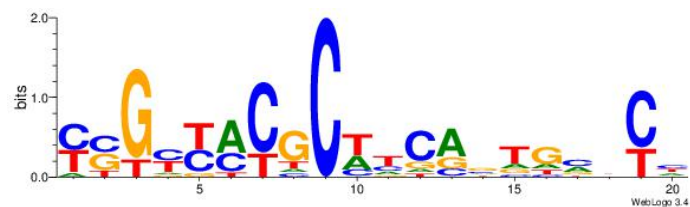
Alignment:

DGVBCABTGDWGCGRRCR
 -----VVCACTTCCGG--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCA BTGBBCD

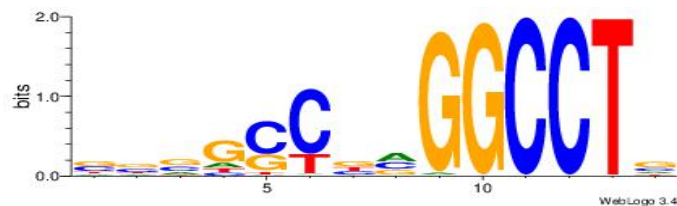


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0457327

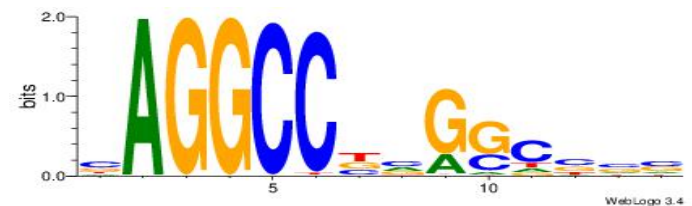
Alignment:

BBVGCCBVGGCCTV
 VVCACTTCCGG---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

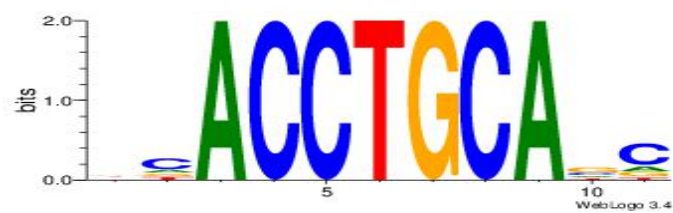


Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0483841

Alignment:
BCACCTGCABC
VVCACTTCCGG

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

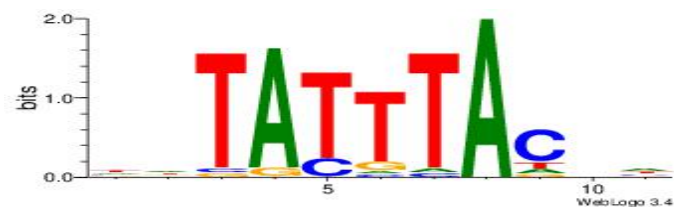


Dataset #: 4
Motif ID: 45
Motif name: wbgTAAATAww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0492127

Alignment:
DBGTAAATAHD
CCGGAAGTG VV

Original motif Consensus sequence: DBGTAAATAHD

Reverse complement motif Consensus sequence: DHTATTTACBD



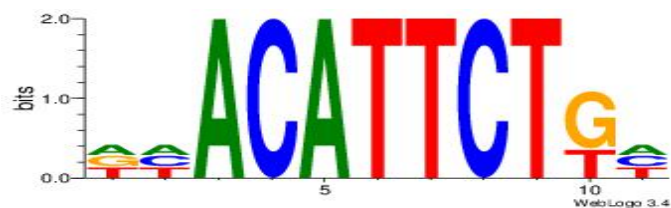
Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0495154

Alignment:

DHACATTCTGH

VVCACTTCCGG

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 5
 Motif ID: 50

Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0504656

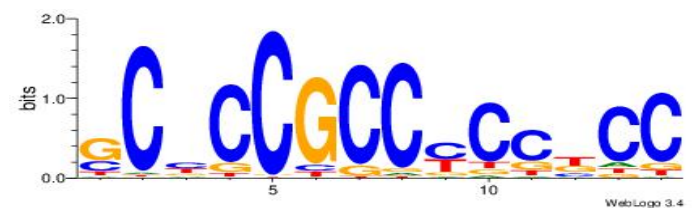
Alignment:

GGMGGRGGCGGVGC
 -CCGGAAGTGVV--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



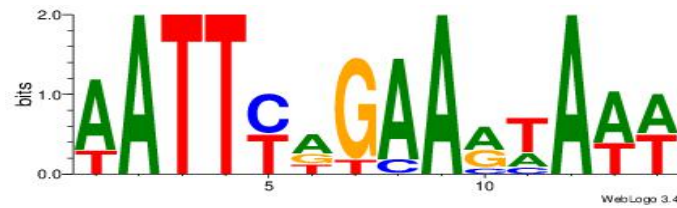
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0518418

Alignment:

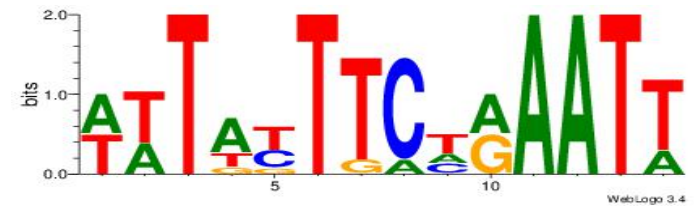
AATTYDGAARTAWW

---CCGGAAGTGVV

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
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:	0.0554249

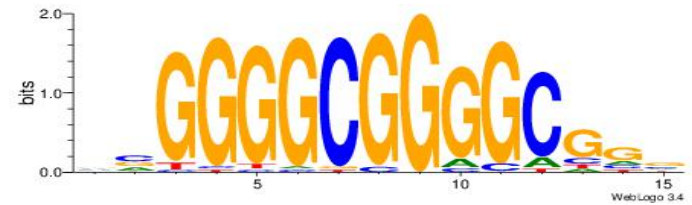
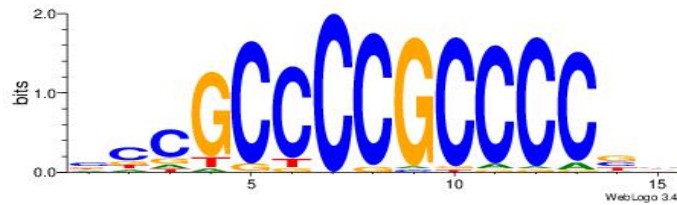
Alignment:

BCCGCCCCGCCCCBB

---VVCACTTCCGG-

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCCGCC



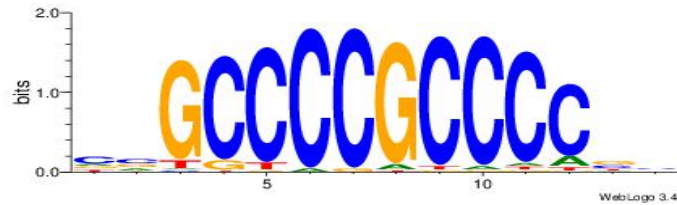
Best Matches for Motif ID 1 (Highest to Lowest)

Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8

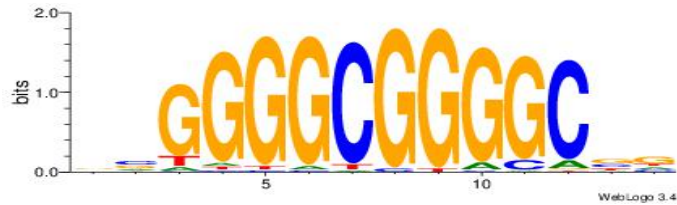
Similarity score: 0

Alignment:
BBGGGGCGGGGCVD
----GGCGGGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

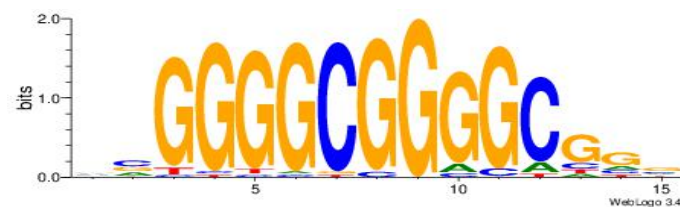
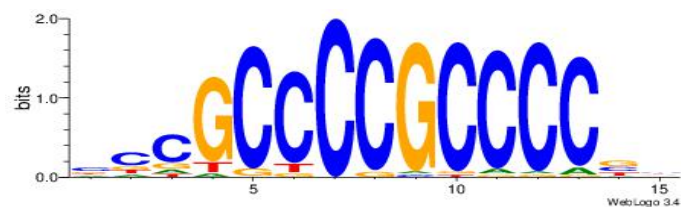


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.00250079

Alignment:
BCCGCCCCGCCCCBB
---GCCCCGCC----

Original motif Consensus sequence: BCCGCCCCGCCCCBB

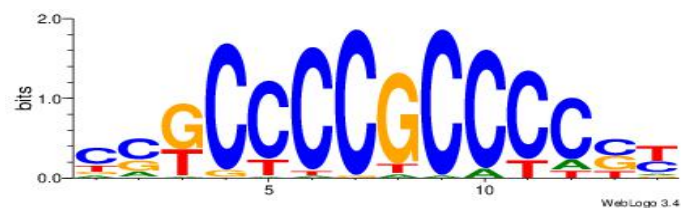
Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



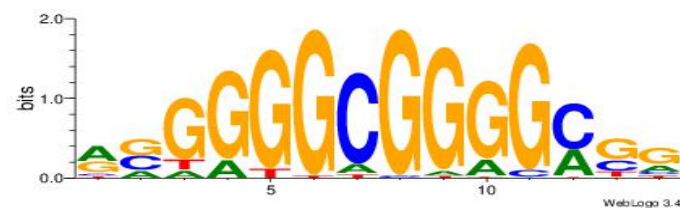
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0149958

Alignment:
 MSGGGGCGGGYSG
 ----GGCGGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY



Dataset #: 5
 Motif ID: 50

Motif name:	TFF11
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:	0.0348969

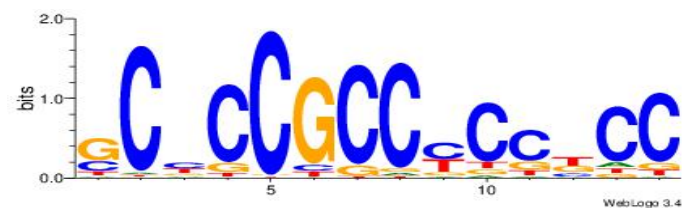
Alignment:

```
GGMGGRGGCGGVGC
-----GGCGGGGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



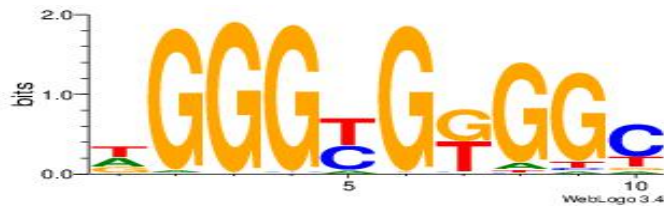
Dataset #:	3
Motif ID:	27
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0349983

Alignment:

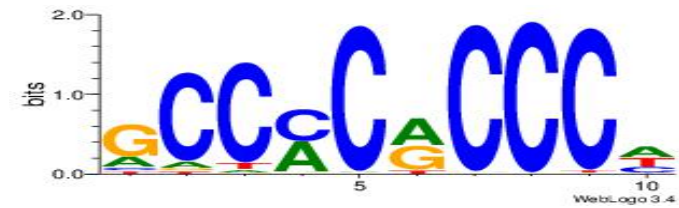
DGGGYGKGGC

--GGCGGGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #:	3
Motif ID:	22
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:	8
Similarity score:	0.0708224

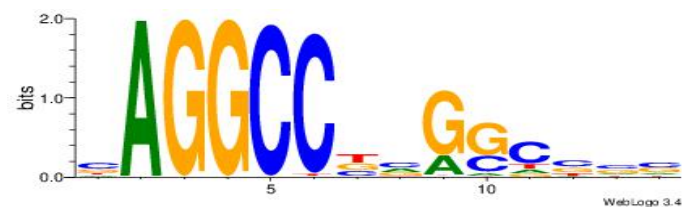
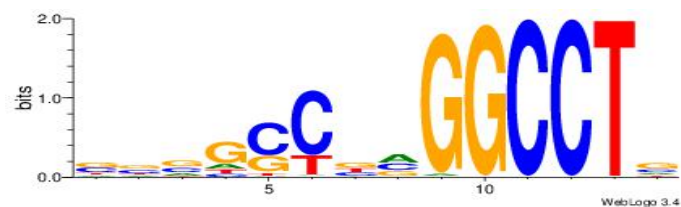
Alignment:

VAGGCCBBGGCVBB

---GCCCGCC---

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Dataset #: 5
 Motif ID: 48
 Motif name: TFW3
 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: 0.071681

Alignment:

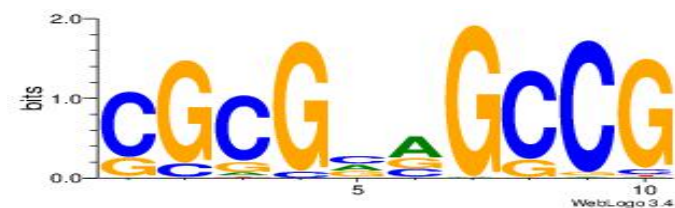
CGCGBMGCCG

-GCCCCGCC-

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

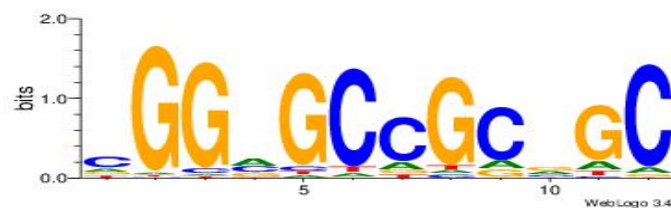


Dataset #: 5
 Motif ID: 49

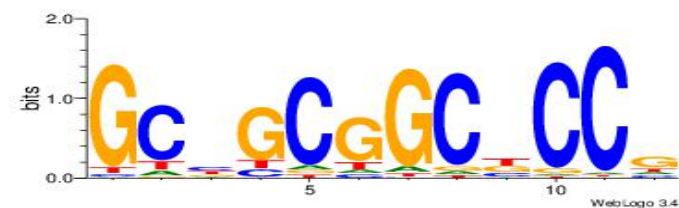
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0803996

Alignment:
CGGVGCCGCVGC
--GCCCCGCC--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



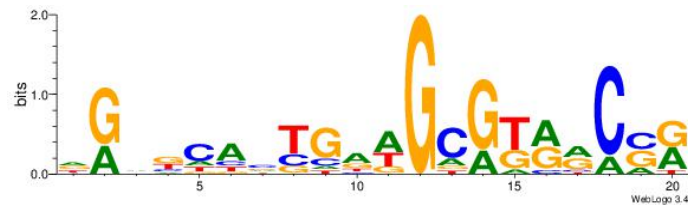
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0853847

Alignment:

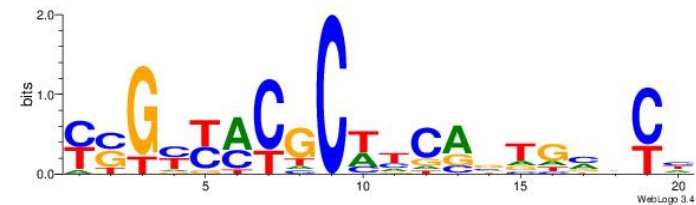
DGVBCABTGDWGCGRRCR

-----GGCGGGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



Dataset #:	3
Motif ID:	23
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:	8
Similarity score:	0.0878731

Alignment:

YCGCCCACGCH

---GCCCGGCC

Original motif Consensus sequence: HGCGTGGGCGK

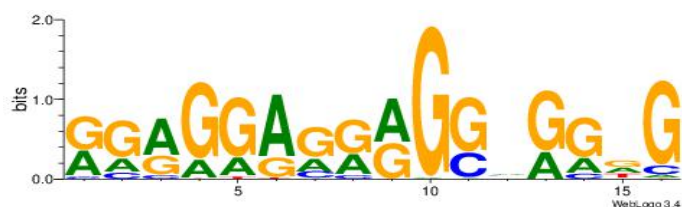
Reverse complement motif Consensus sequence: YCGCCCACGCH



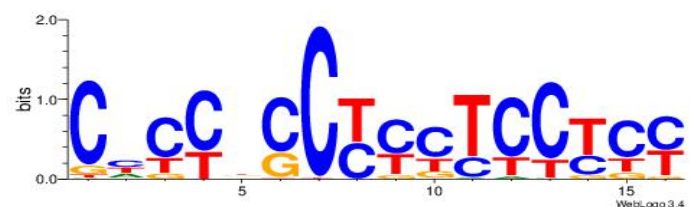
Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0928252

Alignment:
 CHCCBCKMCTCCKCM
 --GCCCCGCC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

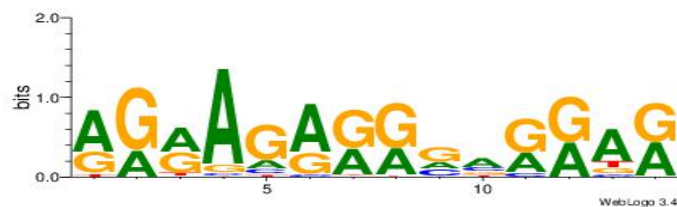


Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

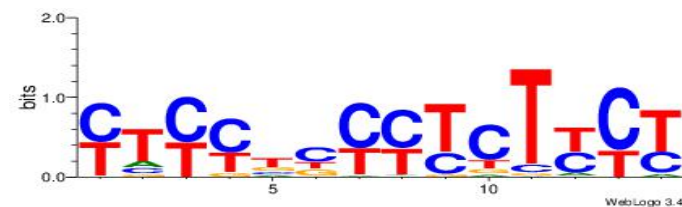


Dataset #: 2 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



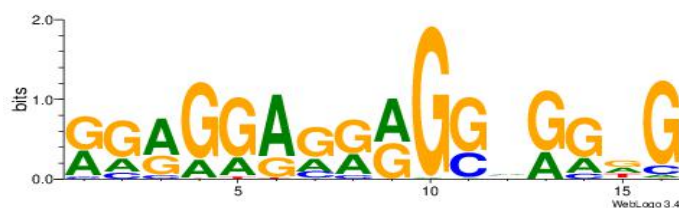
Best Matches for Motif ID 2 (Highest to Lowest)

Dataset #:	5
Motif ID:	51
Motif name:	TFM2
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:	0.00948131

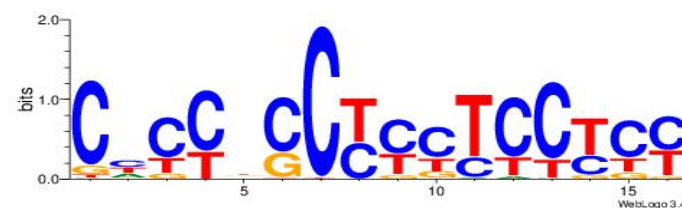
Alignment:

```
RGRGGAGRRGGHGGDG
--RGRAGARRGARRAR
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKM

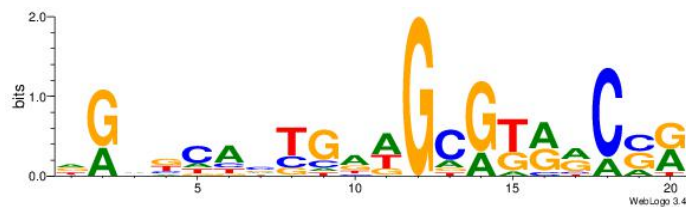


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.047364

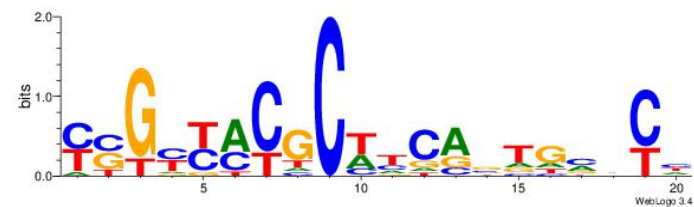
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----MTMMTCMMTCTKCK

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

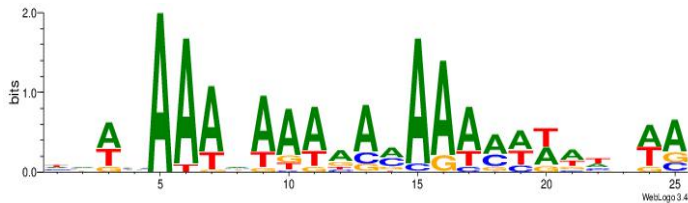


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

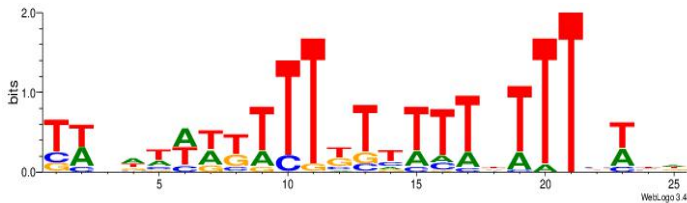
Number of overlap: 14
Similarity score: 0.0541717

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
-----RGRAGARRGARRAR--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



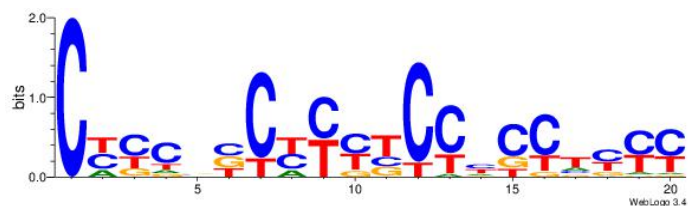
Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH



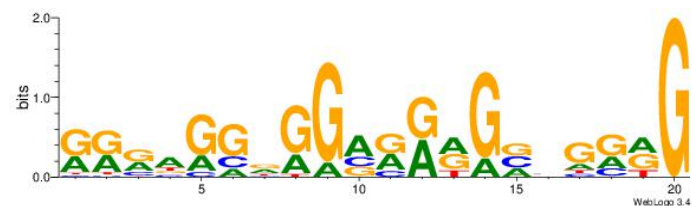
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.0545069

Alignment:
CYVCBBCYYTTCCHCCTYYY
-----MTMMTCMMTCTKCK

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

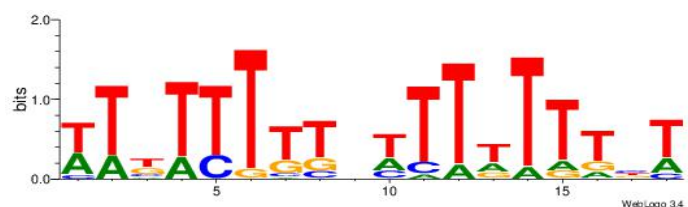


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0558935

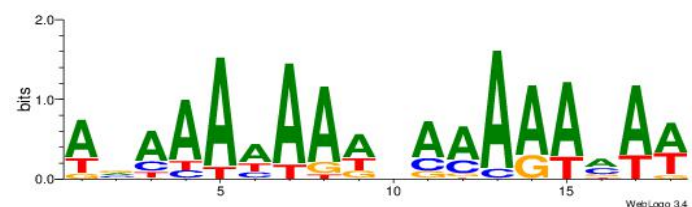
Alignment:

ABAAAAAAWHAAAAARAW
 -RGRAGARRGARRAR---

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW

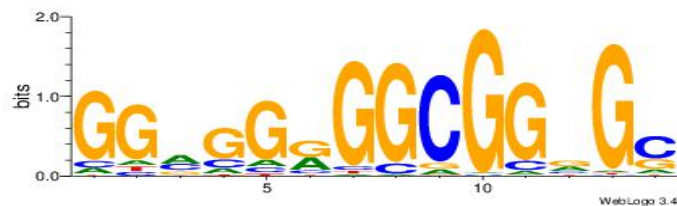


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0689626

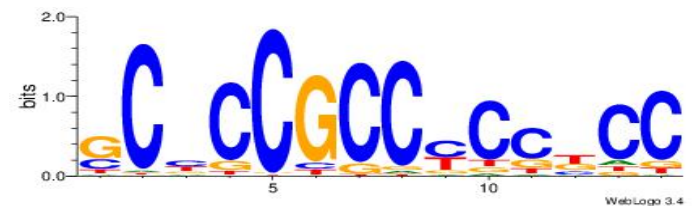
Alignment:

GGMGGRGGCGGVGC
 RGRAGARRGARRAR

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

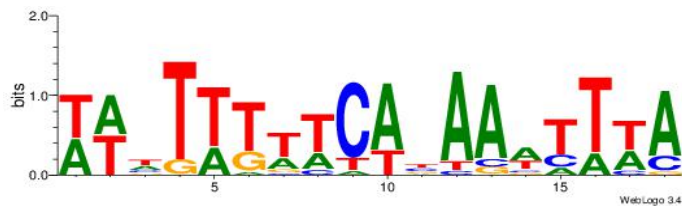


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 14

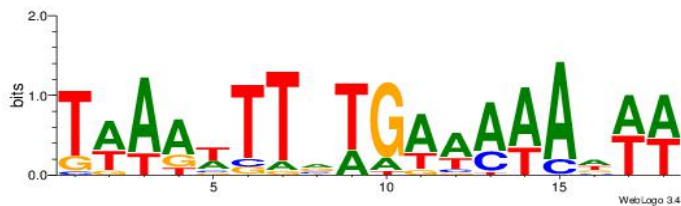
Similarity score: 0.0775356

Alignment:
TWAAWTTVTGAAAAHWW
-RGRAGARRGARRAR---

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

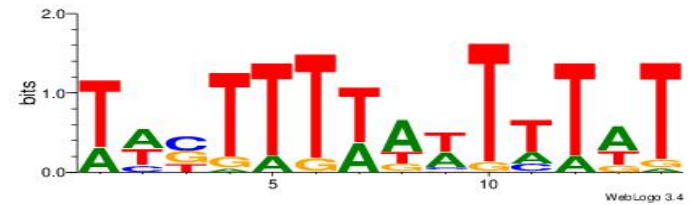
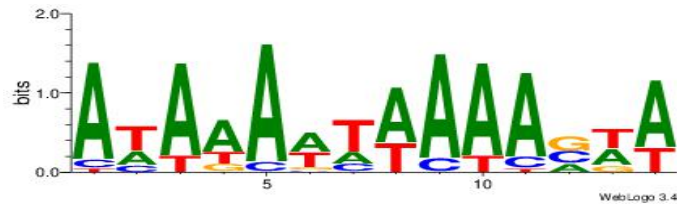


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.57507

Alignment:
AWAAAWTWAAASWA-
-RGRAGARRGARRAR

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTVA

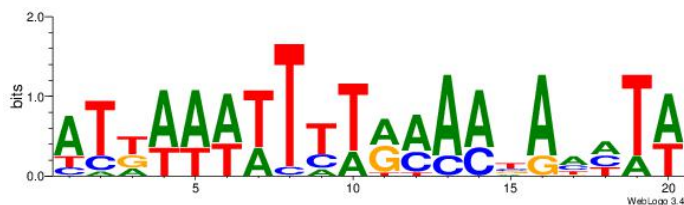


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 12
 Similarity score: 1.0763

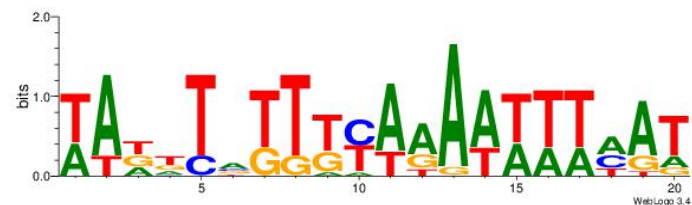
Alignment:

```
ATKAAWTTTTRMAABAHHTW--
-----MTMMTCMMTCTKCK
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATWTRAT

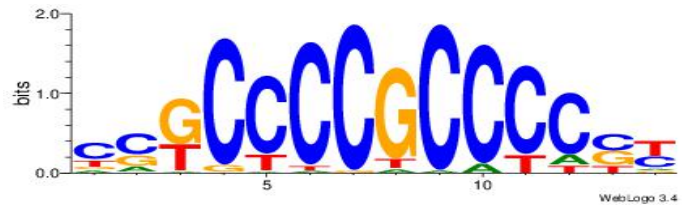


Dataset #: 2

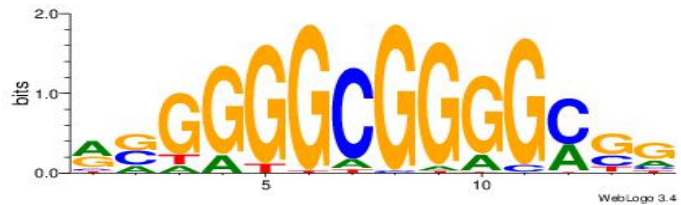
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 1.57133

Alignment:
---MSGGGGCGGGGYSG
RGRAGARRGARRAR---

Original motif Consensus sequence: CSKCCCCGCCCSY

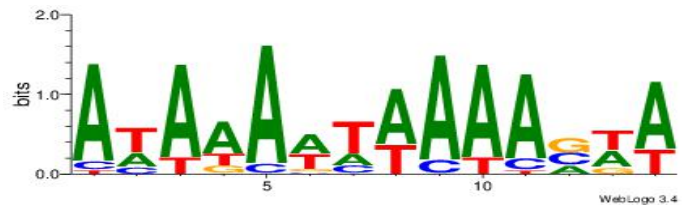


Reverse complement motif Consensus sequence: MSGGGGCGGGGY

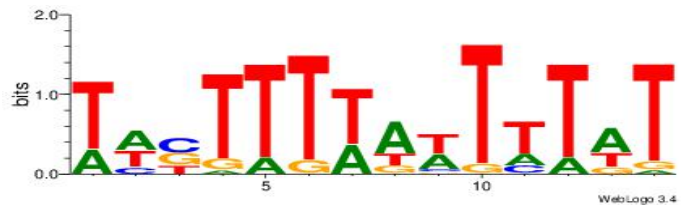


Dataset #: 2 Motif ID: 3 Motif name: Motif 3

Original motif Consensus sequence: AWAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV



Best Matches for Motif ID 3 (Highest to Lowest)

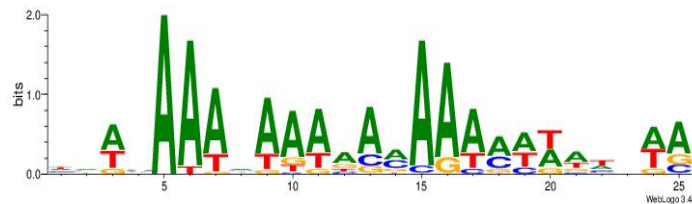
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.0137914

Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA  
-----AWAAAWTWAAASWA-----
```

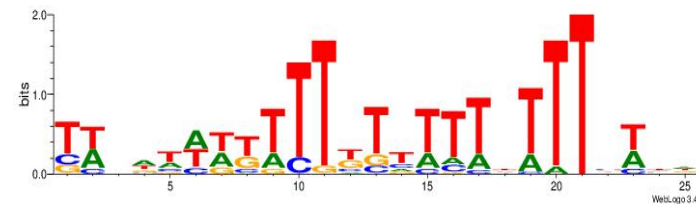
Original motif Consensus sequence:

HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:

TWVHWWYTTTTTTTTTHTTTVWBH

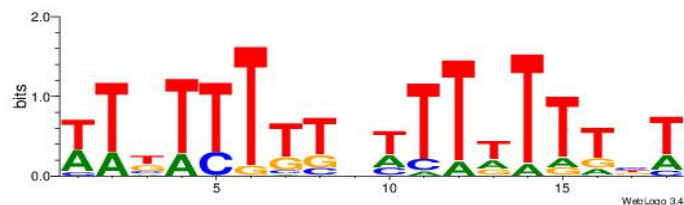


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

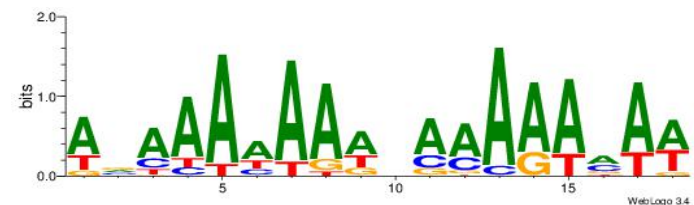
Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0162962

Alignment:
 ABAAAAAWhAAAAARAW
 ----AWAAAWTWAAASWA

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



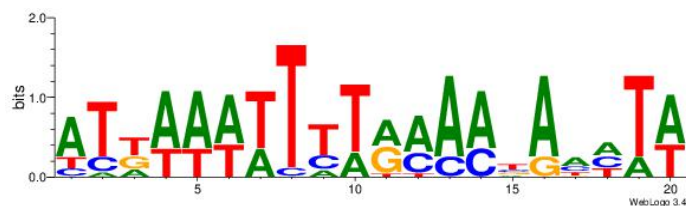
Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW



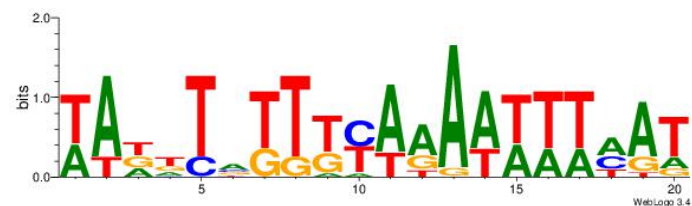
Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.037679

Alignment:
 ATKAAWTTTTRMAABAHHTW
 --AWAAAWTWAAASWA----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



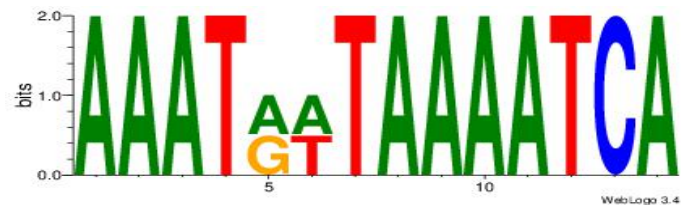
Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0423952

Alignment:

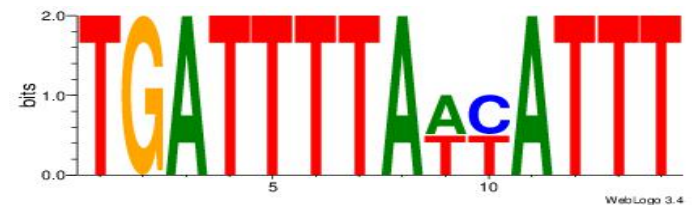
TGATTTTAWKATTT

TWSTTTWAWTTTWT

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT

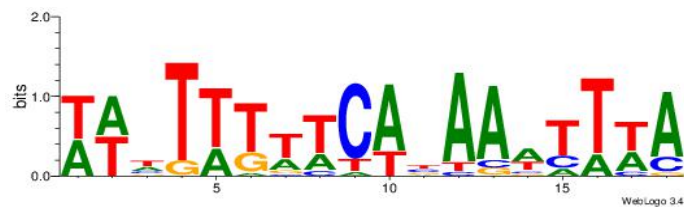


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0456419

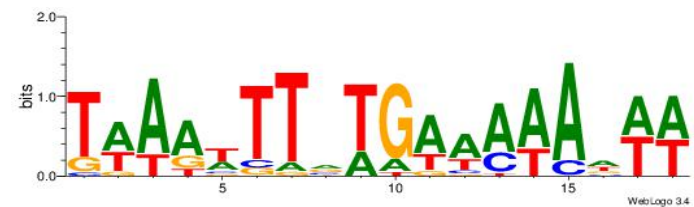
Alignment:

TWAAWTTVTGAAAAHWW
 ----AWAAAWTWAAASWA

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



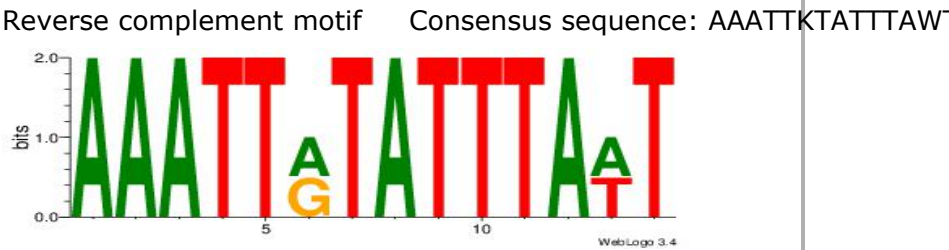
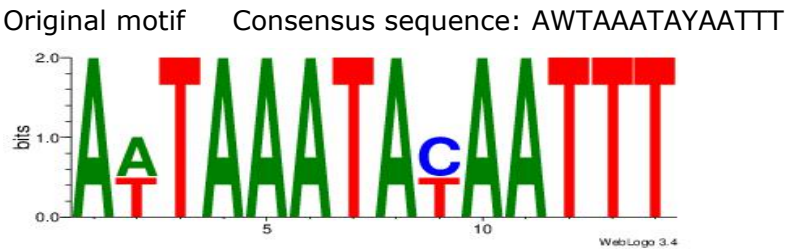
Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 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: 0.0478896

Alignment:
AAATTKTATTTAWT
TWSTTTWAWTTTWT

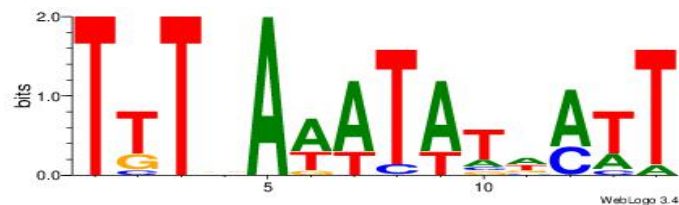
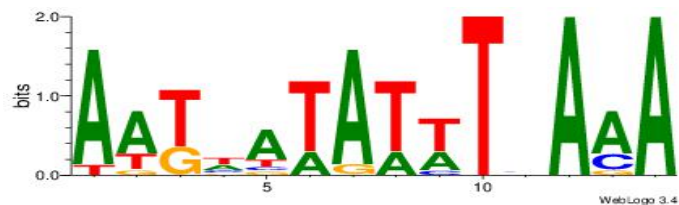


Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0624272

Alignment:
TTTDAWATATHATT
AWAAAWTWAAASWA

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHATT



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 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: 0.0702111

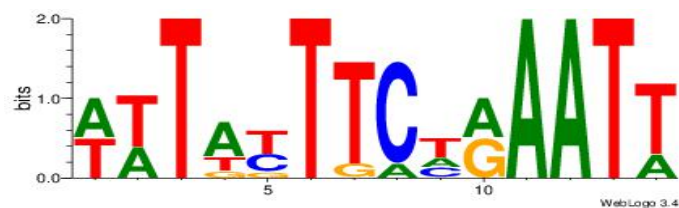
Alignment:

WWTAKTTCDKAATT
 TWSTTTWAWTTTWT

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAATT



Dataset #: 2
 Motif ID: 2

Motif name:	Motif 2
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:	0.567825

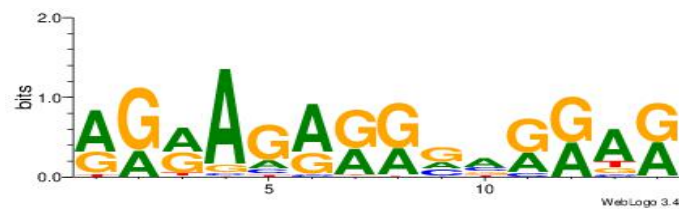
Alignment:

```

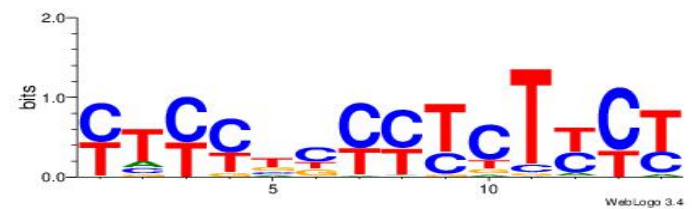
-RGRAGARRGARRAR
AWAAAWTWAAASWA-

```

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



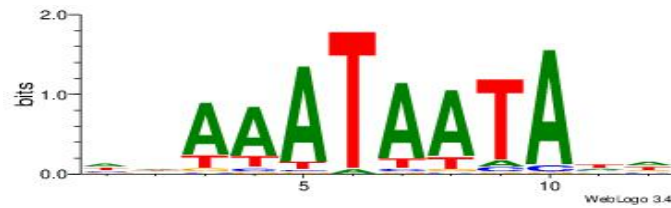
Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	1.0432

Alignment:

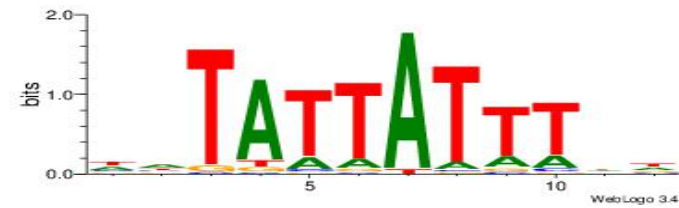
HDAAATAATADD--

AWAAAWTWAAASWA

Original motif Consensus sequence: HDAAATAATADD

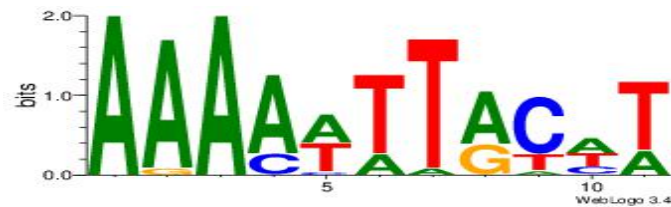


Reverse complement motif Consensus sequence: DDTATTATTDDH



Dataset #: 2 Motif ID: 4 Motif name: Motif 4

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



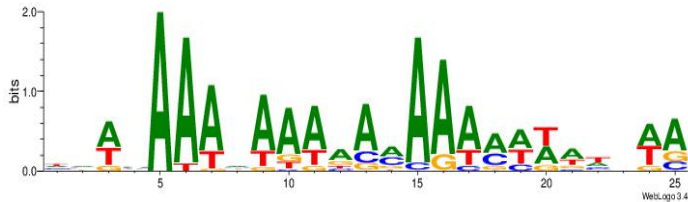
Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2

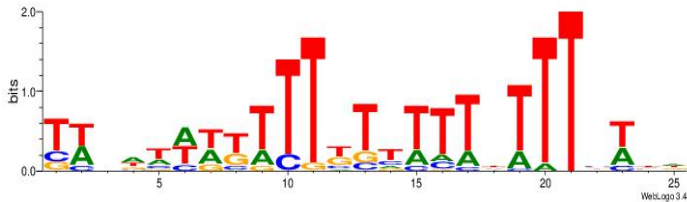
Number of overlap: 11
Similarity score: 0.0718583

Alignment:
HDWVAAAHAAAAAAMAAAMWWWHBWA
-----AAAAWTTRCWT-

Original motif Consensus sequence:
HDWVAAAHAAAAAAMAAAMWWWHBWA



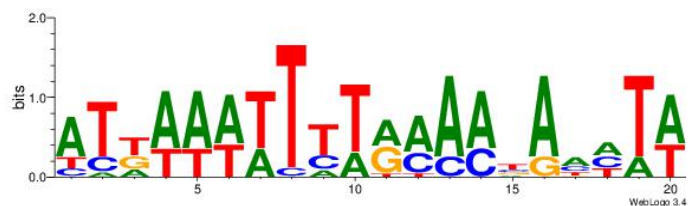
Reverse complement motif Consensus sequence:
TWVHWWYTTTYYTTTTTHTTTVWBH



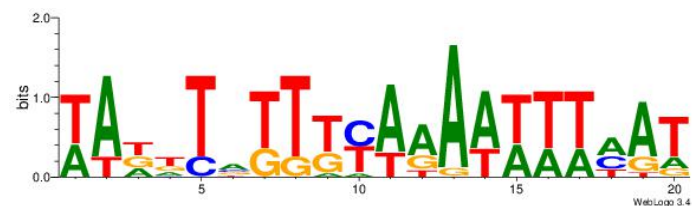
Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 10
Number of overlap: 11
Similarity score: 0.0727073

Alignment:
ATKAAWTTTTRMAABAHHTW
AWGKAAWTTTT-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

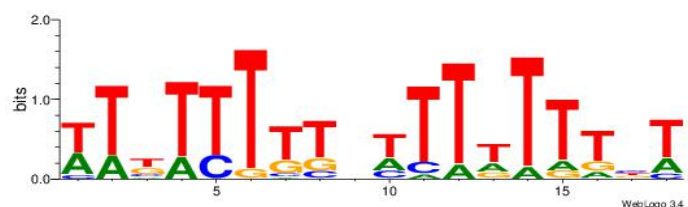


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 11
Similarity score: 0.0748297

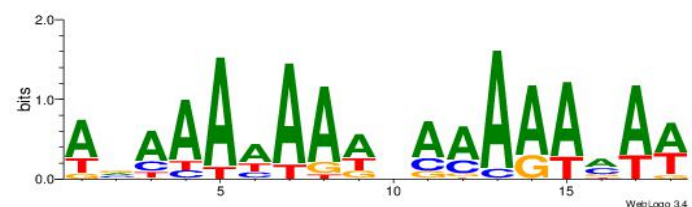
Alignment:

WTKTTTTTHWTTTTTTBT
---AWGKAAWTTTT----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW

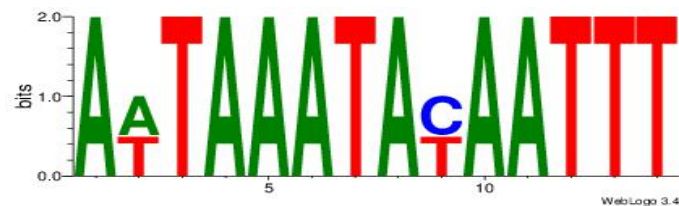


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0786484

Alignment:

AAATTKTATTTAWT
 AAAAWTTRCWT---

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

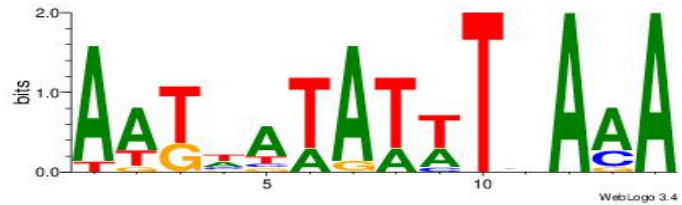


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11

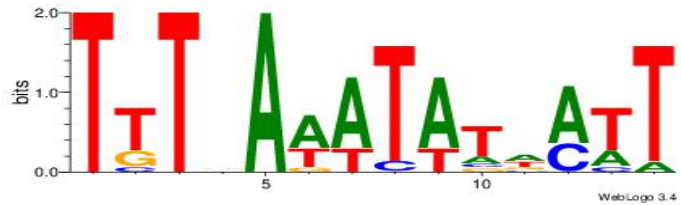
Similarity score: 0.0820375

Alignment:
AATHATATWTHAAA
AWGKAAWTTTT---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

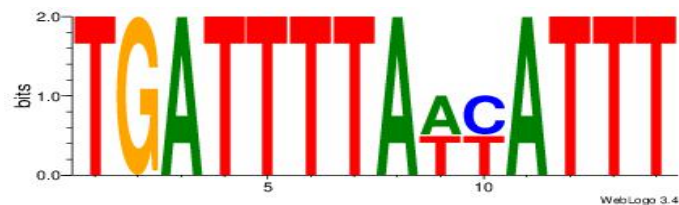
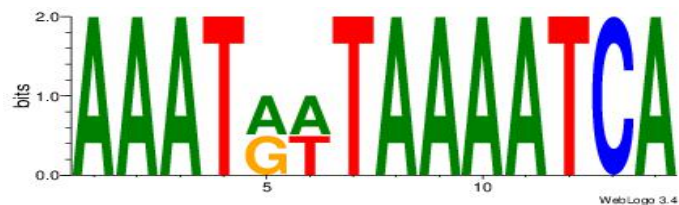


Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.083433

Alignment:
TGATTTTAWKATTT
---AWGKAAWTTTT

Original motif Consensus sequence: AAATRWTAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATTT



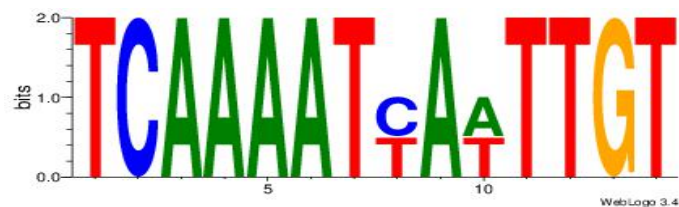
Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0852273

Alignment:
 ACAAWTRATTTTGA
 AAAAWTTRCWT---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #: 5
 Motif ID: 53

Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0858797

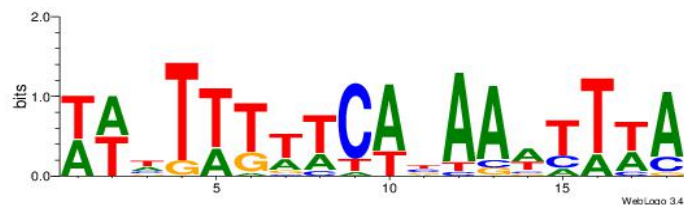
Alignment:

```

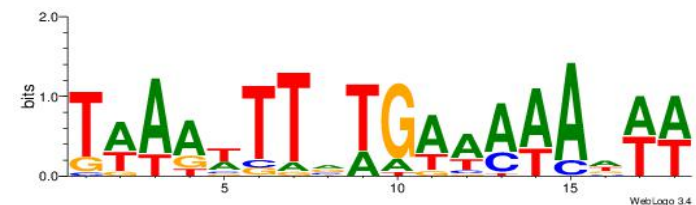
WWHTTTTTCABAAWTTWA
-----AWGKAAWTTT

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Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



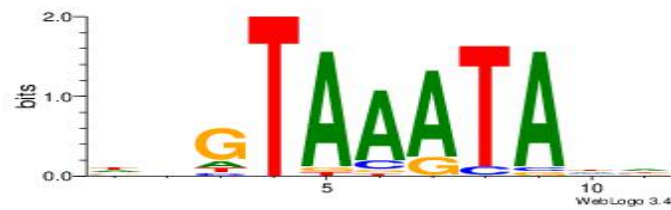
Dataset #:	4
Motif ID:	45
Motif name:	wbgTAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.086338

Alignment:

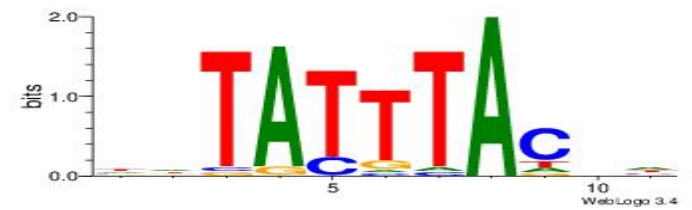
DHTATTTACBD

AAAATTTTCWT

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
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:	0.0867914

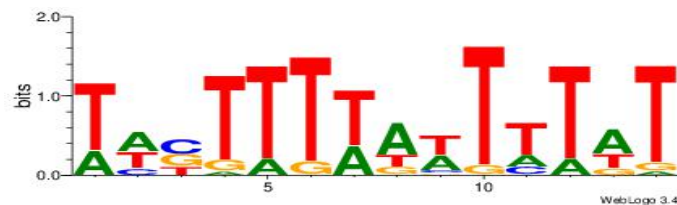
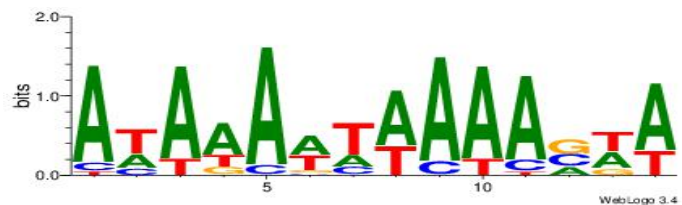
Alignment:

TWSTTTWAWTTTWT

--AWGKAAWTTTT-

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

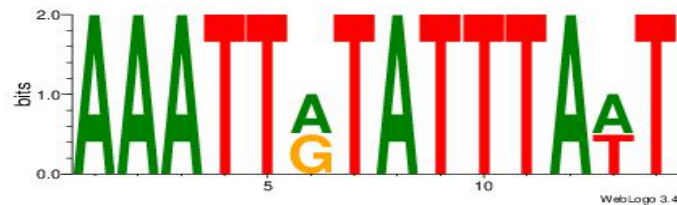


Dataset #: 2 Motif ID: 5 Motif name: Motif 5

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

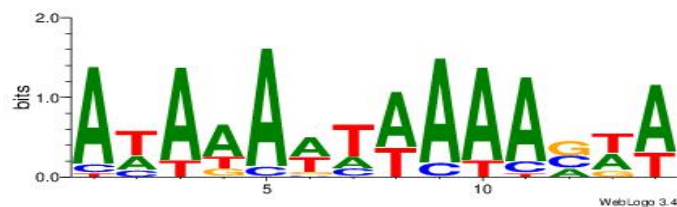


Best Matches for Motif ID 5 (Highest to Lowest)

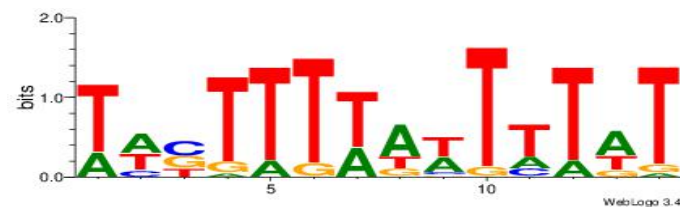
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.101648

Alignment:
 TWSTTTWAWTTTWT
 AAATTKTATTTAWT

Original motif Consensus sequence: AWAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV

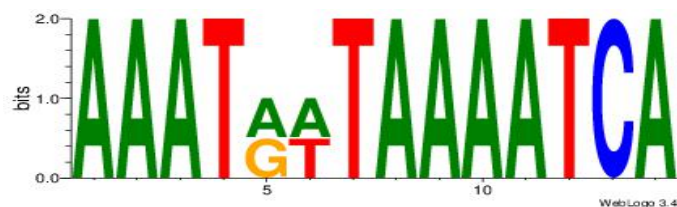


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.107143

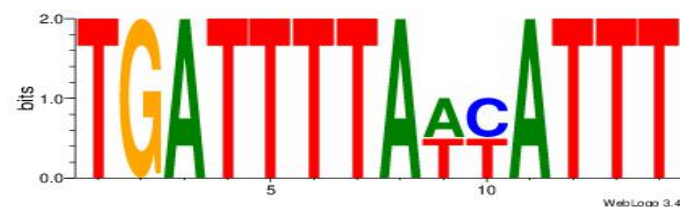
Alignment:

TGATTTTAWKATTT
 AAATTKTATTTAWT

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT

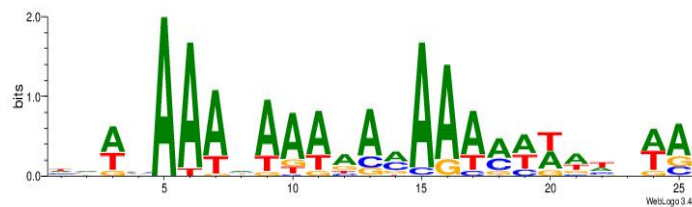


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.109769

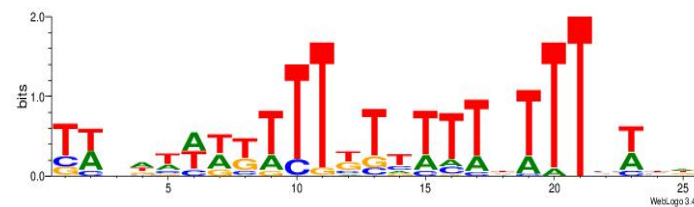
Alignment:

TWVHWWYTTTYYTTTTHTTTVWBH
 -----AAATTKTATTTAWT-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYYTTTTHTTTVWBH

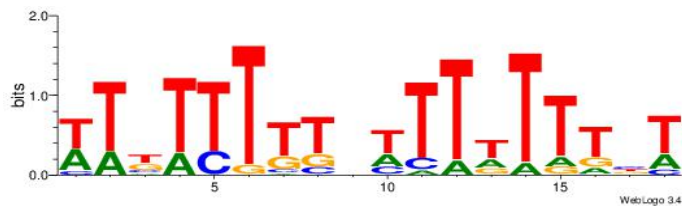


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

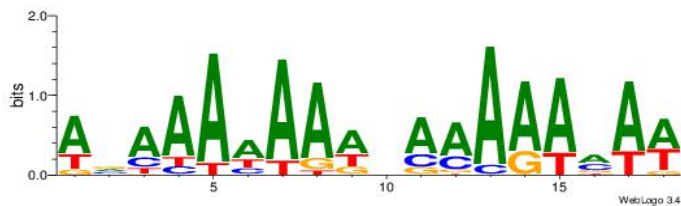
Number of overlap: 14
Similarity score: 0.110348

Alignment:
WTKTTTTTHWTTTTTBT
-AAATTKTATTTAWT---

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW

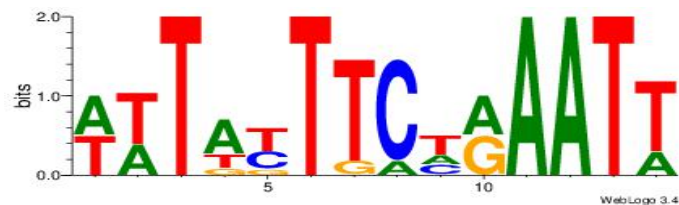


Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.111607

Alignment:
AATTYDGAARTAWW
AAATTKTATTTAWT

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

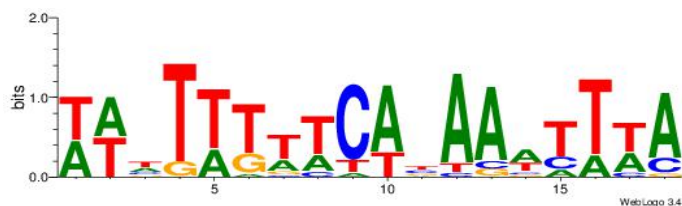


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.124188

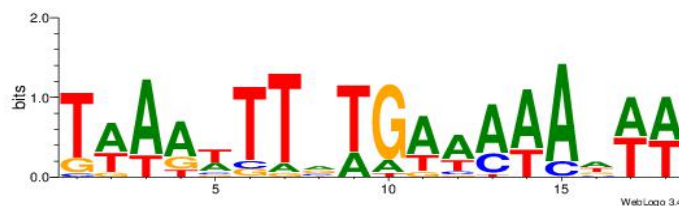
Alignment:

WWHTTTTTTCABAAWTTWA
 --AWTAAATAYAATTT--

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



Dataset #: 2

Motif ID: 16
 Motif name: Motif 16
 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: 0.125

Alignment:

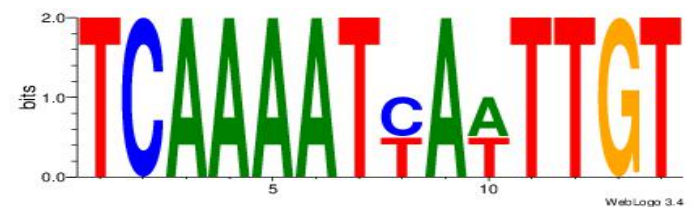
ACAAWTRATTTTGA

AAATTKTATTTAWT

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

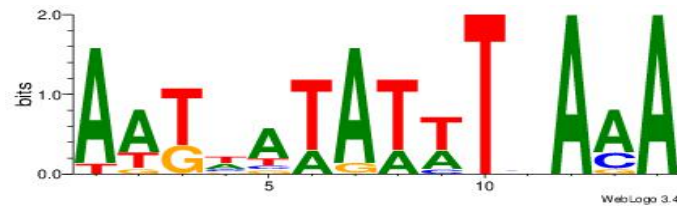


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.596154

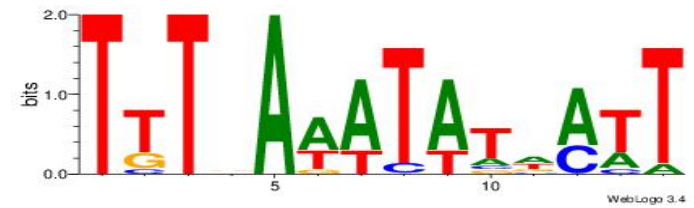
Alignment:

TTTDAWATATHATT-
-AWTAAATAYAATTT

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



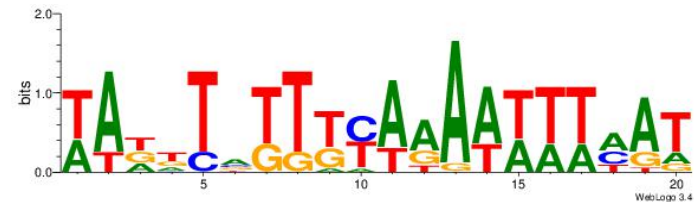
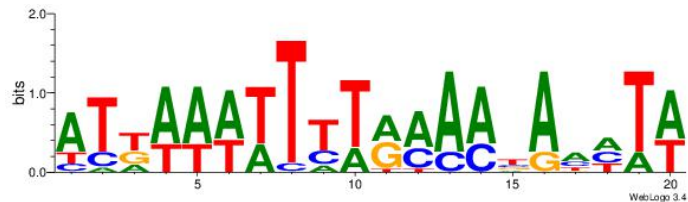
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	12
Similarity score:	1.11736

Alignment:

WAHHTVTTYKAAAWTTRAT--
-----AWTAAATAYAATTT

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAWTTRAT



Dataset #: 2
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 1.125

Alignment:

--TTCWTAGATTAWA
 AWTAAATAYAATTT-

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAAATCTAWGAA

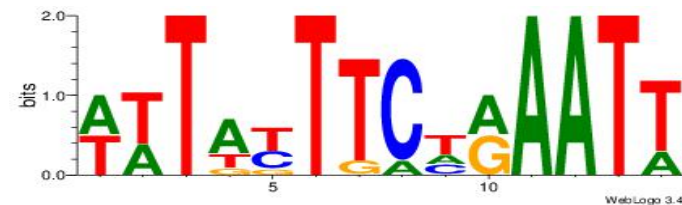


Dataset #: 2 Motif ID: 6 Motif name: Motif 6

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	5
Motif ID:	53
Motif name:	TFM3
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:	0.0325081

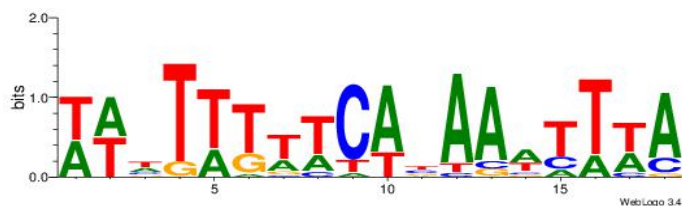
Alignment:

```

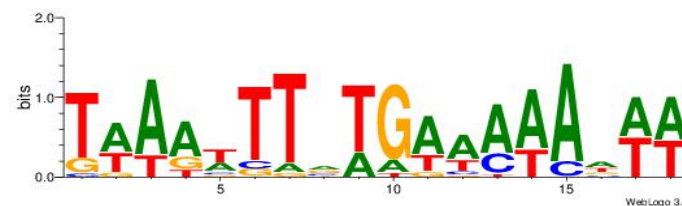
WWHTTTTTTCABAAWTTWA
-WWTAKTTCDKAATT---

```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

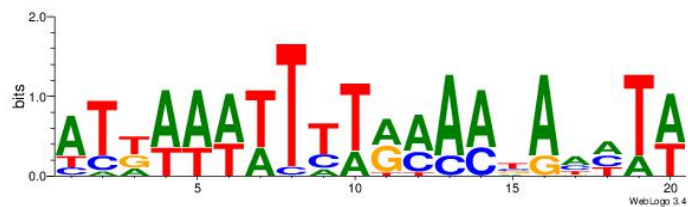


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0349702

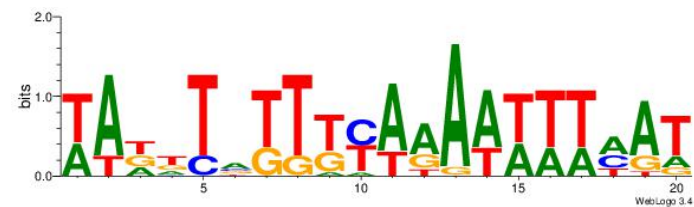
Alignment:

ATKAAWTTTTRMAABAHHTW
 ----AATTYDGAARTAWW--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



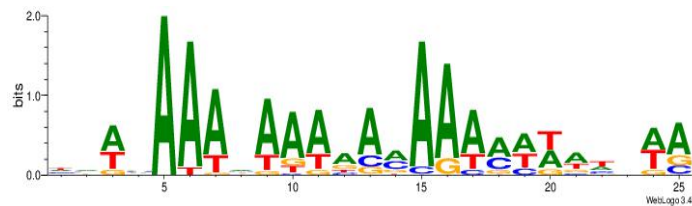
Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9

Number of overlap: 14
 Similarity score: 0.0626838

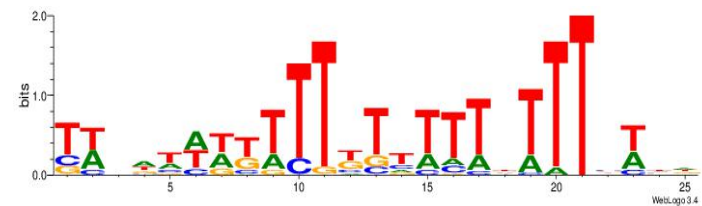
Alignment:

TWVHWWYTTTTYTTTTTHTTTTVWBH
 ---WWTAKTTCDKAATT-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAAMAAAMWWH BW A



Reverse complement motif Consensus sequence:
 TWVHWWYTTTTYTTTTTHTTTTVWBH

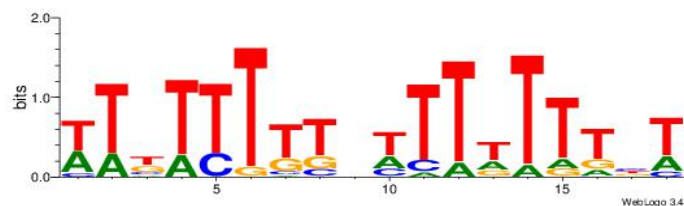


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0667239

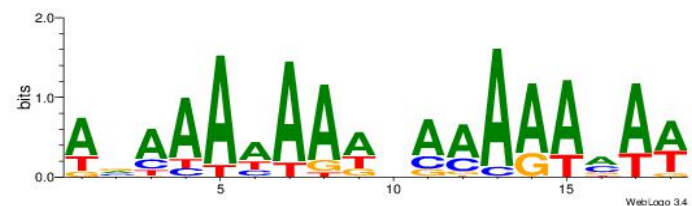
Alignment:

WKTTTTTHWTTTTTTBT
 -WWTAKTTCDKAATT---

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW



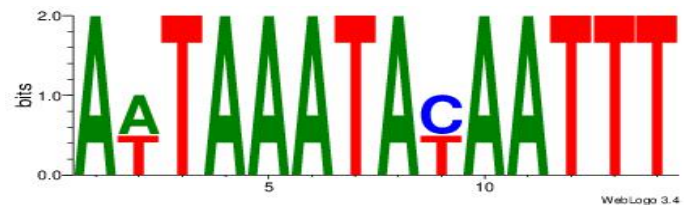
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0741071

Alignment:

AWTAAATAYAATTT

WWTAKTTCDKAATT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

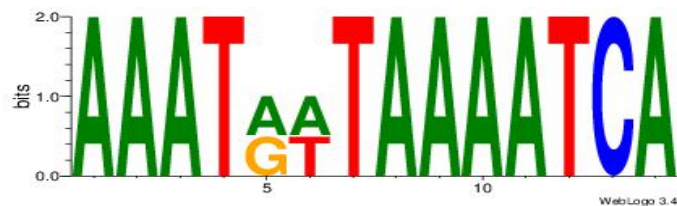


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0763393

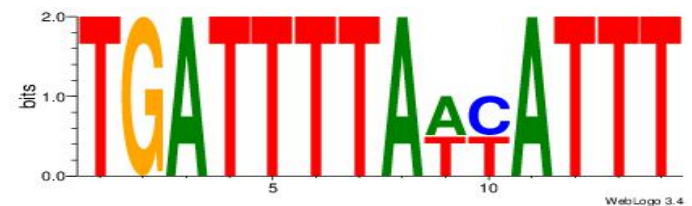
Alignment:

TGATTTTAWKATTT
 WWTAKTTCDKAATT

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT

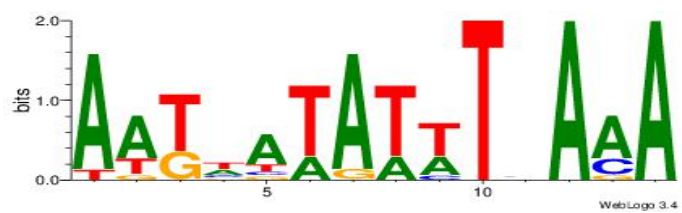


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14

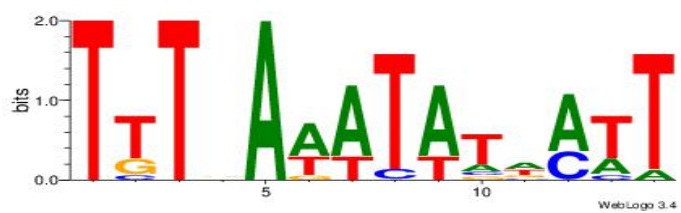
Similarity score: 0.0852679

Alignment:
TTTDAWATATHATT
WWTAKTTCDKAATT

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHATT

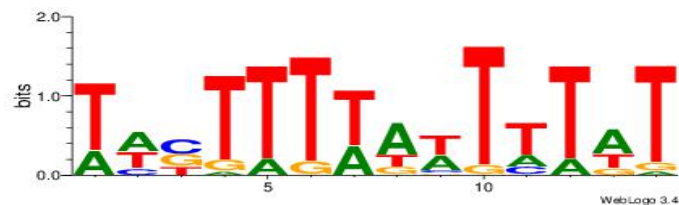
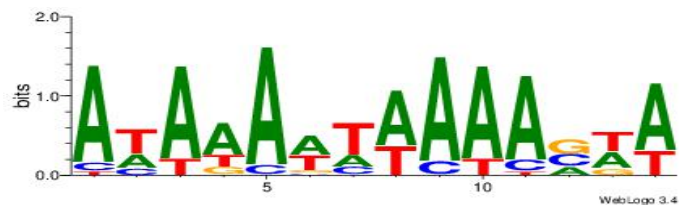


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0864698

Alignment:
TWSTTTWAWTTTWT
WWTAKTTCDKAATT

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT



Dataset #: 2
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 1.06667

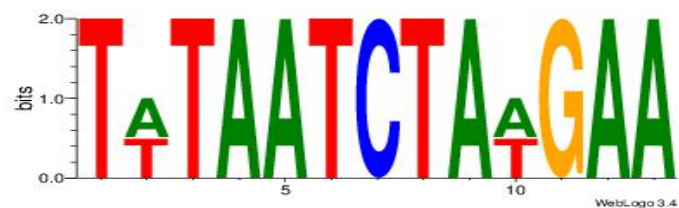
Alignment:

--TTCWTAGATTAWA
 AATTYDGAARTAWW-

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTAWGAA



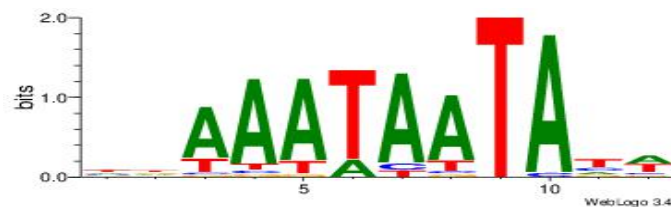
Dataset #: 4
 Motif ID: 37

Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.07587

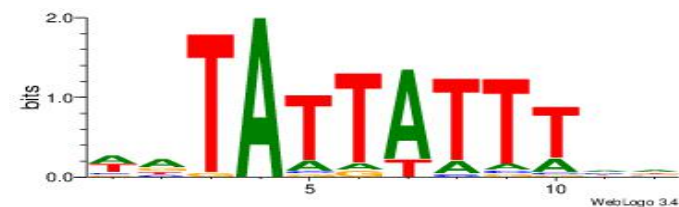
Alignment:

WHTATTATTDDH--
 WWTAKTTCDKAATT

Original motif Consensus sequence: HDAAATAATAHW

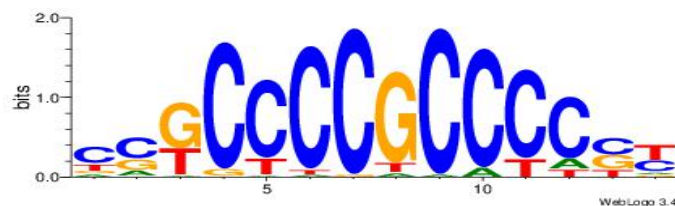


Reverse complement motif Consensus sequence: WHTATTATTDDH

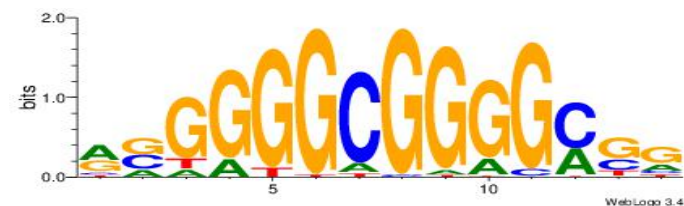


Dataset #: 2 Motif ID: 7 Motif name: Motif 7

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



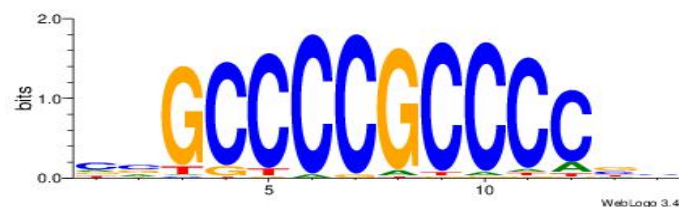
Best Matches for Motif ID 7 (Highest to Lowest)

Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 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

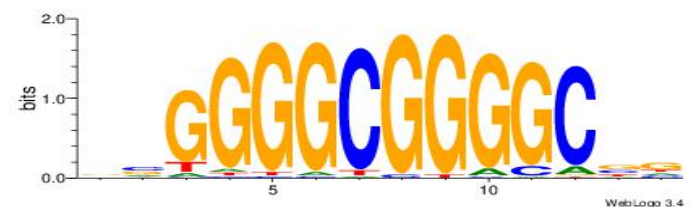
Alignment:

HVGCCCCGCCCCBB
 CSKCCCCGCCCCSY

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14

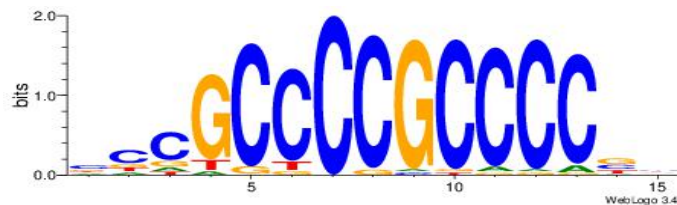
Similarity score: 0.0012818

Alignment:

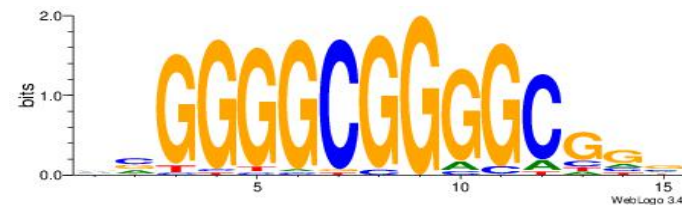
BCCGCCCCGCCCCBB

-CSKCCCCGCCCCSY

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.0537802

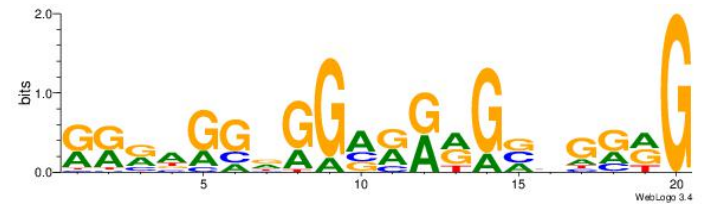
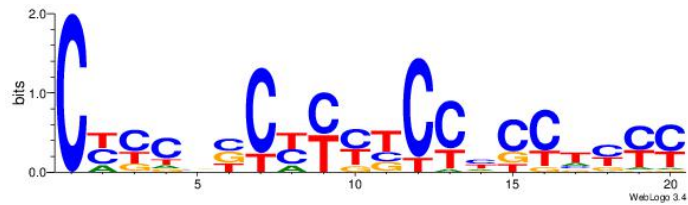
Alignment:

CYYCBBCYYYTCCHCCTYYY

---CSKCCCCGCCCCSY---

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



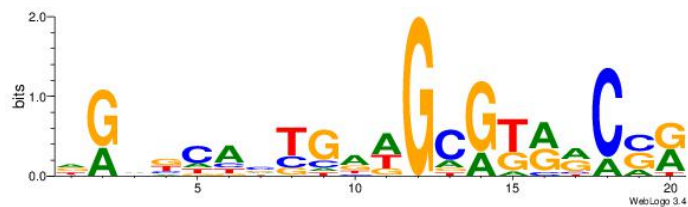
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0662825

Alignment:

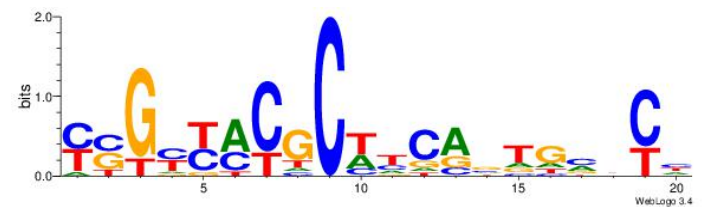
```

DGVBCABTGDWGCGRRCR
-----MSGGGGCGGGYSG
  
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



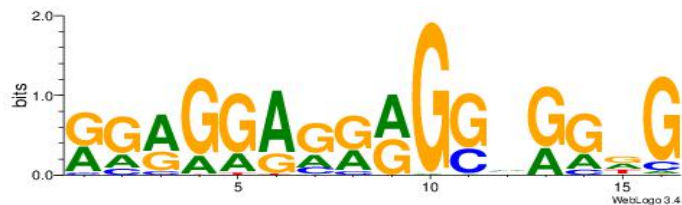
Dataset #: 5

Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0758609

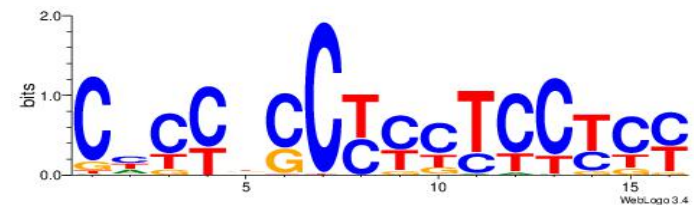
Alignment:

CHCCBCCCKMCTCCKCM
 CSKCCCCGCCCSY--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCCKMCTCCKCM

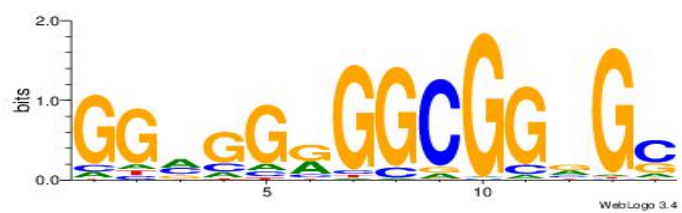


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14

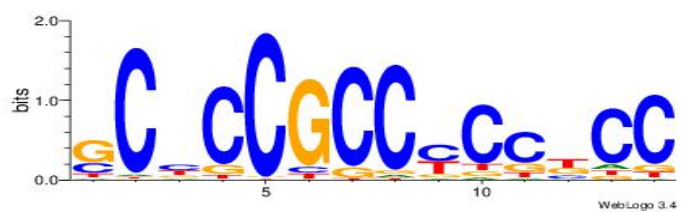
Similarity score: 0.0829042

Alignment:
GCVCCGCCMCCYCC
CSKCCCCGCCCCSY

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

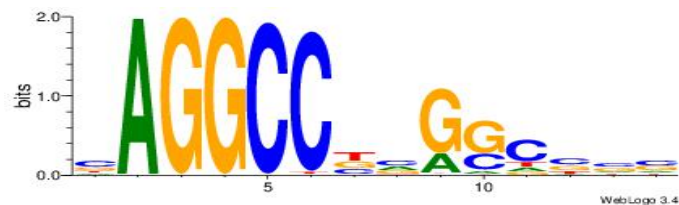
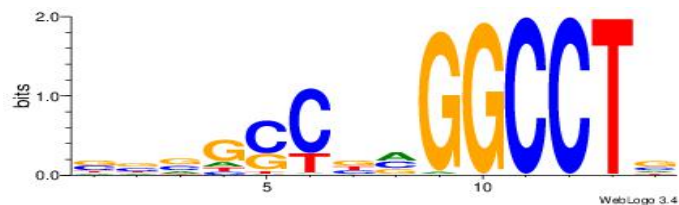


Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0912118

Alignment:
VAGGCCBBGGCVBB
CSKCCCCGCCCCSY

Original motif Consensus sequence: BBVGCCBVGGCCTV

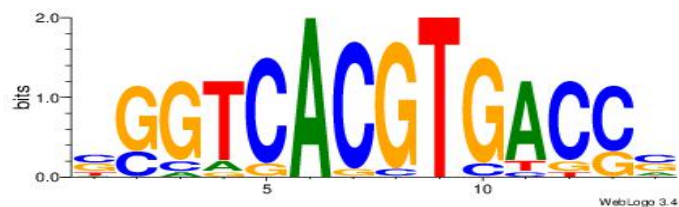
Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



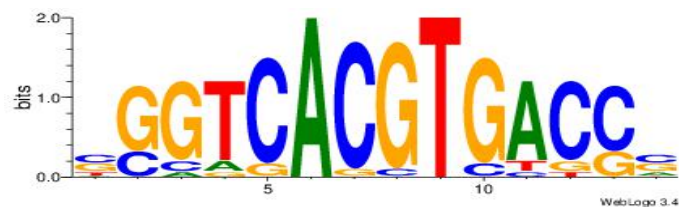
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0948838

Alignment:
 SGGTCACGTGACCS
 MSGGGGCGGGYSG

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 3
 Motif ID: 30

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:	13
Similarity score:	0.590412

Alignment:

```

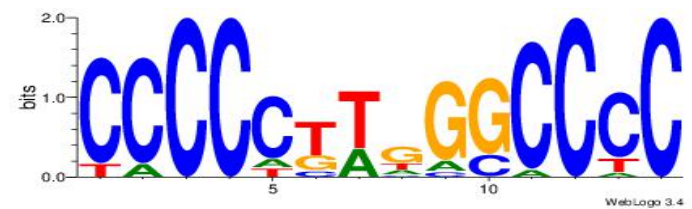
CCCCCTTGGGCCCC-
-CSKCCCCGCCCCSY

```

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC



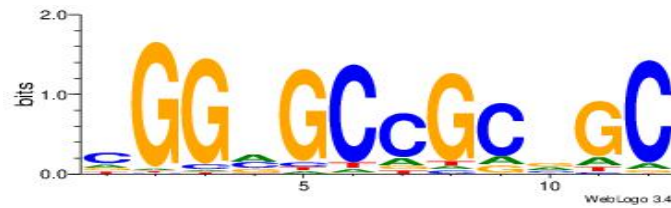
Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	1.07659

Alignment:

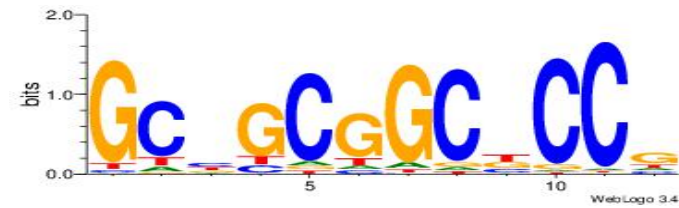
CGGVGCCGCVGC--

MSGGGGCGGGGYSG

Original motif Consensus sequence: CGGVGCCGCVGC

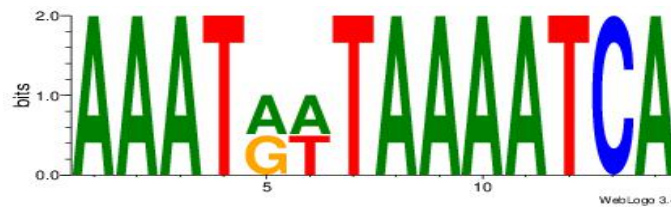


Reverse complement motif Consensus sequence: GCVGCCGCBCCG

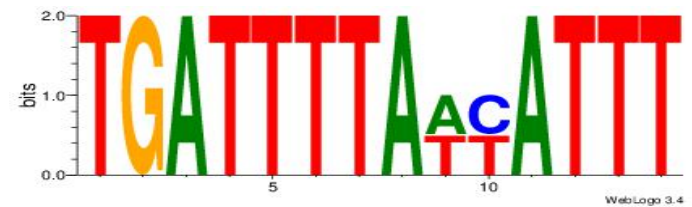


Dataset #: 2 Motif ID: 8 Motif name: Motif 8

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



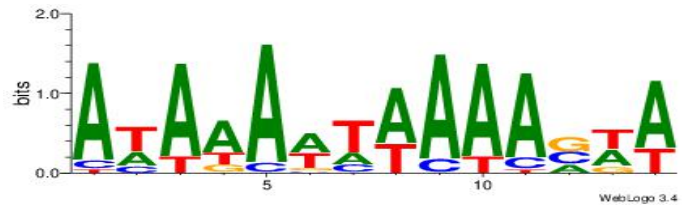
Best Matches for Motif ID 8 (Highest to Lowest)

Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

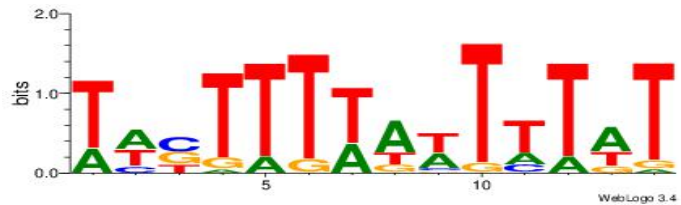
Number of overlap: 14
Similarity score: 0.0961539

Alignment:
TWSTTTWAWTTTWT
TGATTTTAWKATTT

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

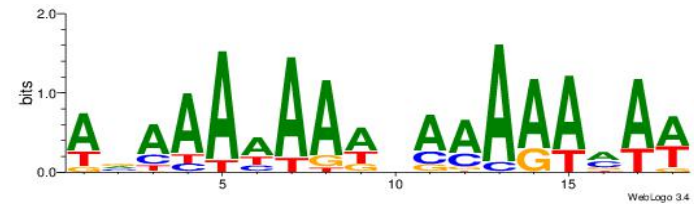
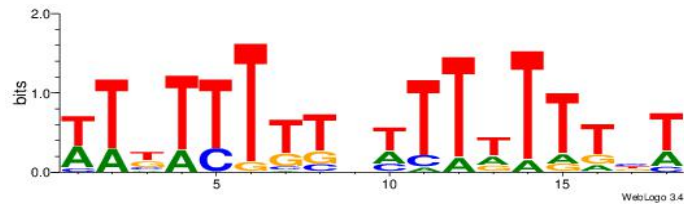


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.10348

Alignment:
WTKTTTTTHWTTTTTBT
-TGATTTTAWKATTT---

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW

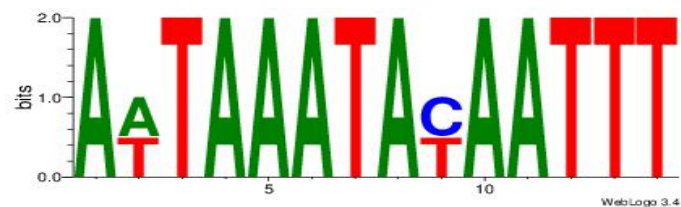


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.107143

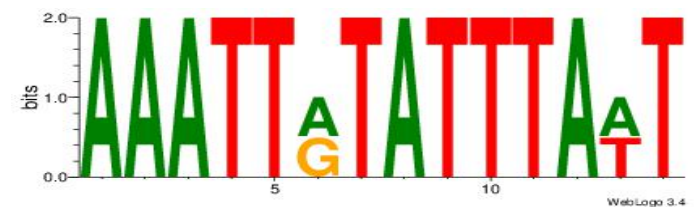
Alignment:

AAATTKTATTTAWT
 TGATTTTAWKATTT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

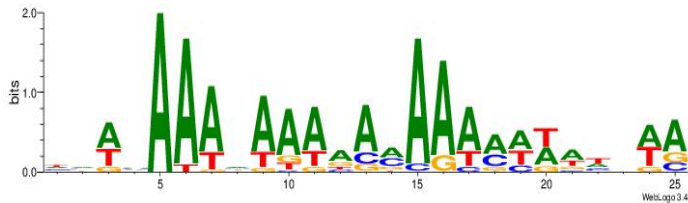


Dataset #: 5
 Motif ID: 56

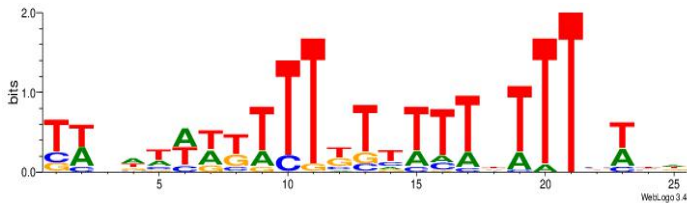
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 14
Similarity score: 0.111345

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
-----AAATRWTAATAATCA-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTTTTTTTHTTTVWBH

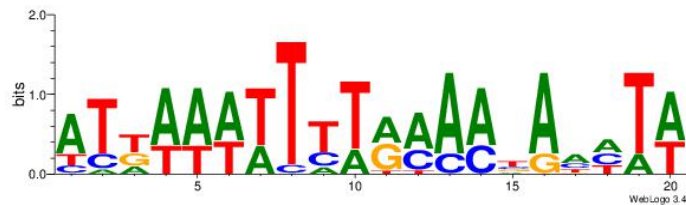


Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.11369

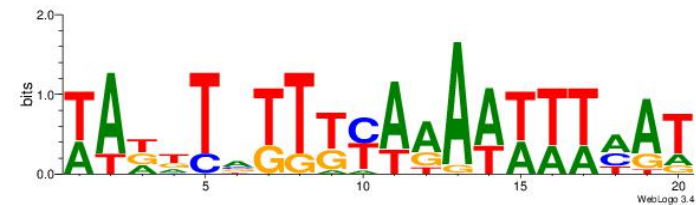
Alignment:

```
WAHHTVTTYKAAAATTRAT
---TGATTTTAWKATTT---
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



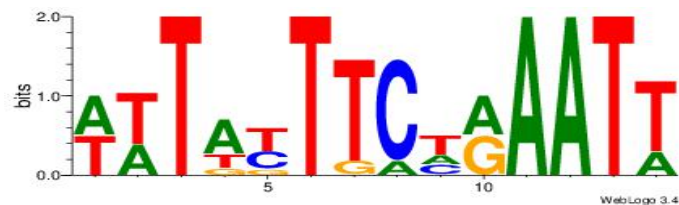
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.113839

Alignment:

```
WWTAKTTCDKAATT
TGATTTTAWKATTT
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAATT

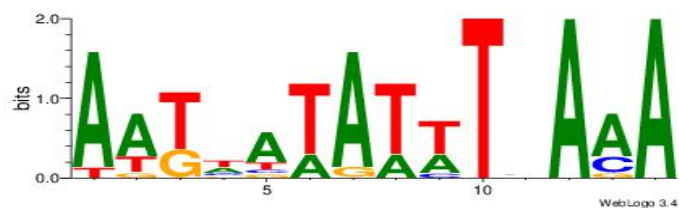


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.625

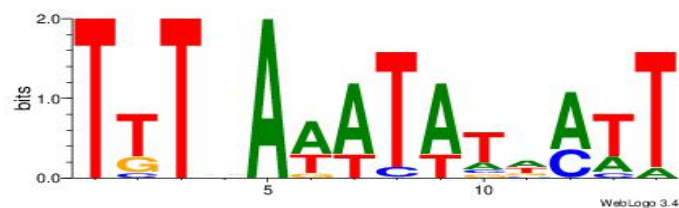
Alignment:

-AATHATATWTHAAA
 AAATRWTAATCA-

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



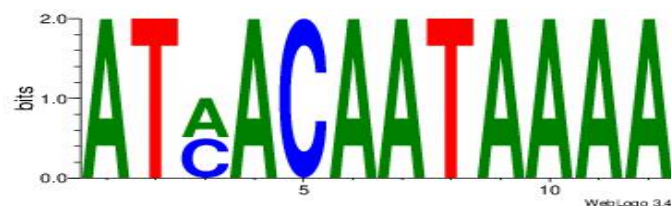
Dataset #: 2
 Motif ID: 15

Motif name:	Motif 15
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:	1.10417

Alignment:

```
--ATMACAATAAAA
AAATRWTAATCA
```

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

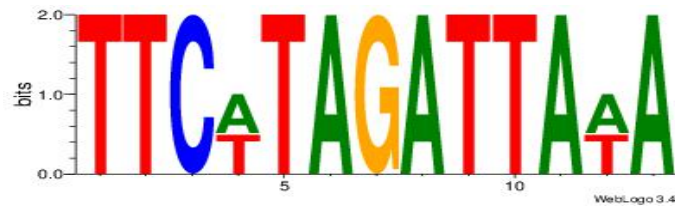


Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	1.10417

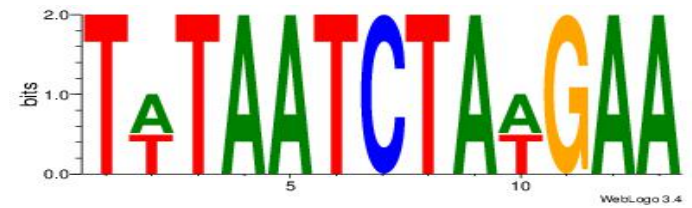
Alignment:

TWTAATCTAWGAA--
-TGATTTTAWKATTT

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAATCTAWGAA



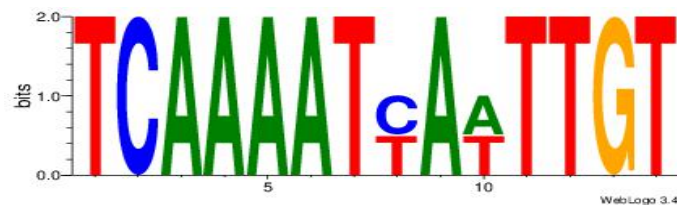
Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	1.125

Alignment:

ACAAWTRATTTTGA--
--AAATRWTAAAATCA

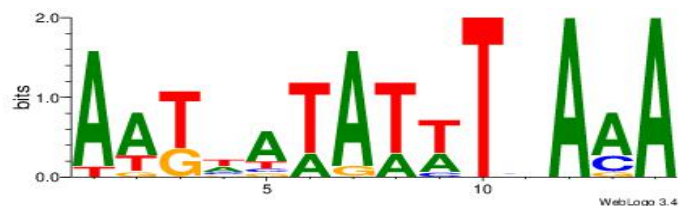
Original motif Consensus sequence: ACAAWTRATTTTGA

Reverse complement motif Consensus sequence: TCAAAATKAWTTG

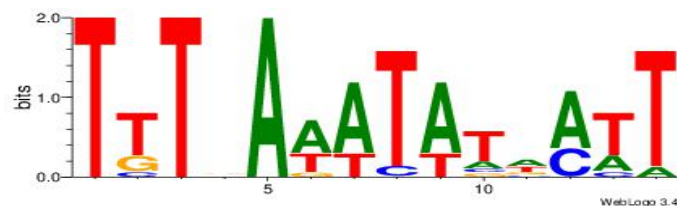


Dataset #: 2 Motif ID: 9 Motif name: Motif 9

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



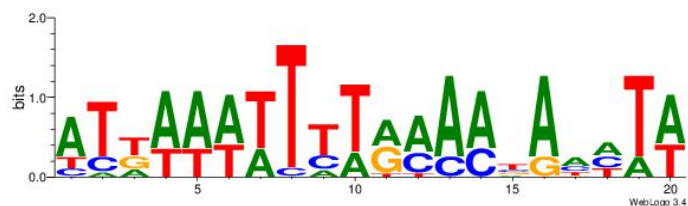
Best Matches for Motif ID 9 (Highest to Lowest)

Dataset #:	5
Motif ID:	55
Motif name:	TFM13
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:	0.0332341

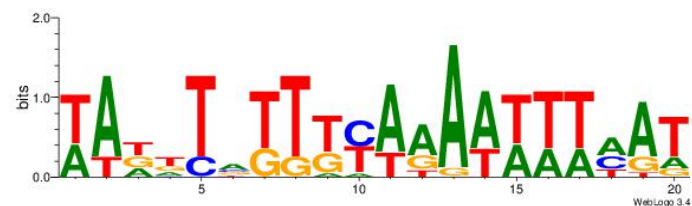
Alignment:

```
WAHHTVTTYKAAAATTRAT
-----TTTDAWATATHATT
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

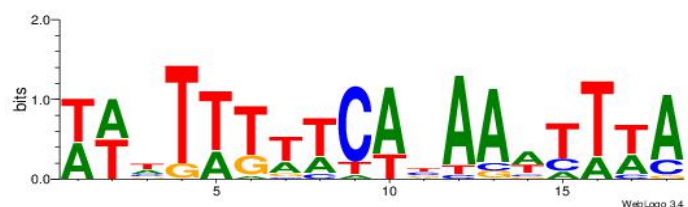


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0486562

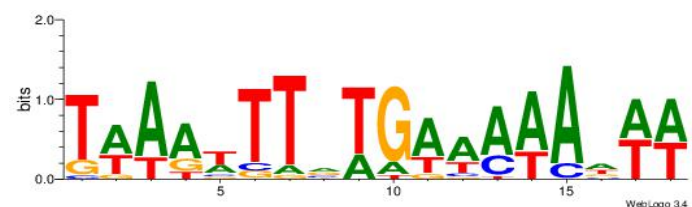
Alignment:

WWHTTTTTCABAAWTTWA
---TTTDAWATATHATT-

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

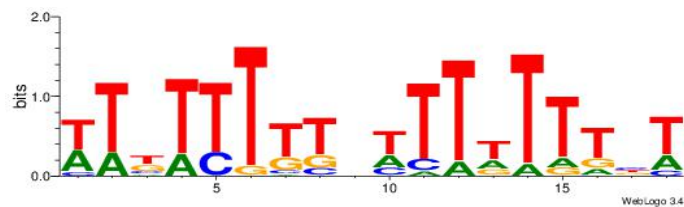


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0528083

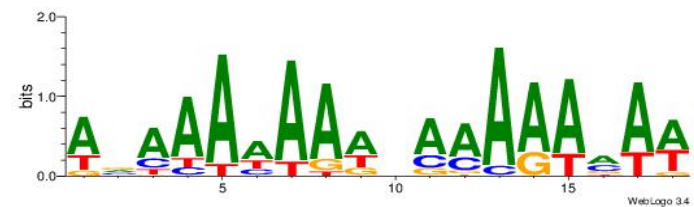
Alignment:

WTKTTTTTHWTTTTTTBT
 ---TTTDAWATATHATT-

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

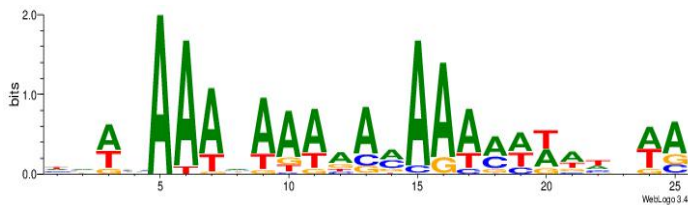


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

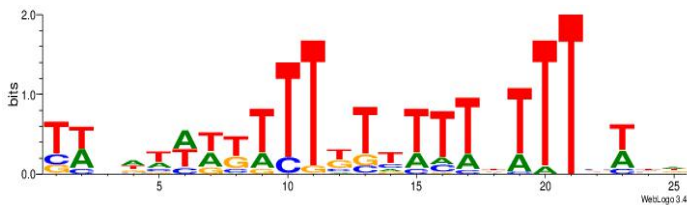
Number of overlap: 14
Similarity score: 0.054155

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
TTTDAWATATHATT-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTTTTTTTHTTTVWBH

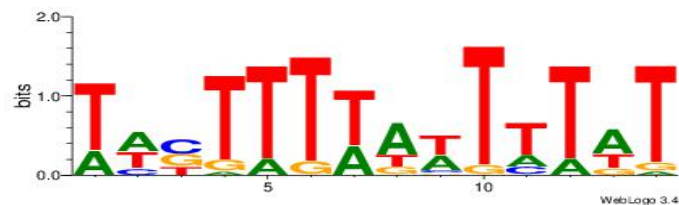
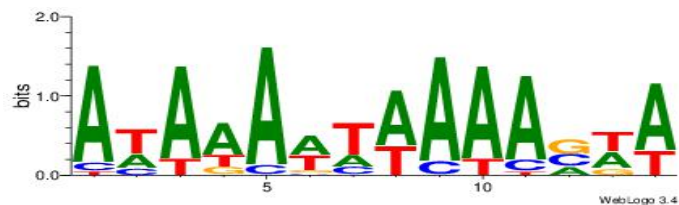


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0675748

Alignment:
TWSTTTWAWTTTWT
AATHATATWTHAAA

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 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: 0.0741568

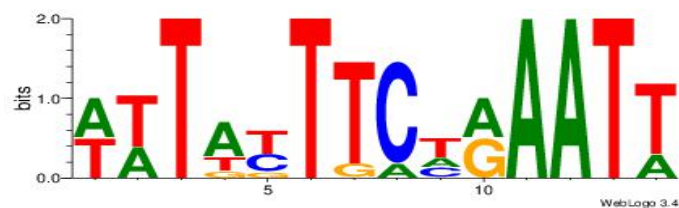
Alignment:

WWTAKTTCDKAATT
 TTTDAWATATHATT

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAATT



Dataset #: 2
 Motif ID: 5

Motif name:	Motif 5
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:	0.547543

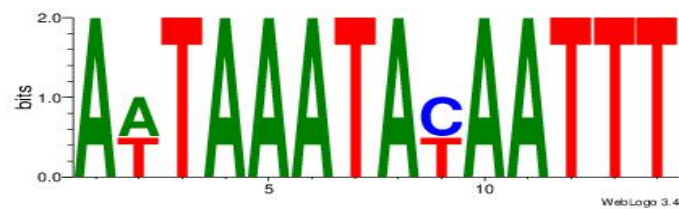
Alignment:

```

-AAATTKTATTTAWT
AATHATATWTHAAA-

```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

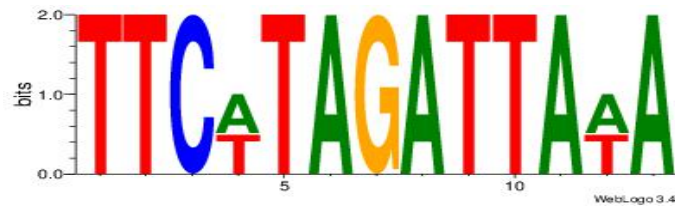


Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0.557158

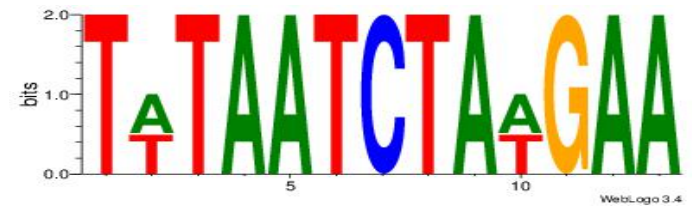
Alignment:

-TTCWTAGATTAWA
AATHATATWTHAAA

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTAWGAA



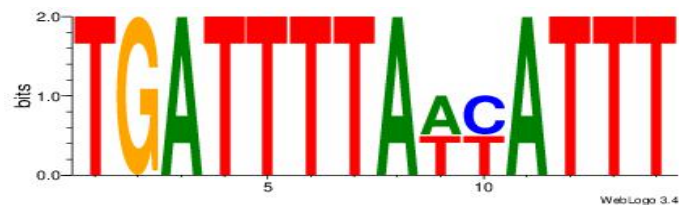
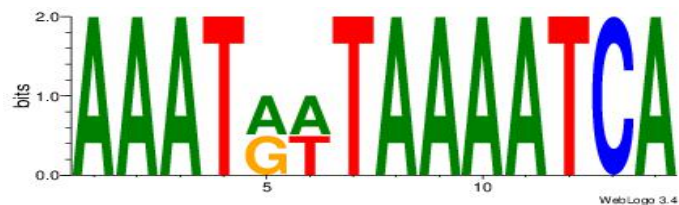
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.576389

Alignment:

-TGATTTTAWKATTT
TTDAWATATHATT-

Original motif Consensus sequence: AAATRWTAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATTT

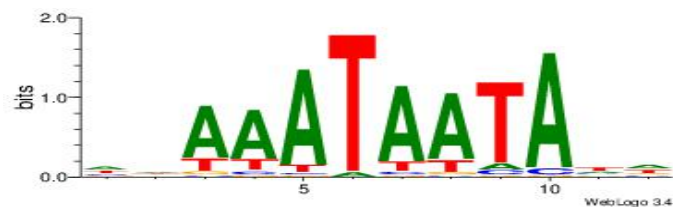


Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.03318

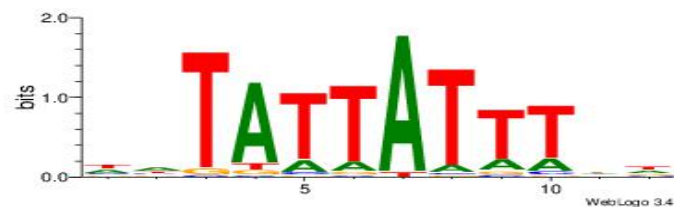
Alignment:

--HDAAATAATADD
 TTTDAWATATHATT

Original motif Consensus sequence: HDAAATAATADD

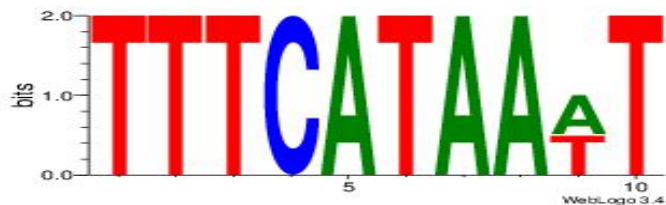


Reverse complement motif Consensus sequence: DDTATTATTTDH

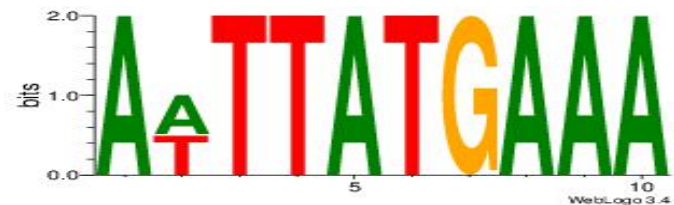


Dataset #: 2 Motif ID: 10 Motif name: Motif 10

Original motif Consensus sequence: TTTCATAAWT



Reverse complement motif Consensus sequence: AWTTATGAAA



Best Matches for Motif ID 10 (Highest to Lowest)

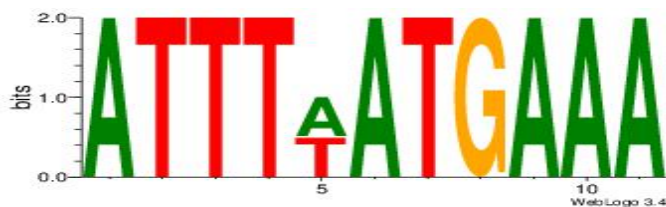
Dataset #:	2
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.01875

Alignment:

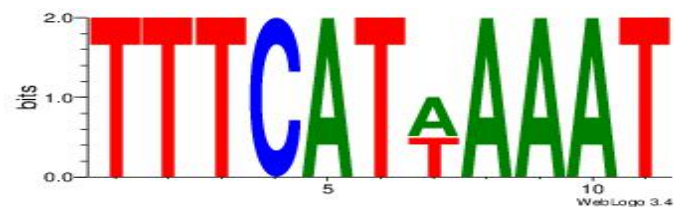
ATTTWATGAAA

-AWTTATGAAA

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 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: 0.0375

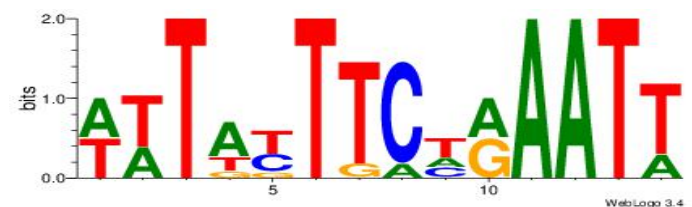
Alignment:

AATTYDGAARTAWW
 ----AWTTATGAAA

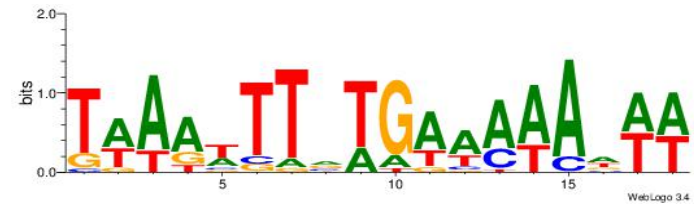
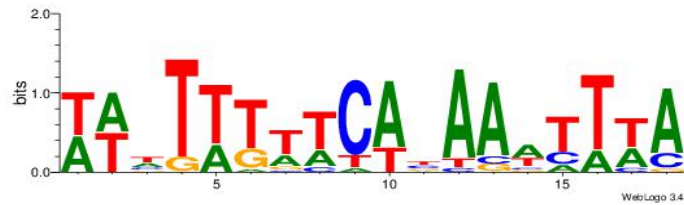
Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10

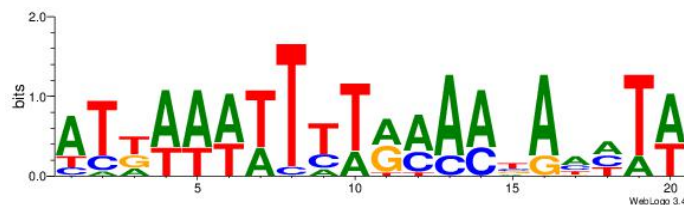


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0545833

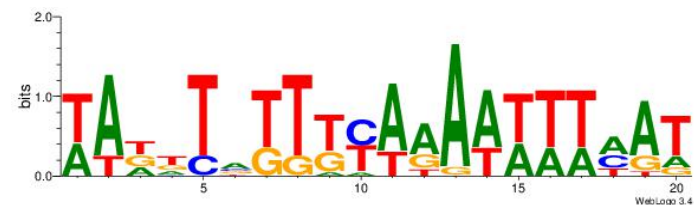
Alignment:

ATKAAWTTTTRMAABAHHTW
 ----AWTTATGAAA-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



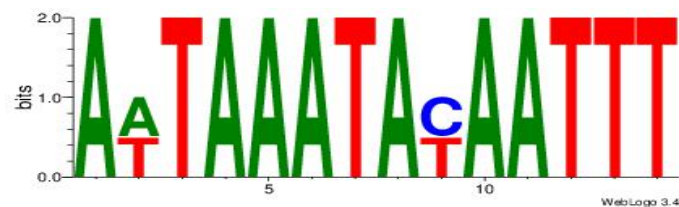
Dataset #: 2

Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.05625

Alignment:

AWTAAATAYAATTT
 ----AWTTATGAAA

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



Dataset #: 2
 Motif ID: 17
 Motif name: Motif 17
 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: 0.05625

Alignment:

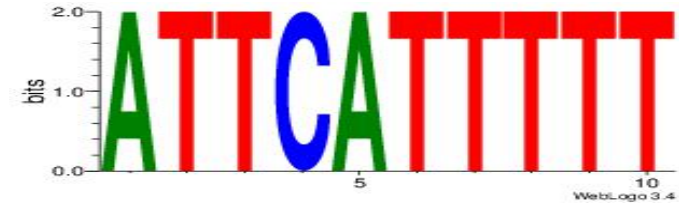
ATTCATTTTT

TTTCATAAWT

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCATTTTT



Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
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:	0.0604166

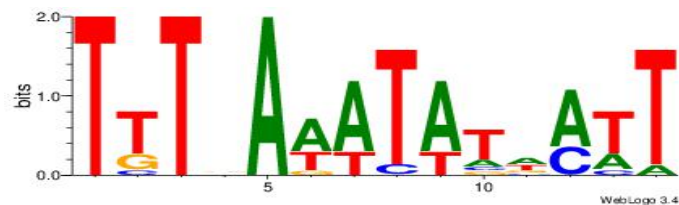
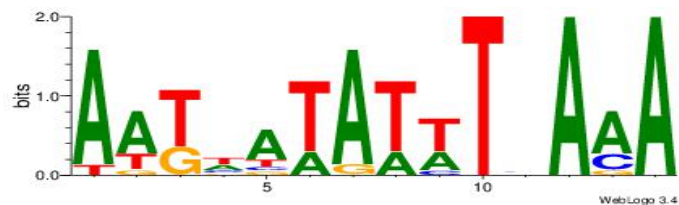
Alignment:

TTTDAWATATHATT

----TTTCATAAWT

Original motif Consensus sequence: AATHATATWTHAAA

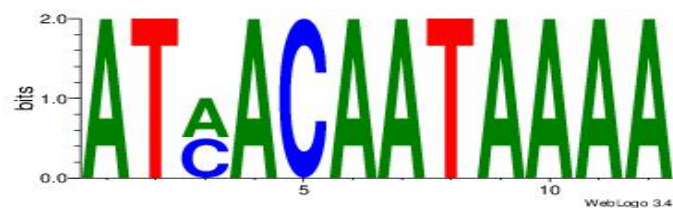
Reverse complement motif Consensus sequence: TTTDAWATATHATT



Dataset #: 2
 Motif ID: 15
 Motif name: Motif 15
 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: 0.06875

Alignment:
 ATMACAATAAAA
 --AWTTATGAAA

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTAT



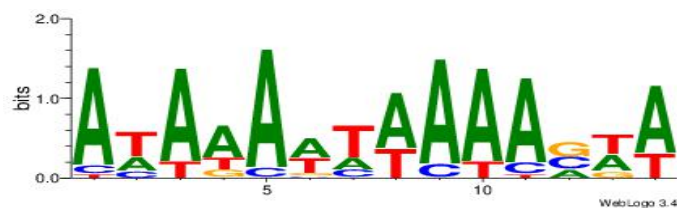
Dataset #: 2
 Motif ID: 3

Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0706731

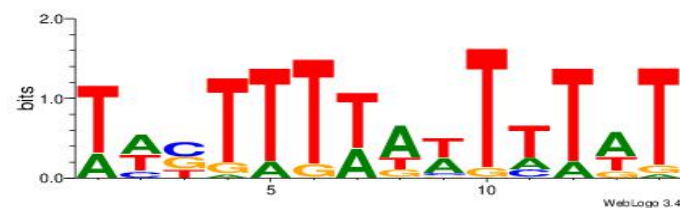
Alignment:

```
AWAAAWTWAAASWA
----AWTTATGAAA
```

Original motif Consensus sequence: AWAAAWTWAAASWA

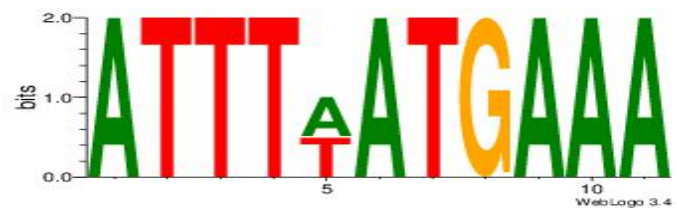


Reverse complement motif Consensus sequence: TWSTTTWAWTTTW

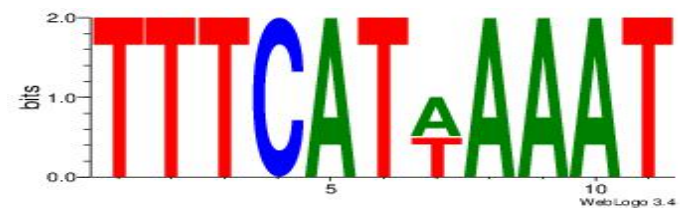


Dataset #: 2 Motif ID: 11 Motif name: Motif 11

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT



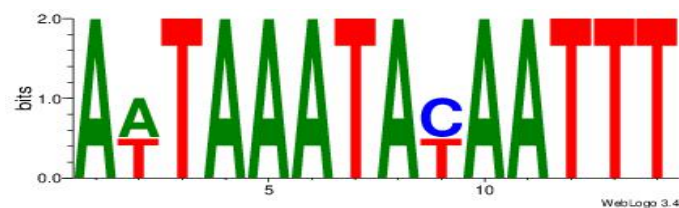
Best Matches for Motif ID 11 (Highest to Lowest)

Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 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: 0.0795455

Alignment:

AAATTKTATTTAWT
 ---TTTCATWAAAT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

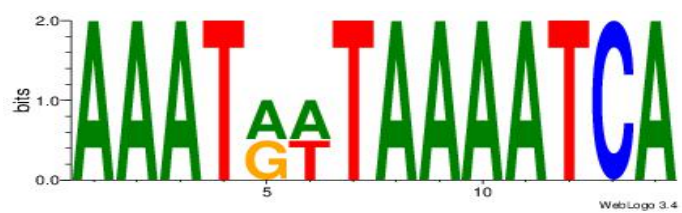


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11

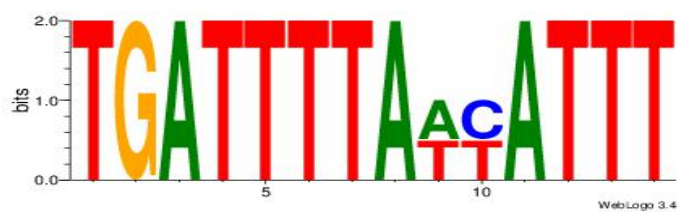
Similarity score: 0.0795455

Alignment:
AAATRWTAATCA
--TTTCATWAAAT--

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

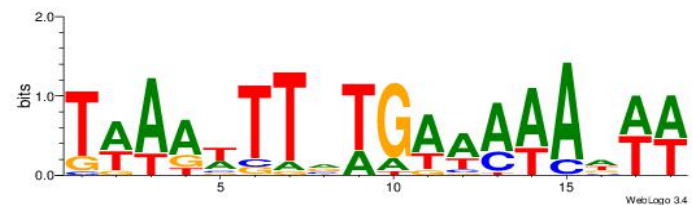
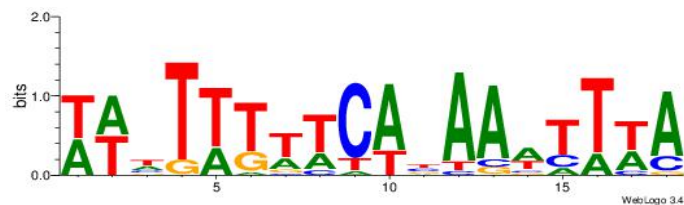


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 11
Similarity score: 0.0991736

Alignment:
WWHTTTTTCABAAWTTWA
-----TTTCATWAAAT--

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TAAWTTVTGAAAAHWW



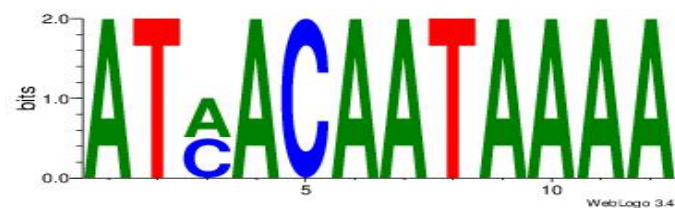
Dataset #: 2
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.102273

Alignment:

ATMACAATAAAA

-TTTCATWAAAT

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTAT



Dataset #: 2
 Motif ID: 18

Motif name:	Motif 18
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.102273

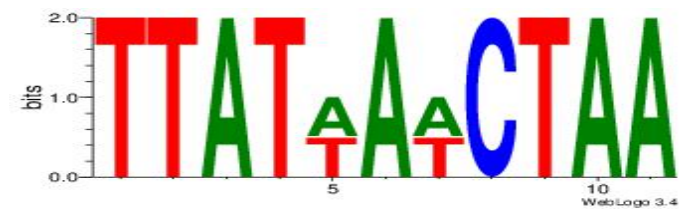
Alignment:

TTATWAWCTAA
ATTTWATGAAA

Original motif Consensus sequence: TTAGWTWATAA



Reverse complement motif Consensus sequence: TTATWAWCTAA

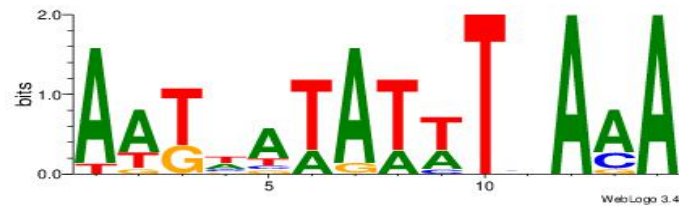


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.109848

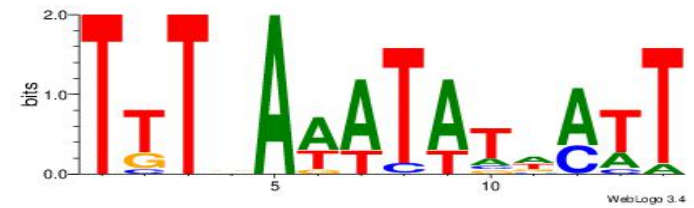
Alignment:

TTTDAWATATHATT
TTTCATWAAAT---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHATT



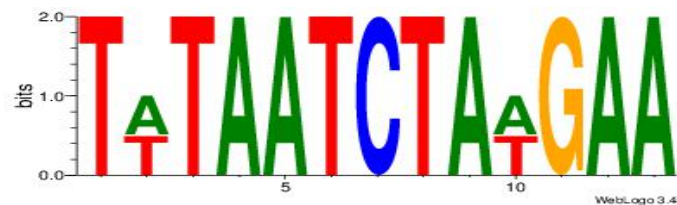
Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.113636

Alignment:

TTCWTAGATTAWA
--ATTTWATGAAA

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAACTAWGAAA



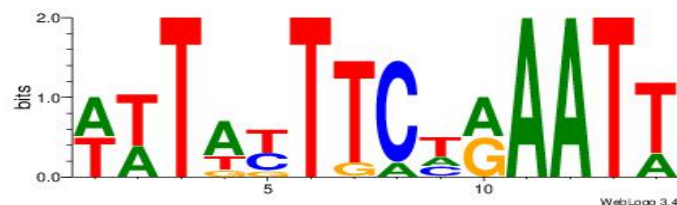
Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.113636

Alignment:
 AATTYDGAARTAWW
 -ATTTWATGAAA--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



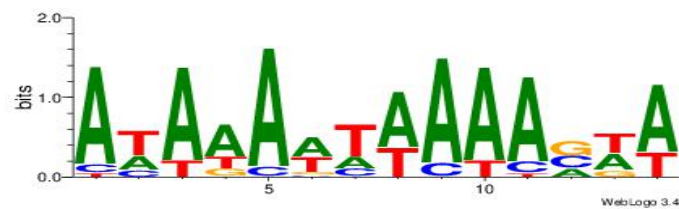
Dataset #: 2
 Motif ID: 3

Motif name:	Motif 3
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:	0.113636

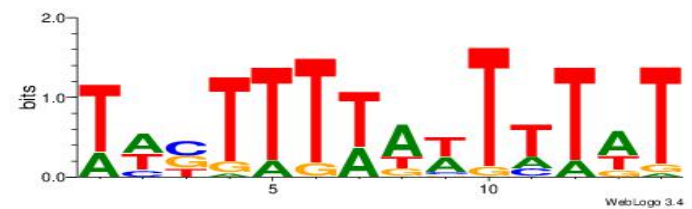
Alignment:

```
AWAAAWTWAAASWA
ATTTWATGAAA---
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



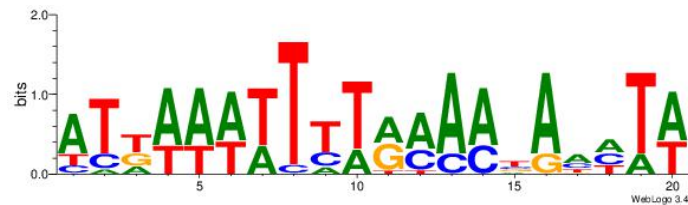
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.114394

Alignment:

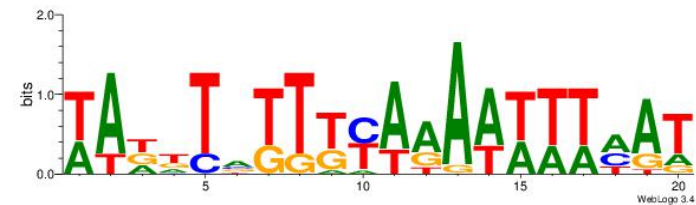
ATKAAWTTTTRMAABAHHTW

---ATTWATGAAA-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



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

Original motif Consensus sequence: AAAACAAA



Reverse complement motif Consensus sequence: TTTGTTTT



Best Matches for Motif ID 12 (Highest to Lowest)

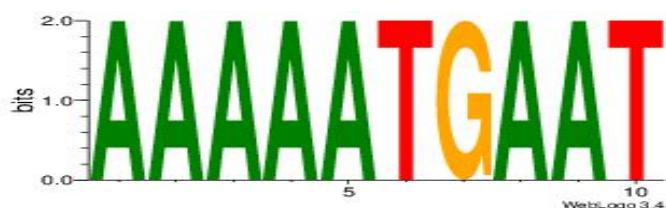
Dataset #:	2
Motif ID:	17
Motif name:	Motif 17
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 2
Number of overlap: 8
Similarity score: 0.0625

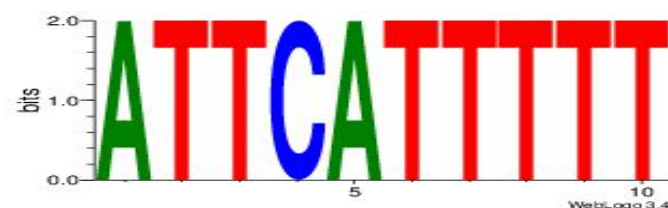
Alignment:

AAAAATGAAT
-AAAACAAA-

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCATTTT



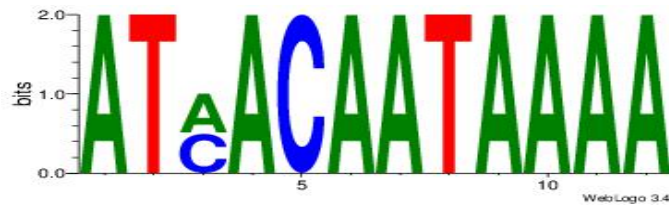
Dataset #: 2
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0625

Alignment:

TTTTATTGTYAT
-TTTGTTTT---

Original motif Consensus sequence: ATMACAATAAAA

Reverse complement motif Consensus sequence: TTTTATTGTYAT



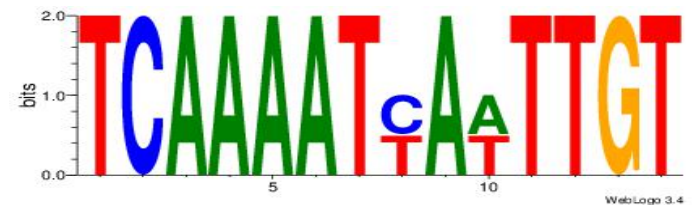
Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.078125

Alignment:
 TCAAAATKAWTTGT
 --AAAACAAA----

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

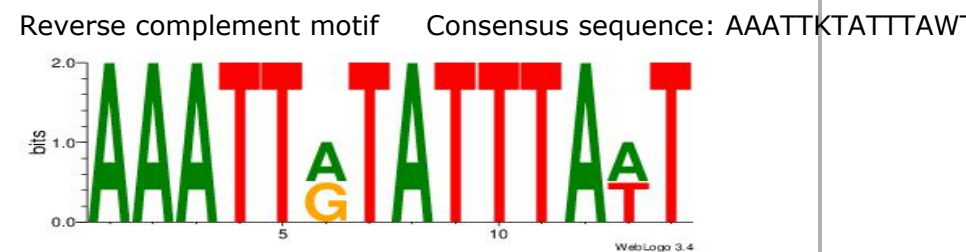
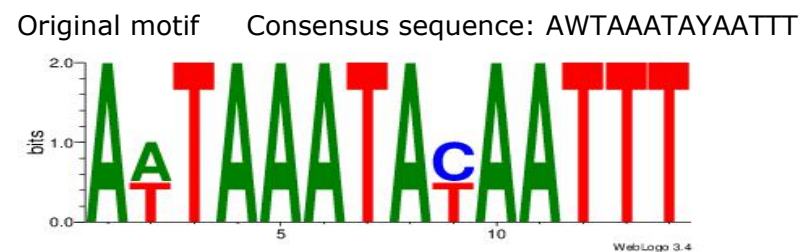


Dataset #: 2

Motif ID:	5
Motif name:	Motif 5
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:	0.078125

Alignment:

```
AWTAAATAYAAATTT
-----AAAACAAA--
```



Dataset #:	2
Motif ID:	14
Motif name:	Motif 14
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.078125

Alignment:
 AWAAATAA
 AAAACAAA

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTTWT

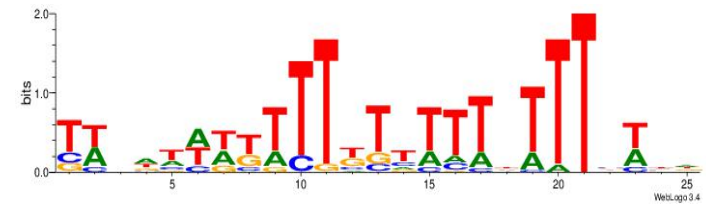
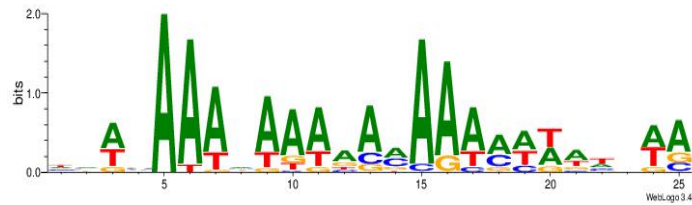


Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	10
Number of overlap:	8
Similarity score:	0.0790441

Alignment:
 HDWVAAAHAAAAAMAAAMWWWHBWA
 -----AAAACAAA-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA

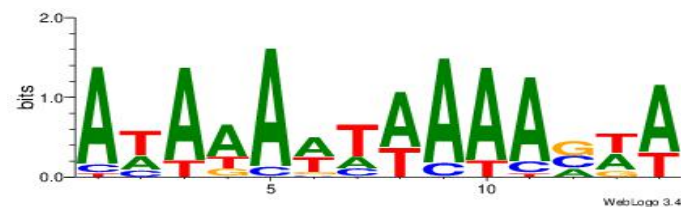
Reverse complement motif Consensus sequence:
 TWVHWWYTTTYYTTTTHTTTVWBH



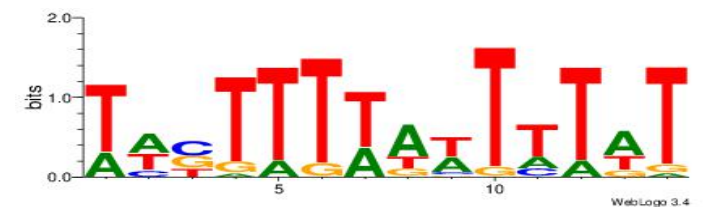
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0805288

Alignment:
 AWAAAWTWAAASWA
 --AAAACAAA----

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV



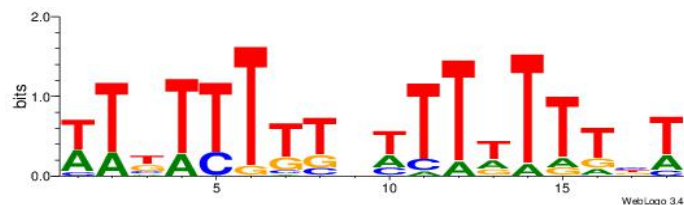
Dataset #: 5
 Motif ID: 52

Motif name: TFM1
 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: 0.0873397

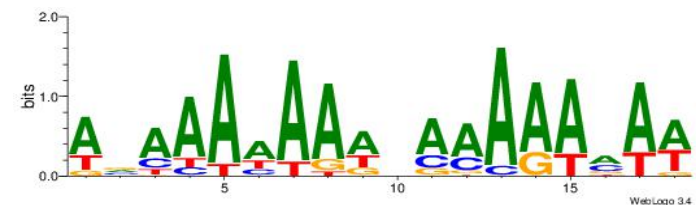
Alignment:

ABAAAAAAWHAAAAARAW
 -----AAAACAAA-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW

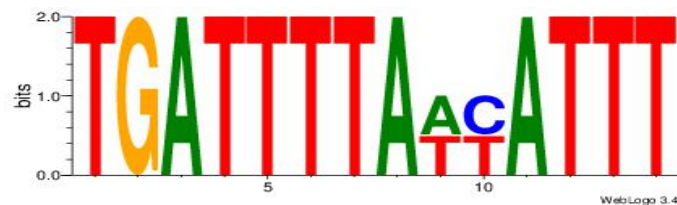
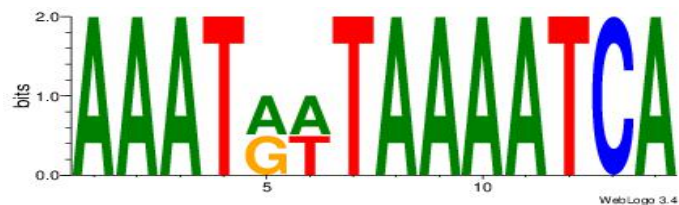


Dataset #: 2
 Motif ID: 18
 Motif name: Motif 18
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.09375

---AAACAAA

-----TTTGTTTT

Reverse complement motif Consensus sequence: TGATTTTAWKATT



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

Original motif Consensus sequence: AAAGATTT



Reverse complement motif Consensus sequence: AAATCTTT



Best Matches for Motif ID 13 (Highest to Lowest)

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

Alignment:

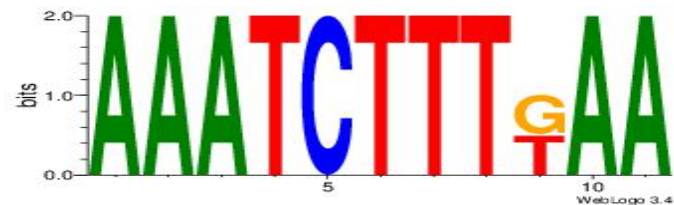
AAATCTTTYAA

AAATCTTT---

Original motif Consensus sequence: TTMAAAGATTT



Reverse complement motif Consensus sequence: AAATCTTTYAA

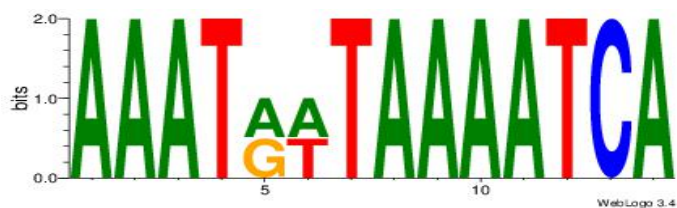


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0625

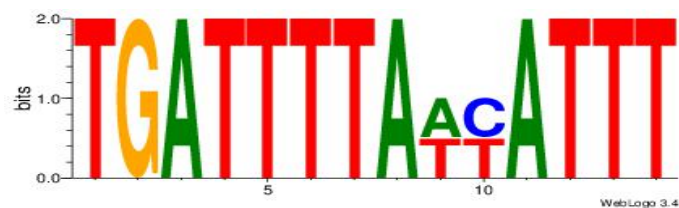
Alignment:

AAATRWTAATCA
 -----AAATCTTT

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTAWKATT



Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0625

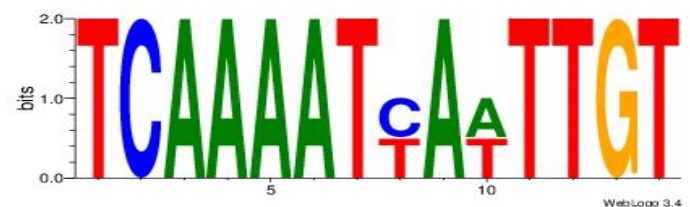
Alignment:

TCAAAATKAWTTGT
 ----AAAGATTT--

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTGT



Dataset #: 2
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8

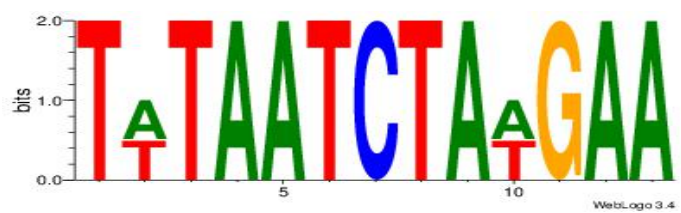
Similarity score: 0.078125

Alignment:
TWTAACTAWGAA
--AAATCTTT---

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTAWGAA

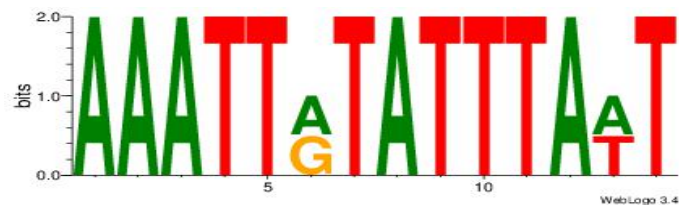
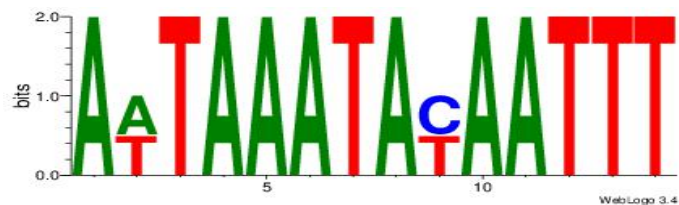


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.078125

Alignment:
AAATTKTATTTAWT
AAATCTTT-----

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAWT

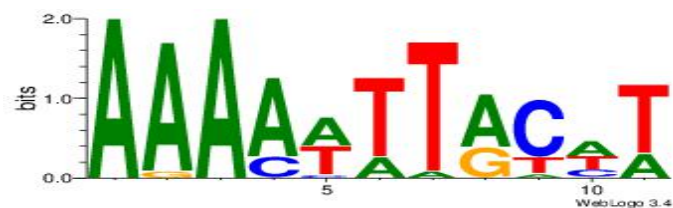


Dataset #: 2
 Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0822369

Alignment:

AWGKAAWTTTT
 ---AAATCTTT

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



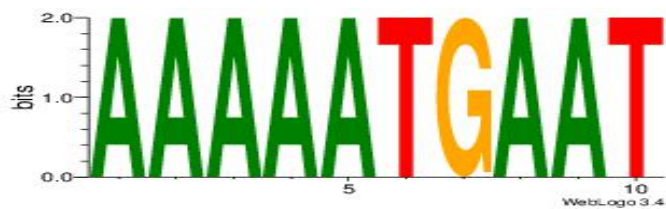
Dataset #: 2
 Motif ID: 17

Motif name:	Motif 17
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.09375

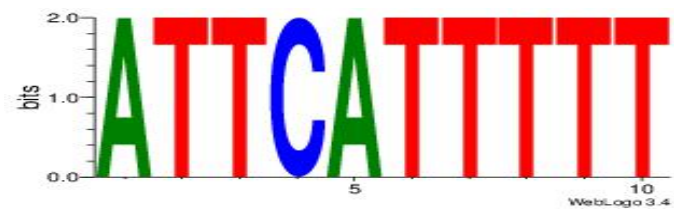
Alignment:

AAAAATGAAT
AAAGATTT--

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCATTTT



Dataset #:	4
Motif ID:	44
Motif name:	dhACATTCTkh
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.104167

Alignment:

DHACATTCTGH

AAAGATTT---

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #:	2
Motif ID:	14
Motif name:	Motif 14
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:	0.109375

Alignment:

AWAAATAA

AAAGATTT

Original motif Consensus sequence: AWAAATAA

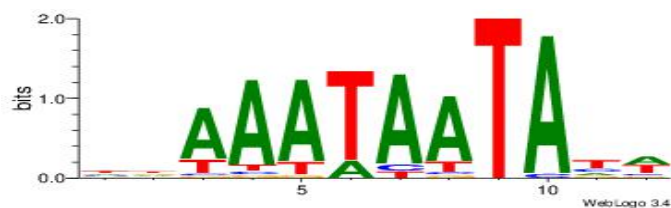
Reverse complement motif Consensus sequence: TTATTTWT



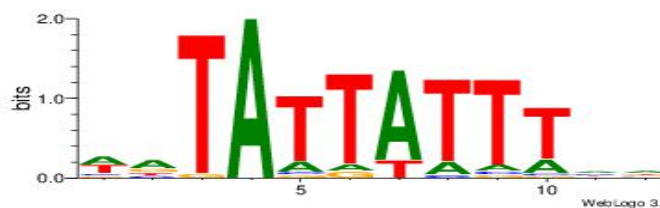
Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.110417

Alignment:
 HDAAATAATAHW
 --AAATCTTT--

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH



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

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTTWT



Best Matches for Motif ID 14 (Highest to Lowest)

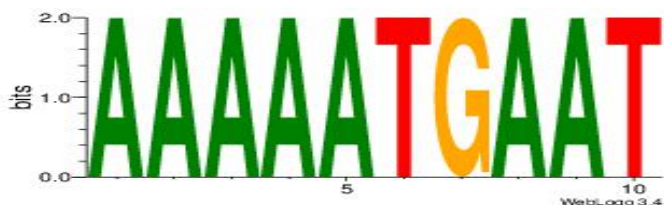
Dataset #:	2
Motif ID:	17
Motif name:	Motif 17
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.046875

Alignment:

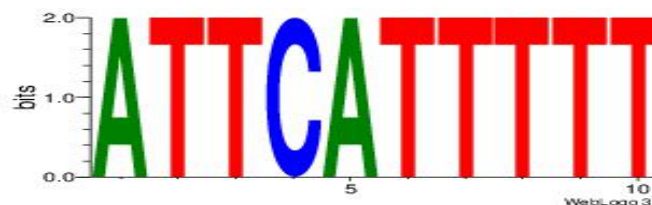
AAAAATGAAT

AWAAATAA--

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCATTTT

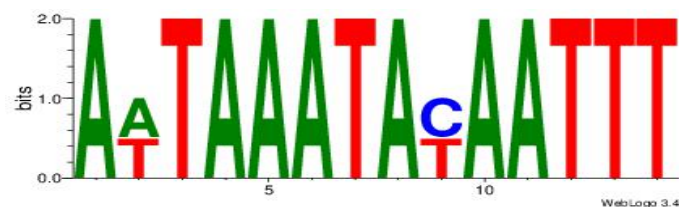


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.046875

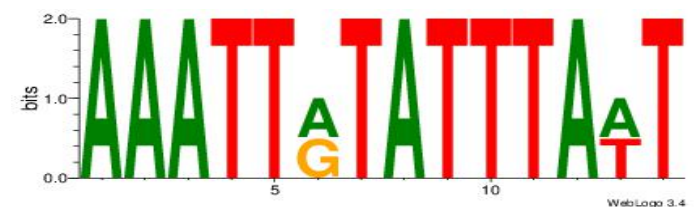
Alignment:

AAATTKTATTTAWT
 -----TTATTTWT-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

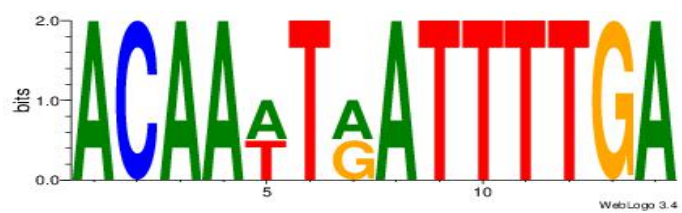


Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8

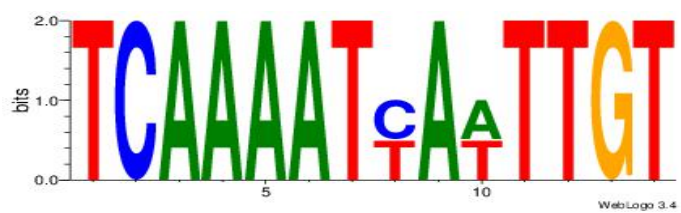
Similarity score: 0.0625

Alignment:
ACAAWTRATTTTGA
AWAAATAA-----

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

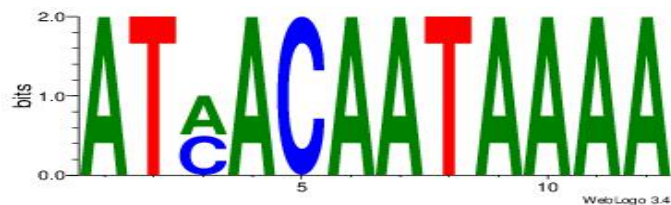


Dataset #: 2
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0625

Alignment:
ATMACAATAAAA
--AWAAATAA--

Original motif Consensus sequence: ATMACAATAAAA

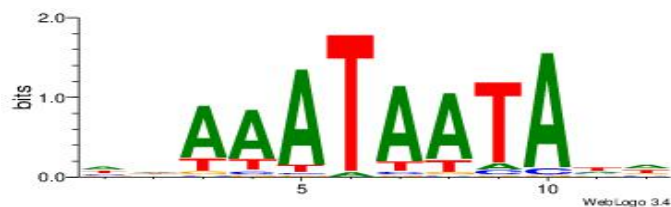
Reverse complement motif Consensus sequence: TTTTATTGTYAT



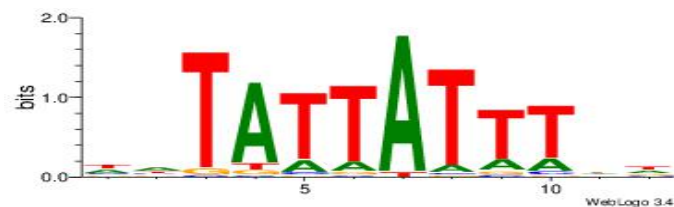
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0636574

Alignment:
 HDAAATAATADD
 AWAAATAA----

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

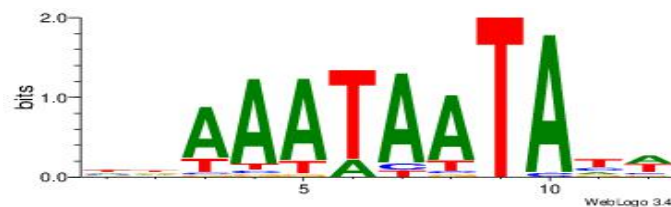


Dataset #: 4
 Motif ID: 37

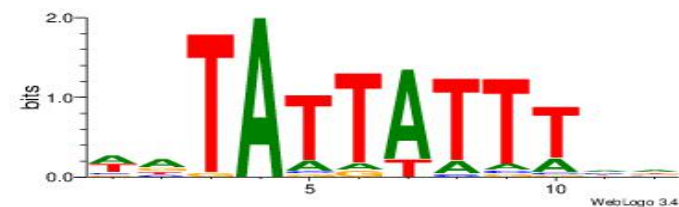
Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0697917

Alignment:
 WHTATTATTTDH
 ----TTATTTWT

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



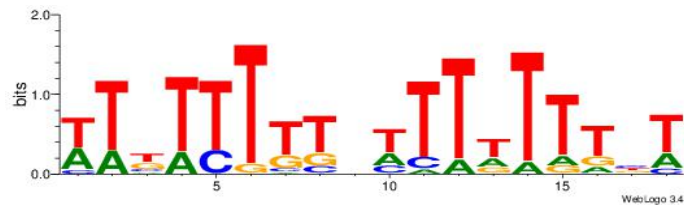
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.078125

Alignment:

WKTTTTTHWTTTTTBT

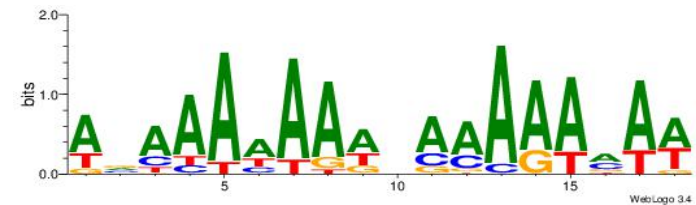
-----TTATTTWT----

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif
ABAAAAAWhAAAAARAW

Consensus sequence:



Dataset #:	2
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:	7
Number of overlap:	8
Similarity score:	0.078125

Alignment:

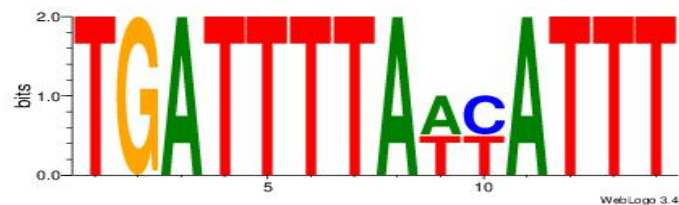
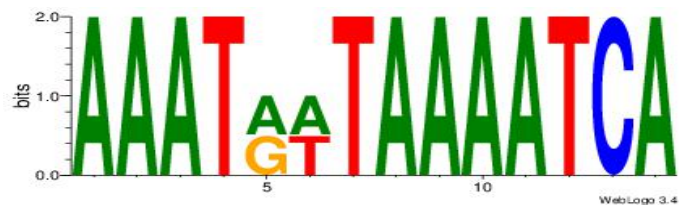
AAATRWTAATCA

-----AWAAATAA

Original motif Consensus sequence: AAATRWTAATCA

Reverse complement motif

Consensus sequence: TGATTTAWKATT



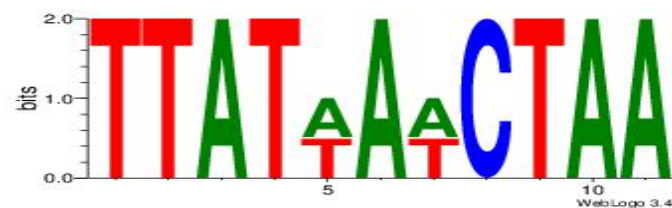
Dataset #: 2
 Motif ID: 18
 Motif name: Motif 18
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.078125

Alignment:
 TTAGWTWATAA
 TTATTTWT---

Original motif Consensus sequence: TTAGWTWATAA



Reverse complement motif Consensus sequence: TTATWAWCTAA



Dataset #: 2
 Motif ID: 12

Motif name:	Motif 12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.078125

Alignment:
AAAACAAA
AWAAATAA

Original motif Consensus sequence: AAAACAAA

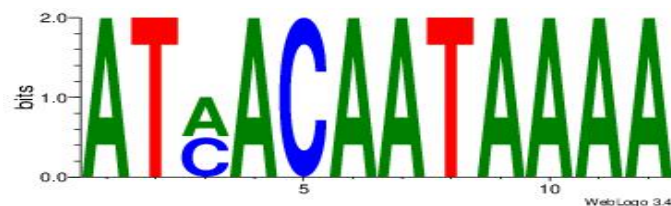


Reverse complement motif Consensus sequence: TTTGTTTT



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

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTAT



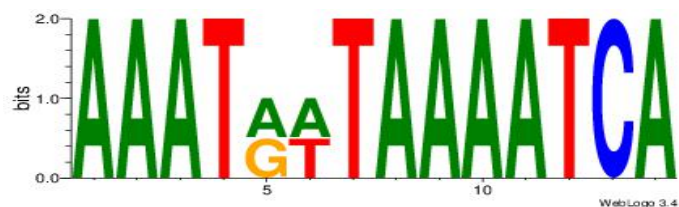
Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #: 2
 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: 3
 Number of overlap: 12
 Similarity score: 0.104167

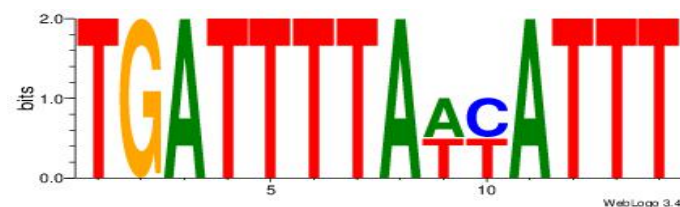
Alignment:

TGATTTTAWKATTT
 TTTTATTGTAT--

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT

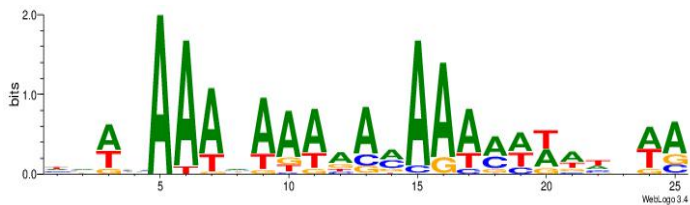


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 12

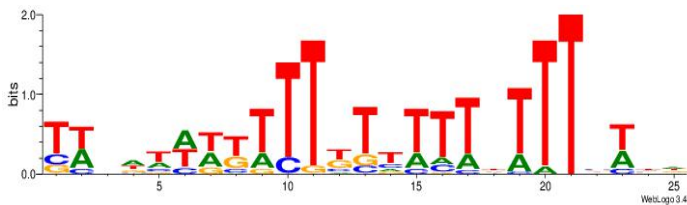
Similarity score: 0.109681

Alignment:
TWVHWWYTTTYTTTTHTTTVWBH
-----TTTATTGTAT-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
TWVHWWYTTTYTTTTHTTTVWBH

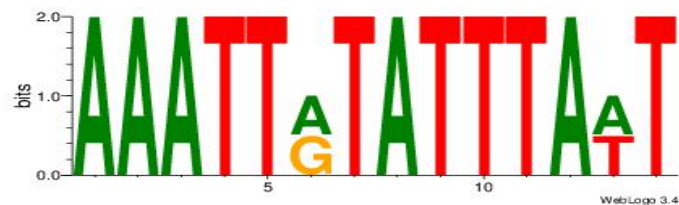
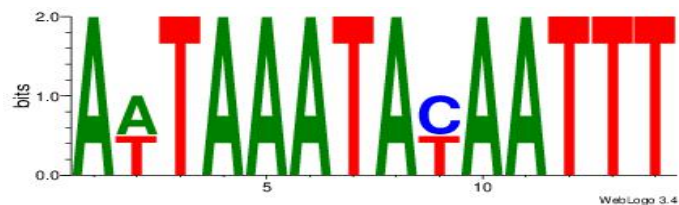


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.114583

Alignment:
AWTAAATAYAATTT
-ATMACAATAAAA-

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKATTTAW



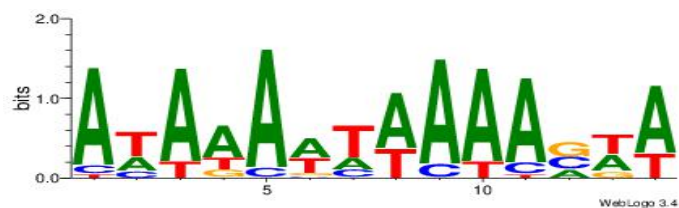
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.114583

Alignment:

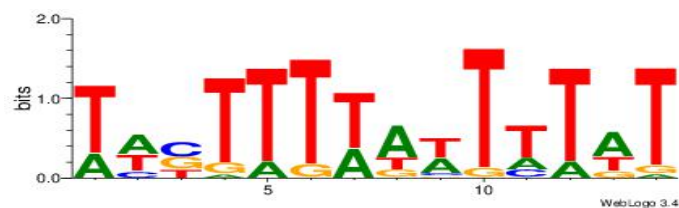
AWAAAWTWAAASWA

ATMACAATAAAA--

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV



Dataset #: 5
 Motif ID: 52

Motif name:	TFM1
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:	0.115652

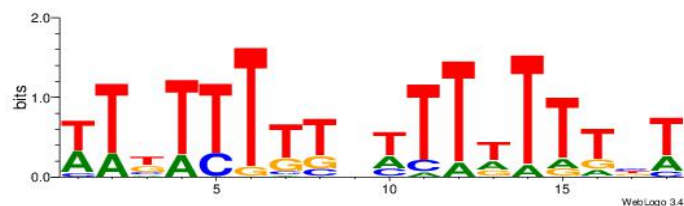
Alignment:

```

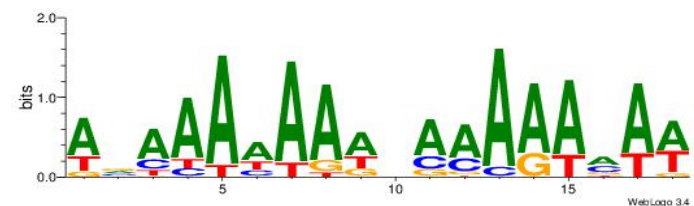
ABAAAAAAWHAAAAARAW
--ATMACAATAAAA-----

```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW



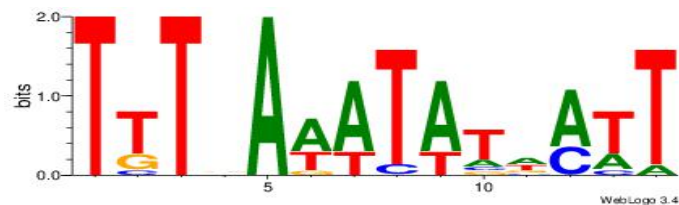
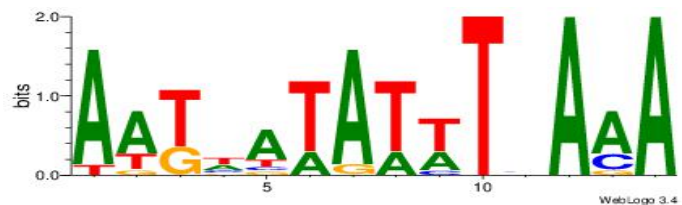
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.119792

WWTAKTTCDKAATT
TTTTATTGTYAT--

Alignment:

```
TTTDAWATATHATT
-TTTTATTGTYAT-
```

Reverse complement motif Consensus sequence: TTTDAWATATHAT

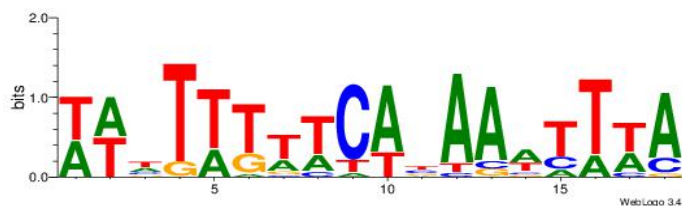


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.125

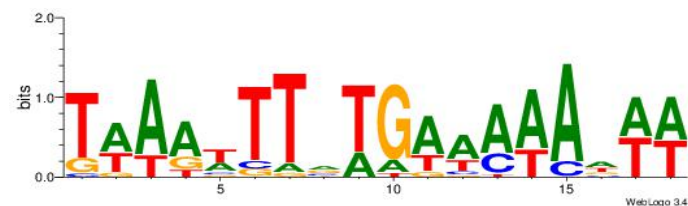
Alignment:

```
WWHTTTTTCABAAWTTWA
-----ATMACAATAAAA
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



Dataset #: 2

Motif ID:	16
Motif name:	Motif 16
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:	0.590909

Alignment:

```

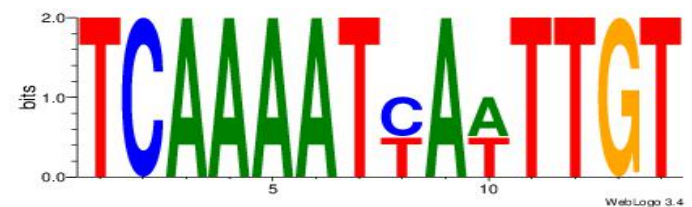
-TCAAATKAWTTGT
ATMACAATAAAA---

```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAATKAWTTG



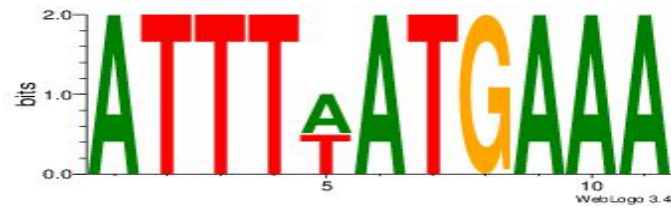
Dataset #:	2
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.602273

Alignment:

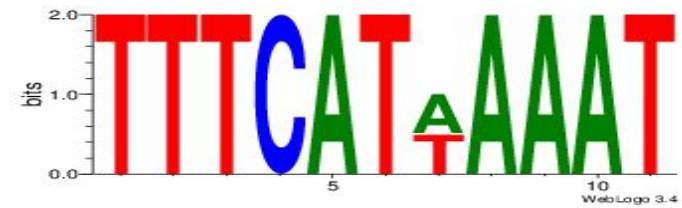
-ATTTWATGAAA

TTTATTGTAT

Original motif Consensus sequence: ATTTWATGAAA

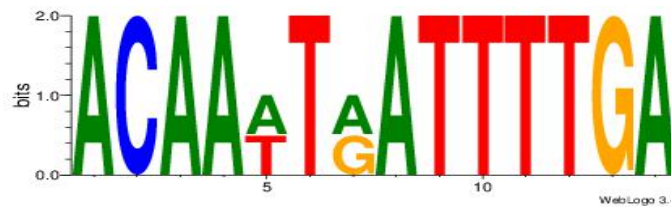


Reverse complement motif Consensus sequence: TTTCATWAAAT

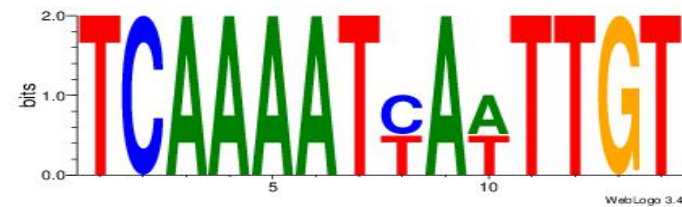


Dataset #: 2 Motif ID: 16 Motif name: Motif 16

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



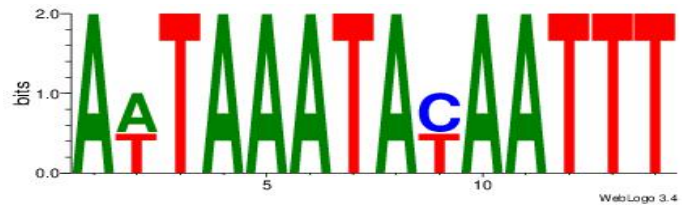
Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

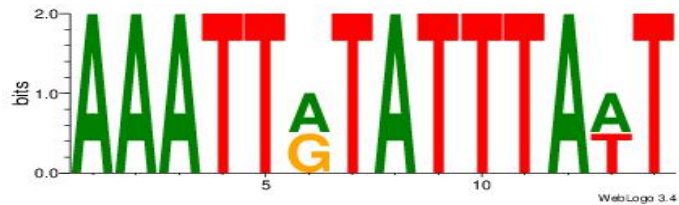
Number of overlap: 14
Similarity score: 0.1

Alignment:
AWTAAATAYAATTT
TCAAAATKAWTTGT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTAW

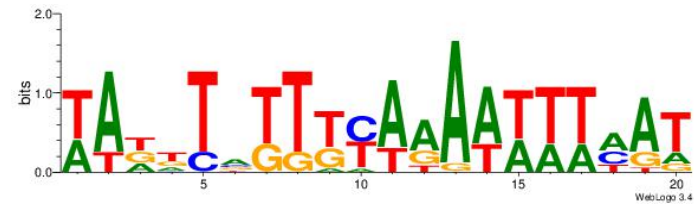
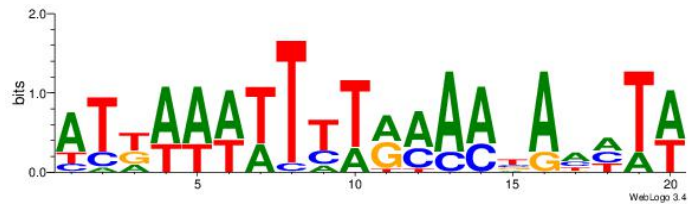


Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 13
Similarity score: 0.599359

Alignment:
ATKAAWTTTTRMAABAHHTW-
-----TCAAAATKAWTTGT

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTTAT

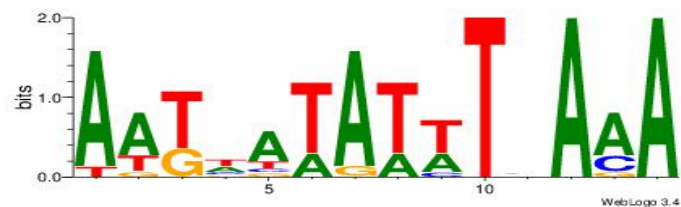


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 1.08264

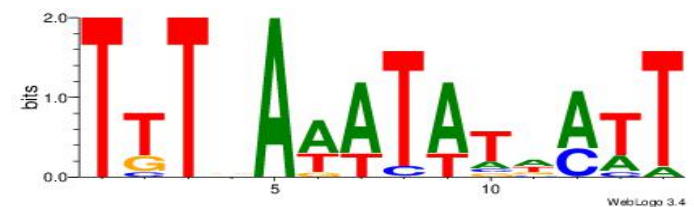
Alignment:

TTTDAWATATHATT--
 --TCAAAATKAWTTGT

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHATT



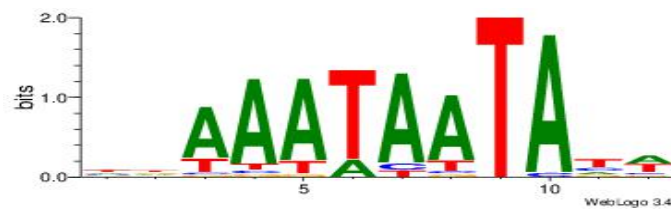
Dataset #: 4
 Motif ID: 37

Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.08403

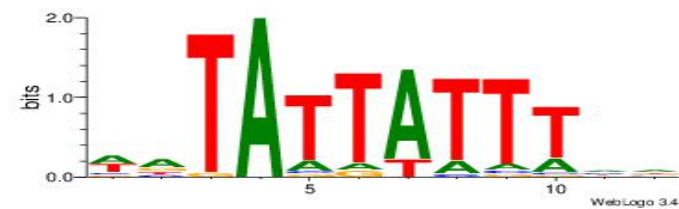
Alignment:

--WHTATTATTDDH
 TCAAAATKAWTTGT

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH

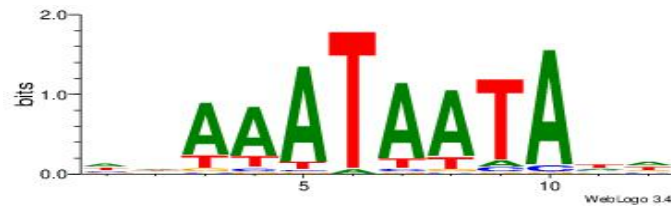


Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.08881

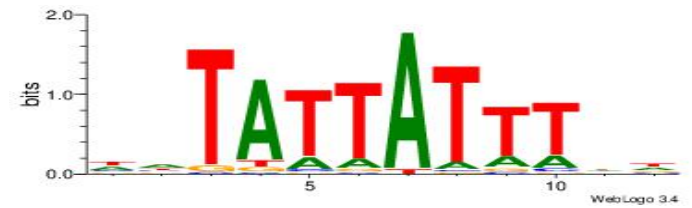
Alignment:

```
--DDTATTATTTDH  
TCAAAATKAWTTGT
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



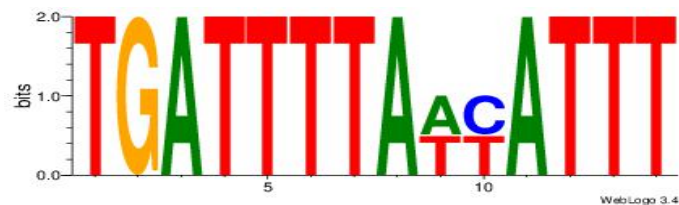
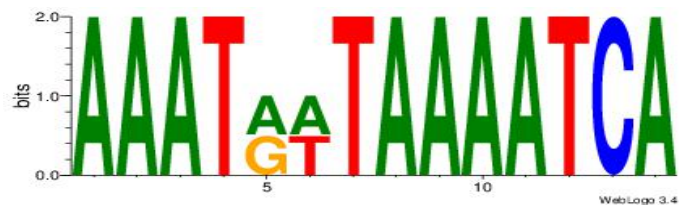
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	1.1

Alignment:

```
TGATTTTAWKATTT--  
--TCAAAATKAWTTGT
```

Original motif Consensus sequence: AAATRWTAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATTT

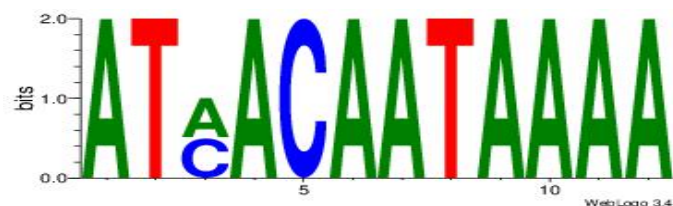


Dataset #: 2
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 1.56591

Alignment:

TTTTATTGTYAT---
 -ACAAWTRATTTTGA

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT



Dataset #: 2
 Motif ID: 6

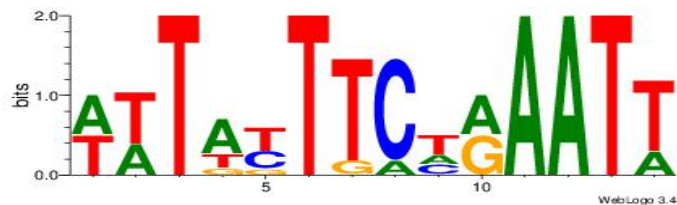
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 1.56875

Alignment:
---AATTYDGAARTAWW
TCAAAATKAWTTGT---

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

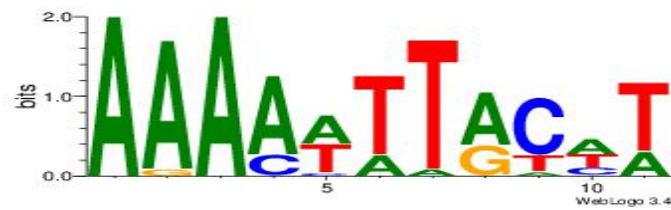


Dataset #: 2
Motif ID: 4
Motif name: Motif 4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 1.57667

Alignment:

AAAATTCRCWT---
ACAAWTRATTTTGA

Original motif Consensus sequence: AAAATTCRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



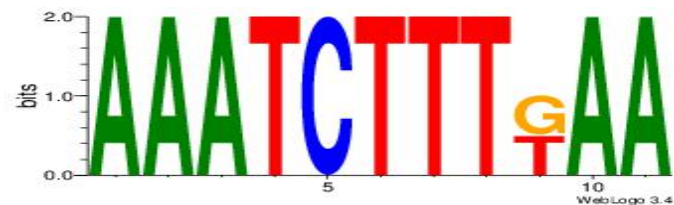
Dataset #:	2
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	1.57727

Alignment:

TTMAAAGATTT---
ACAAWTRATTTTGA

Original motif Consensus sequence: TTMAAAGATTT

Reverse complement motif Consensus sequence: AAATCTTTYAA

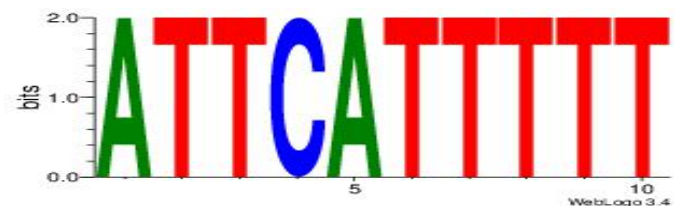


Dataset #: 2 Motif ID: 17 Motif name: Motif 17

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCATTTT



Best Matches for Motif ID 17 (Highest to Lowest)

Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
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:	0.05

Alignment:

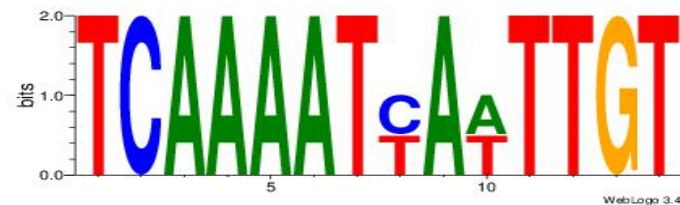
ACAAWTRATTTTGA

-ATTCATTTT---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAAATKAWTTG

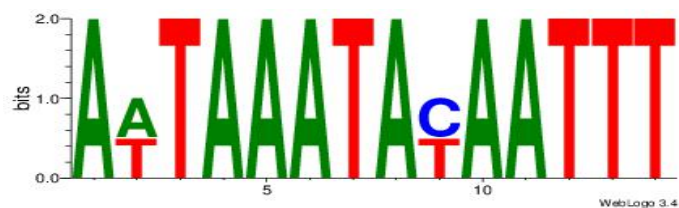


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0875

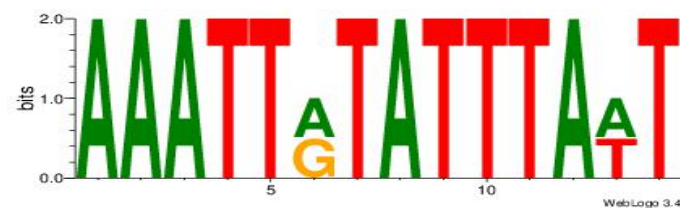
Alignment:

AWTAAATAYAATTT
 ---AAAAATGAAT-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

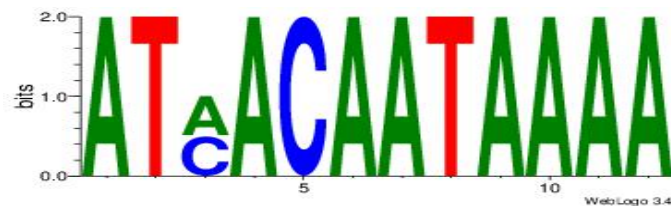


Dataset #: 2
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0875

Alignment:

TTTTATTGTYAT
 ATTCATTTT--

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT



Dataset #: 2
 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: 1
 Number of overlap: 10

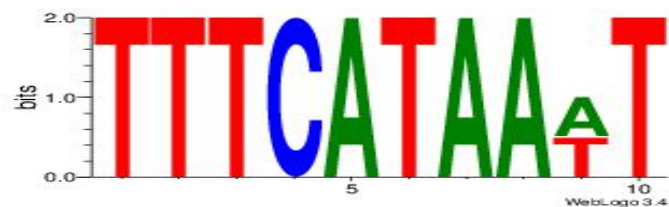
Similarity score: 0.0875

Alignment:

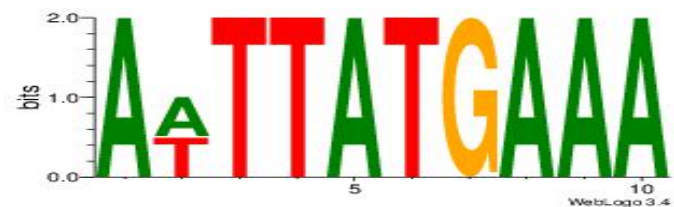
AWTTATGAAA

AAAAATGAAT

Original motif Consensus sequence: TTTCATAAWT



Reverse complement motif Consensus sequence: AWTTATGAAA



Dataset #: 2
Motif ID: 4
Motif name: Motif 4
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: 0.0947369

Alignment:

AWGKAAWTTTT

-ATTCATTTTT

Original motif Consensus sequence: AAAAWTTRCWT

Reverse complement motif Consensus sequence: AWGKAAWTTTT

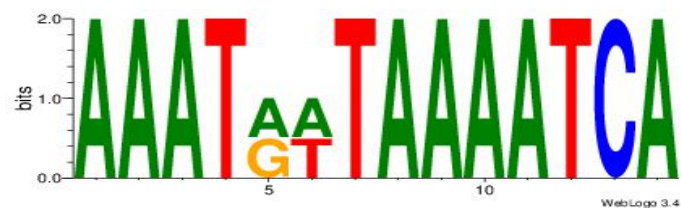


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.1

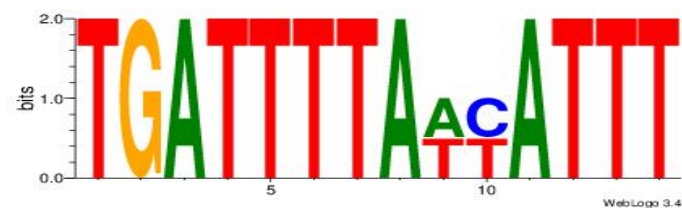
Alignment:

AAATRWTAATCA
 -AAAAATGAAT---

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTAAKATT



Dataset #: 4
 Motif ID: 44

Motif name:	dhACATTCTkh
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:	0.1

Alignment:

DHACATTCTGH
ATTCATTTT-

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

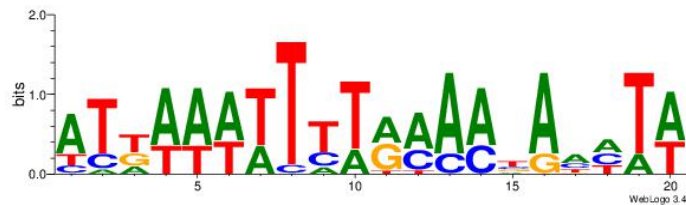


Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	11
Number of overlap:	10
Similarity score:	0.103333

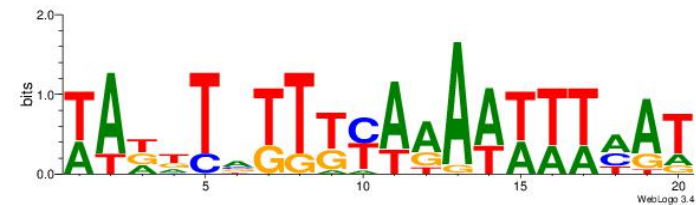
Alignment:

```
WAHHTVTTYKAAAATTRAT
-----AAAAATGAAT
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



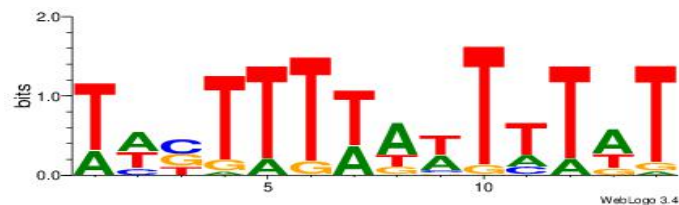
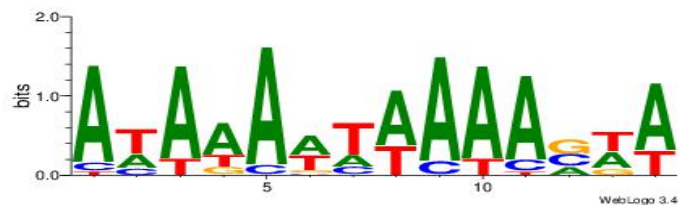
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.104808

Alignment:

```
TWSTTTWAWTTTWT
----ATTCATTTT
```

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

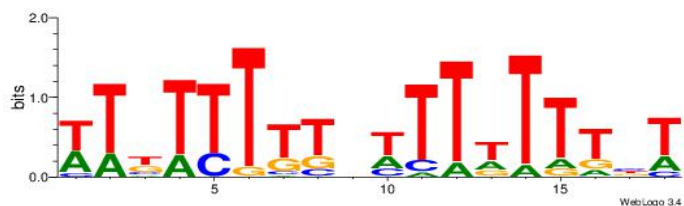


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.105128

Alignment:

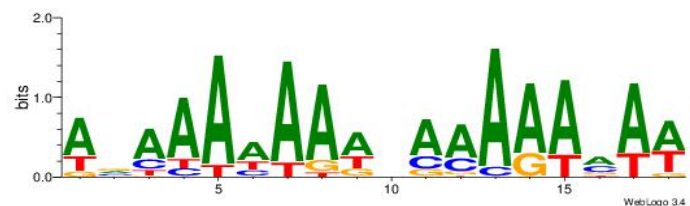
ABAAAAAAWHAAAAARAW
 ----AAAAATGAAT----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif
 ABAAAAAAWHAAAAARAW

Consensus sequence:

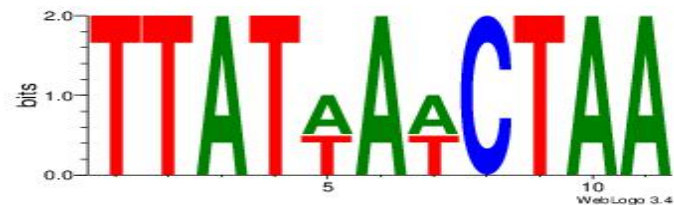


Dataset #: 2 Motif ID: 18 Motif name: Motif 18

Original motif Consensus sequence: TTAGWTWATAA



Reverse complement motif Consensus sequence: TTATWAWCTAA



Best Matches for Motif ID 18 (Highest to Lowest)

Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.09375

Alignment:

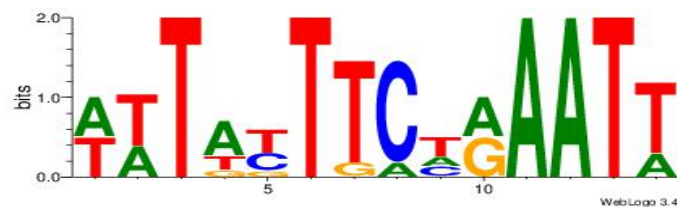
AATTYDGAARTAWW

-TTATWAWCTAA--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

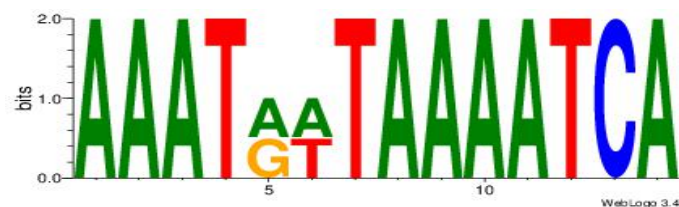


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.102273

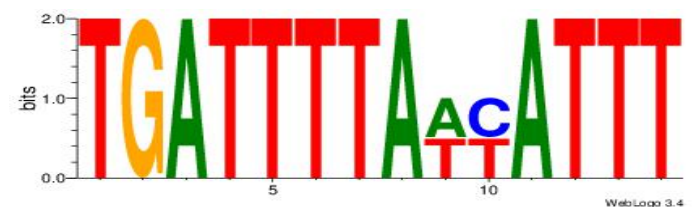
Alignment:

TGATTTTAWKATTT
 ---TTAGWTWATAA

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT



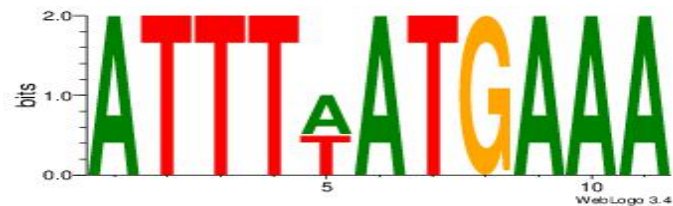
Dataset #: 2
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.102273

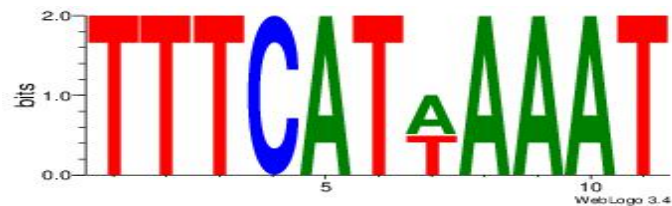
Alignment:

TTTCATWAAAT
TTAGWTWATAA

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT



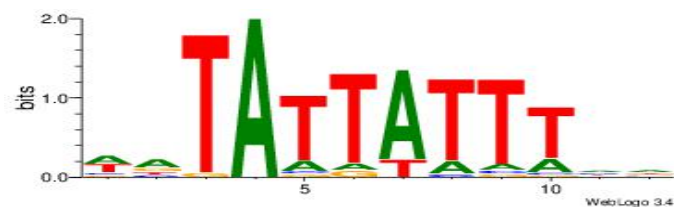
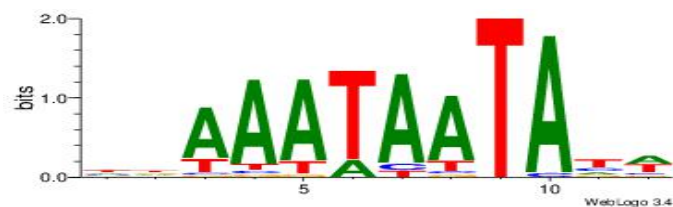
Dataset #: 4
Motif ID: 37
Motif name: tkAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.102273

Alignment:

HDAAATAATAHW
TTAGWTWATAA-

Original motif Consensus sequence: HDAAATAATAHW

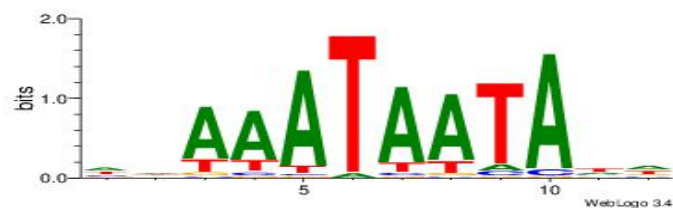
Reverse complement motif Consensus sequence: WHTATTATTTDH



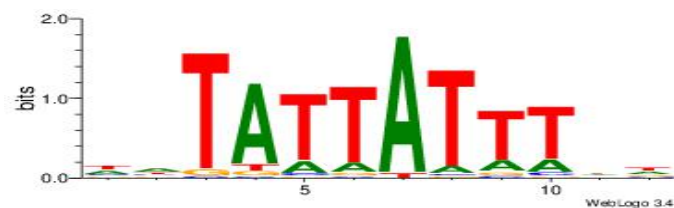
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.104798

Alignment:
 DDTATTATTTDH
 -TTATWAWCTAA

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



Dataset #: 5
 Motif ID: 53

Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.108471

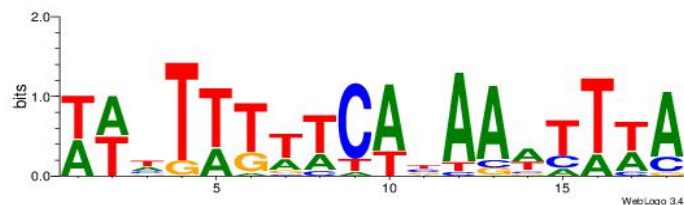
Alignment:

```

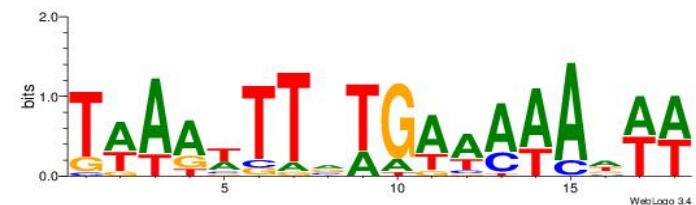
WWHTTTTTCABAAWTTWA
--TTAGWTWATAA-----

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Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

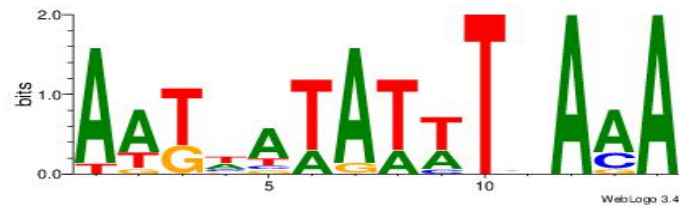


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.109848

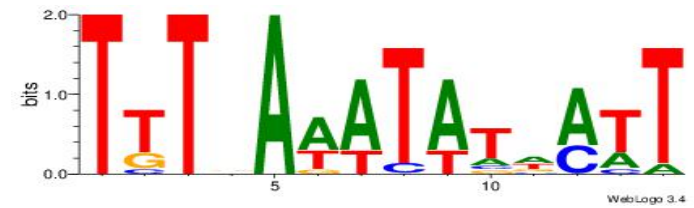
Alignment:

TTTDAWATATHATT
-TTAGWTWATAA--

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHATT



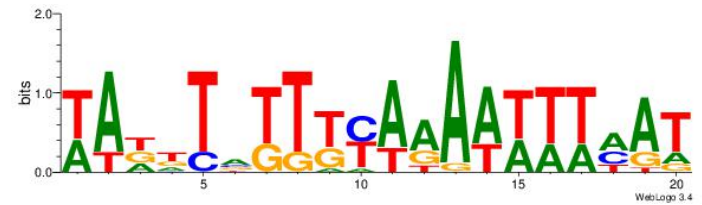
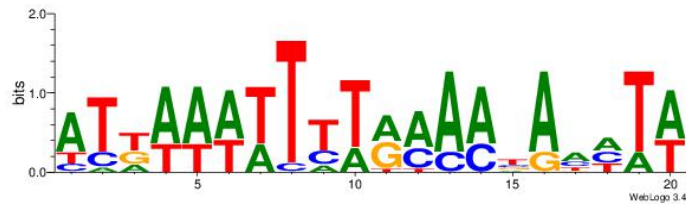
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.109848

Alignment:

ATKAAWTTTTRMAABAHHTW
-----TTATWAWCTAA---

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT



Dataset #: 2
 Motif ID: 19
 Motif name: Motif 19
 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: 0.113636

Alignment:

TTCWTAGATTAWA

TTATWAWCTAA--

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTAWGAA

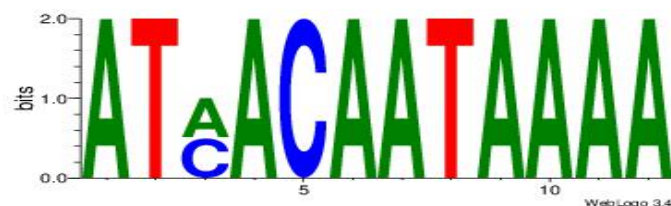


Dataset #: 2
 Motif ID: 15

Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.113636

Alignment:
 ATMACAATAAAA
 -TTAGWTWATAA

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTAT

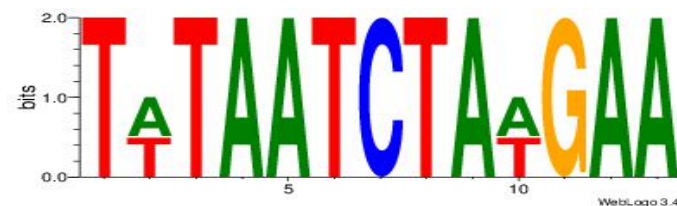


Dataset #: 2 Motif ID: 19 Motif name: Motif 19

Original motif Consensus sequence: TTCWTAGATTAA



Reverse complement motif Consensus sequence: TTAATCTAAGAA



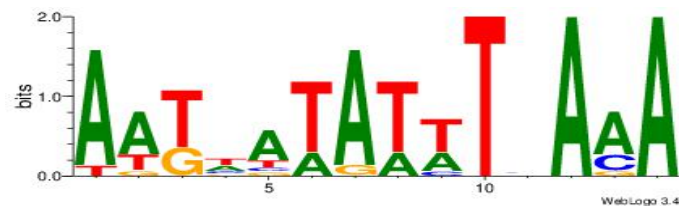
Best Matches for Motif ID 19 (Highest to Lowest)

Dataset #: 2
 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: 2
 Number of overlap: 13
 Similarity score: 0.0641025

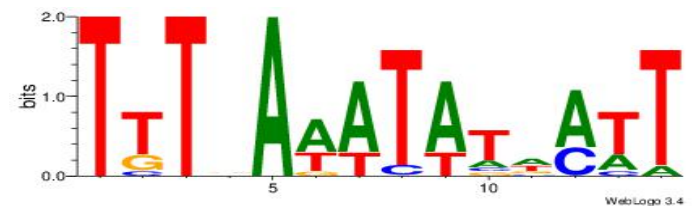
Alignment:

AATHATATWTHAAA
 -TTCWTAGATTAWA

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

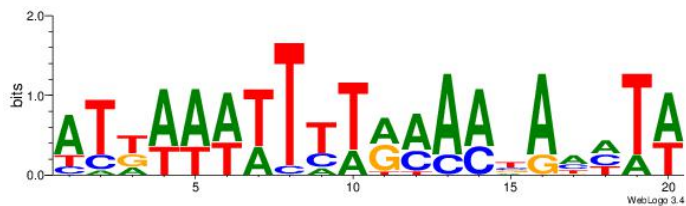


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 13

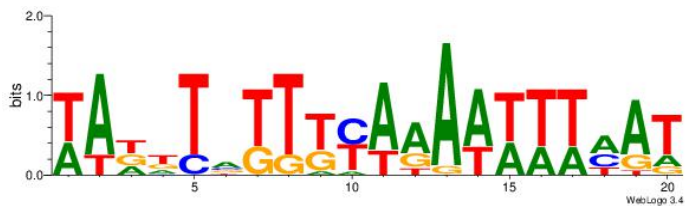
Similarity score: 0.0762821

Alignment:
WAHHTVTTYKAAAAWTTTRAT
-----TTCWTAGATTAWA-

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTTRAT

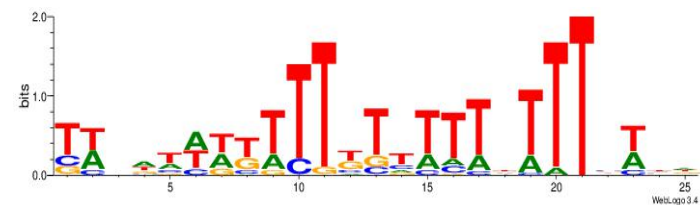


Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 12
Number of overlap: 13
Similarity score: 0.0810709

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
-TWTAAATCTAWGAA-----

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence: TWVHWWYTTTTYTTTTTHTTTVWBH



Alignment:

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TWAAWTTVTGAAAAHWW
-----TTCWTAGATTAWA
```

bits

2.0

1.0

0.0

5 10 15

WebLogo 3.4

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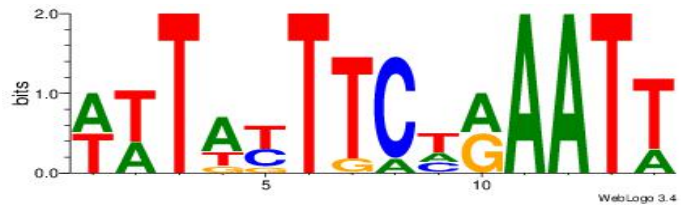
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.5625

Alignment:
AATTYDGAARTAWW-
--TTCWTAGATTAWA

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT

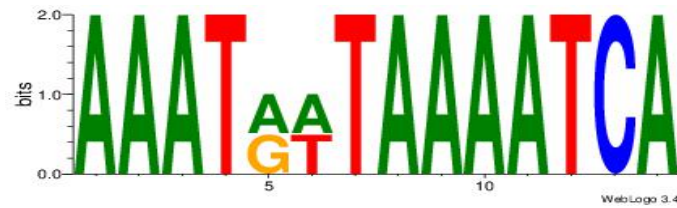


Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.5625

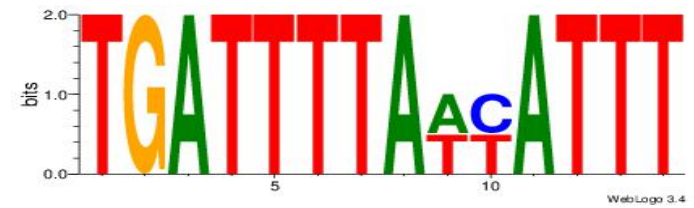
Alignment:

-TGATTTTAWKATTT
TWTAACTAWGAA--

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT



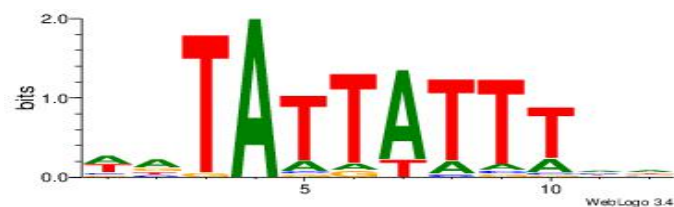
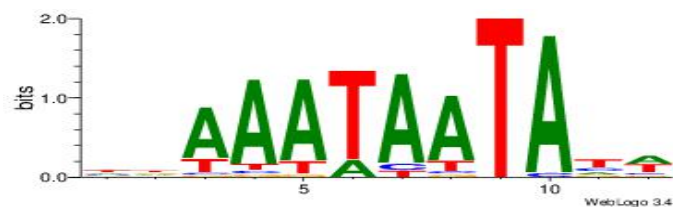
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.577083

Alignment:

WHTATTATTTDH-
TWTAACTAWGAA

Original motif Consensus sequence: HDAAATAATAHW

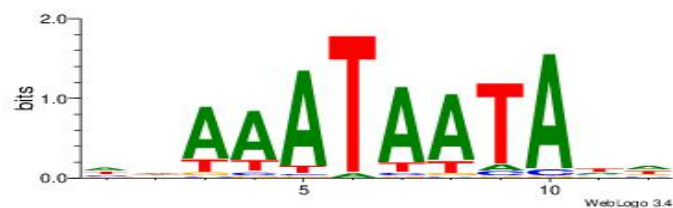
Reverse complement motif Consensus sequence: WHTATTATTTDH



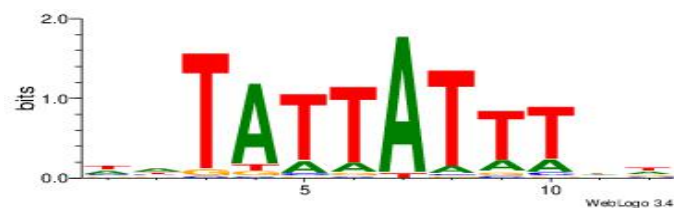
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.58179

Alignment:
 DDTATTATTTDH-
 TWTAACTAWGAA

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



Dataset #: 2
 Motif ID: 5

Motif name:	Motif 5
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:	0.583333

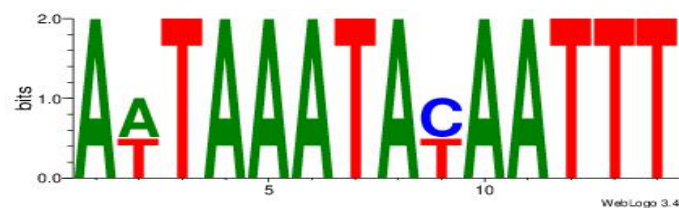
Alignment:

```

-AAATTKTATTTAWT
TWTAAATCTAWGAA--

```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



Dataset #:	2
Motif ID:	20
Motif name:	Motif 20
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:	1.02652

Alignment:

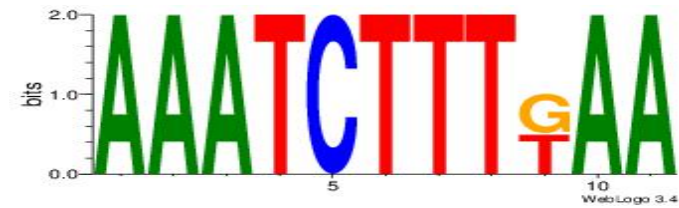
TTMAAAGATTT--

TTCWTAGATTAWA

Original motif Consensus sequence: TTMAAAGATTT



Reverse complement motif Consensus sequence: AAATCTTTYAA

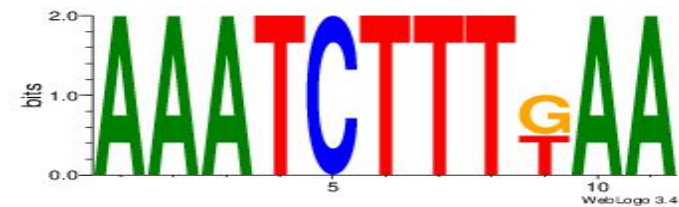


Dataset #: 2 Motif ID: 20 Motif name: Motif 20

Original motif Consensus sequence: TTMAAAGATTT



Reverse complement motif Consensus sequence: AAATCTTTYAA



Best Matches for Motif ID 20 (Highest to Lowest)

Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

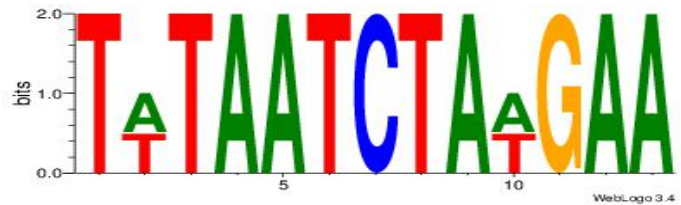
Number of overlap: 11
Similarity score: 0.0681818

Alignment:
TTCWTAGATTAWA
TTMAAAGATT--

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTATGAA

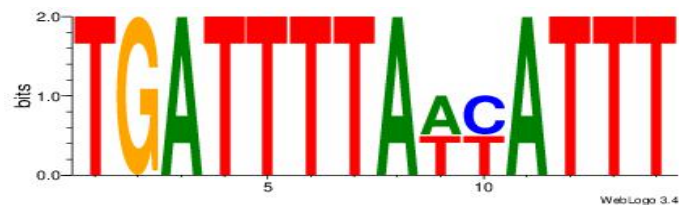
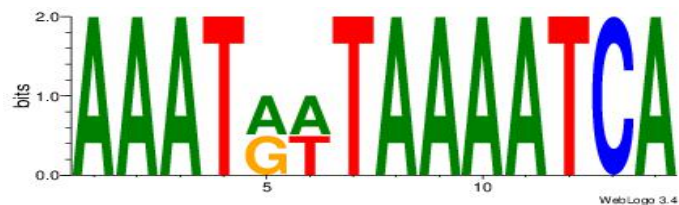


Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0681818

Alignment:
AAATRWATAAATCA
---AAATCTTTYAA

Original motif Consensus sequence: AAATRWATAAATCA

Reverse complement motif Consensus sequence: TGATTTATKATT

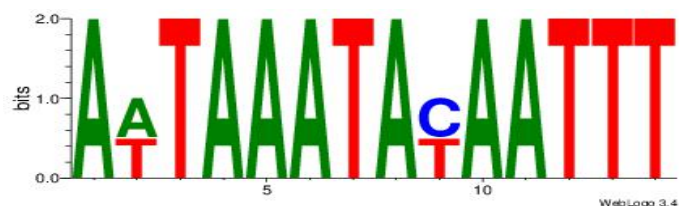


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.102273

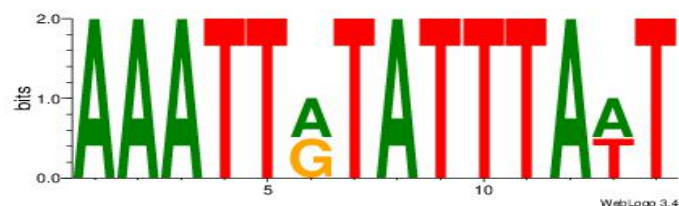
Alignment:

AWTAAATAYAATTT
 --TTMAAAGATTT--

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



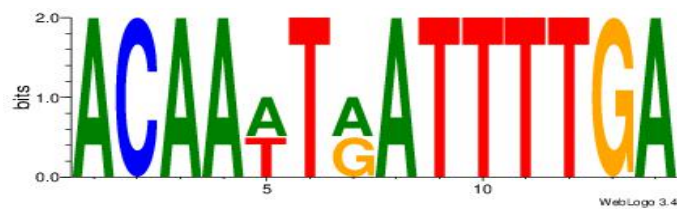
Dataset #: 2
 Motif ID: 16

Motif name:	Motif 16
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:	0.102273

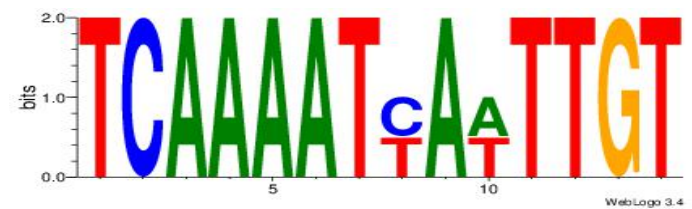
Alignment:

ACAAWTRATTTTGA
TTMAAAGATTT---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



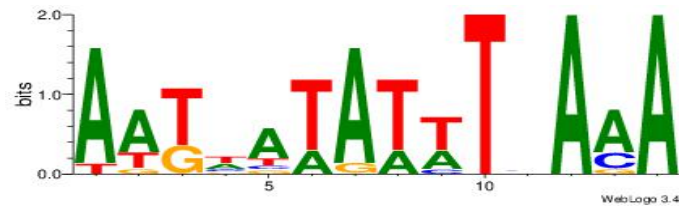
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.106061

Alignment:

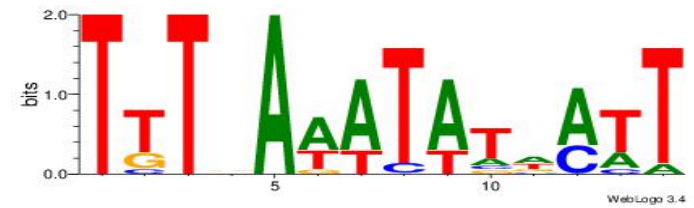
TTTDAWATATHATT

--TTMAAAGATTT--

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHATT



Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.110606

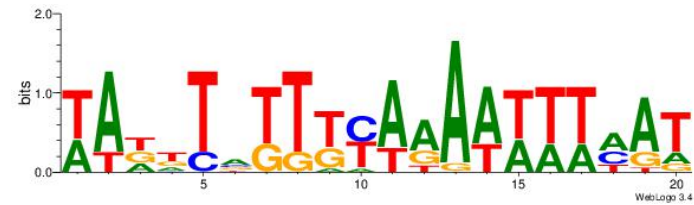
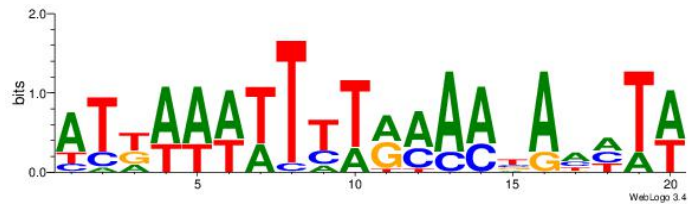
Alignment:

WAHHTVTTYKAAAWTTRAT

-AAATCTTTYAA-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAWTTRAT



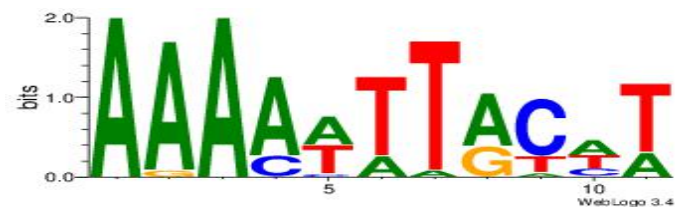
Dataset #: 2
 Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.110646

Alignment:

AWGKAAWTTTT

TTMAAAGATTT

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



Dataset #: 5
 Motif ID: 53

Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	11
Similarity score:	0.113636

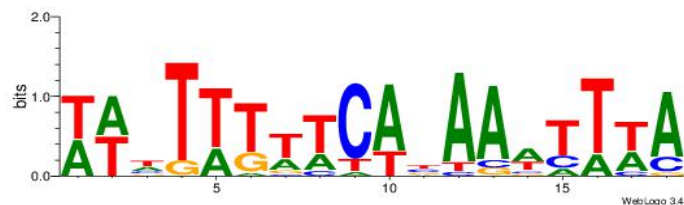
Alignment:

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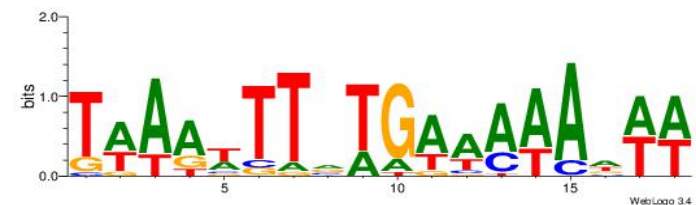
WWHTTTTTCABAAWTTWA
-----TTMAAAGATTT-

```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



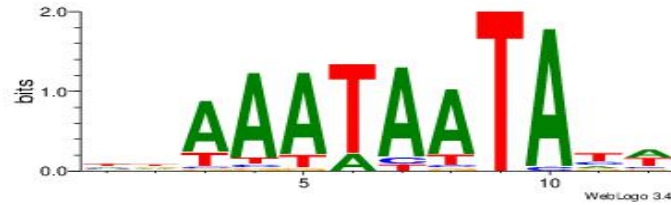
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.124242

Alignment:

WHTATTATTTDH

-AAATCTTTYAA

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.125

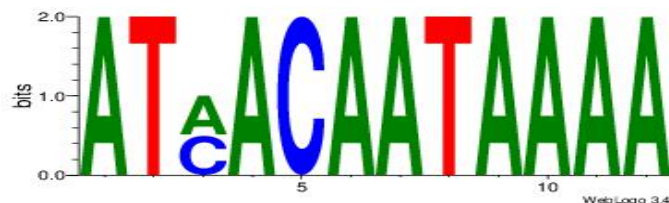
Alignment:

ATMACAATAAAA

-AAATCTTTYAA

Original motif Consensus sequence: ATMACAATAAAA

Reverse complement motif Consensus sequence: TTTTATTGTYAT



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

Original motif Consensus sequence: ATAAAA



Reverse complement motif Consensus sequence: TTTTAT



Best Matches for Motif ID 21 (Highest to Lowest)

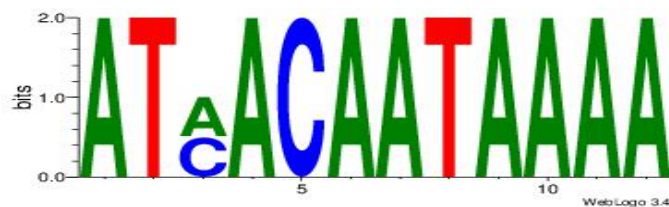
Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0

Alignment:

TTTTATTGTYAT

TTTTAT-----

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

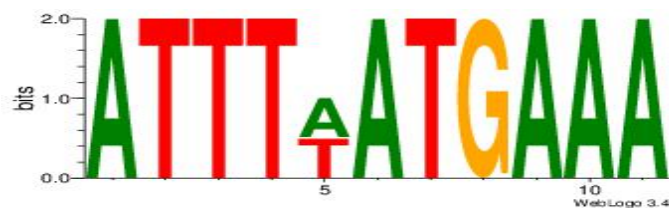


Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0208333

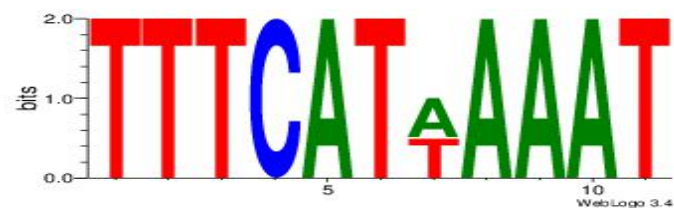
Alignment:

TTTCATWAAAT
-ATAAAA----

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

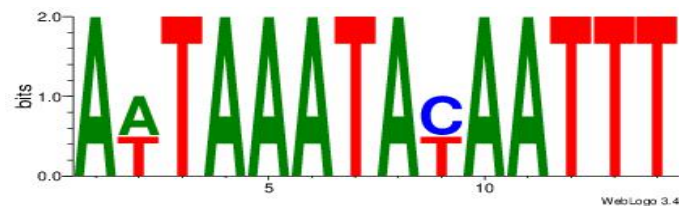


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0208333

Alignment:

AAATTKTATTTAWT
 ---TTTAT-----

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

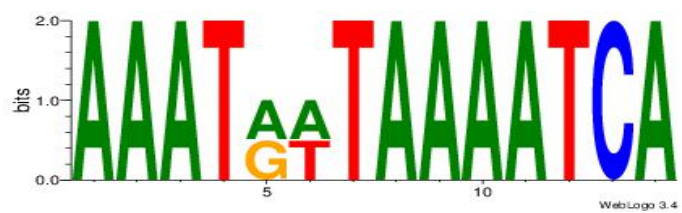


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 6

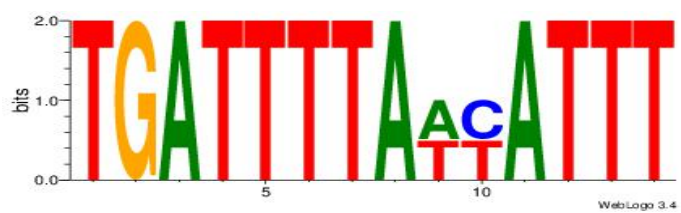
Similarity score: 0.0208333

Alignment:
TGATTTTAWKATT
---TTTAT-----

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

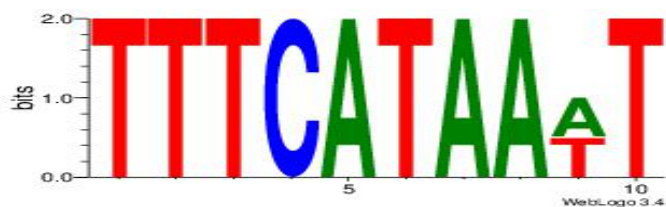


Dataset #: 2
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0416667

Alignment:
TTTCATAAWT
----TTTTAT

Original motif Consensus sequence: TTTCATAAWT

Reverse complement motif Consensus sequence: AWTATGAAA



Dataset #: 2
 Motif ID: 14
 Motif name: Motif 14
 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: 0.0625

Alignment:
 AWAAATAA
 ATAAAA--

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTWT



Dataset #: 2
 Motif ID: 20

Motif name:	Motif 20
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:	0.0625

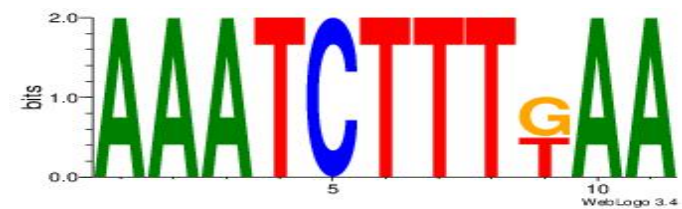
Alignment:

```
TTMAAAGATTT
ATAAAA-----
```

Original motif Consensus sequence: TTMAAAGATTT



Reverse complement motif Consensus sequence: AAATCTTTYAA

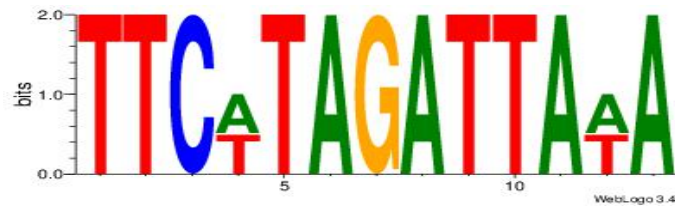


Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	6
Similarity score:	0.0625

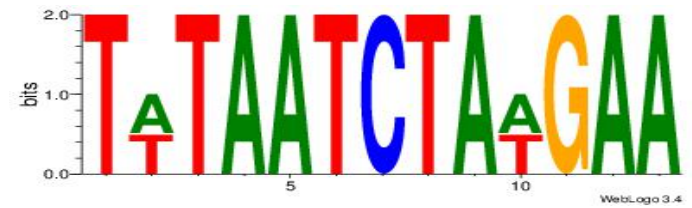
Alignment:

TTCWTAGATTAWA
-----ATAAAA

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTATGAA



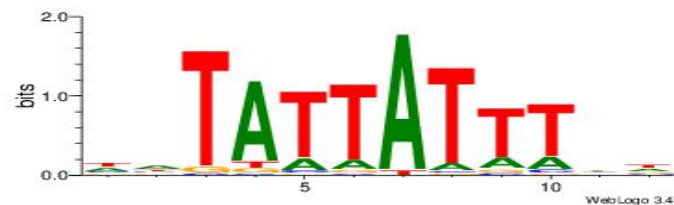
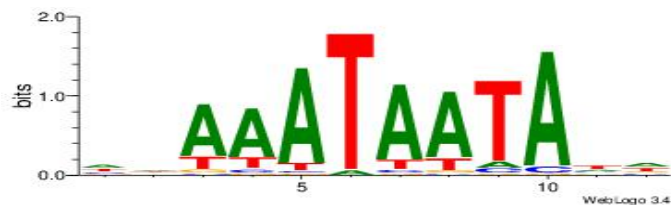
Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0632716

Alignment:

DDTATTATTDDH
--TTTTAT----

Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTDDH

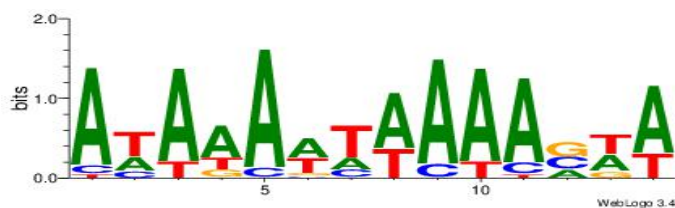


Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0689103

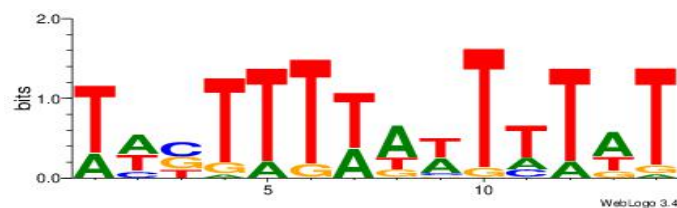
Alignment:

TWSTTTWAWTTTWT
 ---TTTTAT-----

Original motif Consensus sequence: AWAAAWTWAAASWA

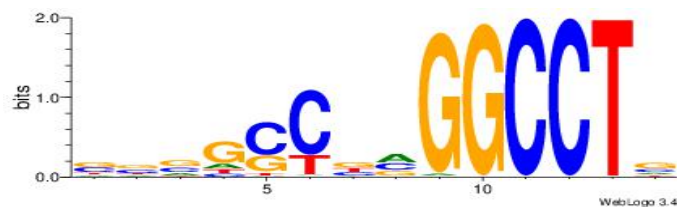


Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

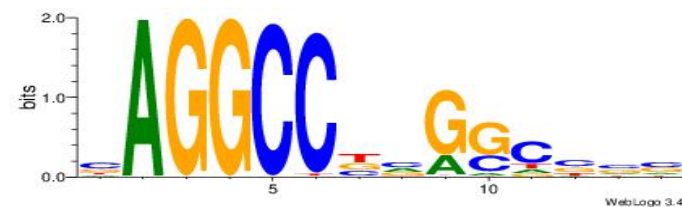


Dataset #: 3 Motif ID: 22 Motif name: Zfx

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



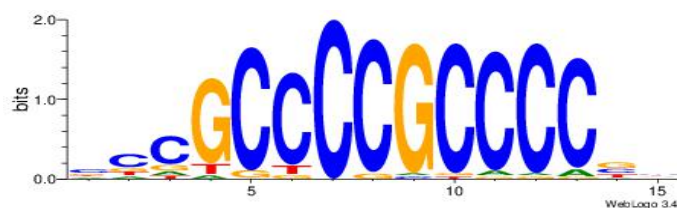
Best Matches for Motif ID 22 (Highest to Lowest)

Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
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:	0.0514008

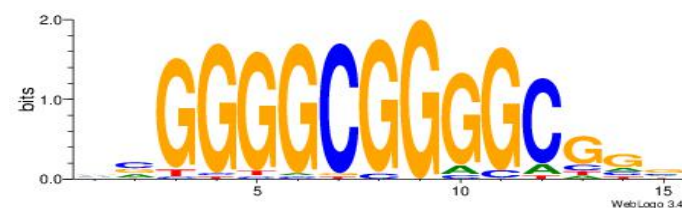
Alignment:

```
BCCGCCCCGCCCCBB
BBVGCCBVGGCCTV-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

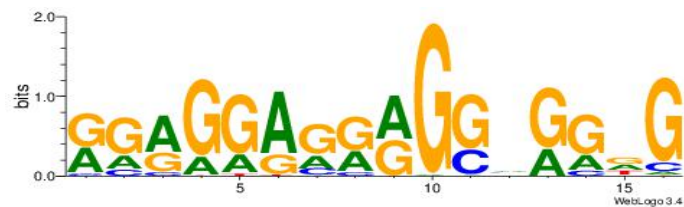


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0590031

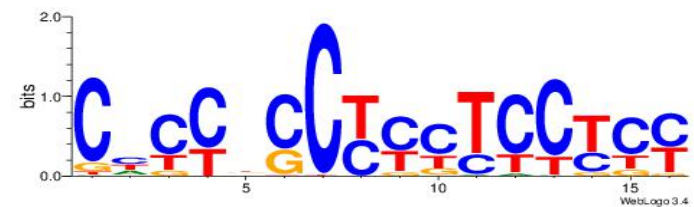
Alignment:

CHCCBCKMCTCCKCM
 -BBVGCCBVGGCCTV-

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

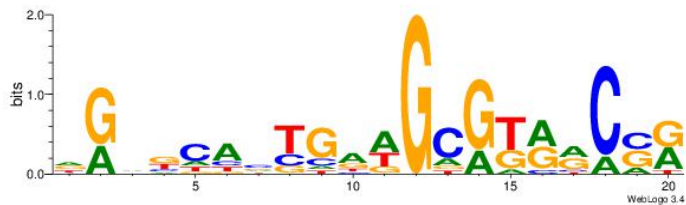


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5

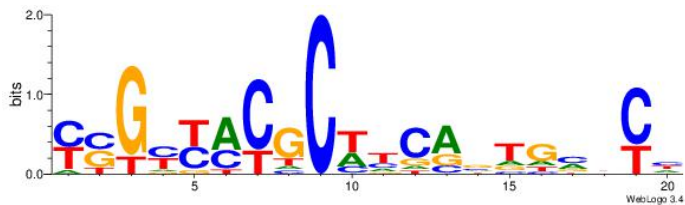
Number of overlap: 14
Similarity score: 0.0611182

Alignment:
DGVBCABTGDWGCGRRCR
--BBVGCCBVGGCCTV----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



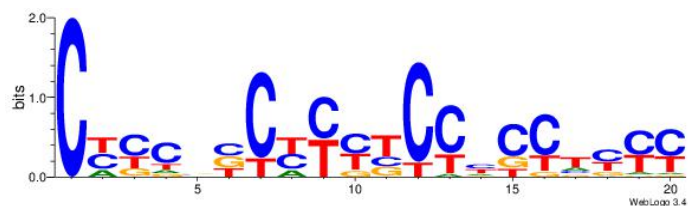
Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBBCD



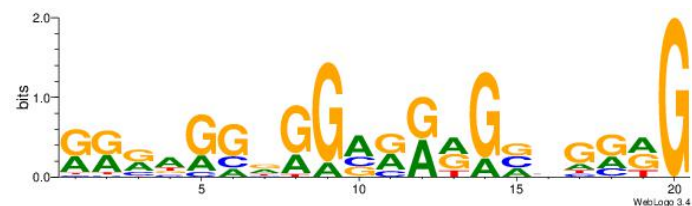
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 14
Similarity score: 0.0629383

Alignment:
KKKAGGDGGAKKMGBBGKMG
-----VAGGCCBBGGCVBB-

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



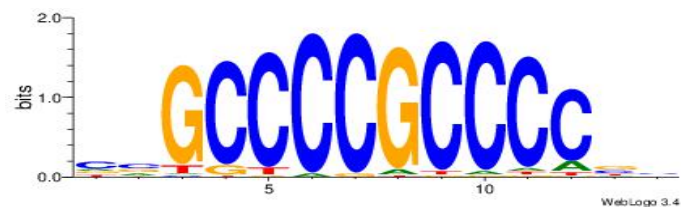
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0654514

Alignment:

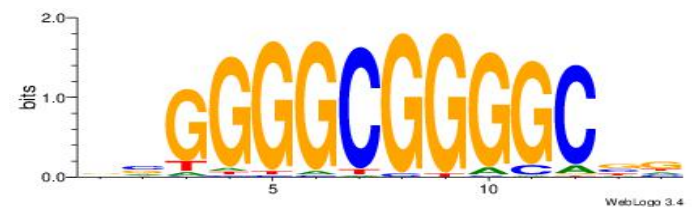
HVCCCCGCCCCBB

VAGGCCBBGGCVBB

Original motif Consensus sequence: HVCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

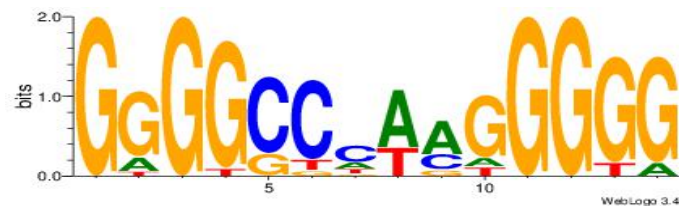


Dataset #: 3
 Motif ID: 30
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0796879

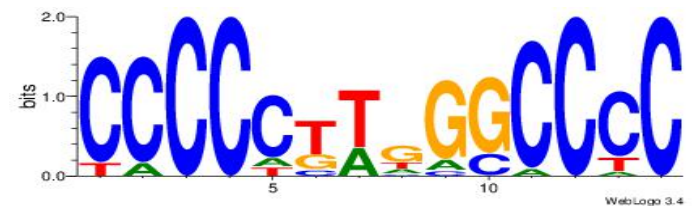
Alignment:

CCCCCTTGGGCCCC
 BBVGCCBVGGCCTV

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC

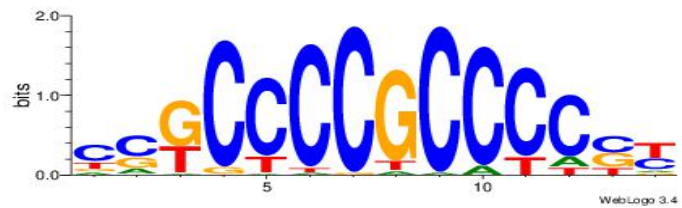


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14

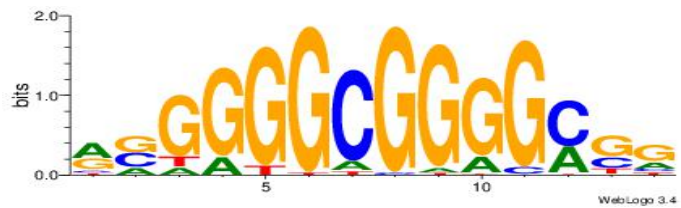
Similarity score: 0.0799116

Alignment:
MSGGGGCGGGYSG
BBVGCCBVGGCCTV

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY

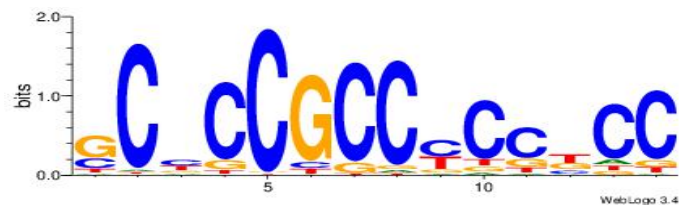
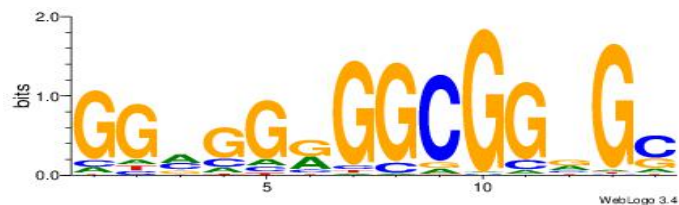


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.583338

Alignment:
-GCVCCGCCMCCYCC
BBVGCCBVGGCCTV-

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY

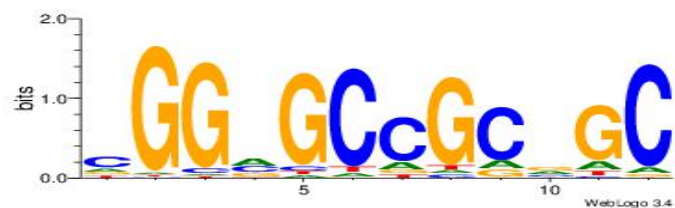


Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 1.55068

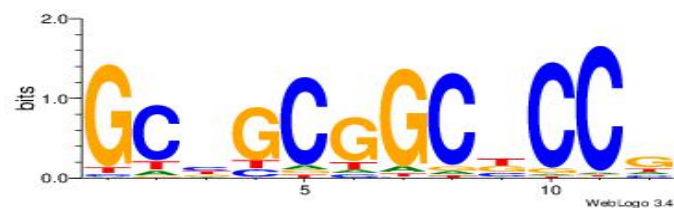
Alignment:

CGGVGCCGCVGC---
 -BBVGCCBVGGCCTV

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



Dataset #: 3
 Motif ID: 35

Motif name: GABPA
 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: 1.57592

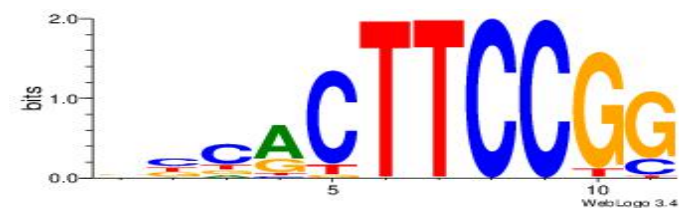
Alignment:

CCGGAAGTGVV---
 VAGGCCBBGGCVBB

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCGG



Dataset #: 3 Motif ID: 23 Motif name: Egr1

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCACGCH



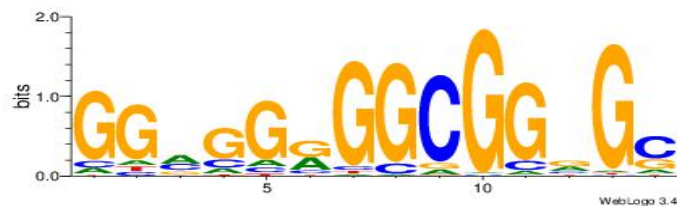
Best Matches for Motif ID 23 (Highest to Lowest)

Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 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: 0.0514701

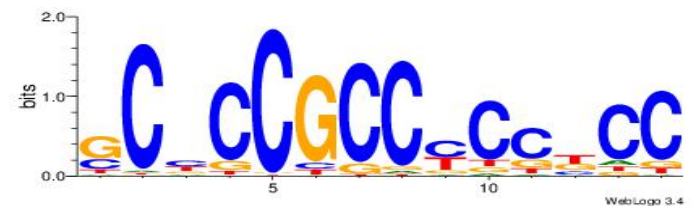
Alignment:

GCVCCGCCMCCYCC
 ---YCGCCCACGCH

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

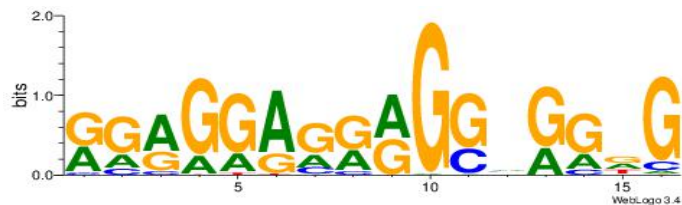


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 11

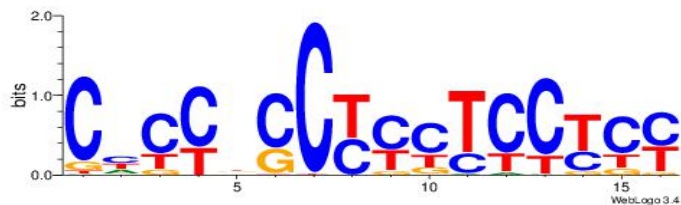
Similarity score: 0.0698683

Alignment:
CHCCBCKMCTCCKCM
-----YCGCCCACGCH

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

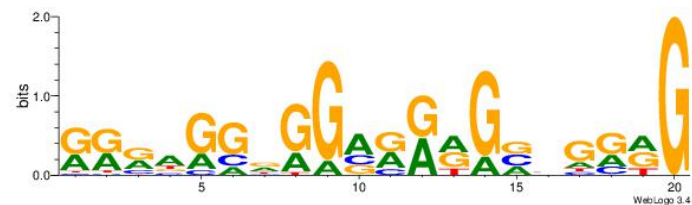
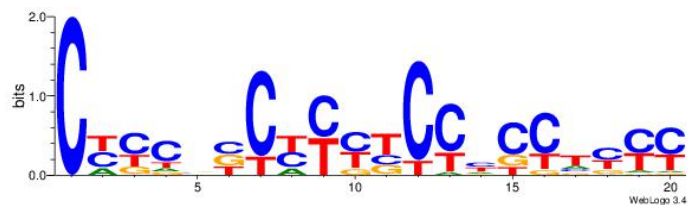


Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0718056

Alignment:
KKKAGGDGGAKKMGBBGKMG
-HGC GTGGGCGK-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

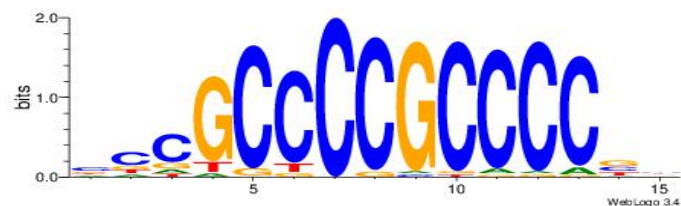


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0730967

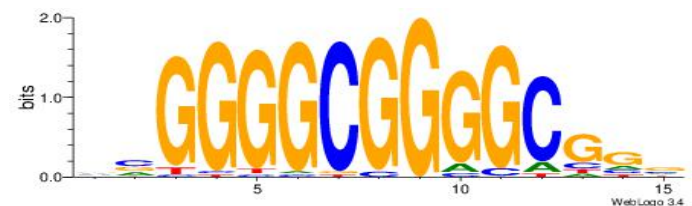
Alignment:

BBGGGGCGGGGCGGB
 ----HCGTGCGK

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



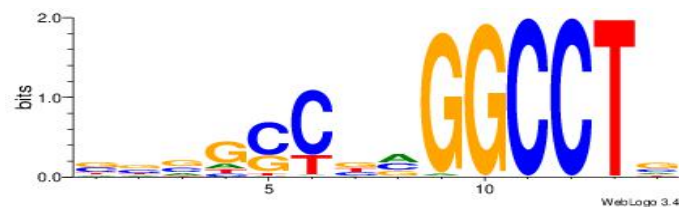
Dataset #: 3

Motif ID: 22
 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

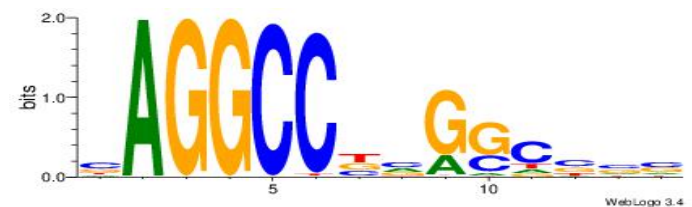
Alignment:

BBVGCCBVGGCCTV
 --HGCGTGGGCGK-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



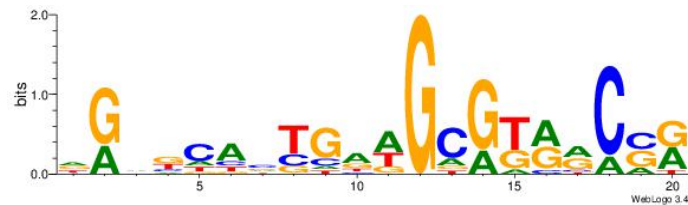
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0765783

Alignment:

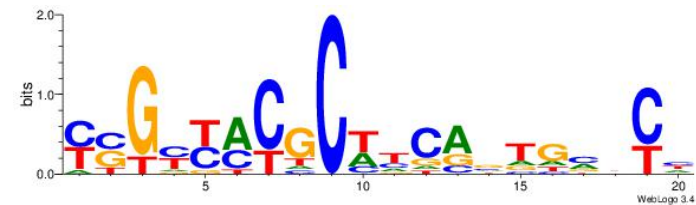
DGVBCABTGDWGCGRRCR

-----HGCCTGGGCGK-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



Dataset #:	2
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:	11
Similarity score:	0.0771215

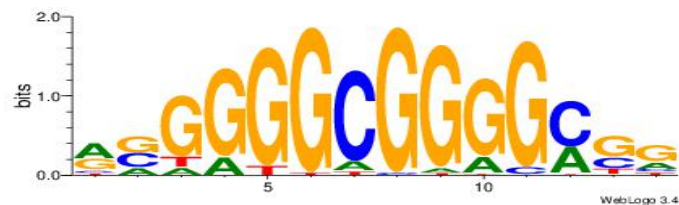
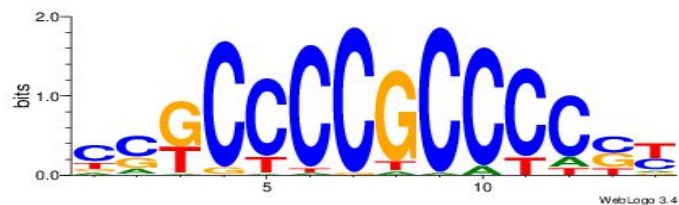
Alignment:

CSKCCCCGCCCSY

-YCGCCACGCH--

Original motif Consensus sequence: CSKCCCCGCCCSY

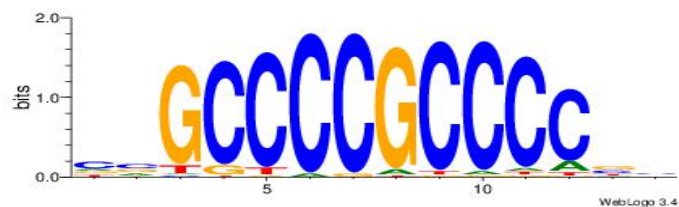
Reverse complement motif Consensus sequence: MSGGGCGGGGY



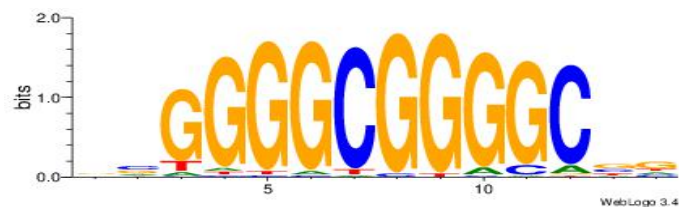
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0825032

Alignment:
 HVGCCCCGCCCCBB
 -YCGCCCACGCH--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



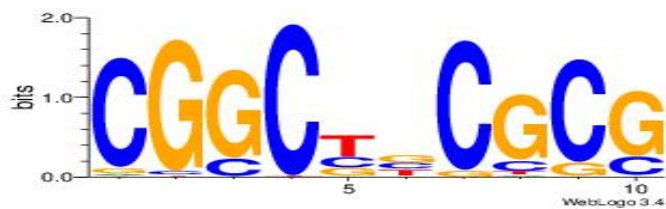
Dataset #: 5
 Motif ID: 48

Motif name:	TFW3
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:	0.550222

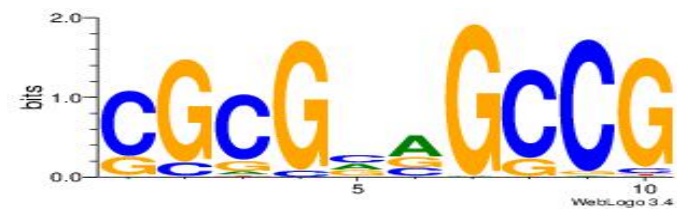
Alignment:

CGCGBMGCCG-
HGCCTGGGCGK

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

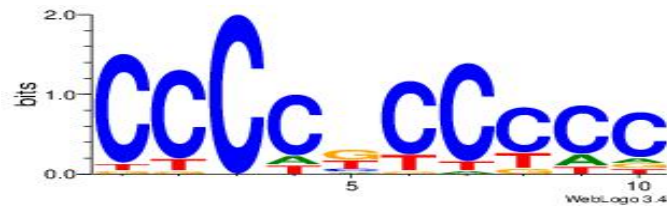


Dataset #:	3
Motif ID:	24
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.572401

Alignment:

GGGGGYGGGG-
HGCGTGGGCGK

Original motif Consensus sequence: CCCCKCCCCC

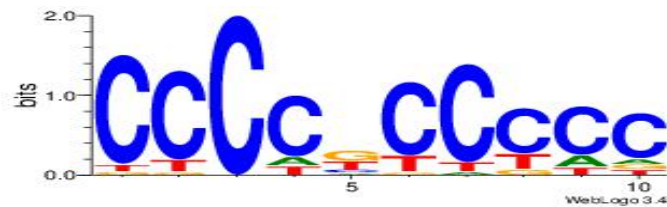


Reverse complement motif Consensus sequence: GGGGGYGGGG



Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



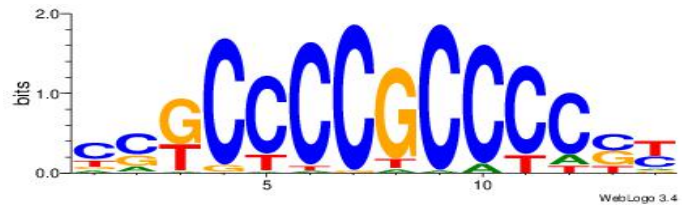
Best Matches for Motif ID 24 (Highest to Lowest)

Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4

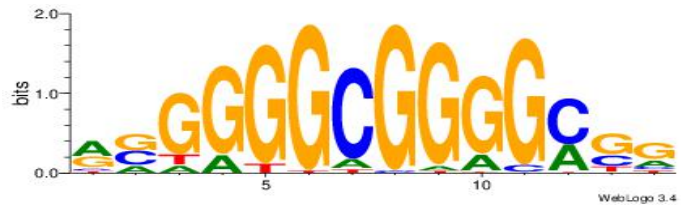
Number of overlap: 10
Similarity score: 0.00451594

Alignment:
MSGGGGCGGGYSG
-GGGGGYGGGG---

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY

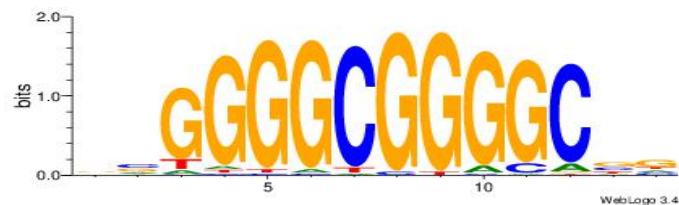
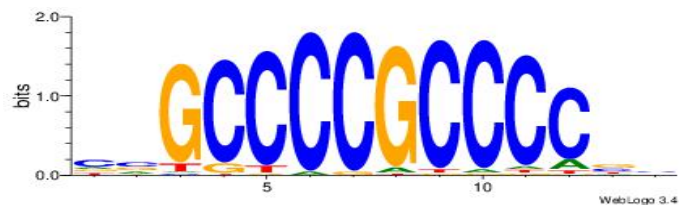


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCS
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.00965796

Alignment:
BBGGGGCGGGCVD
-GGGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCB

Reverse complement motif Consensus sequence: BBGGGGCGGGC

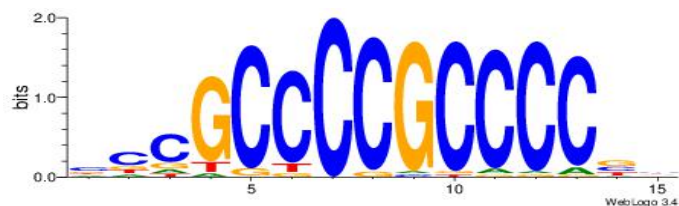


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0127292

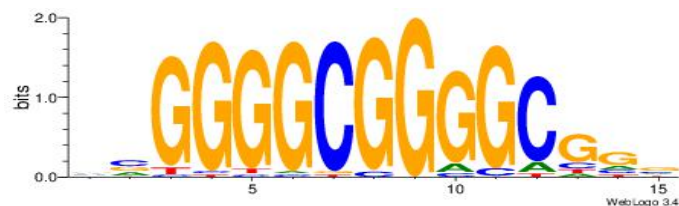
Alignment:

BCCGCCCCGCCCCBB
 ----CCCCKCCCC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



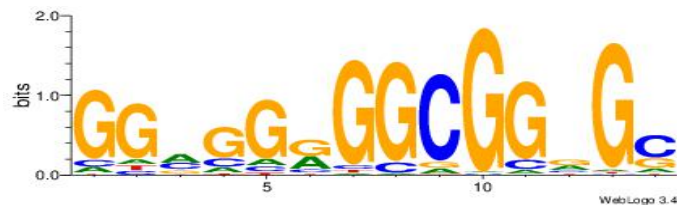
Dataset #: 5

Motif ID: 50
 Motif name: TFF11
 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: 0.0174405

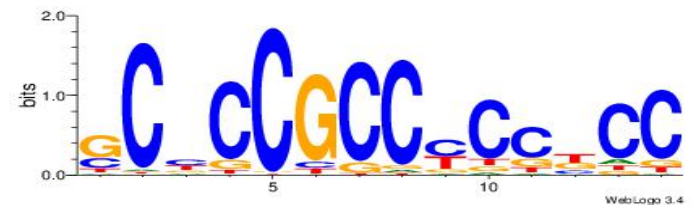
Alignment:

GGMGGRGGCGGVGC
 ---GGGGGYGGG--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

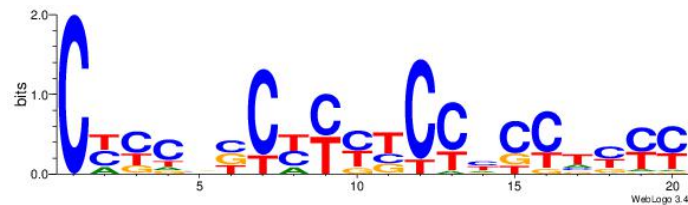


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0301548

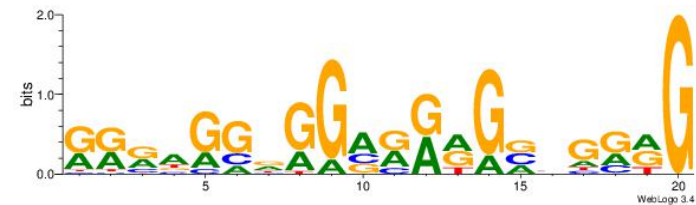
Alignment:

CYYCBBCYYYTCCHCCTYYY
-----CCCCKCCCC-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



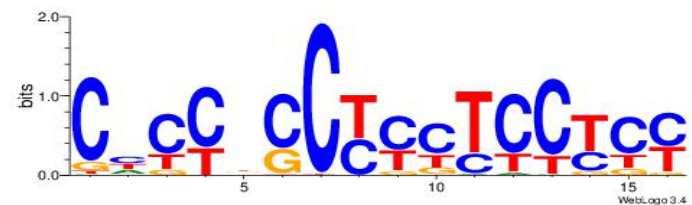
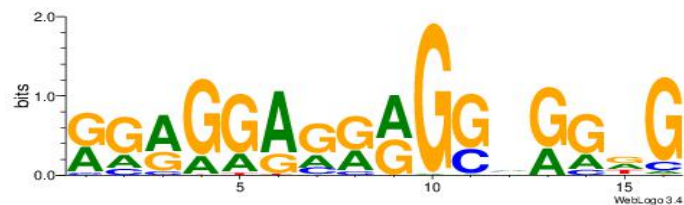
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0329167

Alignment:

RGRGGAGRRGGHGGDG
-----GGGGGYGGGG

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

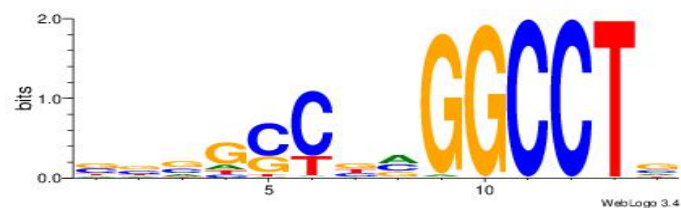
Reverse complement motif Consensus sequence:
CHCCBCKMCTCKCM



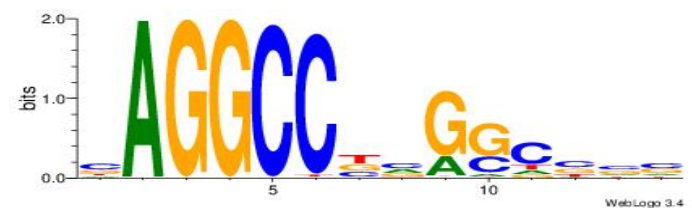
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0540825

Alignment:
 BBVGCCBVGGCCTV
 ----GGGGGYGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



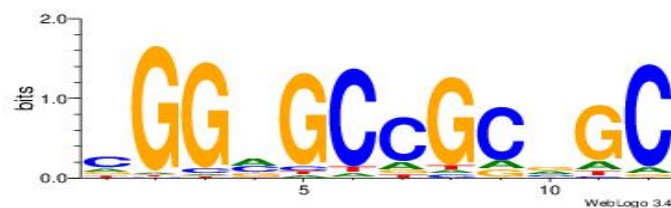
Dataset #: 5
 Motif ID: 49

Motif name:	TFF1
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:	0.0557738

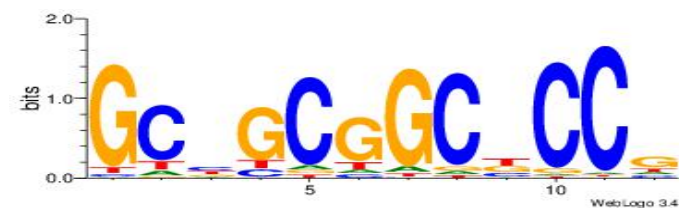
Alignment:

GCVGCGGCBCCG
 -CCCCKCCCCC-

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

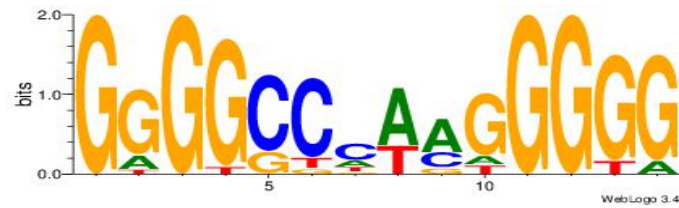


Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.0600992

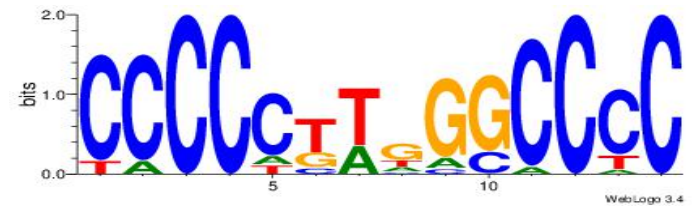
Alignment:

CCCCCTTGGGCCCC
 -CCCCKCCCCC---

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



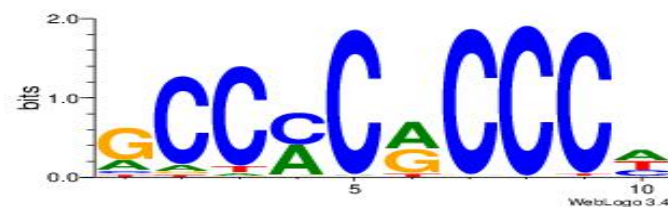
Dataset #:	3
Motif ID:	27
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0637183

Alignment:

GCCYCMCCCD
 CCCCKCCCCC

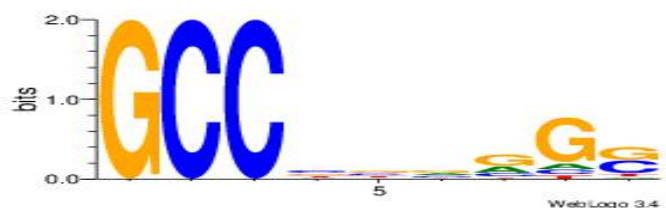
Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

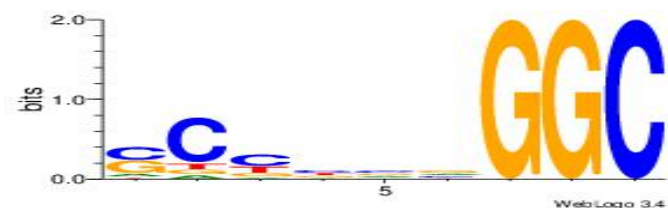


Dataset #: 3 **Motif ID: 25** **Motif name: TFAP2A**

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



Best Matches for Motif ID 25 (Highest to Lowest)

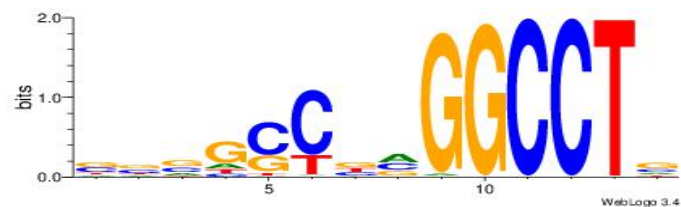
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.0131247

Alignment:

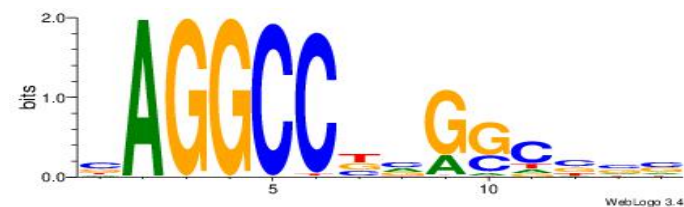
BBVGCCBVGGCTV

---SCMVBBGGC--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

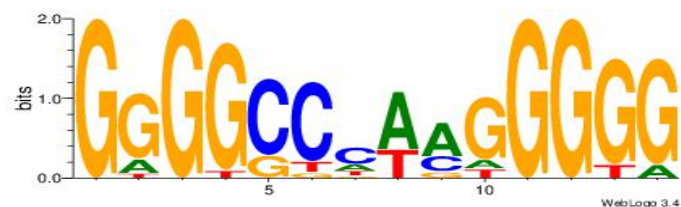


Dataset #: 3
 Motif ID: 30
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0414588

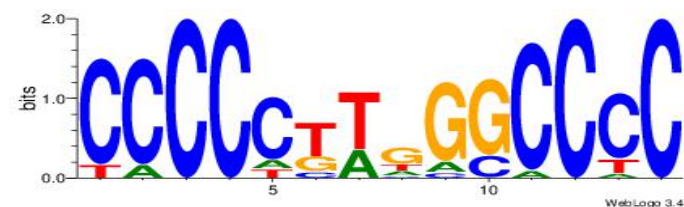
Alignment:

GGGGCCCAAGGGG
 ---GCCBBVRGS---

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

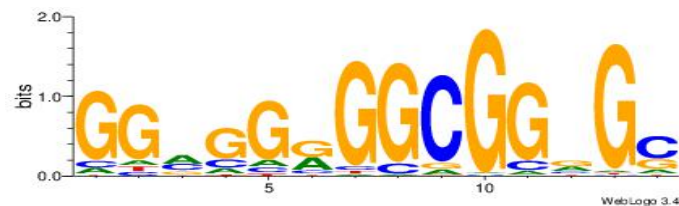


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0415732

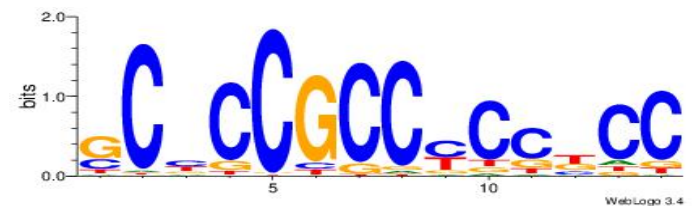
Alignment:

GGMGGRGGCGGVGC
 SCMVBBGGC-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



Dataset #: 3
 Motif ID: 33
 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

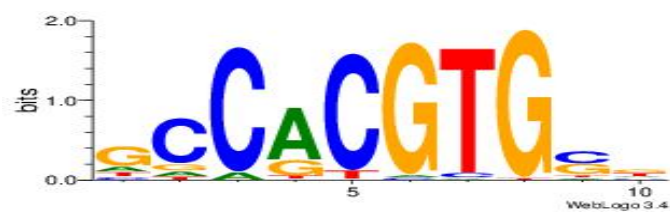
Similarity score: 0.0550803

Alignment:
HSCACGTGGC
-SCMVBBGGC

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

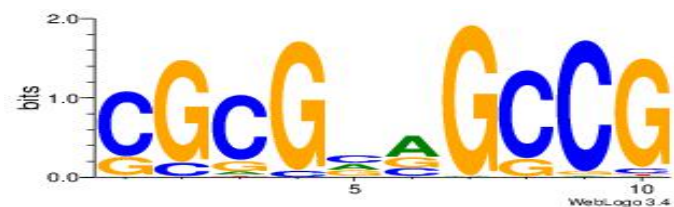
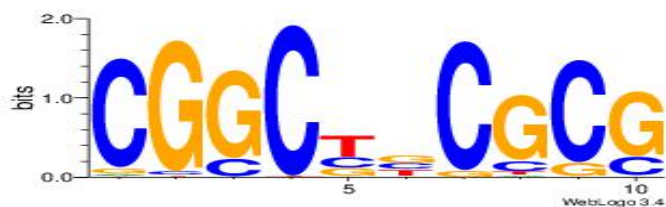


Dataset #: 5
Motif ID: 48
Motif name: TFW3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0552877

Alignment:
CGGCYBCGCG
-GCCBBVRGS

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

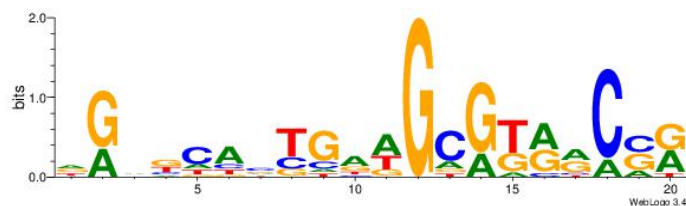


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 9
 Similarity score: 0.0581255

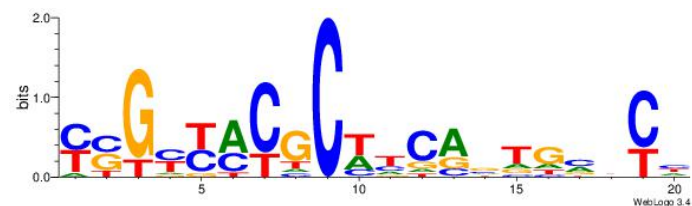
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----GCCBBVRGS-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3

Motif ID: 34
 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

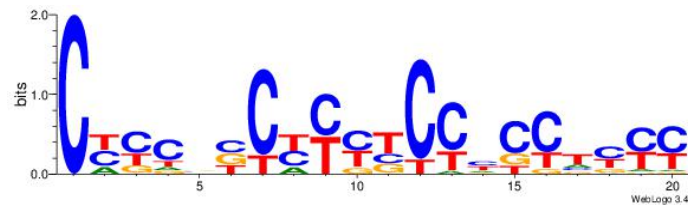


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 9
 Similarity score: 0.0630429

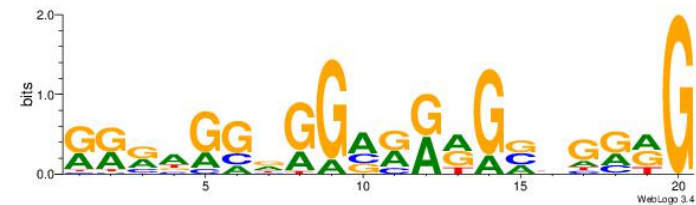
Alignment:

KKKAGGDGGAKKMGBBGKMG
-SCMVBBGGC-----

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



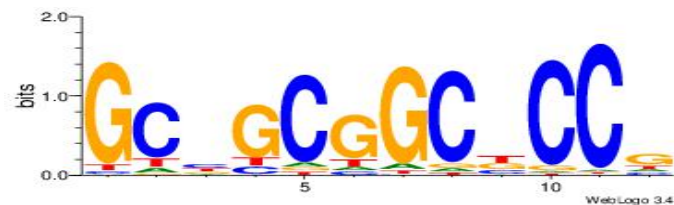
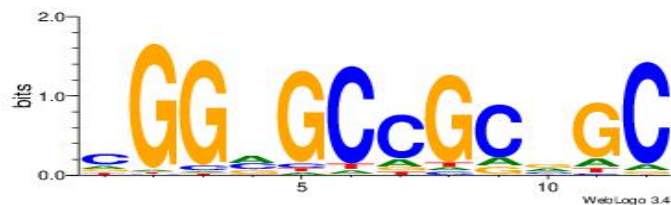
Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.0669772

Alignment:

GCVGCGGCBCCG
SCMVBBGGC---

Original motif Consensus sequence: CGGVGCCGCVGC

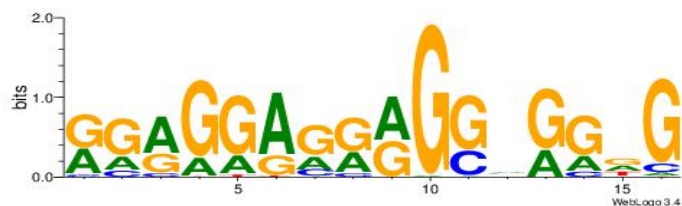
Reverse complement motif Consensus sequence: GCVGCGGCBCCG



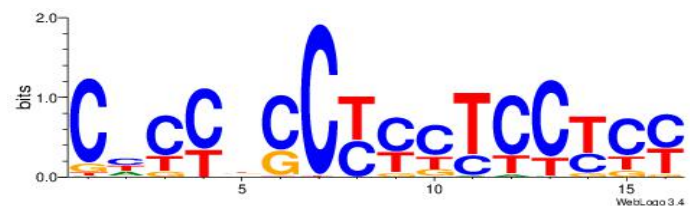
Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 9
 Similarity score: 0.069755

Alignment:
 CHCCBCKMCTCCKCM
 SCMVBBGGC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

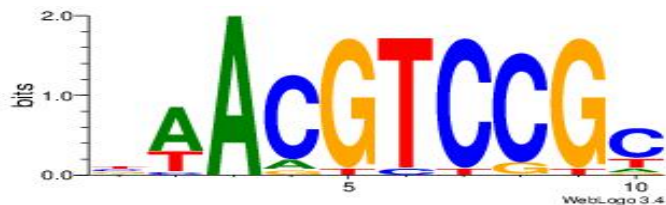


Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



Dataset #: 3 Motif ID: 26 Motif name: MIZF

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



Best Matches for Motif ID 26 (Highest to Lowest)

Dataset #:	3
Motif ID:	35
Motif name:	GABPA
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:	0.0459305

Alignment:

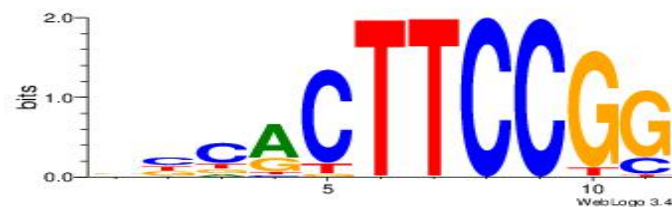
CCGGAAGTGVV

GCGGACGTTT-

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCGG



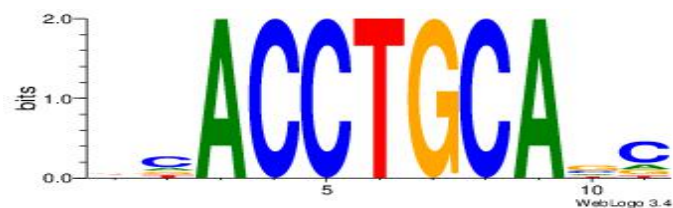
Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0778314

Alignment:

BCACCTGCABC

BAACGTCCGC-

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10

Similarity score: 0.0794339

Alignment:
DHACATTCTGH
BAACGTCCGC-

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

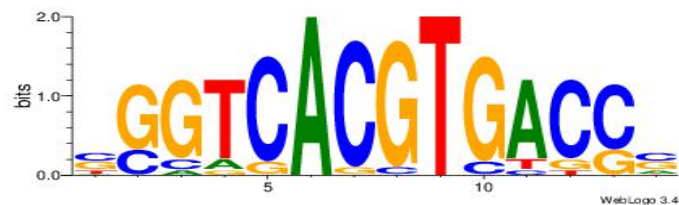
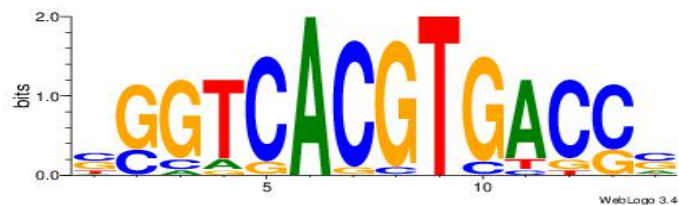


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACCS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0804061

Alignment:
SGGTCACGTGACCS
---BAACGTCCGC-

Original motif Consensus sequence: SGGTCACGTGACCS

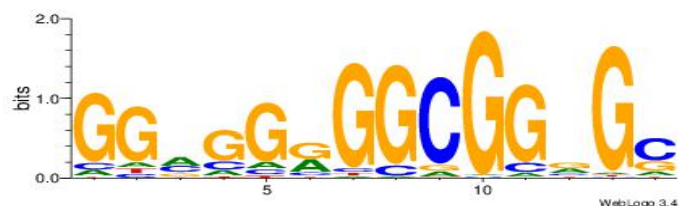
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



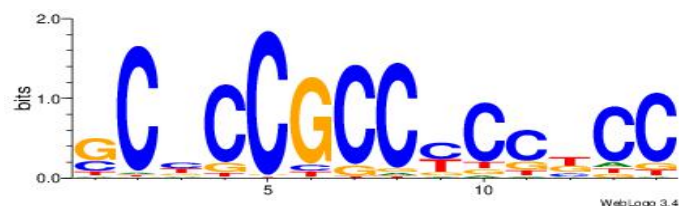
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0861006

Alignment:
 GCVCCGCCMCCYCC
 -BAACGTCCGC---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



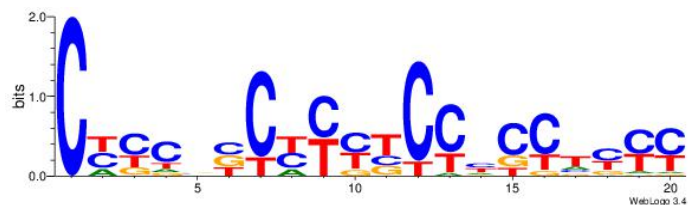
Dataset #: 5
 Motif ID: 54

Motif name: TFM12
 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: 0.0871006

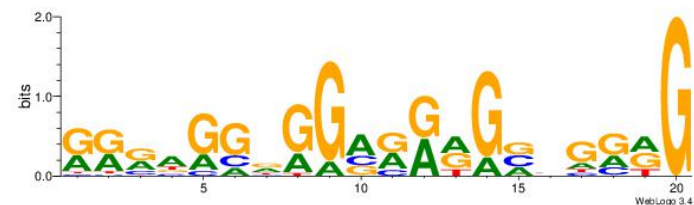
Alignment:

CYYCBBCYYYTCCHCCTYYY
 -----BAACGTCCGC-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

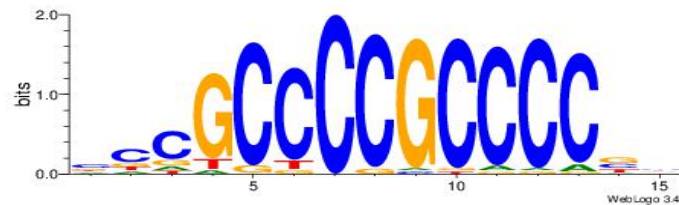


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0877229

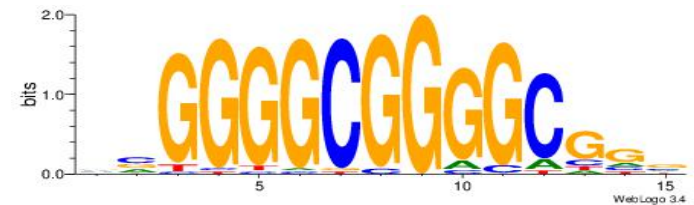
Alignment:

BCCGCCCCGCCCCBB
BAACGTCCGC-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



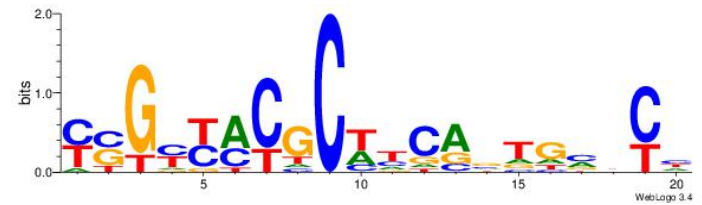
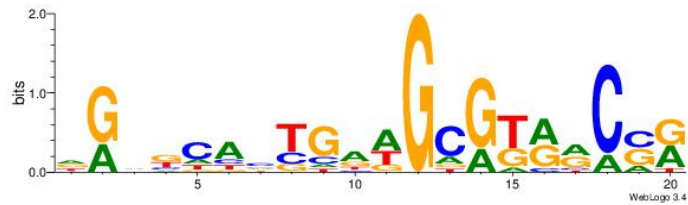
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	10
Number of overlap:	10
Similarity score:	0.0877672

Alignment:

MSGKKRCGCWDCABTGBBCD
-GCGGACGTTV-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

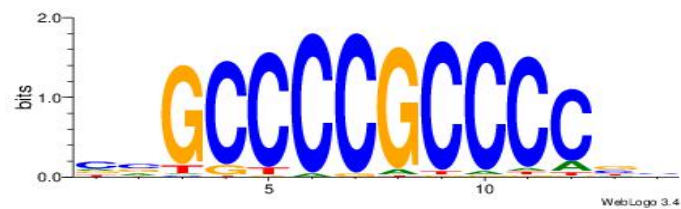
Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



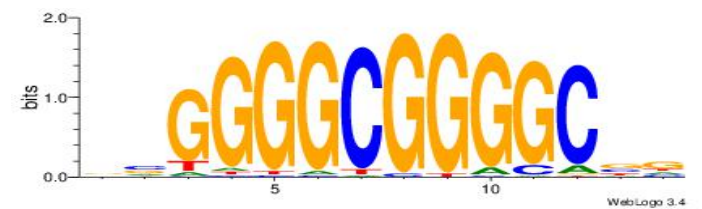
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0884513

Alignment:
 HVGCCCCGCCCCBB
 ---BAACGTCCGC-

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

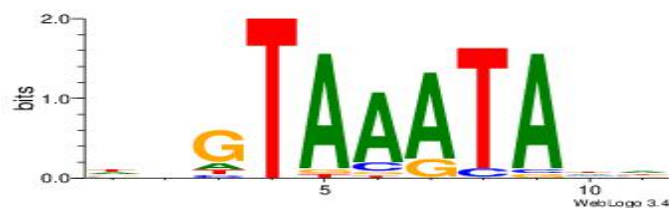


Dataset #: 4
 Motif ID: 45

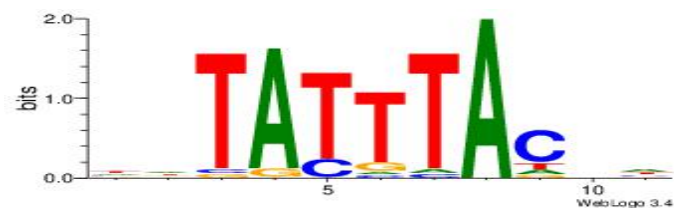
Motif name: wbgTAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0893149

Alignment:
 DBGTAATAHD
 GCGGACGTTV-

Original motif Consensus sequence: DBGTAATAHD

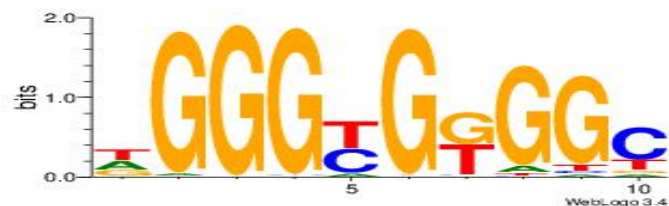


Reverse complement motif Consensus sequence: DHTATTACBD



Dataset #: 3 Motif ID: 27 Motif name: Klf4

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



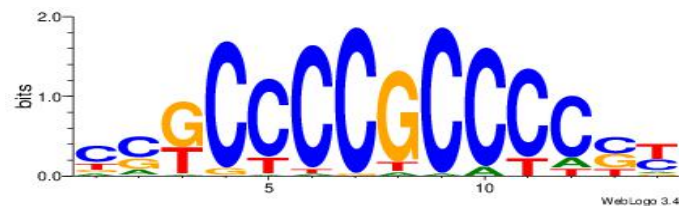
Best Matches for Motif ID 27 (Highest to Lowest)

Dataset #: 2
 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: 3
 Number of overlap: 10
 Similarity score: 0.0152457

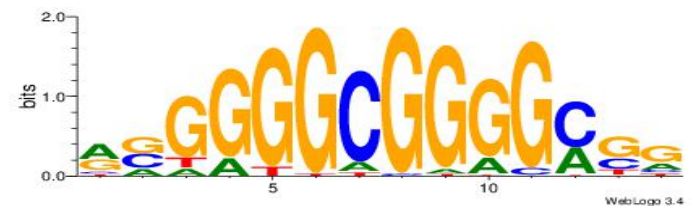
Alignment:

CSKCCCCGCCCSY
 --GCCYCMCCCD--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

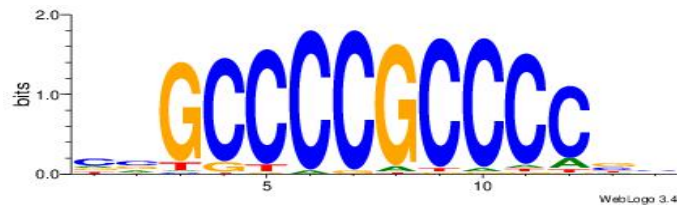


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCSY
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10

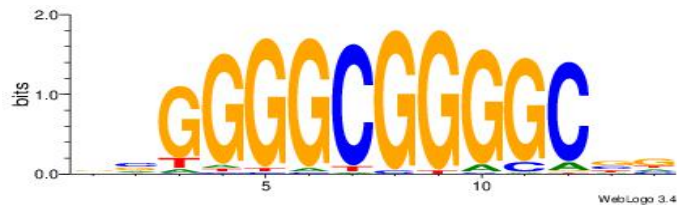
Similarity score: 0.0160185

Alignment:
BBGGGGCGGGGCVD
--DGGGYGKGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

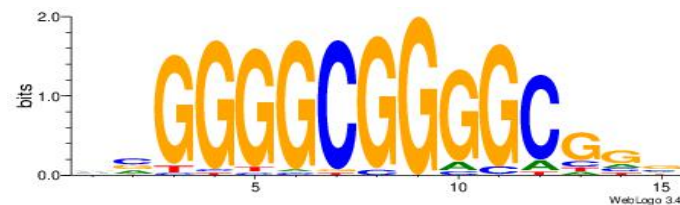
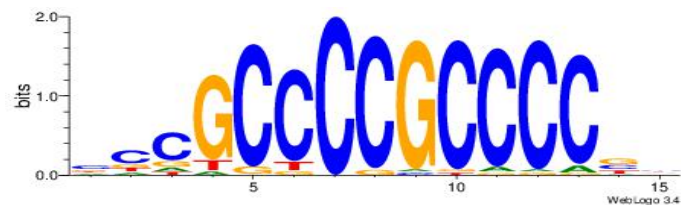


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0194893

Alignment:
BBGGGGCGGGGCGGB
--DGGGYGKGGC---

Original motif Consensus sequence: BCCGCCCCGCCCCBB

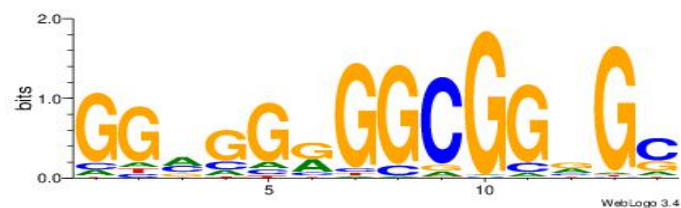
Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



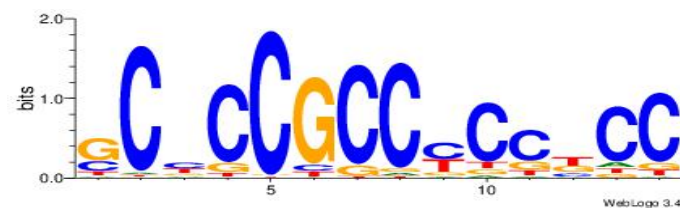
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0402906

Alignment:
 GGMGGRGGCGGVGC
 ----DGGGYGKGGC

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



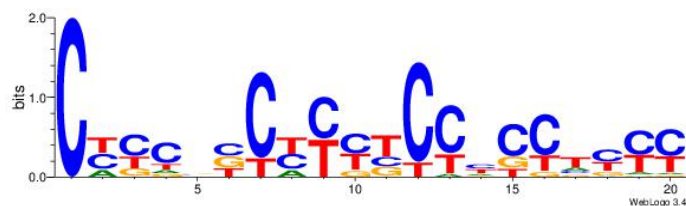
Dataset #: 5
 Motif ID: 54

Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0556427

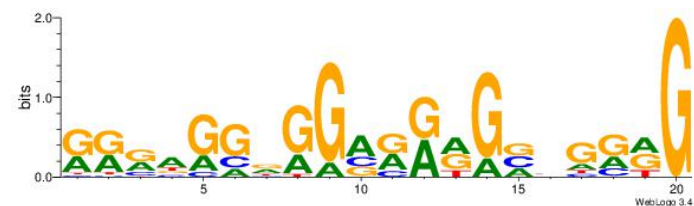
Alignment:

CYYCBBCYYYTCCHCCTYYY
 ----GCCYCMCCCD-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



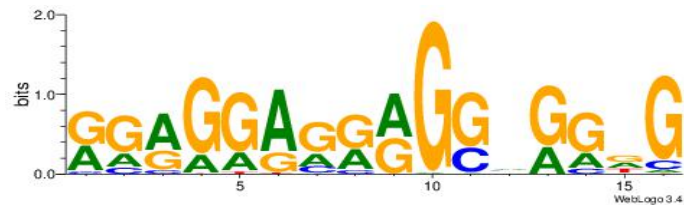
Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0606033

Alignment:

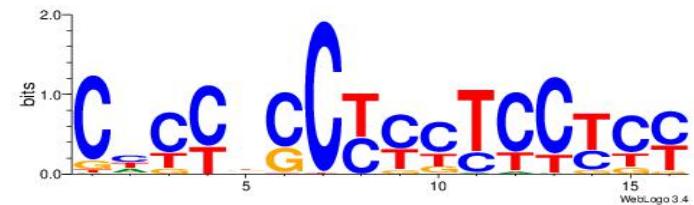
CHCCBCKMCTCCKCM

----GCCYCMCCCD--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



Dataset #:	3
Motif ID:	22
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:	0.0623591

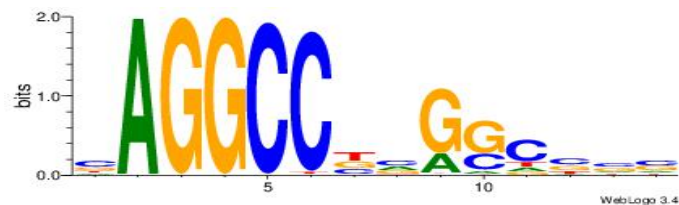
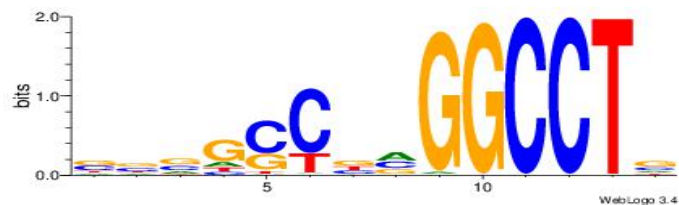
Alignment:

BBVGCCBVGGCCTV

-GCCYCMCCCD---

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



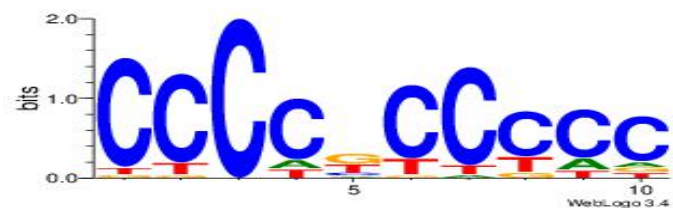
Dataset #: 3
 Motif ID: 24
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0663136

Alignment:

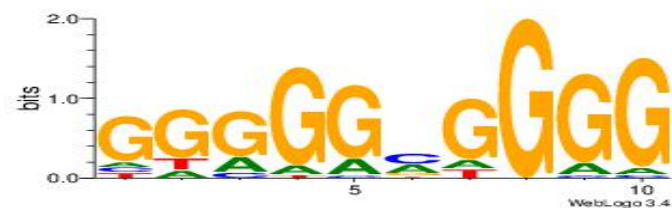
GGGGYGGGG

DGGYGKGGC

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



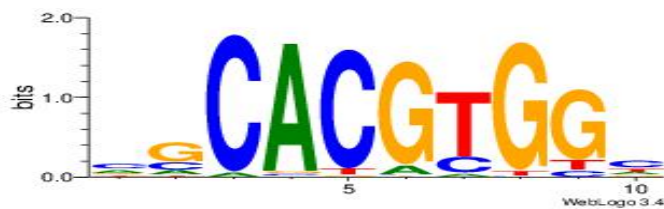
Dataset #: 3
 Motif ID: 34

Motif name:	Myc
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:	0.0686848

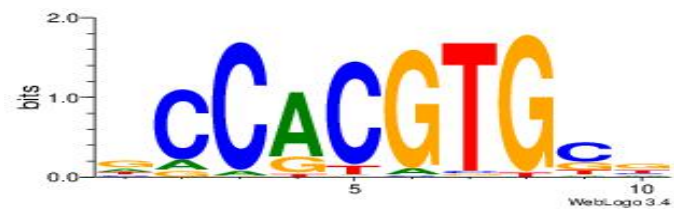
Alignment:

VGCACGTGGH
DGGGYGKGGC

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



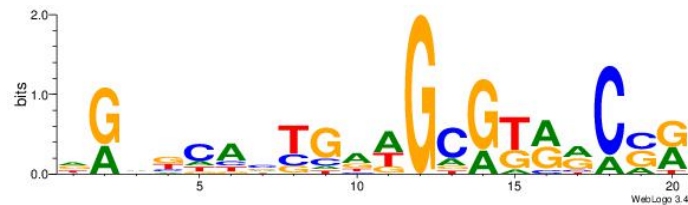
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.06956

Alignment:

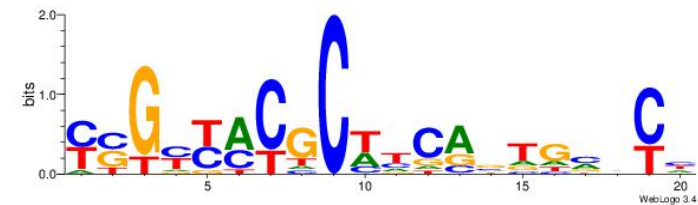
DGVBCABTGDWGCGRRCR

-----DGGGYGKGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3 Motif ID: 28 Motif name: E2F1

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGSAAA



Best Matches for Motif ID 28 (Highest to Lowest)

Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward

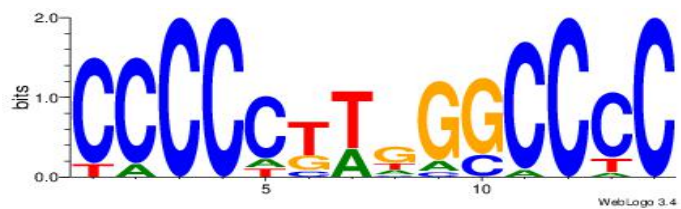
Position number: 2
Number of overlap: 8
Similarity score: 0.0568827

Alignment:
GGGGCCCAAGGGGG
-GCGCSAAA-----

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



Dataset #: 4
Motif ID: 39
Motif name: kCAGCCAATmr
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0624791

Alignment:
MBATTGGCTGH
--TTTSGCGC--

Original motif Consensus sequence: DCAGCCAATVR

Reverse complement motif Consensus sequence: MBATTGGCTGH



Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 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: 0.0781129

Alignment:

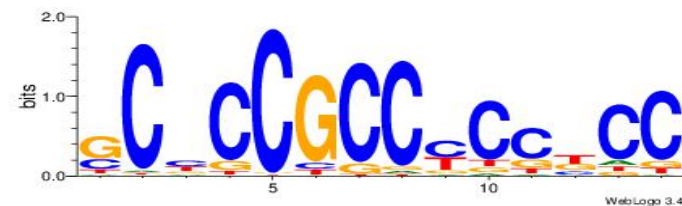
GCVCCGCCMCCYCC

---GCGCSAAA---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 3

Motif ID: 23
 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: 0.0784105

Alignment:

YCGCCCACGCH

GCGCSAAA---

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



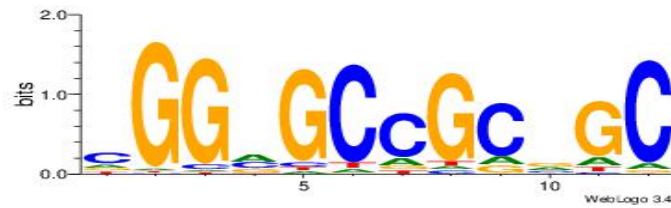
Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0798986

Alignment:

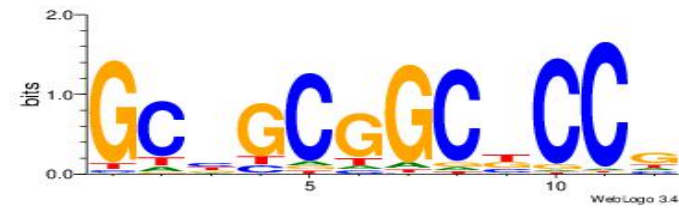
CGGVGCCGCVGC

--GCGCSAAA--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0836188

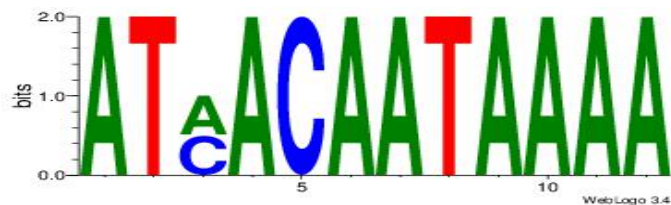
Alignment:

ATMACAATAAAA

-GCGCSAAA---

Original motif Consensus sequence: ATMACAATAAAA

Reverse complement motif Consensus sequence: TTTTATTGTAT



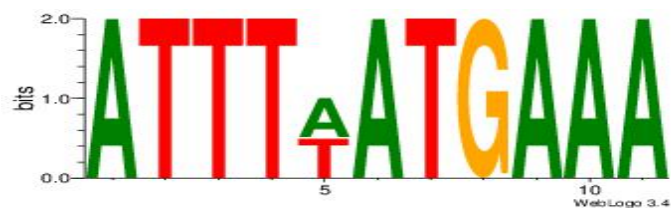
Dataset #: 2
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0836188

Alignment:

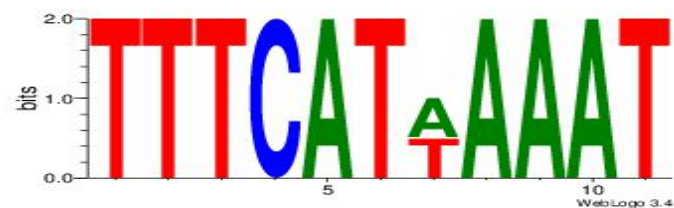
ATTTWATGAAA

-TTTSGCGC--

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTTCATWAAAT



Dataset #: 5
 Motif ID: 56

Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	19
Number of overlap:	7
Similarity score:	0.569963

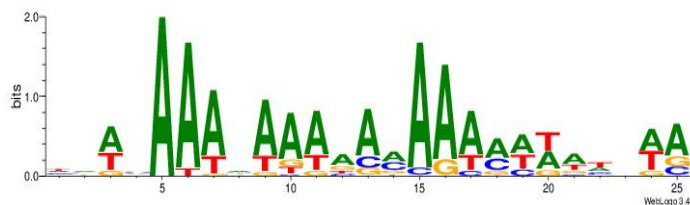
Alignment:

```

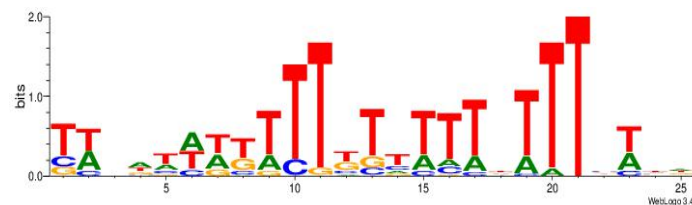
-HDWVAAAHAAAAAAMAAAMWWWHBWA
GCGCSAAA-----

```

Original motif Consensus sequence:
HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH



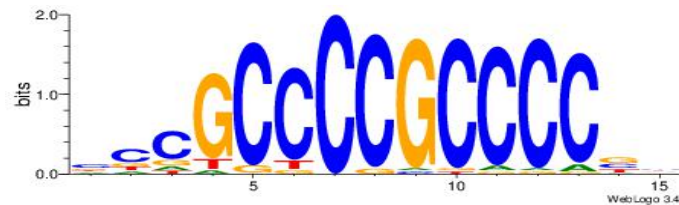
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	7
Similarity score:	0.571005

Alignment:

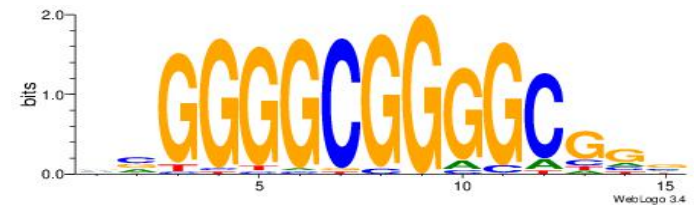
-BBGGGGCGGGGCGGB

TTTSGCGC-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.571119

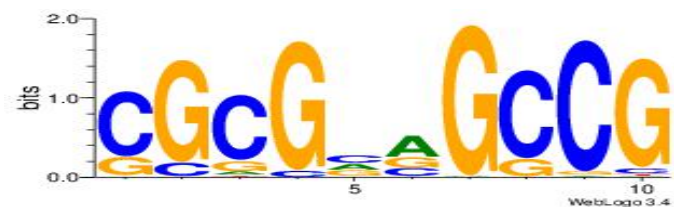
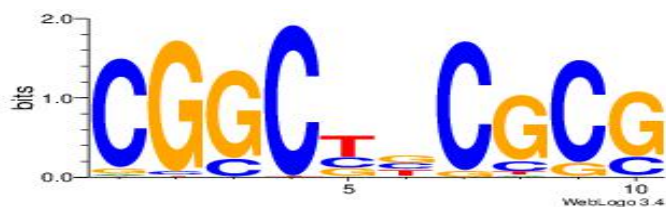
Alignment:

CGGCYBCGCG-

---TTTSGCGC

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG



Dataset #: 3 Motif ID: 29 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Best Matches for Motif ID 29 (Highest to Lowest)

Dataset #:	3
Motif ID:	33
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:	8
Similarity score:	0.0123101

Alignment:

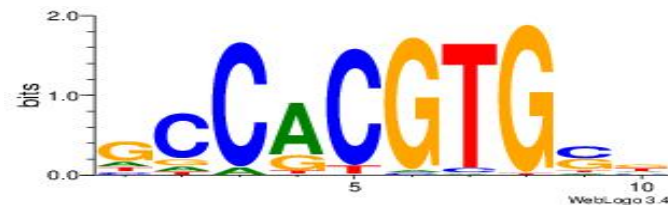
GCCACGTGSD

-VBACGTGV-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 3
Motif ID: 34
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: 8
Similarity score: 0.0144491

Alignment:

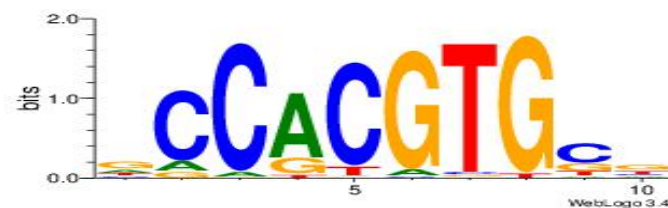
DCCACGTGCV

-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0295473

Alignment:

GBTGCAGGTGB
 ---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

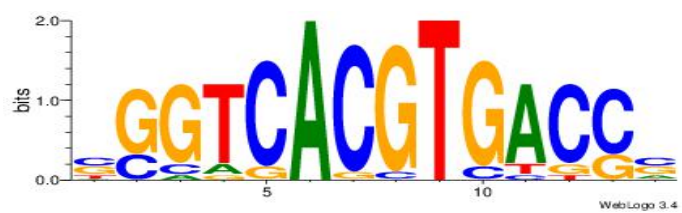


Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACsS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8

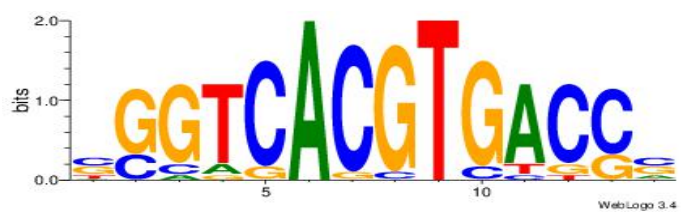
Similarity score: 0.0314837

Alignment:
SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 3
Motif ID: 26
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: 0.0377204

Alignment:
GCGGACGTTV
--VCACGTBV

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

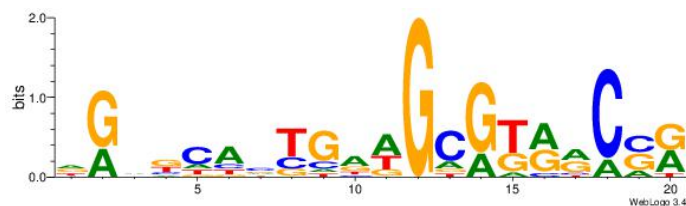


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 8
 Similarity score: 0.0556891

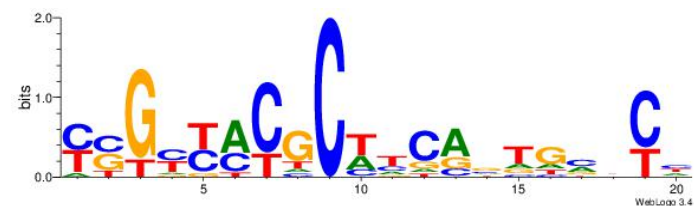
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----VCACGTBV-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 4

Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0640024

Alignment:
 DHACATTCTGH
 VCACGTBV---

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 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: 0.0648153

Alignment:

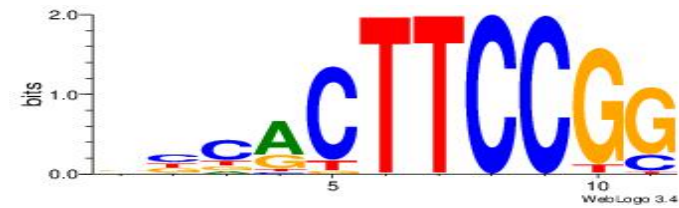
CCGGAAGTGVV

--VCACGTBV--

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACCTCCGG



Dataset #:	5
Motif ID:	47
Motif name:	TFW2
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:	0.0660185

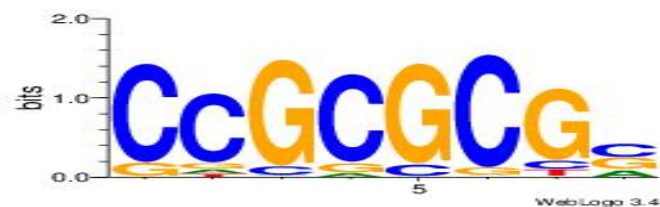
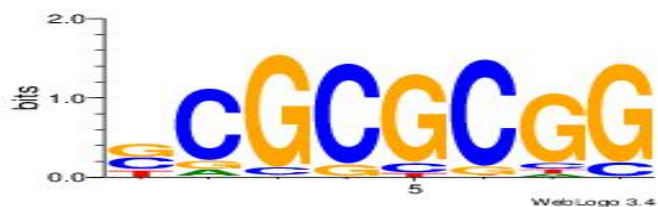
Alignment:

CCGCGCGS

VBACGTGV

Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS



Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.067219

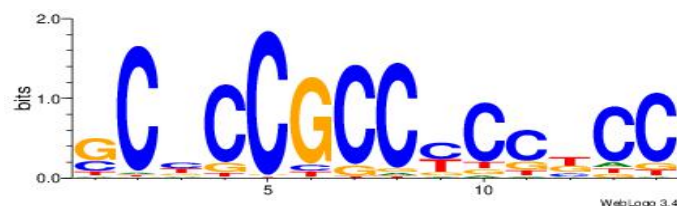
Alignment:

GCVCCGCCMCCYCC
 -----VCACGTBV

Original motif Consensus sequence: GGMGGRGGCGGVGC

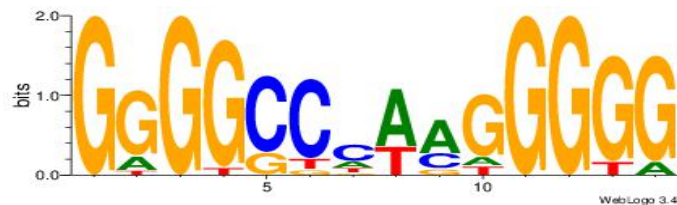


Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

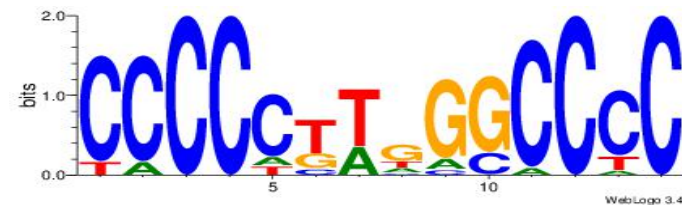


Dataset #: 3 Motif ID: 30 Motif name: PLAG1

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



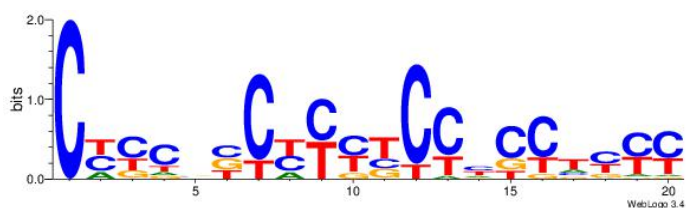
Best Matches for Motif ID 30 (Highest to Lowest)

Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	14
Similarity score:	0.0876918

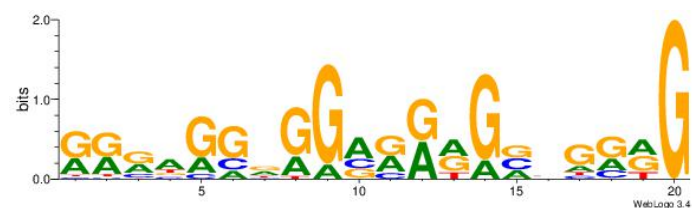
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
-CCCCCTTGGGCCCC-----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

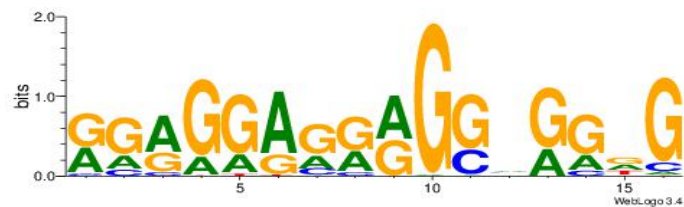


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0880716

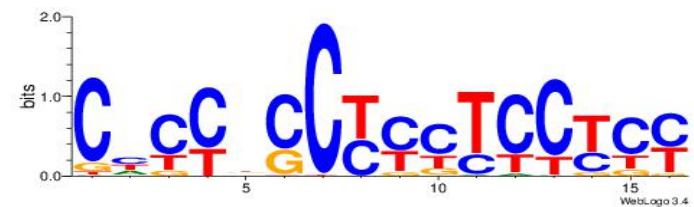
Alignment:

CHCCBCKMCTCCKCM
 --CCCCCTTGGGCCCC

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

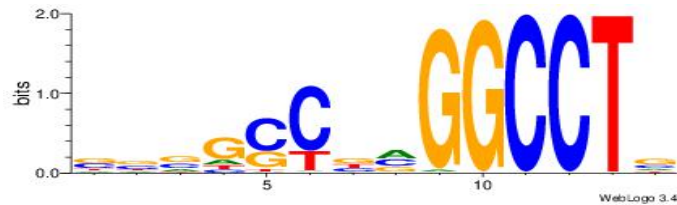


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

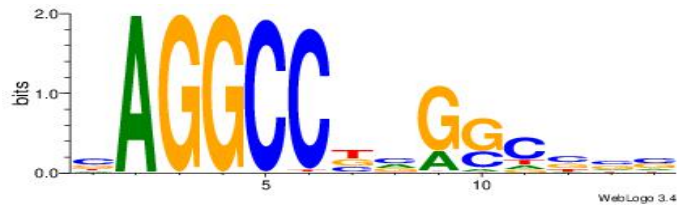
Number of overlap: 14
Similarity score: 0.0886295

Alignment:
VAGGCCBBGGCVBB
GGGGCCCAAGGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

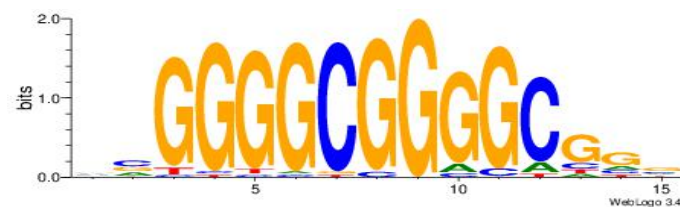
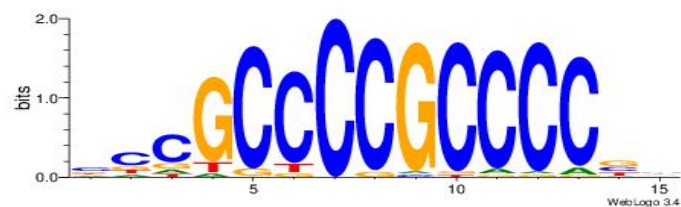


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0904945

Alignment:
BCCGCCCCGCCCCBB
CCCCCTTGGGCCCC-

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

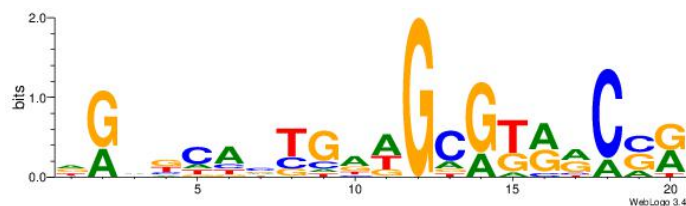


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0943783

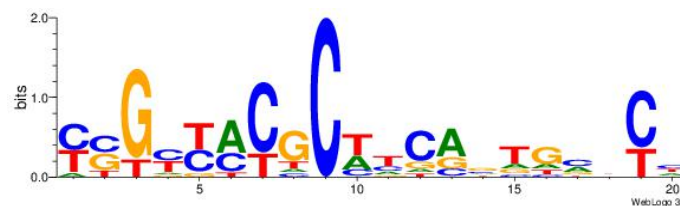
Alignment:

DGVBCABTGDWGCGRRCR
 GGGGCCCAAGGGG-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 2

Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.588053

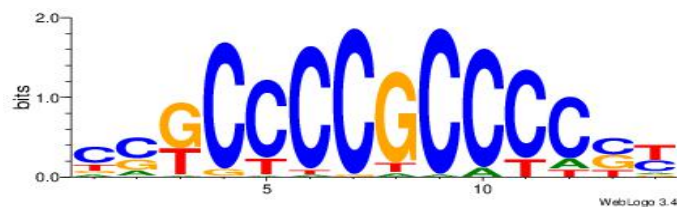
Alignment:

```

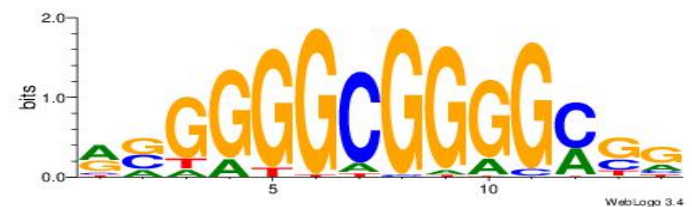
-MSGGGGCGGGGYSG
GGGGCCCAAGGGG-

```

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #:	5
Motif ID:	50
Motif name:	TFF11
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:	0.589357

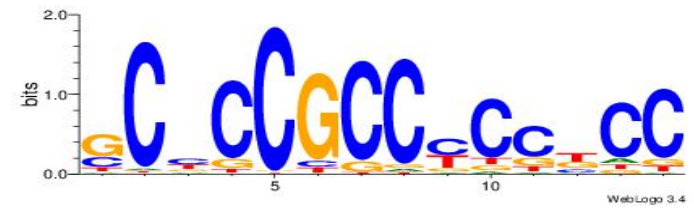
Alignment:

GCVCCGCCMCCYCC-
-CCCCCTTGGGCCCC

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



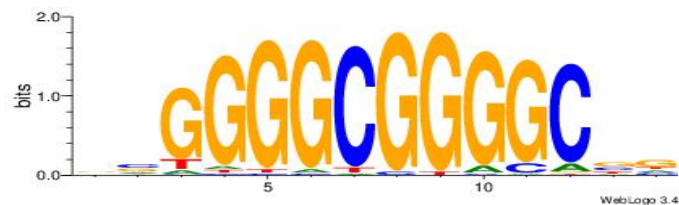
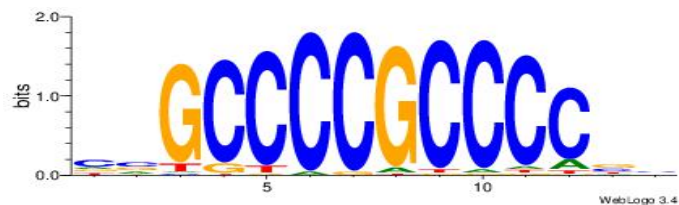
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.595227

Alignment:

-HVGCCCCGCCCCBB
CCCCCTTGGGCCCC-

Original motif Consensus sequence: HVGCCCCGCCCCBB

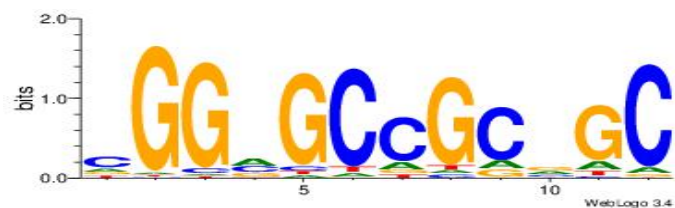
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



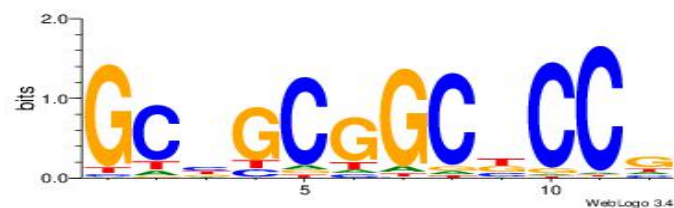
Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.09276

Alignment:
 CGGVGCCGCVGC--
 GGGGCCCAAGGGGG

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



Dataset #: 3
 Motif ID: 24

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:	2.07807

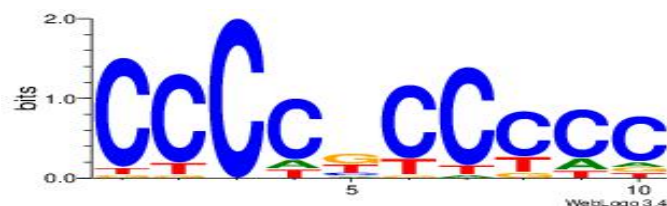
Alignment:

```

-----GGGGGYGGGG
GGGGCCCAAGGGGG

```

Original motif Consensus sequence: CCCCKCCCCC

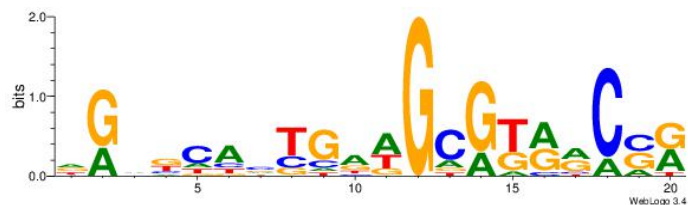


Reverse complement motif Consensus sequence: GGGGGYGGGG

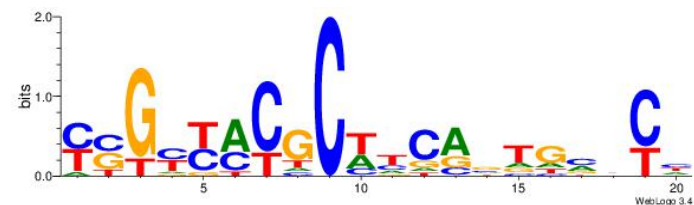


Dataset #: 3 Motif ID: 31 Motif name: Pax5

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBBCD



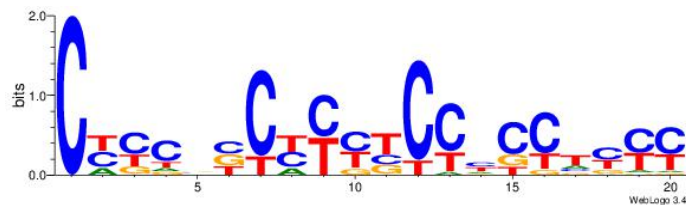
Best Matches for Motif ID 31 (Highest to Lowest)

Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.0373929

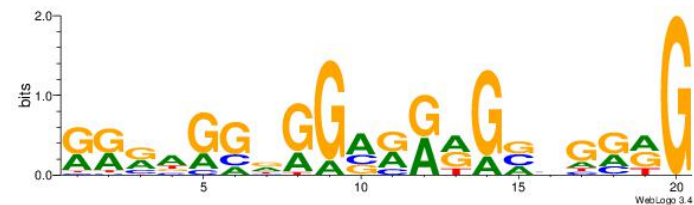
Alignment:

KKKAGGDGGAKKMGBBGKMG
DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

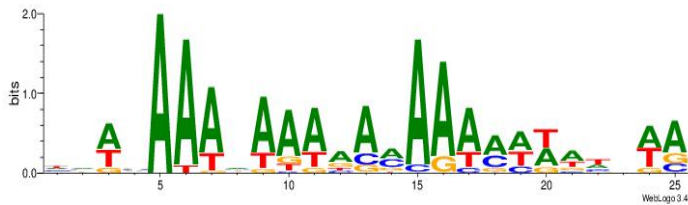


Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

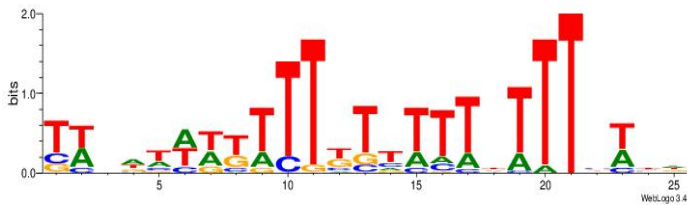
Direction: Backward
Position number: 6
Number of overlap: 20
Similarity score: 0.0546306

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
DGVBCABTGDWGCGRRCR-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



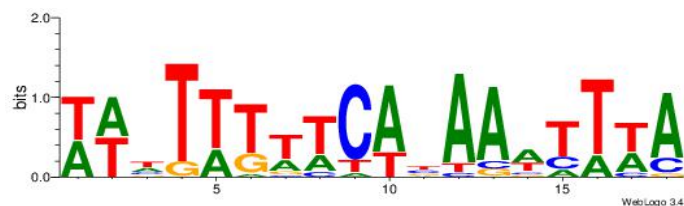
Reverse complement motif Consensus sequence:
TWVHWWYTTTTTTTTTHTTTVWBH



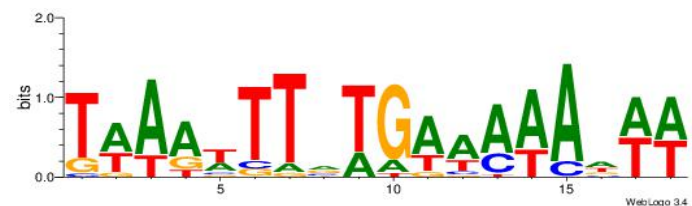
Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 1.5457

Alignment:
TWAAWTTVTGAAAAHWW---
-DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

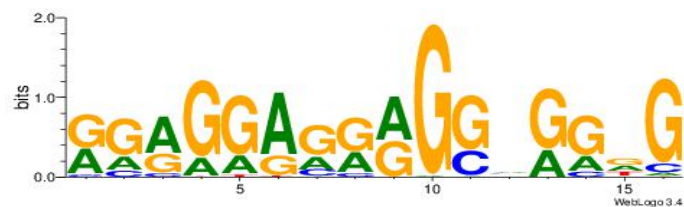


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 2.0519

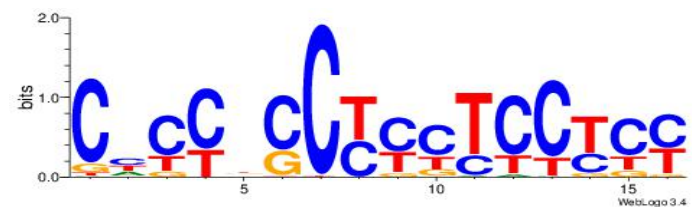
Alignment:

RGRGGAGRRGGHGGDG-----
 MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

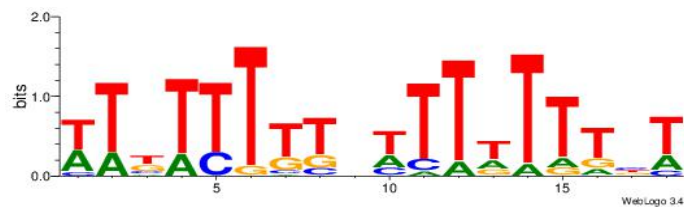


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 2.05456

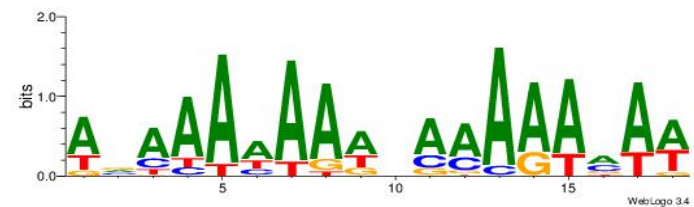
Alignment:

ABAAAAAWhAAAAARAW----
 --DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW



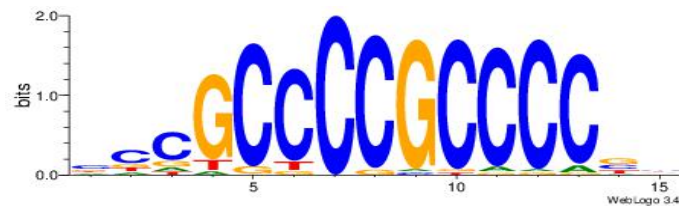
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 15
Similarity score: 2.54483

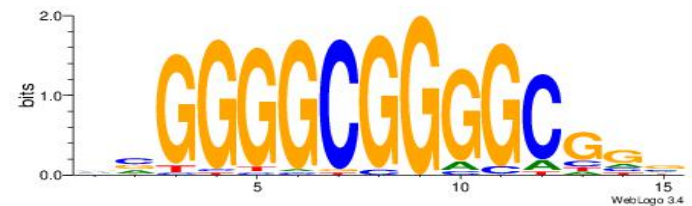
Alignment:

BBGGGGCGGGGCGGB-----
MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

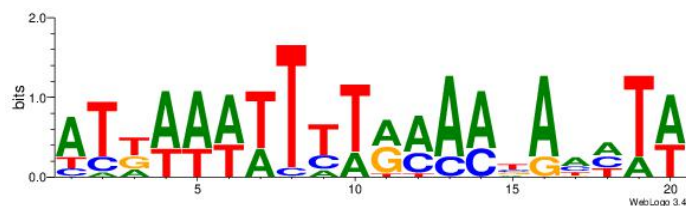


Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 15
Similarity score: 2.55478

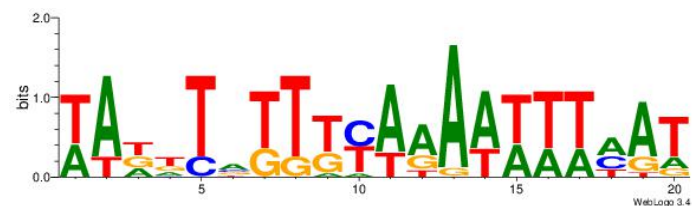
Alignment:

WAHHTVTTYKAAAWTTRAT-----
-----MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

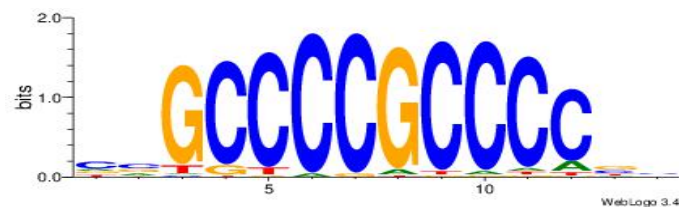


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 3.0203

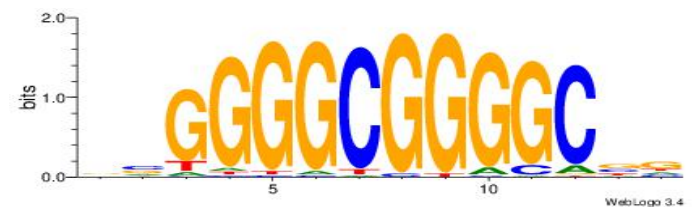
Alignment:

-----BBGGGGCGGGGCVD
 DGVBCABTGDWCGKRRCSR

Original motif Consensus sequence: HVGCCCCGCCCCBB



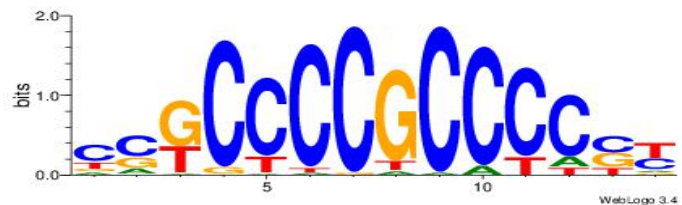
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



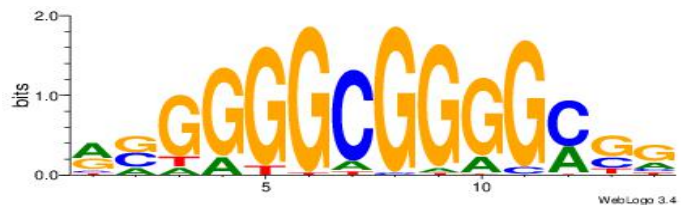
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 3.02361

Alignment:
-----CSKCCCCGCCCSY
MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGCGGGGY

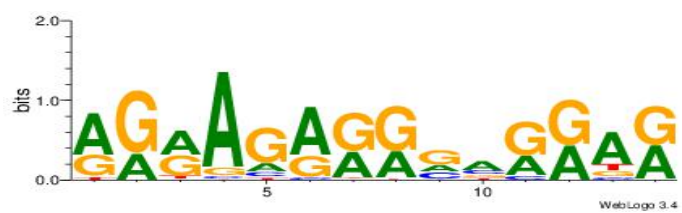


Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14

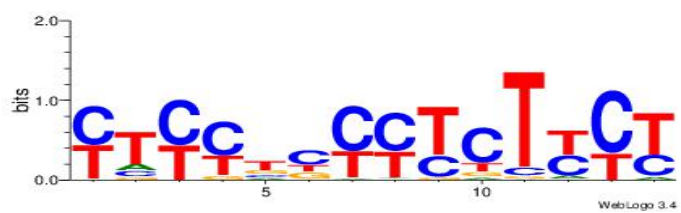
Similarity score: 3.02394

Alignment:
-----MTMMTCMMTCTKCK
MSGKKRRCGCWDCABTGBCD

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



Dataset #: 3 Motif ID: 32 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Best Matches for Motif ID 32 (Highest to Lowest)

Dataset #:	3
Motif ID:	23
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 #: 3
Motif ID: 29
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: 0.0112447

Alignment:
VBACGTGV
-YGCGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV



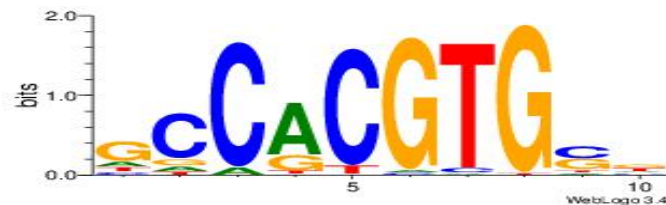
Dataset #: 3
 Motif ID: 33
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0377949

Alignment:
 GCCACGTGSD
 --YGCGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

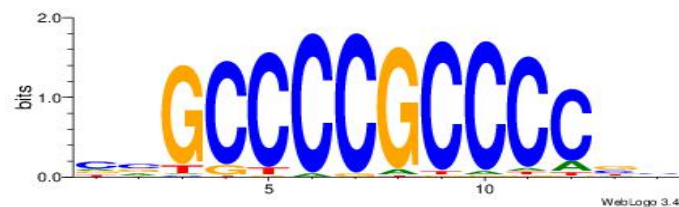


Dataset #: 4

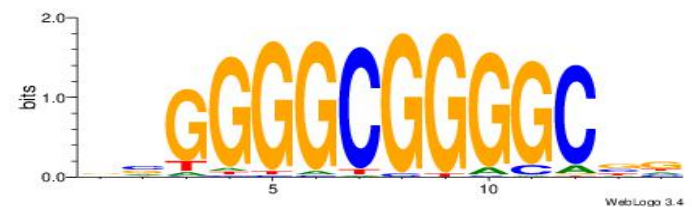
Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0396403

Alignment:
 HVGCCCCGCCCCBB
 ----CACGCM----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



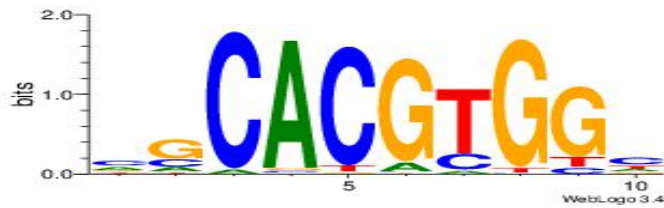
Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0399214

Alignment:

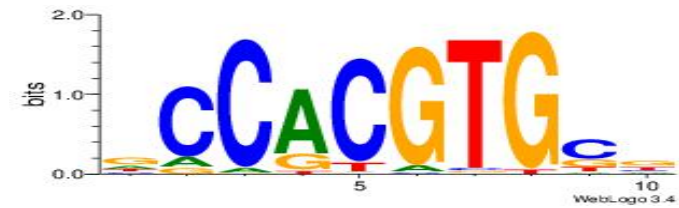
DCCACGTGCV

--YGCGTG--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
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:	0.040625

Alignment:

GCCCCGCC

--CACGCM

Original motif Consensus sequence: GGCGGGGC

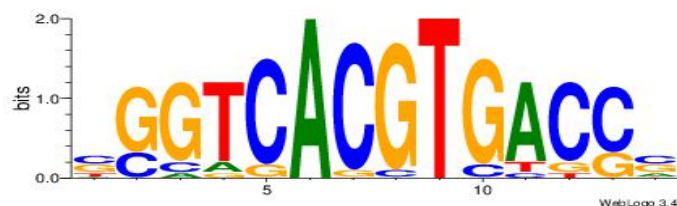
Reverse complement motif Consensus sequence: GCCCCGCC



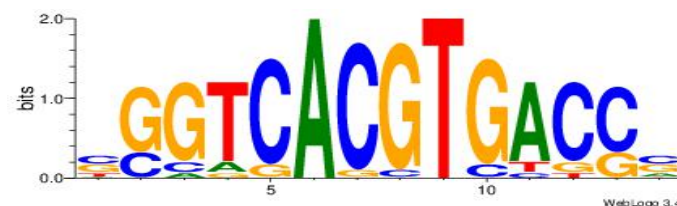
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0412037

Alignment:
 SGGTCACGTGACCS
 ----YGCGTG----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 4
 Motif ID: 38

Motif name:	cccGCCCCGCCCCsb
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:	0.0425089

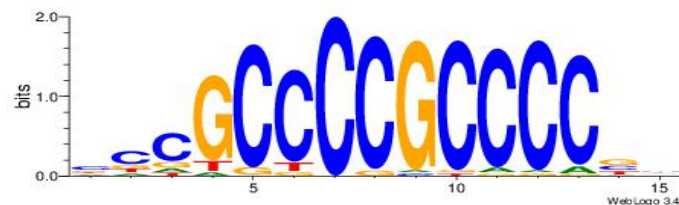
Alignment:

```

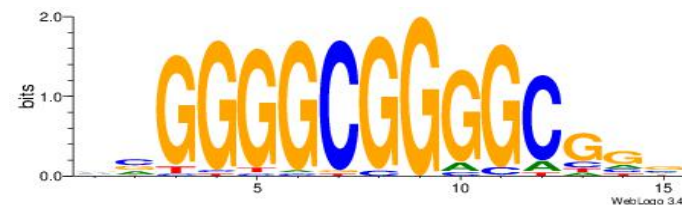
BCCGCCCCGCCCCBB
-----CACGCM-----

```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGCGGB



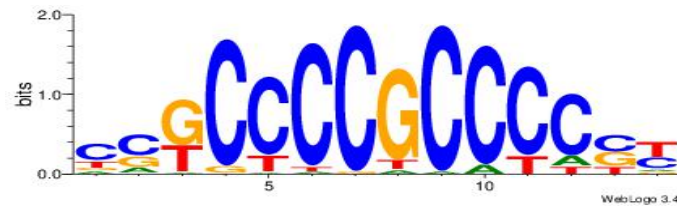
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0465867

Alignment:

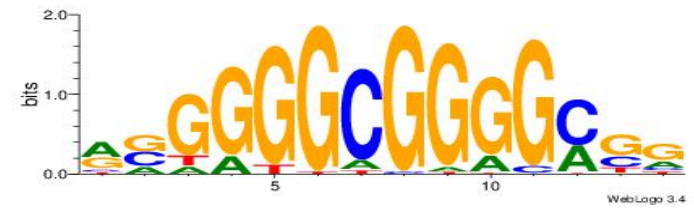
MSGGGGCGGGYSG

-----YGCGTG-----

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY



Dataset #:	5
Motif ID:	47
Motif name:	TFW2
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:	0.0469722

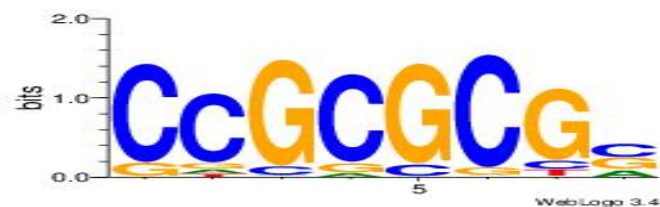
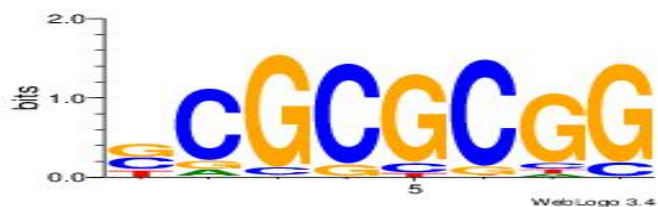
Alignment:

SCGCGCGG

-YGCGTG-

Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS



Dataset #: 3 Motif ID: 33 Motif name: Mycn

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Best Matches for Motif ID 33 (Highest to Lowest)

Dataset #:	3
Motif ID:	34
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



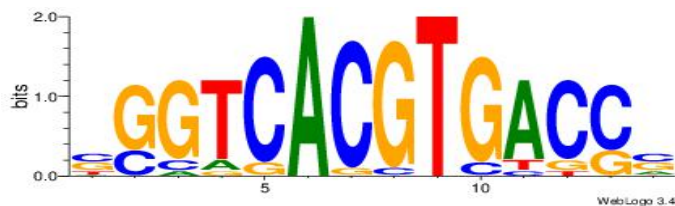
Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSS
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0628441

Alignment:

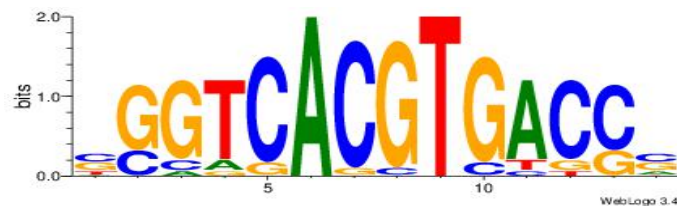
SGGTCACGTGACCS

--GCCACGTGSD--

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 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: 0.0884396

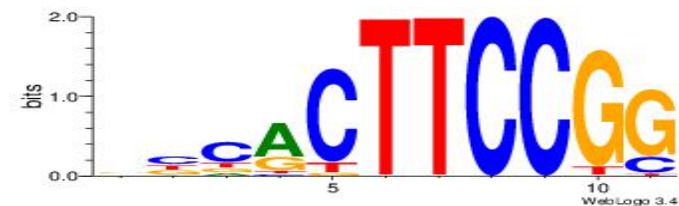
Alignment:

VVCACTTCCGG
 GCCACGTGSD-

Original motif Consensus sequence: CCGGAAGTVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



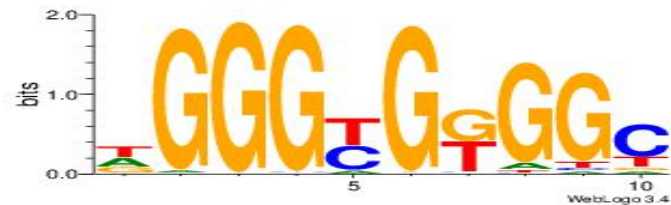
Dataset #: 3
 Motif ID: 27
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0893272

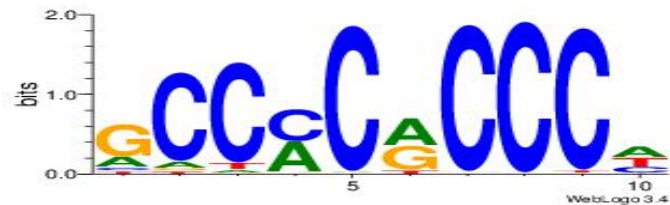
Alignment:

DGGGYGKGGC
HSCACGTGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



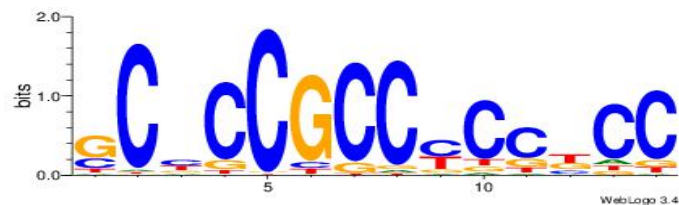
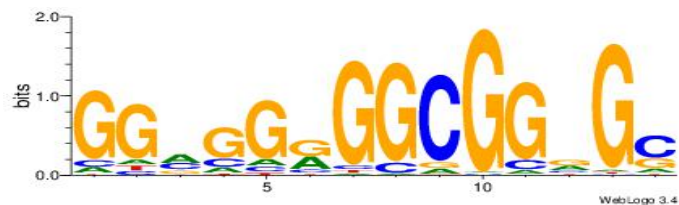
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0895444

Alignment:

GGMGGRGGCGGVGC
--HSCACGTGGC--

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

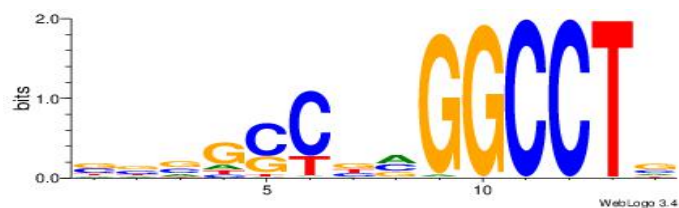


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0899944

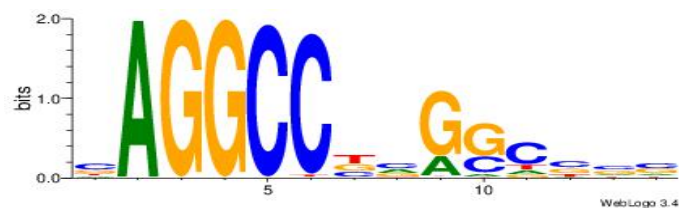
Alignment:

VAGGCCBBGGCVBB
 ---GCCACGTGSD-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Dataset #: 3
 Motif ID: 30

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

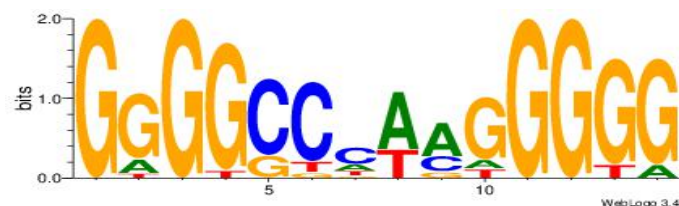
Alignment:

```

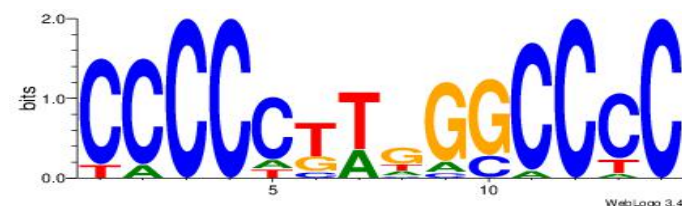
CCCCCTTGGGCCCC
----HSCACGTGGC

```

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC



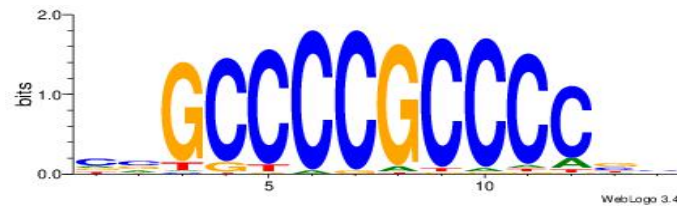
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.093472

Alignment:

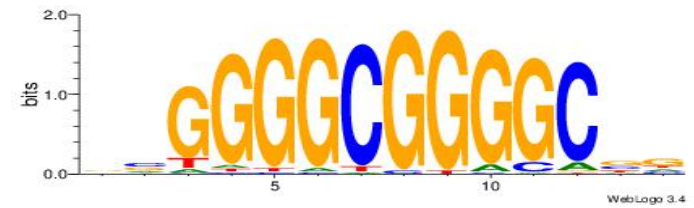
HVGCCCGCCCCBB

--GCCACGTGSD--

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC



Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0964516

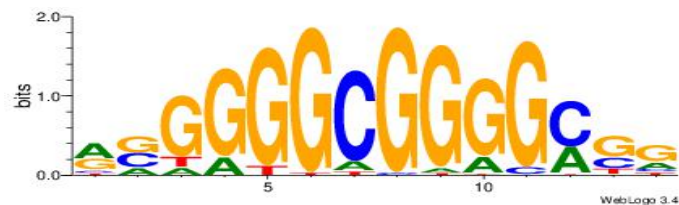
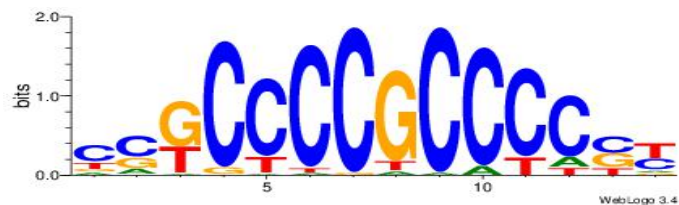
Alignment:

MSGGGGCGGGYSG

--HSCACGTGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY

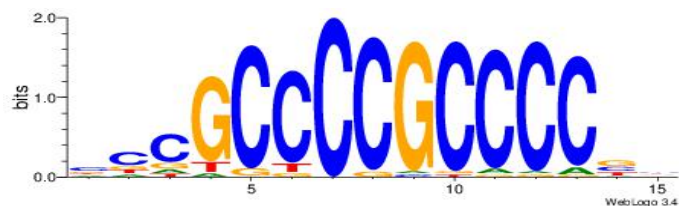
Reverse complement motif Consensus sequence: MSGGGGCGGGY



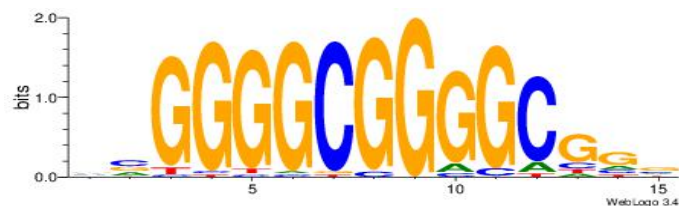
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0979367

Alignment:
 BCCGCCCCGCCCCBB
 ---GCCACGTGSD--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Dataset #: 3 Motif ID: 34 Motif name: Myc

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Best Matches for Motif ID 34 (Highest to Lowest)

Dataset #:	3
Motif ID:	33
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

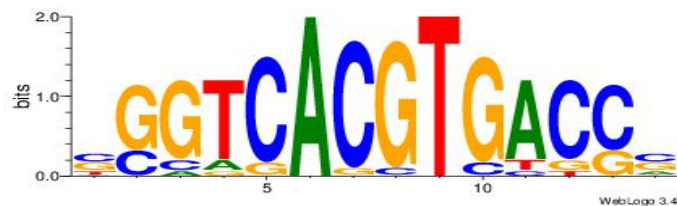


Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0646601

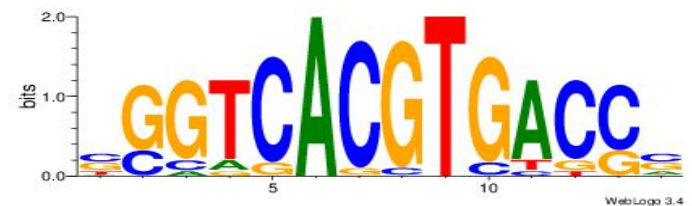
Alignment:

SGGTCACGTGACCS
 --DCCACGTGCV--

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



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

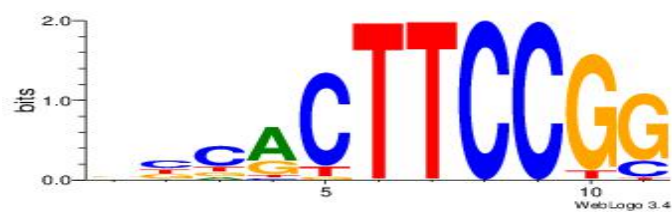
Similarity score: 0.0840341

Alignment:
VVCAC TTCCGG
DCCACGTGCV-

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCAC TTCCGG

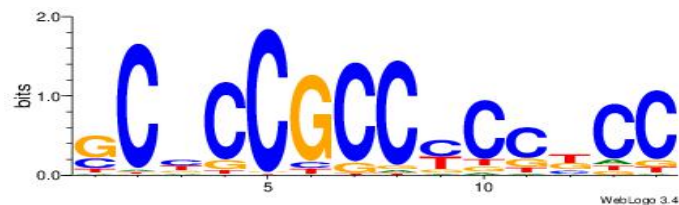
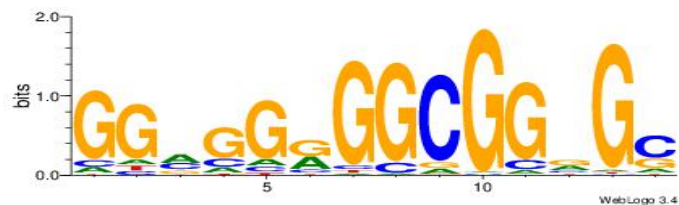


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0851555

Alignment:
GGMGGRGGCGGVGC
--VGCACGTGGH--

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



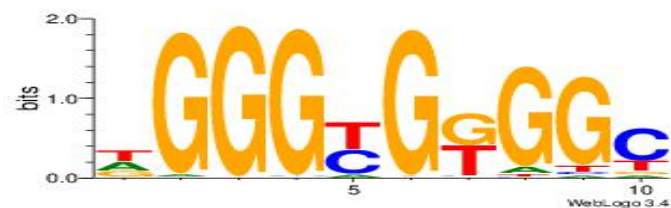
Dataset #: 3
 Motif ID: 27
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0883745

Alignment:

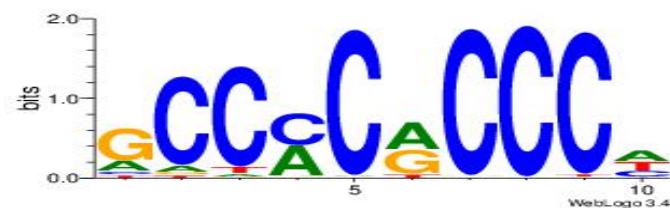
DGGGYGKGGC

VGCACGTGGH

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



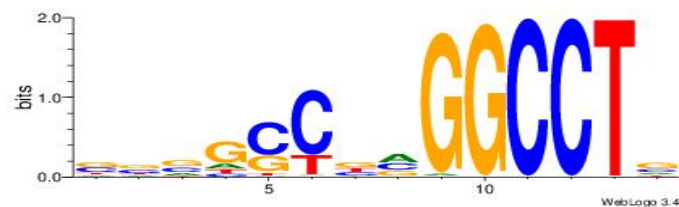
Dataset #: 3
 Motif ID: 22

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

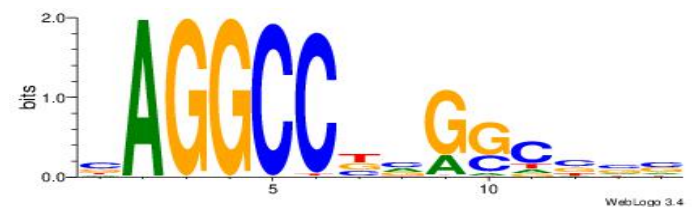
Alignment:

VAGGCCBBGGCVBB
 ---DCCACGTGCV-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



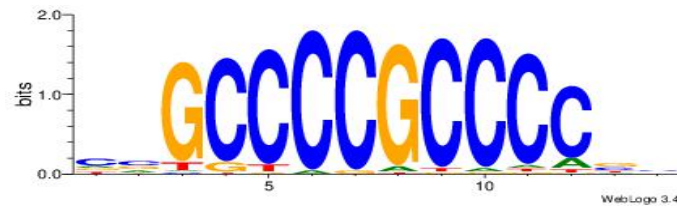
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0928504

Alignment:

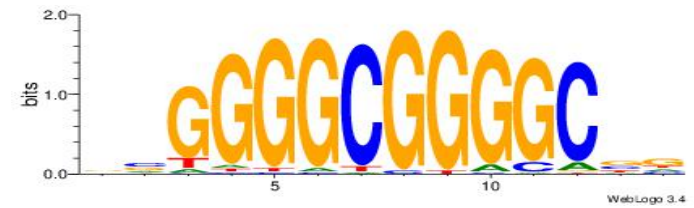
HVGCCCGCCCCBB

--DCCACGTGCV--

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC



Dataset #:	3
Motif ID:	30
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

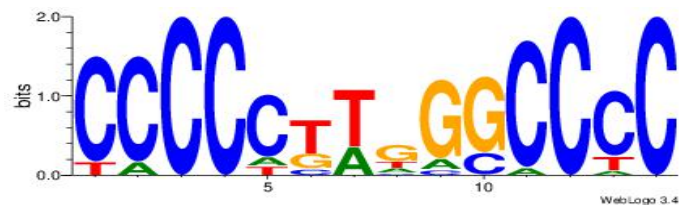
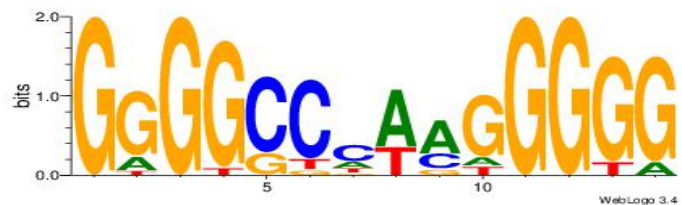
Alignment:

CCCCCTTGGGCCCC

----VGCACGTGGH

Original motif Consensus sequence: GGGGCCCAAGGGG

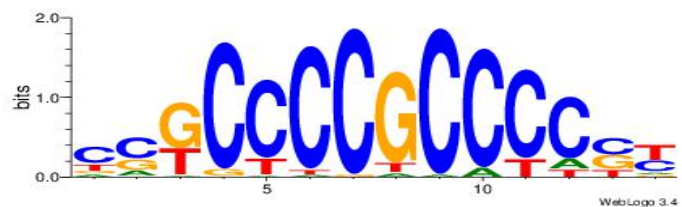
Reverse complement motif Consensus sequence: CCCCCTTGGGCC



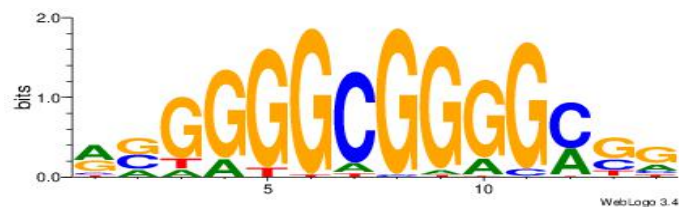
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0941376

Alignment:
 MSGGGGCGGGYSG
 --VGCACGTGGH--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY



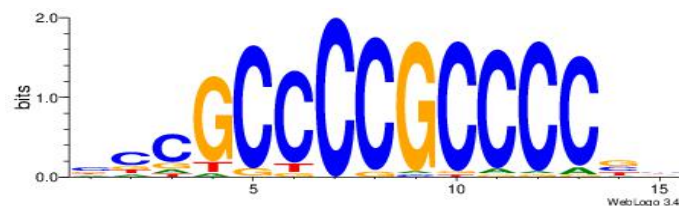
Dataset #: 4
 Motif ID: 38

Motif name: cccGCCCCGCCCCsb
 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: 0.0974172

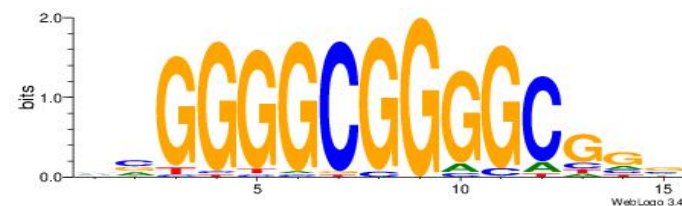
Alignment:

BCCGCCCCGCCCCBB
 ---DCCACGTGCV--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

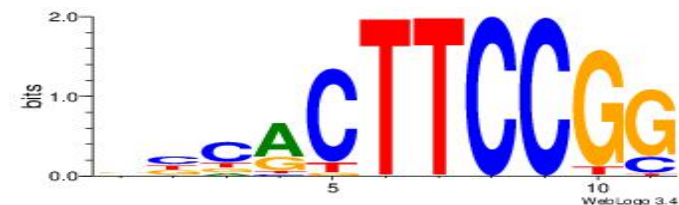


Dataset #: 3 Motif ID: 35 Motif name: GABPA

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCGG



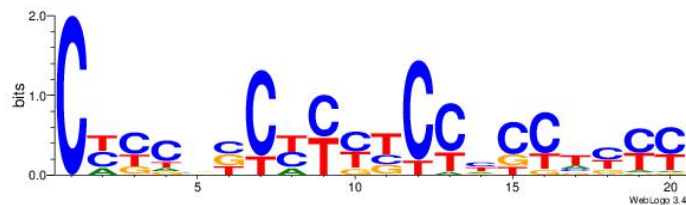
Best Matches for Motif ID 35 (Highest to Lowest)

Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0360984

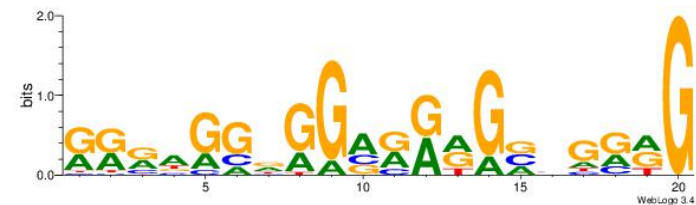
Alignment:

```
CYYCBBCYYYTCCHCCTYYY  
-----VVCACTTCCGG-----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

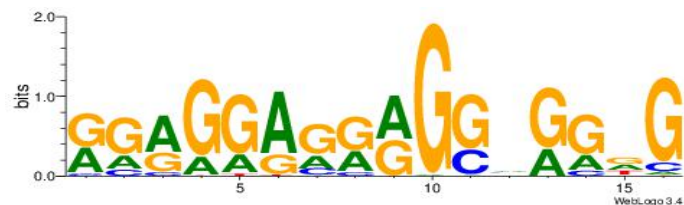


Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

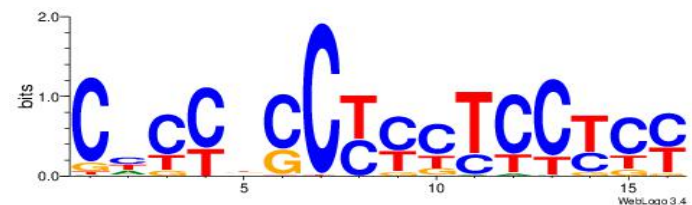
Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0445566

Alignment:
 RGRGGAGRRGGHGGDG
 -CCGGAAGTGVV-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



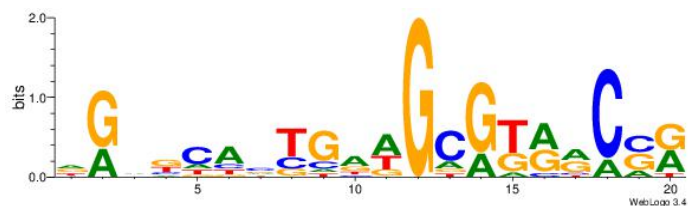
Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



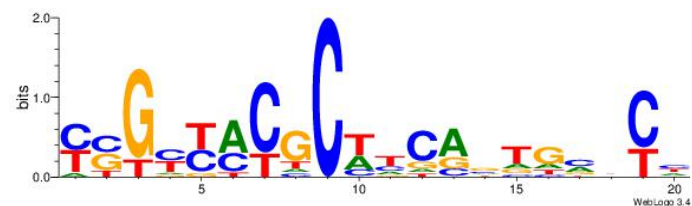
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0446257

Alignment:
 DGVBCABTGDWCGKRRCSR
 -----VVCACTTCCGG--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD



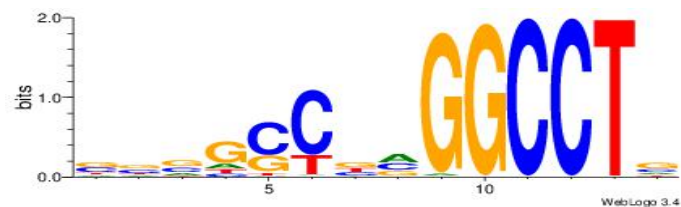
Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0457327

Alignment:

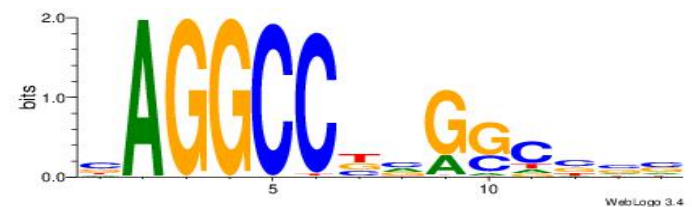
BBVGCCBVGGCCTV

VVCACTTCCGG---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



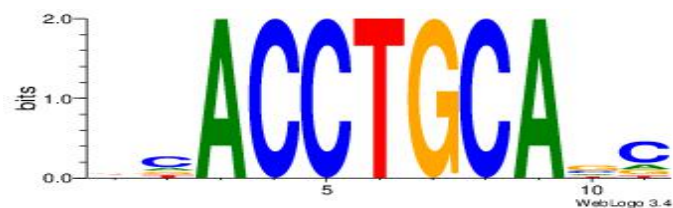
Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0483841

Alignment:

BCACCTGCABC

VVCACTTCCGG

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 4
 Motif ID: 45
 Motif name: wbgTAAATAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11

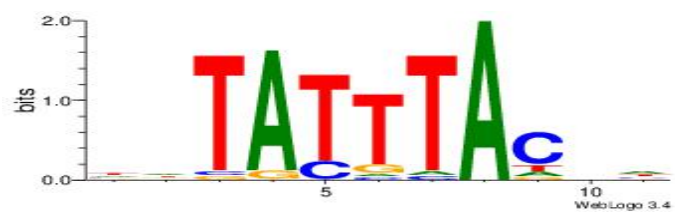
Similarity score: 0.0492127

Alignment:
DBGTAAATAHD
CCGGAAGTGVV

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD

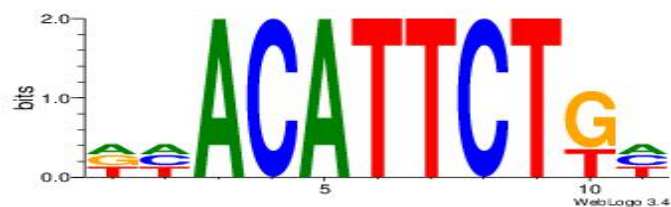


Dataset #: 4
Motif ID: 44
Motif name: dhACATTCTkh
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0495154

Alignment:
DHACATTCTGH
VVCACTTCCGG

Original motif Consensus sequence: DHACATTCTGH

Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0504656

Alignment:

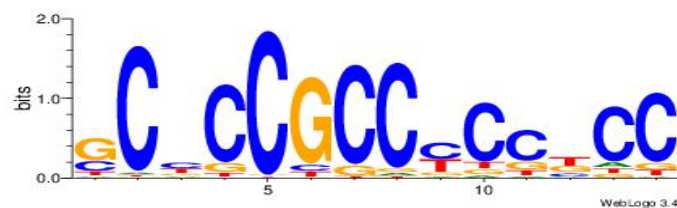
GGMGGRGGCGGVGC

-CCGGAAGTGVV--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 2
 Motif ID: 6

Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0518418

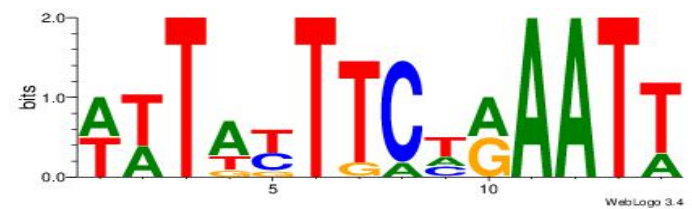
Alignment:

```
AATTYDGAARTAWW
---CCGGAAGTGVV
```

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



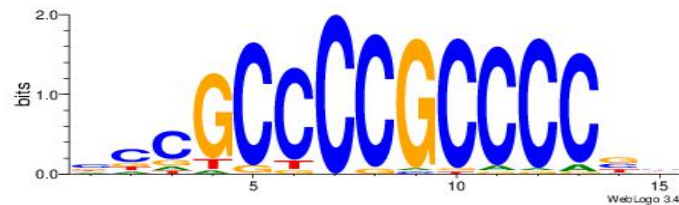
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0554249

Alignment:

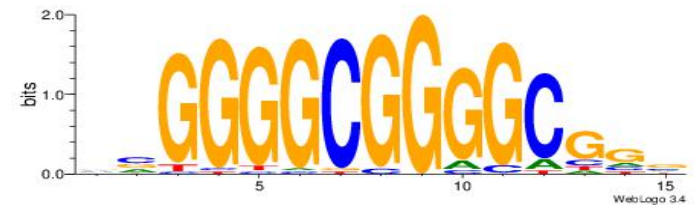
BCCGCCCCGCCCCBB

---VVCACTTCCGG-

Original motif Consensus sequence: BCCGCCCCGCCCCBB

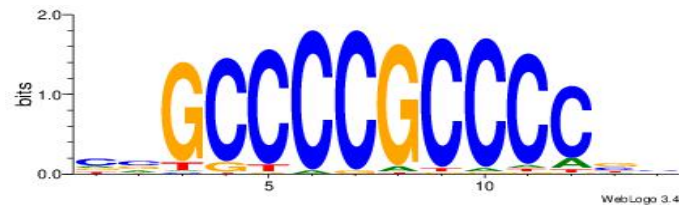


Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

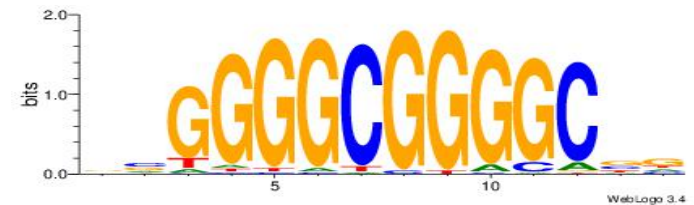


Dataset #: 4 Motif ID: 36 Motif name: csGCCCCGCCCCsc

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Best Matches for Motif ID 36 (Highest to Lowest)

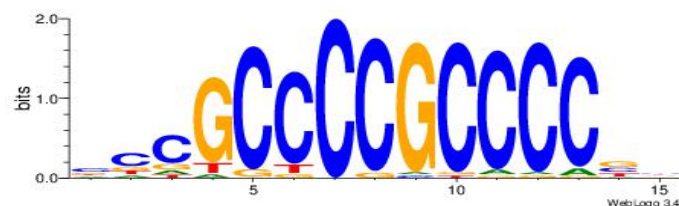
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 1
Number of overlap: 14
Similarity score: 0

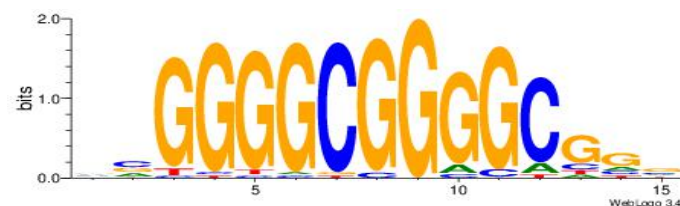
Alignment:

BCCGCCCCGCCCCBB
-HVGCCCCGCCCCBB

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

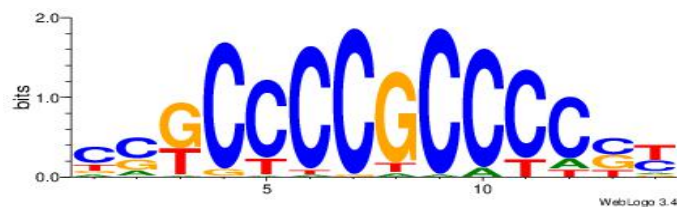


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0117332

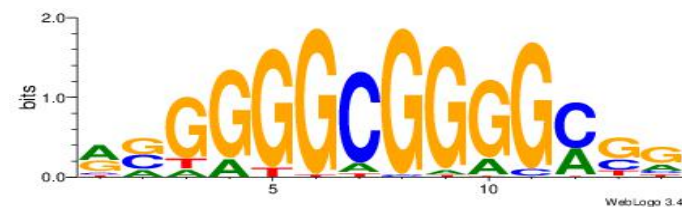
Alignment:

CSKCCCCGCCCCSY
HVGCCCCGCCCCBB

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

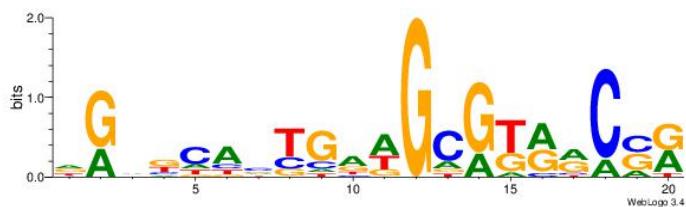


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0747029

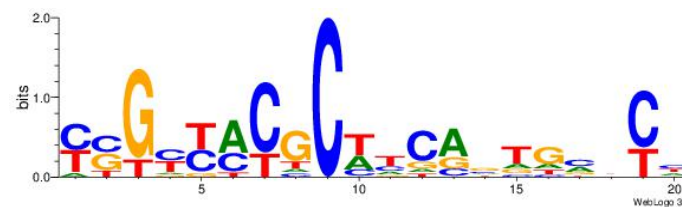
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----HVGCCCCGCCCCBB
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

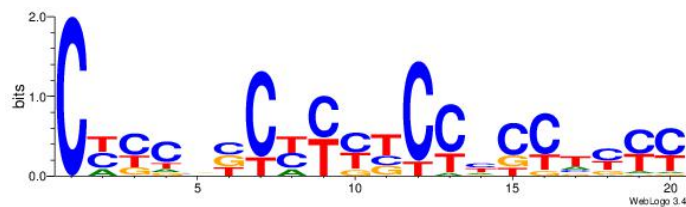


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0777991

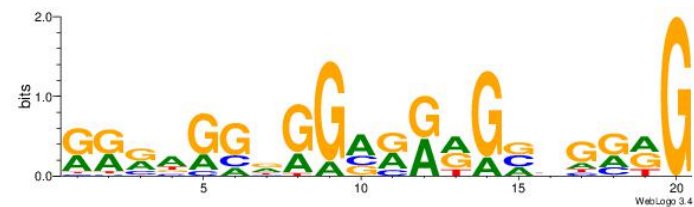
Alignment:

CYYCBBCYYYTCCHCCTYYY
 ---HVGCCCGCCCCBB---

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

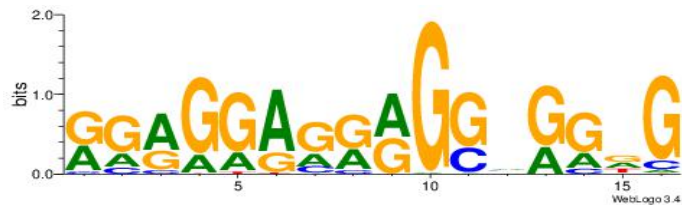


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

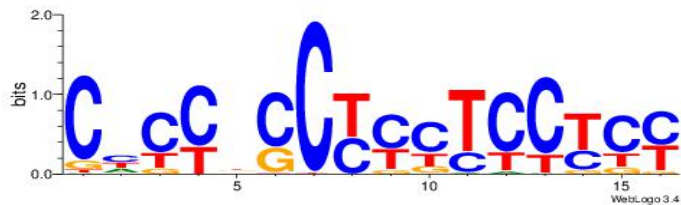
Number of overlap: 14
Similarity score: 0.0880609

Alignment:
RGRGGAGRRGGHGGDG
BBGGGGCGGGGCVD--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM

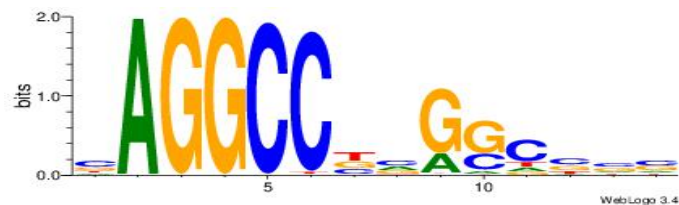
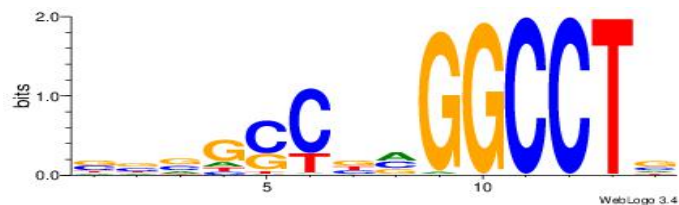


Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0884848

Alignment:
BBVGCCBVGGCCTV
BBGGGGCGGGGCVD

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 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: 0.0937271

Alignment:

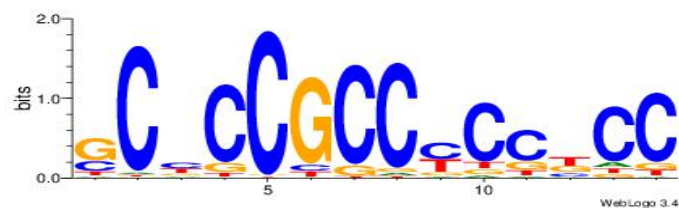
GCVCCGCCMCCYCC

HVGCCCGCCCB

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



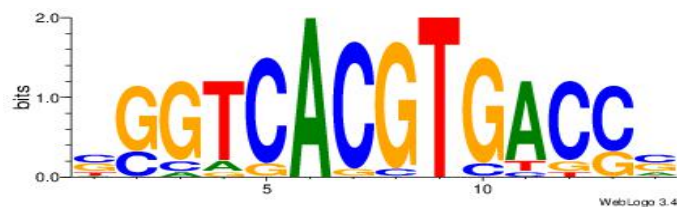
Dataset #: 4
 Motif ID: 42

Motif name:	sSGTCACGTGACSS
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0971132

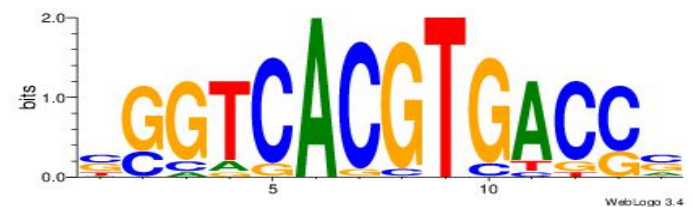
Alignment:

SGGTCACGTGACCS
HVGCCCCGCCCCBB

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

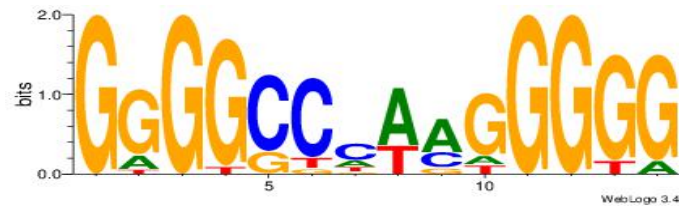


Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.609319

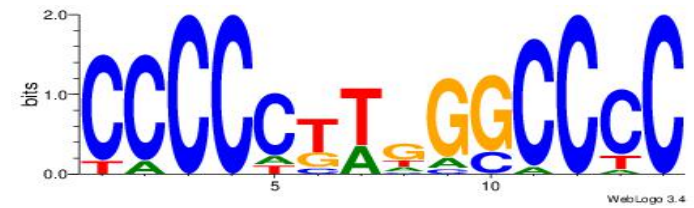
Alignment:

GGGGCCCAAGGGG-
-BBGGGGCGGGGCVD

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



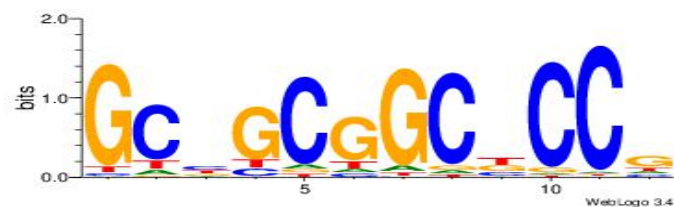
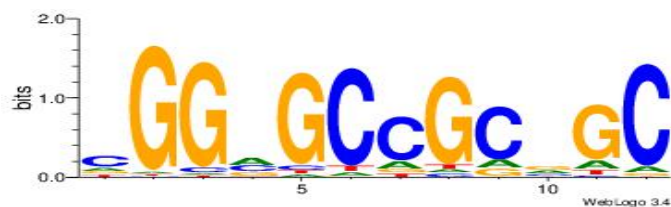
Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	1.08016

Alignment:

CGGVGCCGCVGC--
HVGCCCGCCCCBB

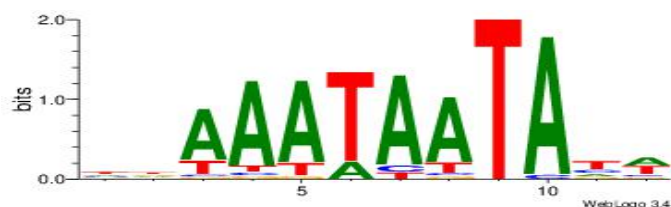
Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCGGCBCCG

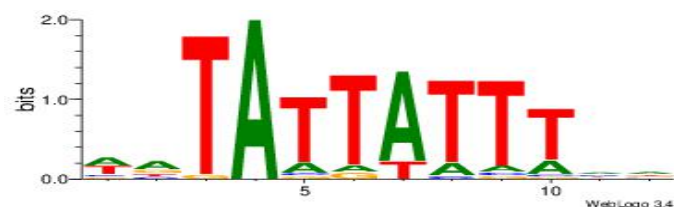


Dataset #: 4 Motif ID: 37 Motif name: tkAAATAATAtw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

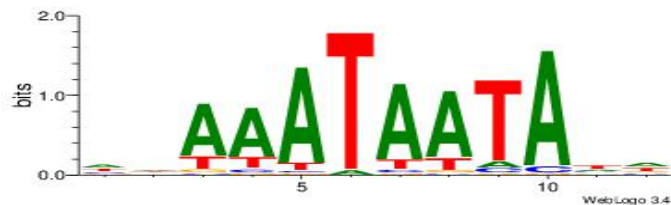


Best Matches for Motif ID 37 (Highest to Lowest)

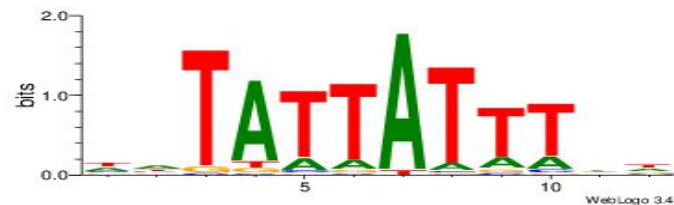
Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:
 HDAAATAATADD
 HDAAATAATAHW

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

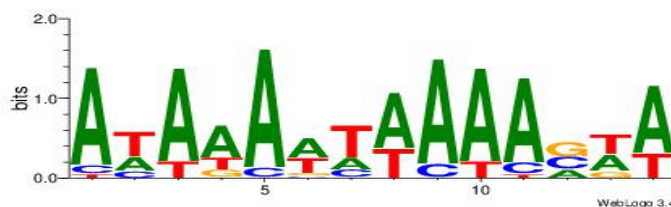


Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0522317

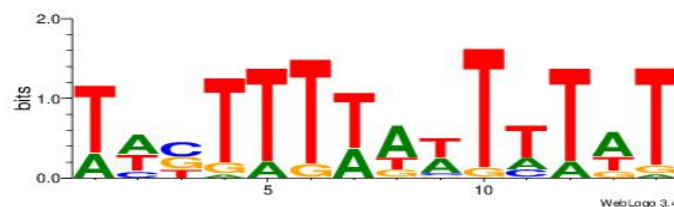
Alignment:

TWSTTTWAWTTTWT
 -WHTATTATTTDH-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV

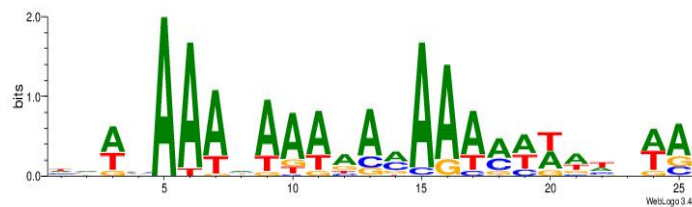


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0590505

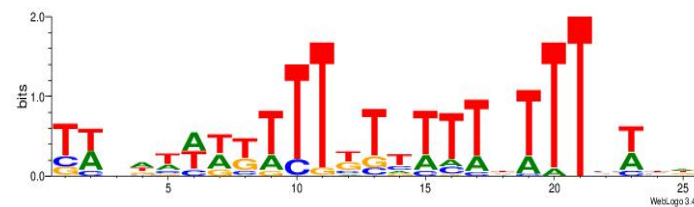
Alignment:

TWVHWWYTTTYYTTTTHTTTVWBH
 -----WHTATTATTTDH--

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYYTTTTHTTTVWBH

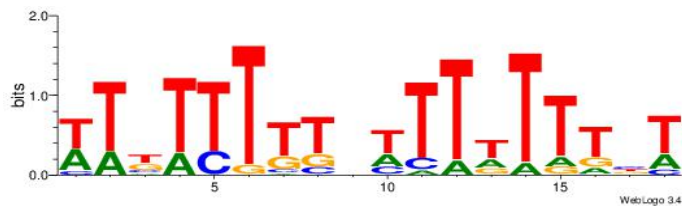


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

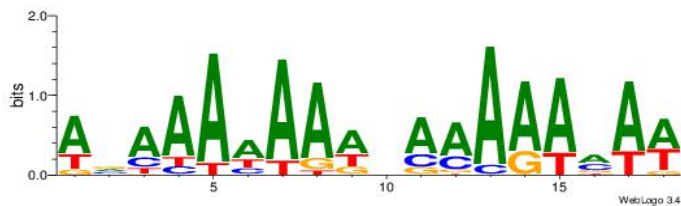
Number of overlap: 12
Similarity score: 0.0637702

Alignment:
ABAAAAAAWHAAAAARAW
HDAAATAATAHW-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW

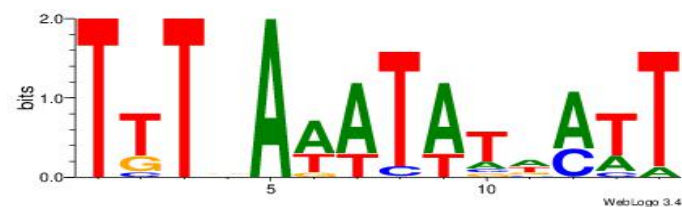
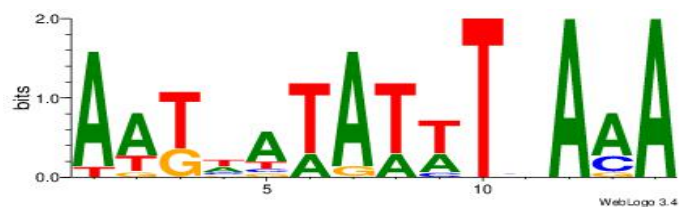


Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0641975

Alignment:
AATHATATWTHAAA
--WHTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTDAWATATHAT



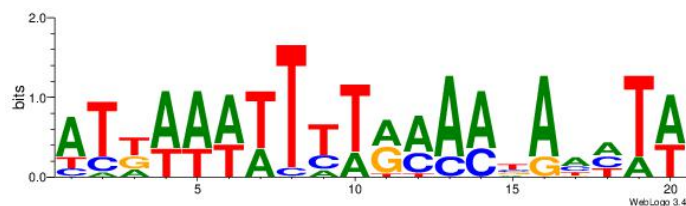
Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 12
 Similarity score: 0.0704475

Alignment:

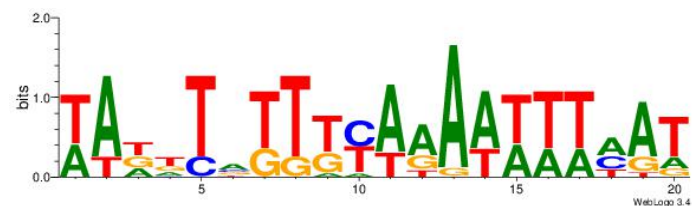
```

WAHHTVTTYKAAAATTRAT
-----HDAAATAATAHW
  
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

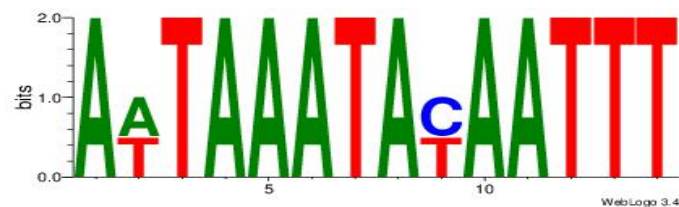


Dataset #: 2

Motif ID: 5
 Motif name: Motif 5
 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: 0.0704475

Alignment:
 AAATTKTATTTAWT
 -WHTATTATTTDH-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

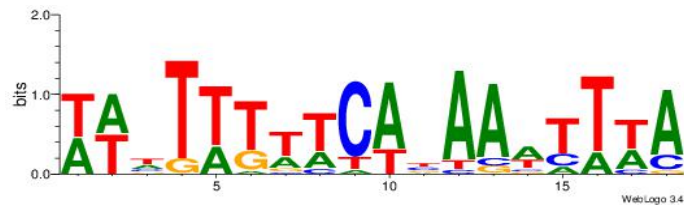


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0763819

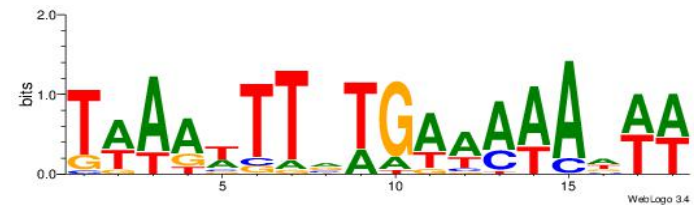
Alignment:

WWHTTTTTCABAAWTTWA
 -----WHTATTATTTDH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
 TAAWTTVTGAAAAHWW



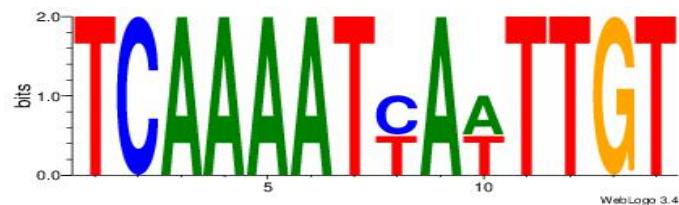
Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0864198

Alignment:

TCAAAATKAWTTGT
 --WHTATTATTTDH

Original motif Consensus sequence: ACAAWTRATTTTGA

Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.09076

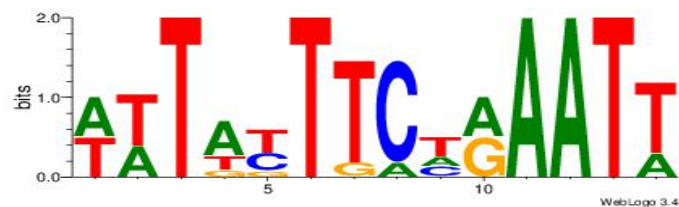
Alignment:

WWTAKTTCDKAATT
 WHTATTATTTDH--

Original motif Consensus sequence: AATTYDGAARTAWW

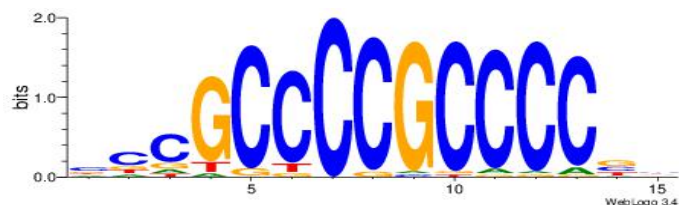


Reverse complement motif Consensus sequence: WWTAKTTCDKAATT

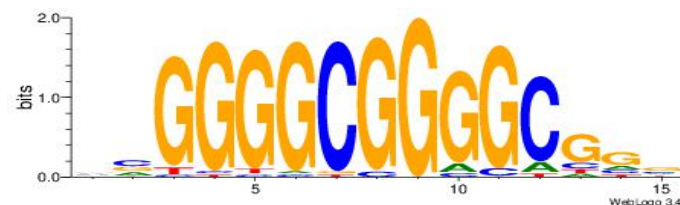


Dataset #: 4 **Motif ID: 38** **Motif name: cccGCCCCGCCCCsb**

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



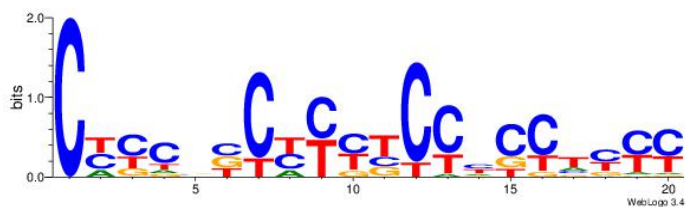
Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #:	5
Motif ID:	54
Motif name:	TFM12
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:	0.0773345

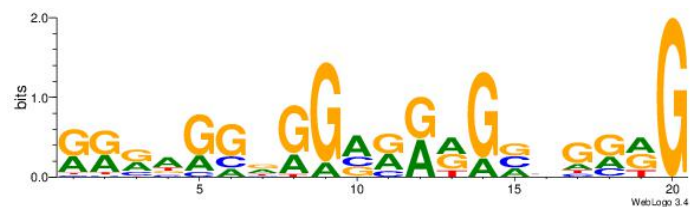
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
--BCCGCCCCGCCCCBB----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



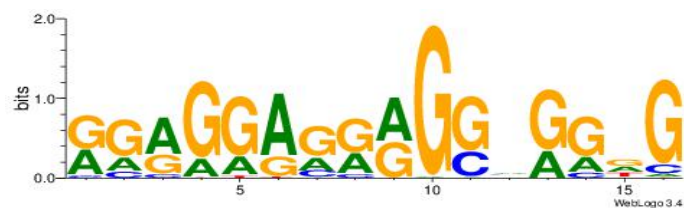
Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0869149

Alignment:

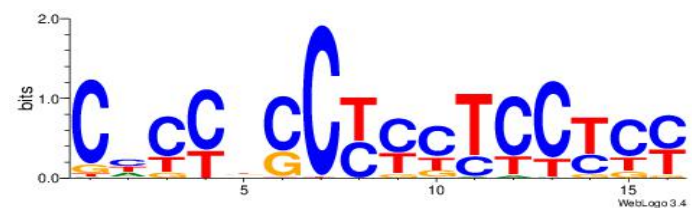
RGRGGAGRRGGHGGDG

BBGGGGCGGGGCGGB-

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



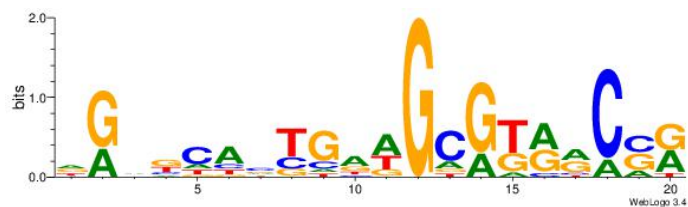
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 1
 Number of overlap: 15
 Similarity score: 0.0992376

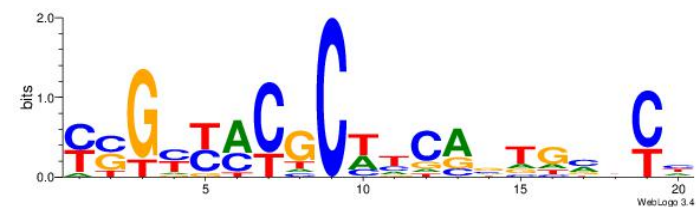
Alignment:

MSGKKRCGCWDCABTGBBCD
 BBGGGGCGGGGCGGB-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

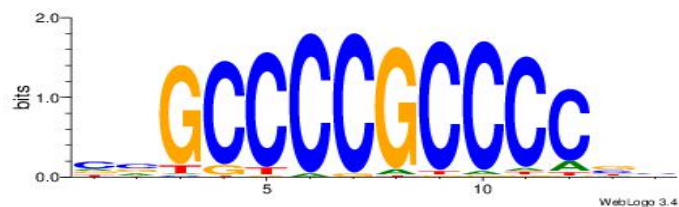


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.5

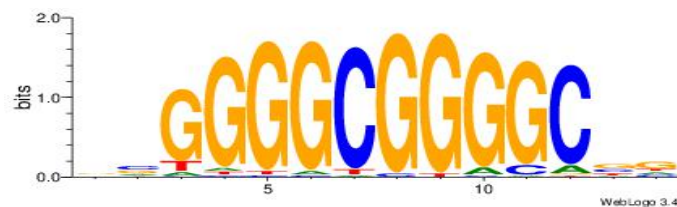
Alignment:

BBGGGGCGGGGCGVD-
 BBGGGGCGGGGCGGB

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

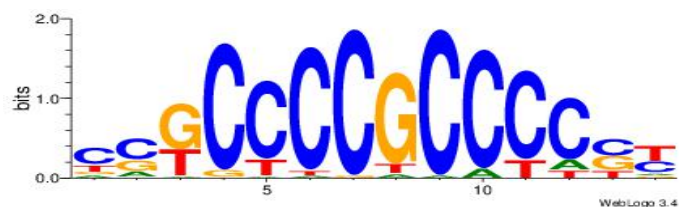


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.513015

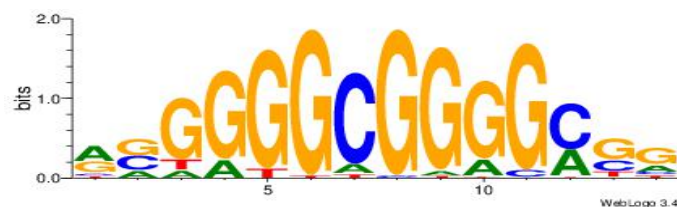
Alignment:

-CSKCCCCGCCCCSY
BCCGCCCCGCCCCBB

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

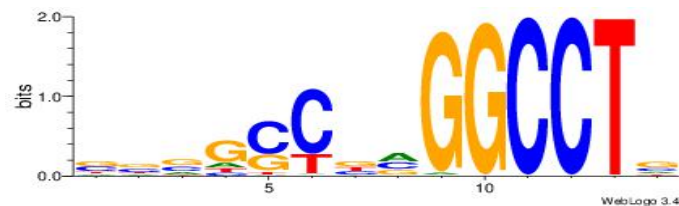


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.574434

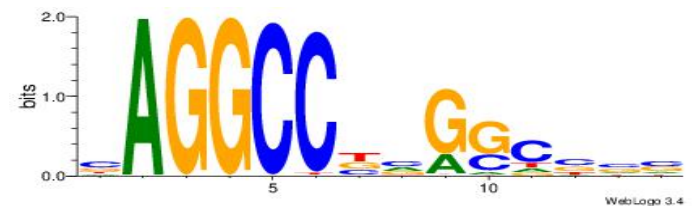
Alignment:

BBVGCCBVGGCCTV-
 BCCGCCCCGCCCCBB

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

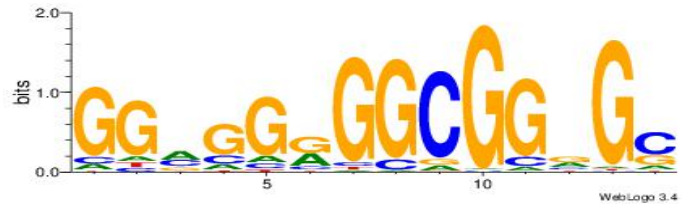


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14

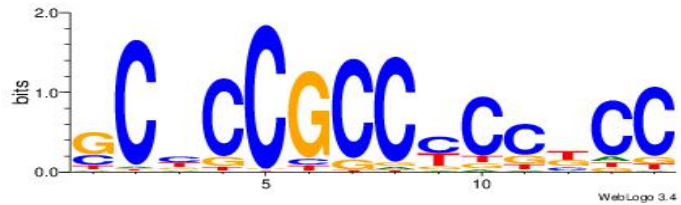
Similarity score: 0.58333

Alignment:
GCVCCGCCMCCYCC-
BCCGCCCCGCCCCBB

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

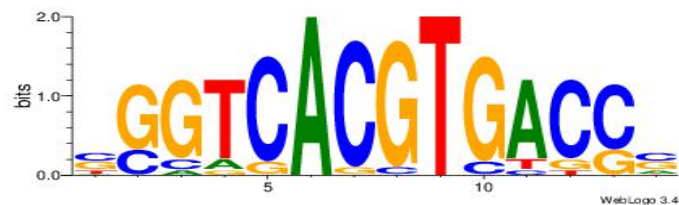
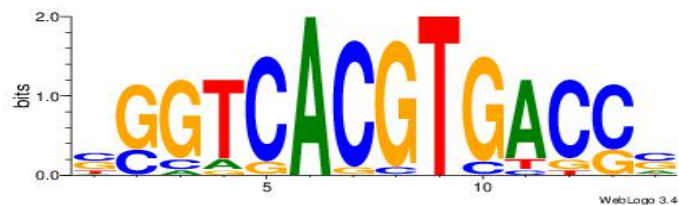


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSS
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.601399

Alignment:
SGGTCACGTGACCS-
BBGGGGCGGGGCGGB

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACCS

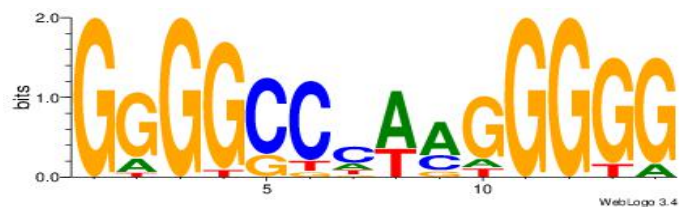


Dataset #: 3
 Motif ID: 30
 Motif name: PLAG1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.604586

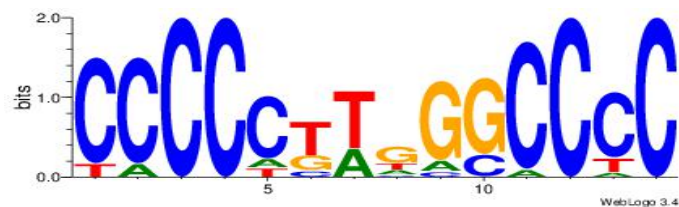
Alignment:

GGGGCCCAAGGGG-
 BBGGGGCGGGCGGB

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



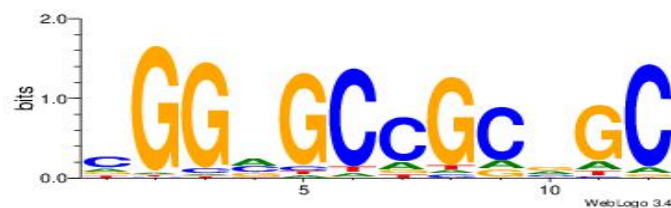
Dataset #: 5
 Motif ID: 49

Motif name: TFF1
 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: 1.58073

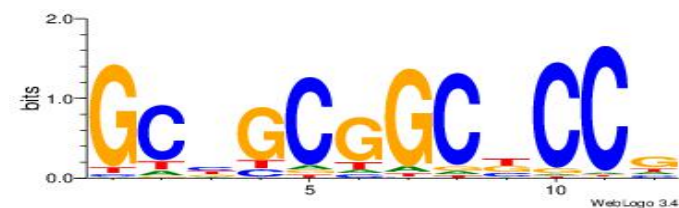
Alignment:

---GCVGCGGCBCCG
 BCCGCCCCGCCCCBB

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #: 4 Motif ID: 39 Motif name: kCAGCCAATmr

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



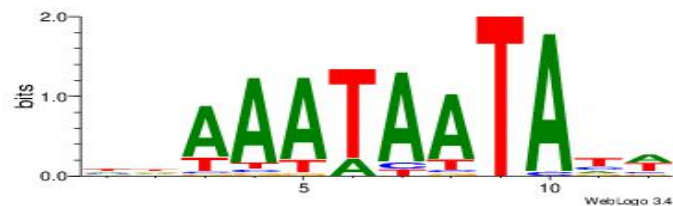
Best Matches for Motif ID 39 (Highest to Lowest)

Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0559269

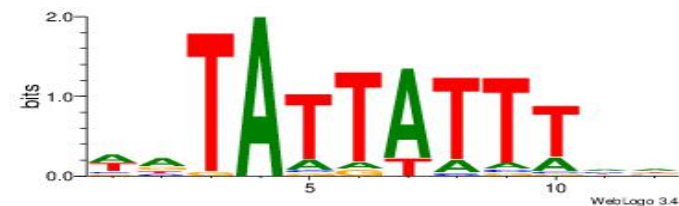
Alignment:

WHTATTATTTDH
 -MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 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: 0.0588235

Alignment:
HCAGAATGTHD
DCAGCCAATVR

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

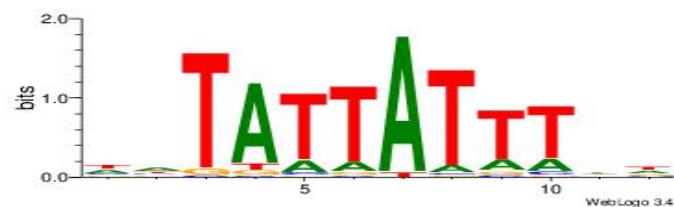
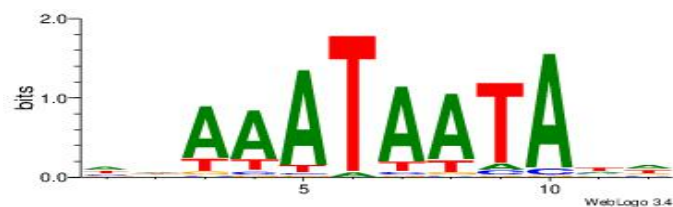


Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0597643

Alignment:
DDTATTATTTDH
-MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTTDH



Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0599548

Alignment:

BCACCTGCABC

MBATTGGCTGH

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 5
 Motif ID: 50

Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0614719

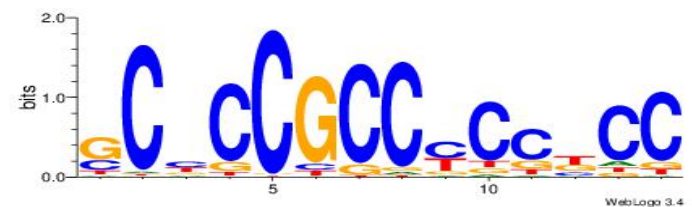
Alignment:

GCVCCGCCMCCYCC
 --DCAGCCAATVR--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

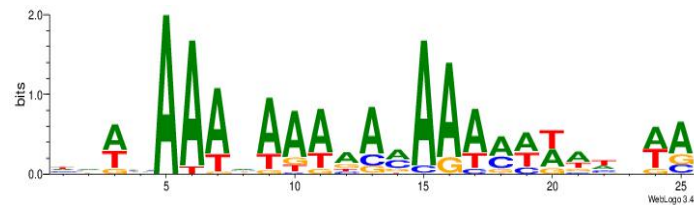


Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	11
Similarity score:	0.0635027

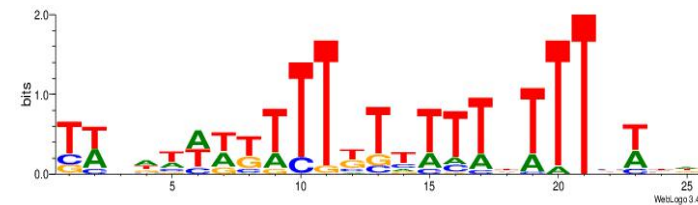
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
-----DCAGCCAATVR-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTTTTTTHTTTVWBH



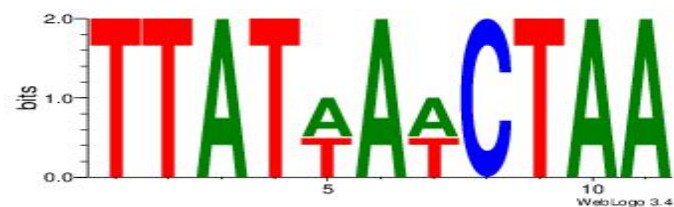
Dataset #:	2
Motif ID:	18
Motif name:	Motif 18
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0661765

Alignment:

TTAGWTWATAA
DCAGCCAATVR

Original motif Consensus sequence: TTAGWTWATAA

Reverse complement motif Consensus sequence: TTATWAWCTAA



Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.56089

Alignment:

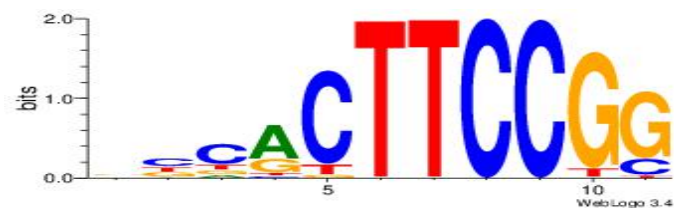
-CCGGAAGTG VV

DCAGCCAATVR-

Original motif Consensus sequence: CCGGAAGTG VV



Reverse complement motif Consensus sequence: VVCACTTC CGG



Dataset #: 4
 Motif ID: 45

Motif name:	wbgTAAATAww
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:	0.561975

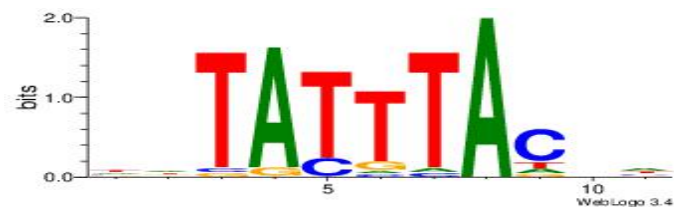
Alignment:

DHTATTTACBD-
-MBATTGGCTGH

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD

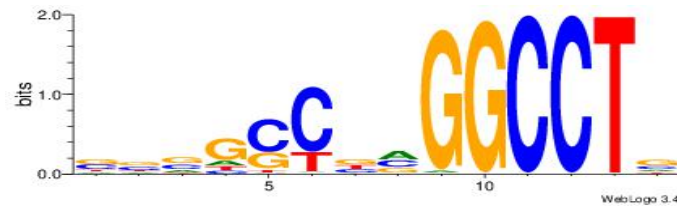


Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.563709

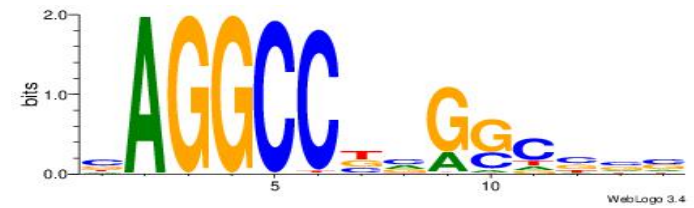
Alignment:

VAGGCCBBGGCVBB-
----DCAGCCAATVR

Original motif Consensus sequence: BBVGCCBVGGCCTV

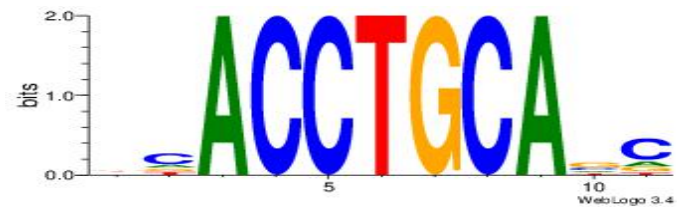


Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Dataset #: 4 Motif ID: 40 Motif name: kcACCTGCAGc

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Best Matches for Motif ID 40 (Highest to Lowest)

Dataset #:	4
Motif ID:	43
Motif name:	wTACwGTAsw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

Number of overlap: 11
Similarity score: 0.0215284

Alignment:
DBTACWGTAVH
BCACCTGCABC

Original motif Consensus sequence: HVTACWGTABD



Reverse complement motif Consensus sequence: DBTACWGTAVH

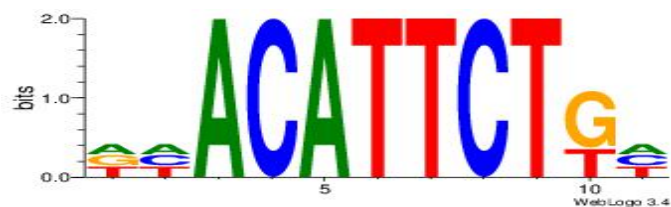


Dataset #: 4
Motif ID: 44
Motif name: dhACATTCTkh
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0254134

Alignment:
DHACATTCTGH
BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH

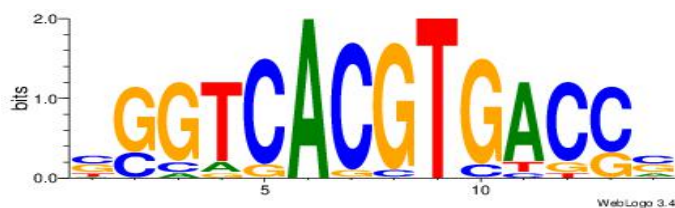
Reverse complement motif Consensus sequence: HCAGAATGTHD



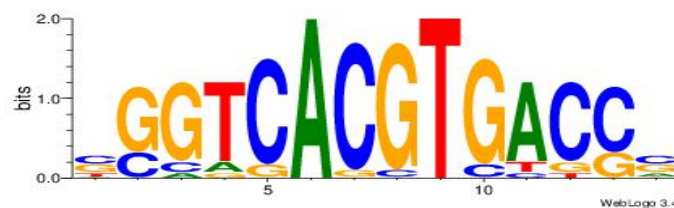
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACCS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.031338

Alignment:
 SGGTCACGTGACCS
 ---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 5
 Motif ID: 50

Motif name:	TFF11
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:	0.034471

Alignment:

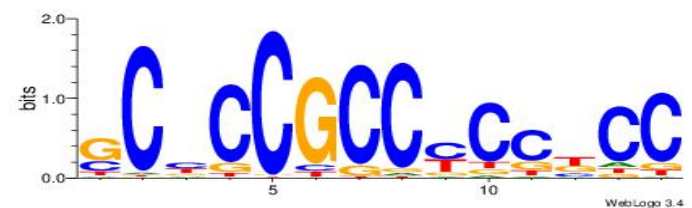
```

GCVCCGCCMCCYCC
BCACCTGCABC---
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

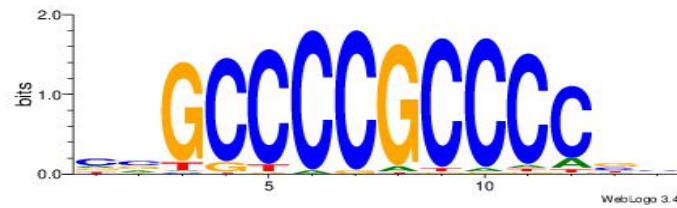


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0402518

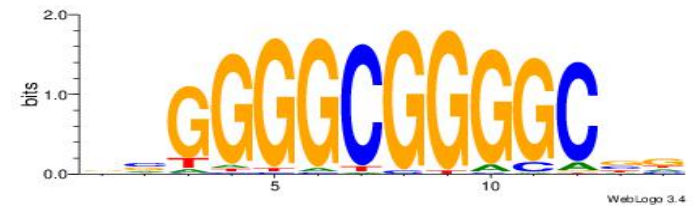
Alignment:

HVGCCCCGCCCCBB
-BCACCTGCABC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



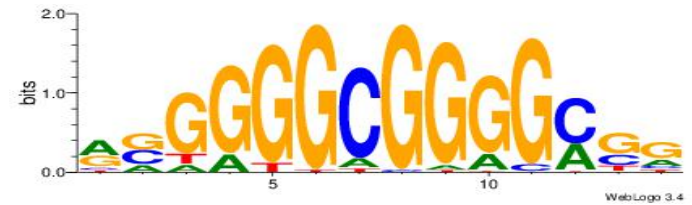
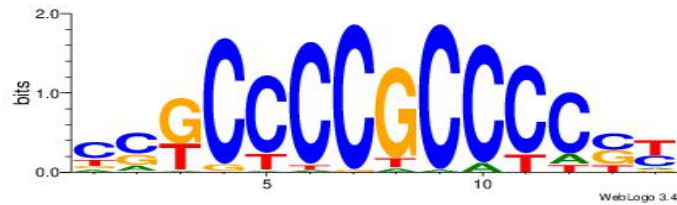
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0411257

Alignment:

CSKCCCCGCCCCSY
-BCACCTGCABC--

Original motif Consensus sequence: CSKCCCCGCCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY

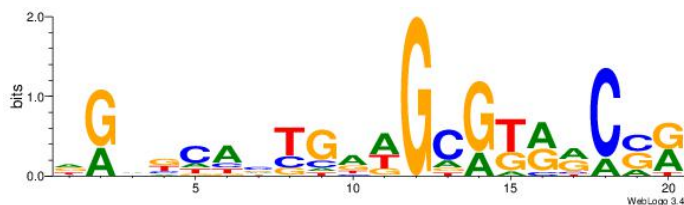


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0420218

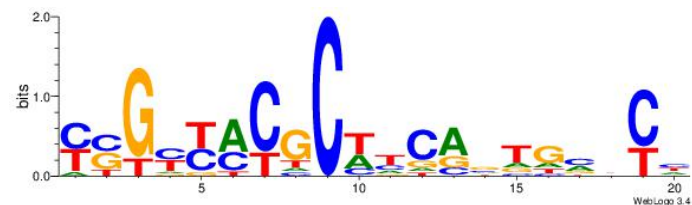
Alignment:

DGVBCABTGDWGCGRRCR
 ----GBTGCAGGTGB-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3

Motif ID: 35
 Motif name: GABPA
 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: 0.0423275

Alignment:

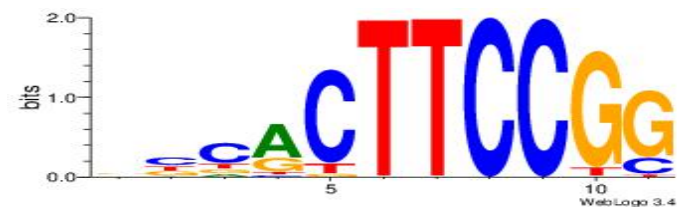
CCGGAAGTGVV

GBTGCAGGTGB

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



Dataset #: 4
 Motif ID: 39
 Motif name: kCAGCCAATmr
 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: 0.0439586

Alignment:

DCAGCCAATVR

GBTGCAGGTGB

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0461444

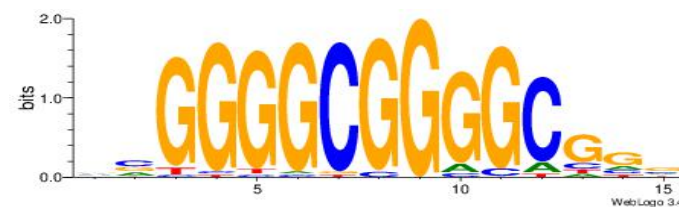
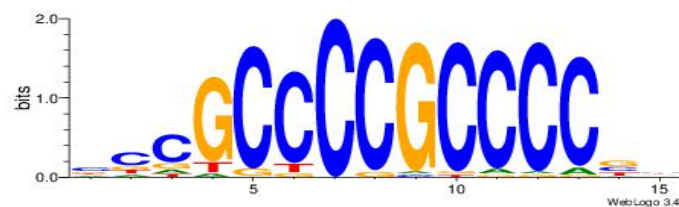
Alignment:

BCCGCCCCGCCCCBB

--BCACCTGCABC--

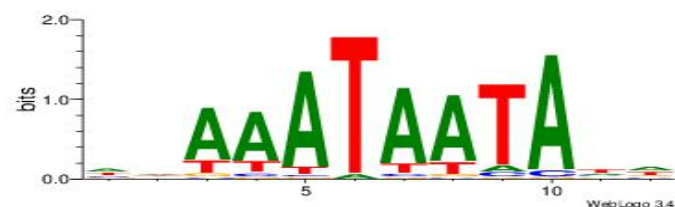
Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

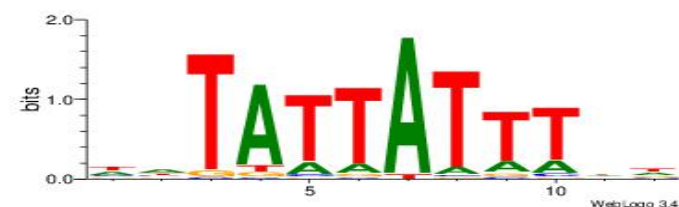


Dataset #: 4 **Motif ID: 41** **Motif name: wwAAATAATAtw**

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

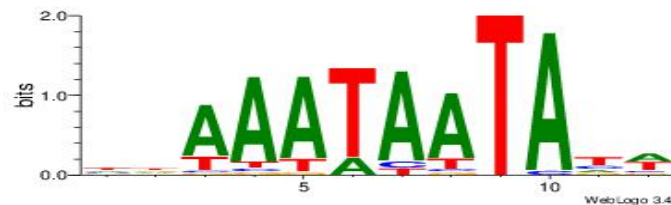


Best Matches for Motif ID 41 (Highest to Lowest)

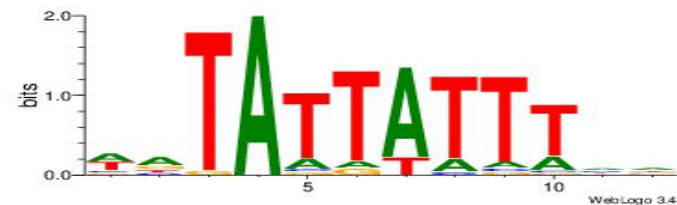
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:
 HDAAATAATAHW
 HDAAATAATADD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



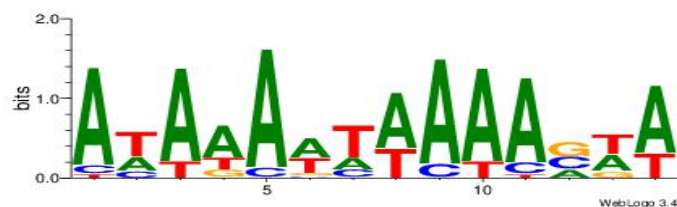
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0536028

Alignment:

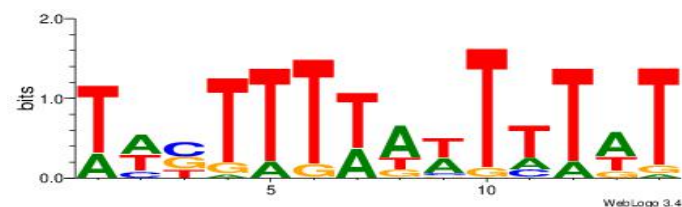
AWAAAWTWAAASWA

-HDAAATAATADD-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV

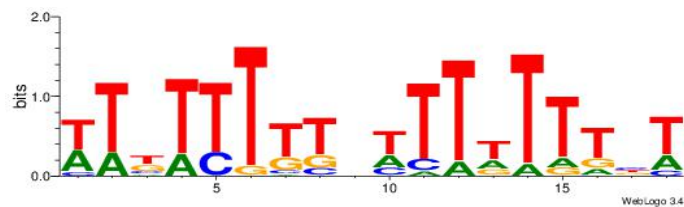


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0565705

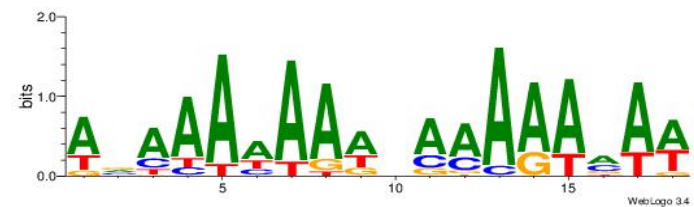
Alignment:

WTKTTTTTHWTTTTTBT
 -----DDTATTATTTDH

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

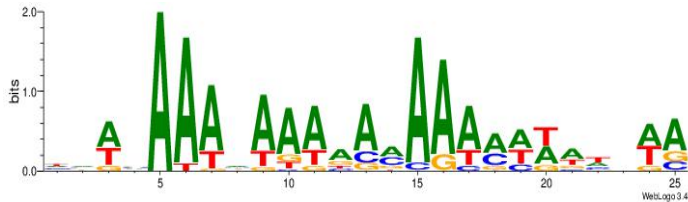


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

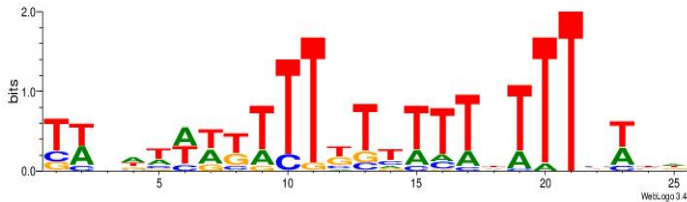
Number of overlap: 12
Similarity score: 0.0575935

Alignment:
HDWVAAAHA AAAA MAAAMWWWHBWA
--HDAAATAATADD-----

Original motif Consensus sequence:
HDWVAAAHA AAAA MAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH

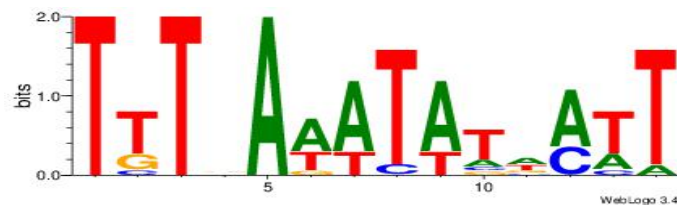
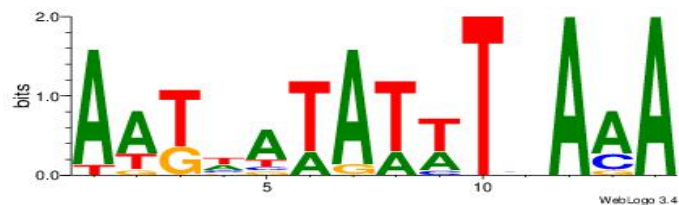


Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0591821

Alignment:
AATHATATWTHAAA
--DDTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT



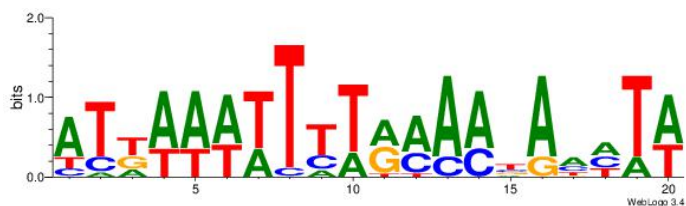
Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0712963

Alignment:

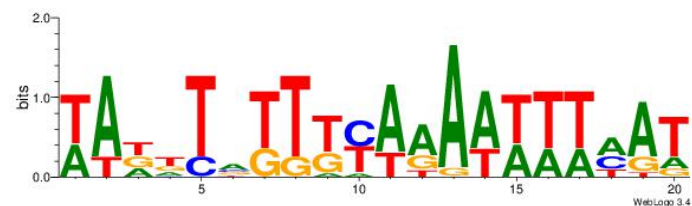
```

WAHHTVTTYKAAAATTRAT
-----HDAAATAATADD
  
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

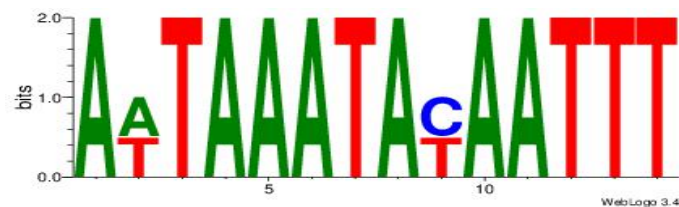


Dataset #: 2

Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0715278

Alignment:
 AAATTKTATTTAWT
 -DDTATTATTTDH-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

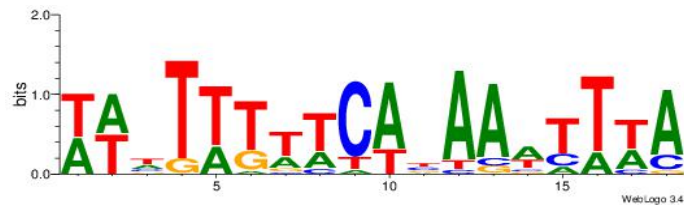


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0733516

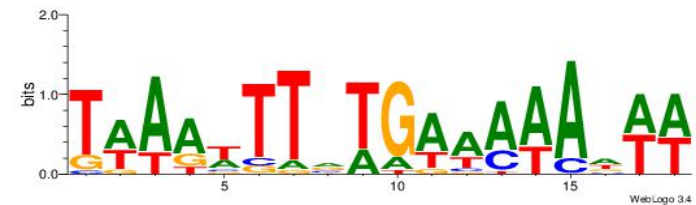
Alignment:

WWHTTTTTCABAAWTTWA
-----DDTATTATTTDH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
TAAWTTVTGAAAAHWW



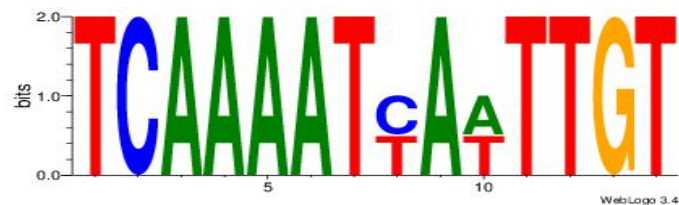
Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0912037

Alignment:

TCAAAATKAWTTGT
--DDTATTATTTDH

Original motif Consensus sequence: ACAAWTRATTTTGA

Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0924576

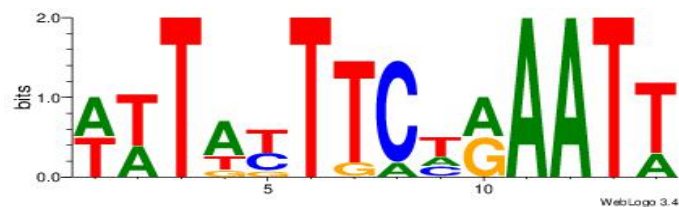
Alignment:

WWTAKTTCDKAATT
 DDTATTATTTDH--

Original motif Consensus sequence: AATTYDGAARTAWW

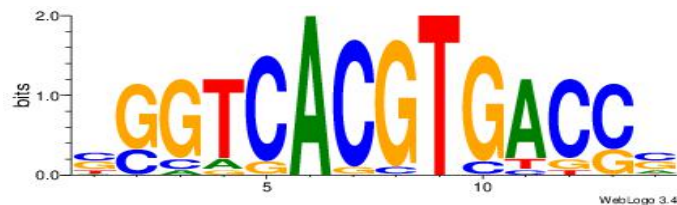


Reverse complement motif Consensus sequence: WWTAKTTCDKAATT

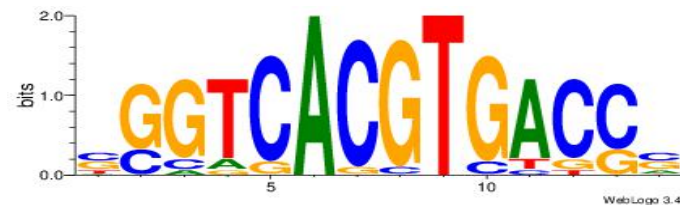


Dataset #: 4 Motif ID: 42 Motif name: sSGTCACGTGACs

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



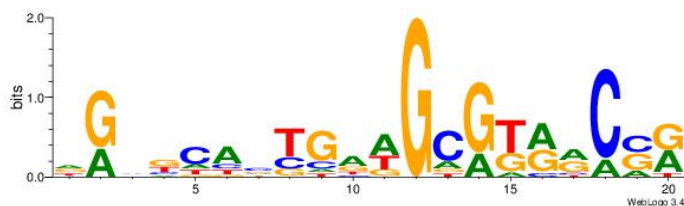
Best Matches for Motif ID 42 (Highest to Lowest)

Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	14
Similarity score:	0.0518737

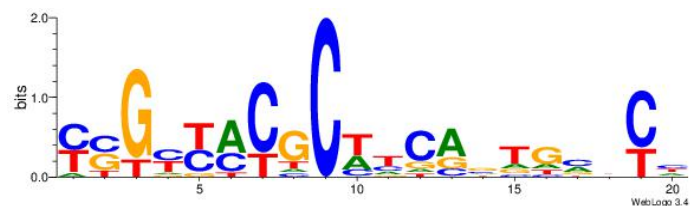
Alignment:

```
DGVBCABTGDWGCGRRCR
-----SGGTCACGTGACCS
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

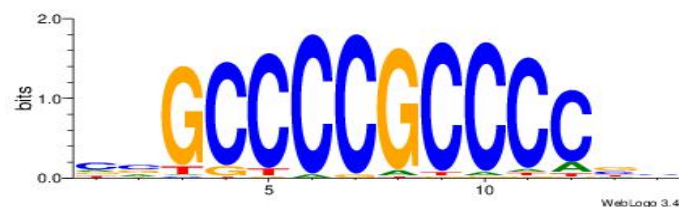


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0539097

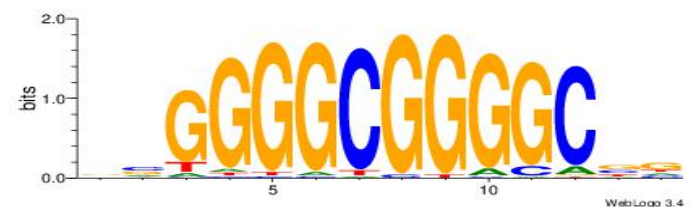
Alignment:

BBGGGGCGGGGCVD
 SGGTCACGTGACCS

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

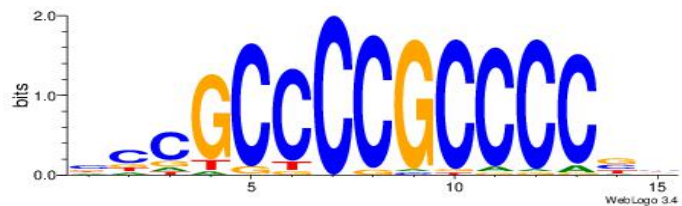


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14

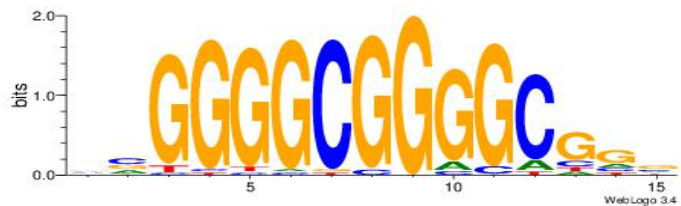
Similarity score: 0.0581955

Alignment:
BCCGCCCCGCCCCBB
SGGTCACGTGACCS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

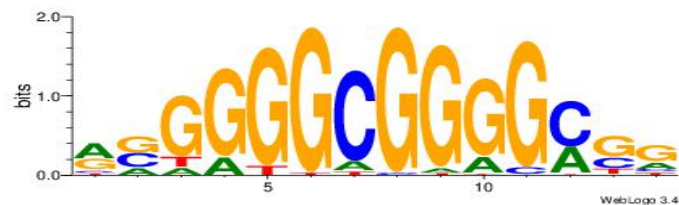
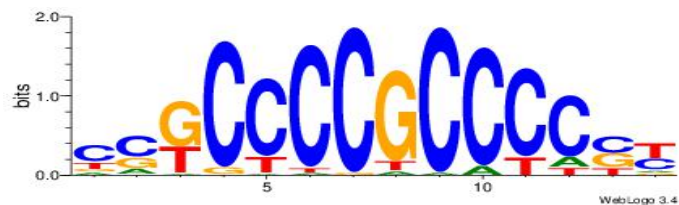


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0634135

Alignment:
MSGGGGCGGGGYSG
SGGTCACGTGACCS

Original motif Consensus sequence: CSKCCCCGCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 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: 1.05855

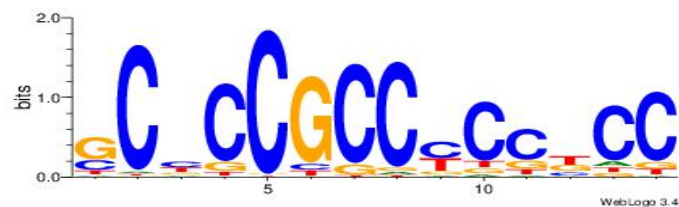
Alignment:

--GCVCCGCCMCCYCC
 SGGTCACGTGACCS--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



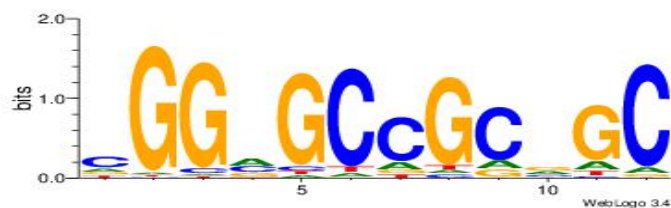
Dataset #: 5
 Motif ID: 49

Motif name:	TFF1
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:	1.06047

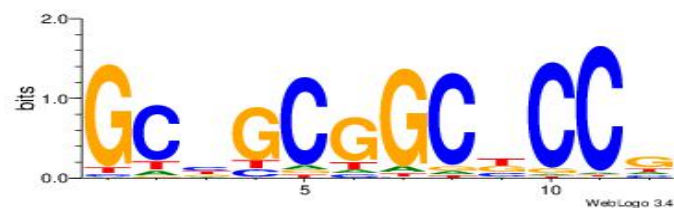
Alignment:

```
--GCVGCGGCBCCG
SGGTACGTGACCS
```

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAGc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	1.54742

Alignment:

---BCACCTGCABC
SGGTCACGTGACCS

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



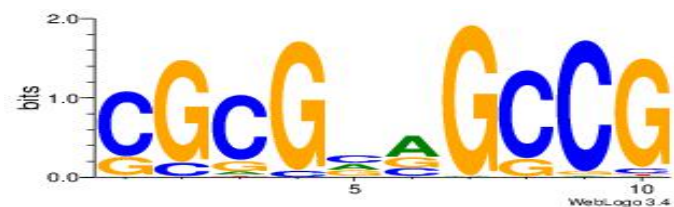
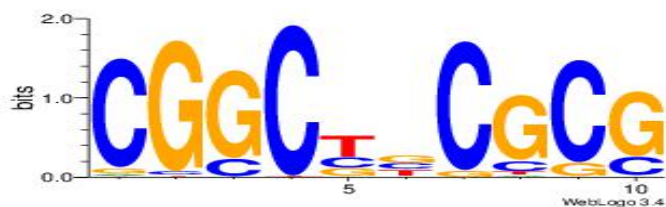
Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	2.05201

Alignment:

----CGCGBMGCCG
SGGTCACGTGACCS

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG



Dataset #: 3
 Motif ID: 23
 Motif name: Egr1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 2.06209

Alignment:

----YCGCCCACGCH
 SGGTCACGTGACCS-

Original motif Consensus sequence: HCGTG GGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



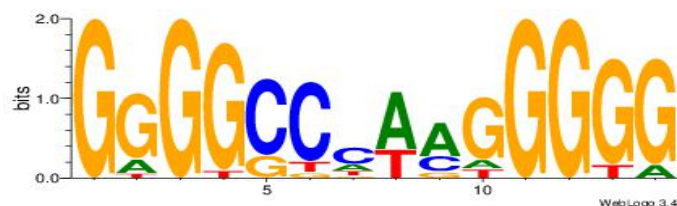
Dataset #: 3
 Motif ID: 30

Motif name: PLAG1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 7
 Similarity score: 3.53253

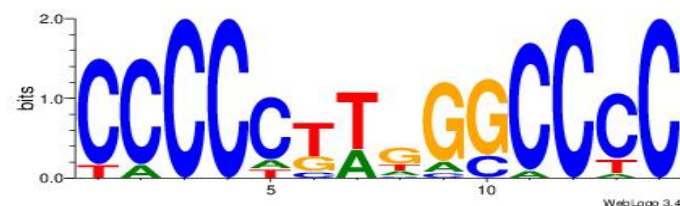
Alignment:

CCCCCTTGGGCCCC-----
 -----SGGTCACGTGACCS

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC



Dataset #: 4 Motif ID: 43 Motif name: wsTACwGTAsw

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



Best Matches for Motif ID 43 (Highest to Lowest)

Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 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: 0.0199592

Alignment:

GBTGCAGGTGB

HVTACWG TABD

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

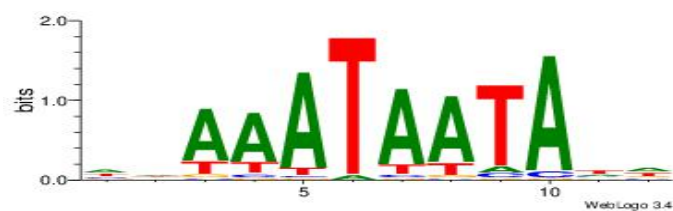


Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

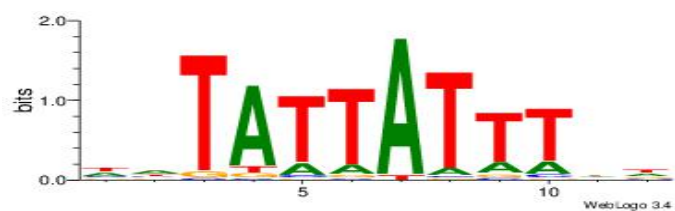
Similarity score: 0.0309343

Alignment:
DDTATTATTTDH
-HVTACWGATABD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

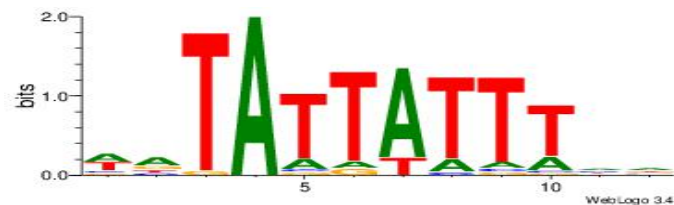
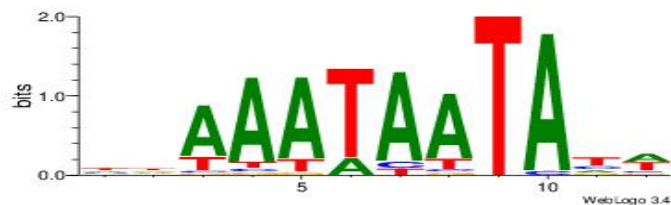


Dataset #: 4
Motif ID: 37
Motif name: tkAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0337121

Alignment:
WHTATTATTTDH
-HVTACWGATABD

Original motif Consensus sequence: HDAAATAATAHW

Reverse complement motif Consensus sequence: WHTATTATTTDH



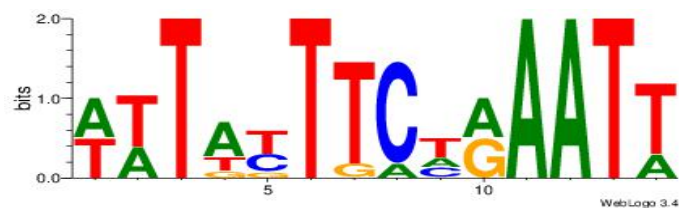
Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0353535

Alignment:
 AATTYDGAARTAWW
 HVTACWGATABD---

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #: 4
 Motif ID: 45

Motif name:	wbgTAAATAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.037518

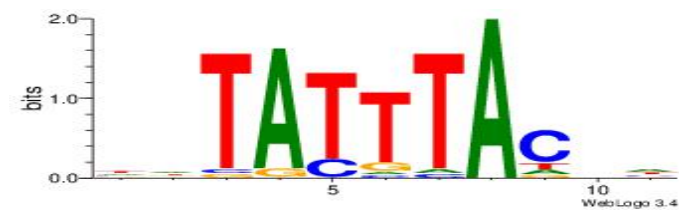
Alignment:

DBGTAAATAHD
DBTACWGTAVH

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD

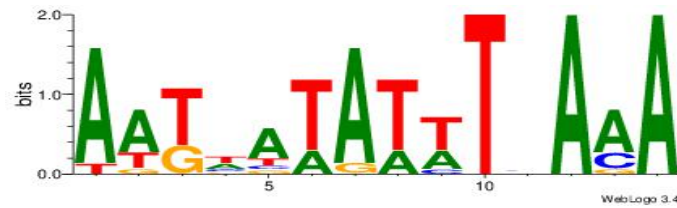


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0397727

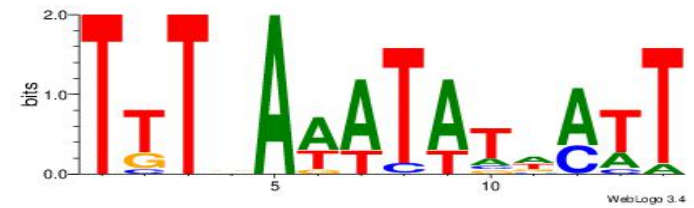
Alignment:

TTTDAWATATHATT
DBTACWGTAVH---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



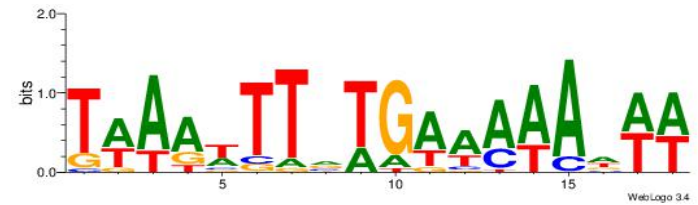
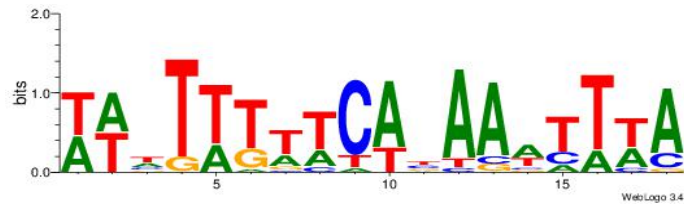
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	11
Similarity score:	0.0413797

Alignment:

TWAAWTTVTGAAAAHWW
---HVTACWGTTABD----

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TWAAWTTVTGAAAAHWW

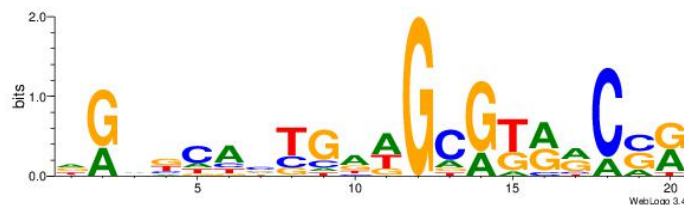


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.042298

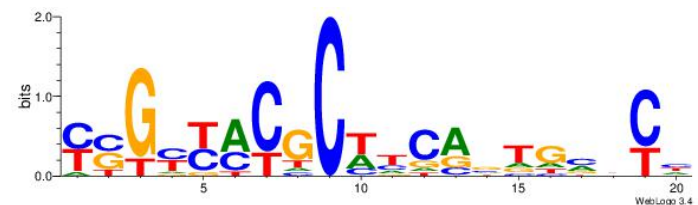
Alignment:

DGVBCABTGDWGCGRRCR
 -----HVTACWG TABD-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTG B B C D



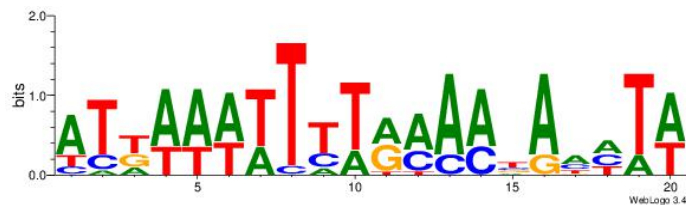
Dataset #: 5

Motif ID: 55
 Motif name: TFM13
 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: 0.0445707

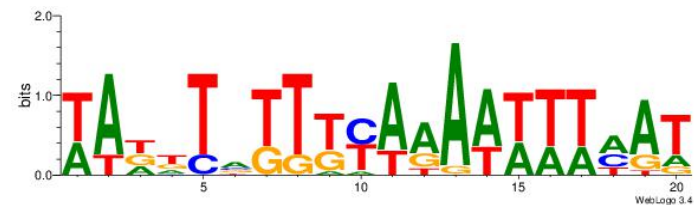
Alignment:

ATKAAWTTTTRMAABAHHTW
 -----DBTACWGTAVH--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2
 Motif ID: 19
 Motif name: Motif 19
 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: 0.0460859

Alignment:

TTCWTAGATTAWA
DBTACWGTAVH--

Original motif Consensus sequence: TTCWTAGATTAWA

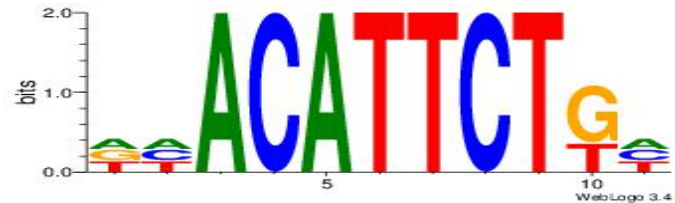


Reverse complement motif Consensus sequence: TWTAACTAWGAA



Dataset #: 4 Motif ID: 44 Motif name: dhACATTCTkh

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Best Matches for Motif ID 44 (Highest to Lowest)

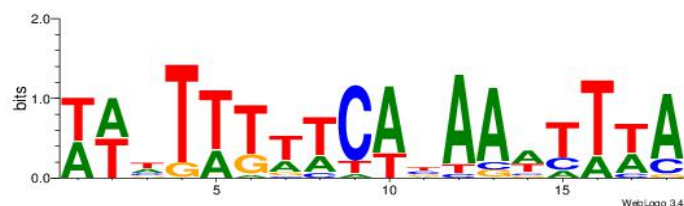
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 8
Number of overlap: 11
Similarity score: 0.0217516

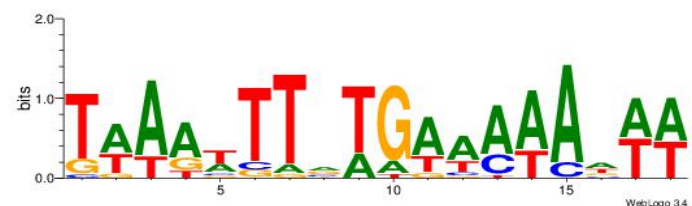
Alignment:

TWAAWTTVTGAAAAHWW
DHACATTCTGH-----

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 4
Motif ID: 40
Motif name: kcACCTGCAGc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0238442

Alignment:

BCACCTGCABC
DHACATTCTGH

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 2
Motif ID: 16
Motif name: Motif 16
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: 0.0258838

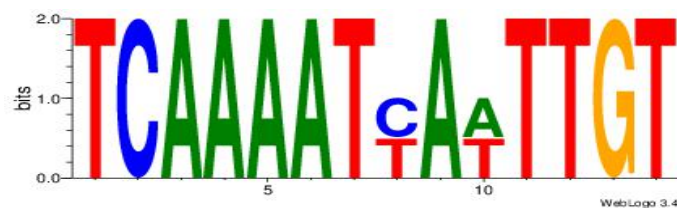
Alignment:

TCAAAATKAWTTGT
HCAGAATGTHD---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

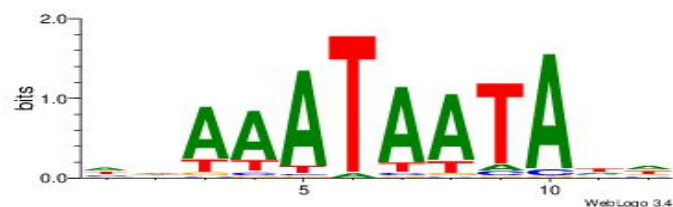


Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0292508

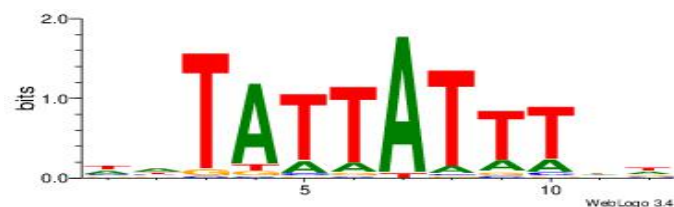
Alignment:

DDTATTATTTDH
 -HCAGAATGTHD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

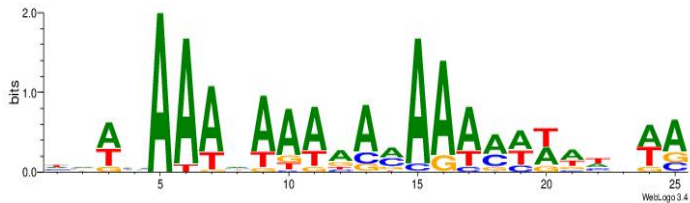


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11

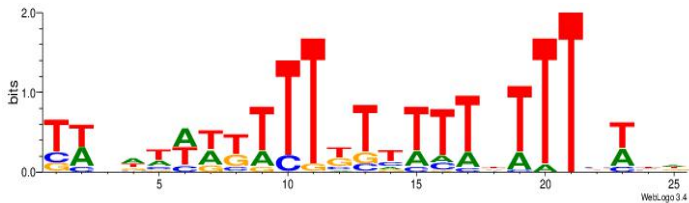
Similarity score: 0.0307858

Alignment:
TWVHWWYTTTTYTTTTHTTTVWBH
----DHACATTCTGH-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTHTTTVWBH

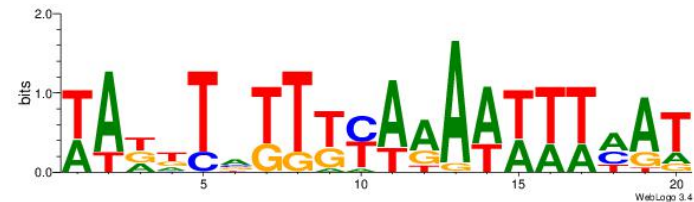
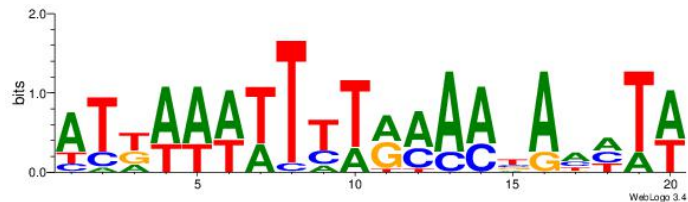


Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 11
Similarity score: 0.0357323

Alignment:
ATKAAWTTTTRMAABAHHTW
-DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

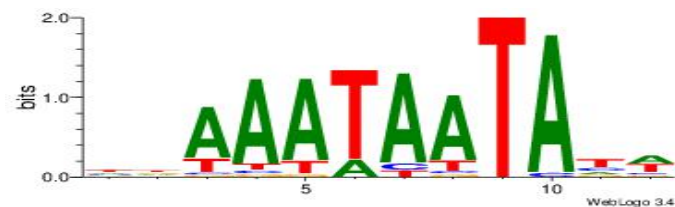
Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT



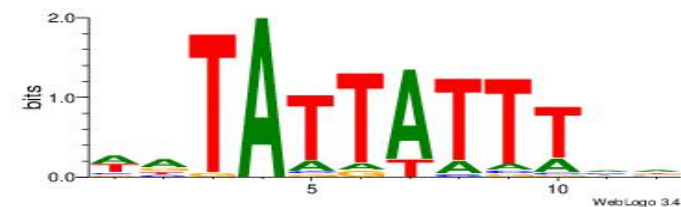
Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0364899

Alignment:
 WHTATTATTDDH
 -HCAGAAATGTHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH



Dataset #: 2
 Motif ID: 6

Motif name:	Motif 6
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:	0.0400884

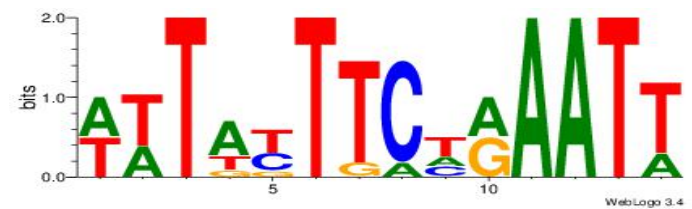
Alignment:

AATTYDGAARTAWW
 HCAGAATGTHD---

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #:	4
Motif ID:	39
Motif name:	kCAGCCAATmr
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:	0.0412582

Alignment:

MBATTGGCTGH

DHACATTCTGH

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



Dataset #:	3
Motif ID:	35
Motif name:	GABPA
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:	0.0418896

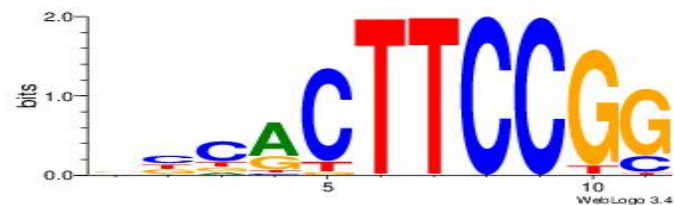
Alignment:

CCGGAAGTGVV

HCAGAATGTHD

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTCCGG

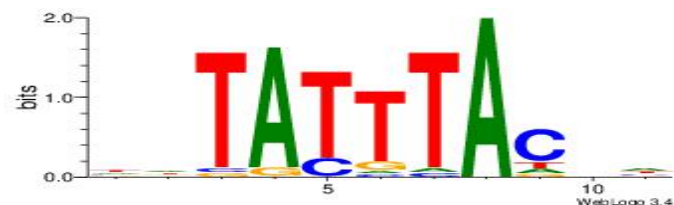


Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Best Matches for Motif ID 45 (Highest to Lowest)

Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0162338

Alignment:
 HDAAATAATAHW
 -DBGTAAATAHD

[illegible]

Alignment:

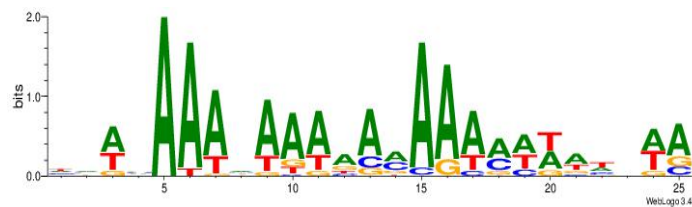
```
DDTATTATTDDH
DHTATTTACBD-
```

Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 11
 Similarity score: 0.0192768

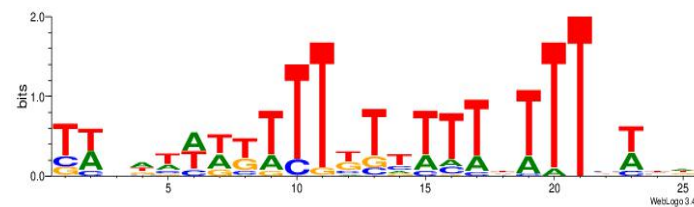
Alignment:

TWVHWWYTTTYYTTTTHTTTVWBH
 -----DHTATTTACBD

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYYTTTTHTTTVWBH

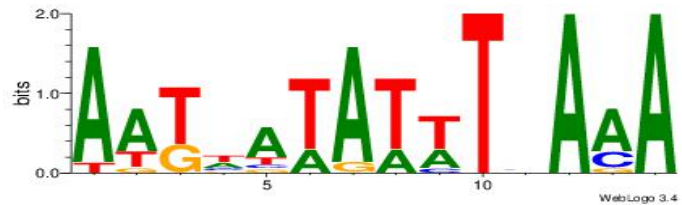


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

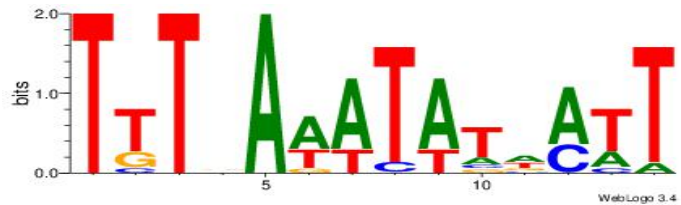
Number of overlap: 11
Similarity score: 0.0250541

Alignment:
AATHATATWTHAAA
DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

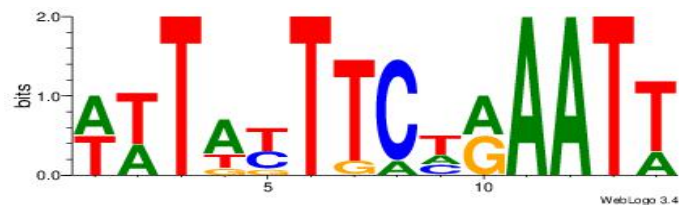


Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.027895

Alignment:
AATTYDGAARTAWW
---DBGTAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

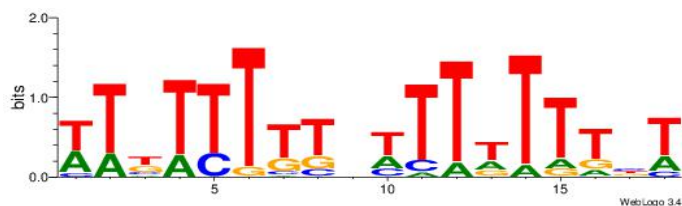


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0283217

Alignment:

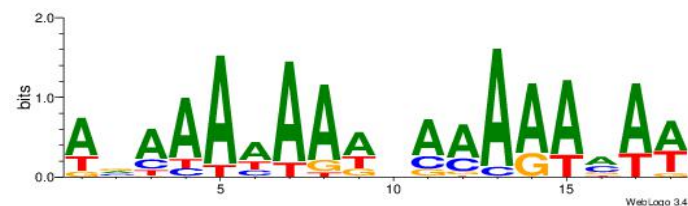
ABAAAAAAWHAAAAARAW
 DBGTAATAHD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif
ABAAAAAAWHAAAAARAW

Consensus sequence:



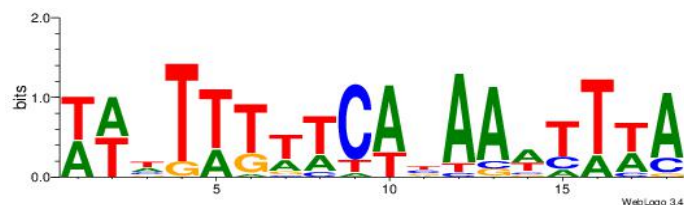
Dataset #: 5

Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0308097

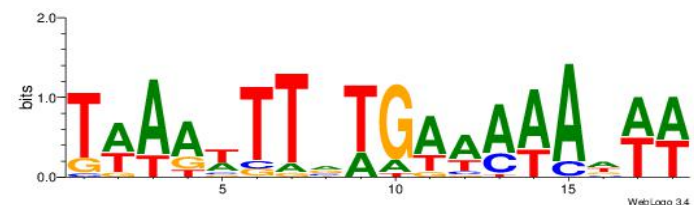
Alignment:

TWAAWTTVTGAAAAHWW
 -----DBGTAATAHD-

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

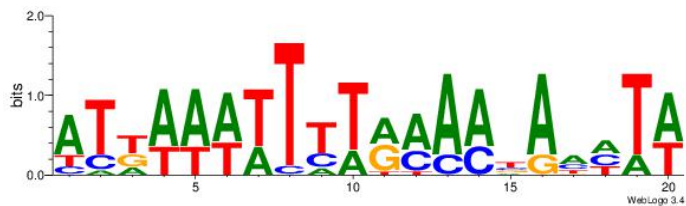


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11

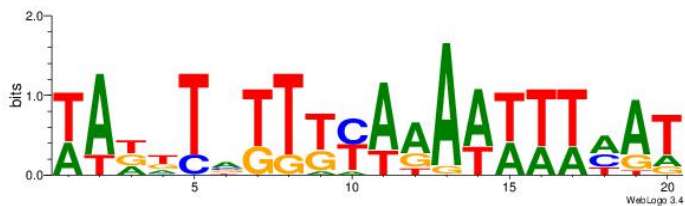
Similarity score: 0.0333874

Alignment:
ATKAAWTTTTRMAABAHHTW
-----DBGTAAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2
Motif ID: 4
Motif name: Motif 4
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: 0.0361187

Alignment:
AAAAWTTTCWT
DHTATTTACBD

Original motif Consensus sequence: AAAAWTTTCWT

Reverse complement motif Consensus sequence: AWGKAAWTTT



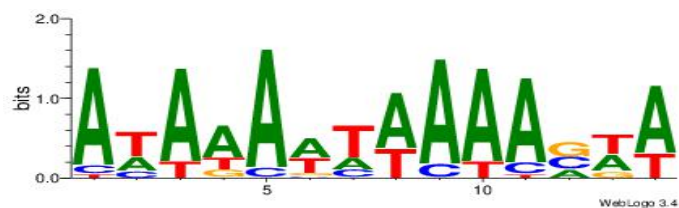
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0410381

Alignment:

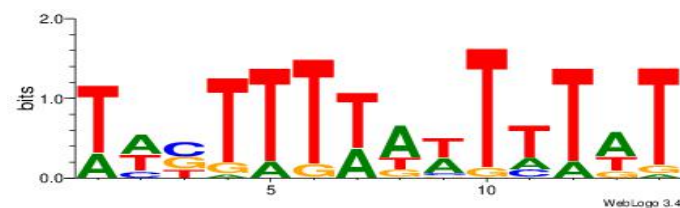
AWAAAWTWAAASWA

--DHTATTTACBD--

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV



Dataset #: 5 Motif ID: 46 Motif name: TFW1

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



Best Matches for Motif ID 46 (Highest to Lowest)

Dataset #:	5
Motif ID:	48
Motif name:	TFW3
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:	0.0350356

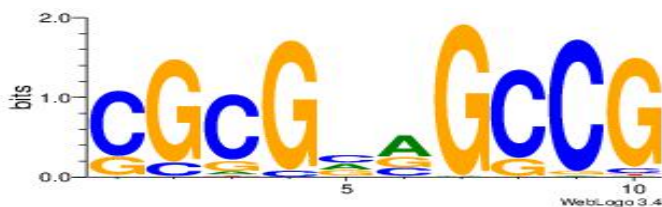
Alignment:

```
CGGCYBCGCG
----GTCGCG
```

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

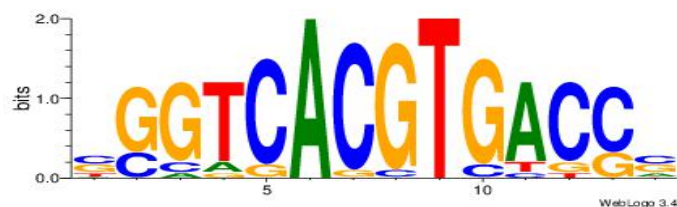


Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSSs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0375102

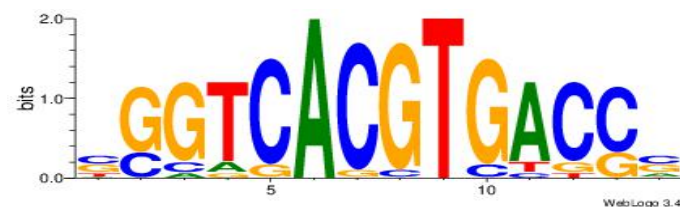
Alignment:

SGGTCACGTGACCS
 --GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

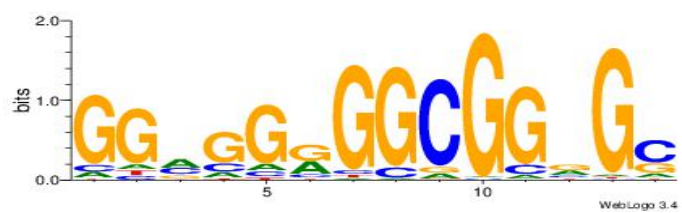


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6

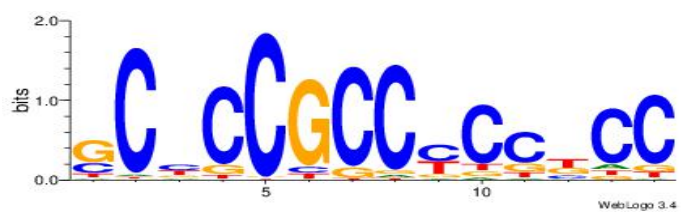
Similarity score: 0.0381641

Alignment:
GCVCCGCCMCCYCC
-----CGCGAC-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

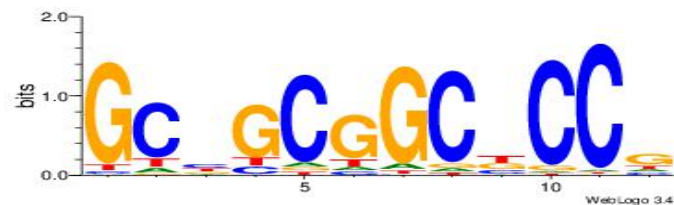
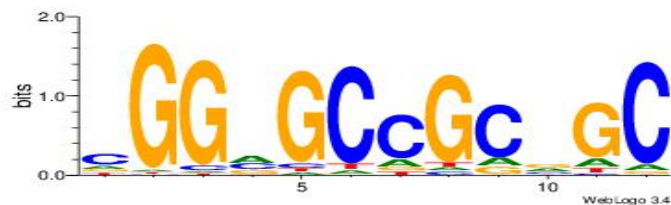


Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 6
Similarity score: 0.0431161

Alignment:
CGGVGCCGCVGC
-----CGCGAC

Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCCGCBCCG



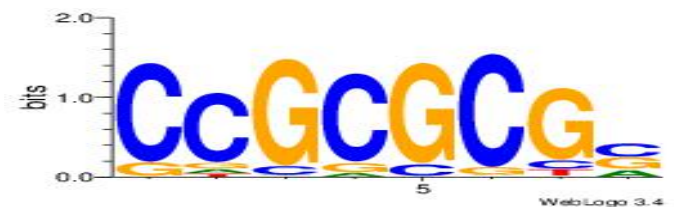
Dataset #: 5
 Motif ID: 47
 Motif name: TFW2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.052047

Alignment:
 CCGCGCGS
 -CGCGAC-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



Dataset #: 3
 Motif ID: 33

Motif name:	Mycn
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:	0.0537993

Alignment:

```

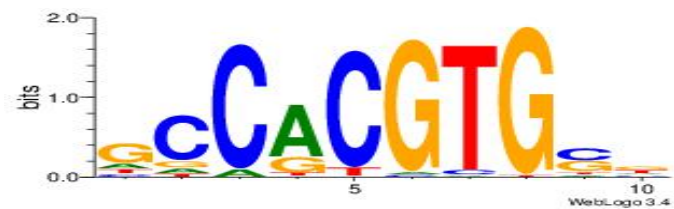
GCCACGTGSD
----GTCGCG

```

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



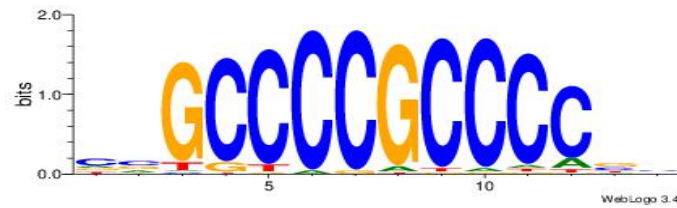
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.0539

Alignment:

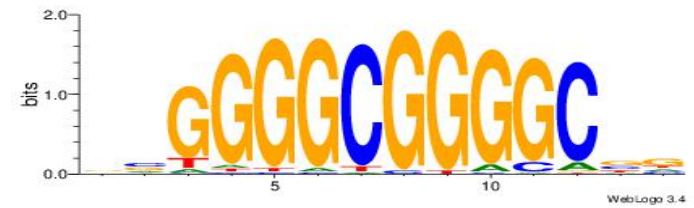
HVGCCCGCCCCBB

--GTCGCG-----

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC



Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
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:	0.0554263

Alignment:

GCCCCGCC

--GTCGCG

Original motif Consensus sequence: GCGGGGC

Reverse complement motif Consensus sequence: GCCCCGCC

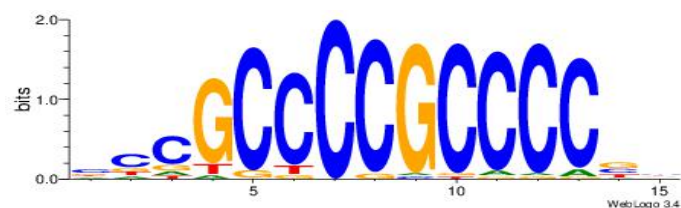


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0558733

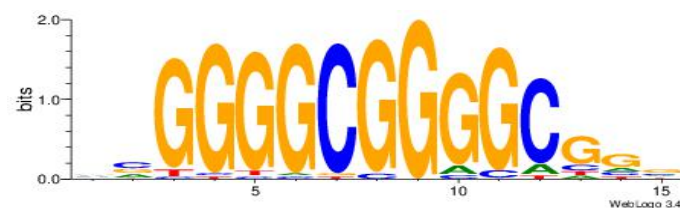
Alignment:

BBGGGGCGGGGCGGB
 -----GTCGCG--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

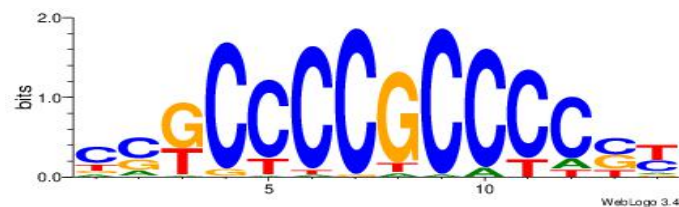


Dataset #: 2

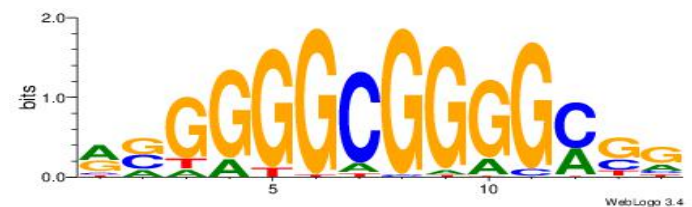
Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0644512

Alignment:
 CSKCCCCGCCCSY
 --CGCGAC-----

Original motif Consensus sequence: CSKCCCCGCCCSY

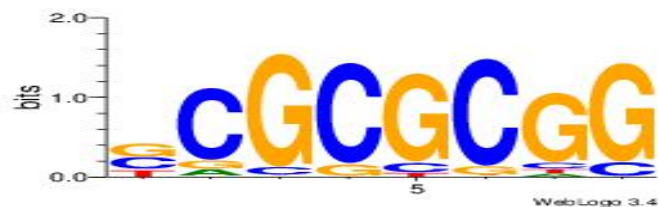


Reverse complement motif Consensus sequence: MSGGGGCGGGGY

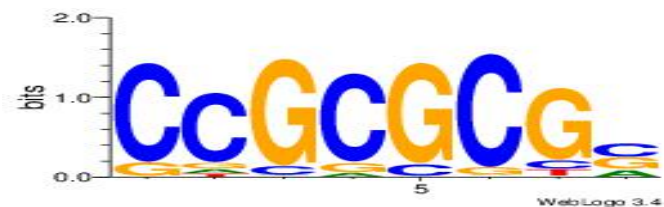


Dataset #: 5 Motif ID: 47 Motif name: TFW2

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



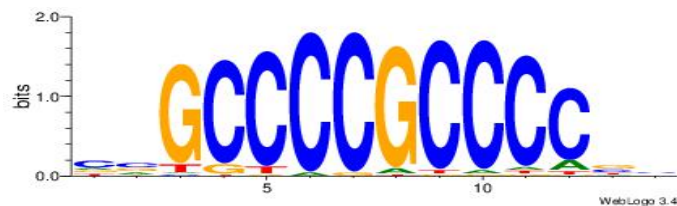
Best Matches for Motif ID 47 (Highest to Lowest)

Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0456233

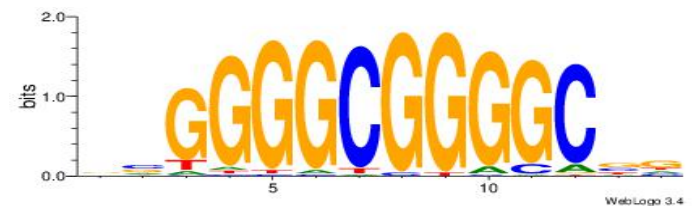
Alignment:

HVCCCCGCCCCBB
-CCGCGCGS-----

Original motif Consensus sequence: HVCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

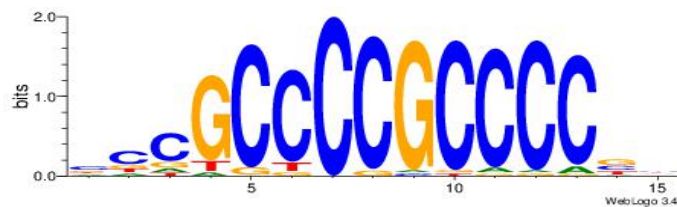


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

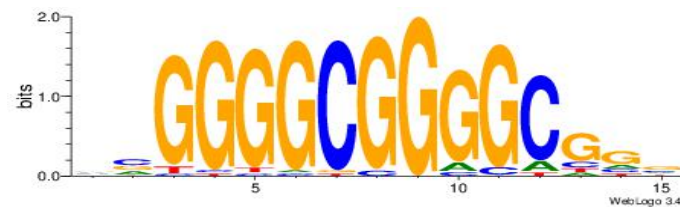
Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

Alignment:
 BBGGGGCGGGCGGB
 -----SCGCGCGG--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



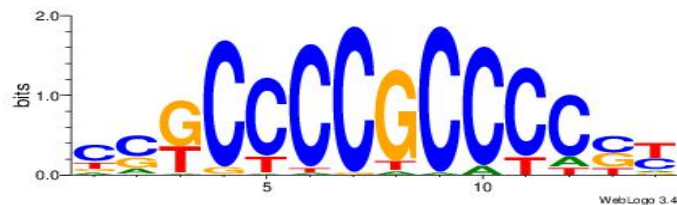
Reverse complement motif Consensus sequence: BBGGGGCGGGCGGB



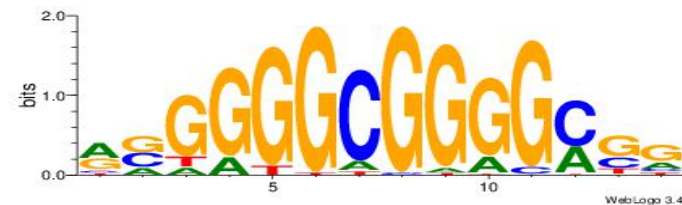
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0504058

Alignment:
 MSGGGGCGGGYSG
 -----SCGCGCGG--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 3
Motif ID: 33
Motif name: Mycn
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: 0.0527532

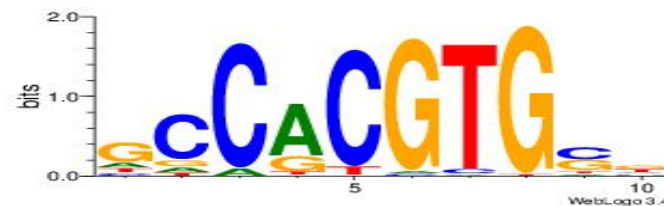
Alignment:

HSCACGTGGC
-SCGCGCGG-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



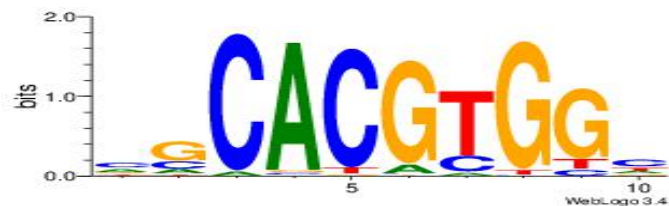
Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0574543

Alignment:

VGCACGTGGH

–SCGCGCGG–

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

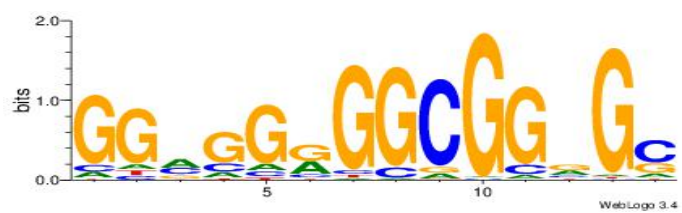


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8

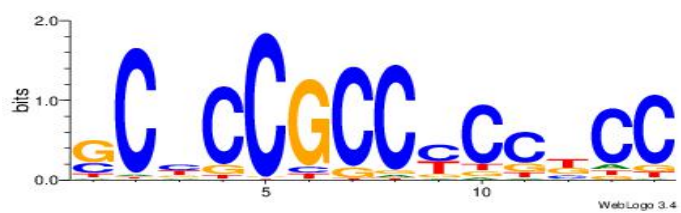
Similarity score: 0.0583967

Alignment:
GGMGGRGGCGGVGC
---SCGCGCGG---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

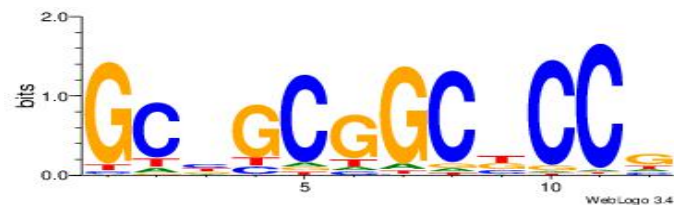
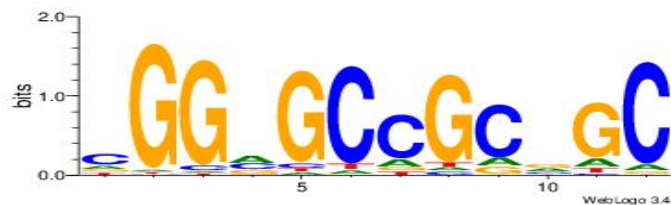


Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.060966

Alignment:
CGGVGCCGCVGC
SCGCGCGG----

Original motif Consensus sequence: CGGVGCCGCVGC

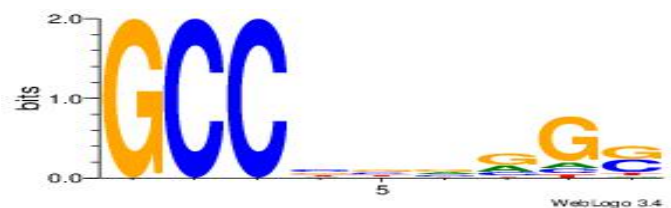
Reverse complement motif Consensus sequence: GCVGCCGCBCCG



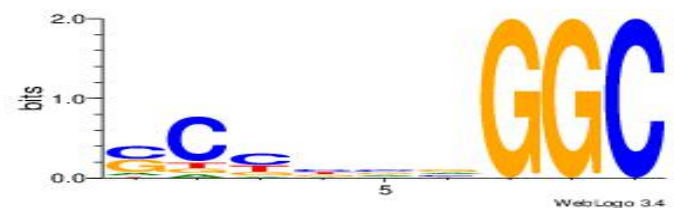
Dataset #: 3
 Motif ID: 25
 Motif name: TFAP2A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0678925

Alignment:
 GCCBBVRGS
 CCGCGCGS-

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



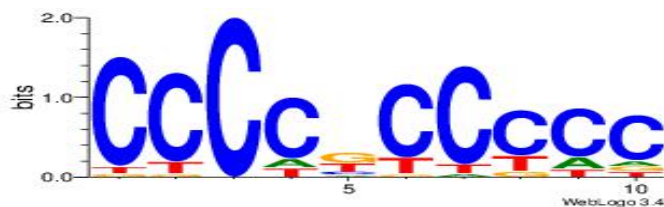
Dataset #: 3
 Motif ID: 24

Motif name:	SP1
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:	0.07018

Alignment:

CCCCKCCCCC
 --CCGCGCGS

Original motif Consensus sequence: CCCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



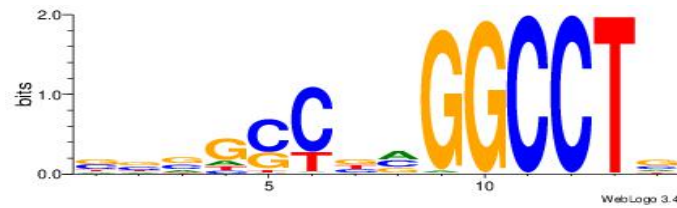
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0710499

Alignment:

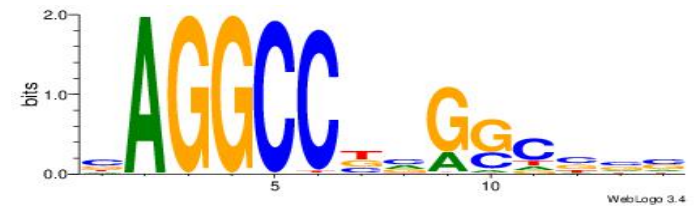
BBVGCCBVGGCCTV

--SCGCGCGG----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

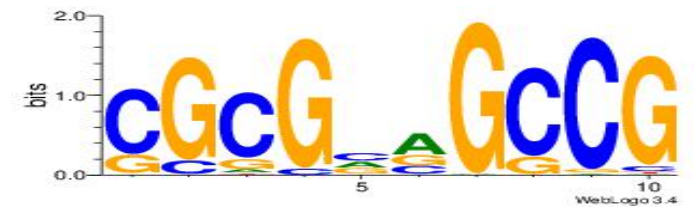


Dataset #: 5 Motif ID: 48 Motif name: TFW3

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



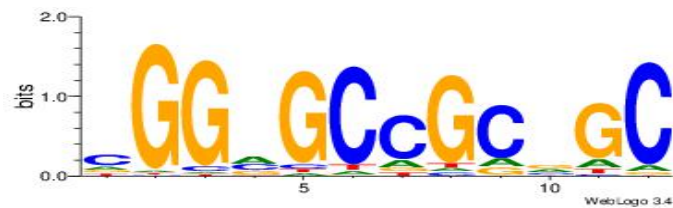
Best Matches for Motif ID 48 (Highest to Lowest)

Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

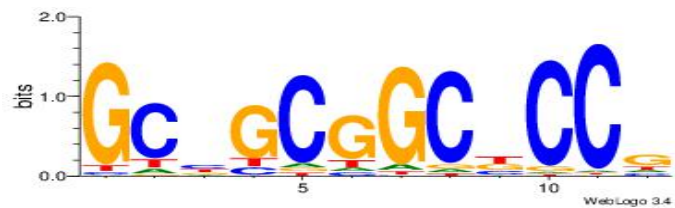
Number of overlap: 10
Similarity score: 0.0623879

Alignment:
CGGVGCCGCVGC
CGGCYBCGCG--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #: 3
Motif ID: 23
Motif name: Egr1
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: 0.0630189

Alignment:
YCGCCCACGCH
CGGCYBCGCG--

Original motif Consensus sequence: HCGTGCGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



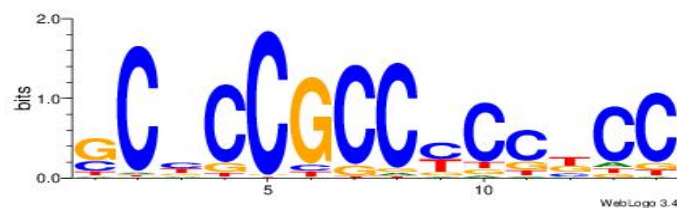
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0645308

Alignment:
 GGMGGRGGCGGVGC
 CGCGBMGCCG----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



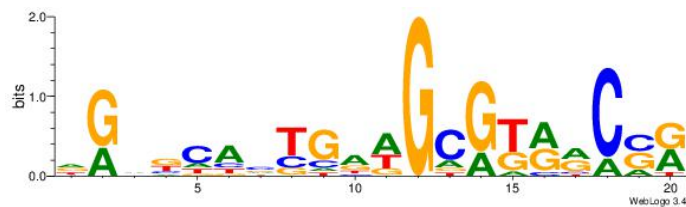
Dataset #: 3
 Motif ID: 31

Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	11
Number of overlap:	10
Similarity score:	0.0714355

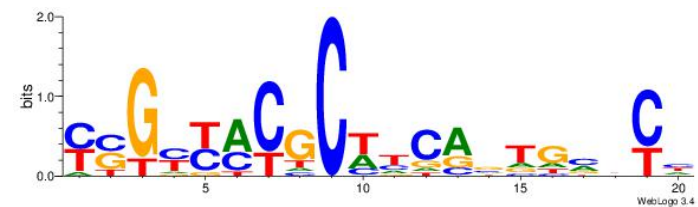
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----CGGCYBCGCG
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

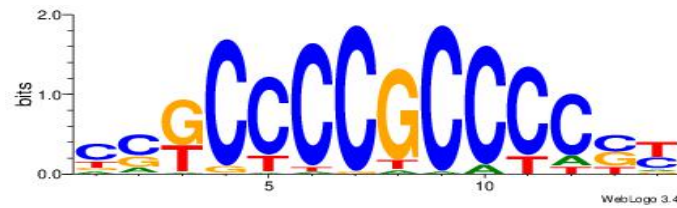


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0717594

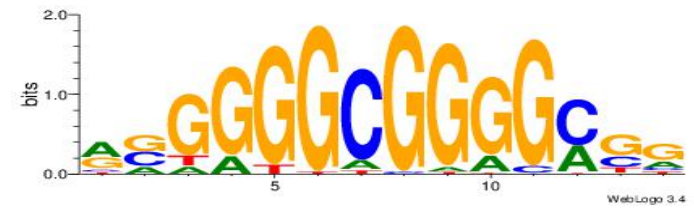
Alignment:

CSKCCCCGCCCCSY
CGGCYBCGCG----

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



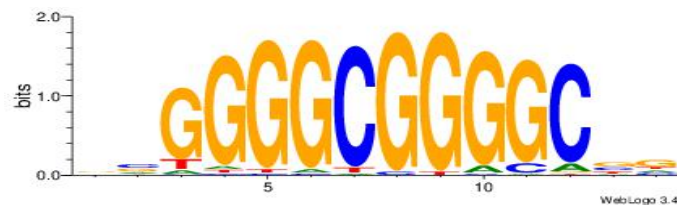
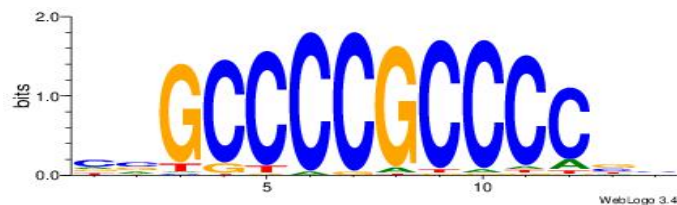
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	10
Similarity score:	0.0718771

Alignment:

HVGCCCCGCCCCBB
CGGCYBCGCG----

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC

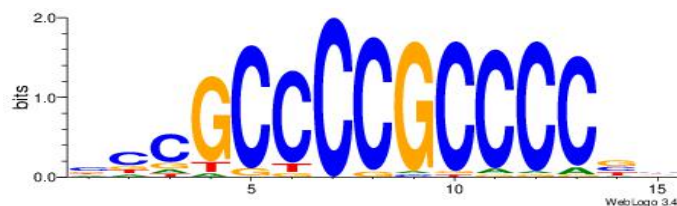


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0719604

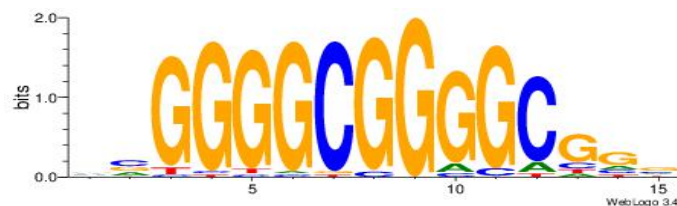
Alignment:

BCCGCCCCGCCCCBB
 -CGGCYBCGCG----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



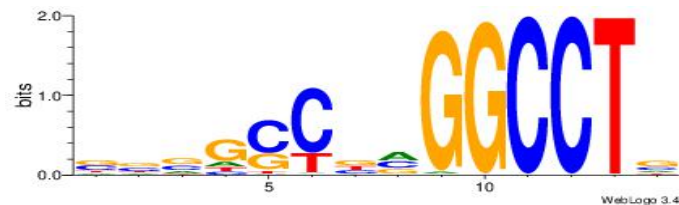
Dataset #: 3

Motif ID: 22
 Motif name: Zfx
 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: 0.0766755

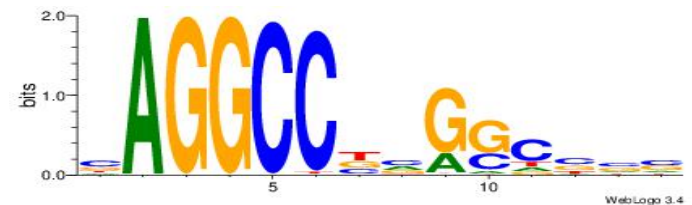
Alignment:

VAGGCCBBGGCVBB
 --CGGCYBCGCG--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

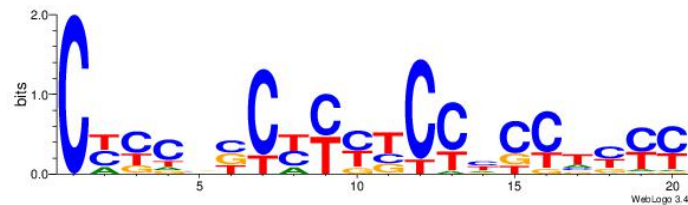


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0767689

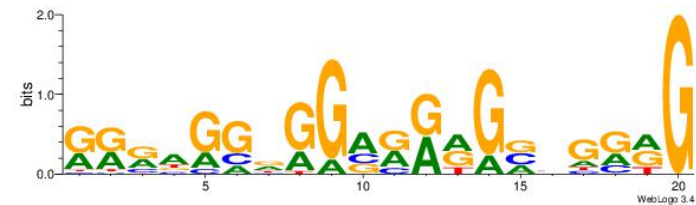
Alignment:

KKKAGGDGGAKKMGBBGKMG
-----CGCGBMGCCG

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



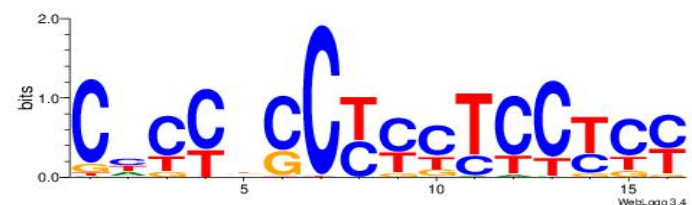
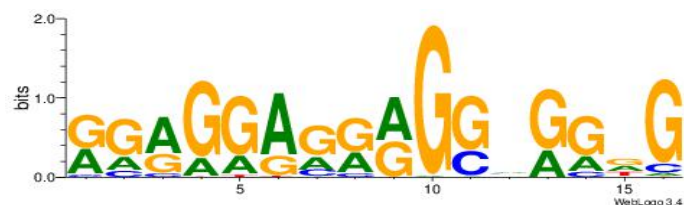
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0814831

Alignment:

CHCCBCKMCTCCKCM
CGGCYBCGCG-----

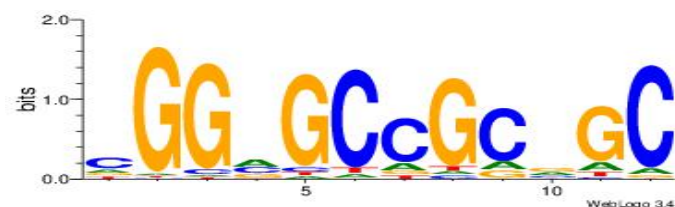
Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM

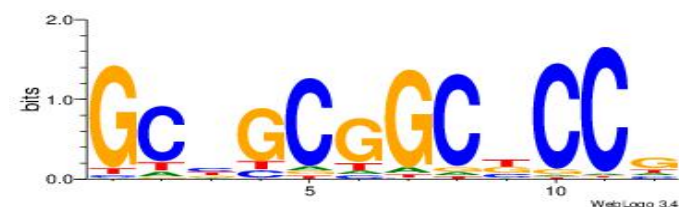


Dataset #: 5 Motif ID: 49 Motif name: TFF1

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



Best Matches for Motif ID 49 (Highest to Lowest)

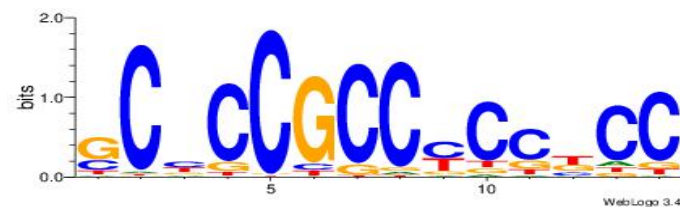
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0292081

Alignment:
 GGMGGRGGCGGVGC
 --CGGVGCCGCVGC

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

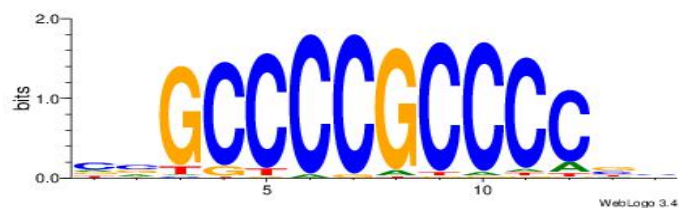


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0542674

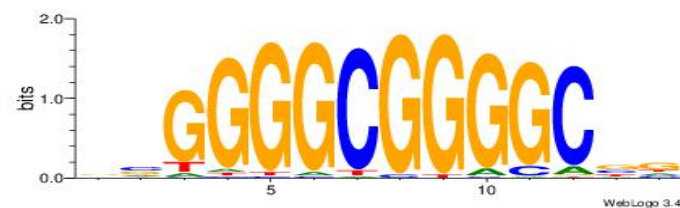
Alignment:

HVGCCCCGCCCCBB
 CGGVGCCGCVGC---

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

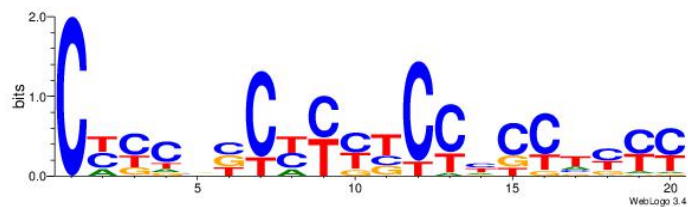


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0543272

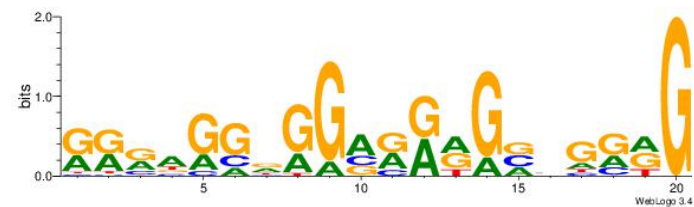
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -----CGGVGCCGCVGC--

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



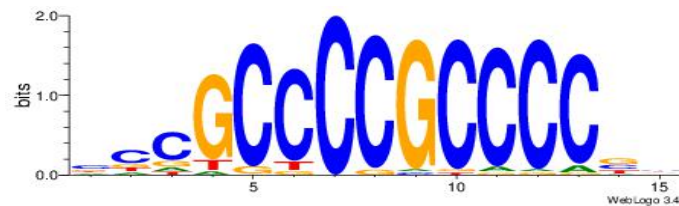
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4

Number of overlap: 12
Similarity score: 0.0548371

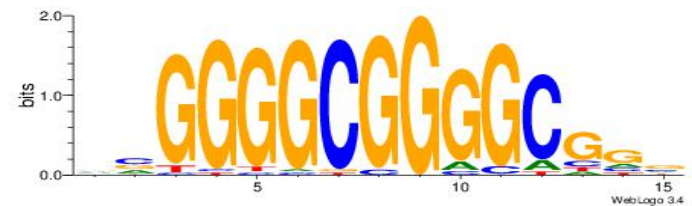
Alignment:

BBGGGGCGGGGCGGB
---CGGVGCCGCVGC

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

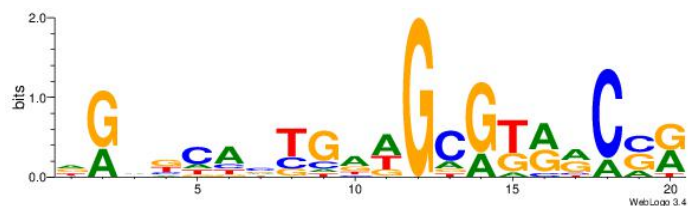


Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 12
Similarity score: 0.0556962

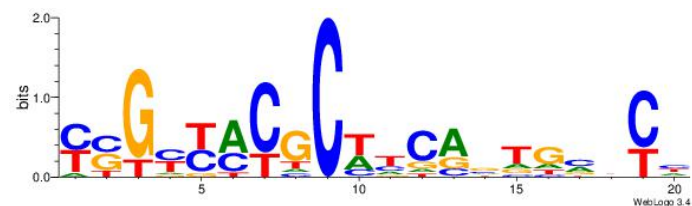
Alignment:

DGVBCABTGDWCGKRRCSR
GCVGCGGCBCCG-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBB

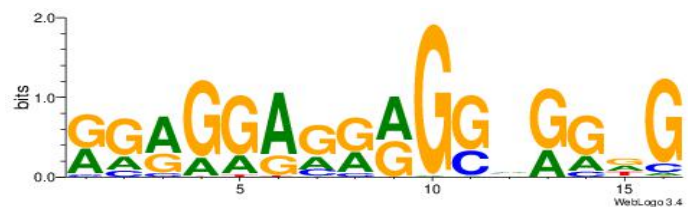


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0594165

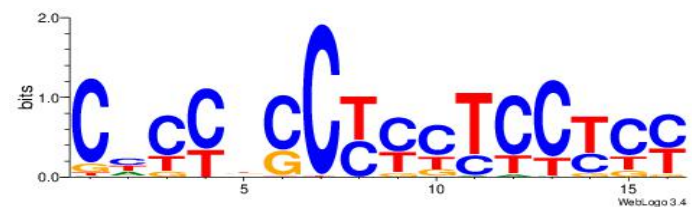
Alignment:

CHCCBCKMCTCCKCM
 --GCVGCGGCBCG--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

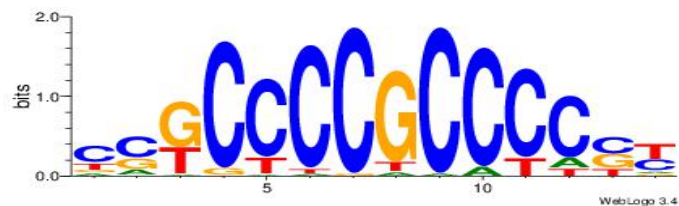


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0624366

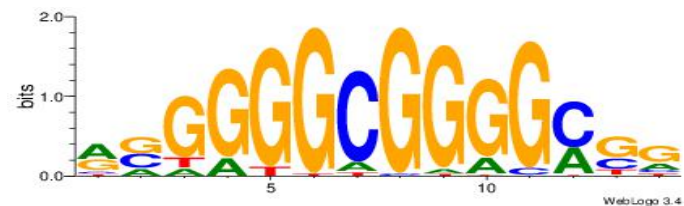
Alignment:

CSKCCCCGCCCCSY
 GCVGCGGCBCCG--

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

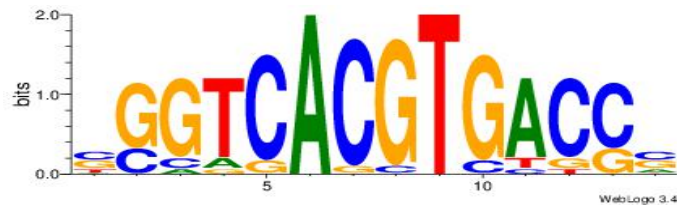


Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12

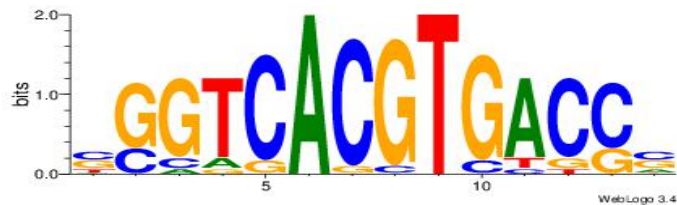
Similarity score: 0.0777862

Alignment:
SGGTCACGTGACCS
--CGGVGCCGCVGC

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

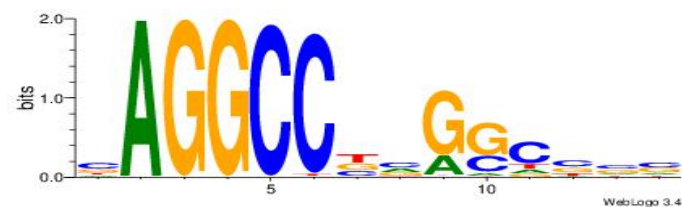
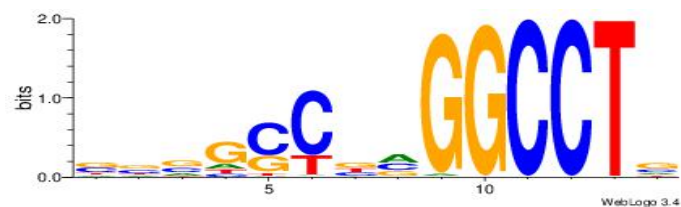


Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0779228

Alignment:
BBVGCCBVGGCCTV
-GCVGCGGCBCCG-

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCV

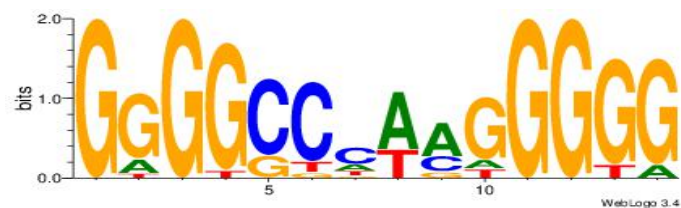


Dataset #: 3
 Motif ID: 30
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0809608

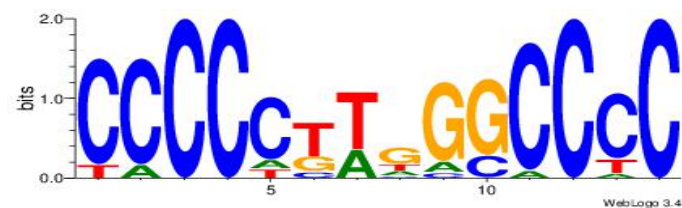
Alignment:

GGGGCCCAAGGGGG
 CGGVGCCGCVGC--

Original motif Consensus sequence: GGGGCCCAAGGGGG

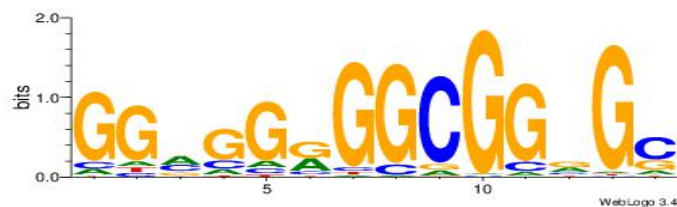


Reverse complement motif Consensus sequence: CCCCCTTGGGCC

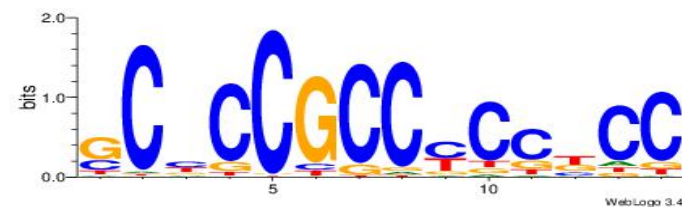


Dataset #: 5 **Motif ID: 50** **Motif name: TFF11**

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



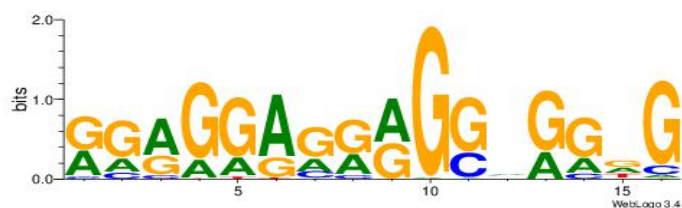
Best Matches for Motif ID 50 (Highest to Lowest)

Dataset #:	5
Motif ID:	51
Motif name:	TFM2
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:	0.033716

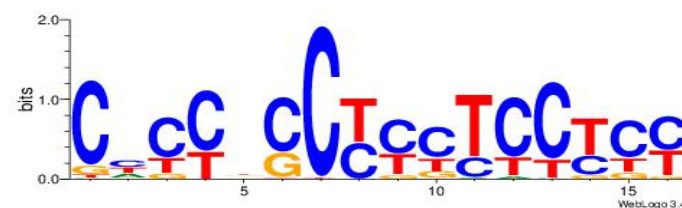
Alignment:

```
RGRGGAGRRGGHGGDG
GGMGGRGGCGGVGC--
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKM

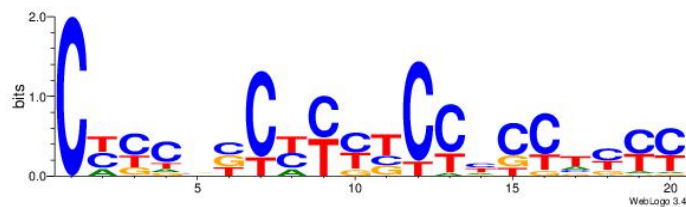


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0386905

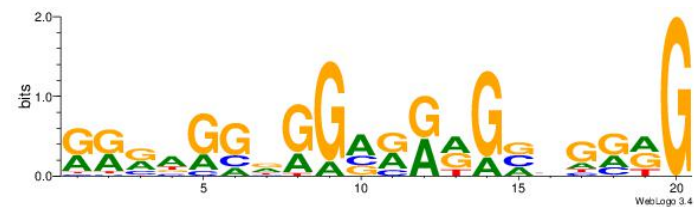
Alignment:

CYYCBBCYYYTCCHCCTYYY
 -----GCVCCGCCMCCYCC-

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

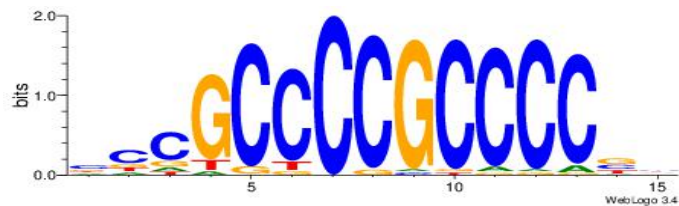


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

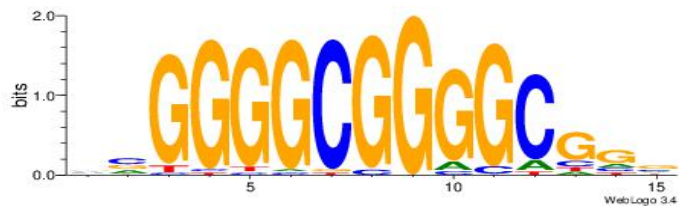
Number of overlap: 14
Similarity score: 0.0548198

Alignment:
BBGGGGCGGGGCGGB
GGMGRRGGCGGVGC-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



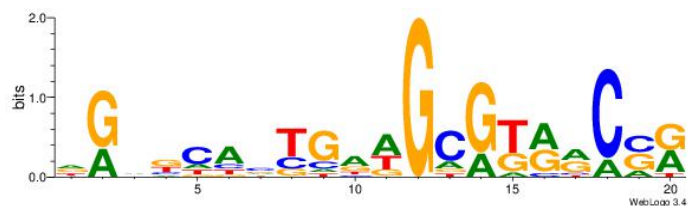
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



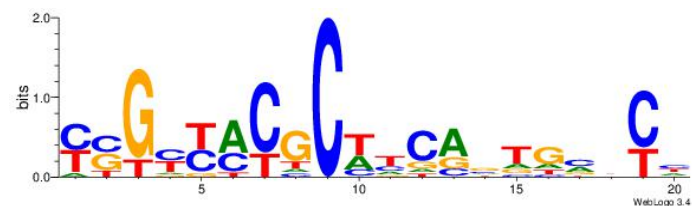
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0573129

Alignment:
DGVBCABTGDWCGKRRCSR
----GGMGRRGGCGGVGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBBCD



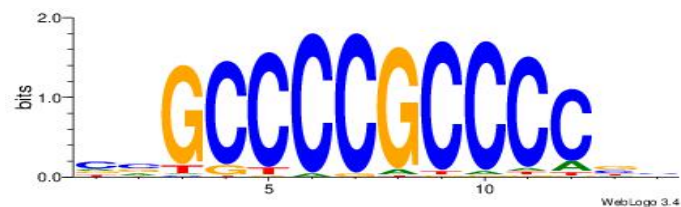
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0652173

Alignment:

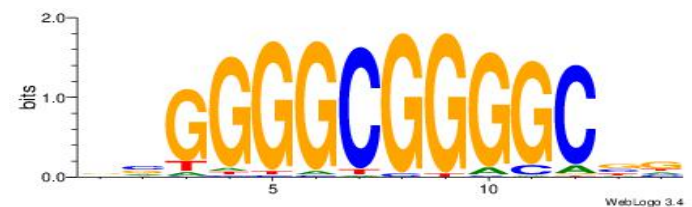
BBGGGGCGGGGCVD

GGMGGRGGCGGVGC

Original motif Consensus sequence: HVGCCCCGCCCCBB



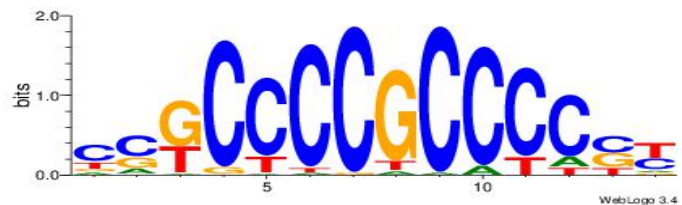
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



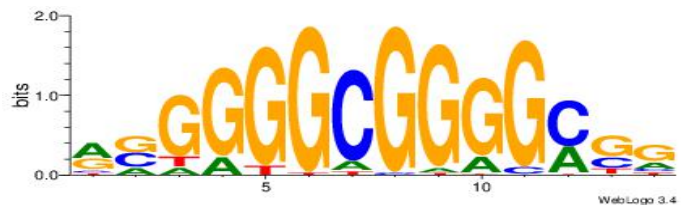
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0661275

Alignment:
MSGGGGCGGGYSG
GGMGRRGGCGGVGC

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY

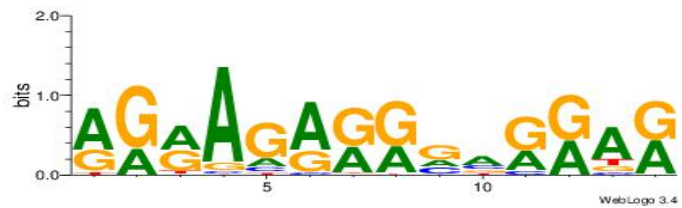


Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14

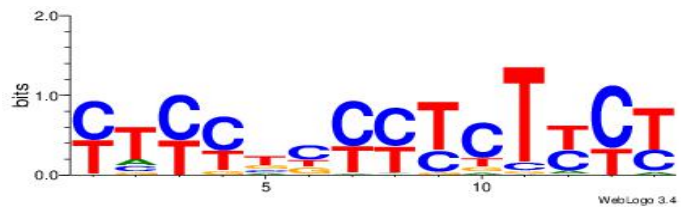
Similarity score: 0.0714286

Alignment:
RGRAGARRGARRAR
GGMGGRGGCGGVGC

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

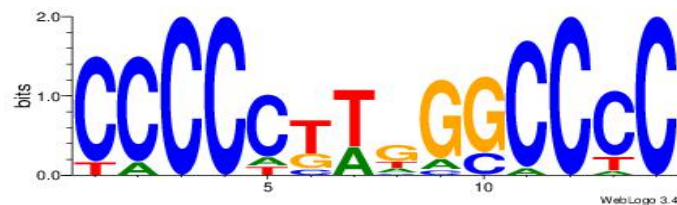
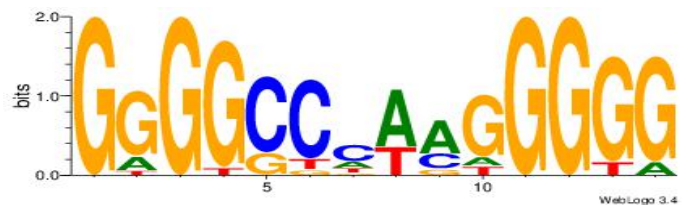


Dataset #: 3
Motif ID: 30
Motif name: PLAG1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.574939

Alignment:
-CCCCCTTGGGCCCC
GCVCCGCCMCCYCC-

Original motif Consensus sequence: GGGGCCCAAGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCC

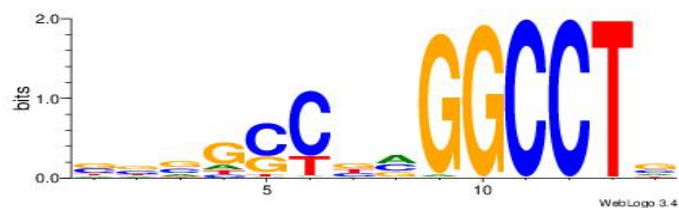


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.577861

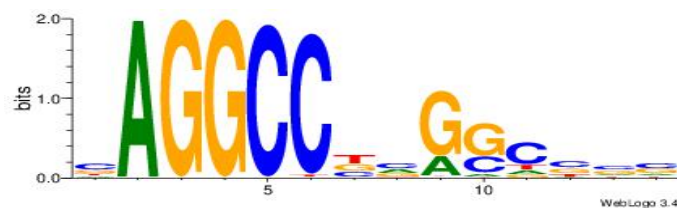
Alignment:

VAGGCCBBGGCVBB-
 -GGMGGRGGCGGVGC

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



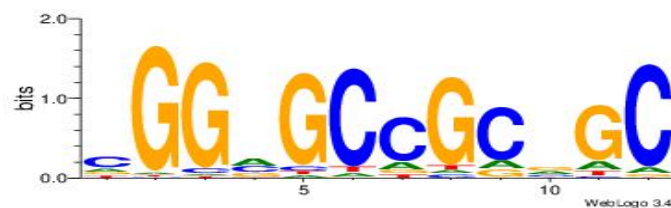
Dataset #: 5
 Motif ID: 49

Motif name: TFF1
 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: 1.02659

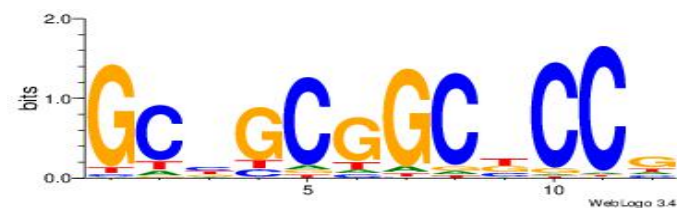
Alignment:

--CGGVGCCGCVGC
 GGMGGRGGCGGVGC

Original motif Consensus sequence: CGGVGCCGCVGC

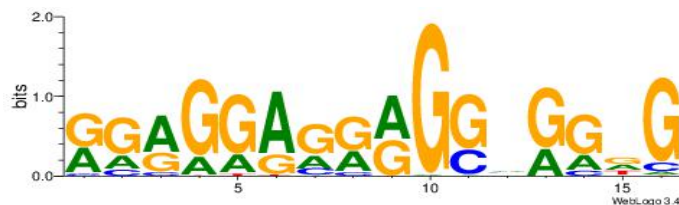


Reverse complement motif Consensus sequence: GCVGCGGCBCCG

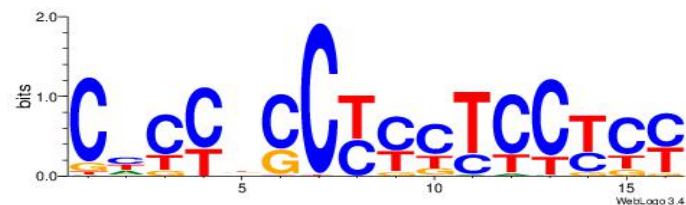


Dataset #: 5 Motif ID: 51 Motif name: TFM2

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



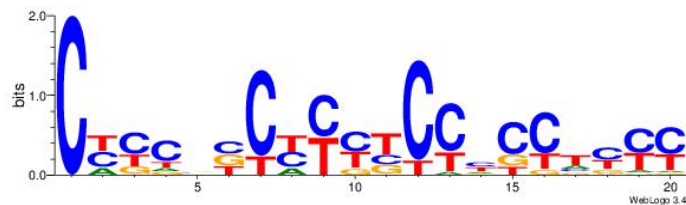
Best Matches for Motif ID 51 (Highest to Lowest)

Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0331473

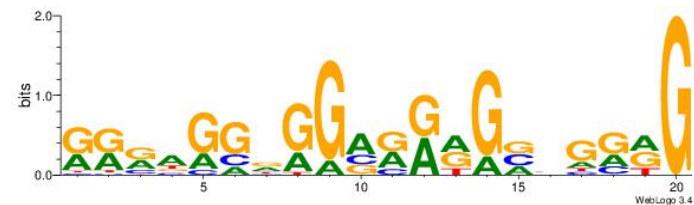
Alignment:

```
CYYCBBCYYYTCCHCCTYYY  
CHCCBCKMCTCCKCM----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



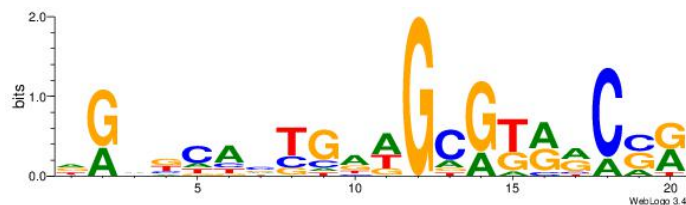
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0668155

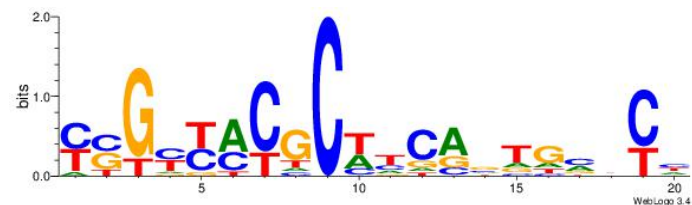
Alignment:

DGVBCABTGDWGCGRRCR
 -RGRGGAGRRGGHGGDG---

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBB

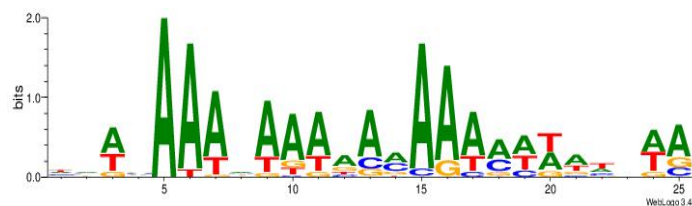


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 16
 Similarity score: 0.0794752

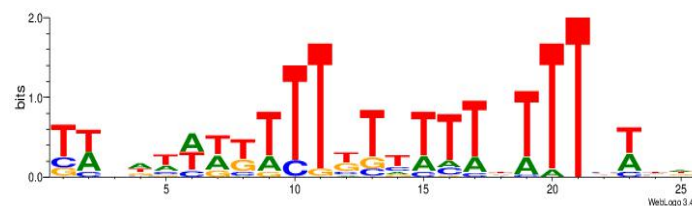
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 -----RGRGGAGRRGGHGGDG--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH

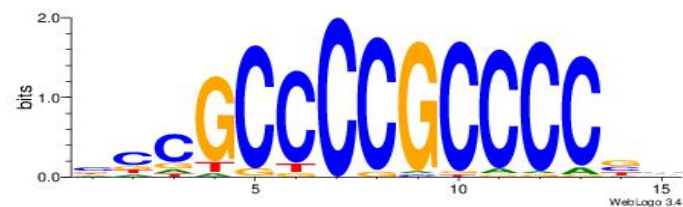


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.558405

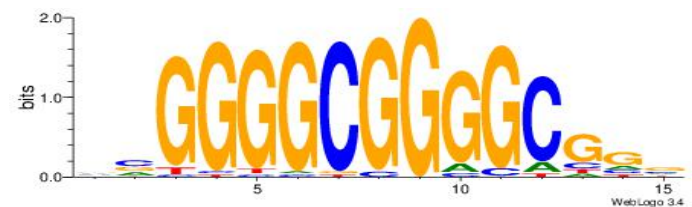
Alignment:

BCCGCCCCGCCCCBB-
CHCCBCKMCTCCKCM

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

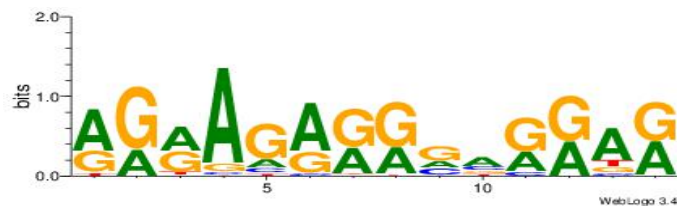


Dataset #: 2
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 1.01195

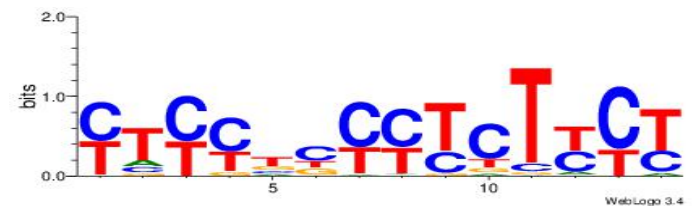
Alignment:

--RGRAGARRGARRAR
 RGRGGAGRRGGHGGDG

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

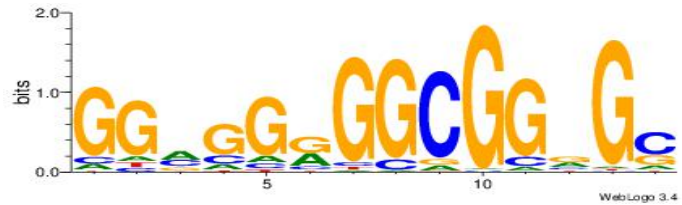


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14

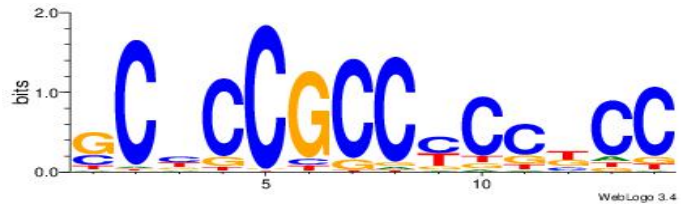
Similarity score: 1.03372

Alignment:
GGMGGRGGCGGVGC--
RGRGGAGRRGGHGGDG

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

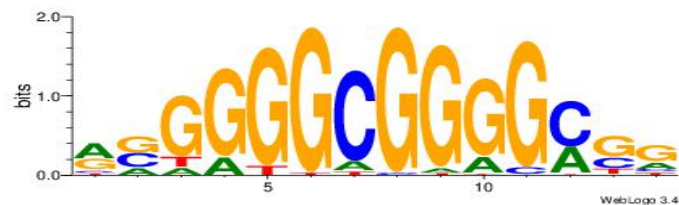
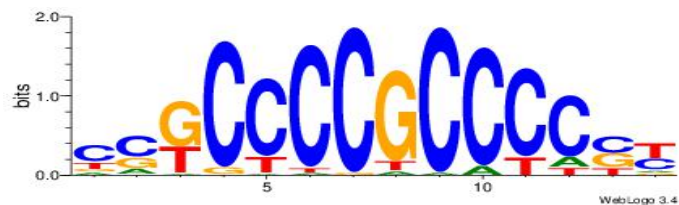


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 1.05908

Alignment:
MSGGGGCGGGYSG--
RGRGGAGRRGGHGGDG

Original motif Consensus sequence: CSKCCCCGCCCSY

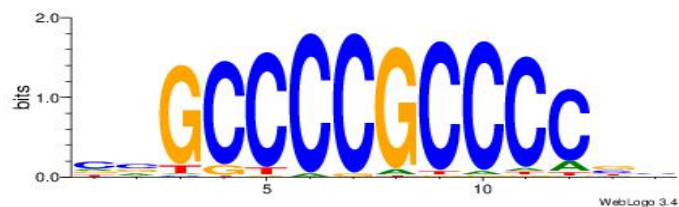
Reverse complement motif Consensus sequence: MSGGGGCGGGY



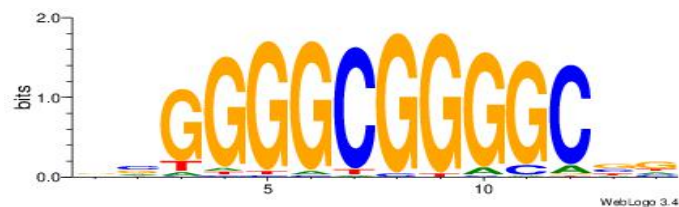
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 1.05955

Alignment:
 HVGCCCGCCCCBB--
 CHCCBCKMCTCCKCM

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGc



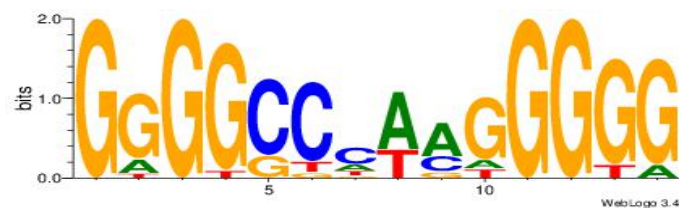
Dataset #: 3
 Motif ID: 30

Motif name:	PLAG1
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:	1.07365

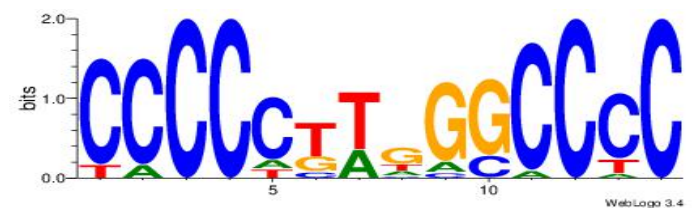
Alignment:

```
--CCCCCTTGGGCCCC
CHCCBCKMCTCCKCM
```

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

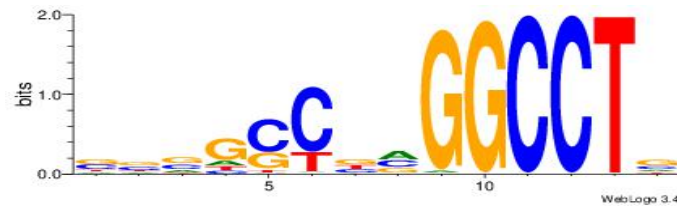


Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	2.06908

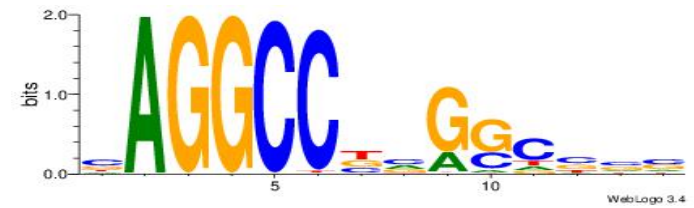
Alignment:

VAGGCCBBGGCVBB-----
--RGRGGAGRRGGHGGDG

Original motif Consensus sequence: BBVGCCBVGGCCTV

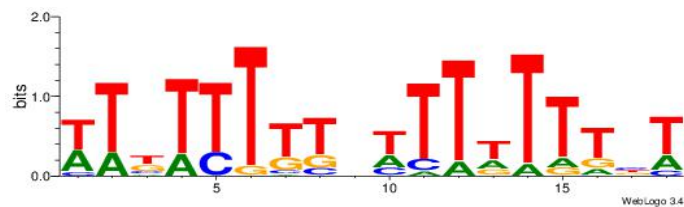


Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

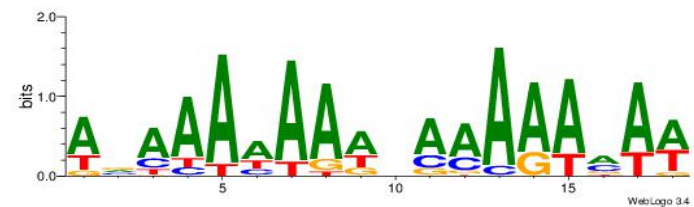


Dataset #: 5 Motif ID: 52 Motif name: TFM1

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWHAAAAARAW



Best Matches for Motif ID 52 (Highest to Lowest)

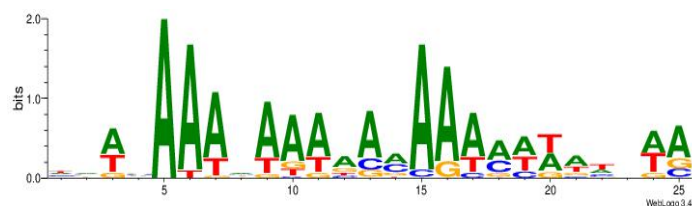
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 6
 Number of overlap: 18
 Similarity score: 0

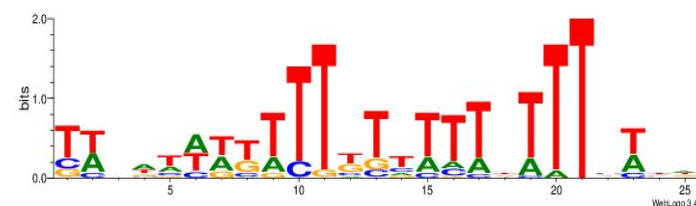
Alignment:

TWVHWWYTTTYTTTTTHTTTVWBH
 -----WTKTTTTTHWTTTTTTBT--

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTTHTTTVWBH

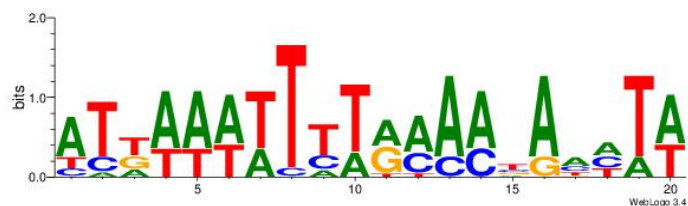


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0364672

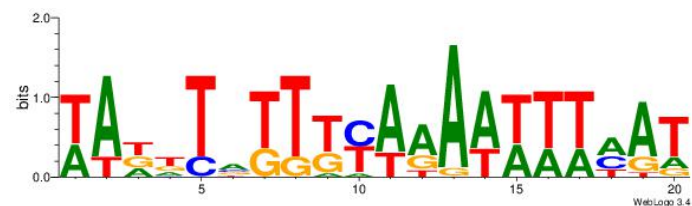
Alignment:

ATKAAWTTTTTRMAABAHHTW
 ABAAAAAWhAAAAARAW--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

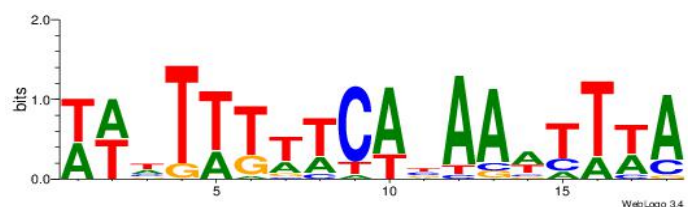


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.0456974

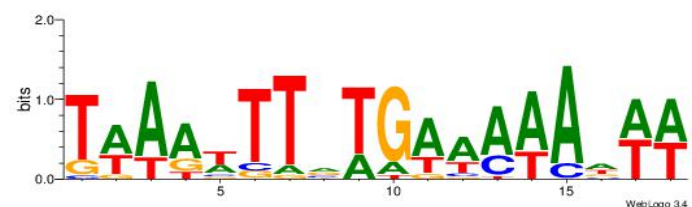
Alignment:

WWHTTTTTCABAAWTTWA
WTKTTTTTHWTTTTTTBT

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

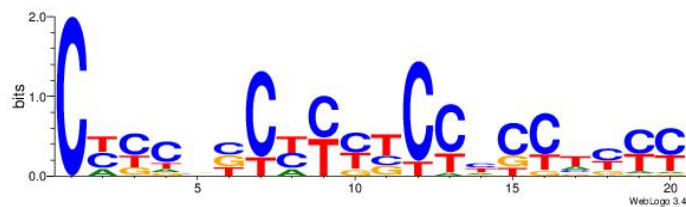


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.572783

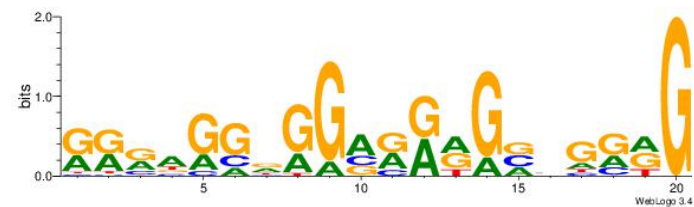
Alignment:

CYYCBBCYYYTCCHCCTYYY-
 ---WTKTTTTTHWTTTTTTBT

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

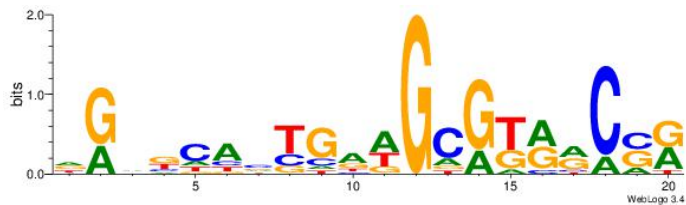


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5

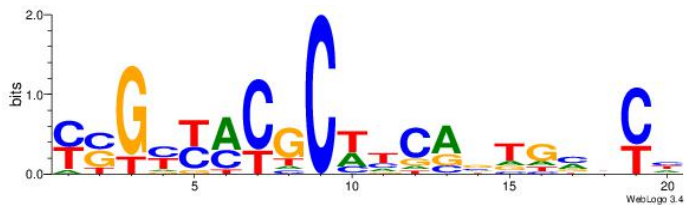
Number of overlap: 16
Similarity score: 1.07322

Alignment:
--MSGKKRCGCWDCABTGBBCD
WTKTTTTTHWTTTTTTBT----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

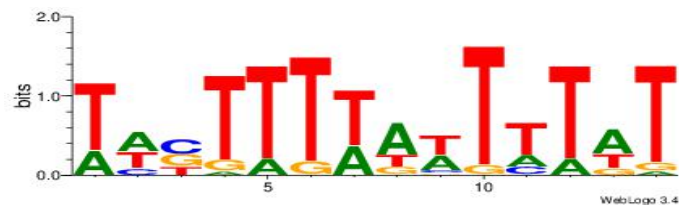
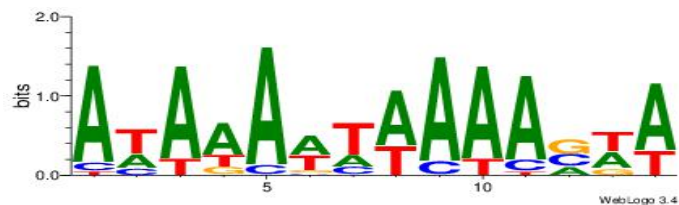


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 2.01877

Alignment:
----TWSTTTWAWTTTWT
WTKTTTTTHWTTTTTTBT

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

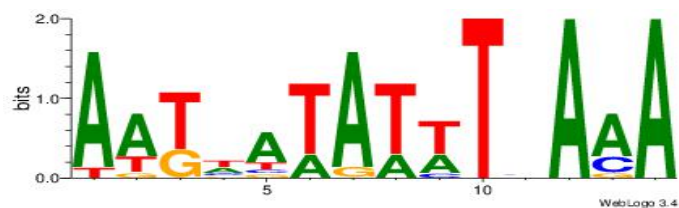


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 2.05025

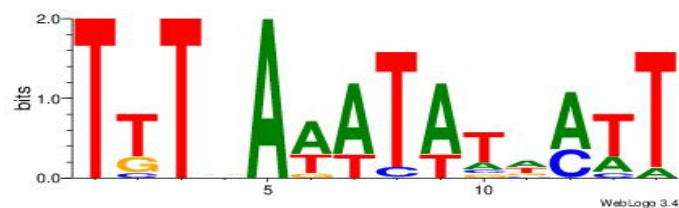
Alignment:

----AATHATATWTHAAA
 ABAAAAAAWHAAAAARAW

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

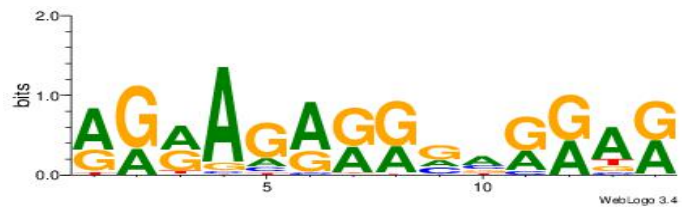


Dataset #: 2
 Motif ID: 2

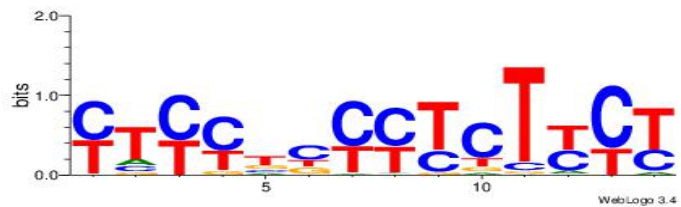
Motif name:	Motif 2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	2.05187

Alignment:
MTMMTCMMTCTKCK-----
WTKTTTTTHWTTTTTTBT

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK

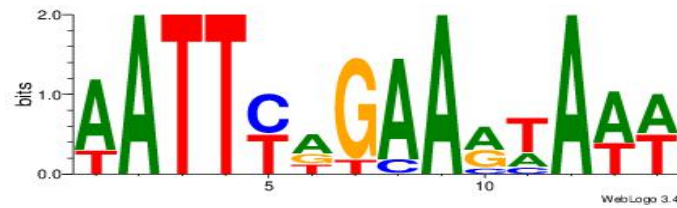


Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	2.0566

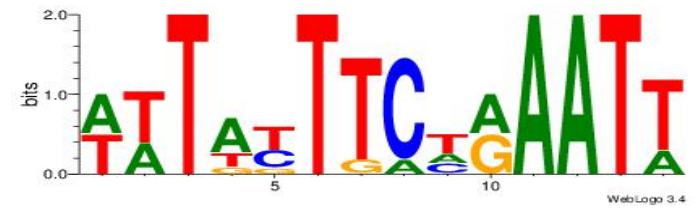
Alignment:

AATTYDGAARTAWW-----
ABAAAAAAWHAAAAARAW

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



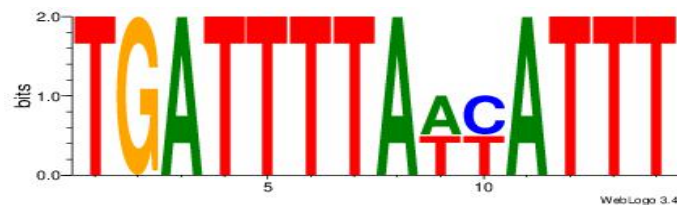
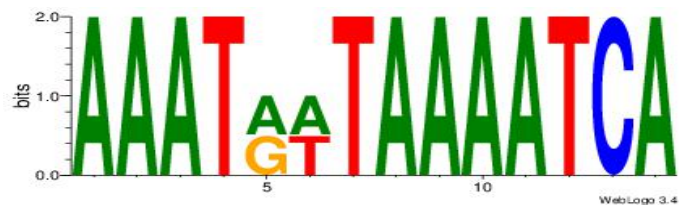
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	2.07166

Alignment:

-----TGATTTTAWKATTT
WTKTTTTTHWTTTTTTBT

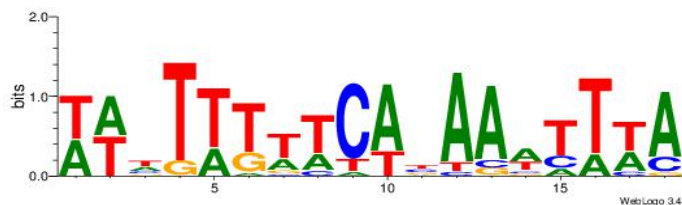
Original motif Consensus sequence: AAATRWTAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATTT

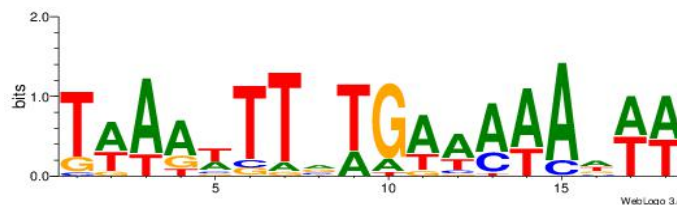


Dataset #: 5 **Motif ID: 53** **Motif name: TFM3**

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



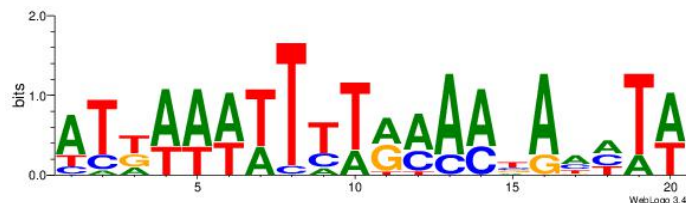
Best Matches for Motif ID 53 (Highest to Lowest)

Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	18
Similarity score:	0.013876

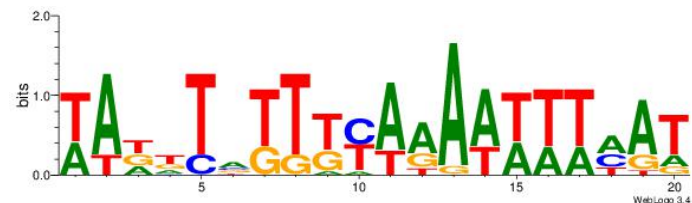
Alignment:

ATKAAWTTTTRMAABAHHTW
 -TAAWTTVTGAAAAHWW-

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



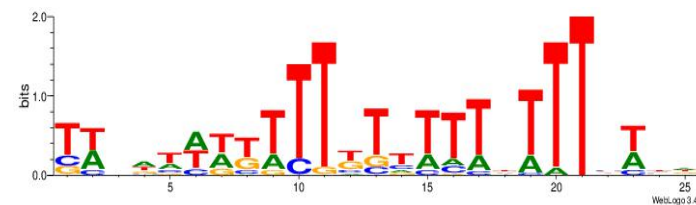
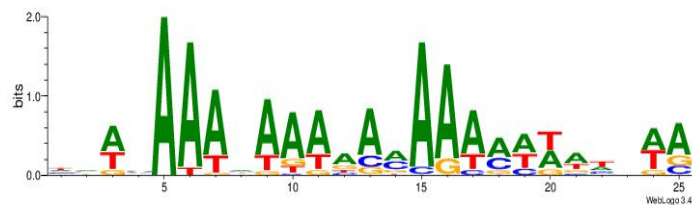
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	18
Similarity score:	0.0402327

Alignment:

```
TWVHWWYTTTYTTTTHTTTVWBH
----WWHTTTTTCABAAWTTWA----
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTHTTTVWBH

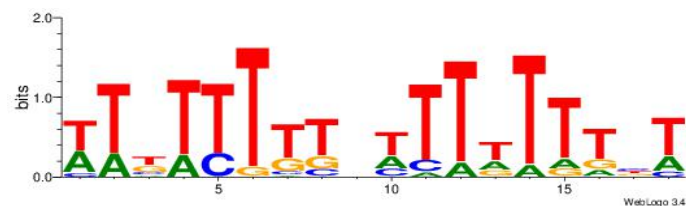


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0432207

Alignment:

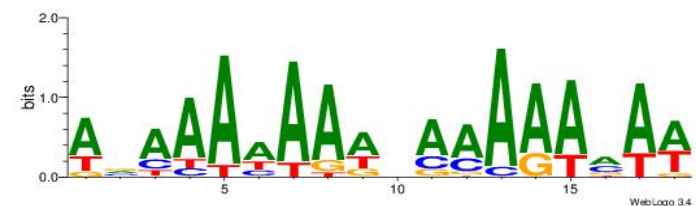
WTKTTTTTHWTTTTTTBT
 WWHTTTTTTCABAAWTTWA

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif
 ABAAAAAAWHAAAAARAW

Consensus sequence:



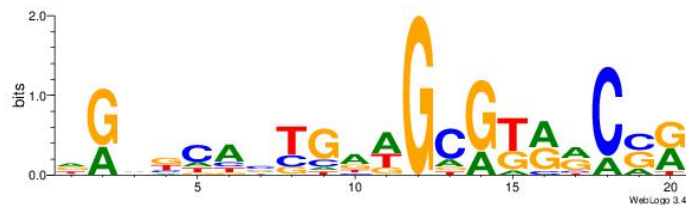
Dataset #: 3

Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	17
Similarity score:	0.561883

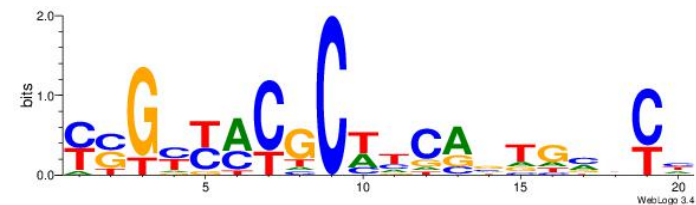
Alignment:

-MSGKKRCGCWDCABTGBB
 CD
 WWHTTTTTTCABAAWTTWA---

Original motif Consensus sequence: DGVBCABTGDWGCGRRC



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBB

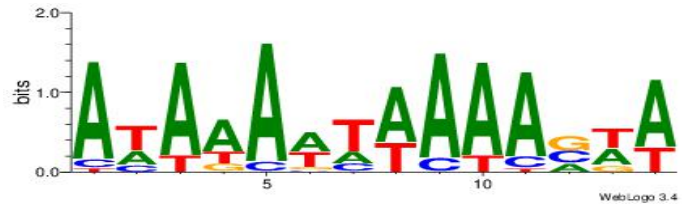


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14

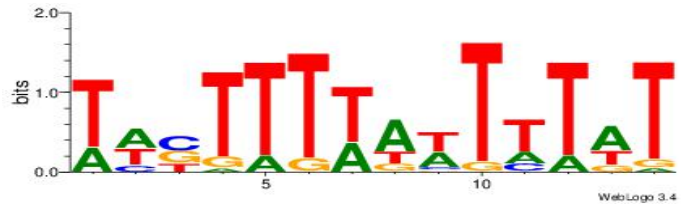
Similarity score: 2.04564

Alignment:
----TWSTTTWAWTTTWT
WWHTTTTTTCABAAWTTWA

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

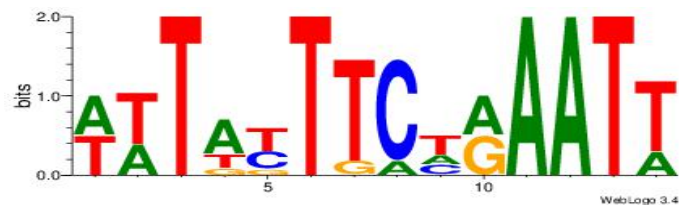


Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 2.04628

Alignment:
WWTAKTTCDKAATT----
TWAAWTTVTGAAAAAHWW

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAATT

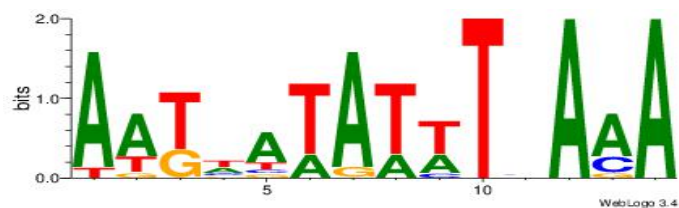


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 2.04784

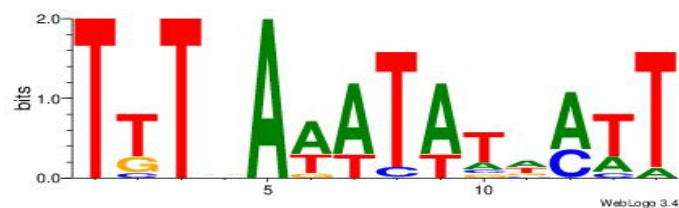
Alignment:

AATHATATWTHAAA----
 WWHTTTTTTCABAAWTTWA

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

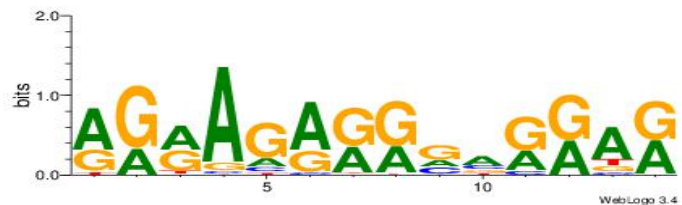


Dataset #: 2
 Motif ID: 2

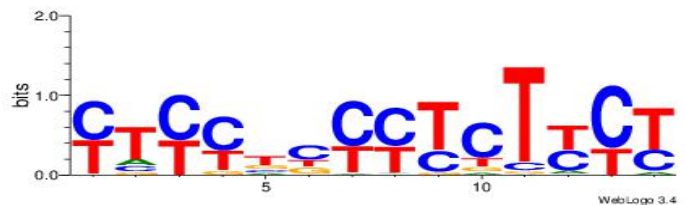
Motif name: Motif 2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 2.56928

Alignment:
-----RGRAGARRGARRAR
TWAAWTTVTGAAAAHWW-

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

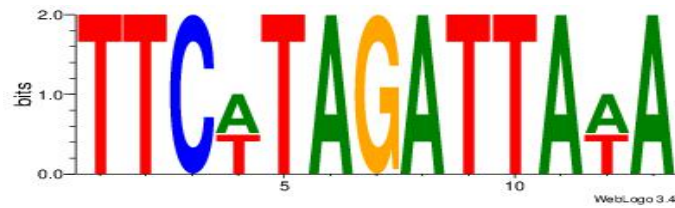


Dataset #: 2
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 2.56949

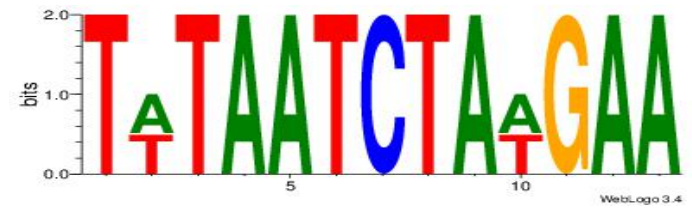
Alignment:

-----TWTAACTAWGAA
WWHTTTTTTCABAAWTTWA

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTAWGAA



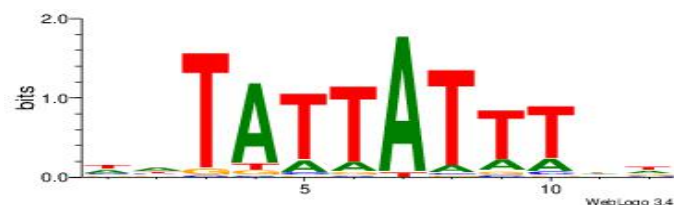
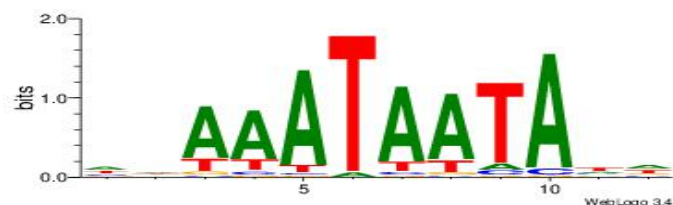
Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	3.0422

Alignment:

-----HDAAATAATADD
TWAAWTTVTGAAAAHWW

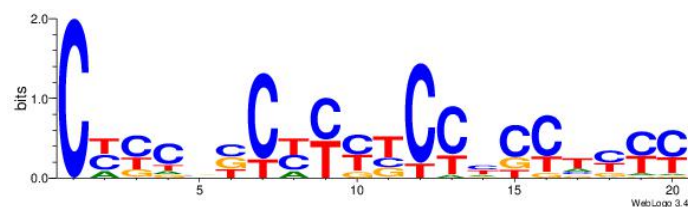
Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTDH

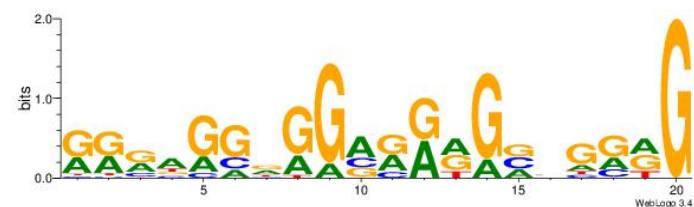


Dataset #: 5 Motif ID: 54 Motif name: TFM12

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



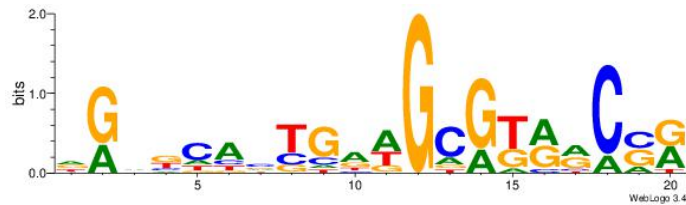
Best Matches for Motif ID 54 (Highest to Lowest)

Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0458155

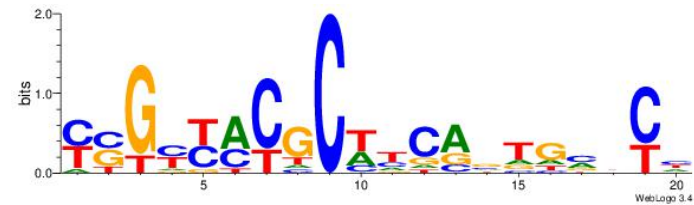
Alignment:

MSGKKRCGCWDCABTGBBCD
CYYCBCYYYTCCHCCTYYY

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



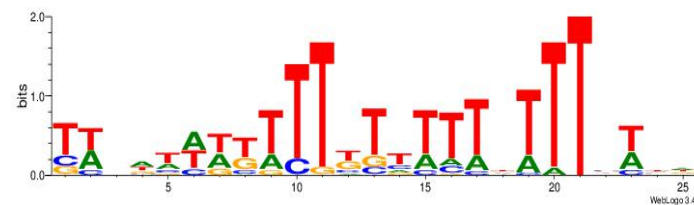
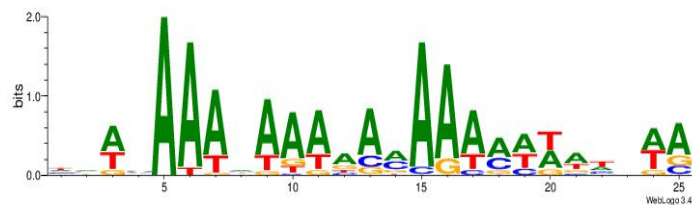
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	20
Similarity score:	0.0573204

Alignment:

TWVHWWYTTTTYTTTTTHTTTVWBH
CYYCBCYYYTCCHCCTYYY-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBBWA

Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTTHTTTVWBH



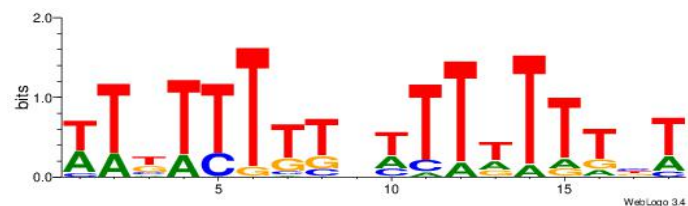
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 1.56255

Alignment:

```

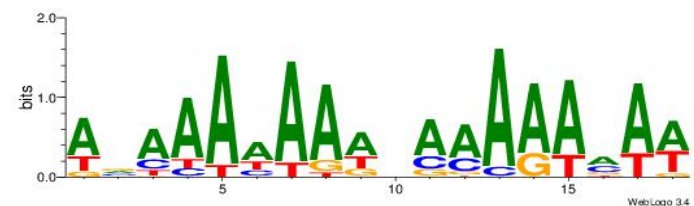
---WTKTTTTTHWTTTTTBT
CYVCBBCYYTTCCHCCTYYY-
  
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif
 ABAAAAA WHAAAAA RAW

Consensus sequence:



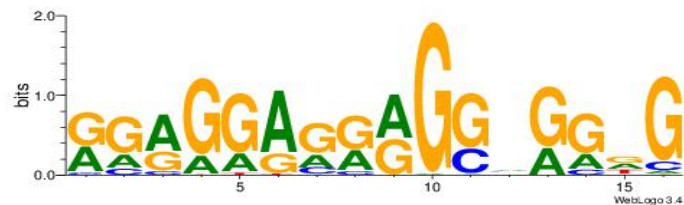
Dataset #: 5

Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 2.01568

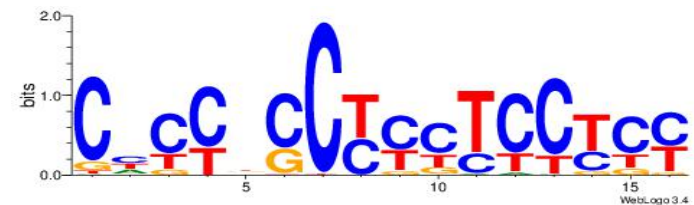
Alignment:

RGRGGAGRRGGHGGDG-----
 KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

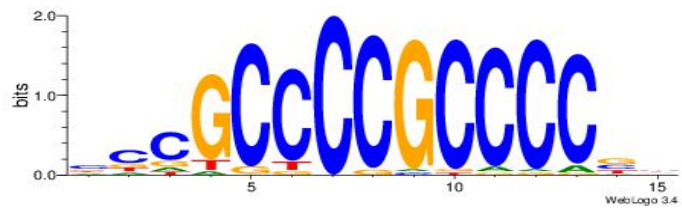


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15

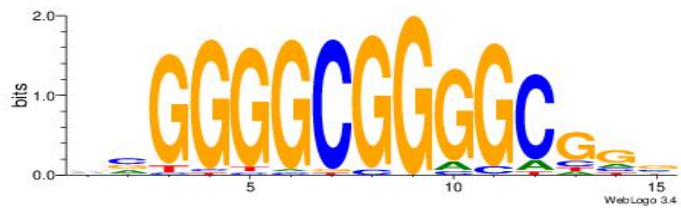
Similarity score: 2.55221

Alignment:
-----BCCGCCCCGCCCCBB
CYYCBBCYYYTCCHCCTYYY

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

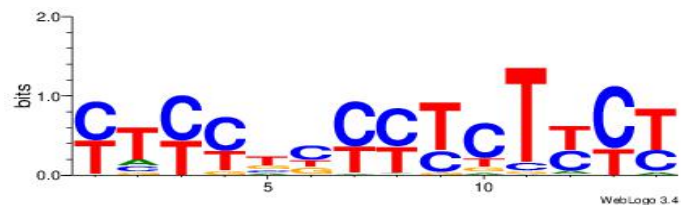
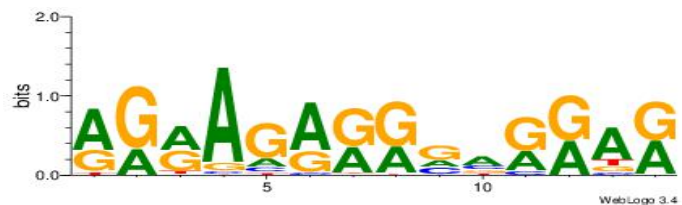


Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 3.0395

Alignment:
-----RGRAGARRGARRAR
KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTK

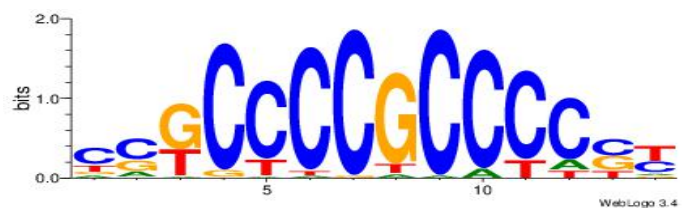


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 3.04463

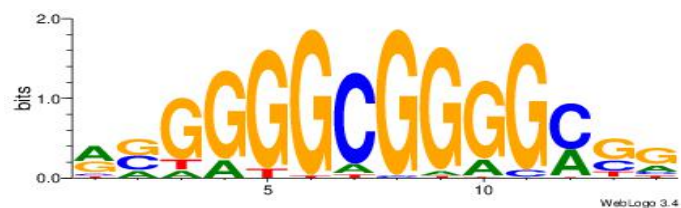
Alignment:

```
-----CSKCCCCGCCCSY
CYICBBCYYYTCCHCCTYYY
```

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



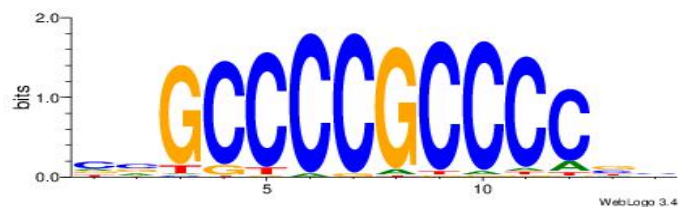
Dataset #: 4
 Motif ID: 36

Motif name: csGCCCCGCCCCsc
 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: 3.05024

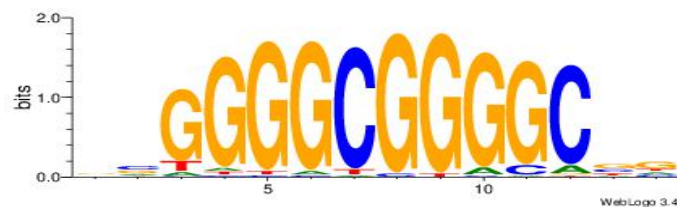
Alignment:

-----BBGGGGCGGGGCVD
 KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 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: 3.0542

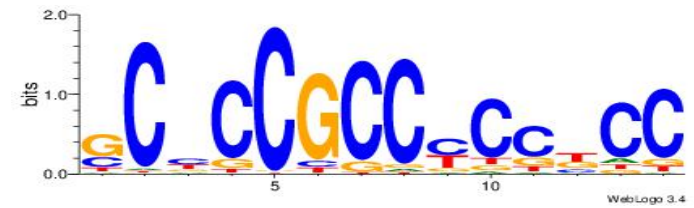
Alignment:

GGMGGRGGCGGVGC-----
KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



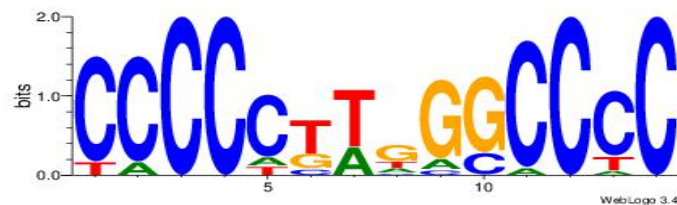
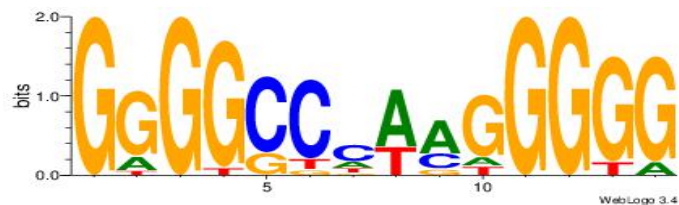
Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	3.06074

Alignment:

GGGGCCCAAGGGG-----
KKKAGGDGGAKKMGBBGKMG

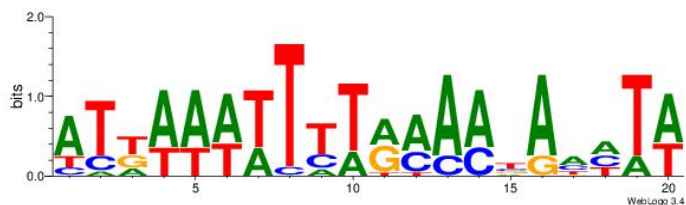
Original motif Consensus sequence: GGGGCCCAAGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCC

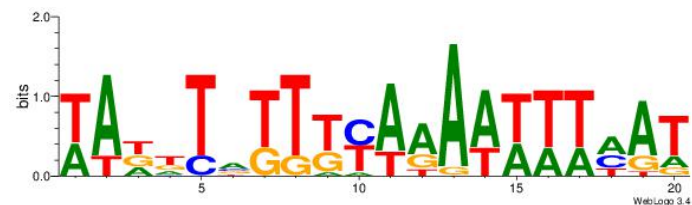


Dataset #: 5 Motif ID: 55 Motif name: TFM13

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



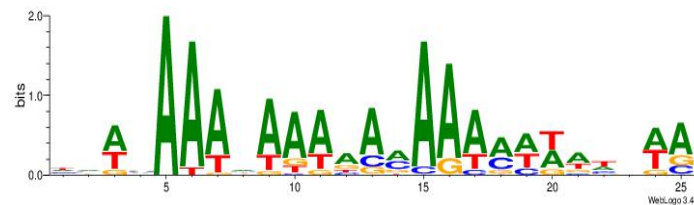
Best Matches for Motif ID 55 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	20
Similarity score:	0.0352451

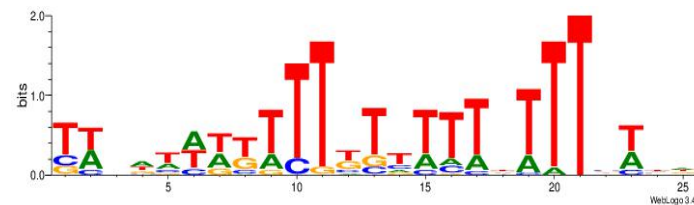
Alignment:

TWVHWWYTTTYTTTTTHTTTVWBH
 ----WAHHTVTTYKAAAAWTTRAT-

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTTHTTTVWBH

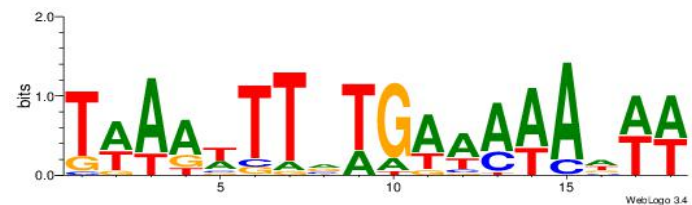
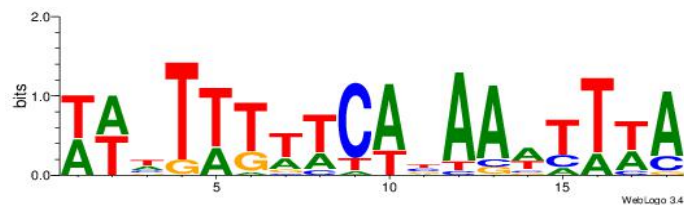


Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	1.02254

Alignment:
 TWAAWTTVTGAAAAHWW--
 ATKAAWTTTTRMAABAHHTW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
 TWAAWTTVTGAAAAHWW

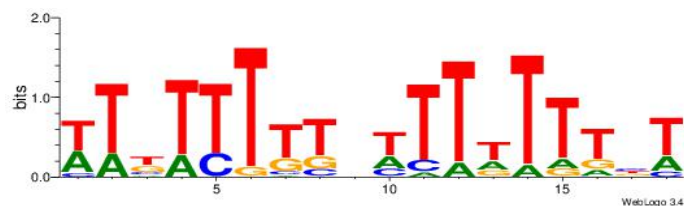


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.02868

Alignment:

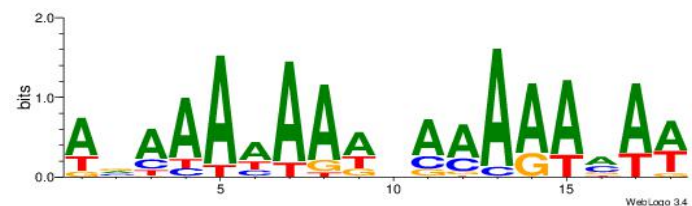
WTKTTTTTHWTTTTTTBT--
 WAHHTVTTYKAAAATTRAT

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif
 ABAAAAAWHAAAAARAW

Consensus sequence:



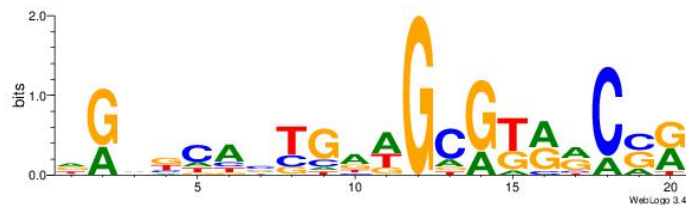
Dataset #: 3

Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 15
 Similarity score: 2.56565

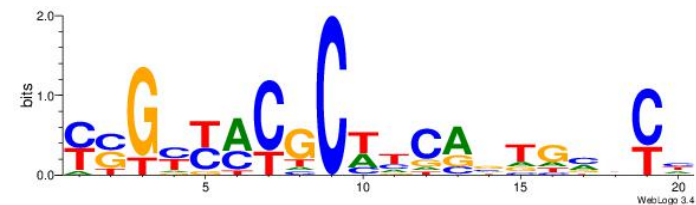
Alignment:

-----MSGKKRCGCWDCABTGBBCD
 WAHHTVTTYKAAAATTRAT-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

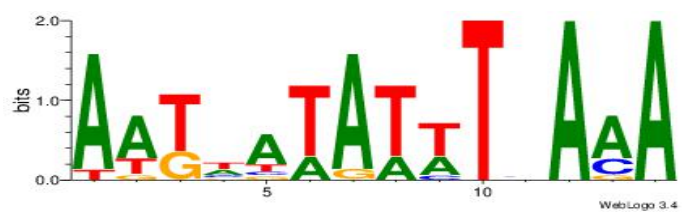


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14

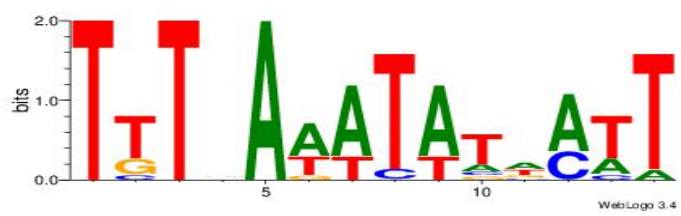
Similarity score: 3.02278

Alignment:
-----TTTDAWATATHATT
WAHHTVTTYKAAAATTRAT

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHATT

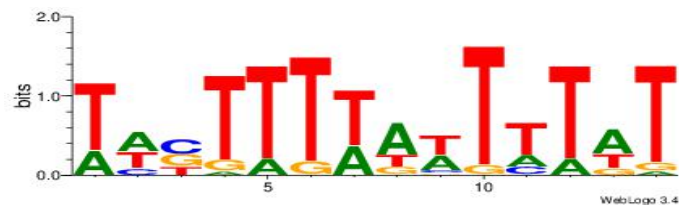
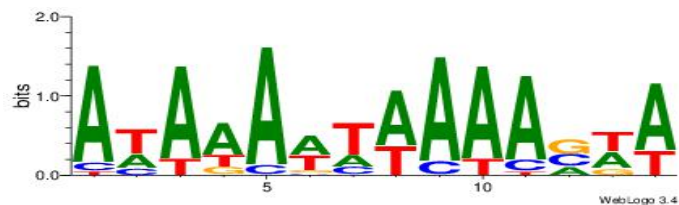


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 3.04317

Alignment:
AWAAAWTWAAASW-----
ATKAAWTTTTRMAABAHHTW

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 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: 3.05135

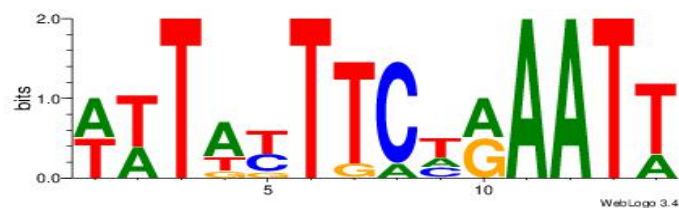
Alignment:

WWTAKTTCDKAATT-----
 WAHHTVTTYKAAAATTTTAT

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAATT



Dataset #: 2
 Motif ID: 19

Motif name:	Motif 19
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:	3.56273

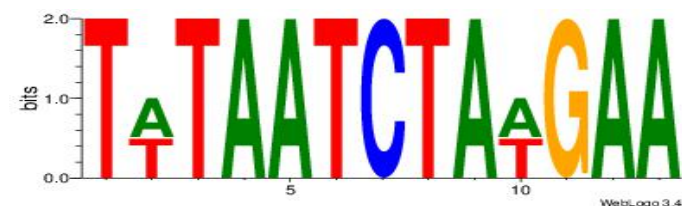
Alignment:

```
TTCWTAGATTAWA-----
WAHHTVTTYKAAAWTTRAT
```

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTAWGAA



Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
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:	3.56529

-----ACAAWTRATTTTGA
WAHHTVTTYKAAAWTTRAT-

bits

A C A A A T T A A T T T T G A

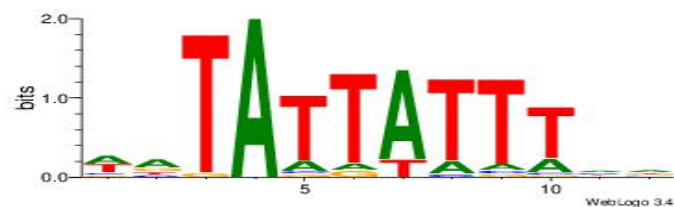
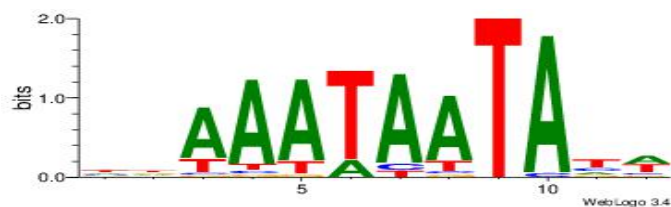
5 10

WebLogo 3.4

Alignment:

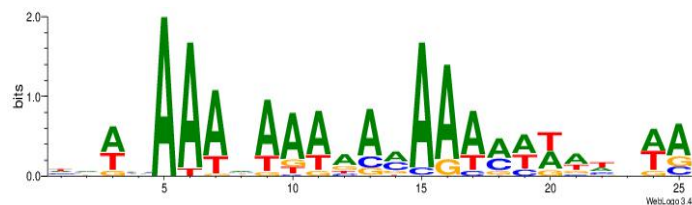
```
-----WHTATTATTTDH
ATKAAWTTTTRMAABAHTW
```

Reverse complement motif Consensus sequence: WHTATTATTTDH

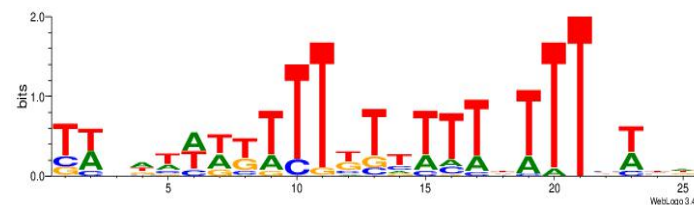


Dataset #: 5 Motif ID: 56 Motif name: TFM11

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTTTTHVWBH



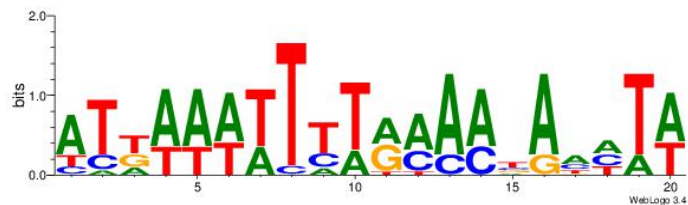
Best Matches for Motif ID 56 (Highest to Lowest)

Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0486765

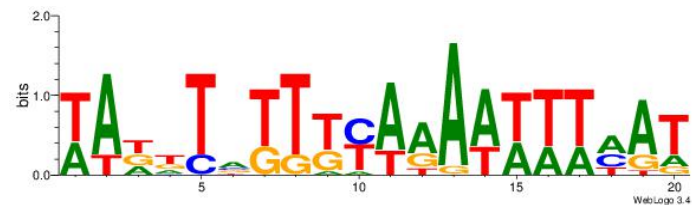
Alignment:

WAHHTVTTYKAAAATTRAT-----
 TWVHWWYTTYTTTTTHTTTVWBH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence:
 WAHHTVTTYKAAAATTRAT

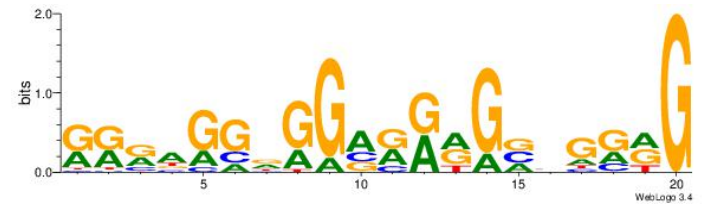
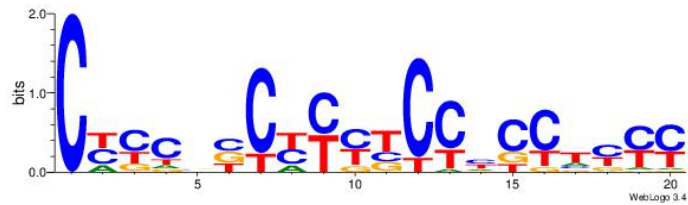


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0693284

Alignment:
 KKKAGGDGGAKKMGBBGKMG-----
 HDWVAAAHAAAAAMAAAMWWHBWA

Original motif Consensus sequence: CYCBBCTTTTCCHCCTTTT

Reverse complement motif Consensus sequence:
 KKKAGGDGGAKKMGBBGKMG

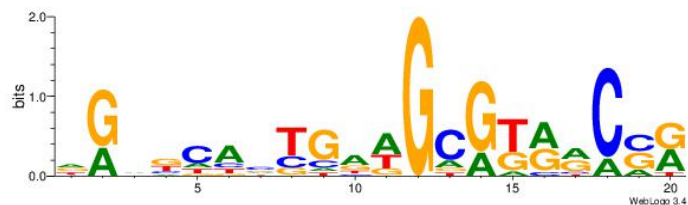


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0750613

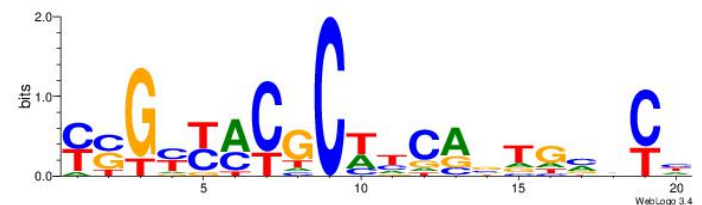
Alignment:

DGVBCABTGDWGCGRRCR-----
 HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 5

Alignment:

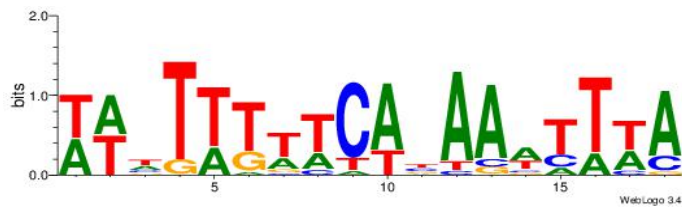
```
-----ABAAAAAAWHAAAAARAW
HDWVAAAHAAAAAMAAAMWWWHBWA
```

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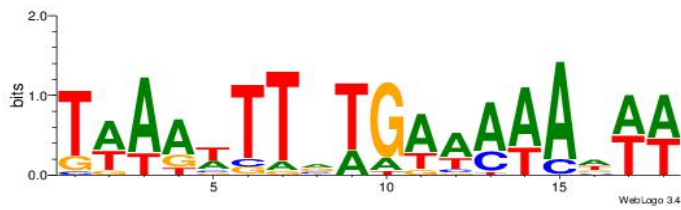
Similarity score: 1.05388

Alignment:
WWHTTTTTCABAAWTTWA-----
TWVHWWYTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

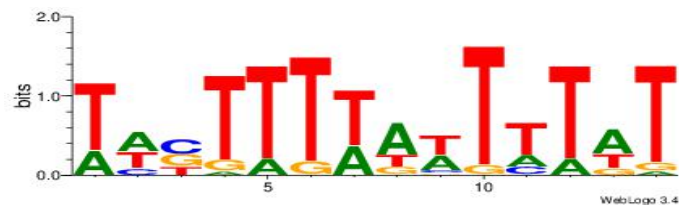
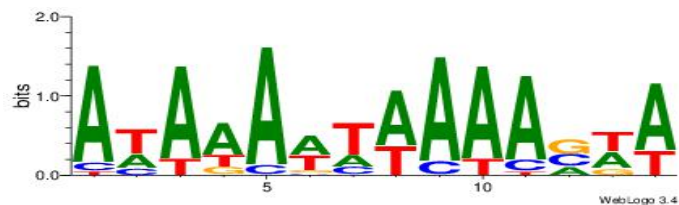


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 3.04236

Alignment:
TWSTTTWAWTTTWT-----
TWVHWWYTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: AWAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

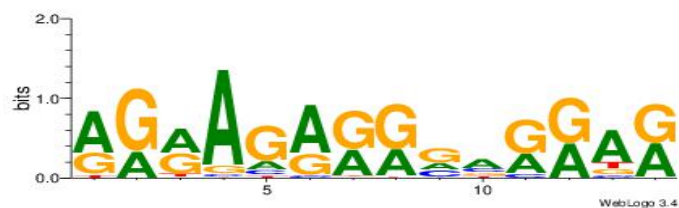


Dataset #: 2
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 3.05212

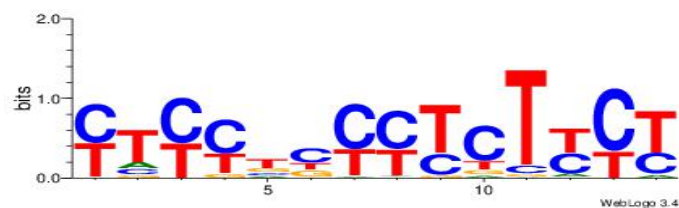
Alignment:

-----RGRAGARRGARRAR
 HDWVAAAHA AAAA MA AAMWWH BWA

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



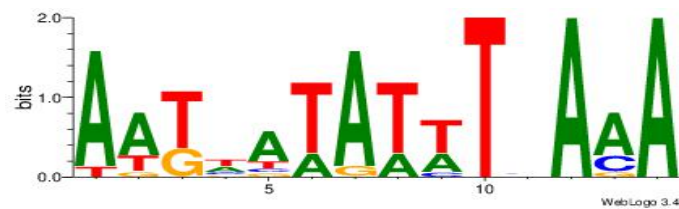
Dataset #: 2
 Motif ID: 9

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:	14
Similarity score:	3.05326

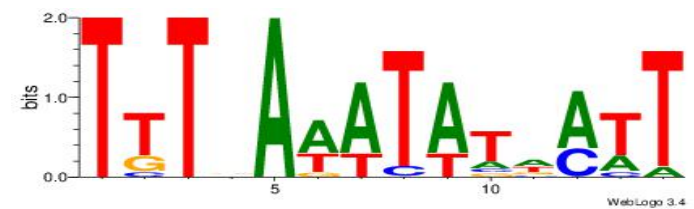
Alignment:

AATHATATWTHAAA-----
TWVHWWWYTTYTTTTHTTTVWBH

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

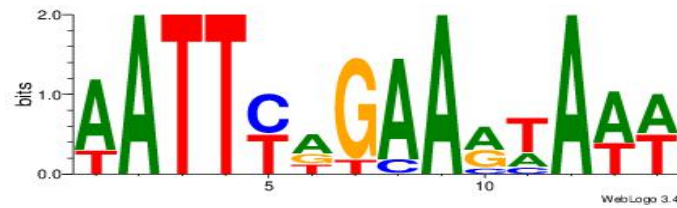


Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	3.06919

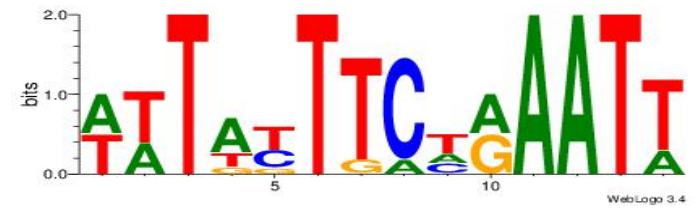
Alignment:

WWTAKTTCDKAATT-----
TWVHWWYTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



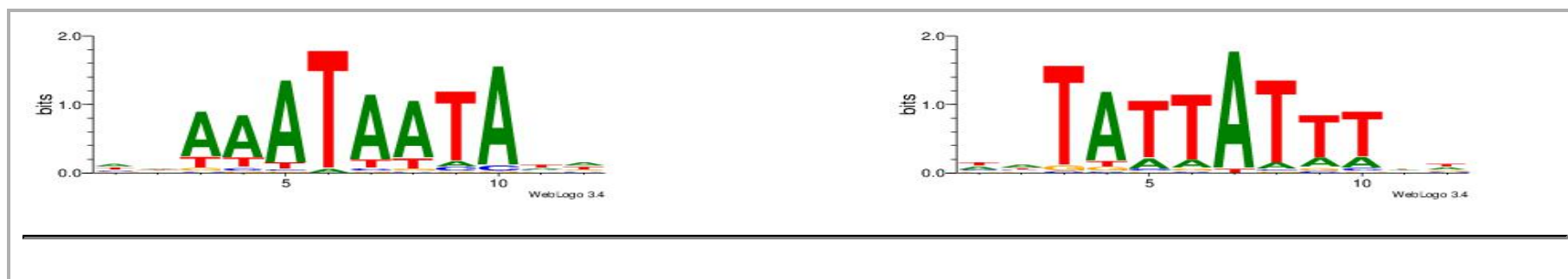
Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 4.03464

Alignment:

HDAAATAATADD-----
HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTTDH



Results created by MOTIFSIM on 06-19-2018 08:41:08
Runtime: 819.17 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
Motif logo generated by [weblogo](#)