



# 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

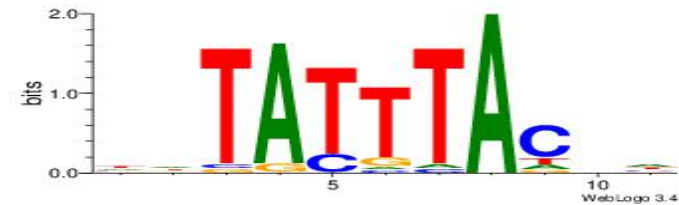
### Top 10 Significant Motifs - Global Matching (Highest to Lowest)

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

Original motif      Consensus sequence: DBGTAATAHD



Reverse complement motif      Consensus sequence: DHTATTTACBD



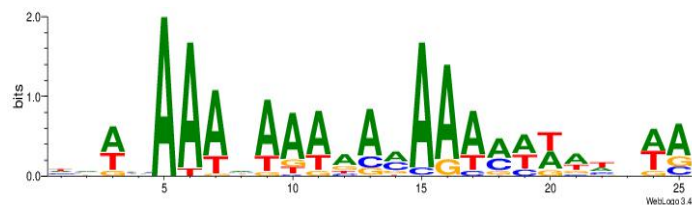
### Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

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

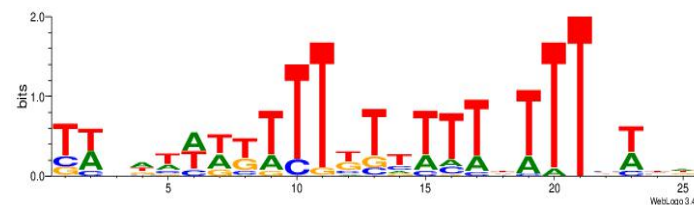
Alignment:

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

Original motif    Consensus sequence:  
HDWVAAAHAAAAAMAAAMWWHBBWA



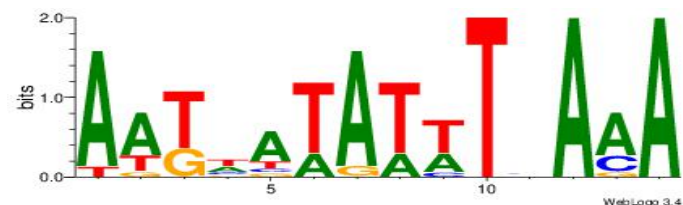
Reverse complement motif    Consensus sequence:  
TWVHWWYTTTTYTTTTTHTTTVWBH



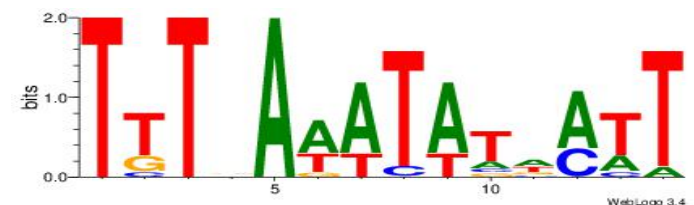
Dataset #: 2  
Motif ID: 9  
Motif name: Motif 9  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0250541

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

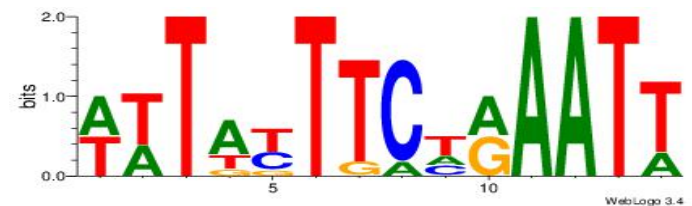
Alignment:

AATTYDGAARTAWW  
 ---DBGTAATAHD

Original motif      Consensus sequence: AATTYDGAARTAWW



Reverse complement motif      Consensus sequence: WWTAKTTCDKAAT

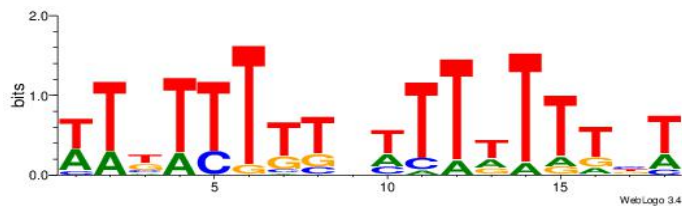


Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11

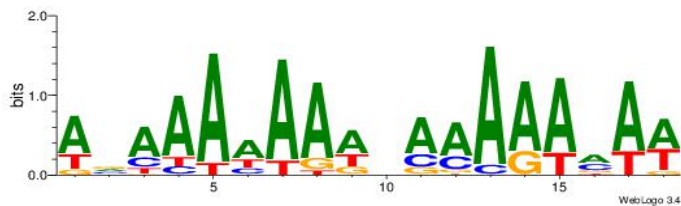
Similarity score: 0.0283217

Alignment:  
ABAAAAAAWHAAAAARAW  
DBGTAATAHD-----

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif      Consensus sequence:  
ABAAAAAAWHAAAAARAW

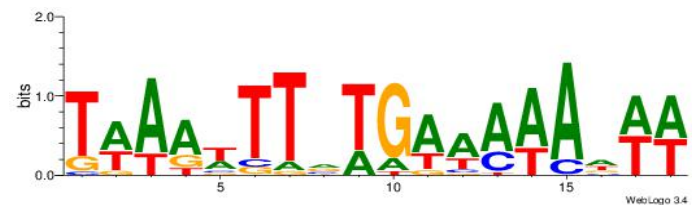
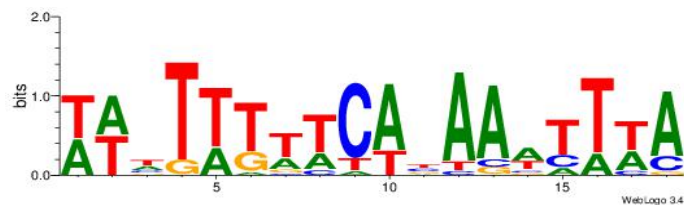


Dataset #: 5  
Motif ID: 53  
Motif name: TFM3  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.0308097

Alignment:  
TWAAWTTVTGAAAAHWW  
-----DBGTAATAHD-

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif      Consensus sequence:  
TWAAWTTVTGAAAAHWW

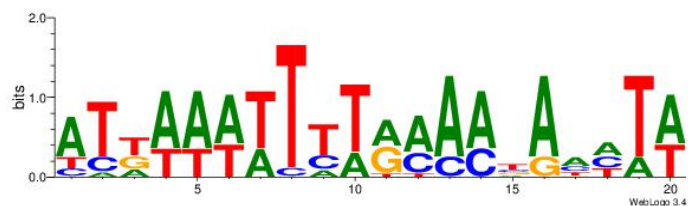


Dataset #: 5  
 Motif ID: 55  
 Motif name: TFM13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0333874

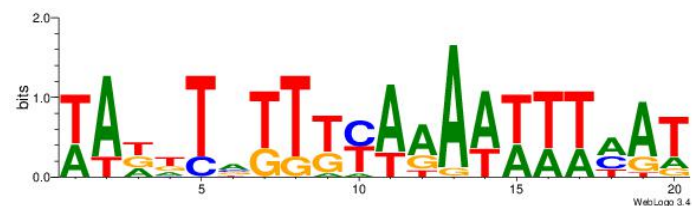
Alignment:

ATKAAWTTTTRMAABAHHTW  
 -----DBGTAATAHD--

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2

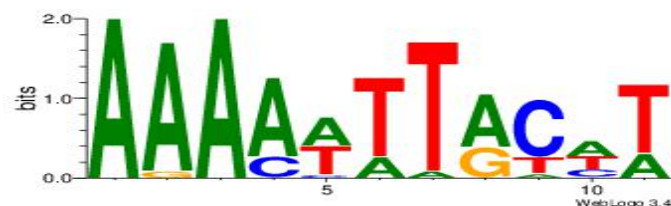
Motif ID: 4  
 Motif name: Motif 4  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0361187

Alignment:

AAAWTTTCWT

DHTATTTACBD

Original motif      Consensus sequence: AAAAWTTTCWT



Reverse complement motif      Consensus sequence: AWGKAAWTTT



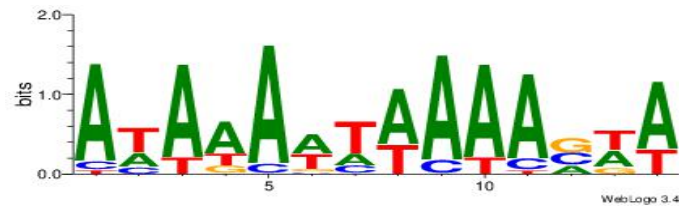
Dataset #: 2  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0410381

Alignment:

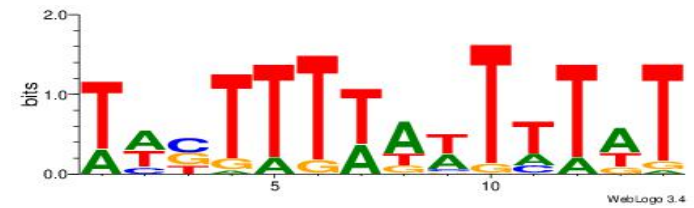
AWAAAWTWAAASWA

--DHTATTTACBD-

Original motif      Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif      Consensus sequence: TWSTTTWAWTTTV



Dataset #:	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:

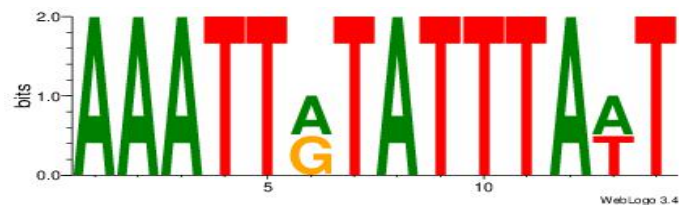
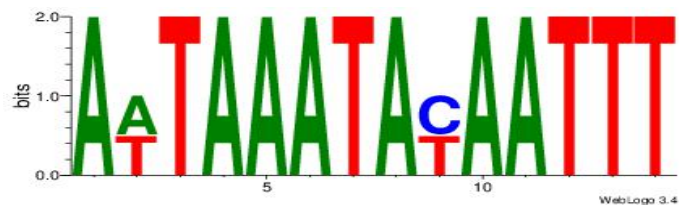
AWTAAATAYAATTT

---DHTATTTACBD

Original motif      Consensus sequence: AWTAAATAYAATTT

Reverse complement motif      Consensus sequence: AAATTKTATTTAW



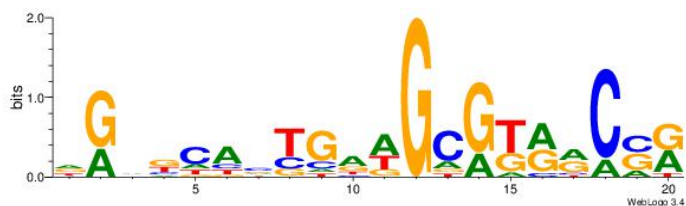


Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0512987

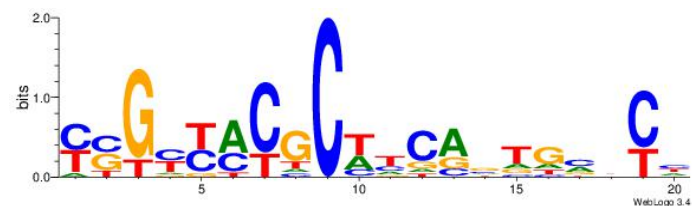
#### Alignment:

DGVBCABTGDWGCGRRCR  
 DBGTAATAHD-----

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR

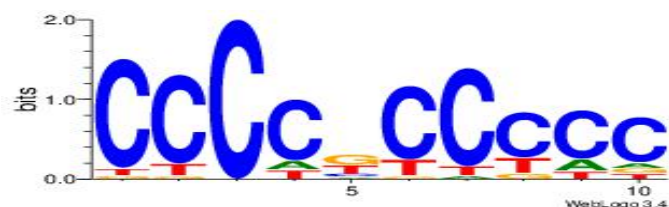


Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD

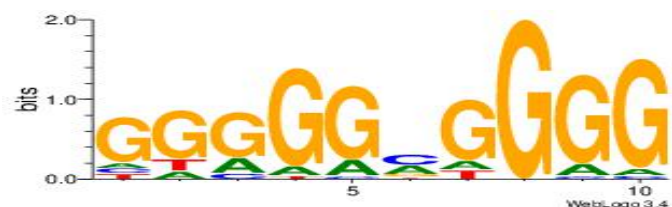


**Dataset #: 3      Motif ID: 24      Motif name: SP1**

Original motif      Consensus sequence: CCCCKCCCCC



Reverse complement motif      Consensus sequence: GGGGGYGGGG



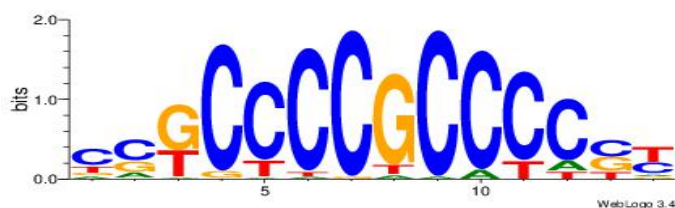
### Best Matches for Top Significant Motif ID 24 (Highest to Lowest)

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

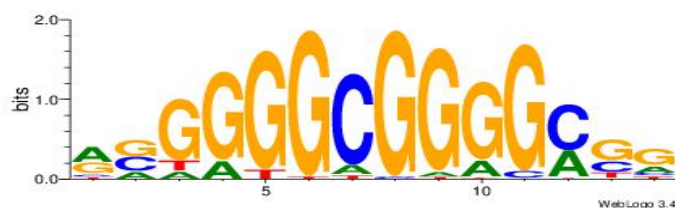
Alignment:

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

Original motif      Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif      Consensus sequence: MSGGGGCGGGGY

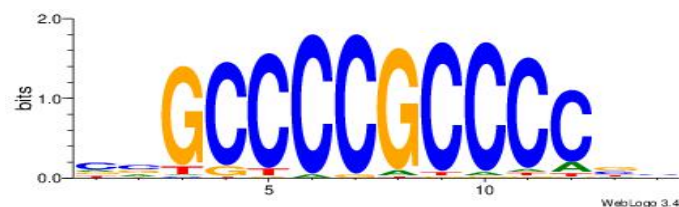


Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.00965796

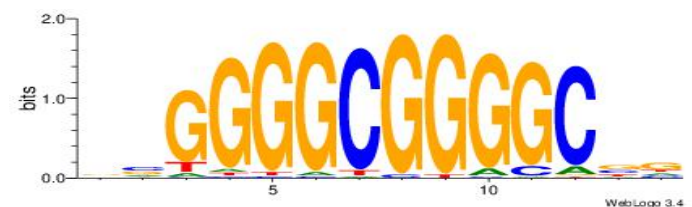
Alignment:

BBGGGGCGGGGCVD  
 -GGGGGYGGGG---

Original motif      Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC

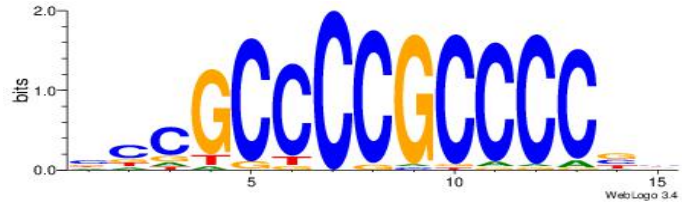


Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 10

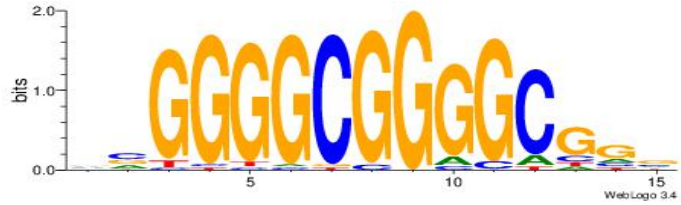
Similarity score: 0.0127292

Alignment:  
BBGGGGCGGGGCGGB  
-GGGGGYGGGG----

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

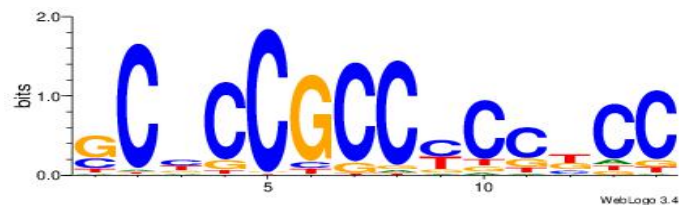


Dataset #: 5  
Motif ID: 50  
Motif name: TFF11  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 10  
Similarity score: 0.0174405

Alignment:  
GGMGGRGGCGGVGC  
---GGGGGYGGGG-

Original motif      Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif      Consensus sequence: GCVCCGCCMCCY

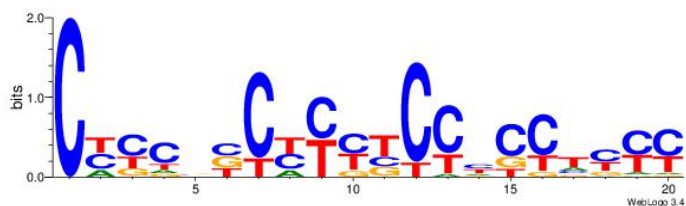


Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.0301548

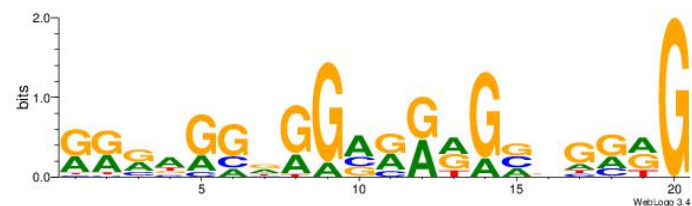
Alignment:

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

Original motif      Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG



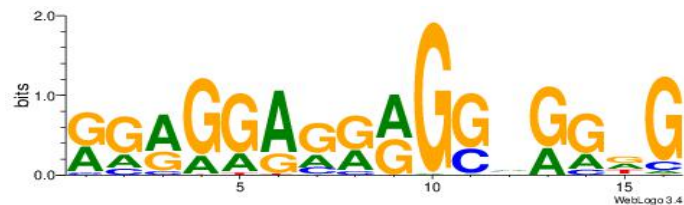
Dataset #: 5

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

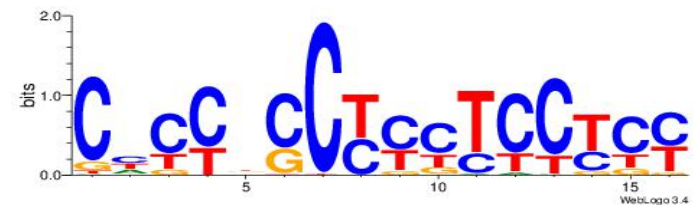
Alignment:

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

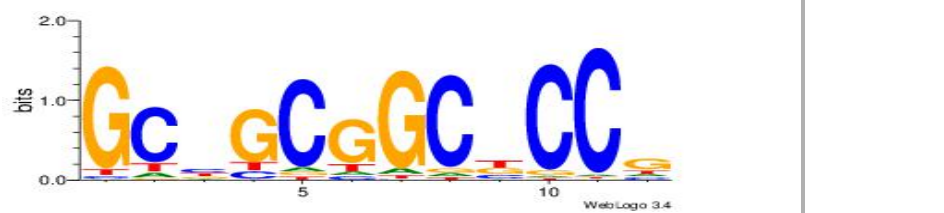
Similarity score: 0.0557738

Alignment:  
GCVGCGGCBCCG  
-CCCCKCCCCC-

Original motif      Consensus sequence: CGGVGCCGCVGC



Reverse complement motif      Consensus sequence: GCVGCGGCBCCG

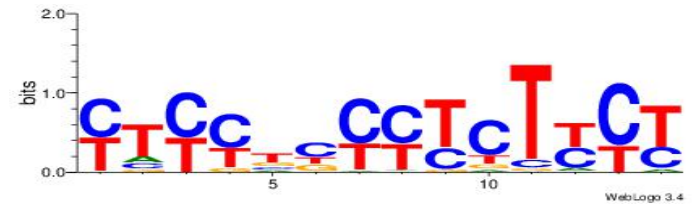
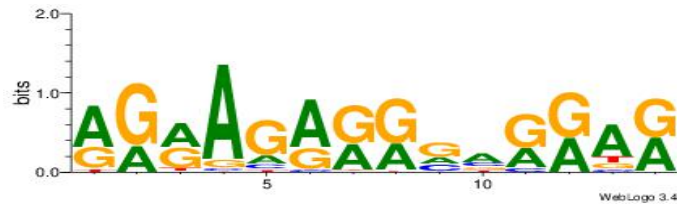


Dataset #: 2  
Motif ID: 2  
Motif name: Motif 2  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 10  
Similarity score: 0.0648214

Alignment:  
MTMMTCMMTCTKCK  
----CCCCKCCCCC

Original motif      Consensus sequence: RGRAGARRGARRAR

Reverse complement motif      Consensus sequence: MTMMTCMMTCTKCK



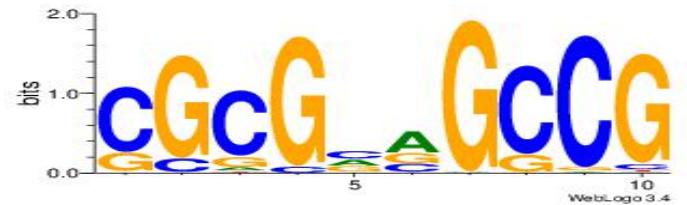
Dataset #: 5  
 Motif ID: 48  
 Motif name: TFW3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0762976

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



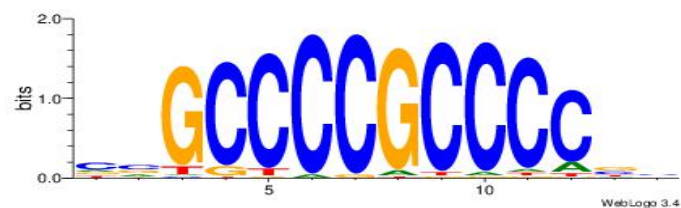
**Best Matches for Top Significant Motif ID 32 (Highest to Lowest)**

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

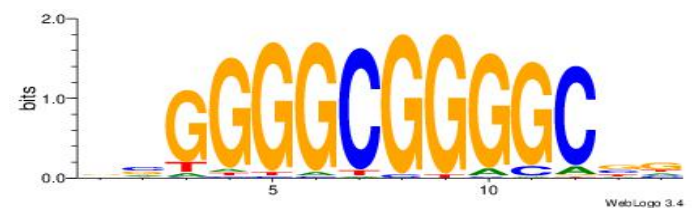
Alignment:

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



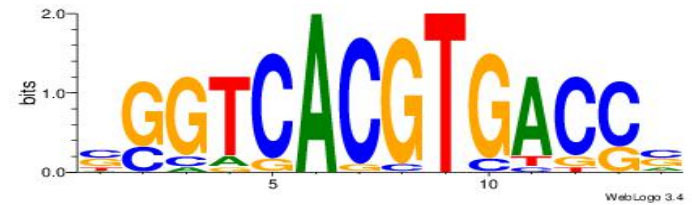
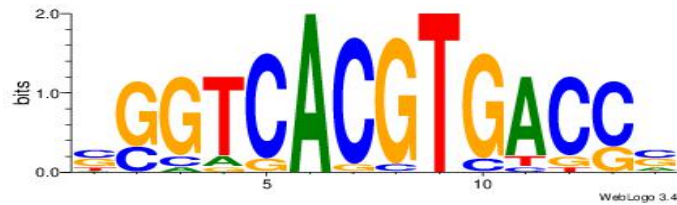
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Dataset #: 4  
Motif ID: 42  
Motif name: sSGTCACGTGACSS  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 5  
Number of overlap: 6  
Similarity score: 0.0412037

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

Original motif      Consensus sequence: SGGTCACGTGACCS

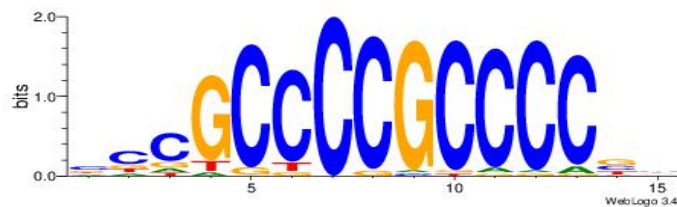
Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



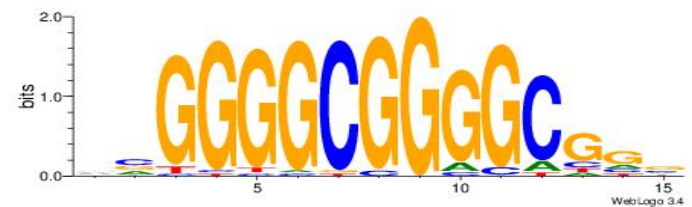
Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 6  
 Similarity score: 0.0425089

Alignment:  
 BCCGCCCCGCCCCBB  
 -----CACGCM-----

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

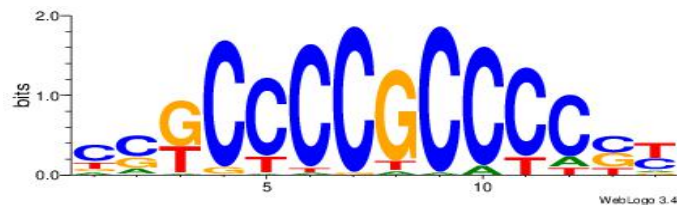


Dataset #: 2

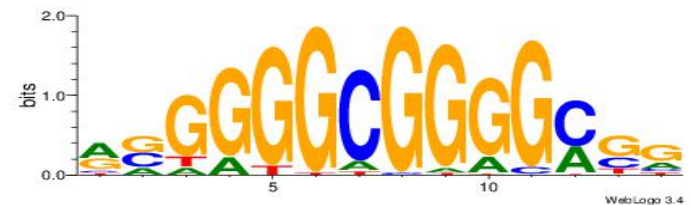
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0465867

Alignment:  
MSGGGGCGGGGYSG  
-----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

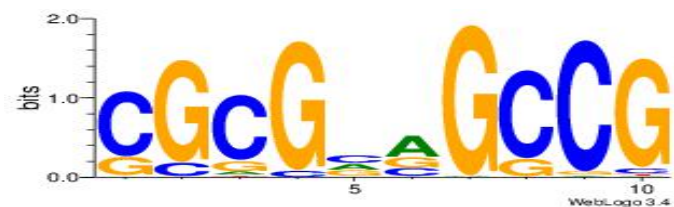


Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0586806

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



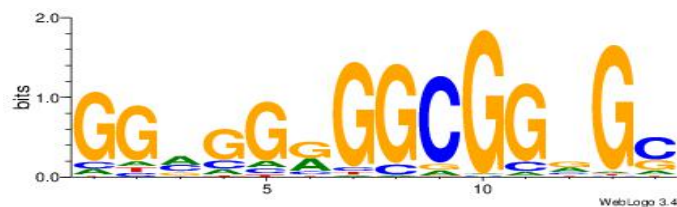
Dataset #: 5  
 Motif ID: 50

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

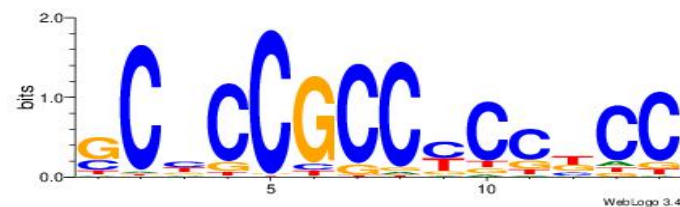
Alignment:

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



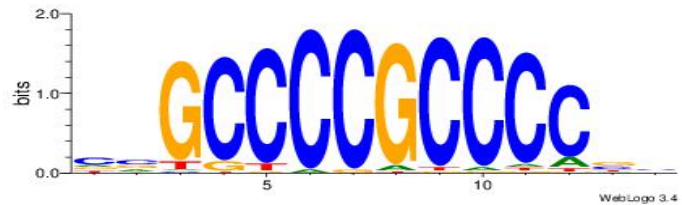
### Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

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

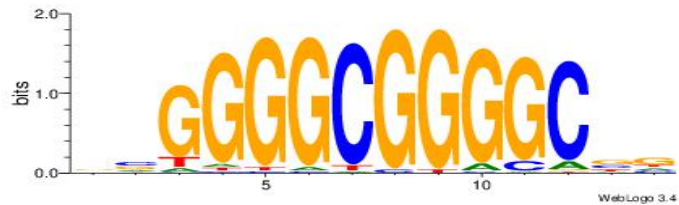
Number of overlap: 8  
Similarity score: 0

Alignment:  
BBGGGGCGGGGCVD  
----GGCGGGGC--

Original motif      Consensus sequence: HVGCCCCGCCCB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC

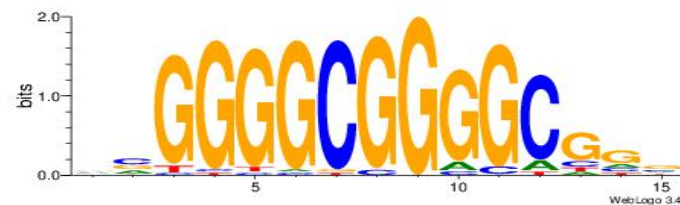
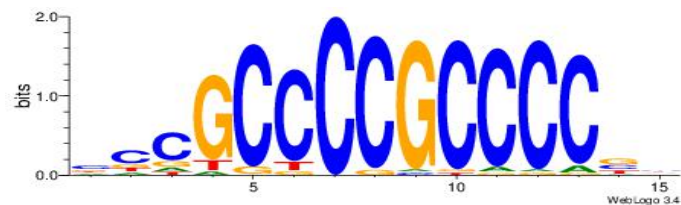


Dataset #: 4  
Motif ID: 38  
Motif name: cccGCCCCGCCCBsb  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 5  
Number of overlap: 8  
Similarity score: 0.00250079

Alignment:  
BCCGCCCCGCCCB  
---GCCCGCC---

Original motif      Consensus sequence: BCCGCCCCGCCCB

Reverse complement motif      Consensus sequence:  
BBGGGGCGGGGCGGB



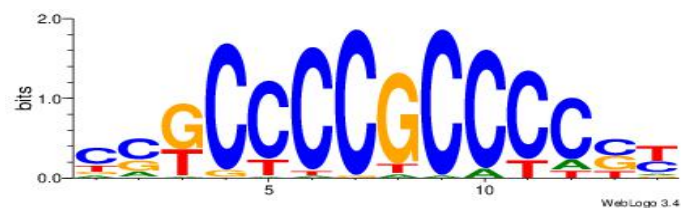
Dataset #: 2  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.0149958

Alignment:

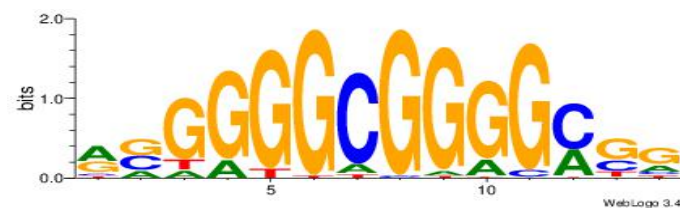
MSGGGGCGGGYSG

----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

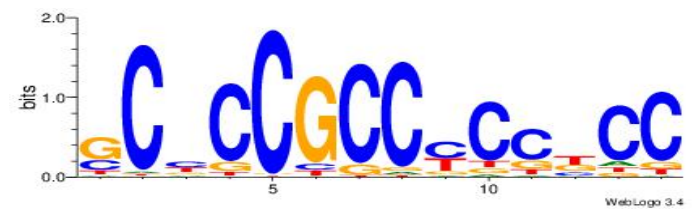
Alignment:

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

Original motif      Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYC



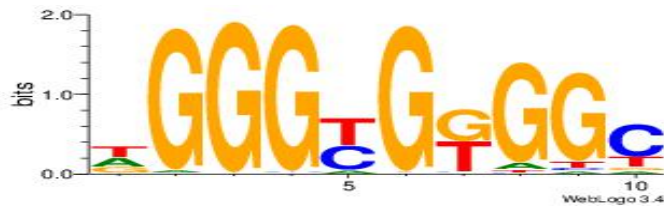
Dataset #:	3
Motif ID:	27
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0349983

Alignment:

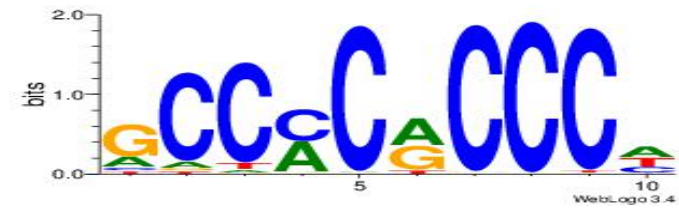
DGGGYGKGGC

--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

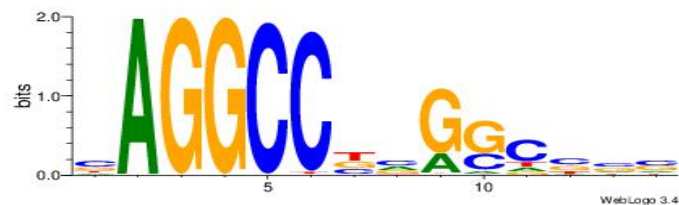
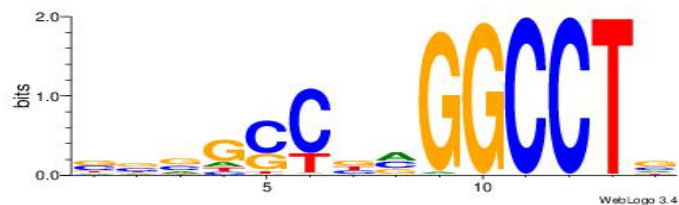
Alignment:

VAGGCCBBGGCVBB

---GCCCGGCC---

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:

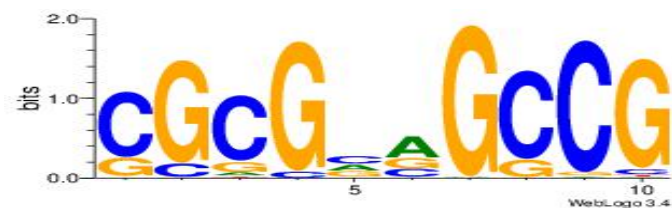
CGCGBMGCCG

-GCCCCGCC-

Original motif      Consensus sequence: CGGCYBCGCG



Reverse complement motif      Consensus sequence: CGCGBMGCCG



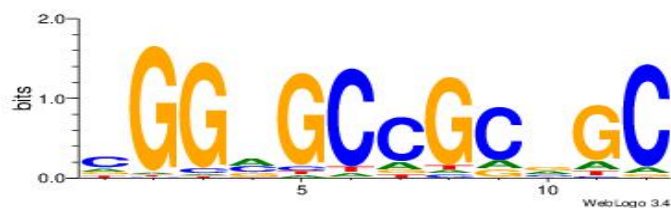
Dataset #: 5  
 Motif ID: 49

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

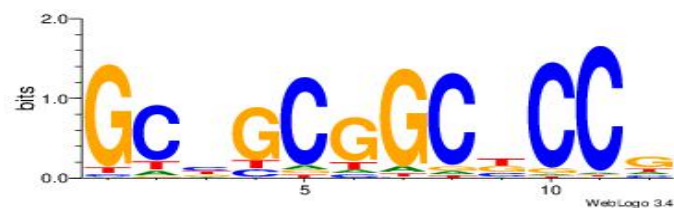
Alignment:

CGGVGCCGCVGC  
 --GCCCCGCC--

Original motif      Consensus sequence: CGGVGCCGCVGC



Reverse complement motif      Consensus sequence: GCVGCGGCBCCG



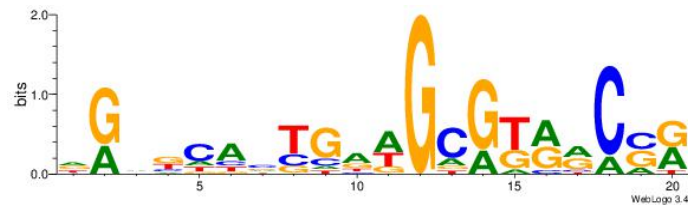
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0853847

Alignment:

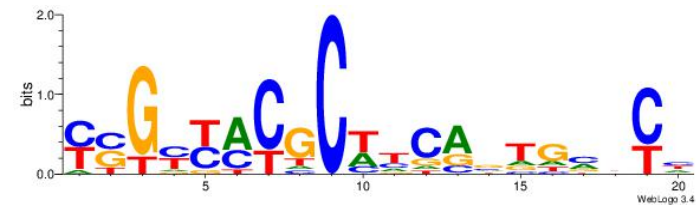
DGVBCABTGDWGCGRRCR

-----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

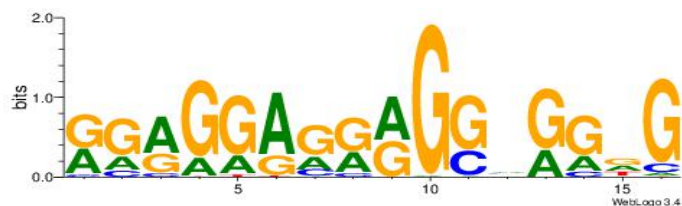




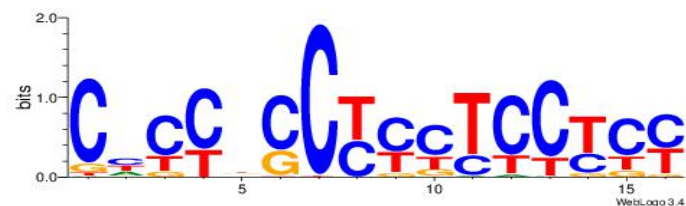
Dataset #: 5  
 Motif ID: 51  
 Motif name: TFM2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 8  
 Similarity score: 0.0928252

Alignment:  
 CHCCBCKMCTCCKCM  
 --GCCCCGCC-----

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif      Consensus sequence: CHCCBCKMCTCCKCM



**Dataset #: 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)

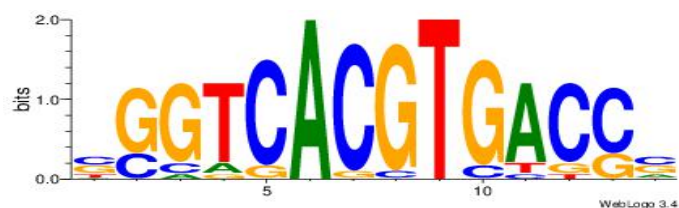
Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACCS
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0375102

Alignment:

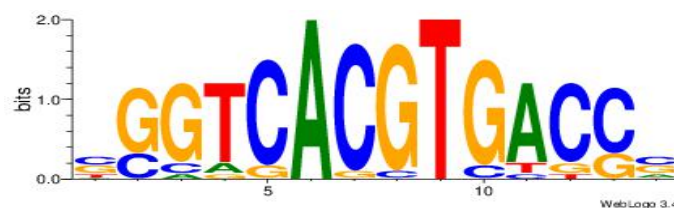
SGGTCACGTGACCS

--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

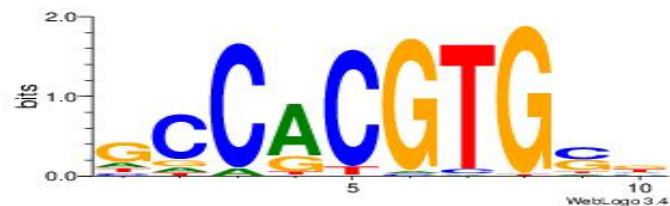
Alignment:

GCCACGTGSD  
 ----GTCGCG

Original motif      Consensus sequence: HSCACGTGGC



Reverse complement motif      Consensus sequence: GCCACGTGSD

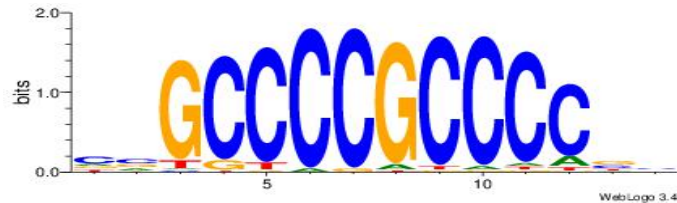


Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 6

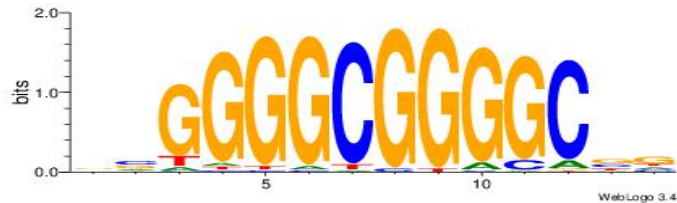
Similarity score: 0.0539

Alignment:  
HVGCCCGCCCCBB  
--GTCGCG-----

Original motif      Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC



---

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: GGCGGGGC

Reverse complement motif      Consensus sequence: GCCCGGCC

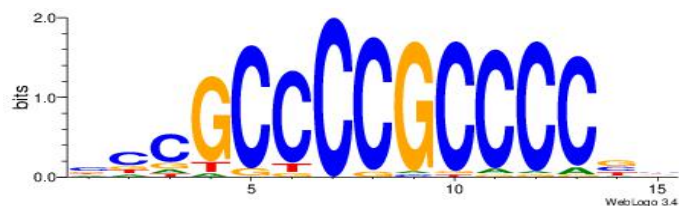


Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 6  
 Similarity score: 0.0558733

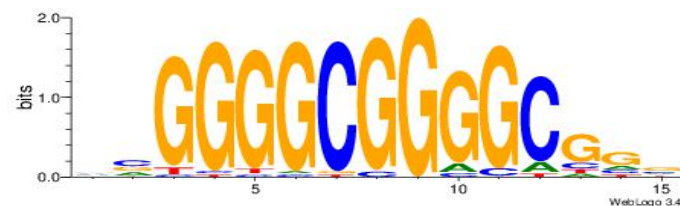
#### Alignment:

BBGGGGCGGGGCGGB  
 -----GTCGCG--

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB



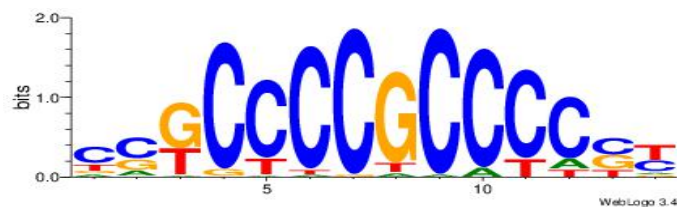
Dataset #: 2

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

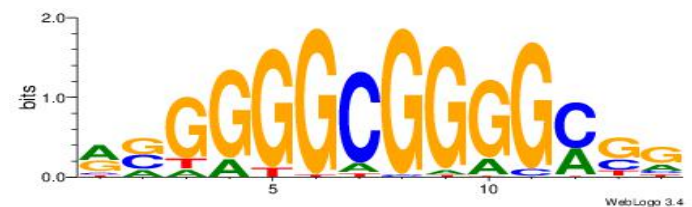
Alignment:

CSKCCCCGCCCSY  
 --CGCGAC-----

Original motif      Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif      Consensus sequence: MSGGGGCGGGGY



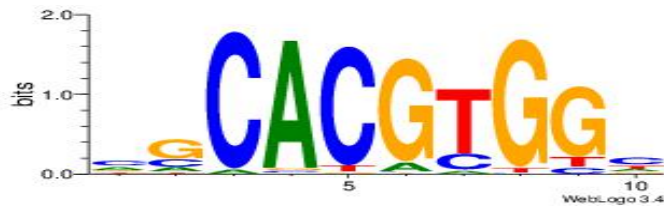

---

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

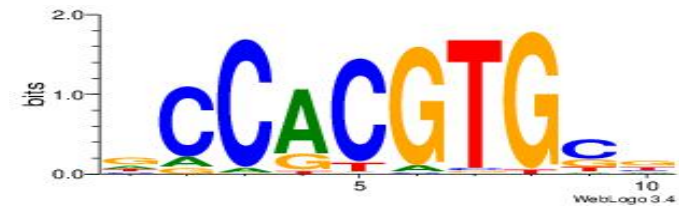
Alignment:

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

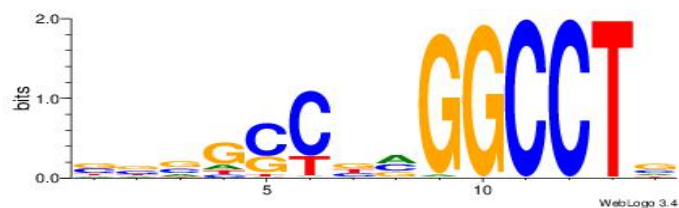
Reverse complement motif      Consensus sequence: GCGCSAAA



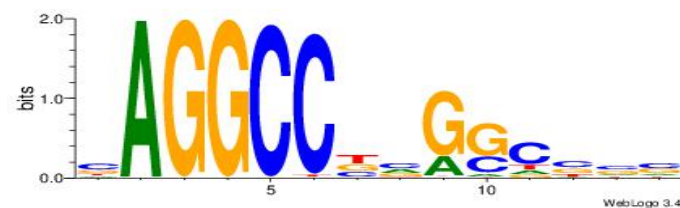
Dataset #: 3  
 Motif ID: 22  
 Motif name: Zfx  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 6  
 Similarity score: 0.069909

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

Original motif      Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCV



Dataset #: 3  
 Motif ID: 31

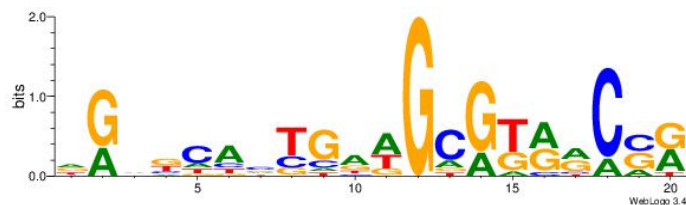


Motif name: Pax5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 6  
 Similarity score: 0.072456

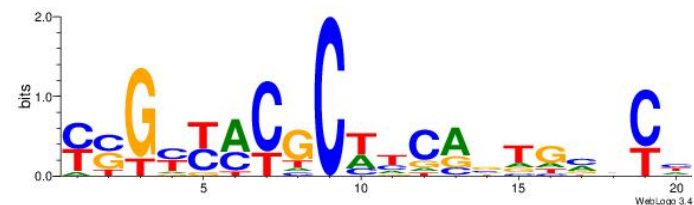
**Alignment:**

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

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR

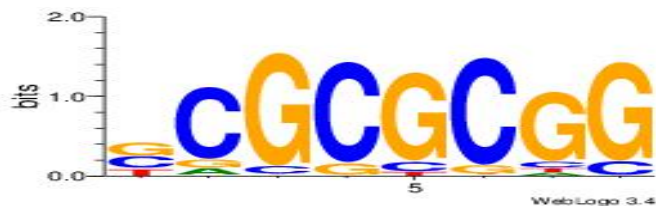


Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD



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

Original motif      Consensus sequence: SCGCGCGG



Reverse complement motif      Consensus sequence: CCGCGCGS



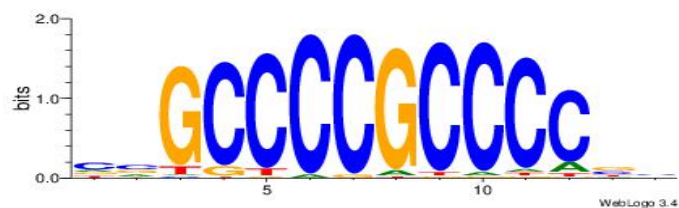
## Best Matches for Top Significant Motif ID 47 (Highest to Lowest)

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

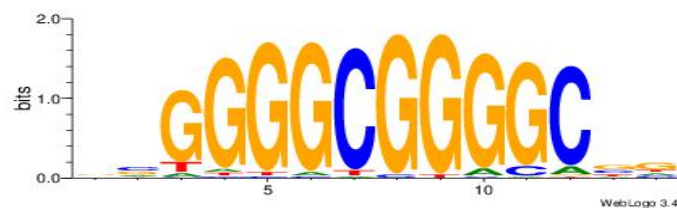
### Alignment:

HVGCCCCGCCCCBB  
 -CCGCGCGS-----

Original motif      Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC

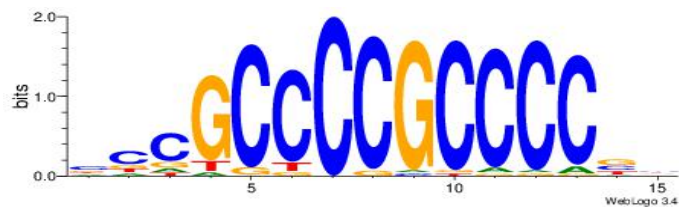


Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement

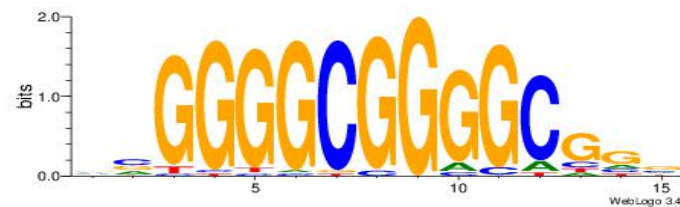
Direction: Forward  
 Position number: 7  
 Number of overlap: 8  
 Similarity score: 0.045686

Alignment:  
 BBGGGGCGGGGCGGB  
 -----SCGCGCGG--

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



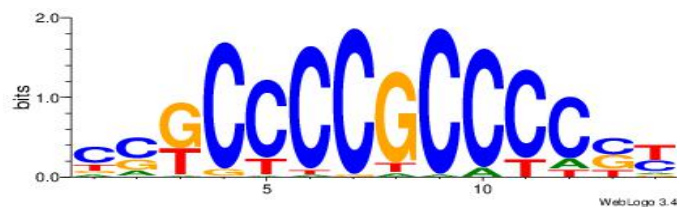
Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB



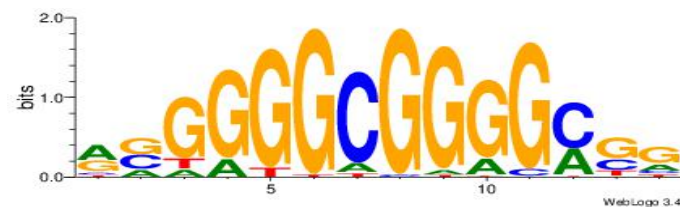
Dataset #: 2  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 8  
 Similarity score: 0.0504058

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

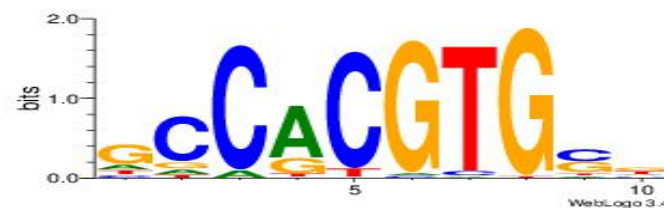
Alignment:

HSCACGTGGC  
 -SCGCGCGG-

Original motif      Consensus sequence: HSCACGTGGC



Reverse complement motif      Consensus sequence: GCCACGTGSD



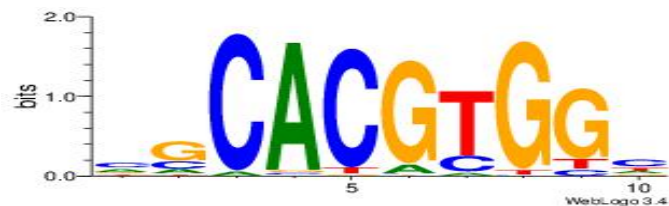
Dataset #: 3  
 Motif ID: 34  
 Motif name: Myc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 8  
 Similarity score: 0.0574543

Alignment:

VGCACGTGGH

–SCGCGCGG–

Original motif      Consensus sequence: VGCACGTGGH



Reverse complement motif      Consensus sequence: DCCACGTGCV

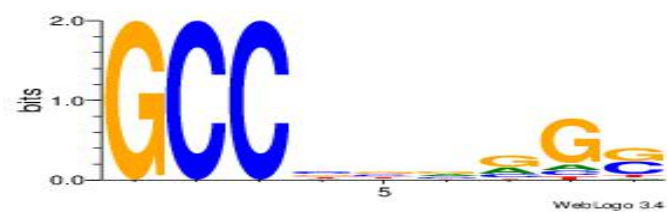


Dataset #: 3  
 Motif ID: 25  
 Motif name: TFAP2A  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 8

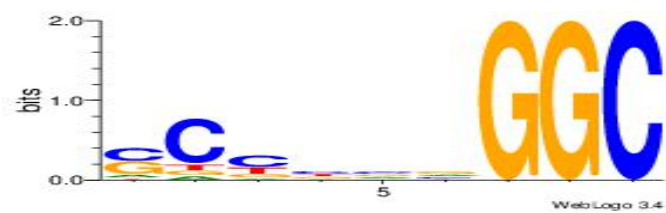
Similarity score: 0.0678925

Alignment:  
SCMVBBGGC  
-SCGCGCGG

Original motif      Consensus sequence: GCCBBVRGS



Reverse complement motif      Consensus sequence: SCMVBBGGC



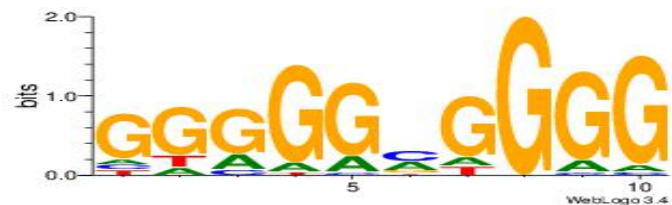
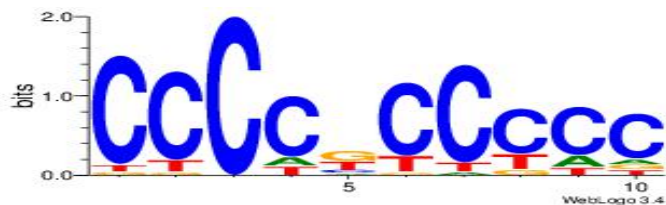
---

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

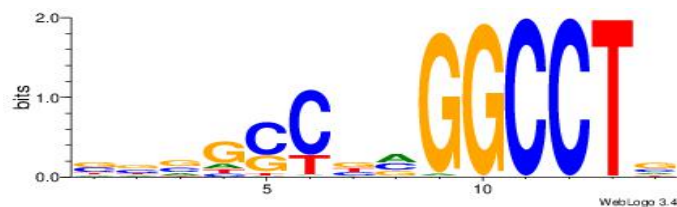


Dataset #: 3  
 Motif ID: 22  
 Motif name: Zfx  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 8  
 Similarity score: 0.0710499

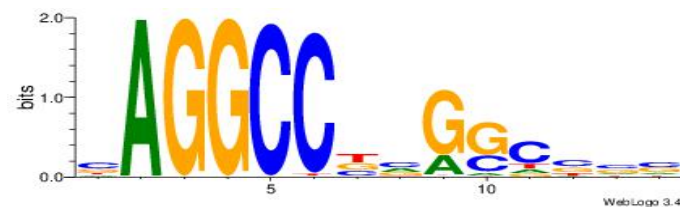
#### Alignment:

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

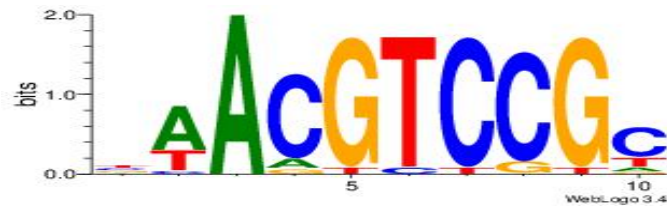


Alignment:

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

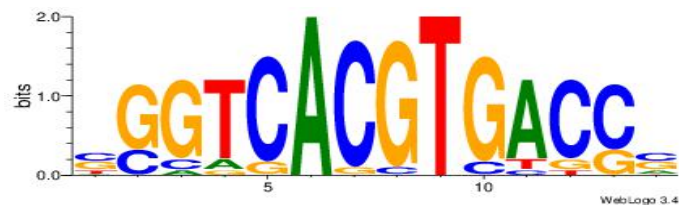
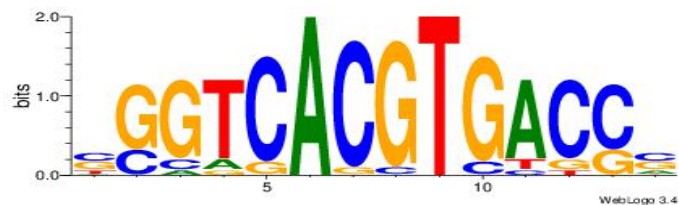


Dataset #: 4  
Motif ID: 42  
Motif name: sSGTCACGTGACSS  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 8  
Similarity score: 0.0314837

Alignment:  
SGGTCACGTGACCS  
---VCACGTBV---

Original motif      Consensus sequence: SGGTCACGTGACCS

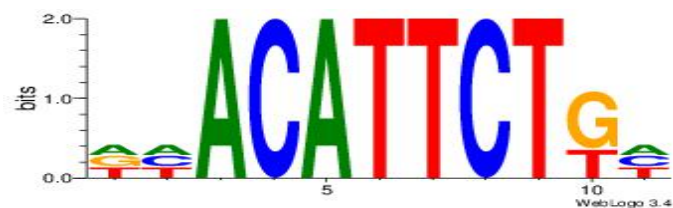
Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



Dataset #: 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

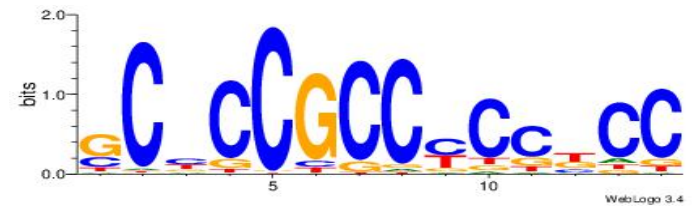
Alignment:

GCVCCGCCMCCYCC  
 -----VCACGTBV

Original motif      Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYCC



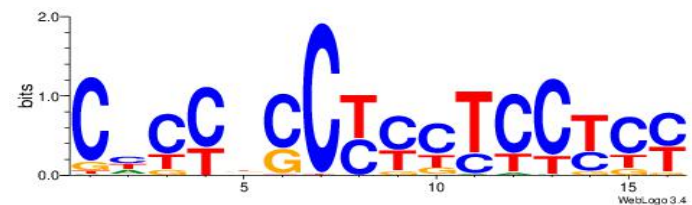
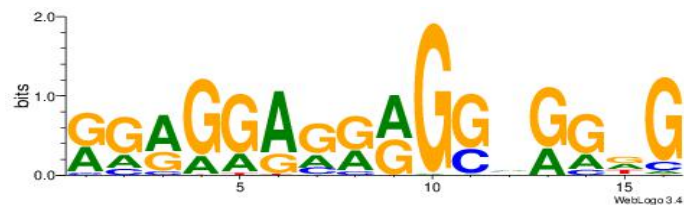
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0698117

Alignment:

RGRGGAGRRGGHGGDG  
 ----VBACGTGV-----

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG

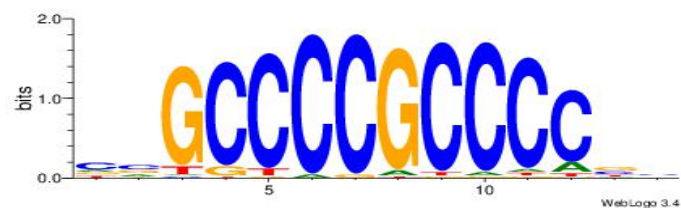
Reverse complement motif      Consensus sequence:  
 CHCCBCKMCTCCKCM



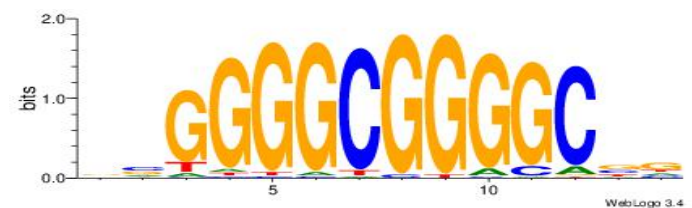
Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 8  
 Similarity score: 0.0711168

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

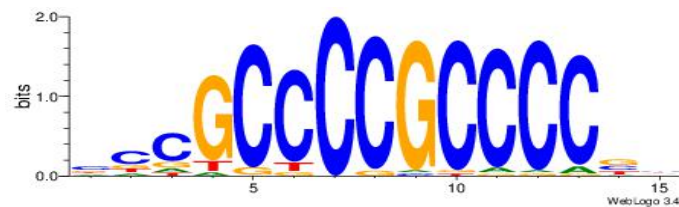
**Alignment:**

```

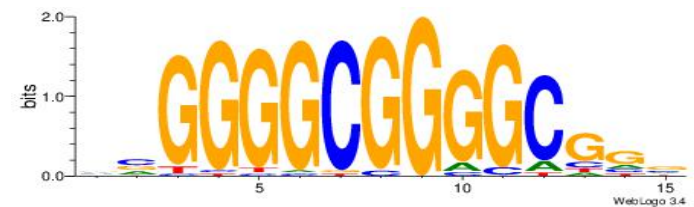
BBGGGGCGGGGCGGB
---VBACGTGV-----

```

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

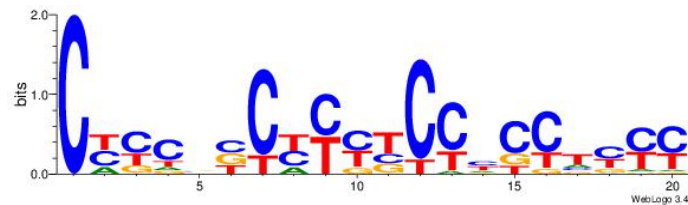


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	12
Number of overlap:	8
Similarity score:	0.0757612

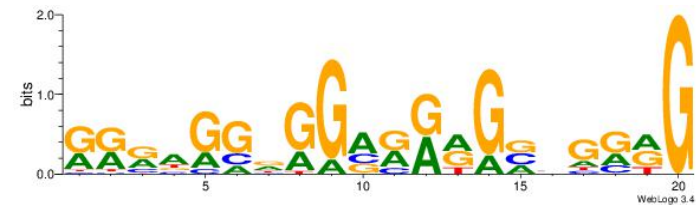
Alignment:

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

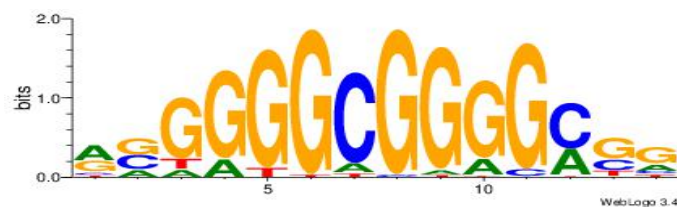
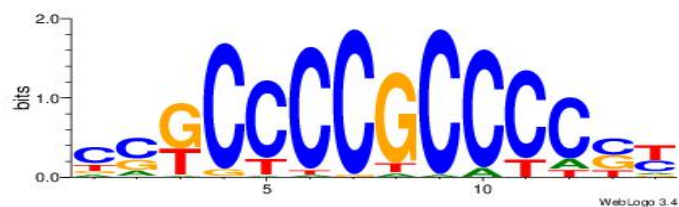
Alignment:

CSKCCCCGCCCSY  
---VCACGTBV---

Original motif      Consensus sequence: CSKCCCCGCCCSY

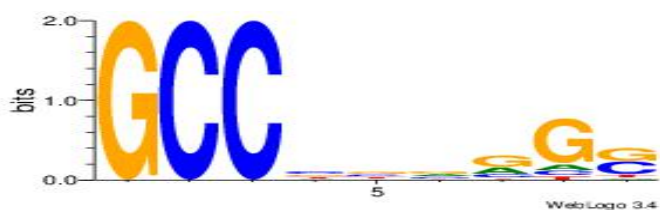
Reverse complement motif      Consensus sequence: MSGGGGCGGGGY



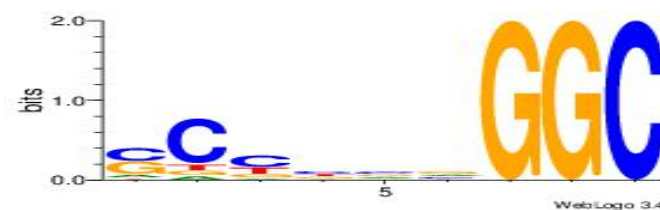


**Dataset #: 3**      **Motif ID: 25**      **Motif name: TFAP2A**

Original motif      Consensus sequence: GCCBBVRGS



Reverse complement motif      Consensus sequence: SCMVBGGC



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

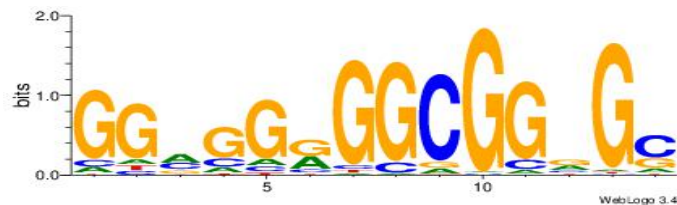
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.0415732

Alignment:

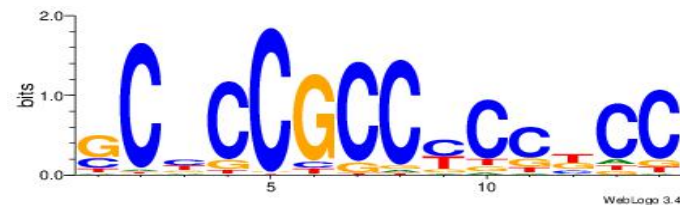
GGMGGRGGCGGVGC

SCMVBBGGC-----

Original motif      Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYC

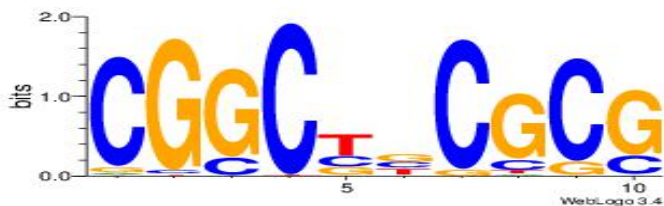


Dataset #: 5  
 Motif ID: 48  
 Motif name: TFW3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 9  
 Similarity score: 0.0552877

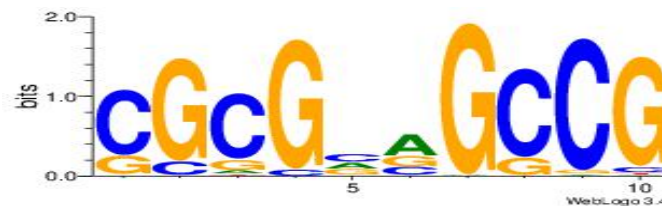
Alignment:

CGGCYBCGCG  
 -GCCBBVRGS

Original motif      Consensus sequence: CGGCYBCGCG



Reverse complement motif      Consensus sequence: CGCGBMGCCG

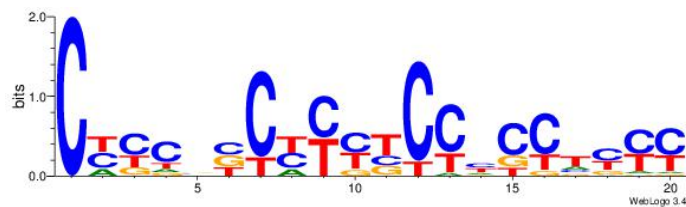


Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 9  
 Similarity score: 0.0630429

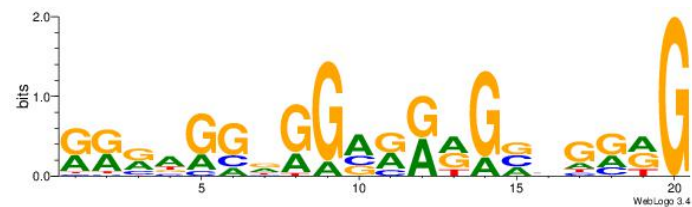
Alignment:

KKKAGGDGGAKKMGBBGKMG  
 -SCMVBBGGC-----

Original motif      Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

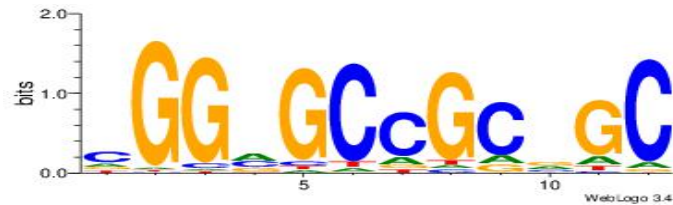


Dataset #: 5  
 Motif ID: 49  
 Motif name: TFF1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1

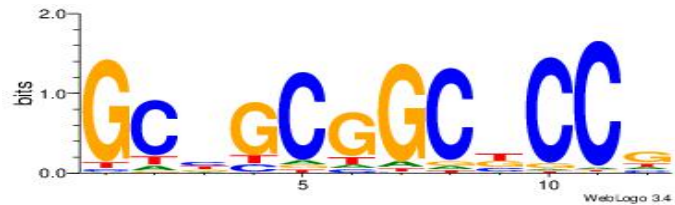
Number of overlap: 9  
Similarity score: 0.0669772

Alignment:  
GCVGCGGCBCCG  
SCMVBBGGC---

Original motif      Consensus sequence: CGGVGCCGCVGC



Reverse complement motif      Consensus sequence: GCVGCGGCBCCG

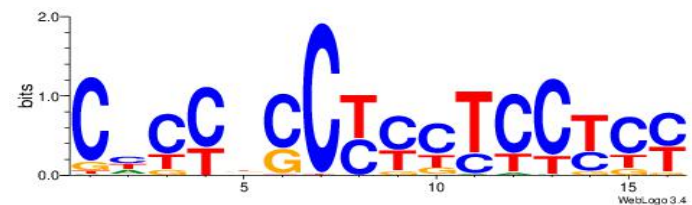
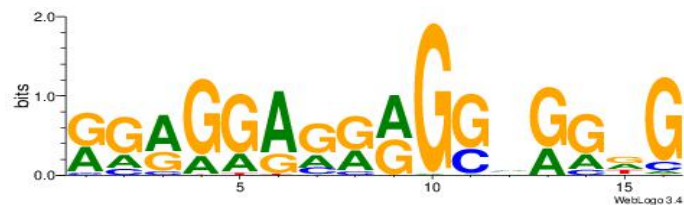


Dataset #: 5  
Motif ID: 51  
Motif name: TFM2  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 8  
Number of overlap: 9  
Similarity score: 0.069755

Alignment:  
CHCCBCKMCTCCKCM  
SCMVBBGGC-----

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif      Consensus sequence:  
CHCCBCKMCTCCKCM



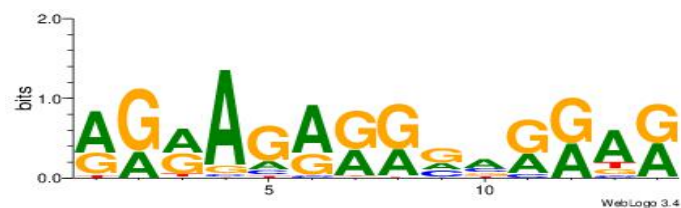
Dataset #: 2  
 Motif ID: 2  
 Motif name: Motif 2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 9  
 Similarity score: 0.0715961

#### Alignment:

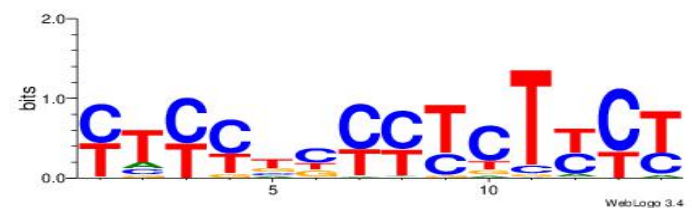
MTMMTCMMTCTKCK

----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

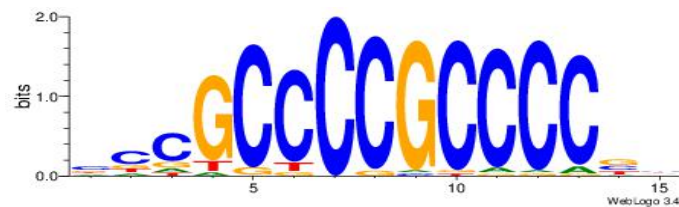
**Alignment:**

```

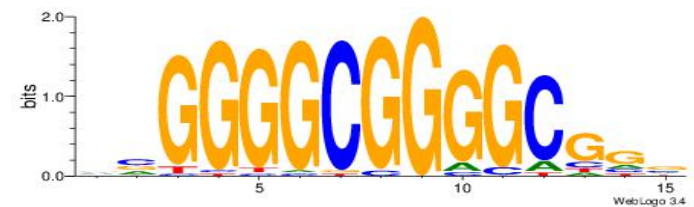
BBGGGGCGGGGCGGB
-----GCCBBVRGS-

```

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

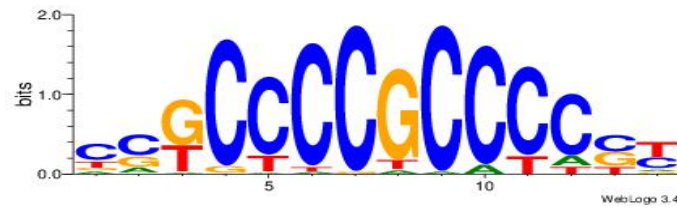


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0781606

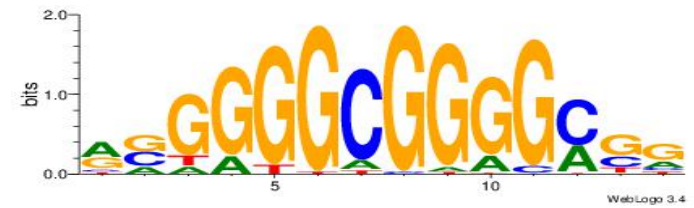
Alignment:

CSKCCCCGCCCCSY  
 -----SCMVBBGGC

Original motif      Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif      Consensus sequence: MSGGGGCGGGGY



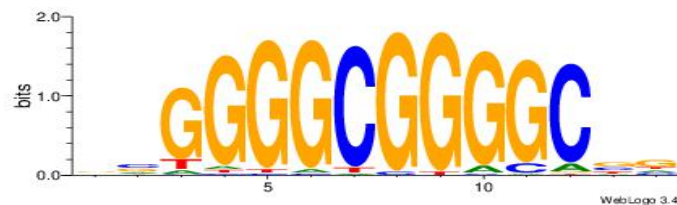
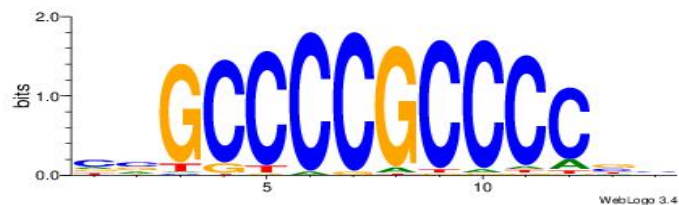
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0800026

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



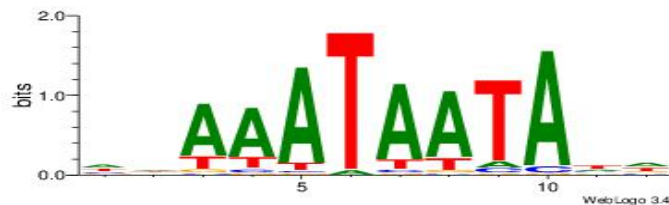
Reverse complement motif Consensus sequence: GBTGCAGGTGB



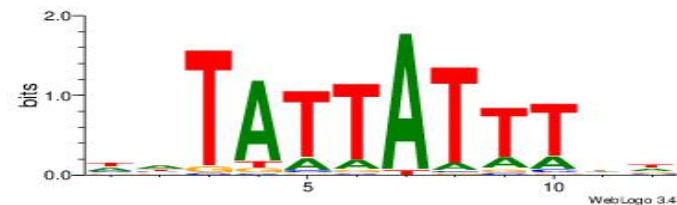
**Dataset #: 4**      **Motif ID: 41**      **Motif name: wwAAATAATAtw**



Original motif      Consensus sequence: HDAAATAATADD



Reverse complement motif      Consensus sequence: DDTATTATTDDH



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

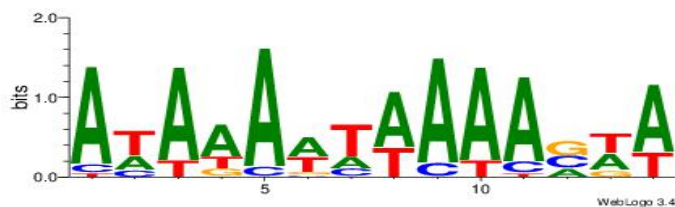
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0536028

Alignment:

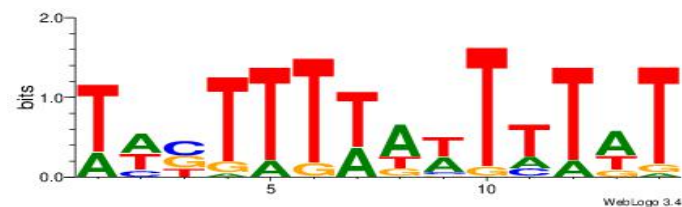
AWAAAWTWAAASWA

-HDAAATAATADD-

Original motif      Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif      Consensus sequence: TWSTTTWAWTTTV

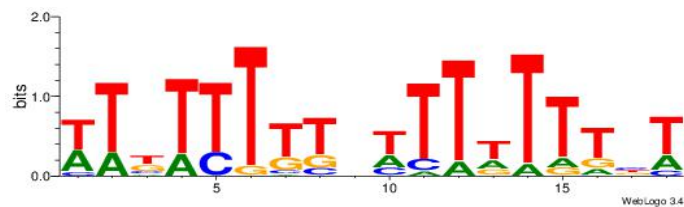


Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 12  
 Similarity score: 0.0565705

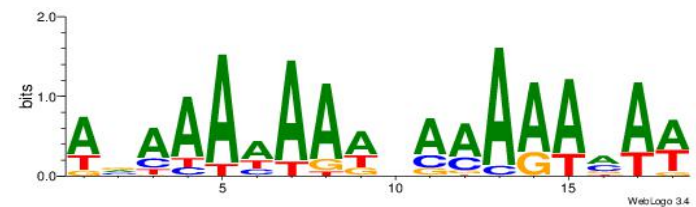
Alignment:

WTKTTTTTHWTTTTTBT  
 -----DDTATTATTTDH

Original motif      Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAAWHAAAAARAW

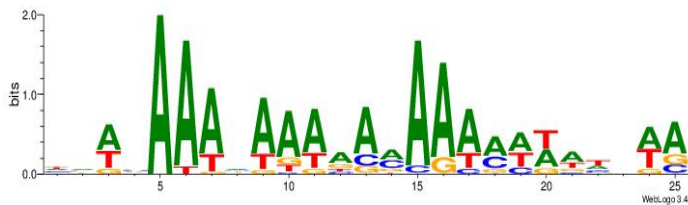


Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3

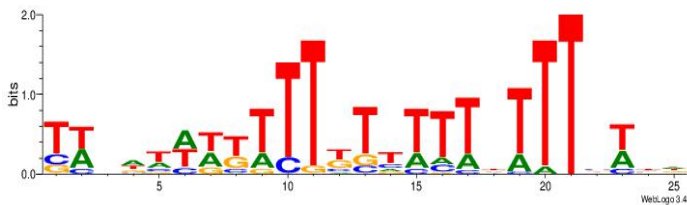
Number of overlap: 12  
Similarity score: 0.0575935

Alignment:  
HDWVAAAHAAAAAAMAAAMWWWHBWA  
--HDAAATAATADD-----

Original motif    Consensus sequence:  
HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
TWVHWWYTTTTTTTTTHTTTVWBH

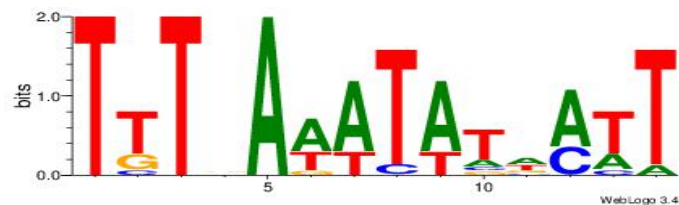
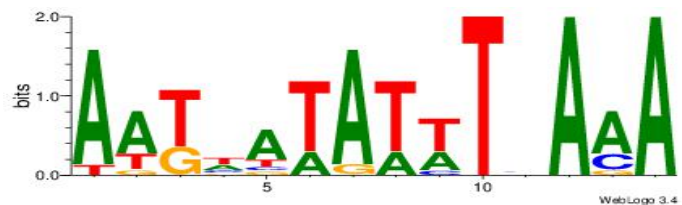


Dataset #: 2  
Motif ID: 9  
Motif name: Motif 9  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 12  
Similarity score: 0.0591821

Alignment:  
AATHATATWTHAAA  
--DDTATTATTTDH

Original motif    Consensus sequence: AATHATATWTHAAA

Reverse complement motif    Consensus sequence: TTTDAWATATHAT



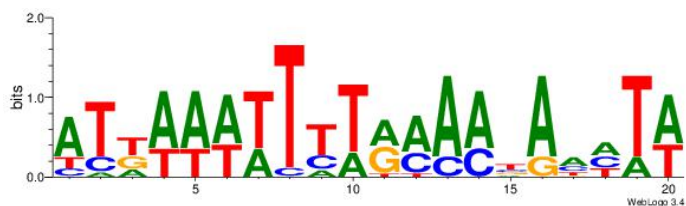
Dataset #: 5  
 Motif ID: 55  
 Motif name: TFM13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0712963

#### Alignment:

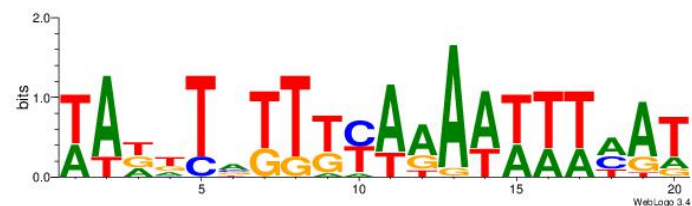
```

WAHHTVTTYKAAAATTRAT
-----HDAAATAATADD
  
```

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



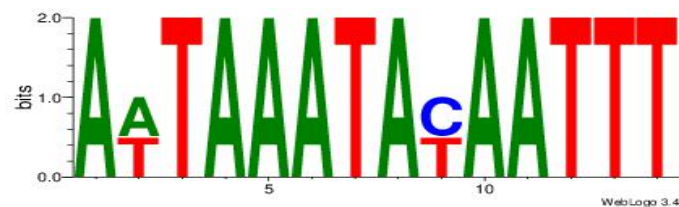
Dataset #: 2

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



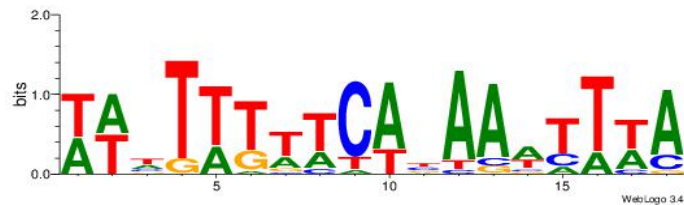
Dataset #: 5  
 Motif ID: 53  
 Motif name: TFM3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0733516

Alignment:

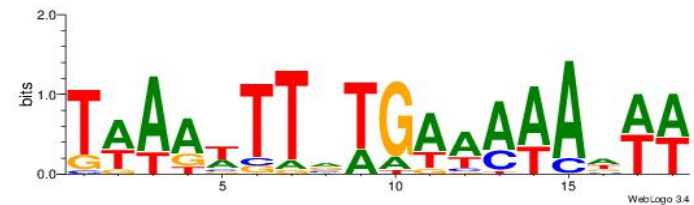
WWHTTTTTCABAAWTTWA

-----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

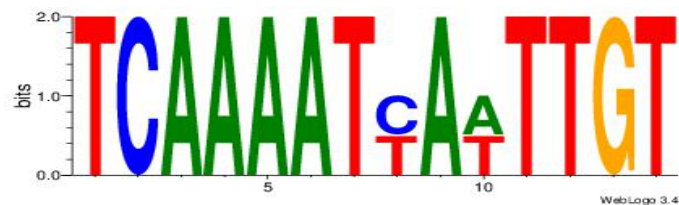
Alignment:

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

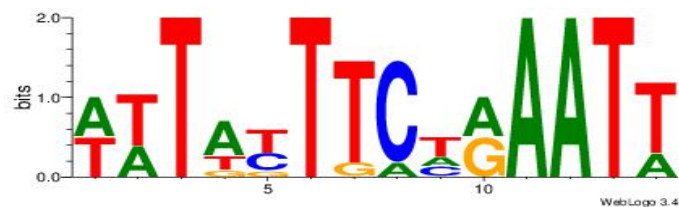
#### Alignment:

WWTAKTTCDKAATT  
 DDTATTATTTDH--

Original motif      Consensus sequence: AATTYDGAARTAWW



Reverse complement motif      Consensus sequence: WWTAKTTCDKAATT



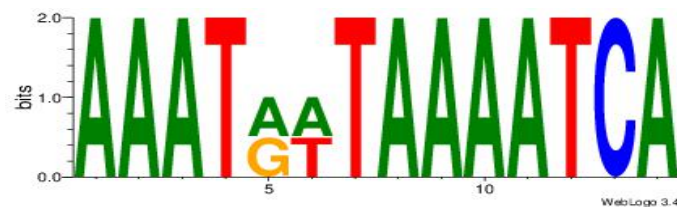
Dataset #: 2  
 Motif ID: 8

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

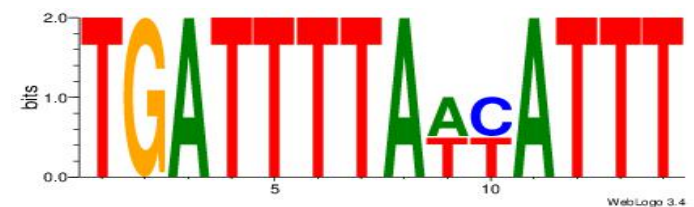
Alignment:

TGATTTTAWKATTT  
 -DDTATTATTTDH-

Original motif      Consensus sequence: AAATRWTA<sup>+</sup>AAATCA

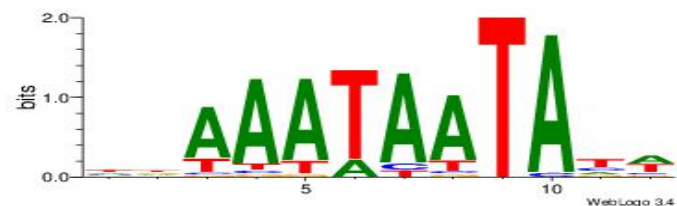


Reverse complement motif      Consensus sequence: TGATTITAWKATT

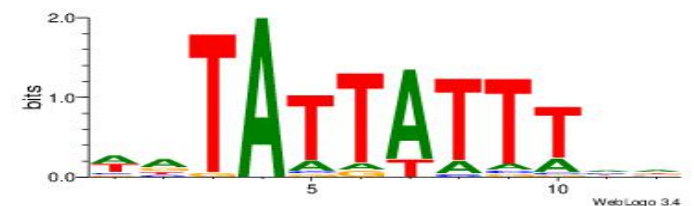


**Dataset #: 4**      **Motif ID: 37**      **Motif name: tkAAATAATAtw**

Original motif      Consensus sequence: HDAAATAATAHW



Reverse complement motif      Consensus sequence: WHTATTATTTDH



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

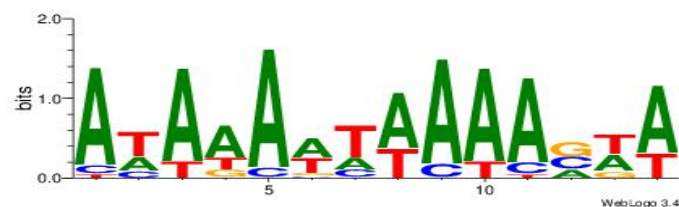


Dataset #: 2  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0522317

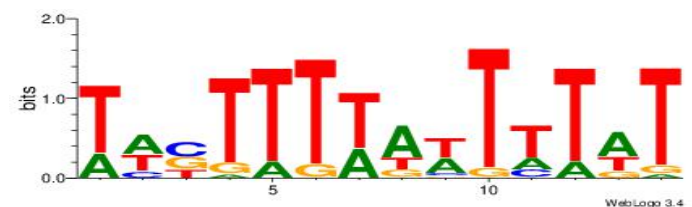
Alignment:

TWSTTTWAWTTTWT  
 -WHTATTATTTDH-

Original motif      Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif      Consensus sequence: TWSTTTWAWTTTWT

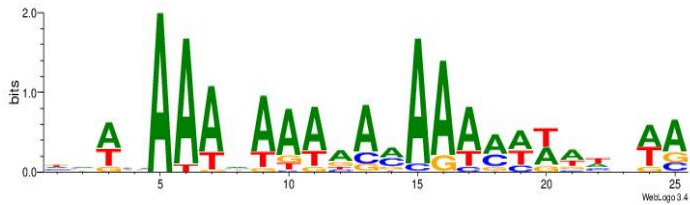


Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 12  
 Number of overlap: 12

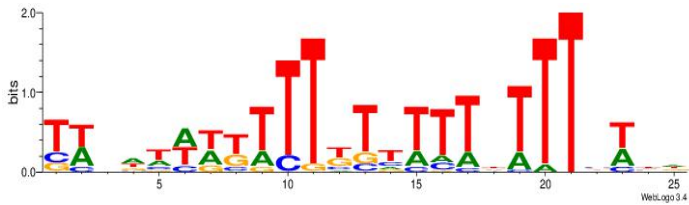
Similarity score: 0.0590505

Alignment:  
TWVHWWYTTTYTTTTHTTTVWBH  
-----WHTATTATTTDH--

Original motif    Consensus sequence:  
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
TWVHWWYTTTYTTTTHTTTVWBH

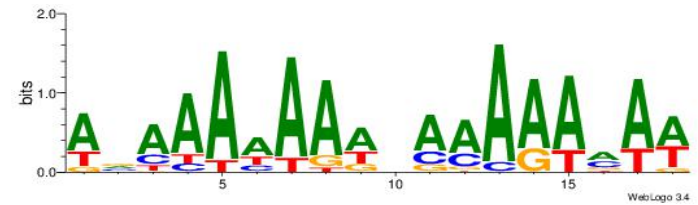
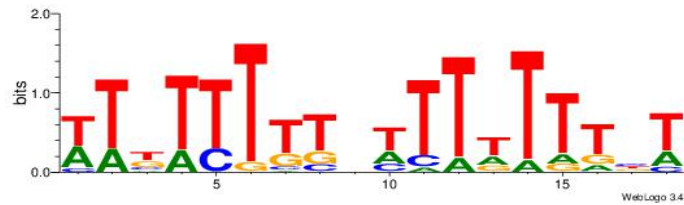


Dataset #: 5  
Motif ID: 52  
Motif name: TFM1  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 12  
Similarity score: 0.0637702

Alignment:  
ABAAAAAWhAAAAARAW  
HDAAATAATAHW-----

Original motif    Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif    Consensus sequence:  
ABAAAAAWhAAAAARAW

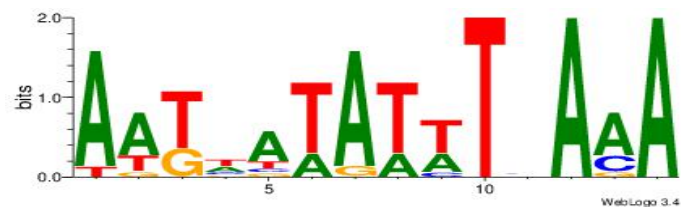


Dataset #: 2  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0641975

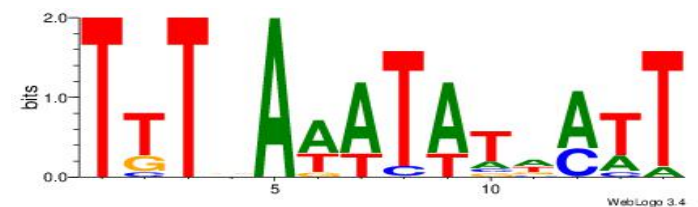
Alignment:

AATHATATWTHAAA  
 --WHTATTATTTDH

Original motif      Consensus sequence: AATHATATWTHAAA



Reverse complement motif      Consensus sequence: TTTDAWATATHAT



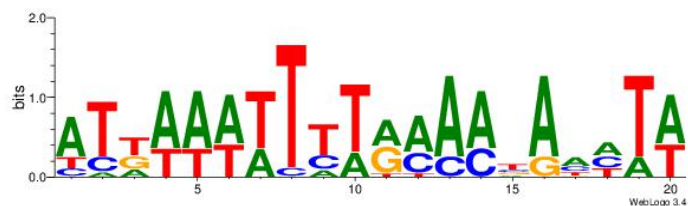
Dataset #: 5  
 Motif ID: 55

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

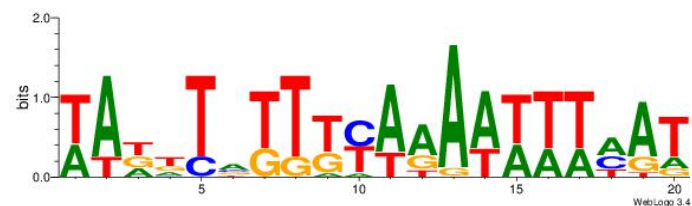
Alignment:

WAHHTVTTYKAAAATTRAT  
 -----HDAAATAATAHW

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



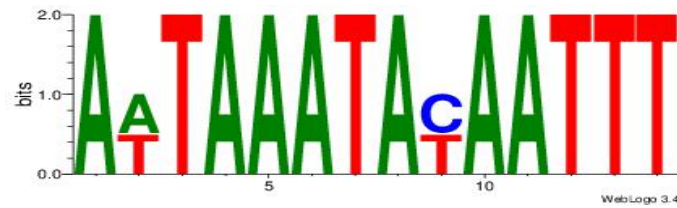
Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0704475

Alignment:

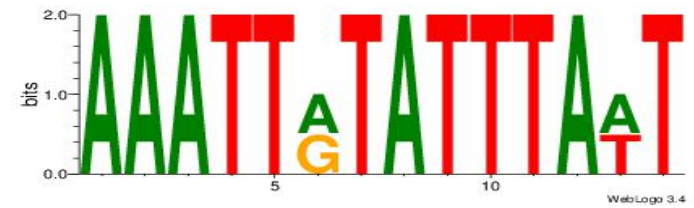
AAATTKTATTTAWT

-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

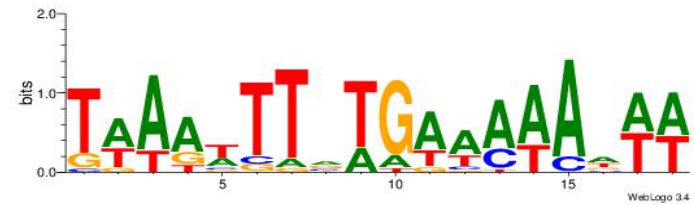
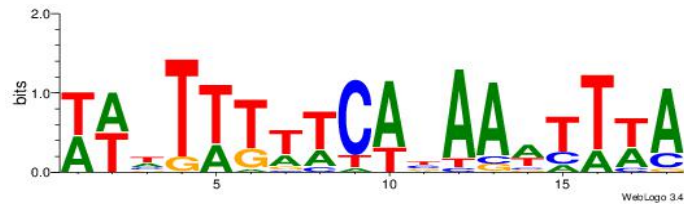
Alignment:

WWHTTTTTCABAAWTTWA

-----WHTATTATTTDH

Original motif      Consensus sequence: WWHTTTTTCABAAWTTWA

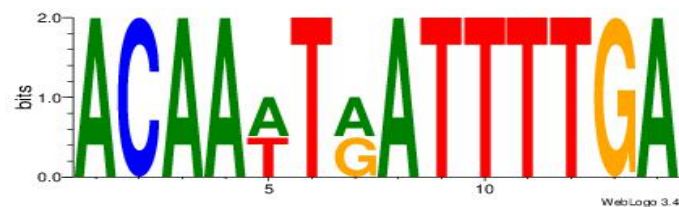
Reverse complement motif      Consensus sequence:  
TAAWTTVTGAAAAHWW



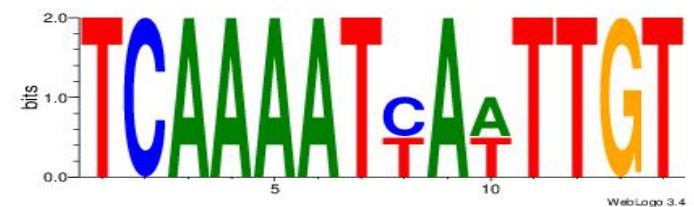
Dataset #: 2  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0864198

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

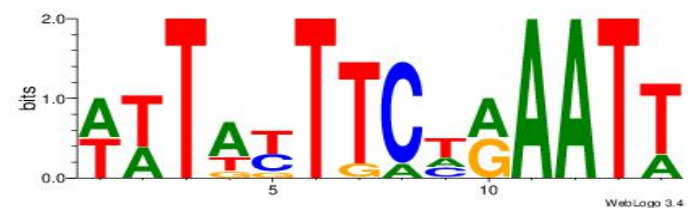
Alignment:

WWTAKTTCDKAATT  
WHTATTATTTDH--

Original motif      Consensus sequence: AATTYDGAARTAWW



Reverse complement motif      Consensus sequence: WWTAKTTCDKAATT



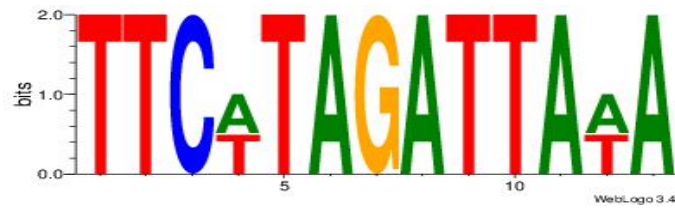
Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.096142

Alignment:

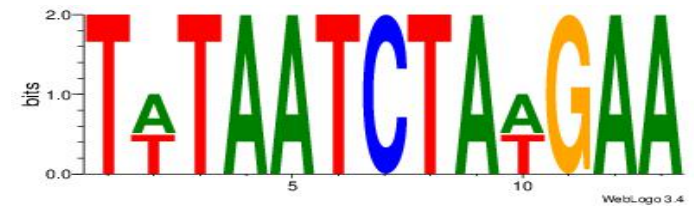
TWTAATCTAWGAA

WHTATTATTTDH-

Original motif      Consensus sequence: TTCWTAGATTAWA



Reverse complement motif      Consensus sequence: TWTAATCTAWGAA



Results created by MOTIFSIM on 06-19-2018 08:41:08

Runtime: 819.17 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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