



# MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

## INPUT

### Input Parameters

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

### Input files and motif counts

File name	Count of motifs	Dataset number
W-ChIPMotifs_DM230.txt	11	1
RSAT_peak-motifs_DM230.txt	10	2

## RESULTS

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

<b>Dataset #: 1</b>	<b>Motif ID: 1</b>	<b>Motif name: TFW1</b>
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Original motif      Consensus sequence: GTCGCG



Reverse complement motif      Consensus sequence: CGCGAC

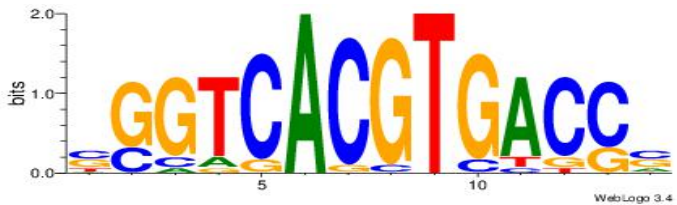


### Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

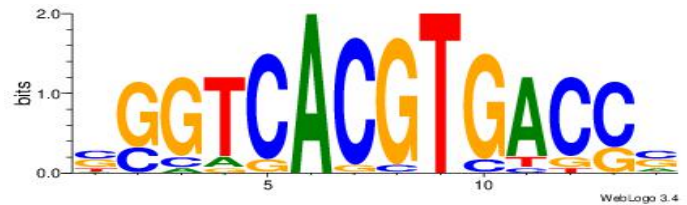
Dataset #: 2  
 Motif ID: 18  
 Motif name: sSGTCACGTGACCS  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 6  
 Similarity score: 0.0375102

Alignment:  
 SGGTCACGTGACCS  
 --GTCGCG-----

Original motif      Consensus sequence: SGGTCACGTGACCS



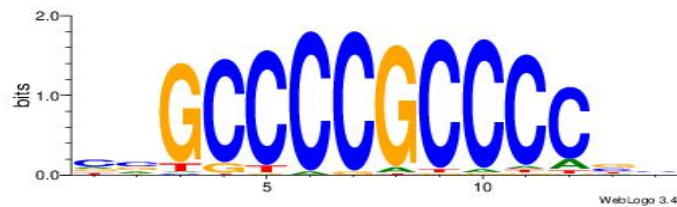
Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



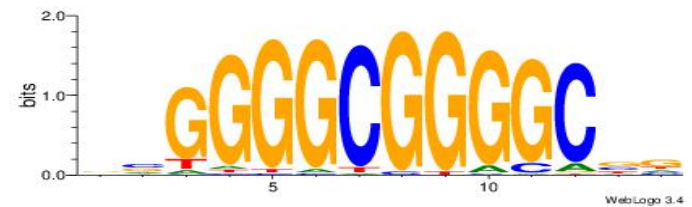
Dataset #: 2  
 Motif ID: 12  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 6  
 Similarity score: 0.0539

Alignment:  
 HVGCCCCGCCCCBB  
 --GTCGCG-----

Original motif      Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC



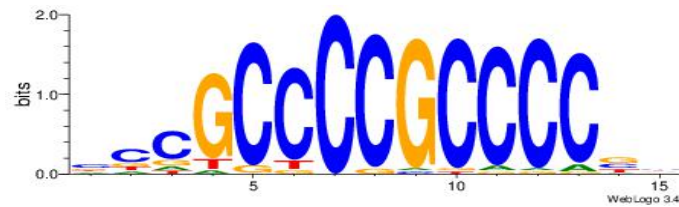
Dataset #: 2  
 Motif ID: 14  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 6

Similarity score: 0.0558733

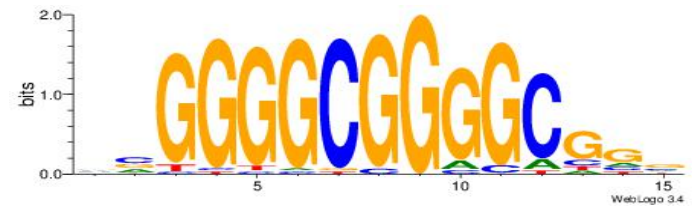
Alignment:

BCCGCCCCGCCCCBB  
-----CGCGAC--

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence:  
BBGGGGCGGGGCGGB



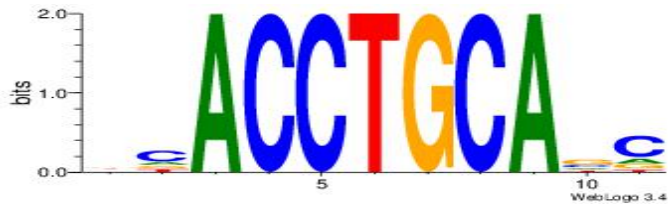
Dataset #: 2  
Motif ID: 16  
Motif name: kcACCTGCAGc  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 6  
Number of overlap: 6  
Similarity score: 0.0980422

Alignment:

BCACCTGCABC  
-----CGCGAC

Original motif      Consensus sequence: BCACCTGCABC

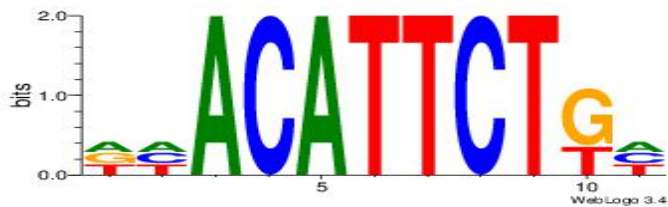
Reverse complement motif      Consensus sequence: GBTGCAGGTGB



Dataset #: 2  
 Motif ID: 20  
 Motif name: dhACATTCTkh  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 4  
 Similarity score: 1.09467

Alignment:  
 HCAGAATGTHD--  
 -----GTCGCG

Original motif      Consensus sequence: DHACATTCTGH



Reverse complement motif      Consensus sequence: HCAGAATGTHD

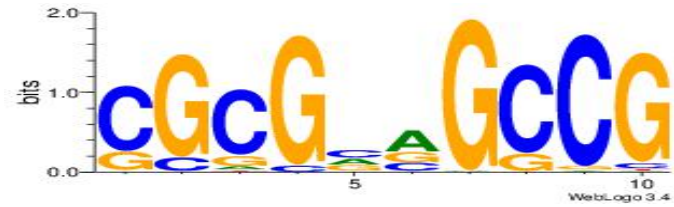


**Dataset #: 1      Motif ID: 3      Motif name: TFW3**

Original motif      Consensus sequence: CGGCYBCGCG



Reverse complement motif      Consensus sequence: CGCGBMGCCG



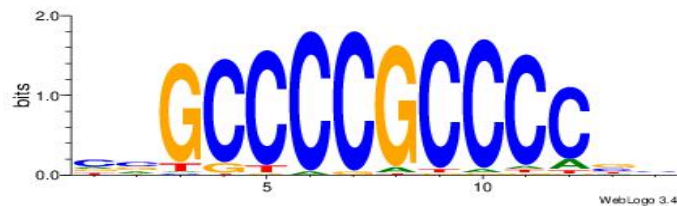
### Best Matches for Top Significant Motif ID 3 (Highest to Lowest)

Dataset #: 2  
 Motif ID: 12  
 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

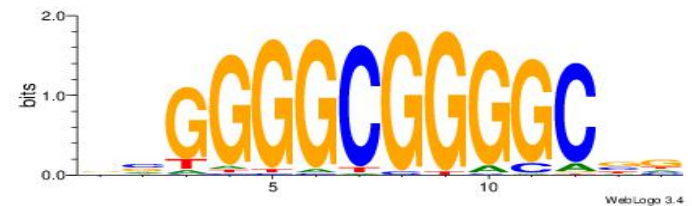
#### Alignment:

HVCCCCGCCCCBB  
 CGGCYBCGCG----

Original motif      Consensus sequence: HVCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC

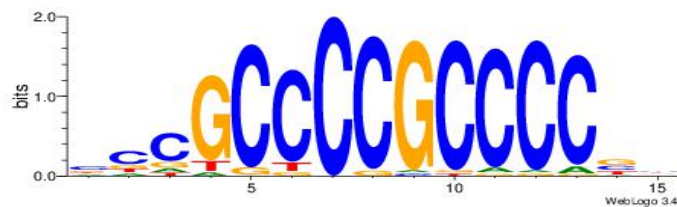


Dataset #: 2  
 Motif ID: 14  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 10  
 Similarity score: 0.0719604

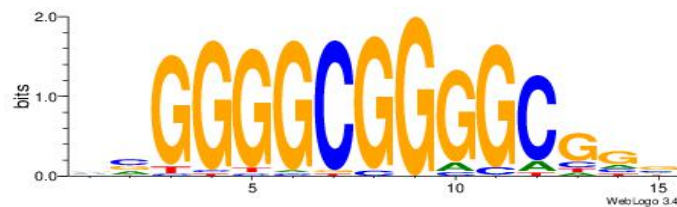
Alignment:

BCCGCCCCGCCCCBB  
 -CGGCYBCGCG-----

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

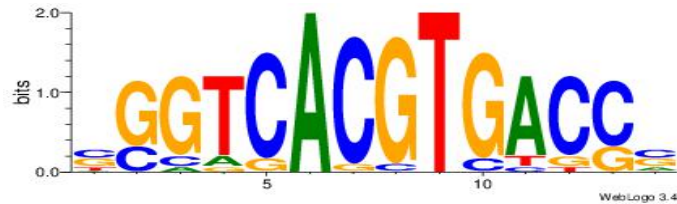


Dataset #: 2  
 Motif ID: 18  
 Motif name: sSGTCACGTGACSS  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5

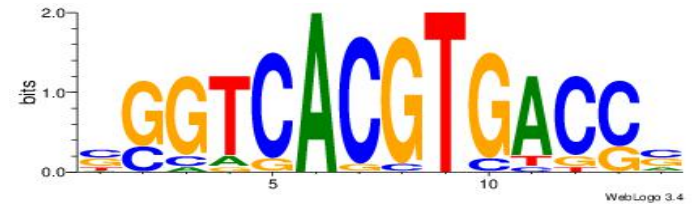
Number of overlap: 10  
Similarity score: 0.0895189

Alignment:  
SGGTCACGTGACCS  
----CGCGBMGCCG

Original motif      Consensus sequence: SGGTCACGTGACCS



Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



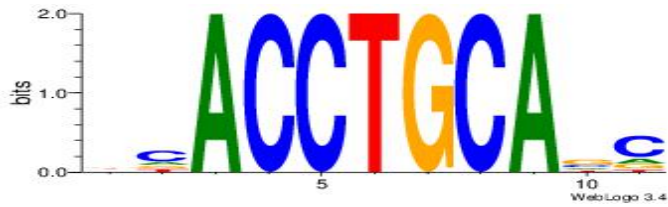
Dataset #: 2  
Motif ID: 16  
Motif name: kcACCTGCAGc  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 8  
Similarity score: 1.10343

Alignment:  
BCACCTGCABC--  
----CGCGBMGCCG

Original motif      Consensus sequence: BCACCTGCABC

Reverse complement motif      Consensus sequence: GBTGCAGGTGB





Dataset #: 2  
 Motif ID: 15  
 Motif name: kCAGCCAATmr  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 7  
 Similarity score: 1.57732

Alignment:

---DCAGCCAATVR  
 CGCGBMGCCG----

Original motif      Consensus sequence: DCAGCCAATVR

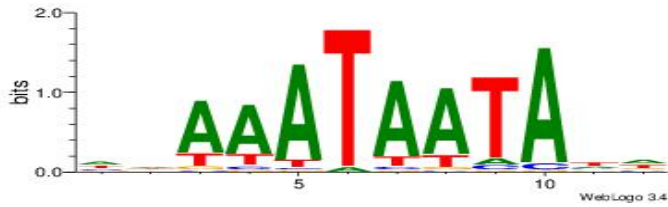


Reverse complement motif      Consensus sequence: MBATTGGCTGH

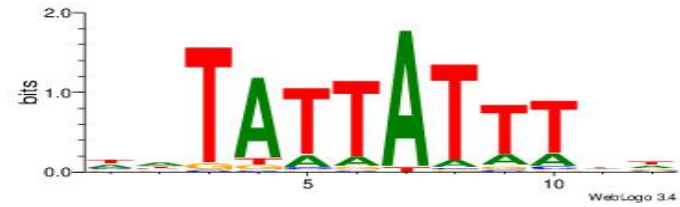


**Dataset #: 2      Motif ID: 17      Motif name: wwAAATAATAtw**

Original motif      Consensus sequence: HDAAATAATADD



Reverse complement motif      Consensus sequence: DDTATTATTTDH



### Best Matches for Top Significant Motif ID 17 (Highest to Lowest)

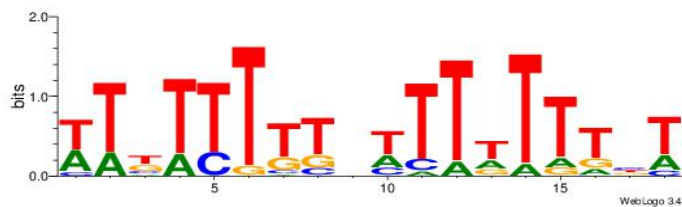
Dataset #:	1
Motif ID:	7
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	12
Similarity score:	0.0565705

Alignment:

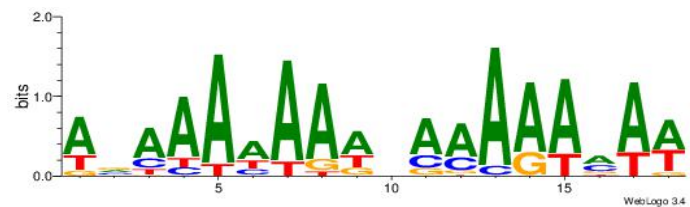
```

ABAAAAAWhAAAAARAW
-----HDAAATAATADD
  
```

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAAWhAAAAARAW

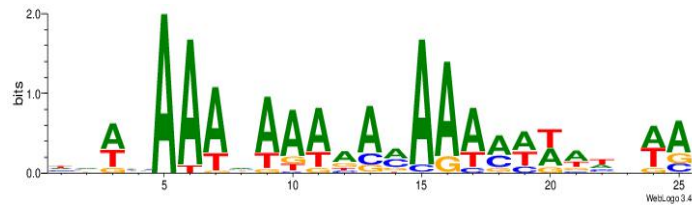


Dataset #: 1  
 Motif ID: 11  
 Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.0575935

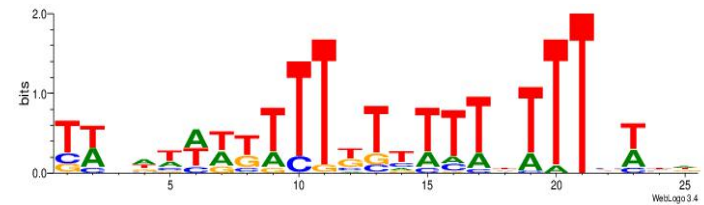
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA  
 --HDAAATAATADD-----

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTTTTTTHTTTVWBH



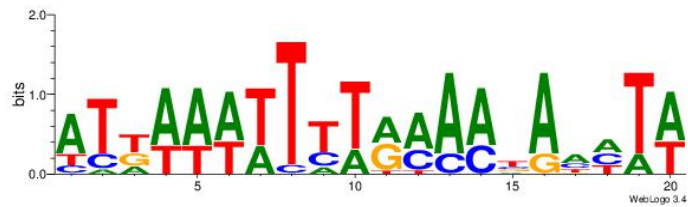
Dataset #: 1  
 Motif ID: 10  
 Motif name: TFM13  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1

Number of overlap: 12  
Similarity score: 0.0712963

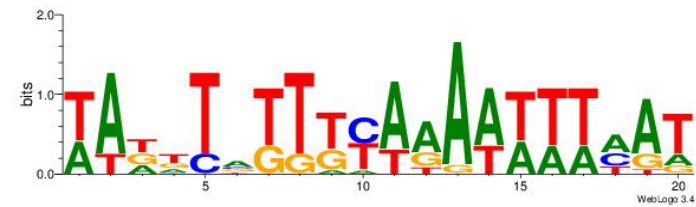
Alignment:

ATKAAWTTTTTRMAABAHTW  
-----DDTATTATTTDH

Original motif      Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif      Consensus sequence:  
WAHHTVTTYKAAAATTRAT

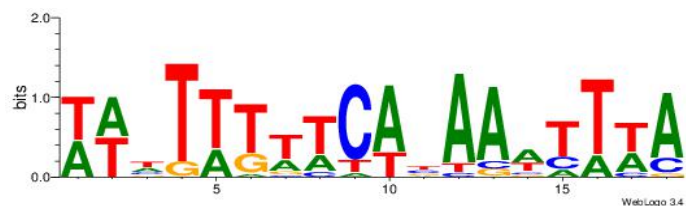


Dataset #: 1  
Motif ID: 8  
Motif name: TFM3  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 12  
Similarity score: 0.0733516

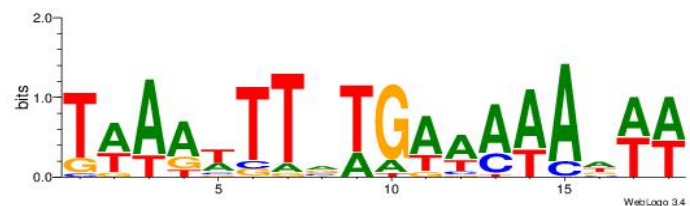
Alignment:

TWAAWTTVTGAAAAAHWW  
-----HDAAATAATADD

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif      Consensus sequence: TWAAWTTVTGAAAAHWW

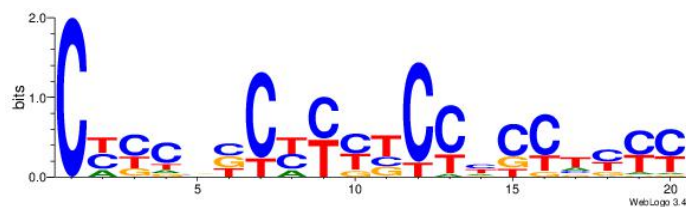


Dataset #: 1  
Motif ID: 9  
Motif name: TFM12  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 16  
Number of overlap: 5  
Similarity score: 3.59569

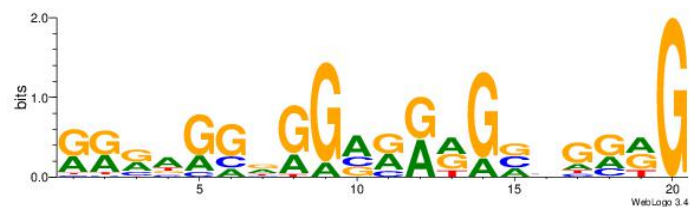
Alignment:

-----KKKAGGDGGAKKMGBBGKMG  
DDTATTATTTDH-----

Original motif      Consensus sequence: CYYCBCYYYTCCHCCTYYY

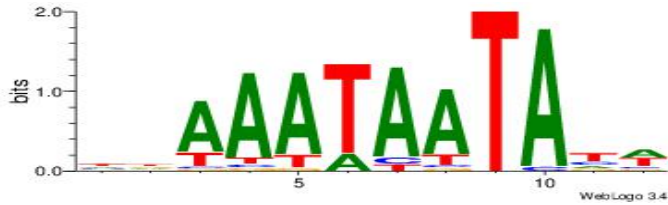


Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG



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

Original motif      Consensus sequence: HDAAATAATAHW



Reverse complement motif      Consensus sequence: WHTATTATTTDH



**Best Matches for Top Significant Motif ID 13 (Highest to Lowest)**

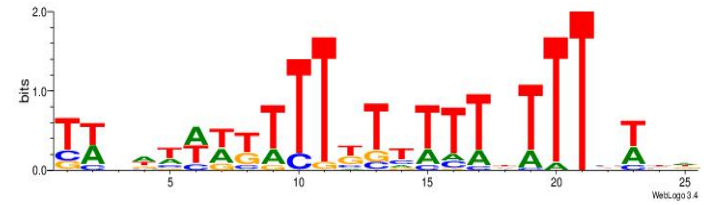
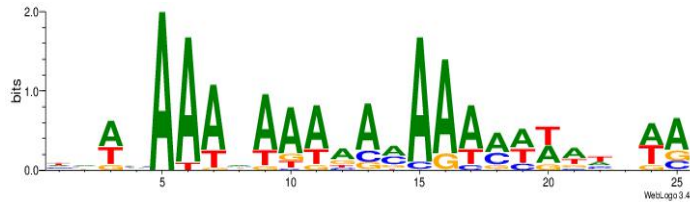
Dataset #: 1  
 Motif ID: 11  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.0590505

**Alignment:**

TWVHWWWYTTTTYTTTTTHTTTTVWBH  
 -----WHTATTATTTDH--

Original motif      Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA

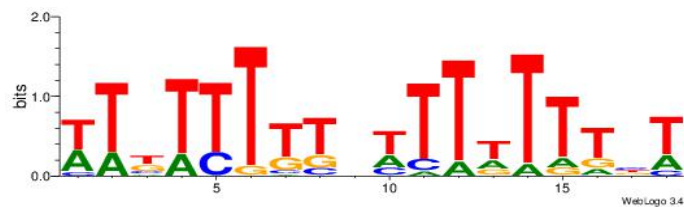
Reverse complement motif      Consensus sequence:  
 TWVHWWWYTTTTYTTTTTHTTTTVWBH



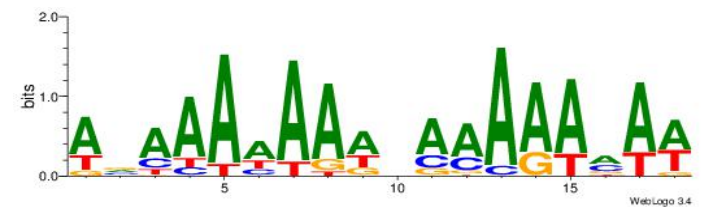
Dataset #: 1  
 Motif ID: 7  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0637702

Alignment:  
 WKTTTTTHWTTTTTBT  
 WHTATTATTTDH-----

Original motif      Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAAWHAAAAARAW



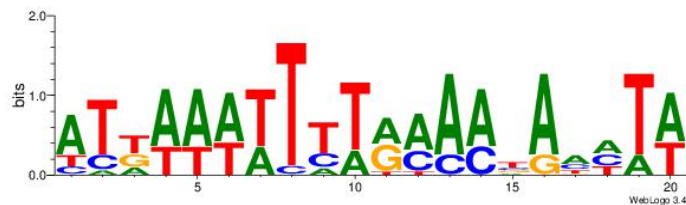
Dataset #: 1

Motif ID: 10  
 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: 0.0704475

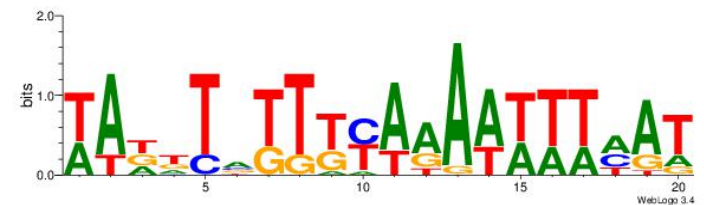
Alignment:

ATKAAWTTTTTRMAABAHTW  
 -----WHTATTATTTDH

Original motif      Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 1  
 Motif ID: 8  
 Motif name: TFM3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12

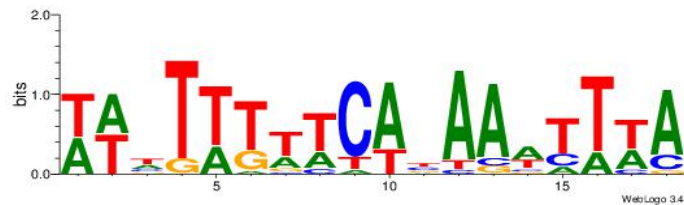


Similarity score: 0.0763819

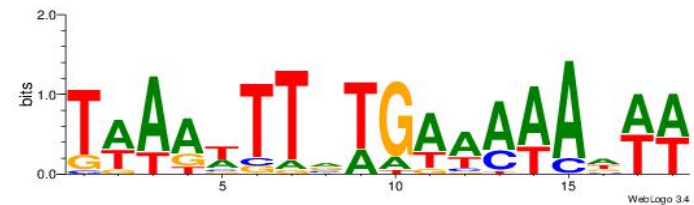
Alignment:

TWAAWTTVTGAAAAHWW  
-----HDAAATAATAHW

Original motif    Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif    Consensus sequence:  
TAAWTTVTGAAAAHWW



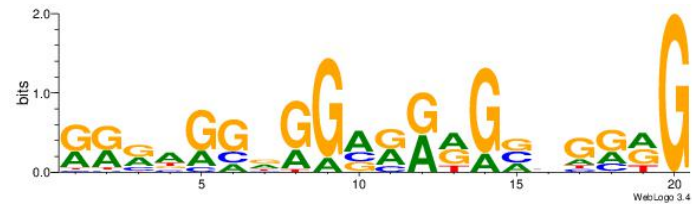
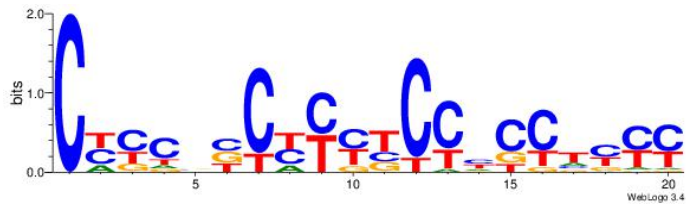
Dataset #: 1  
Motif ID: 9  
Motif name: TFM12  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 16  
Number of overlap: 5  
Similarity score: 3.59273

Alignment:

-----KKKAGGDGGAKKMGBBGKMG  
WHTATTATTDH-----

Original motif    Consensus sequence: CYYCBCYYYTCCHCCTYYY

Reverse complement motif    Consensus sequence:  
KKKAGGDGGAKKMGBBGKMG



**Dataset #: 1      Motif ID: 2      Motif name: TFW2**

Original motif      Consensus sequence: SCGCGCGG



Reverse complement motif      Consensus sequence: CCGCGCGS

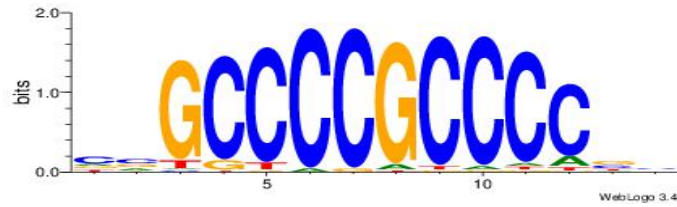


**Best Matches for Top Significant Motif ID 2 (Highest to Lowest)**

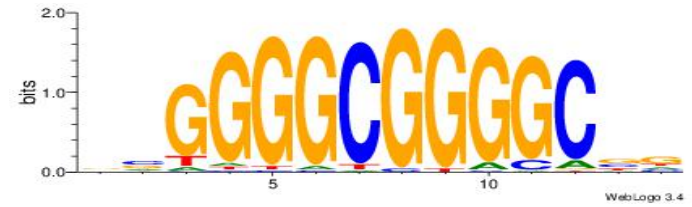
Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0456233

Alignment:  
 BBGGGGCGGGGCVD  
 -SCGCGCGG-----

Original motif      Consensus sequence: HVGCCCCGCCCB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC

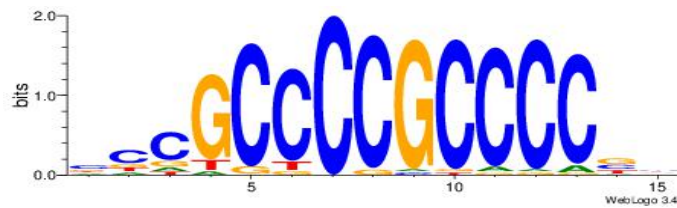


Dataset #: 2  
 Motif ID: 14  
 Motif name: cccGCCCCGCCCBsb  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 8  
 Similarity score: 0.045686

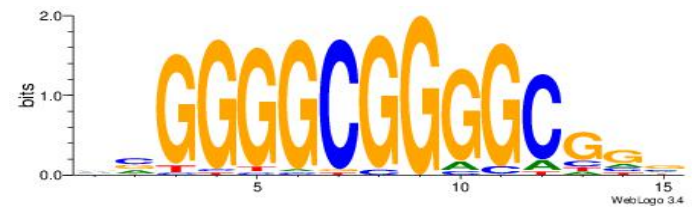
Alignment:

```
BCCGCCCCGCCCB
-----CCGCGCS-
```

Original motif      Consensus sequence: BCCGCCCCGCCCB



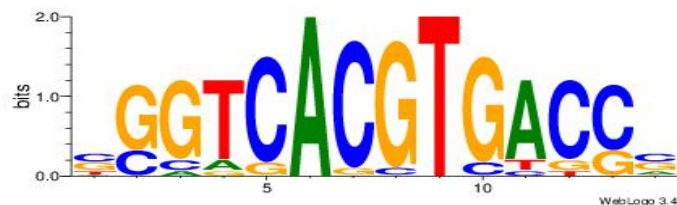
Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGB



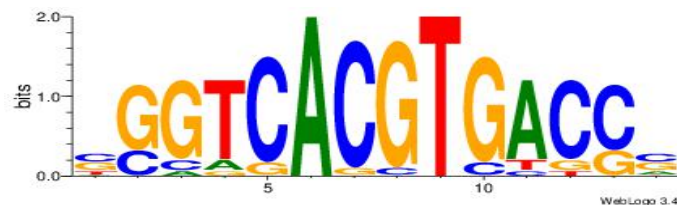
Dataset #: 2  
 Motif ID: 18  
 Motif name: sSGTCACGTGACSS  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 8  
 Similarity score: 0.0988223

Alignment:  
 SGGTCACGTGACCS  
 ---SCGCGCGG---

Original motif      Consensus sequence: SGGTCACGTGACCS



Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



Dataset #: 2  
 Motif ID: 16  
 Motif name: kcACCTGCAGc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 4

Similarity score: 2.08456

Alignment:

----GBTGCAGGTGB  
SCGCGCGG-----

Original motif      Consensus sequence: BCACCTGCABC



Reverse complement motif      Consensus sequence: GBTGCAGGTGB



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Dataset #: 2  
Motif ID: 15  
Motif name: kCAGCCAATmr  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 8  
Number of overlap: 4  
Similarity score: 2.0901

Alignment:

MBATTGGCTGH----  
-----CCGCGCGS

Original motif      Consensus sequence: DCAGCCAATVR

Reverse complement motif      Consensus sequence: MBATTGGCTGH



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

Original motif      Consensus sequence: DBGTAATAHD



Reverse complement motif      Consensus sequence: DHTATTTACBD



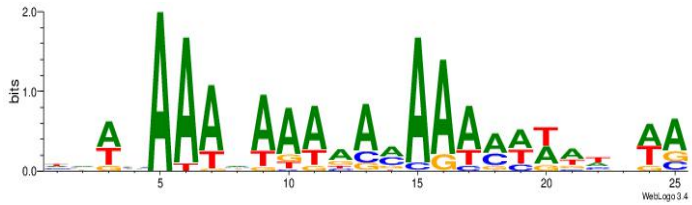
**Best Matches for Top Significant Motif ID 21 (Highest to Lowest)**

Dataset #:	1
Motif ID:	11
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

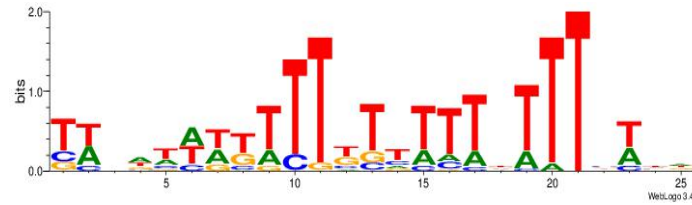
Alignment:

```
TWVHWWWYTTTYTTTTHTTTVWBH
-----DHTATTTACBD
```

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTTTTTTHTTTVWBH

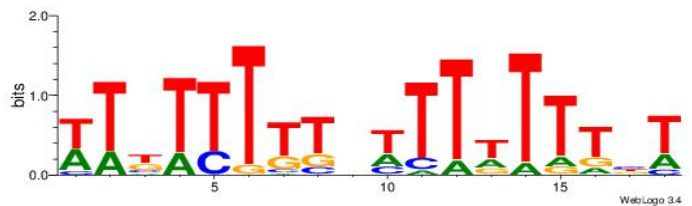


Dataset #: 1  
 Motif ID: 7  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0283217

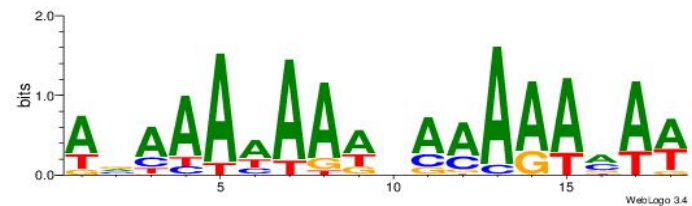
Alignment:

WTKTTTTTHWTTTTTTBT  
 DHTATTTACBD-----

Original motif    Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif    Consensus sequence:  
 ABAAAAAWHAAAAARAW

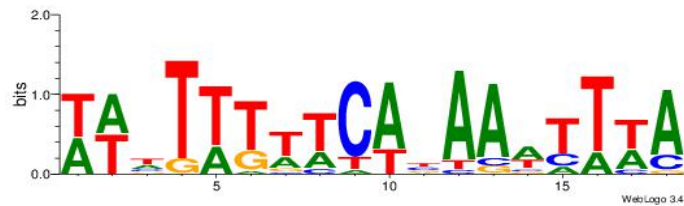


Dataset #: 1  
 Motif ID: 8  
 Motif name: TFM3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0308097

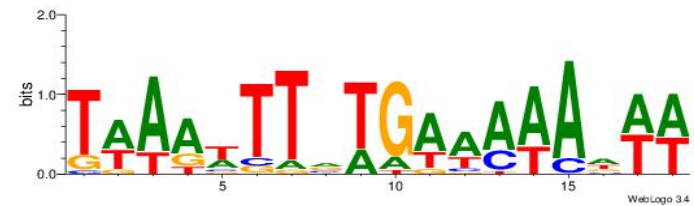
Alignment:

WWHTTTTTTCABAAWTTWA  
 -----DHTATTTACBD-

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif      Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 1  
 Motif ID: 10  
 Motif name: TFM13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3

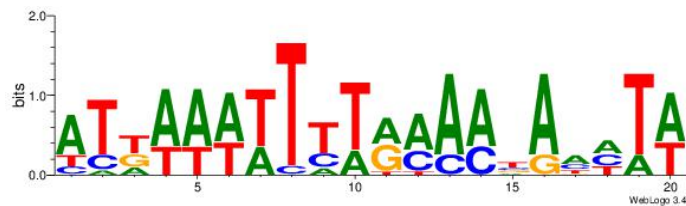


Number of overlap: 11  
 Similarity score: 0.0333874

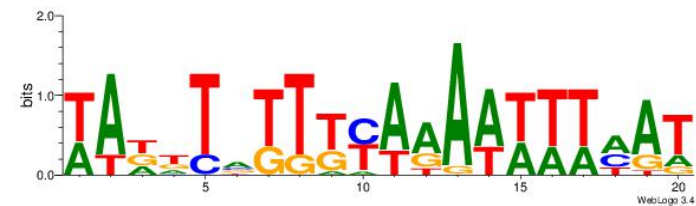
Alignment:

ATKAAWTTTTTRMAABAHTW  
 -----DBGTAAATAHD--

Original motif      Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif      Consensus sequence:  
 WAHHTVTTYKAAAATTRAT

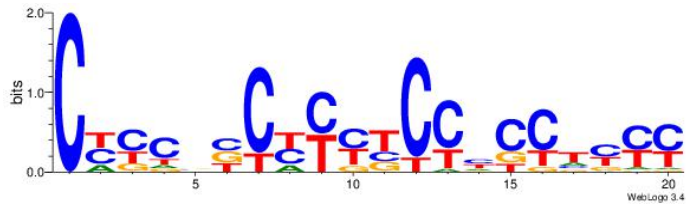


Dataset #: 1  
 Motif ID: 9  
 Motif name: TFM12  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 14  
 Number of overlap: 7  
 Similarity score: 2.0544

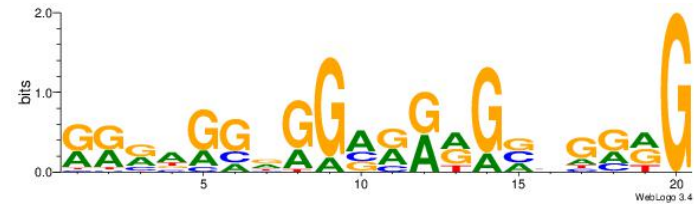
Alignment:

----KKKAGGDGGAKKMGBBGKMG  
 DHTATTTACBD-----

Original motif      Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

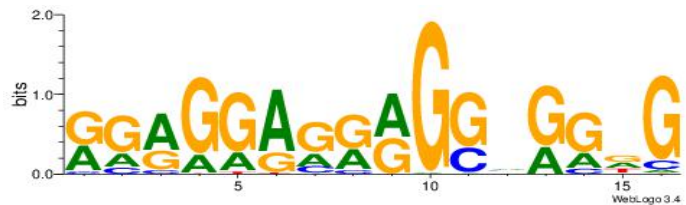


Dataset #: 1  
Motif ID: 6  
Motif name: TFM2  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 12  
Number of overlap: 5  
Similarity score: 3.05714

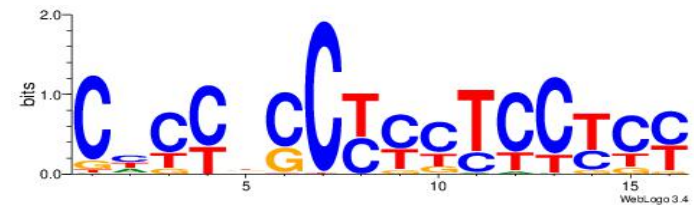
Alignment:

-----CHCCBCCKMCTCCKCM  
DHTATTTACBD-----

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif      Consensus sequence: CHCCBCCKMCTCCKCM

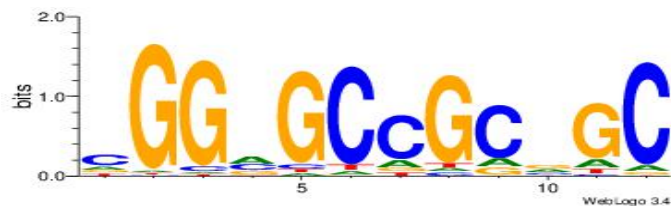


Dataset #: 1  
 Motif ID: 4  
 Motif name: TFF1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 4  
 Similarity score: 3.54896

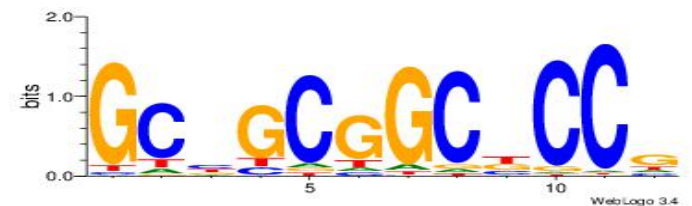
Alignment:

-----GCVGCGGCBCCG  
 DHTATTTACBD-----

Original motif    Consensus sequence: CGGVGCCGCVGC



Reverse complement motif    Consensus sequence: GCVGCGGCBCCG



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

Original motif    Consensus sequence: HVTACWG TABD



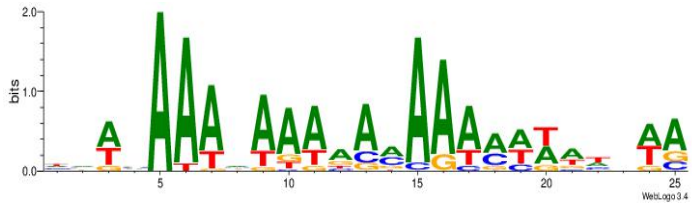
Reverse complement motif    Consensus sequence: DBTACWG TAVH



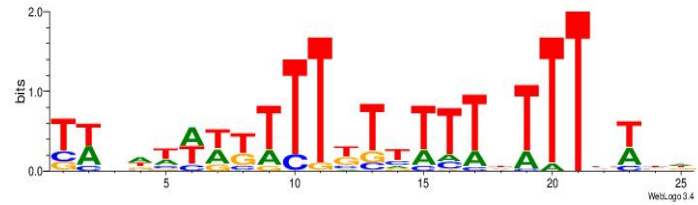




Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTTTTTTHTTTTWWBH



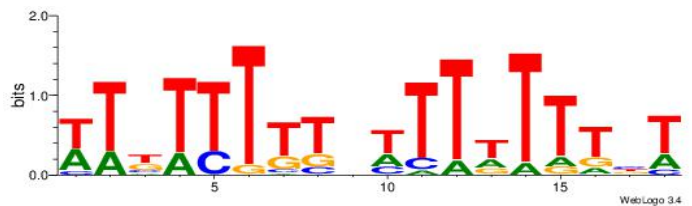
Dataset #: 1  
 Motif ID: 7  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 9  
 Similarity score: 1.04742

Alignment:

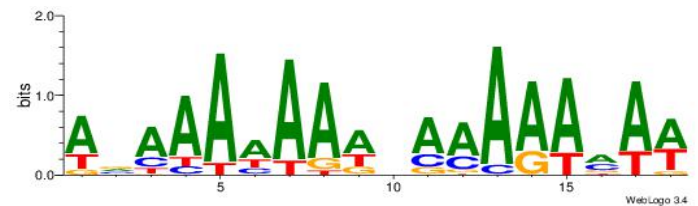
```

WTKTTTTTHWTTTTTTBT--
-----DBTACWGTAVH
  
```

Original motif    Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif    Consensus sequence:  
 ABAAAAAWHAAAAARAW

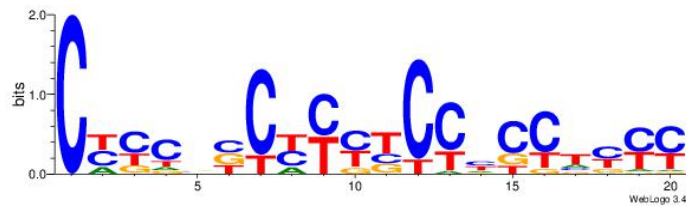


Dataset #: 1  
 Motif ID: 9  
 Motif name: TFM12  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 15  
 Number of overlap: 6  
 Similarity score: 2.54736

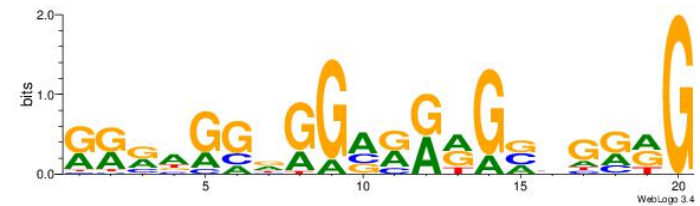
Alignment:

-----CYYCBBCYYYYTCCHCCTYYY  
 DBTACWGTAVH-----

Original motif      Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG



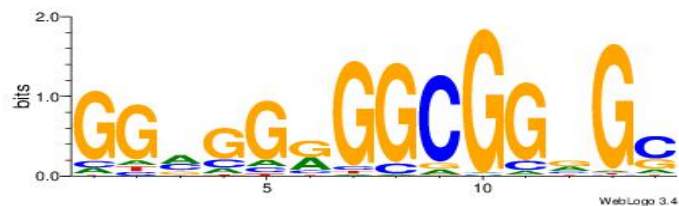
Dataset #: 1  
 Motif ID: 5  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10

Number of overlap: 5  
Similarity score: 3.04599

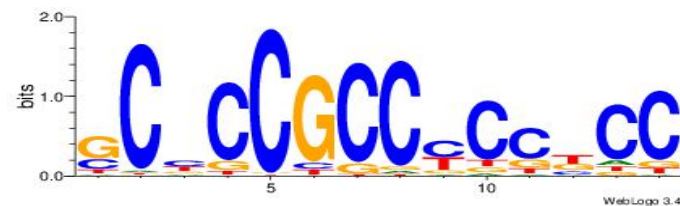
Alignment:

GGMGGRGGCGGVGC-----  
-----DBTACWGTAVH

Original motif      Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYC



Dataset #: 1  
Motif ID: 6  
Motif name: TFM2  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 12  
Number of overlap: 5  
Similarity score: 3.04861

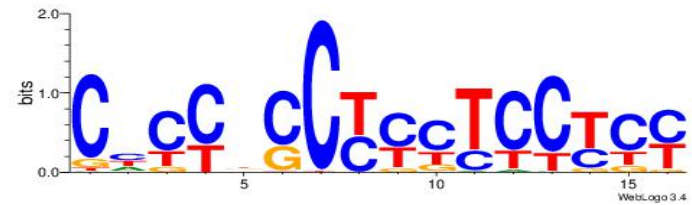
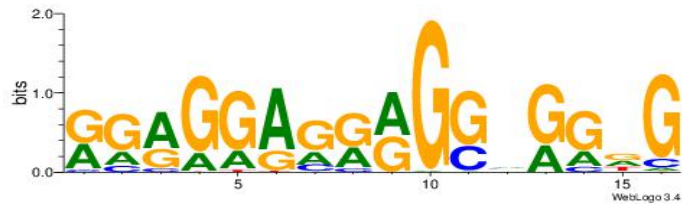
Alignment:

RGRGGAGRRGGHGGDG-----  
-----DBTACWGTAVH

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif      Consensus sequence:  
CHCCBCKMCTCKCM





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

Original motif      Consensus sequence: BCACCTGCABC



Reverse complement motif      Consensus sequence: GBTGCAGGTGB

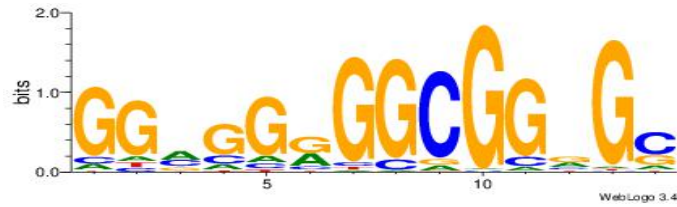


**Best Matches for Top Significant Motif ID 16 (Highest to Lowest)**

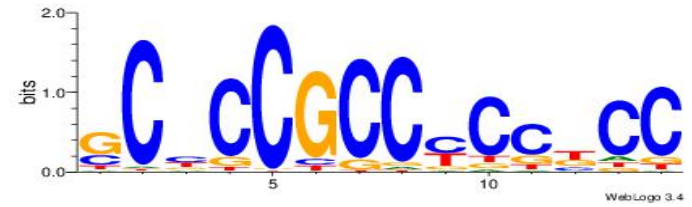
Dataset #:	1
Motif ID:	5
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0312321

Alignment:  
 GGMGGRGGCGGVGC  
 GBTGCAGGTGB---

Original motif      Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYC



Dataset #: 1  
 Motif ID: 9  
 Motif name: TFM12  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 11  
 Similarity score: 0.0444938

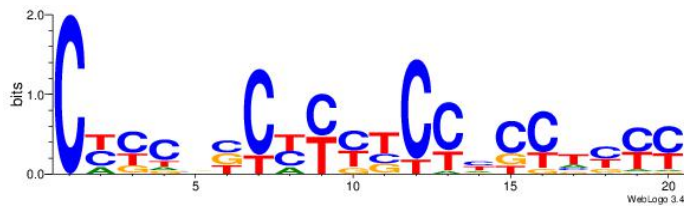
Alignment:

```

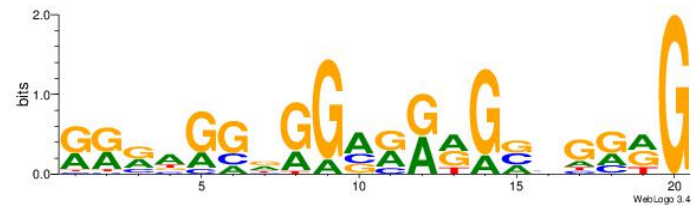
KKKAGGDGGAKKMGBBGKMG
----GBTGCAGGTGB-----

```

Original motif      Consensus sequence: CYYCBBYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

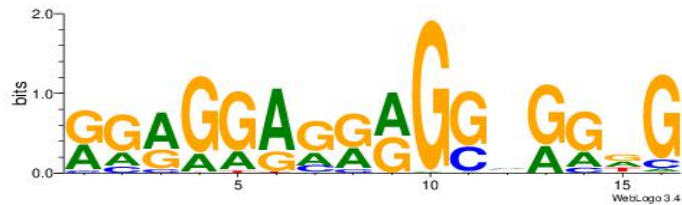


Dataset #: 1  
 Motif ID: 6  
 Motif name: TFM2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.538471

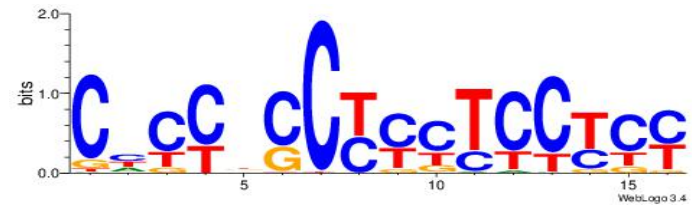
Alignment:

-RGRGGAGRRGGHGGDG  
 GBTGCAGGTGB-----

Original motif    Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif    Consensus sequence: CHCCBCKMCTCCKCM

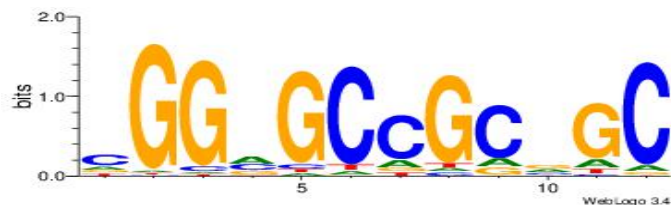


Dataset #: 1  
 Motif ID: 4  
 Motif name: TFF1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5

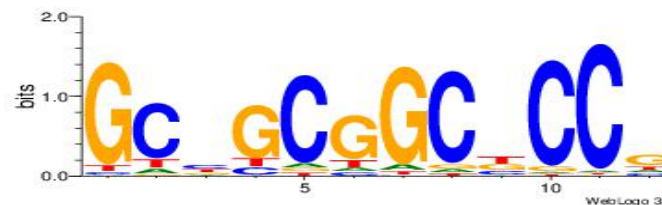
Number of overlap: 8  
 Similarity score: 1.54364

Alignment:  
 GCVGCGGCBCCG---  
 ----BCACCTGCABC

Original motif    Consensus sequence: CGGVGCCGCVGC



Reverse complement motif    Consensus sequence: GCVGCGGCBCCG

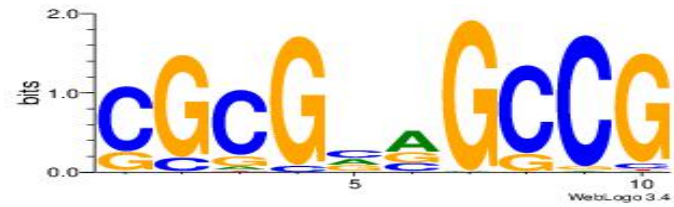


Dataset #: 1  
 Motif ID: 3  
 Motif name: TFW3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 8  
 Similarity score: 1.5466

Alignment:  
 ---CGGCYBCGCG  
 GBTGCAGGTGB--

Original motif    Consensus sequence: CGGCYBCGCG

Reverse complement motif    Consensus sequence: CGCGBMGCCG



Dataset #: 1  
 Motif ID: 1  
 Motif name: TFW1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 6  
 Similarity score: 2.54121

Alignment:  
 CGCGAC-----  
 BCACCTGCABC

Original motif    Consensus sequence: GTCGCG



Reverse complement motif    Consensus sequence: CGCGAC



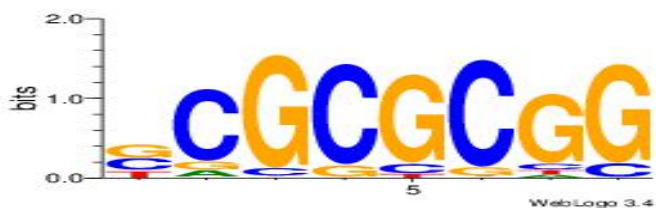
Dataset #: 1  
 Motif ID: 2

Motif name: TFW2  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 4  
 Similarity score: 3.53211

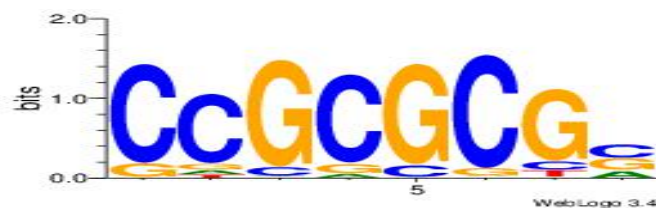
Alignment:

CCGCGCGS-----  
 ----BCACCTGCABC

Original motif    Consensus sequence: SCGCGCGG



Reverse complement motif    Consensus sequence: CCGCGCGS



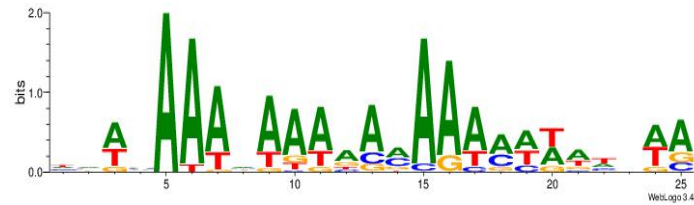

---

Dataset #: 1  
 Motif ID: 11  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 22  
 Number of overlap: 4  
 Similarity score: 3.53789

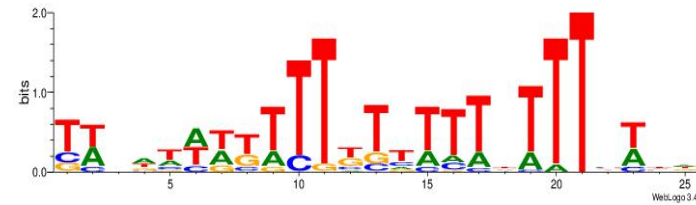
Alignment:

-----TWVHWWYTTTTYTTTTTHTTTTVWBH  
GBTGCAGGTGB-----

Original motif    Consensus sequence:  
HDWVAAAHAAAAAMAAAMWWWHBWA

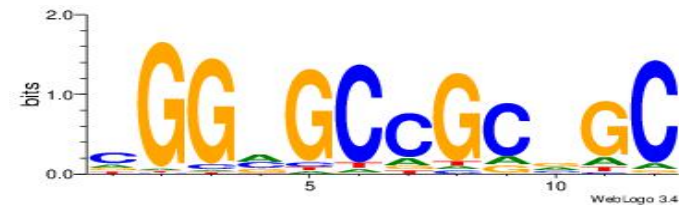


Reverse complement motif    Consensus sequence:  
TWVHWWYTTTTYTTTTTHTTTTVWBH

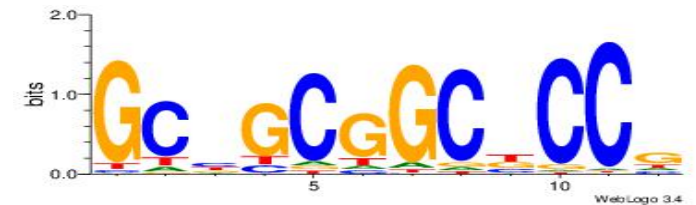


**Dataset #: 1      Motif ID: 4      Motif name: TFF1**

Original motif    Consensus sequence: CGGVGCCGCVGC



Reverse complement motif    Consensus sequence: GCVGCGGCBCCG



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

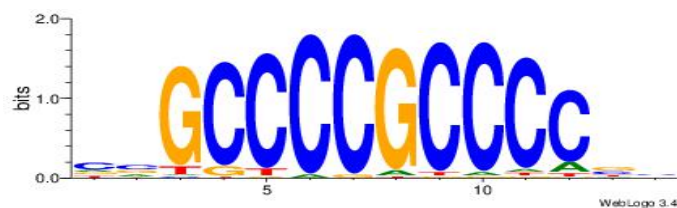
Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 1  
Number of overlap: 12  
Similarity score: 0.0542674

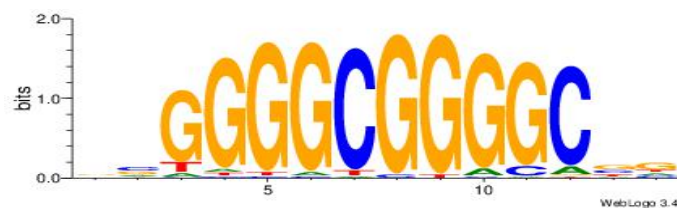
Alignment:

HVGCCCCGCCCCBB  
CGGVGCCGCVGC--

Original motif    Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC



---

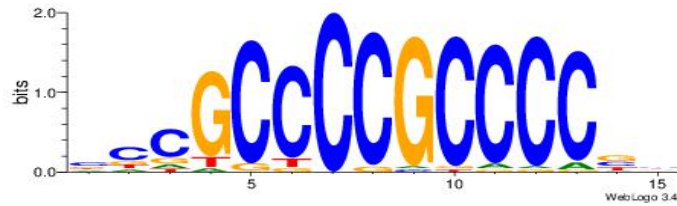
Dataset #: 2  
Motif ID: 14  
Motif name: cccGCCCCGCCCCsb  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 12  
Similarity score: 0.0548371

Alignment:

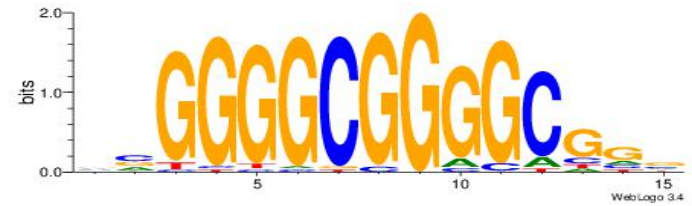
BCCGCCCCGCCCCBB  
---GCVGCGGCBCCG



Original motif      Consensus sequence: BCGCCCCGCCCB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

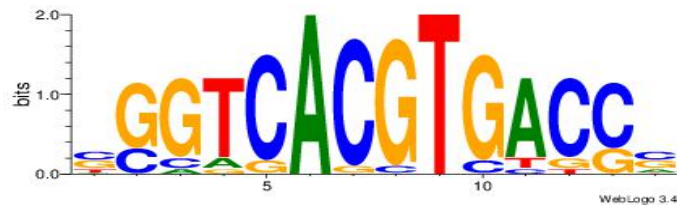


Dataset #: 2  
Motif ID: 18  
Motif name: sSGTCACGTGACCS  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 12  
Similarity score: 0.0777862

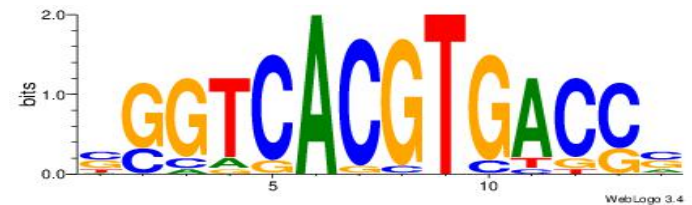
Alignment:

SGGTCACGTGACCS  
--GCVGCGGCBCCG

Original motif      Consensus sequence: SGGTCACGTGACCS



Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



Dataset #: 2  
 Motif ID: 16  
 Motif name: kcACCTGCAGc  
 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: 2.08028

Alignment:

----GBTGCAGGTGB  
 CGGVGCCGCVGC----

Original motif      Consensus sequence: BCACCTGCABC



Reverse complement motif      Consensus sequence: GBTGCAGGTGB



Dataset #: 2  
 Motif ID: 15  
 Motif name: kCAGCCAATmr  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 5

Similarity score: 3.54126

Alignment:

-----DCAGCCAATVR  
CGGVGCCGCVGC-----

Original motif      Consensus sequence: DCAGCCAATVR



Reverse complement motif      Consensus sequence: MBATTGGCTGH



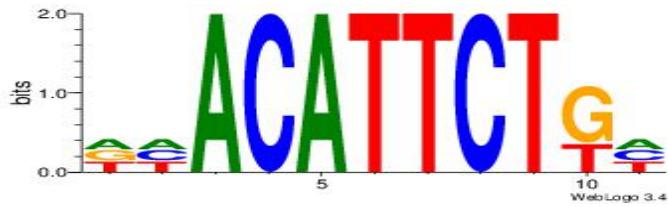
Dataset #: 2  
Motif ID: 20  
Motif name: dhACATTCTkh  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 8  
Number of overlap: 4  
Similarity score: 4.07107

Alignment:

HCAGAATGTHD-----  
-----GCVGCGGCBCCG

Original motif      Consensus sequence: DHACATTCTGH

Reverse complement motif      Consensus sequence: HCAGAATGTHD



Dataset #: 2  
 Motif ID: 21  
 Motif name: wbgTAAATAww  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 4  
 Similarity score: 4.0742

Alignment:  
 DHTATTTACBD-----  
 -----GCVGCGGCBCCG

Original motif      Consensus sequence: DBGTAATAHD

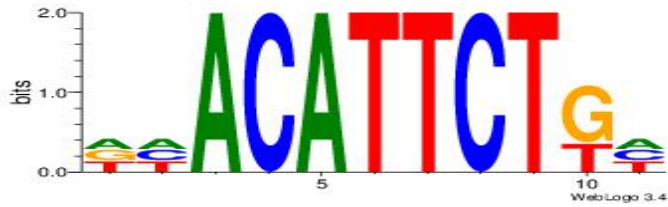


Reverse complement motif      Consensus sequence: DHTATTTACBD



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

Original motif      Consensus sequence: DHACATTCTGH



Reverse complement motif      Consensus sequence: HCAGAATGTHD



### Best Matches for Top Significant Motif ID 20 (Highest to Lowest)

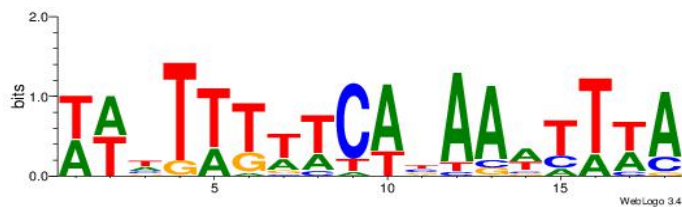
Dataset #: 1  
 Motif ID: 8  
 Motif name: TFM3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.00522383

Alignment:

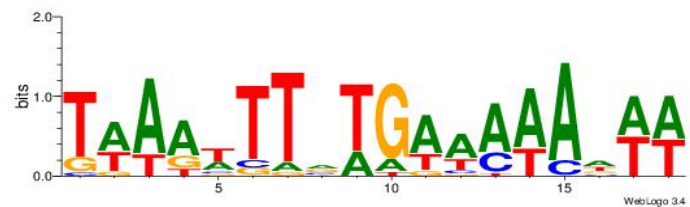
```

WWHTTTTTTCABAAWTTWA
HCAGAATGTHD-----
  
```

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif      Consensus sequence: TAAWTTVTGAAAAHWW

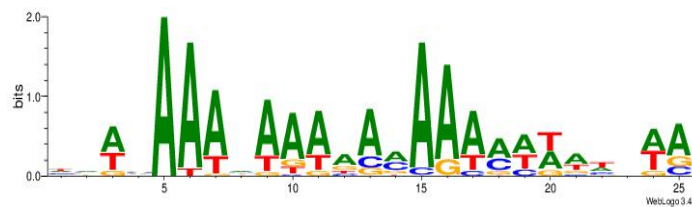


Dataset #: 1  
 Motif ID: 11  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 11  
 Similarity score: 0.014258

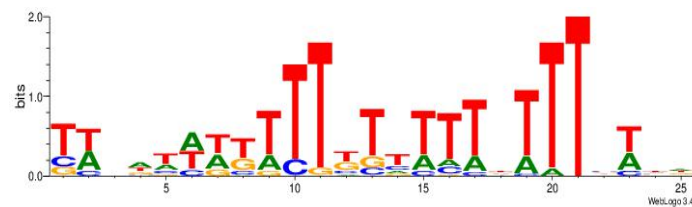
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA  
 ----HCAGAATGTHD-----

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTTTTTHTTTVWBH



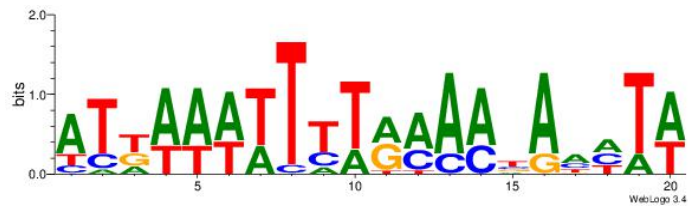
Dataset #: 1  
 Motif ID: 10  
 Motif name: TFM13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 9

Number of overlap: 11  
Similarity score: 0.0192045

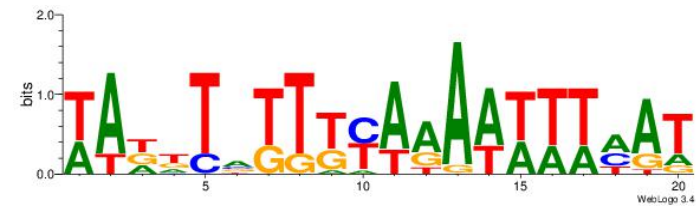
Alignment:

ATKAAWTTTTTRMAABAHTW  
-DHACATTCTGH-----

Original motif    Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif    Consensus sequence:  
WAHHTVTTYKAAAATTRAT

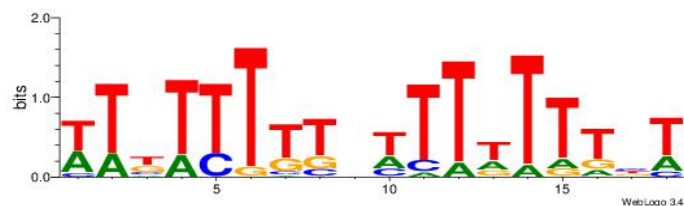


Dataset #: 1  
Motif ID: 7  
Motif name: TFM1  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 9  
Number of overlap: 10  
Similarity score: 0.519904

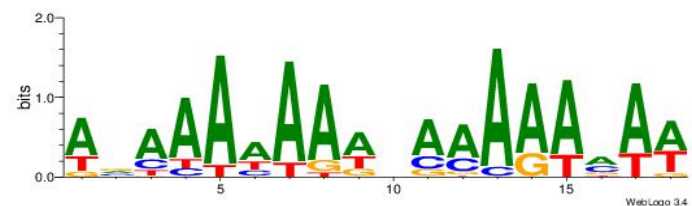
Alignment:

ABAAAAAWhAAAAARAW-  
-----HCAGAATGTHD

Original motif      Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAAWHAAAAARAW

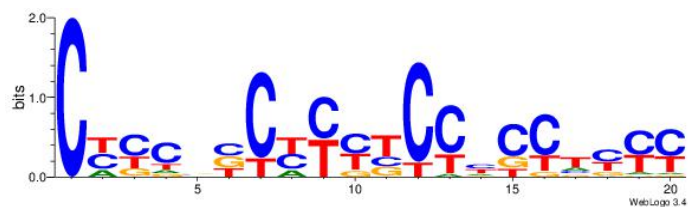


Dataset #: 1  
 Motif ID: 9  
 Motif name: TFM12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 17  
 Number of overlap: 4  
 Similarity score: 3.5

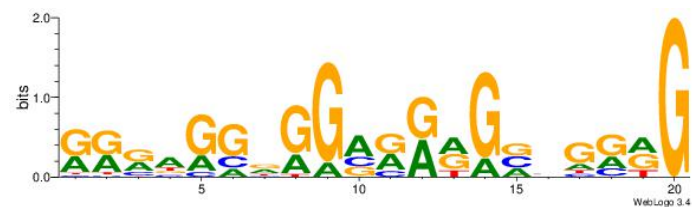
Alignment:

```
-----CYYCBBCYYYYTCCHCCTYYY
DHACATTCTGH-----
```

Original motif      Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG



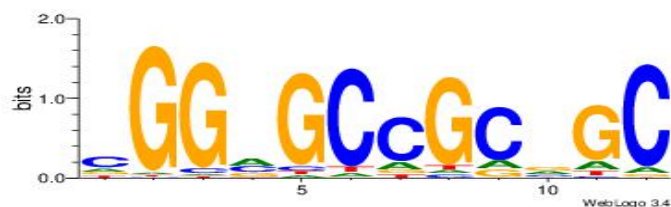


Dataset #: 1  
 Motif ID: 4  
 Motif name: TFF1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 4  
 Similarity score: 3.51958

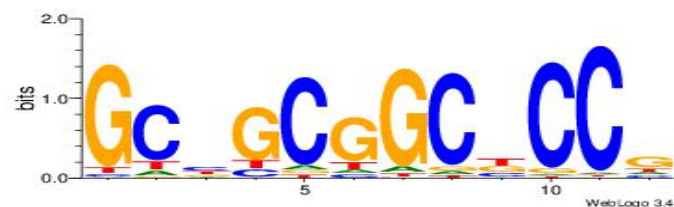
Alignment:

-----GCVGCGGCBCCG  
 HCAGAAATGTHD-----

Original motif    Consensus sequence: CGGVGCCGCVGC



Reverse complement motif    Consensus sequence: GCVGCGGCBCCG



Dataset #: 1  
 Motif ID: 1  
 Motif name: TFW1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 4

Similarity score: 3.52299

Alignment:

-----CGCGAC  
DHACATTCTGH--

Original motif    Consensus sequence: GTCGCG



Reverse complement motif    Consensus sequence: CGCGAC



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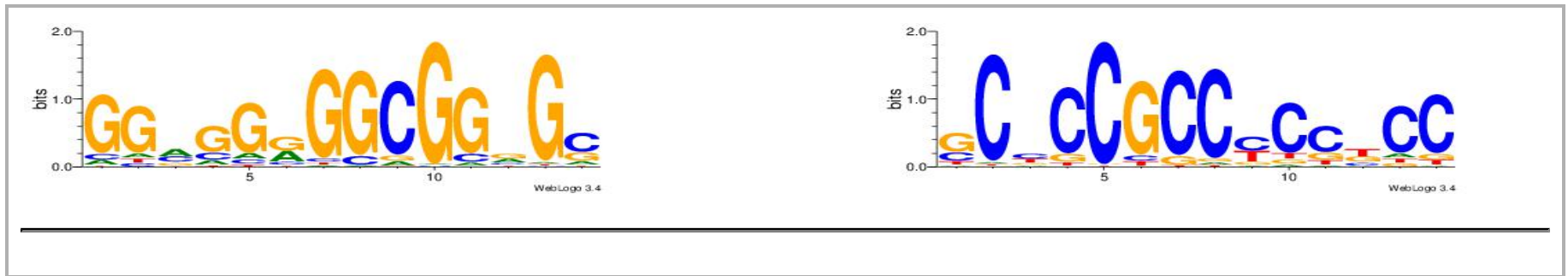
Dataset #: 1  
Motif ID: 5  
Motif name: TFF11  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 11  
Number of overlap: 4  
Similarity score: 3.52554

Alignment:

-----GCVCCGCCMCCYCC  
DHACATTCTGH-----

Original motif    Consensus sequence: GGMGRRGGCGGVGC

Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC



Results created by MOTIFSIM on 11-20-2016 20:47:38  
Runtime: 651.925 seconds

MOTIFSIM is written by Ngoc Tam L. Tran  
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