



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

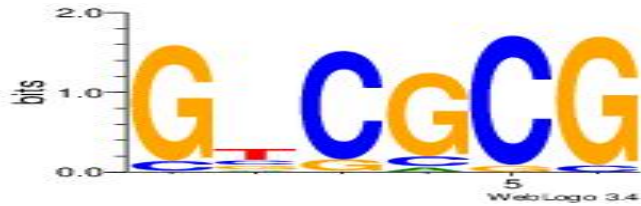
File name	Count of motifs	Dataset number
W-ChIPMotifs_DM230.txt	11	1
RSAT_peak-motifs_DM230.txt	10	2

RESULTS

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

Dataset #: 1 Motif ID: 1 Motif name: TFW1

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



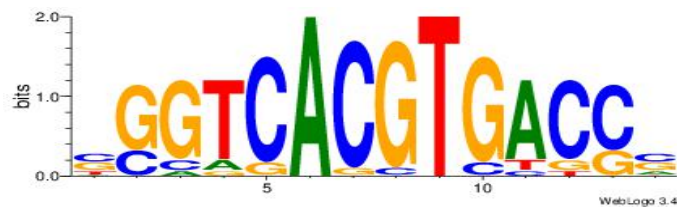
Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

Dataset #: 2
Motif ID: 18
Motif name: sSGTCACGTGACCS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0375102

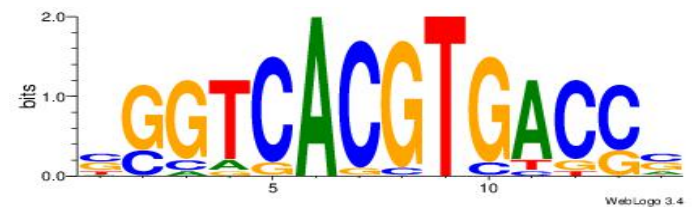
Alignment:

```
SGGTCACGTGACCS  
--GTCGCG-----
```

Original motif Consensus sequence: SGGTCACGTGACCS



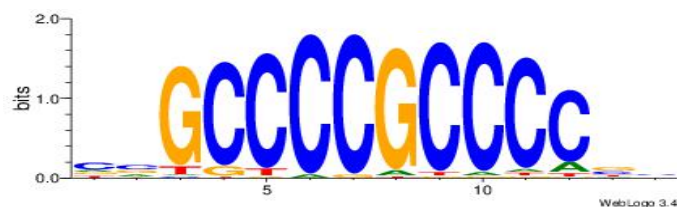
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



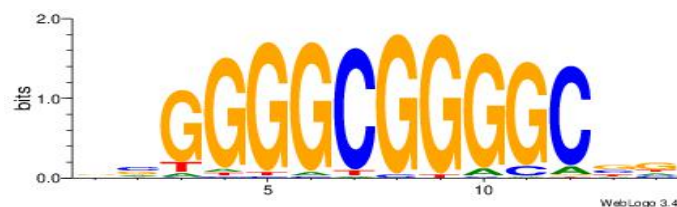
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0539

Alignment:
 HVGCCCCGCCCCBB
 --GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



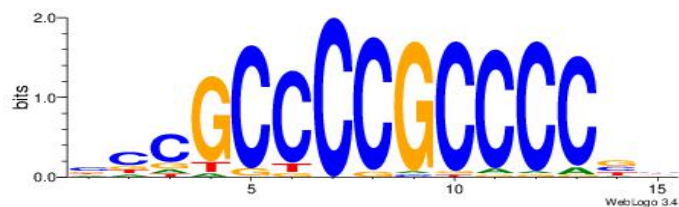
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 6

Similarity score: 0.0558733

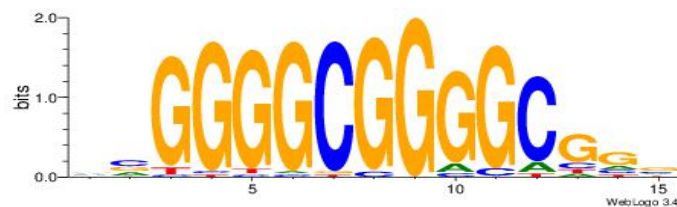
Alignment:

BCCGCCCCGCCCCBB
-----CGCGAC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



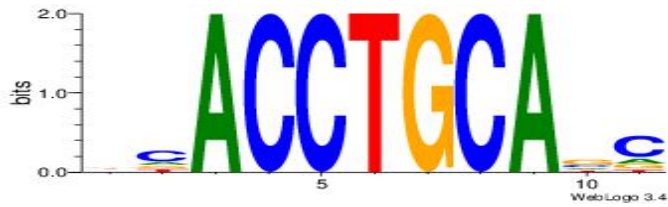
Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 6
Similarity score: 0.0980422

Alignment:

GBTGCAGGTGB
GTCGCG-----

Original motif Consensus sequence: BCACCTGCABC

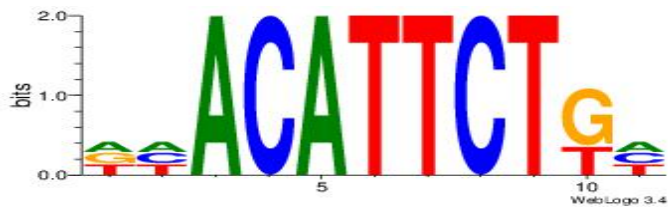
Reverse complement motif Consensus sequence: GBTGCAGGTGB



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

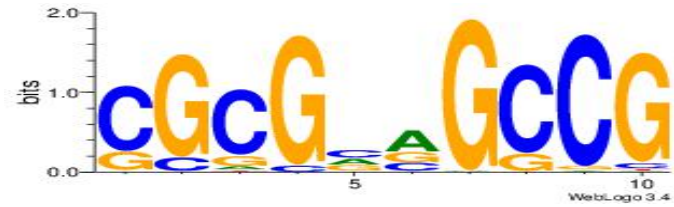


Dataset #: 1 Motif ID: 3 Motif name: TFW3

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



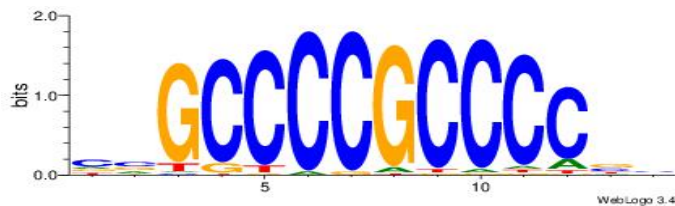
Best Matches for Top Significant Motif ID 3 (Highest to Lowest)

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

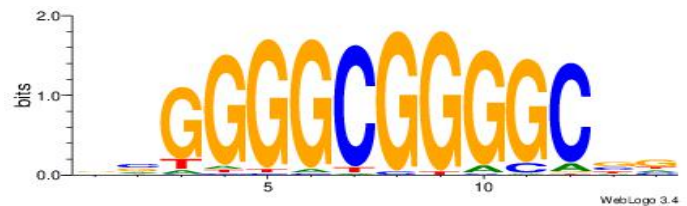
Alignment:

```
HVGCCCCGCCCCBB  
CGGCYBCGCG-----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

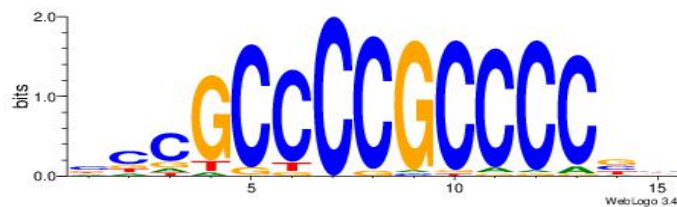


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0719604

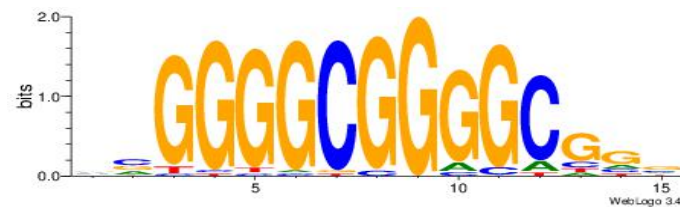
Alignment:

BCCGCCCCGCCCCBB
 -CGGCYBCGCG-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

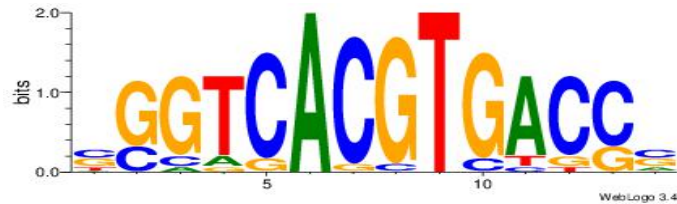


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

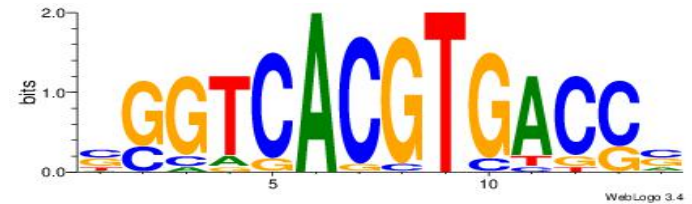
Number of overlap: 10
 Similarity score: 0.0895189

Alignment:
 SGGTCACGTGACCS
 ----CGCGBMGCCG

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

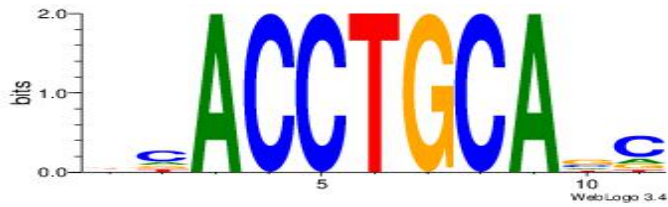


Dataset #: 2
 Motif ID: 16
 Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 1.10343

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

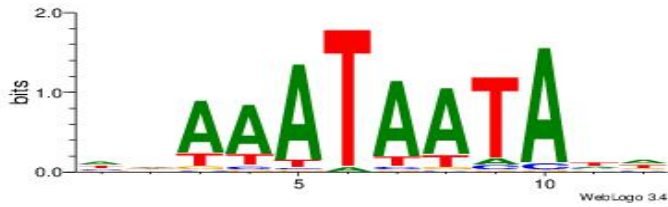


Reverse complement motif Consensus sequence: MBATTGGCTGH

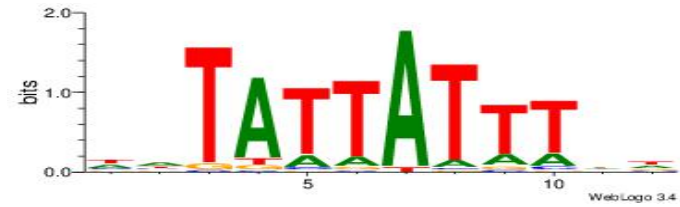


Dataset #: 2 Motif ID: 17 Motif name: wwAAATAATAtw

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

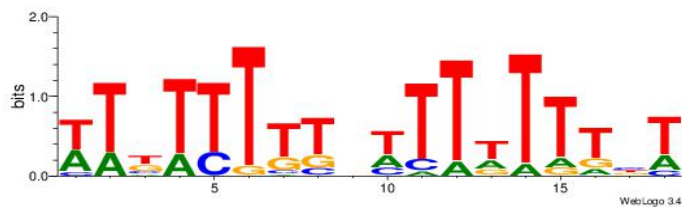
Alignment:

```

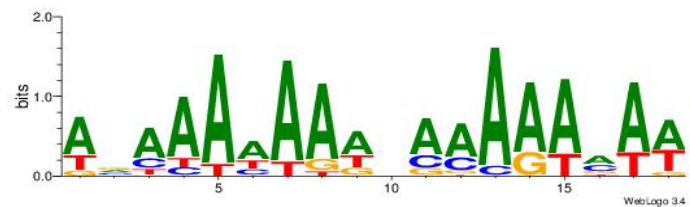
ABAAAAAWHAAAAARAW
-----HDAAATAATADD

```

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

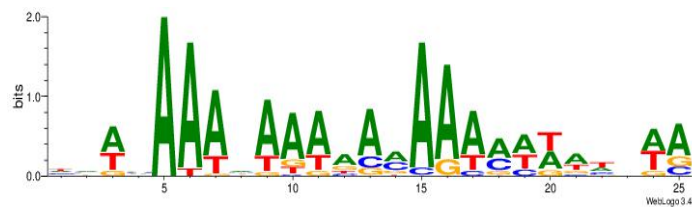


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0575935

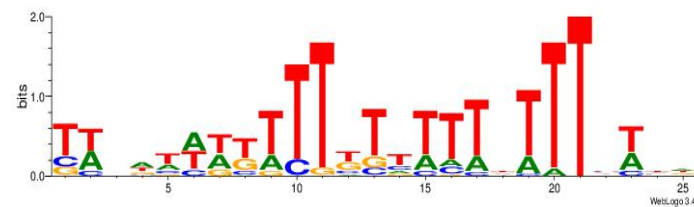
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 --HDAAATAATADD-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTHTTTVWBH



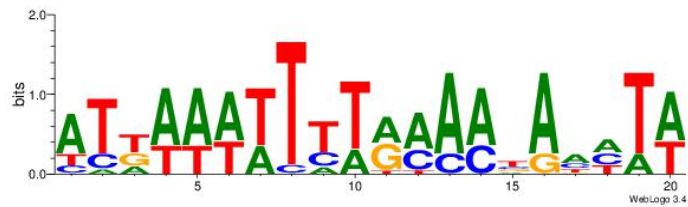
Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0712963

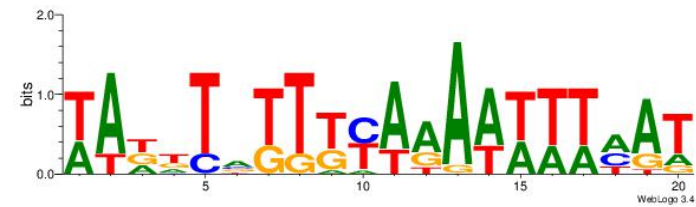
Alignment:

ATKAAWTTTTTRMAABAHTW
-----DDTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT

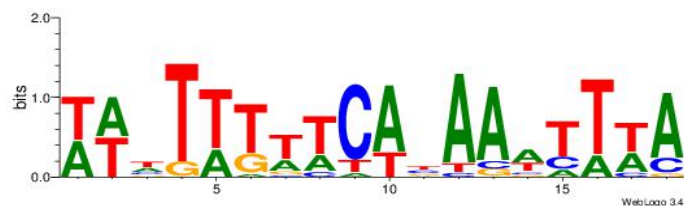


Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0733516

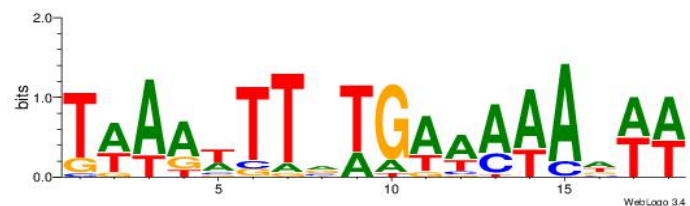
Alignment:

TWAAWTTVTGAAAAHWW
-----HDAAATAATADD

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

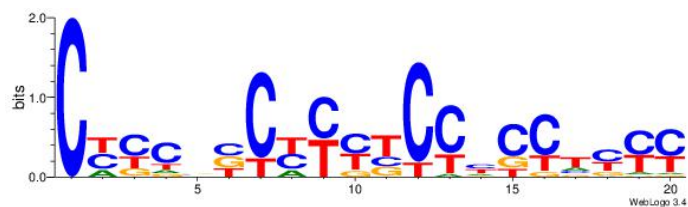


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 16
Number of overlap: 5
Similarity score: 3.59569

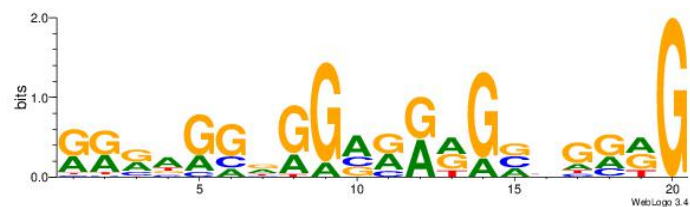
Alignment:

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

Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY

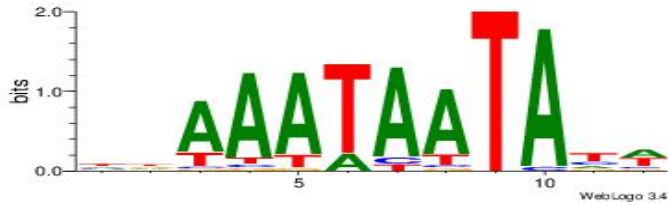


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



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)

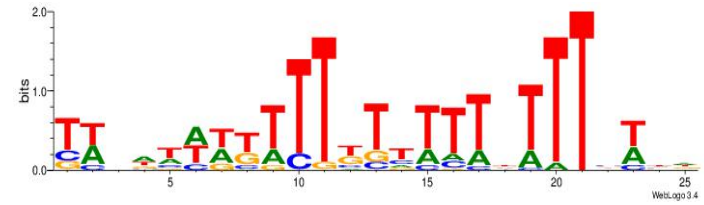
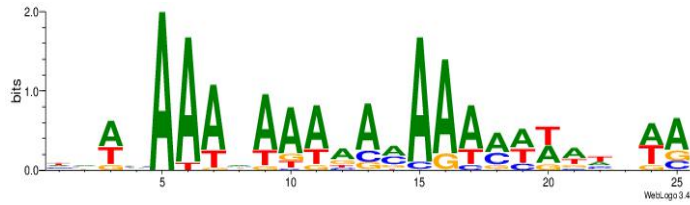
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 12
 Similarity score: 0.0590505

Alignment:

```
TWVHWWWYTTTTYTTTTTHTTTVWBH
-----WHTATTATTTDH--
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA

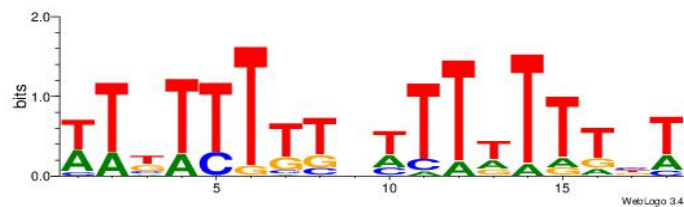
Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTTHTTTVWBH



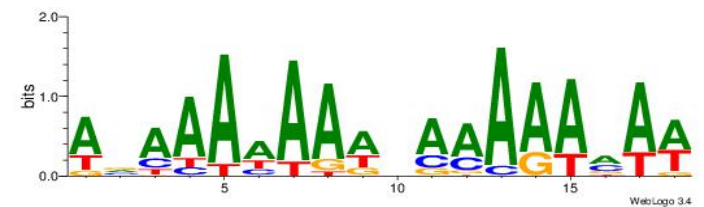
Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0637702

Alignment:
 WKTTTTTHWTTTTTBT
 WHTATTATTTDH-----

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW



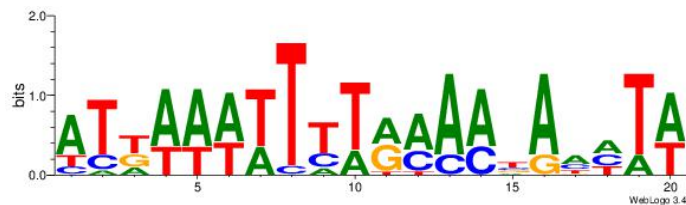
Dataset #: 1

Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0704475

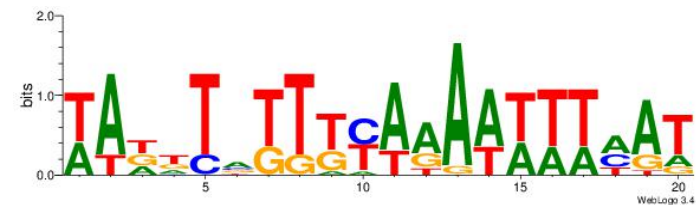
Alignment:

WAHHTVTTYKAAAATTRAT
 HDAAATAATAHW-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



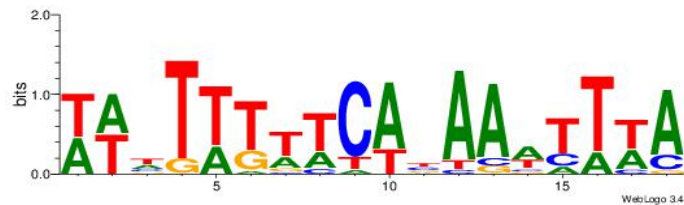
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12

Similarity score: 0.0763819

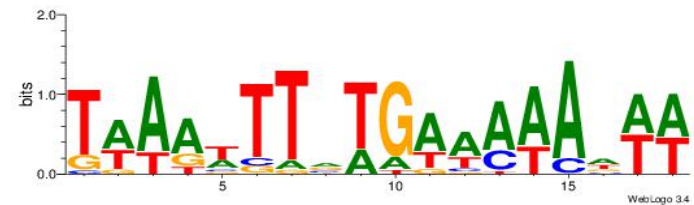
Alignment:

TWAAWTTVTGAAAAHWW
-----HDAAATAATAHW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
TAAWTTVTGAAAAHWW



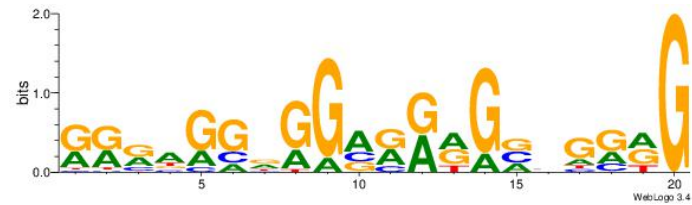
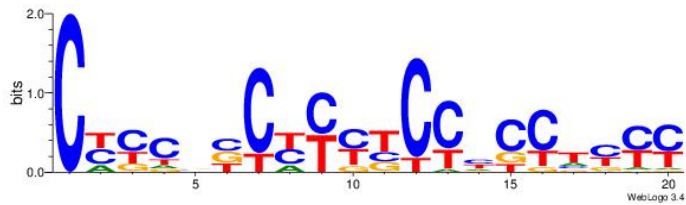
Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 16
Number of overlap: 5
Similarity score: 3.59273

Alignment:

-----KKKAGGDGGAKKMGBBGKMG
WHTATTATTTDH-----

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

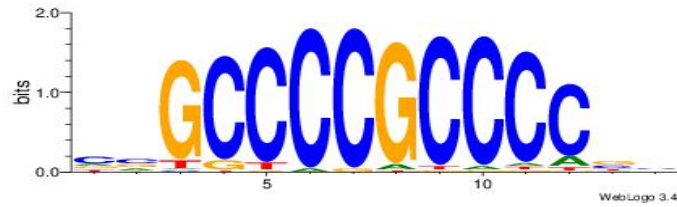


Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

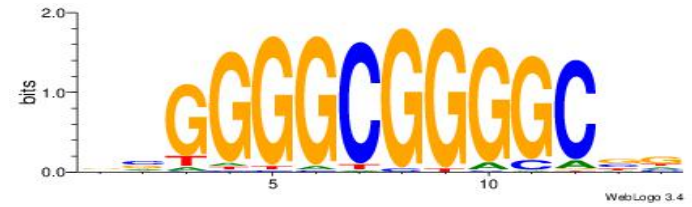
Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0456233

Alignment:
 BBGGGGCGGGGCVD
 -SCGCGCGG-----

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

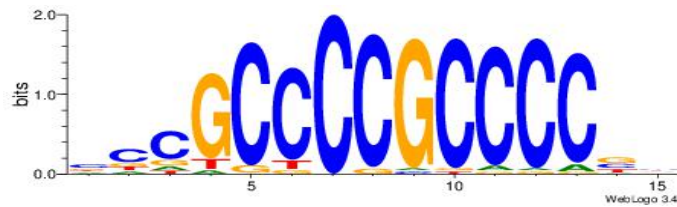


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCBsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

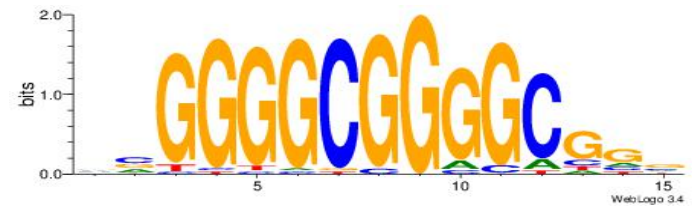
Alignment:

BCCGCCCCGCCCB
 -----CCGCGCS-

Original motif Consensus sequence: BCCGCCCCGCCCB



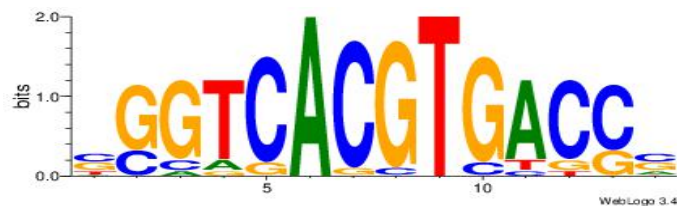
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGB



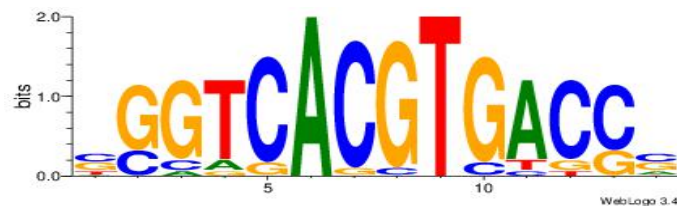
Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0988223

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



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



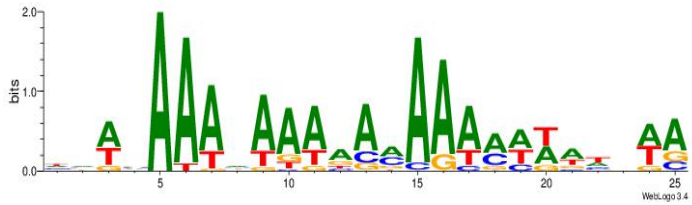
Best Matches for Top Significant Motif ID 21 (Highest to Lowest)

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

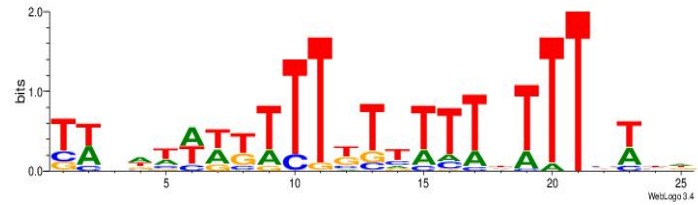
Alignment:

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

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



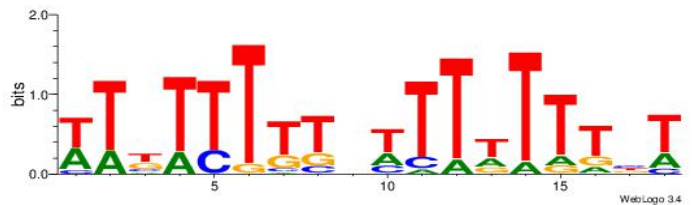
Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



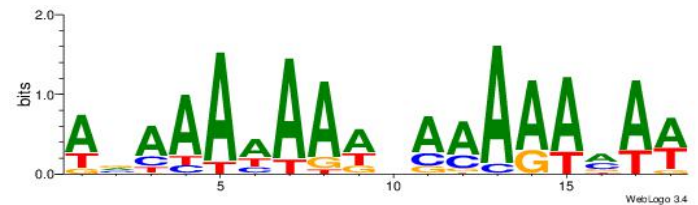
Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0283217

Alignment:
 WTKTTTTTHWTTTTTTBT
 DHTATTTACBD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
 ABAAAAAWHAAAAARAW

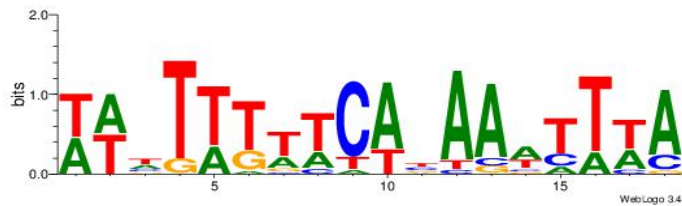


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0308097

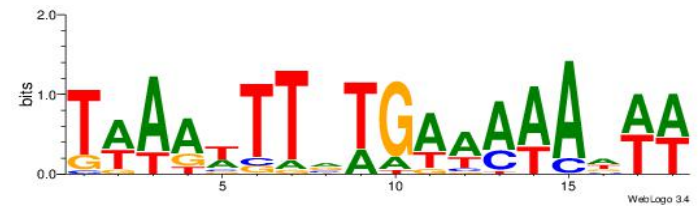
Alignment:

WWHTTTTTTCABAAWTTWA
 -----DHTATTTACBD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



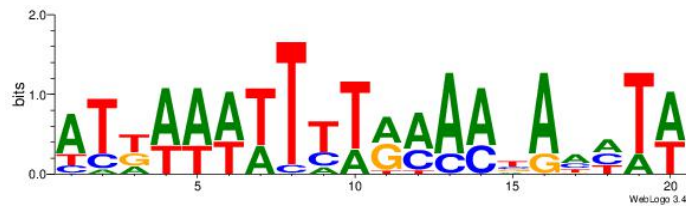
Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

Number of overlap: 11
 Similarity score: 0.0333874

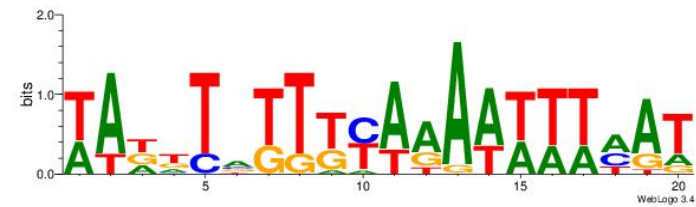
Alignment:

ATKAAWTTTTTRMAABAHTW
 -----DBGTAAATAHD--

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

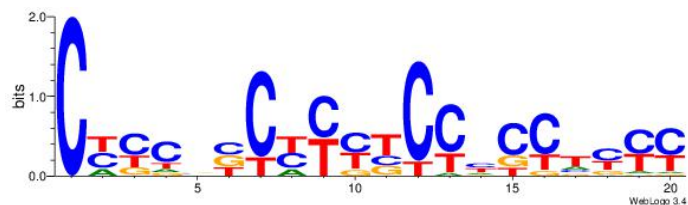


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 14
 Number of overlap: 7
 Similarity score: 2.0544

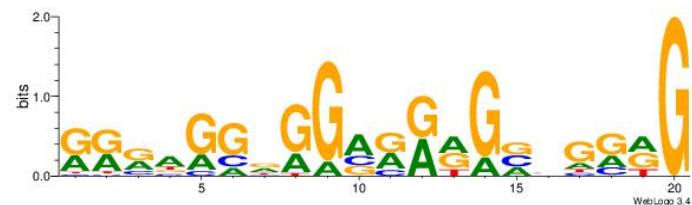
Alignment:

----KKKAGGDGGAKKMGBBGKMG
 DHTATTTACBD-----

Original motif Consensus sequence: CYCBBCYYYYTCCHCCTYYY



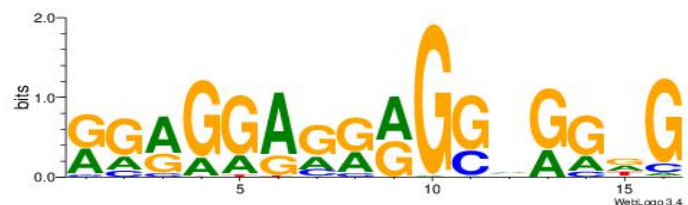
Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



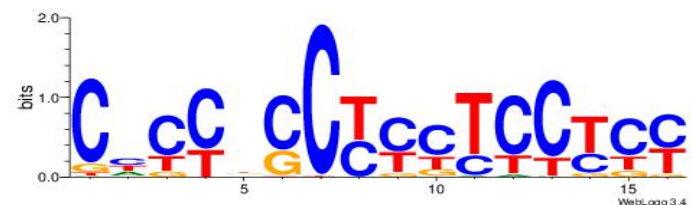
Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 12
 Number of overlap: 5
 Similarity score: 3.05714

Alignment:
 -----CHCCBCCKMCTCCKCM
 DHTATTTACBD-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

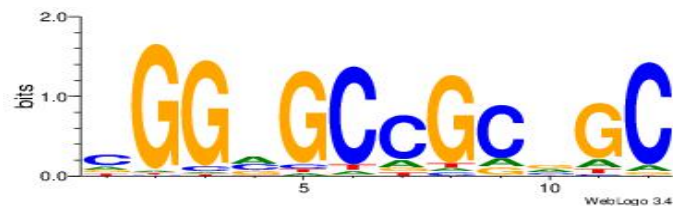


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 4
 Similarity score: 3.54896

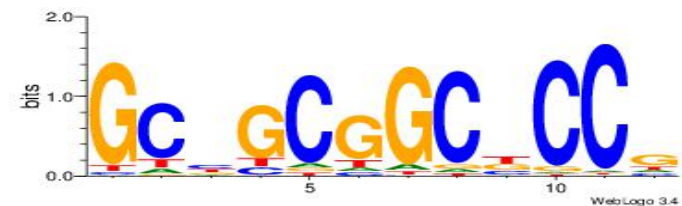
Alignment:

-----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: DBTACWGTAVH



Best Matches for Top Significant Motif ID 19 (Highest to Lowest)

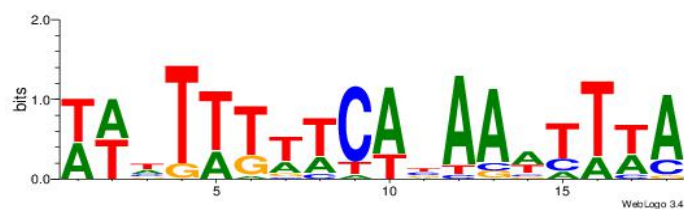
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0413797

Alignment:

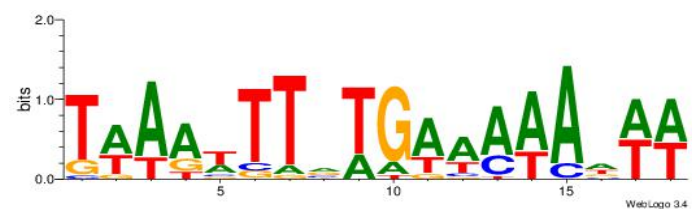
```

WWHTTTTTTCABAAWTTWA
---DBTACWGTAVH-----
  
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

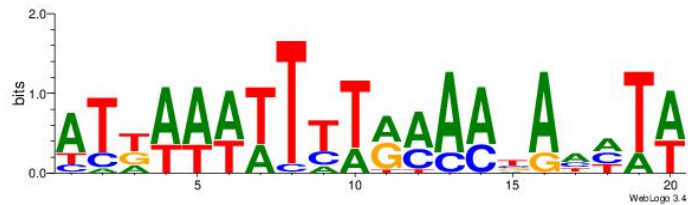


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement

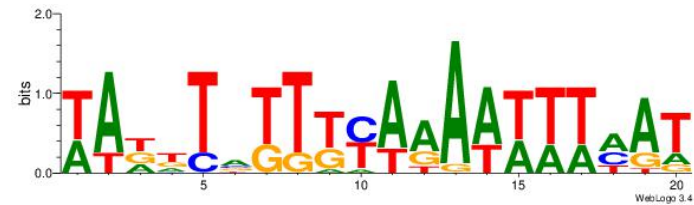
Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0445707

Alignment:
 WAHHTVTTYKAAAATTRAT
 -----HVTACWG TABD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



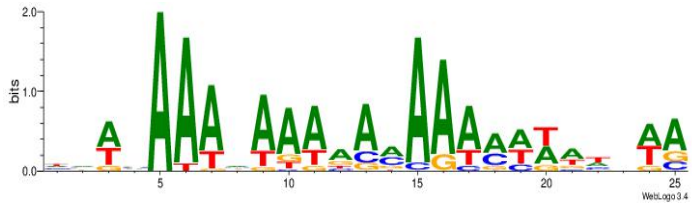
Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



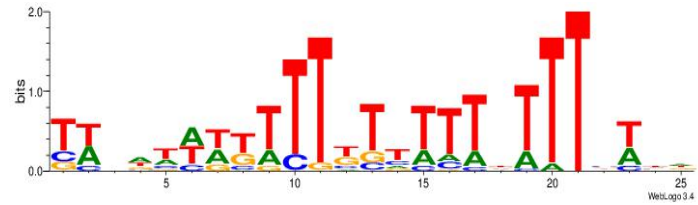
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0472742

Alignment:
 HDWVAAAHA AAAAAMAAAMWWWHBWA
 ---DBTACWG TAVH-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



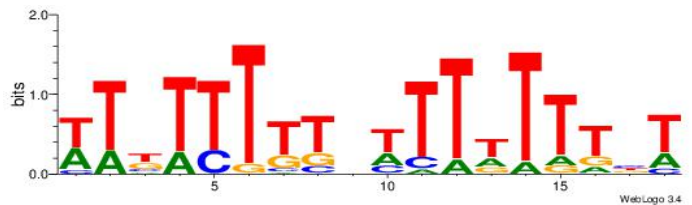
Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 9
 Similarity score: 1.04742

Alignment:

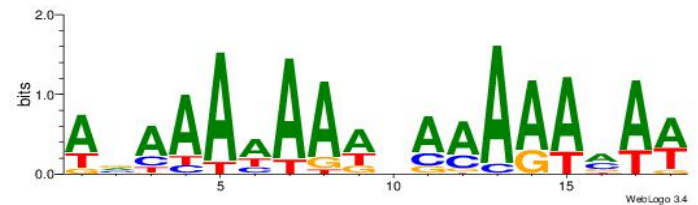
```

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

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
 ABAAAAAWhAAAAARAW

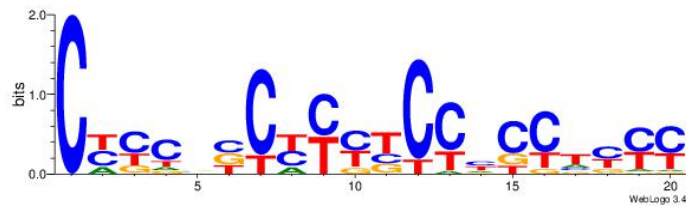


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 15
 Number of overlap: 6
 Similarity score: 2.54736

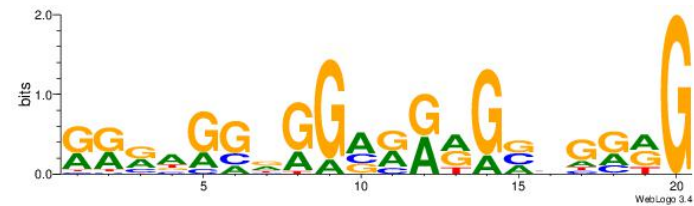
Alignment:

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

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



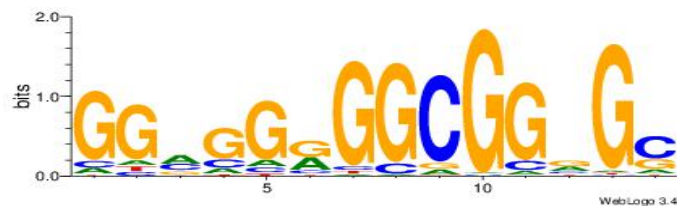
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10

Number of overlap: 5
Similarity score: 3.04599

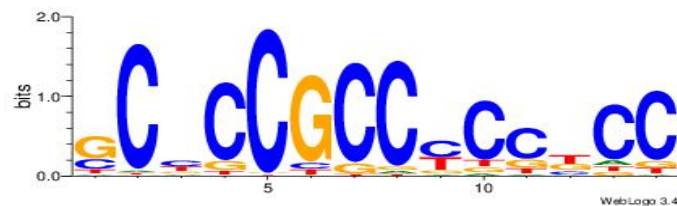
Alignment:

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

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



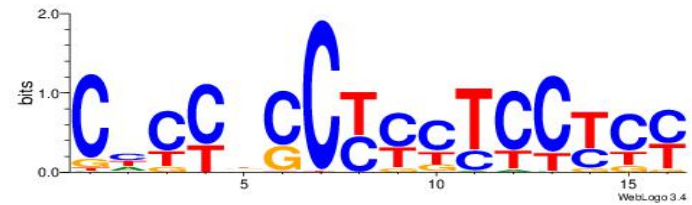
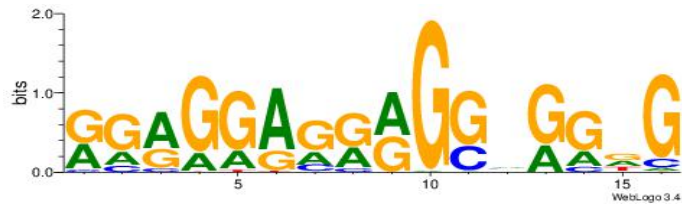
Dataset #: 1
Motif ID: 6
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 12
Number of overlap: 5
Similarity score: 3.04861

Alignment:

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

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM



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

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

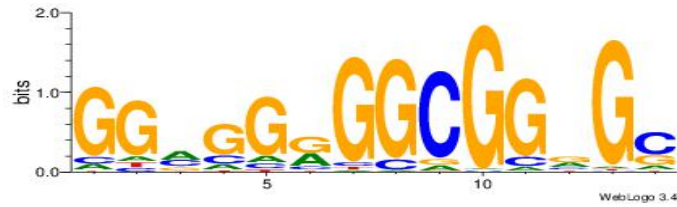


Best Matches for Top Significant Motif ID 16 (Highest to Lowest)

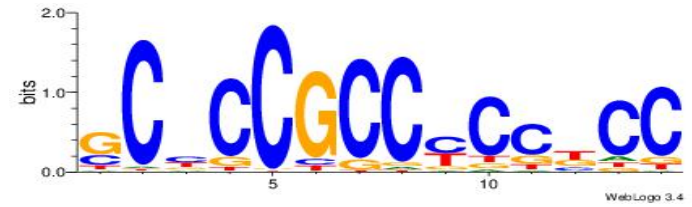
Dataset #:	1
Motif ID:	5
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0312321

Alignment:
 GGMGGRGGCGGVGC
 GBTGCAGGTGB---

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

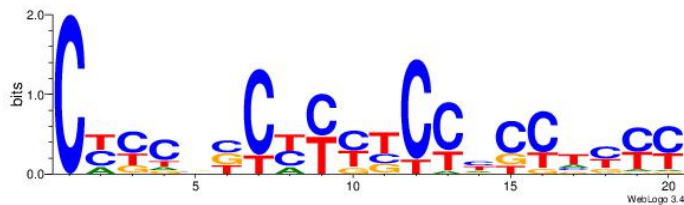


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 11
Similarity score: 0.0444938

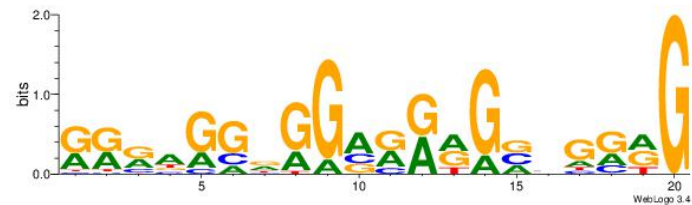
Alignment:

```
KKKAGGDGGAKKMGBBGKMG  
----GBTGCAGGTGB-----
```

Original motif Consensus sequence: CYYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

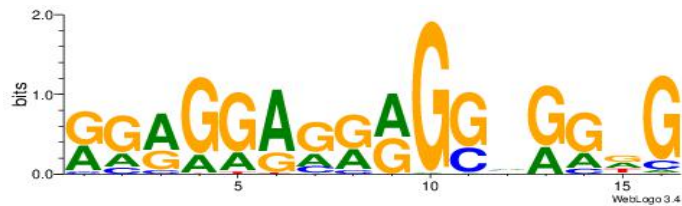


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.538471

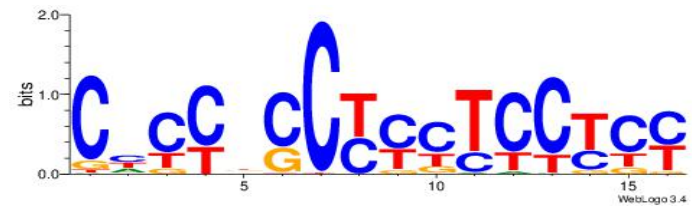
Alignment:

-RGRGGAGRRGGHGGDG
 GBTGCAGGTGB-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

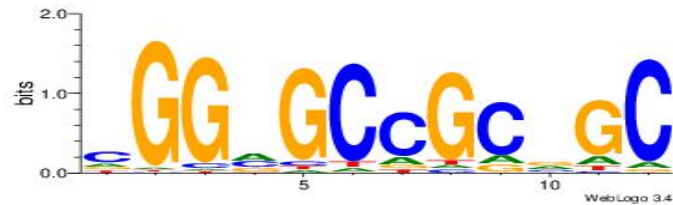


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

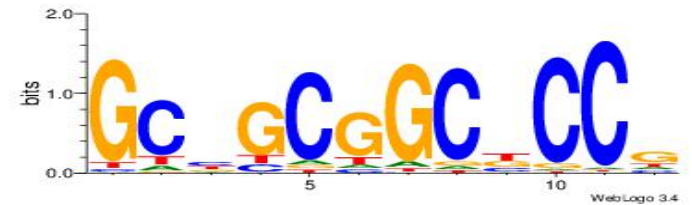
Number of overlap: 8
Similarity score: 1.54364

Alignment:
GCVGCGGCBCCG---
----BCACCTGCABC

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

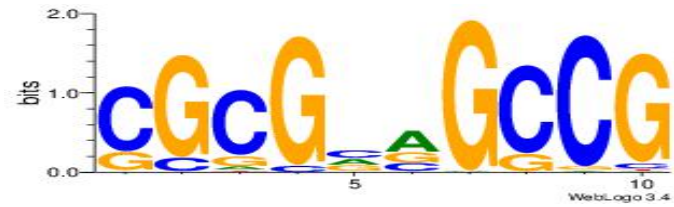


Dataset #: 1
Motif ID: 3
Motif name: TFW3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 1.5466

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



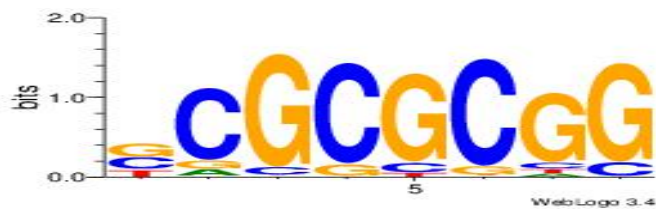
Dataset #: 1
 Motif ID: 2

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

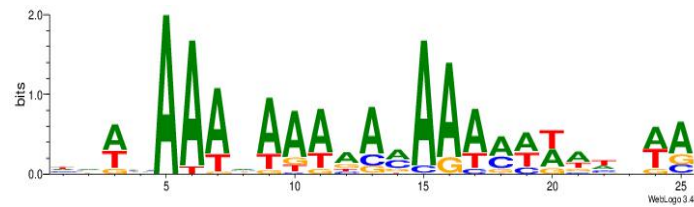


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 22
 Number of overlap: 4
 Similarity score: 3.53789

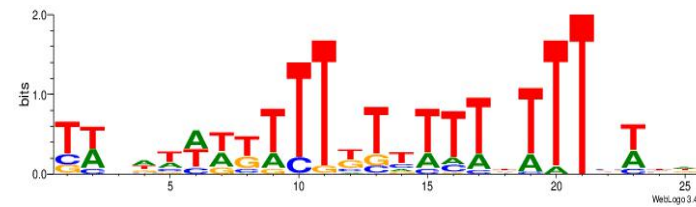
Alignment:

-----TWVHWWYTTTTYTTTTTHTTTVWBH
GBTGCAGGTGB-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

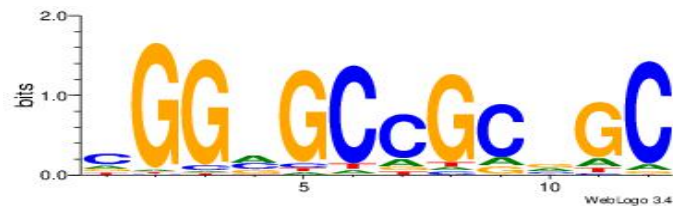


Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTTHTTTVWBH

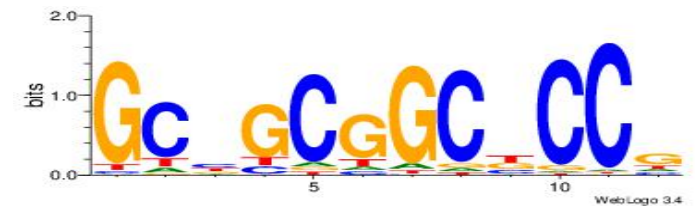


Dataset #: 1 Motif ID: 4 Motif name: TFF1

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



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

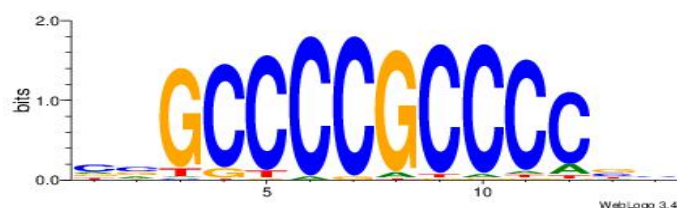
Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

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

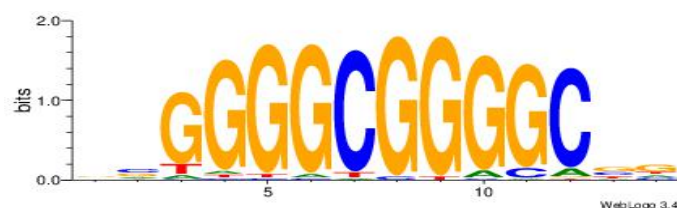
Alignment:

HVGGCCCGCCCCBB
CGGVGCCGCVGC--

Original motif Consensus sequence: HVGGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

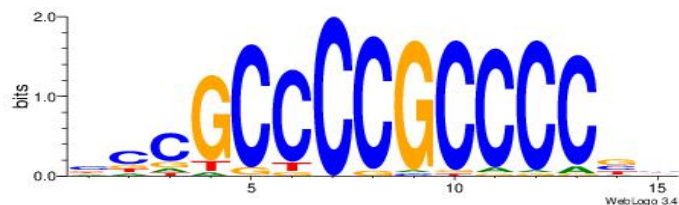


Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0548371

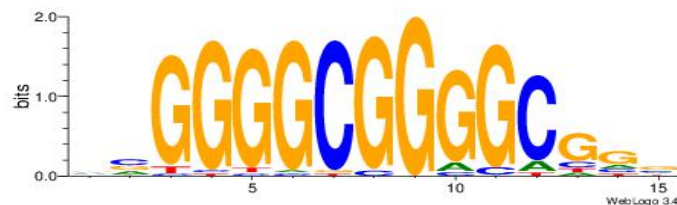
Alignment:

BCCGCCCCGCCCCBB
---GCVGCGGCBCCG

Original motif Consensus sequence: BCCGCCCCGCCCCBB



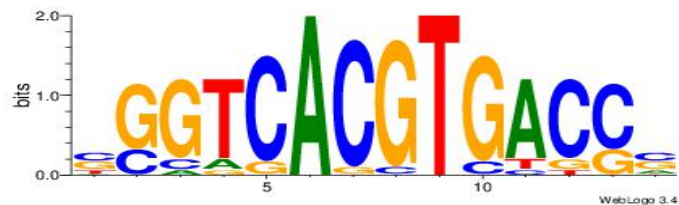
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



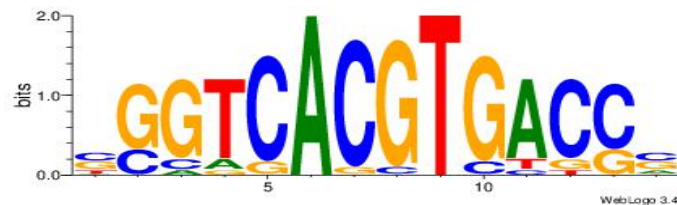
Dataset #: 2
Motif ID: 18
Motif name: sSGTCACGTGACCS
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0777862

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



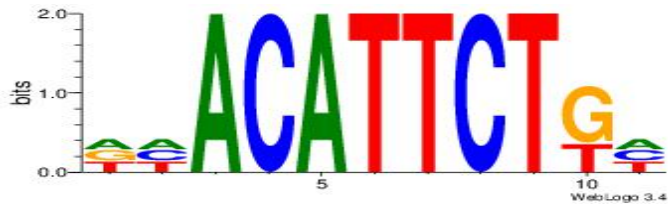
Dataset #: 2
Motif ID: 20
Motif name: dhACATTCTkh
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 4
Similarity score: 4.07107

Alignment:

HCAGAATGTHD-----
-----GCVGCCGCBCCG

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

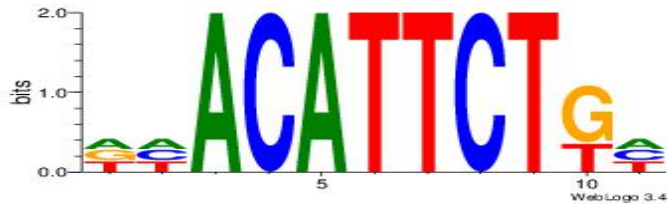


Reverse complement motif Consensus sequence: DHTATTTACBD



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)

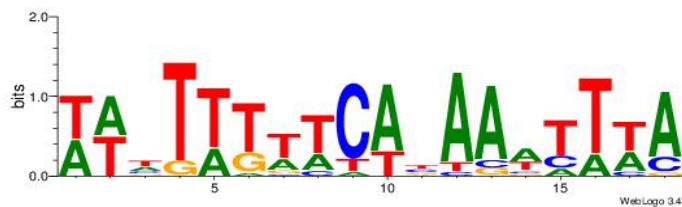
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.00522383

Alignment:

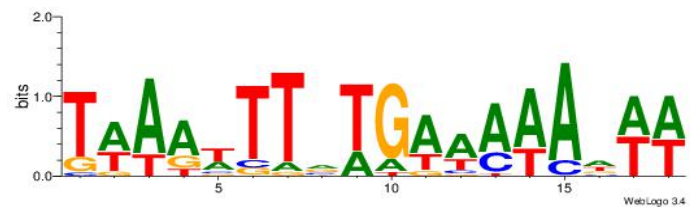
```

WWHTTTTTTCABAAWTTWA
HCAGAATGTHD-----
  
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

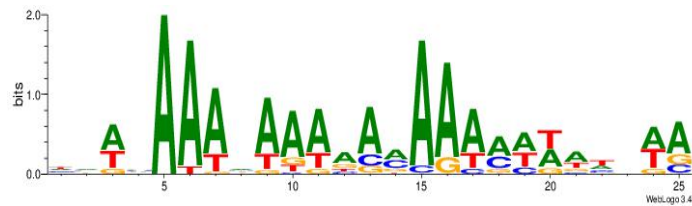


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.014258

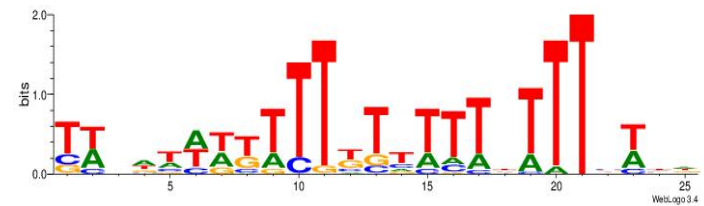
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 ----HCAGAATGTHD-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH

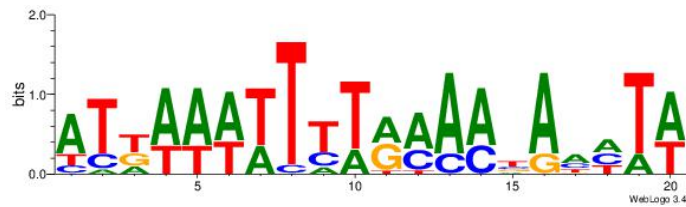


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

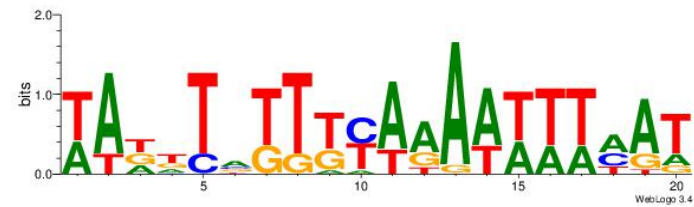
Number of overlap: 11
 Similarity score: 0.0192045

Alignment:
 ATKAAWTTTTTRMAABAHTW
 -DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW



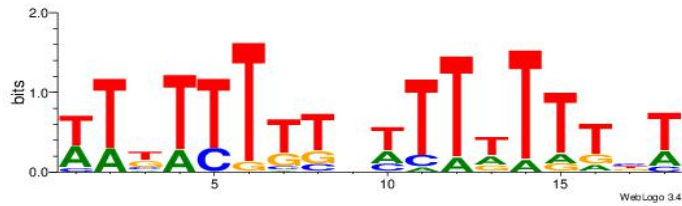
Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



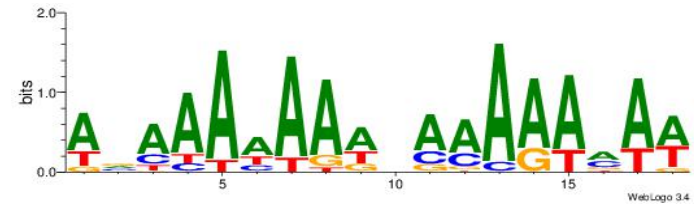
Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.519904

Alignment:
 ABAAAAAWhAAAAARAW-
 -----HCAGAATGTHD

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

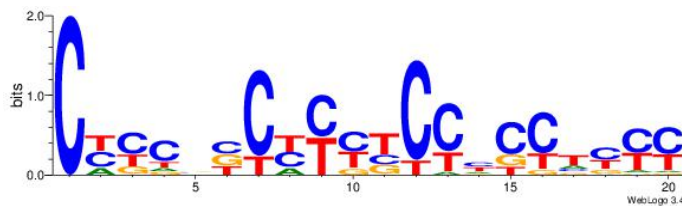


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 17
Number of overlap: 4
Similarity score: 3.5

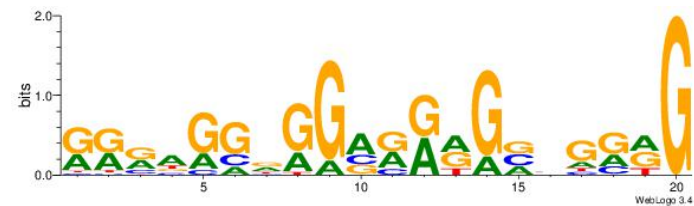
Alignment:

-----CYYCBBCYYYYTCCHCCTYYY
DHACATTCTGH-----

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

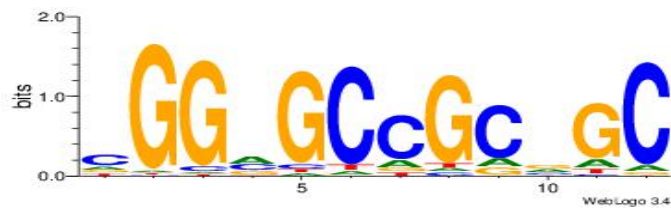


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 4
 Similarity score: 3.51958

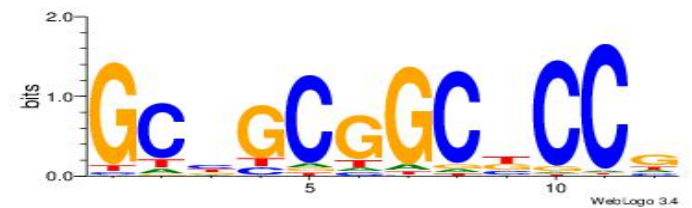
Alignment:

-----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



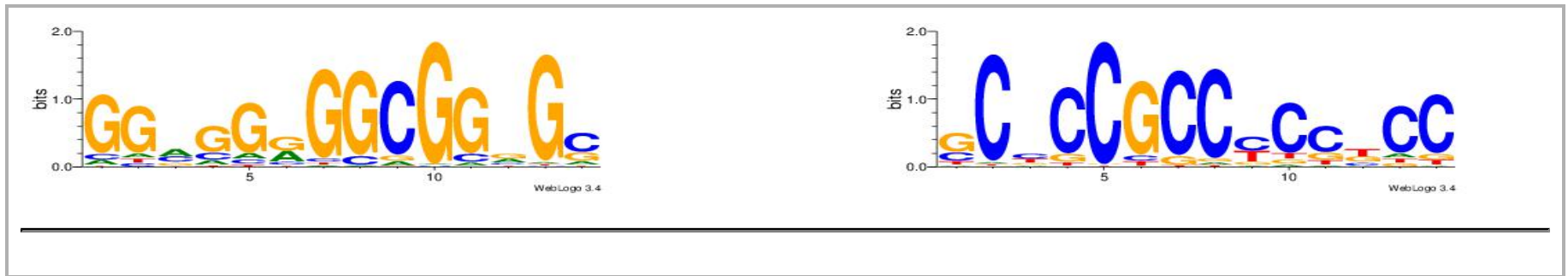
Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 11
Number of overlap: 4
Similarity score: 3.52554

Alignment:

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

Original motif Consensus sequence: GGMGRRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Results created by MOTIFSIM on 11-20-2016 13:21:41
Runtime: 601.6 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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