



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

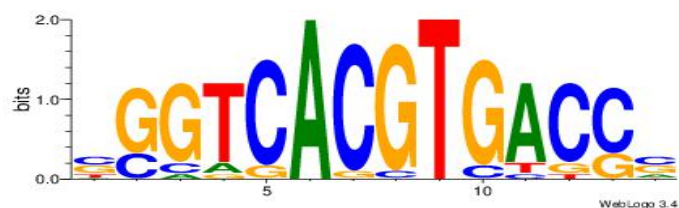


Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

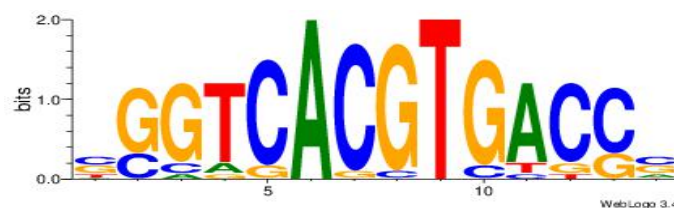
Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACCS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0375102

Alignment:
 SGGTCACGTGACCS
 --GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

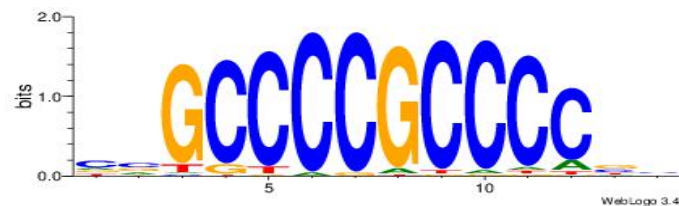


Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0539

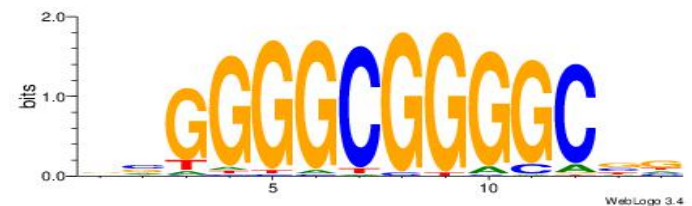
Alignment:

HVGCCCCGCCCCBB
 --GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

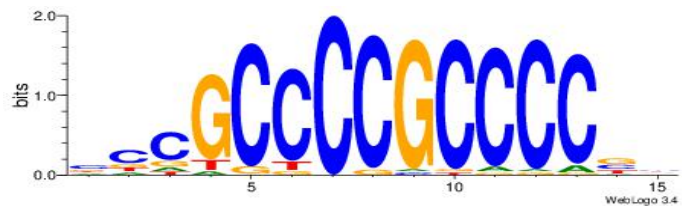


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 6

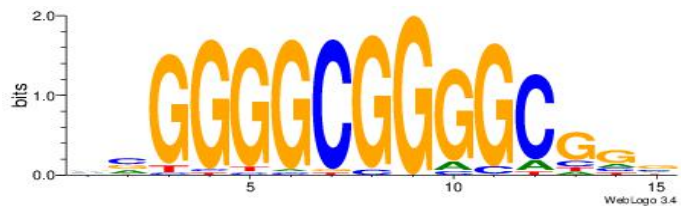
Similarity score: 0.0558733

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



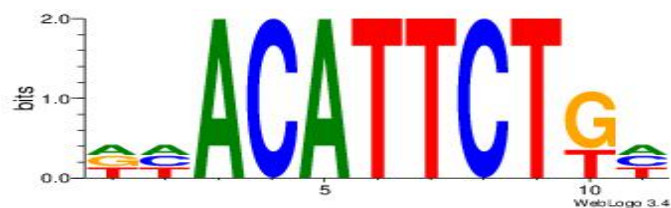
Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 4
 Similarity score: 1.09467

Alignment:

HCAGAATGTHD--

-----GTCGCG

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

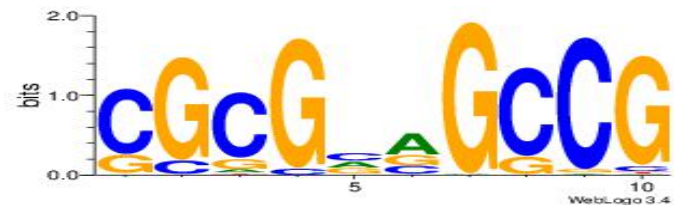


Dataset #: 1 Motif ID: 3 Motif name: TFW3

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



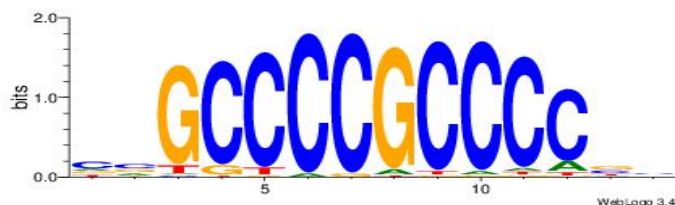
Best Matches for Top Significant Motif ID 3 (Highest to Lowest)

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

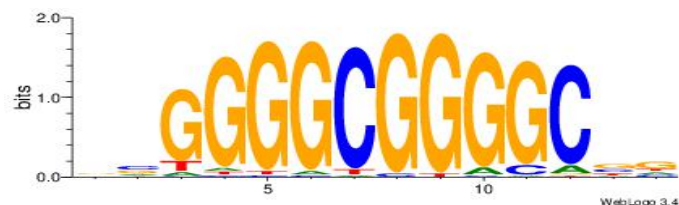
Alignment:

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

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

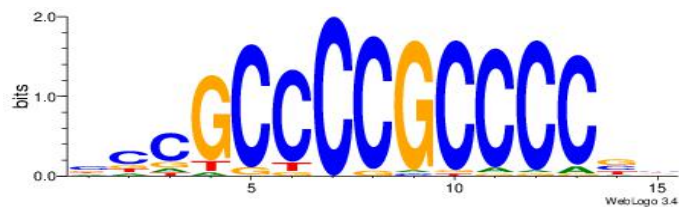


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0719604

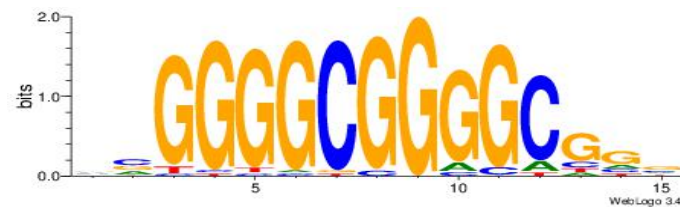
Alignment:

BCCGCCCCGCCCCBB
 -CGGCYBCGCG-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

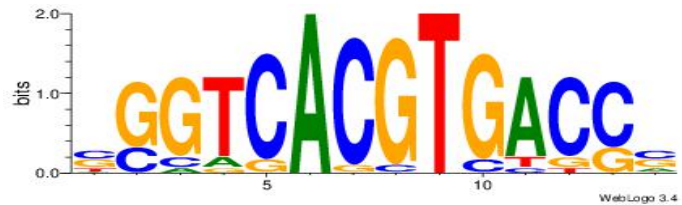


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

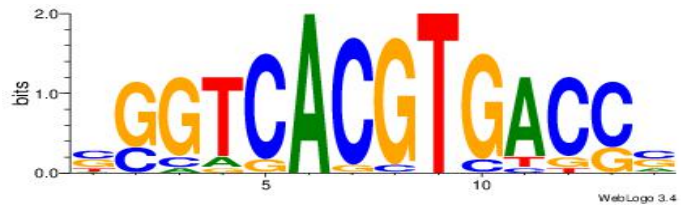
Number of overlap: 10
Similarity score: 0.0895189

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

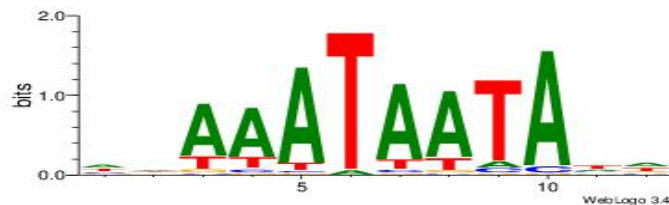


Reverse complement motif Consensus sequence: MBATTGGCTGH

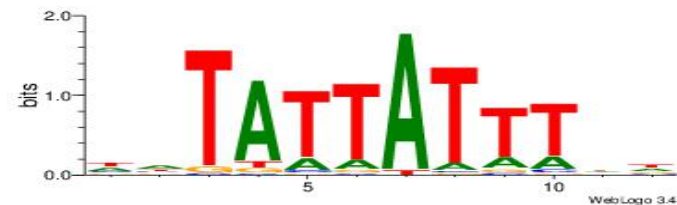


Dataset #: 2 Motif ID: 17 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTDDH



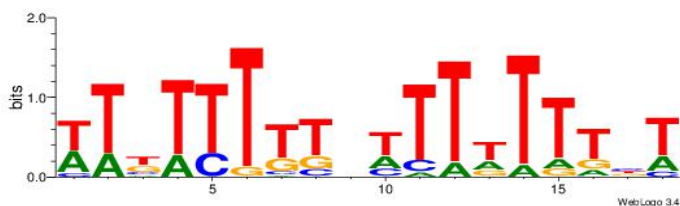
Best Matches for Top Significant Motif ID 17 (Highest to Lowest)

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

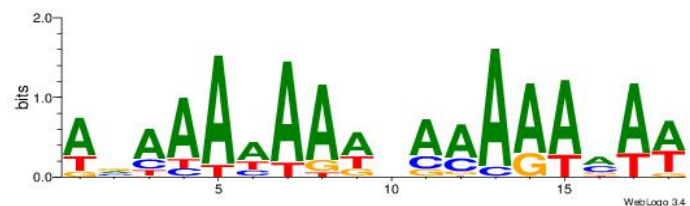
Alignment:

```
ABAAAAAWhAAAAARAW
-----HDAAATAATADD
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW

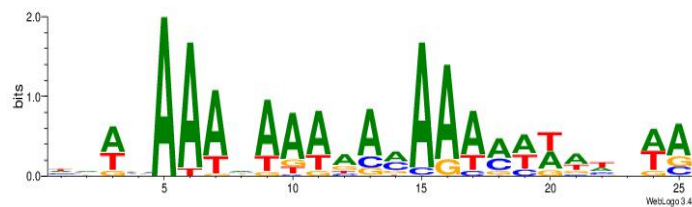


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0575935

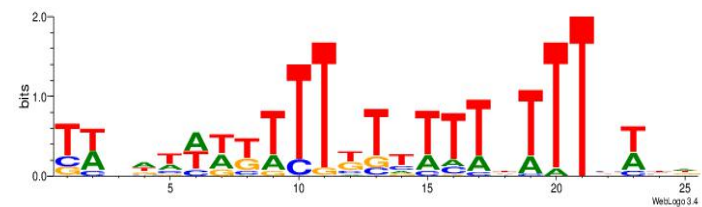
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 --HDAAATAATADD-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTHTTTVWBH

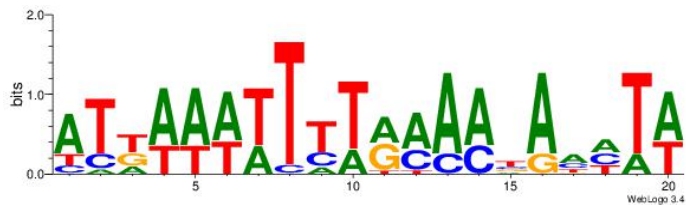


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

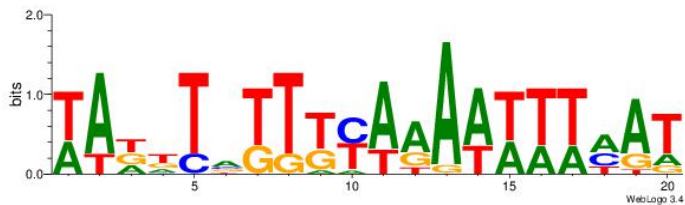
Number of overlap: 12
Similarity score: 0.0712963

Alignment:
ATKAAWTTTTRMAABAHHTW
-----DDTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



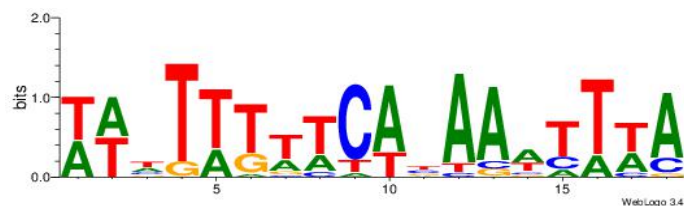
Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



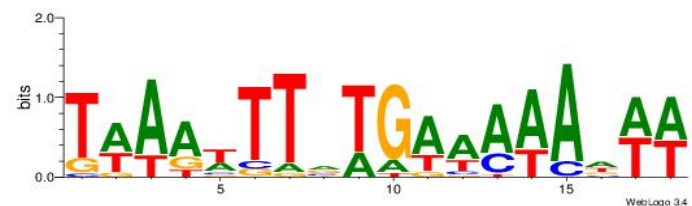
Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0733516

Alignment:
TWAAWTTVTGAAAAHWW
-----HDAAATAATADD

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

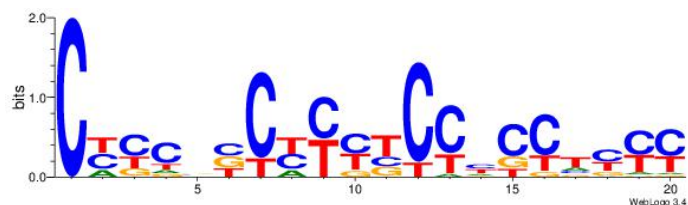


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 16
 Number of overlap: 5
 Similarity score: 3.59569

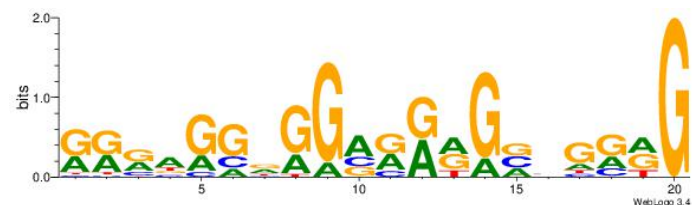
Alignment:

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

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

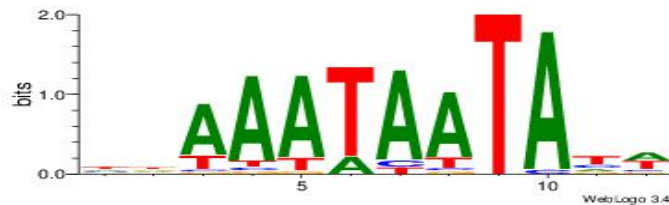


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

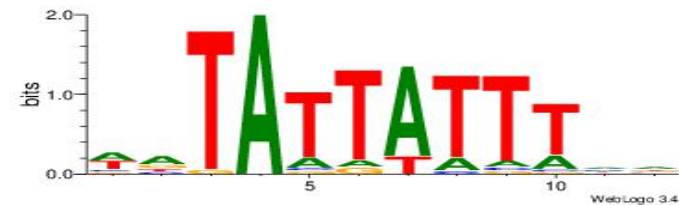


Dataset #: 2 **Motif ID: 13** **Motif name: tkAAATAATAtw**

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH



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

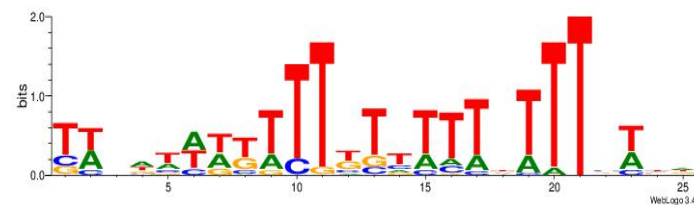
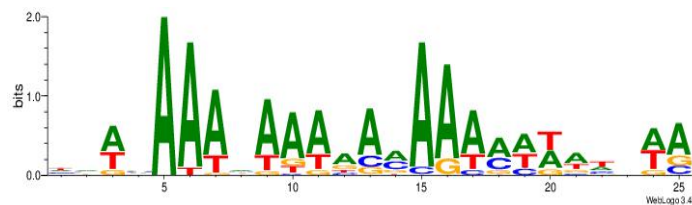
Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	12
Number of overlap:	12
Similarity score:	0.0590505

Alignment:

```
TWVHWWYTTTYTTTTTHTTTVWBH
-----WHTATTATTDDH--
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
TWVHWWYTTTYTTTTTHTTTVWBH

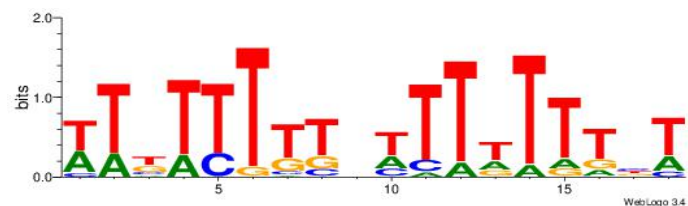


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0637702

Alignment:

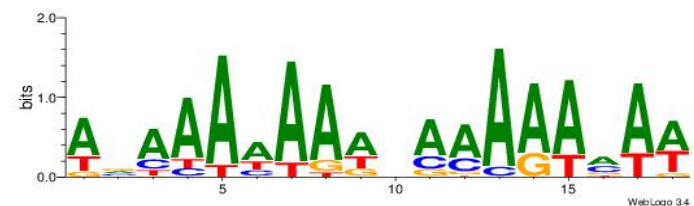
WTKTTTTTHWTTTTTBT
 WHTATTATTTDH-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif
 ABAAAAAWhAAAAARAW

Consensus sequence:



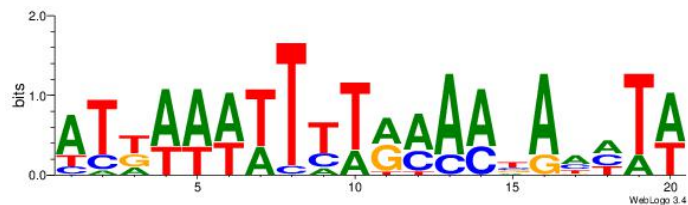
Dataset #: 1

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

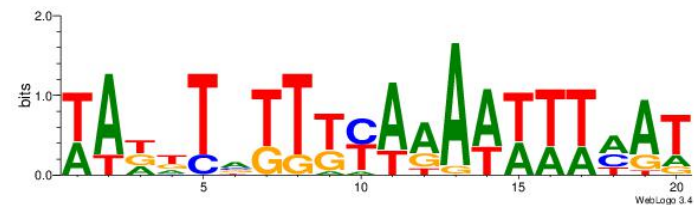
Alignment:

WAHHTVTTYKAAAATTRAT
 HDAAATAATAHW-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



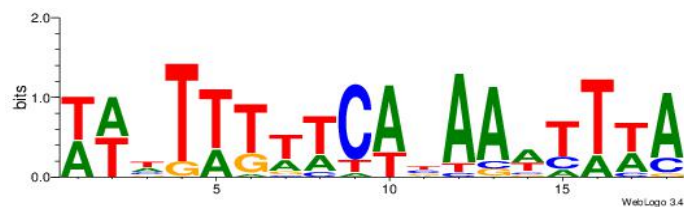
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12

Similarity score: 0.0763819

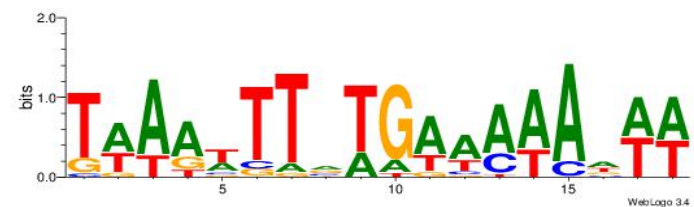
Alignment:

TWAAWTTVTGAAAAHWW
-----HDAAATAATAHW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
TWAAWTTVTGAAAAHWW



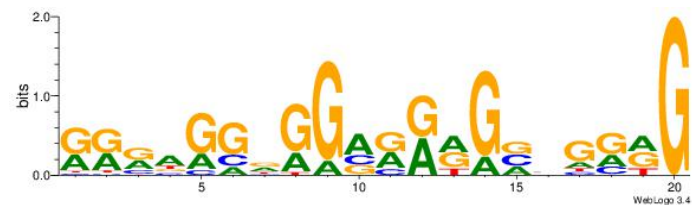
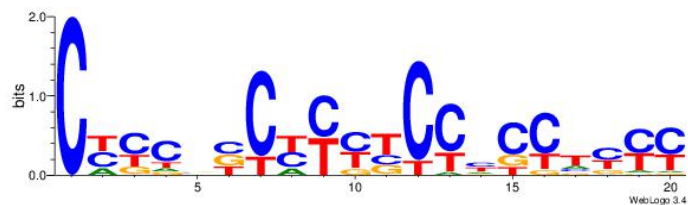
Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 16
Number of overlap: 5
Similarity score: 3.59273

Alignment:

-----KKKAGGDGGAKKMGBBGKMG
WHTATTATTDDH-----

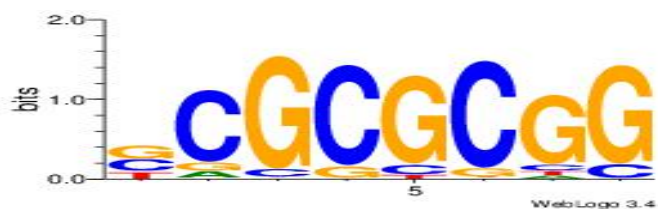
Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY

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)

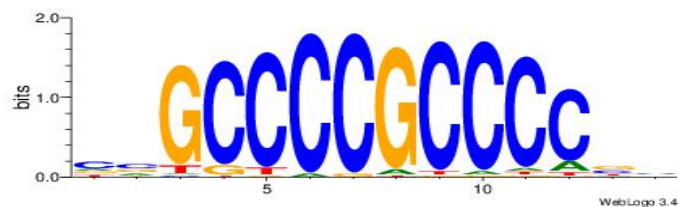
Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0456233

Alignment:

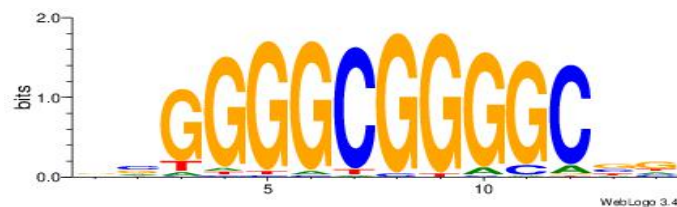
BBGGGGCGGGCVD

-SCGCGCGG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

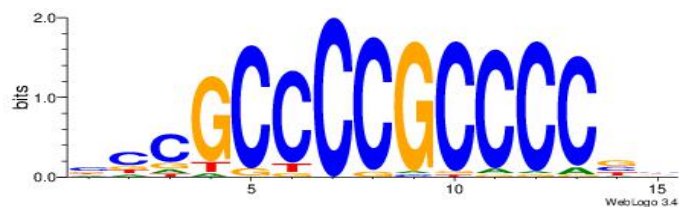


Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.045686

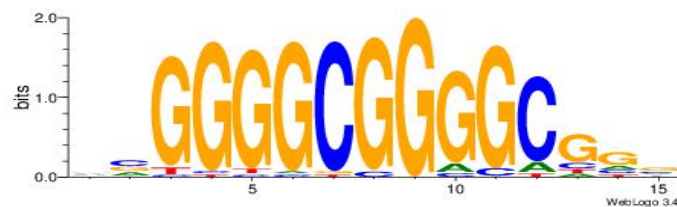
Alignment:

BCCGCCCCGCCCCBB
-----CCGCGCGS--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

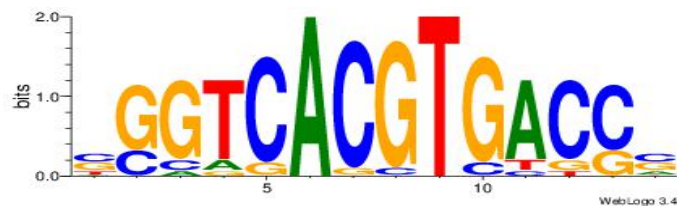


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0988223

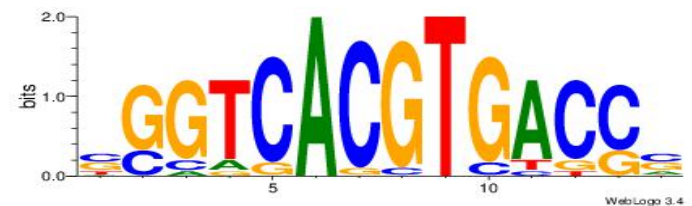
Alignment:

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

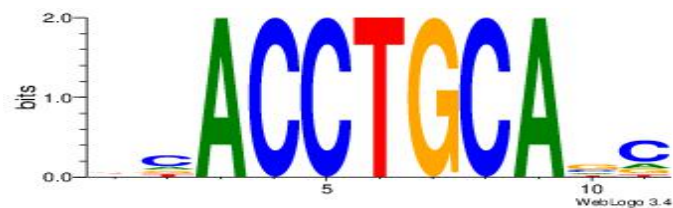
Similarity score: 2.08456

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



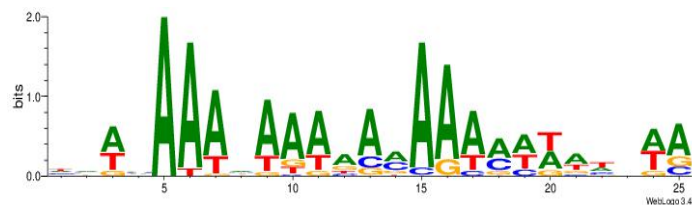
Best Matches for Top Significant Motif ID 21 (Highest to Lowest)

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

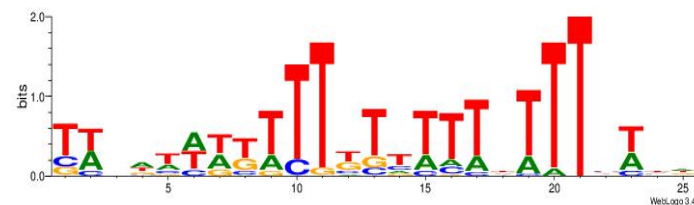
Alignment:

```
TWVHWWYTTTYTTTTHTTTVWBH
-----DHTATTTACBD
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWTYYYYTTTTTHTTTVWBH

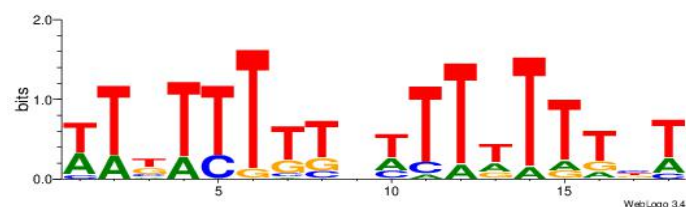


Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0283217

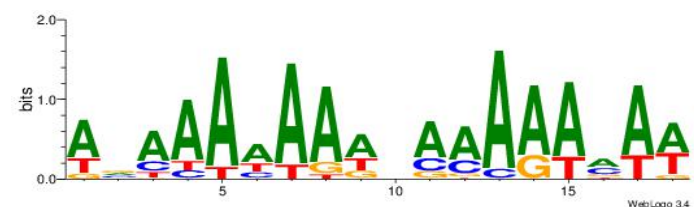
Alignment:

WTKTTTTTHWTTTTTTBT
DHTATTTACBD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW

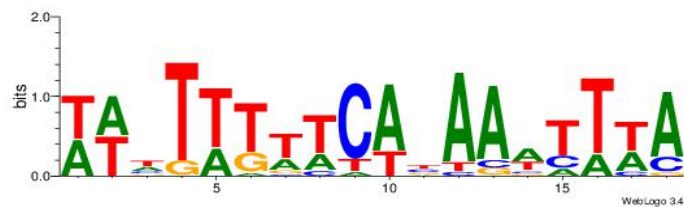


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0308097

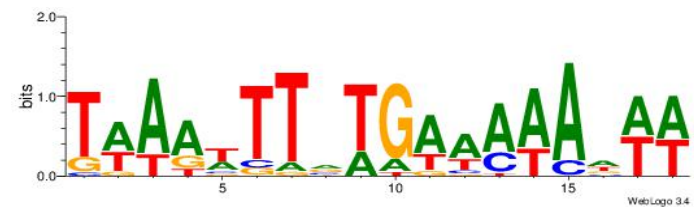
Alignment:

WWHTTTTTTCABAAWTTWA
 -----DHTATTTACBD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

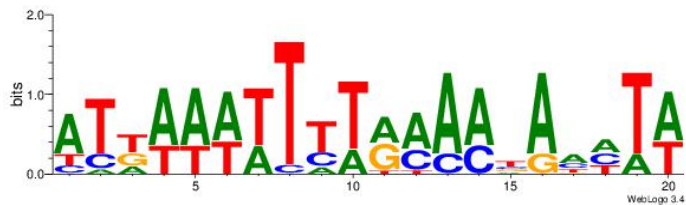


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

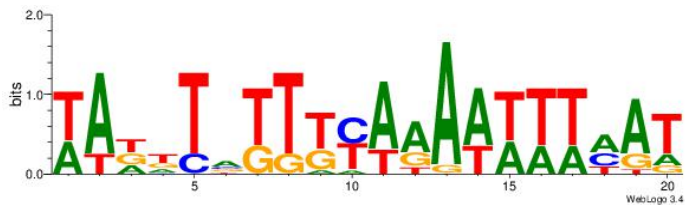
Number of overlap: 11
Similarity score: 0.0333874

Alignment:
ATKAAWTTTTRMAABAHHTW
-----DBGTAAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



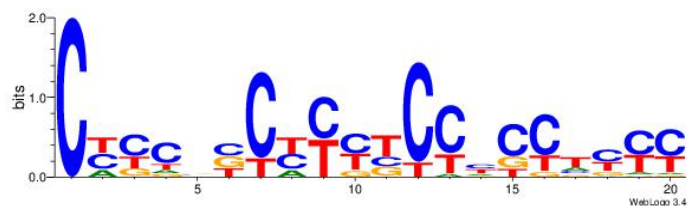
Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



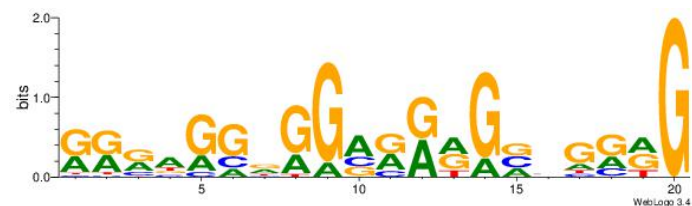
Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 14
Number of overlap: 7
Similarity score: 2.0544

Alignment:
----KKKAGGDGGAKKMGBBGKMG
DHTATTTACBD-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

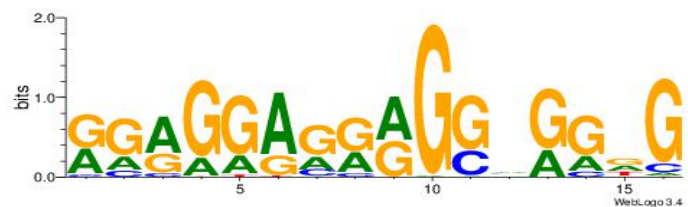


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 12
 Number of overlap: 5
 Similarity score: 3.05714

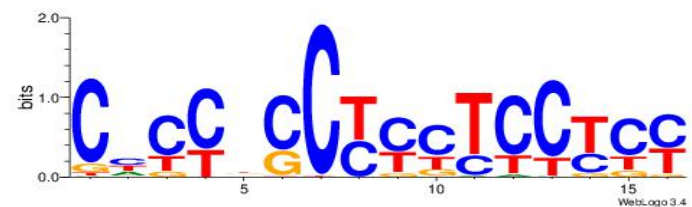
Alignment:

-----CHCCBCKMCTCCKCM
 DHTATTTACBD-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

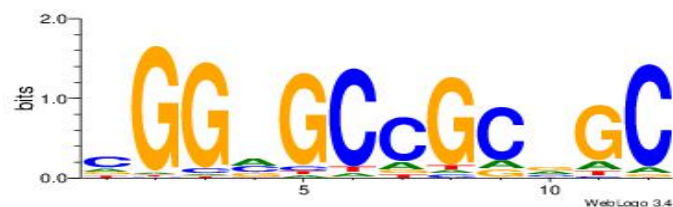


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 4
 Similarity score: 3.54896

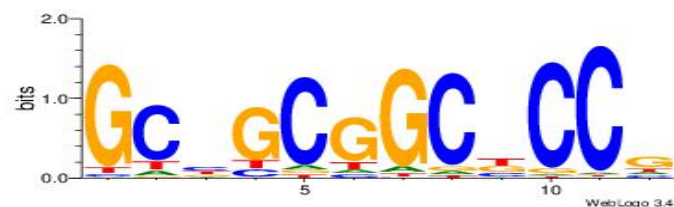
Alignment:

-----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: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



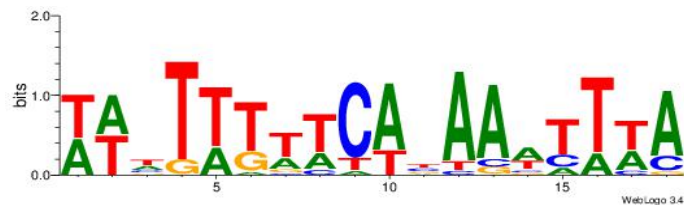
Best Matches for Top Significant Motif ID 19 (Highest to Lowest)

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

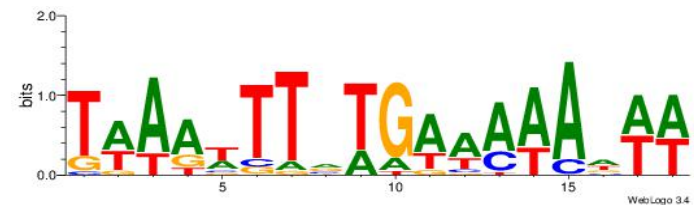
Alignment:

WWHTTTTTCABAAWTTWA
---DBTACWGTAVH----

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



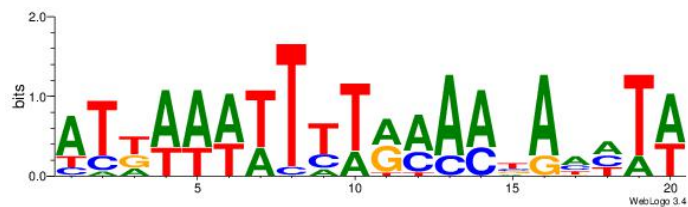
Dataset #: 1
Motif ID: 10
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

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

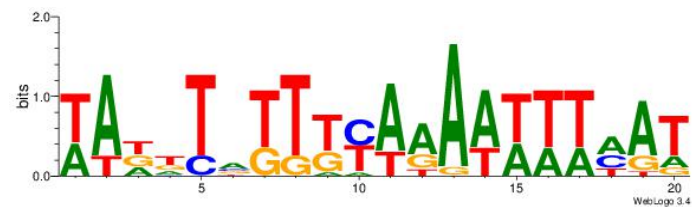
Alignment:

WAHHTVTTYKAAAWTTRAT
 -----HVTACWGATABD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAWTTRAT

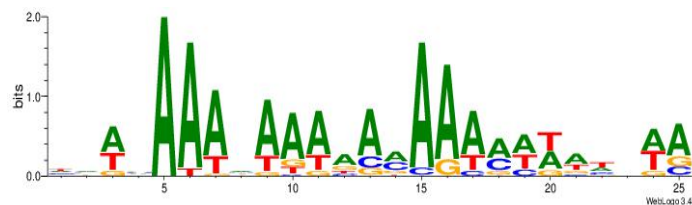


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0472742

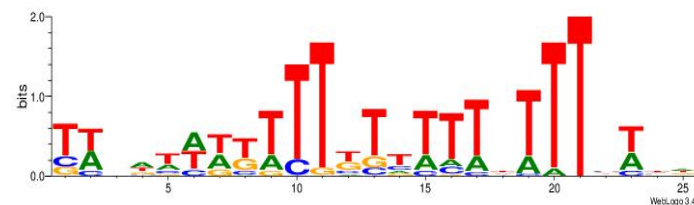
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 ---DBTACWGTA VH-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH

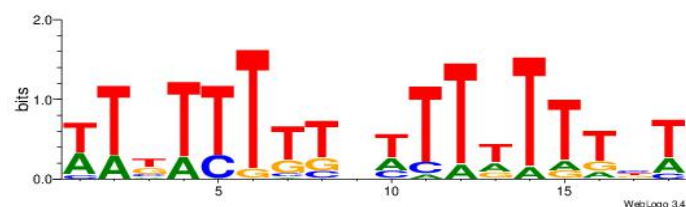


Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 9
Similarity score: 1.04742

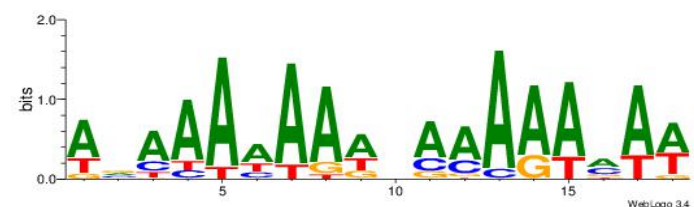
Alignment:

WTKTTTTTHWTTTTTTBT--
-----DBTACWGTAHV

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW

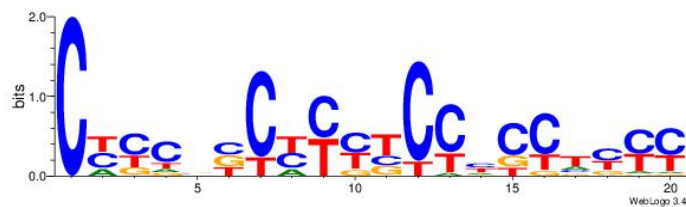


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 15
 Number of overlap: 6
 Similarity score: 2.54736

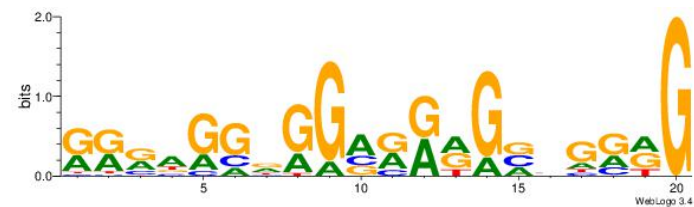
Alignment:

-----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

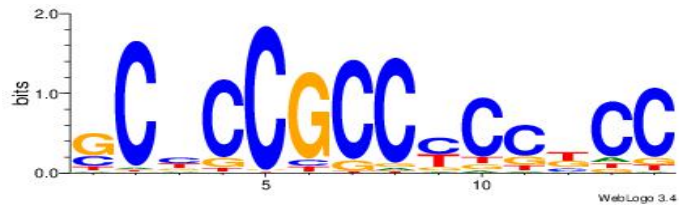
Number of overlap: 5
Similarity score: 3.04599

Alignment:
GGMGGRGGCGGVGC-----
-----DBTACWGTAVH

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

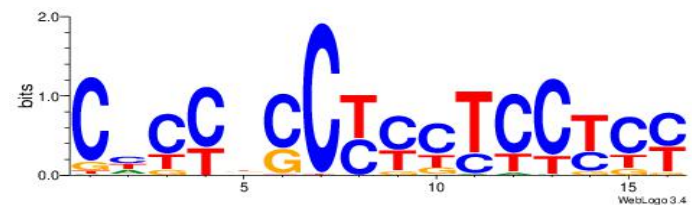
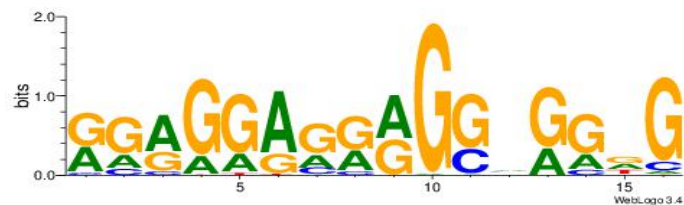


Dataset #: 1
Motif ID: 6
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 12
Number of overlap: 5
Similarity score: 3.04861

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)

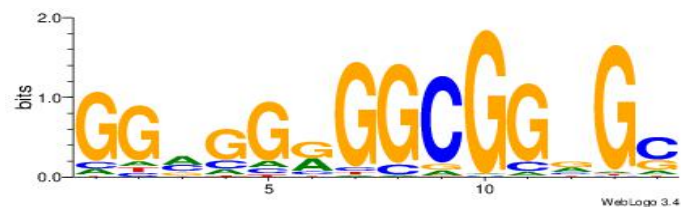
Dataset #:	1
Motif ID:	5
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0312321

Alignment:

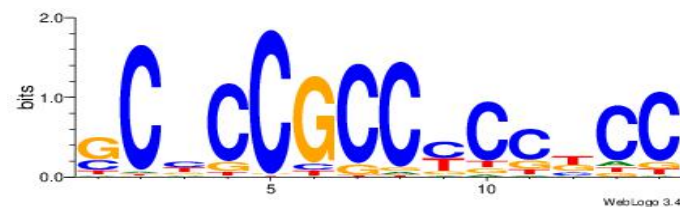
GGMGGRGGCGGVC

GBTGCAGGTGB---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

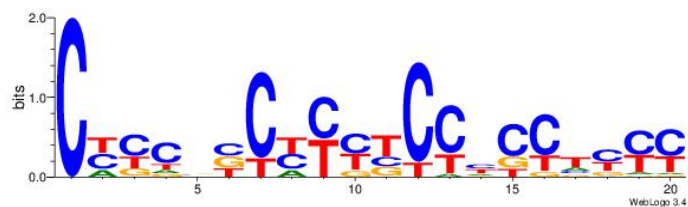


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0444938

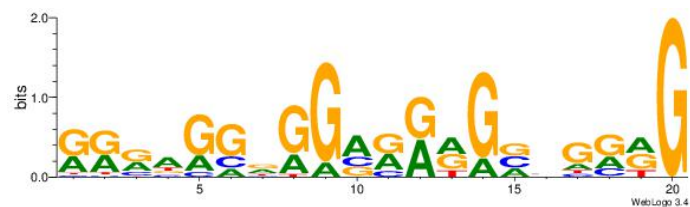
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -----GBTGCAGGTGB-----

Original motif Consensus sequence: CYCBB CYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

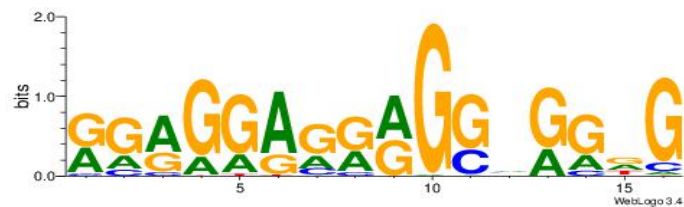


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.538471

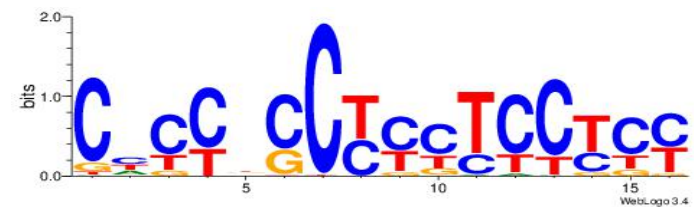
Alignment:

-RGRGGAGRRGGHGGDG
 GBTGCAGGTGB-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

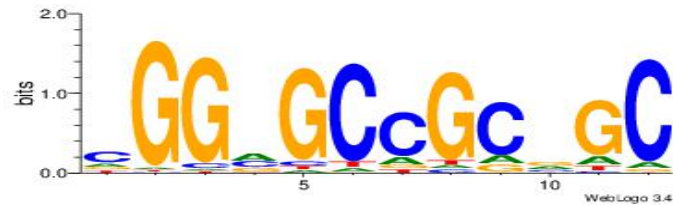


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

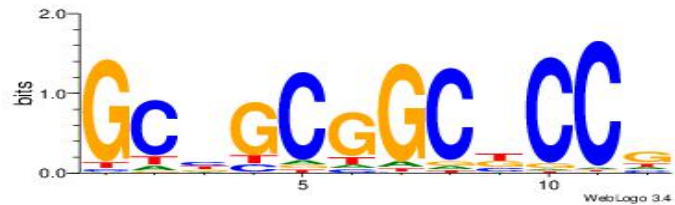
Number of overlap: 8
Similarity score: 1.54364

Alignment:
GCVGCGGCBCCG---
----BCACCTGCABC

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

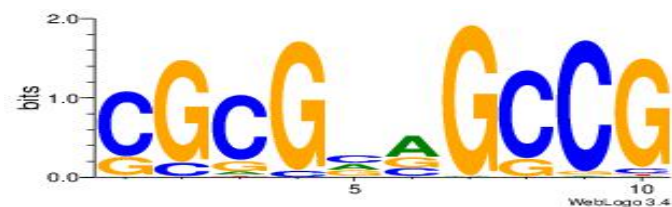
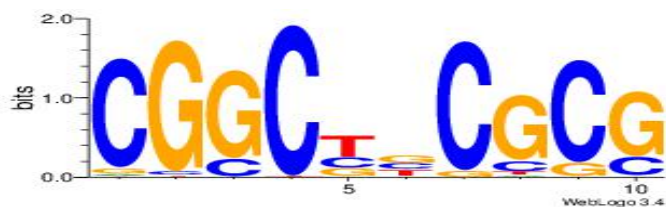


Dataset #: 1
Motif ID: 3
Motif name: TFW3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 1.5466

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



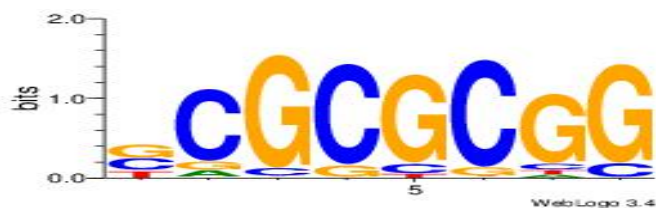
Dataset #: 1
 Motif ID: 2

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

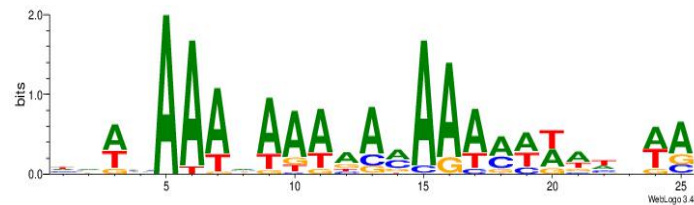


Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	22
Number of overlap:	4
Similarity score:	3.53789

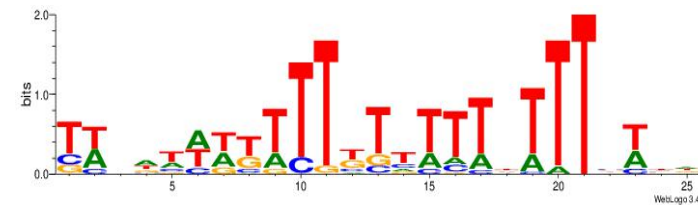
Alignment:

```
-----TWVHWWYTTTTYTTTTTHTTTTVWBH
GBTGCAGGTGB-----
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

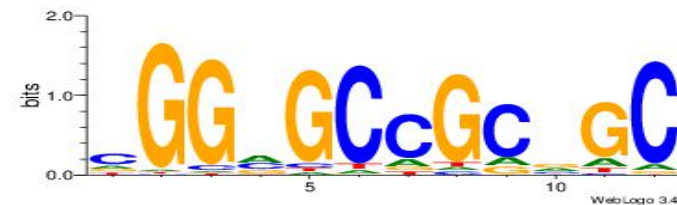


Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTTHTTTTVWBH

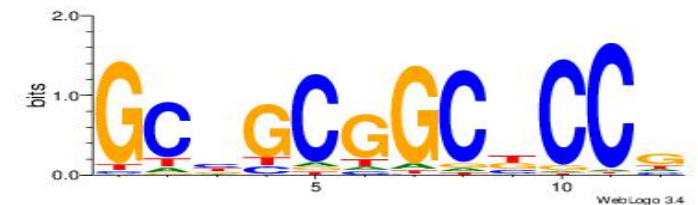


Dataset #: 1 Motif ID: 4 Motif name: TFF1

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



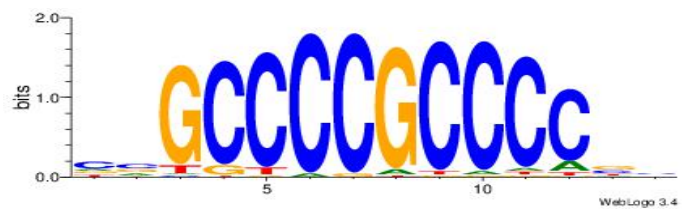
Best Matches for Top Significant Motif ID 4 (Highest to Lowest)

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

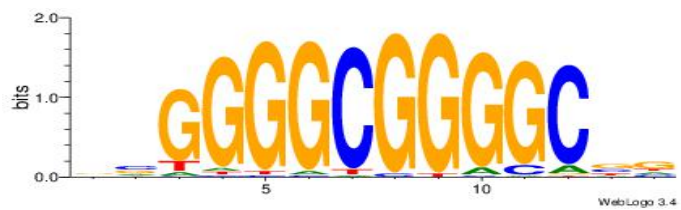
Position number: 1
Number of overlap: 12
Similarity score: 0.0542674

Alignment:
HVGCCCCGCCCCBB
CGGVGCCGCVGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



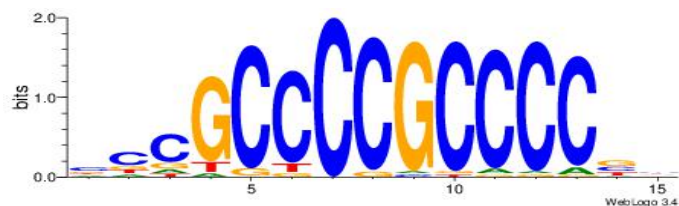
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



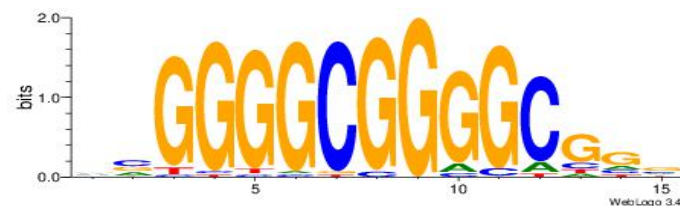
Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0548371

Alignment:
BCCGCCCCGCCCCBB
---GCVGCGGCBCCG

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



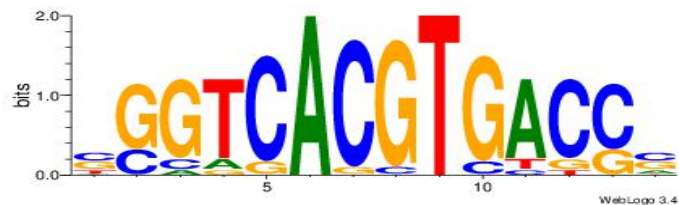
Dataset #: 2
Motif ID: 18
Motif name: sSGTCACGTGACSS
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0777862

Alignment:

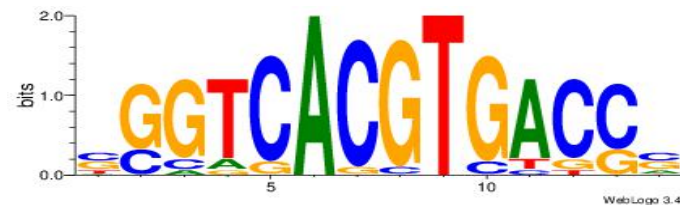
SGGTCACGTGACCS

--GCVGCGGCBCCG

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

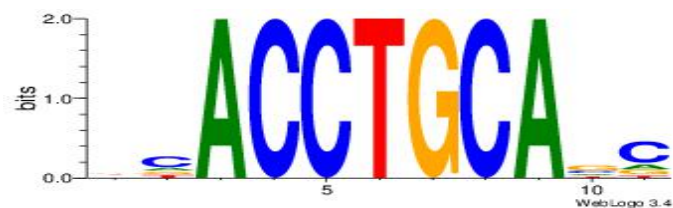


Dataset #: 2
 Motif ID: 16
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 2.08028

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

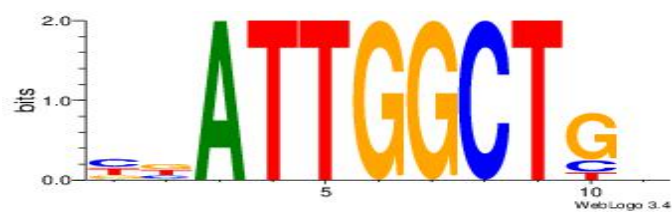
Similarity score: 3.54126

Alignment:
-----DCAGCCAATVR
CGGVGCCGCVGC-----

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH

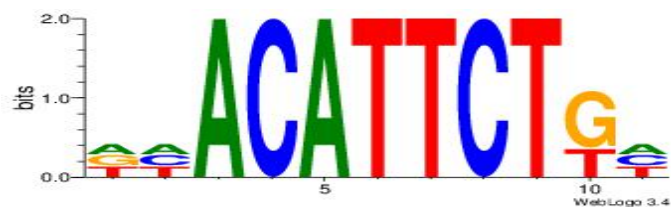


Dataset #: 2
Motif ID: 20
Motif name: dhACATTCTkh
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 4
Similarity score: 4.07107

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

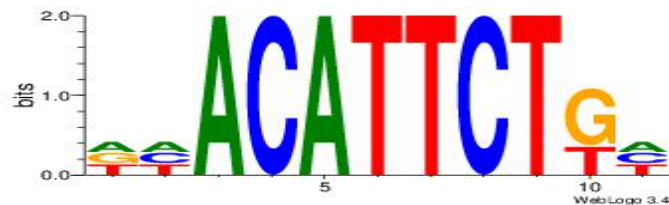


Reverse complement motif Consensus sequence: DHTATTTACBD



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)

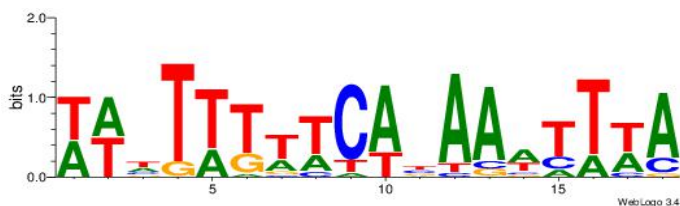
Dataset #:	1
Motif ID:	8
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	8
Number of overlap:	11
Similarity score:	0.00522383

Alignment:

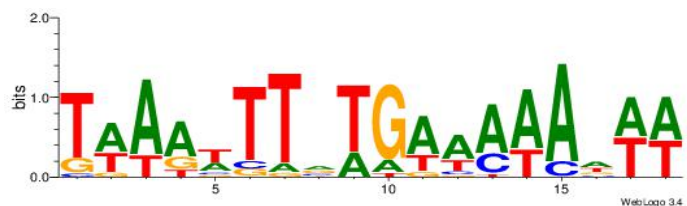
```

WWHTTTTTCABAAWTTWA
HCAGAATGTHD-----
  
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

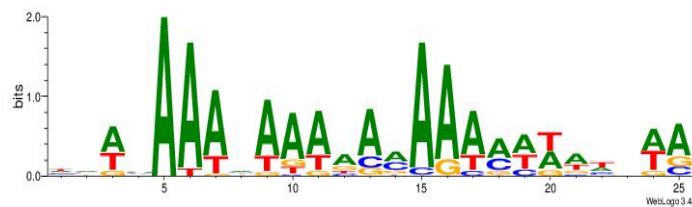


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.014258

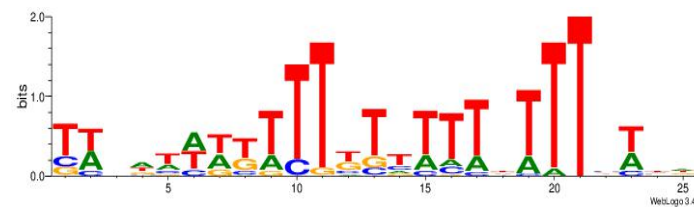
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 ----HCAGAATGTHD-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



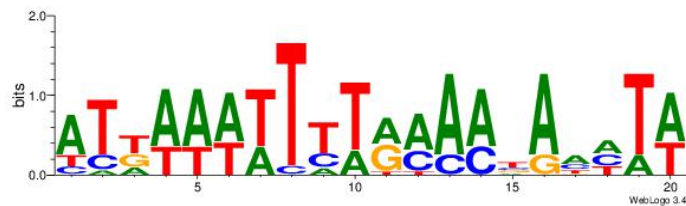
Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 11
Similarity score: 0.0192045

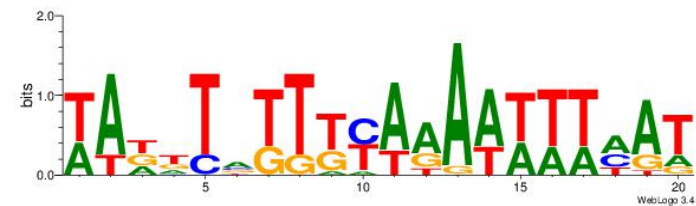
Alignment:

ATKAAWTTTTRMAABAHHTW
-DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT

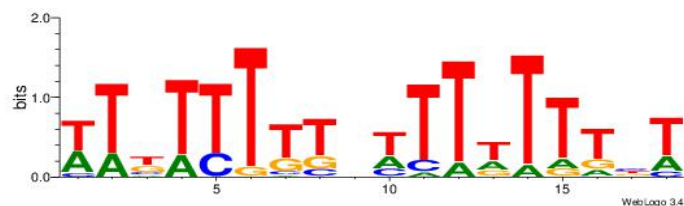


Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 0.519904

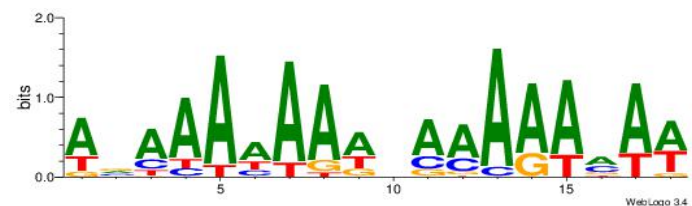
Alignment:

ABAAAAAWhAAAAARAW-
-----HCAGAATGTHD

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

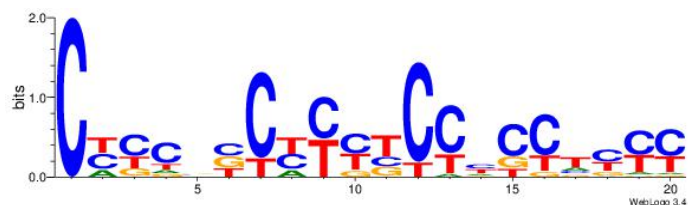


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 17
 Number of overlap: 4
 Similarity score: 3.5

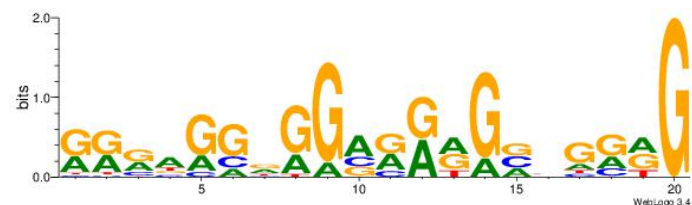
Alignment:

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

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

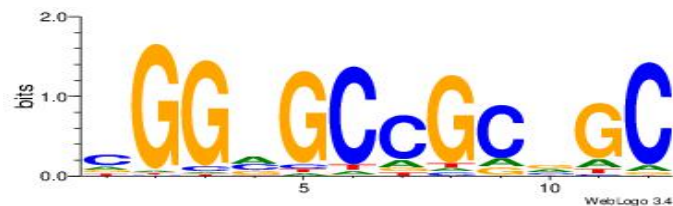


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 4
 Similarity score: 3.51958

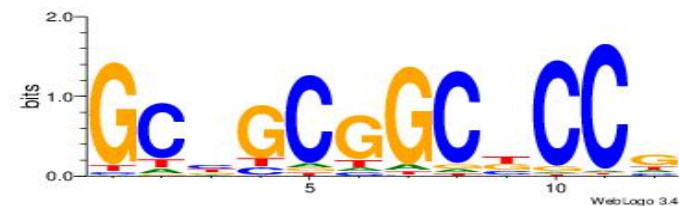
Alignment:

-----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

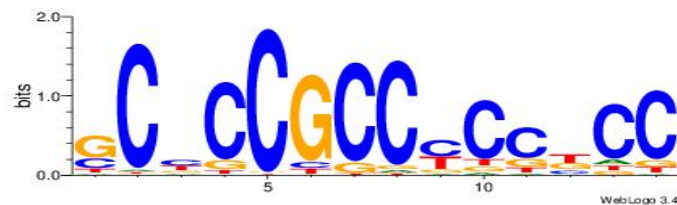
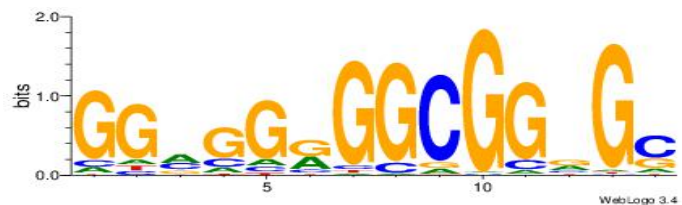


Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 11
Number of overlap: 4
Similarity score: 3.52554

Alignment:
-----GCVCCGCCMCCYCC
DHACATTCTGH-----

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



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

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

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



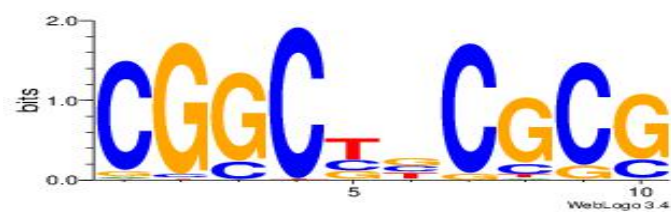
Best Matches for Significant Motif ID 1 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6

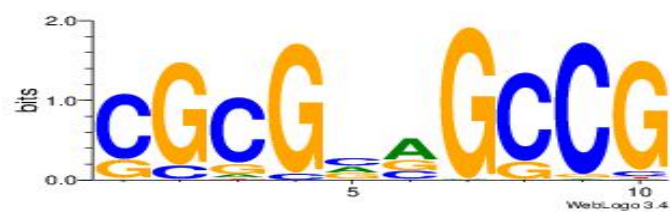
Similarity score: 0.0350356

Alignment:
CGGCYBCGCG
----GTCGCG

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

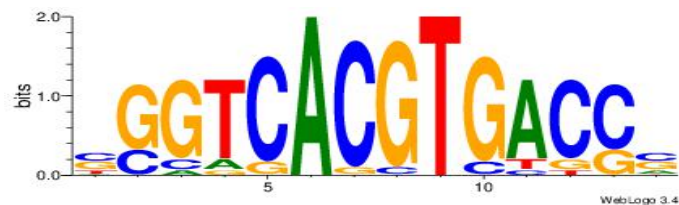
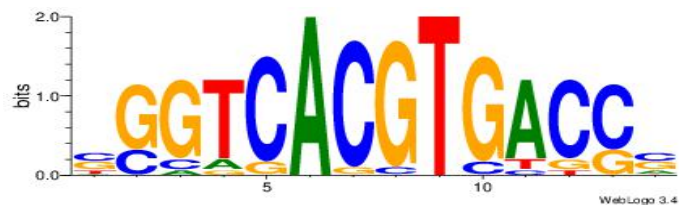


Dataset #: 2
Motif ID: 18
Motif name: sSGTCACGTGACSS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0375102

Alignment:
SGGTCACGTGACCS
--GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACCS



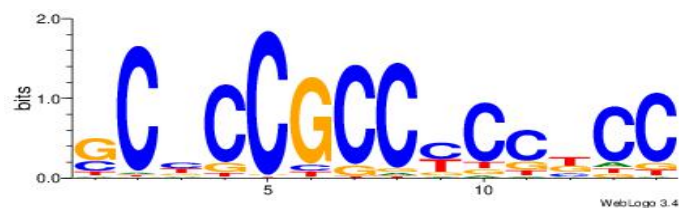
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0381641

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

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



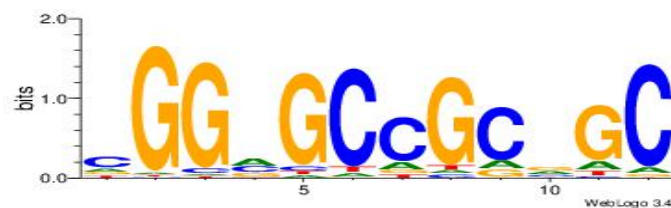
Dataset #: 1
 Motif ID: 4

Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0431161

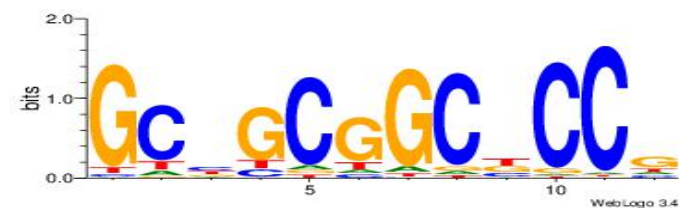
Alignment:

```
CGGVGCCGCVGC
-----CGCGAC
```

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #:	1
Motif ID:	2
Motif name:	TFW2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.052047

Alignment:
CCGCGCGS
-CGCGAC-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS

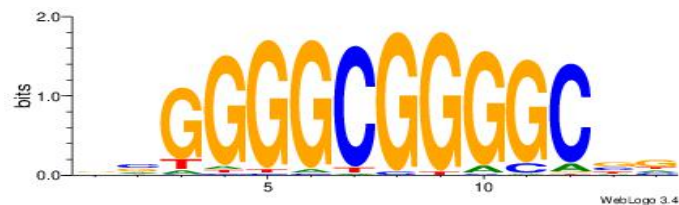
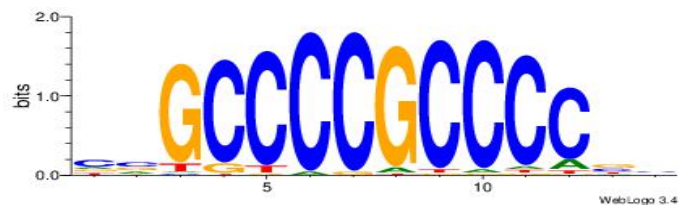


Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.0539

Alignment:
HVGCCCCGCCCCBB
--GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC

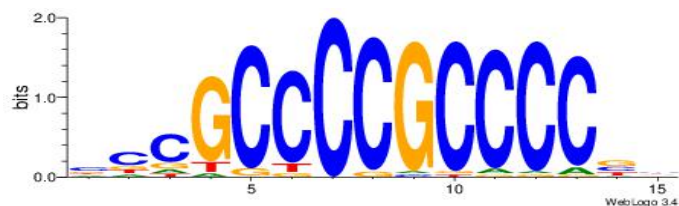


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0558733

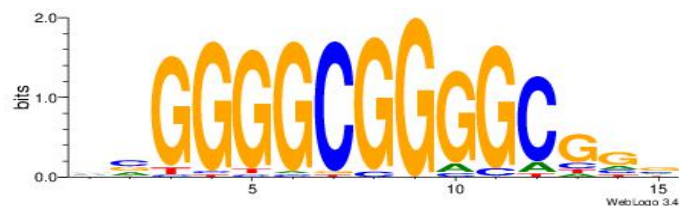
Alignment:

BCCGCCCCGCCCCBB
 -----CGCGAC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



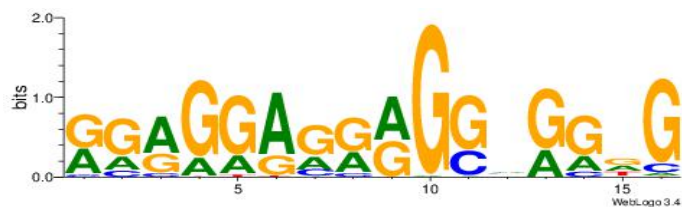
Dataset #: 1

Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0877631

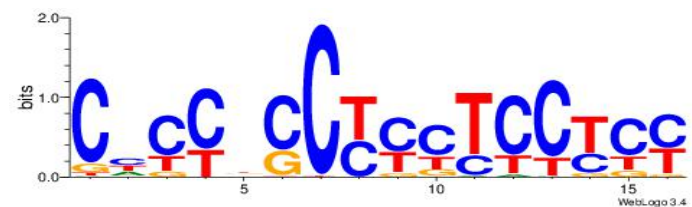
Alignment:

CHCCBCCCKMCTCCKCM
 -----CGCGAC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCCKMCTCCKCM

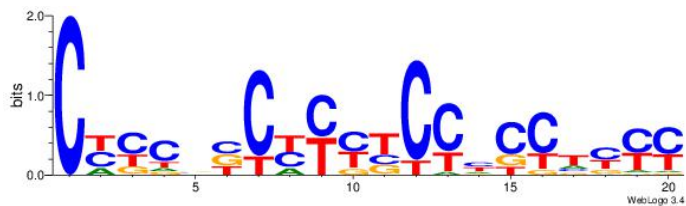


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 6

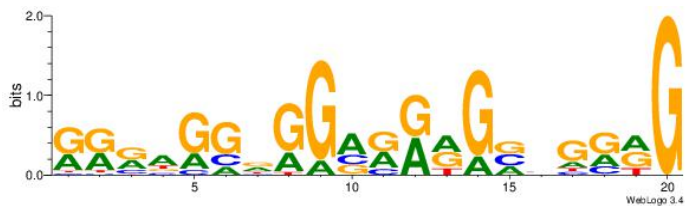
Similarity score: 0.089121

Alignment:
KKKAGGDGGAKKMGBBGKMG
-----GTCGCG-----

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



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

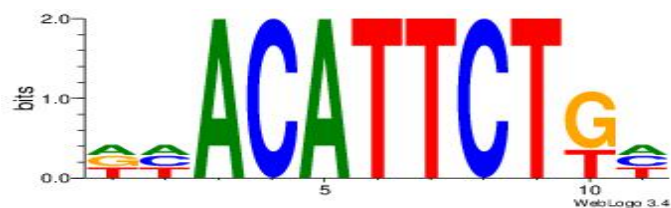
Reverse complement motif Consensus sequence: GBTGCAGGTGB



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 #: 2 Motif ID: 16 Motif name: kcACCTGCAGc

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



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

Dataset #:	2
Motif ID:	19
Motif name:	wsTACwGTAsw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0182895

Alignment:

DBTACWGTAVH

BCACCTGCABC

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH

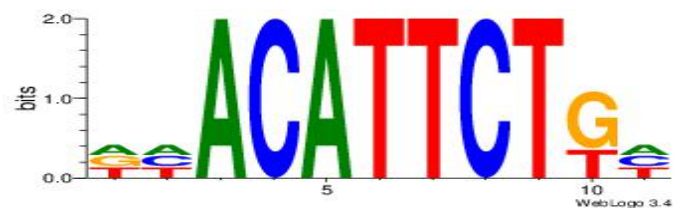


Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0221745

Alignment:

DHACATTCTGH
 BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

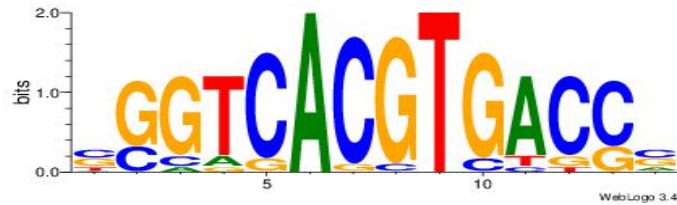


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11

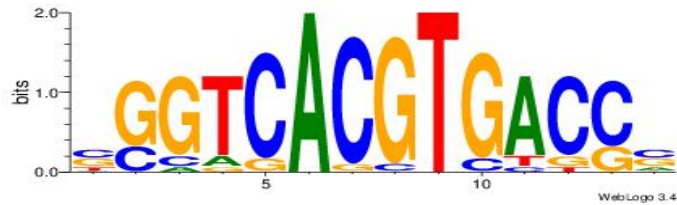
Similarity score: 0.0280991

Alignment:
SGGTCACGTGACCS
---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

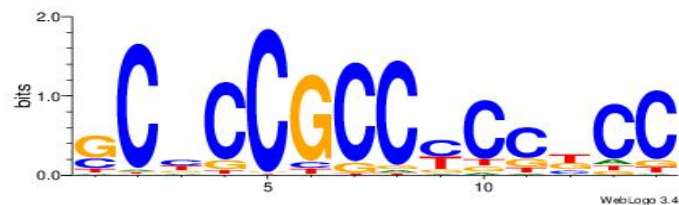
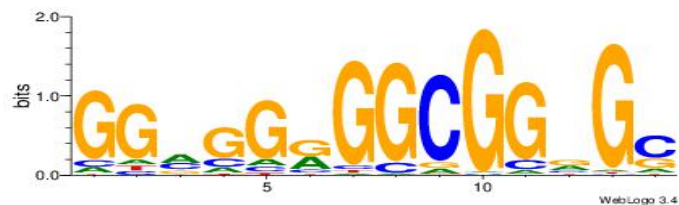


Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0312321

Alignment:
GGMGGRGGCGGVGC
GBTGCAGGTGB---

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

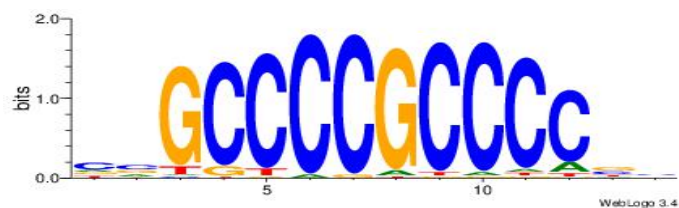


Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0370129

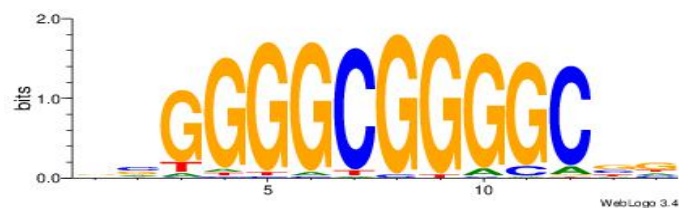
Alignment:

HVGCCCCGCCCCBB
 -BCACCTGCABC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 2
 Motif ID: 15

Motif name:	kCAGCCAATmr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0407197

Alignment:

DCAGCCAATVR
GBTGCAGGTGB

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



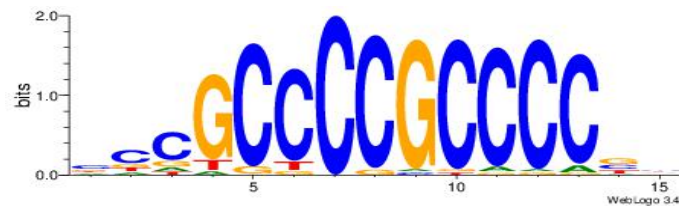
Dataset #:	2
Motif ID:	14
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0429055

Alignment:

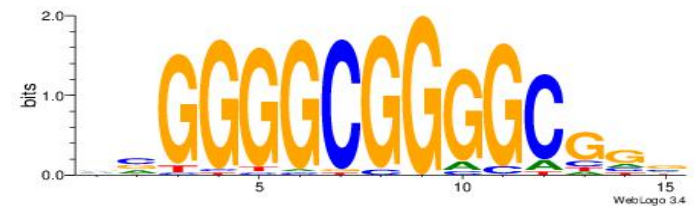
BCCGCCCCGCCCCBB

--BCACCTGCABC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



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

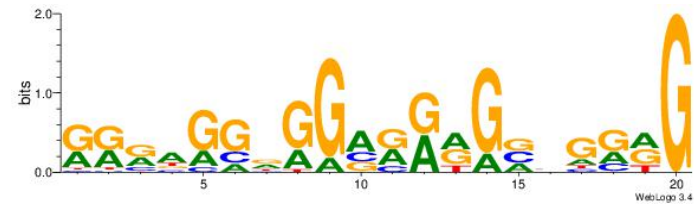
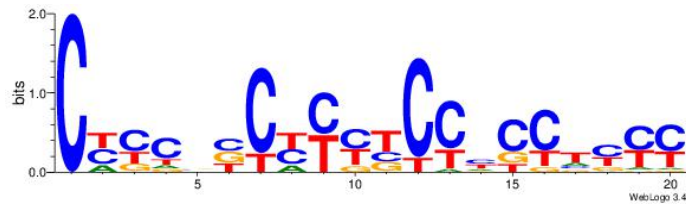
Alignment:

KKKAGGDGGAKKMGBBGKMG

----GBTGCAGGTGB-----

Original motif Consensus sequence: CYCBBCYYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

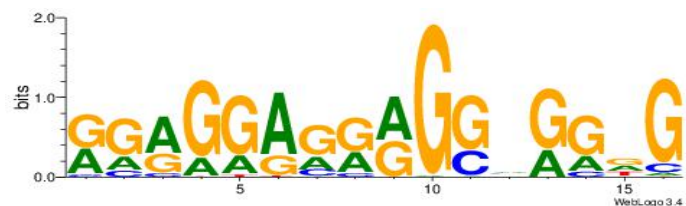


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.538471

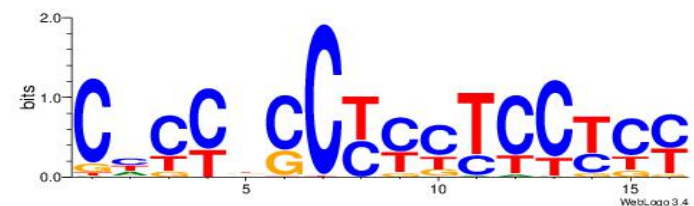
Alignment:

-RGRGGAGRRGGHGGDG
 GBTGCAGGTGB-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



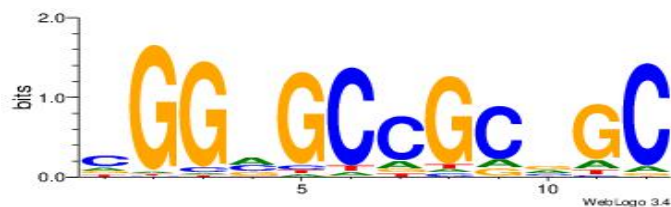
Dataset #: 1

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

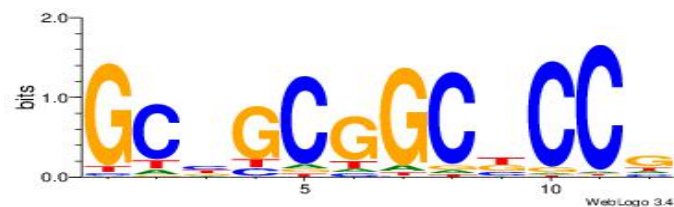
Alignment:

GCVGCGGCBCCG---
 ----BCACCTGCABC

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

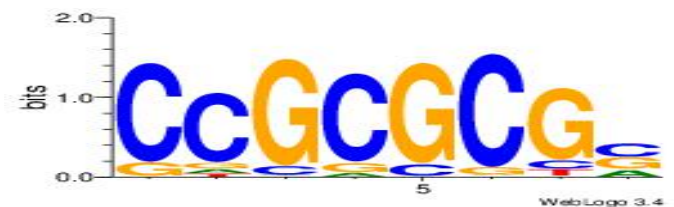


Dataset #: 1 Motif ID: 2 Motif name: TFW2

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



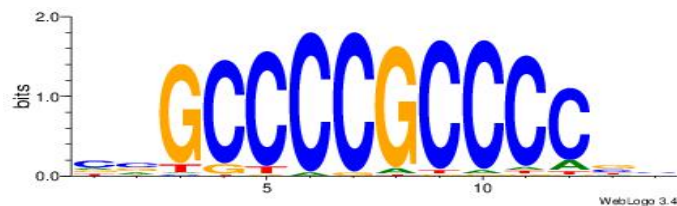
Best Matches for Significant Motif ID 2 (Highest to Lowest)

Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0456233

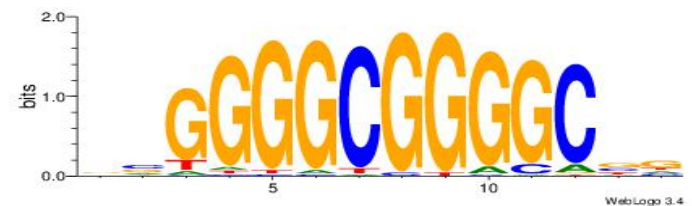
Alignment:

BBGGGGCGGGGCVD
 -SCGCGCGG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

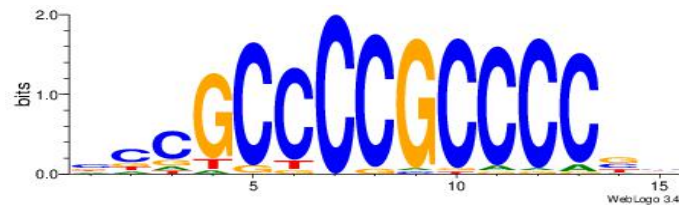


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif

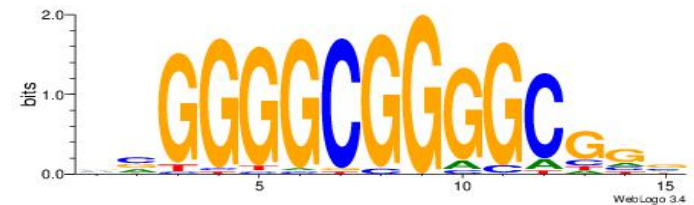
Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

Alignment:
 BCCGCCCCGCCCCBB
 -----CCGCGCGS--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



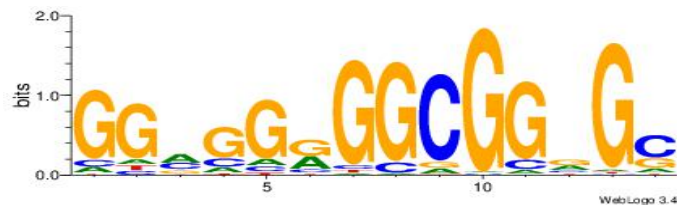
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



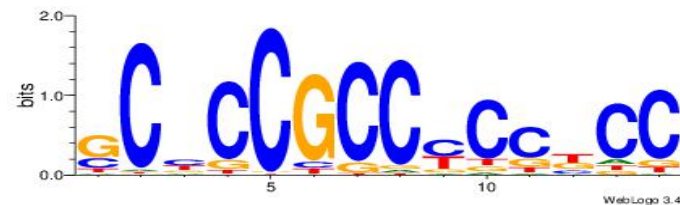
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0583967

Alignment:
 GCVCCGCCMCCYCC
 ---CCGCGCGS---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

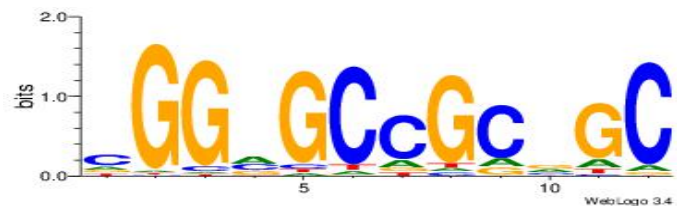


Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.060966

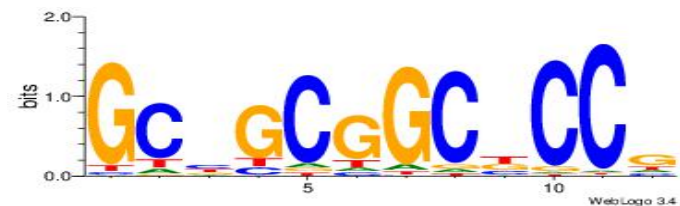
Alignment:

CGGVGCCGCVGC
SCGCGCGG----

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0906073

Alignment:

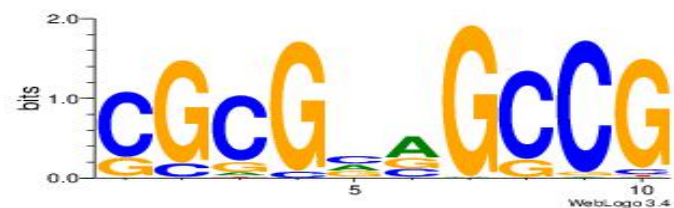
CGCGBMGCCG

--SCGCGCGG

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

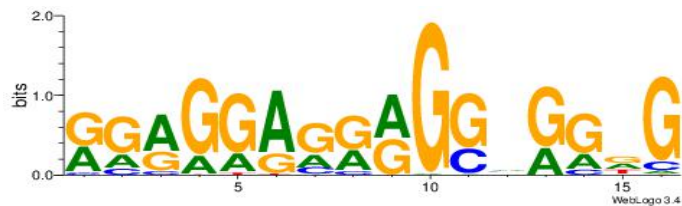


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 8

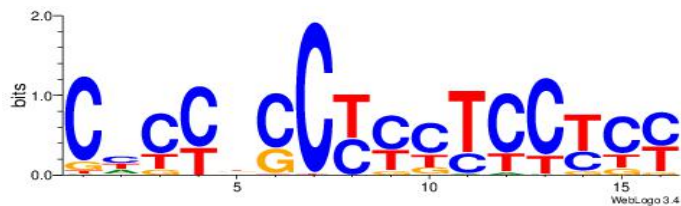
Similarity score: 0.0910301

Alignment:
CHCCBCKMCTCCKCM
---CCGCGCGS-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

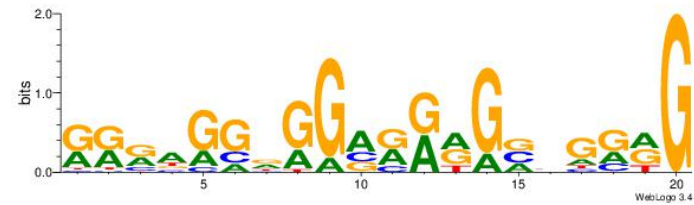
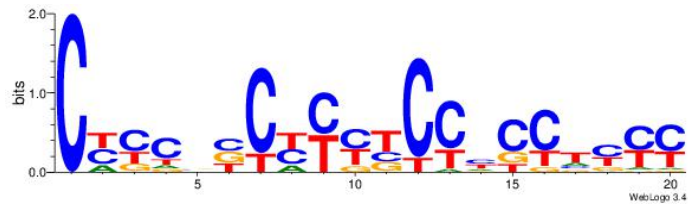


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.094473

Alignment:
KKKAGGDGGAKKMGBBGKMG
-----SCGCGCGG----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

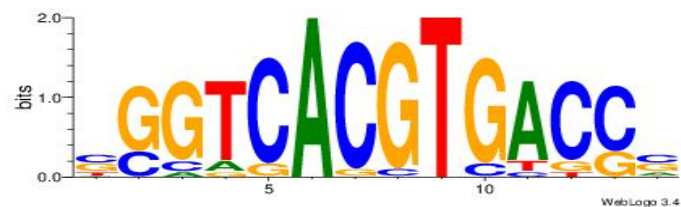
Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



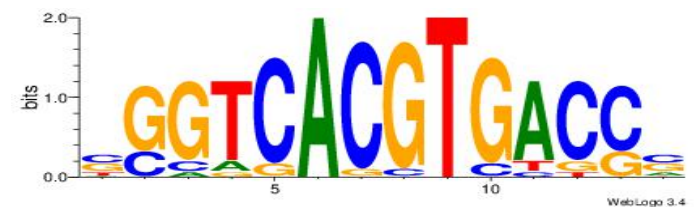
Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACCS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0988223

Alignment:
 SGGTCACGTGACCS
 ---SCGCGCGG---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 1
 Motif ID: 1

Motif name:	TFW1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	5
Similarity score:	1.5088

Alignment:

GTCGCG---
 -SCGCGCGG

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



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 #: 1 Motif ID: 3 Motif name: TFW3

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



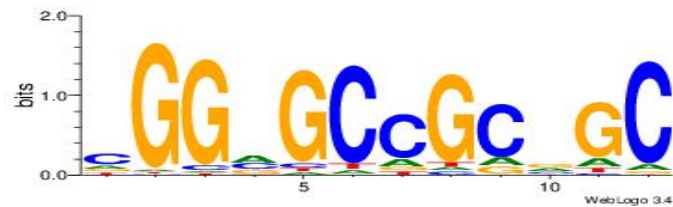
Best Matches for Significant Motif ID 3 (Highest to Lowest)

Dataset #:	1
Motif ID:	4
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

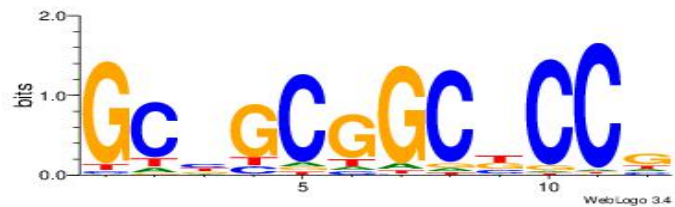
Number of overlap: 10
Similarity score: 0.0623879

Alignment:
CGGVGCCGCVGC
CGGCYBCGCG--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

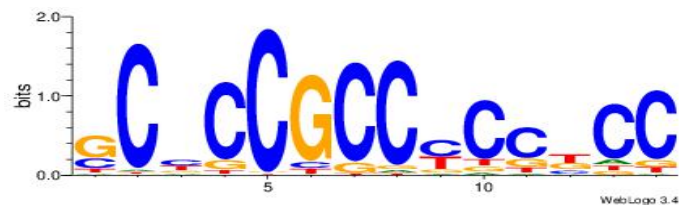
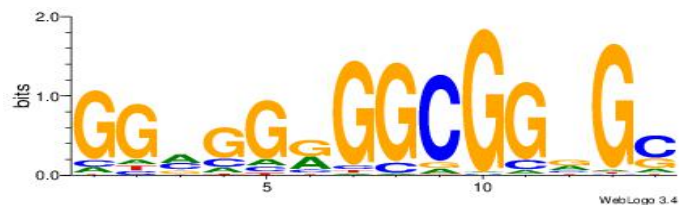


Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0645308

Alignment:
GGMGGRGGCGGVGC
CGCGBMGCCG----

Original motif Consensus sequence: GGMGGRGGCGGVGC

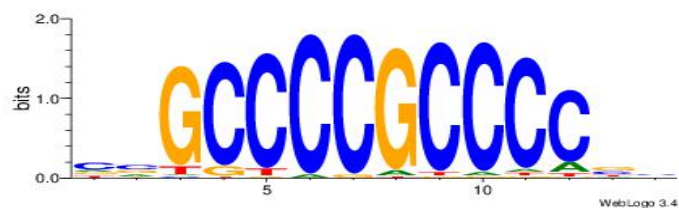
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



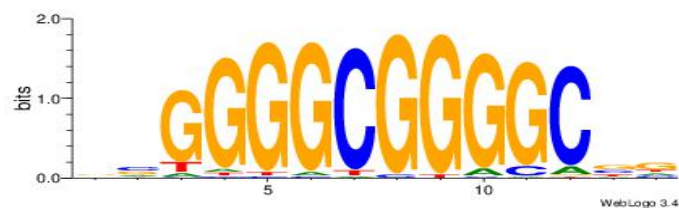
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0718771

Alignment:
 HVGCCCCGCCCCBB
 CGGCYBCGCG----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



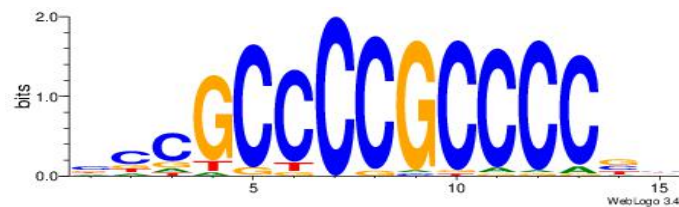
Dataset #: 2
 Motif ID: 14

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

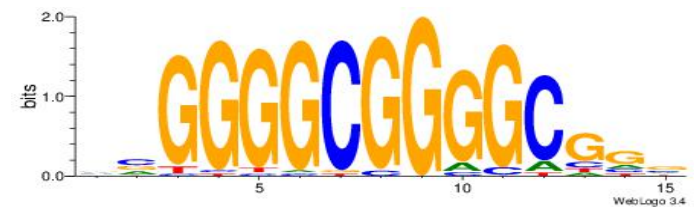
Alignment:

BCCGCCCCGCCCCBB
 -CGGCYBCGCG----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGCGGB

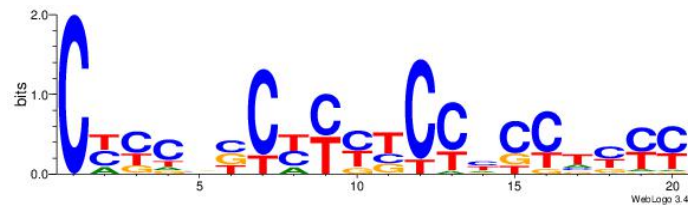


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0767689

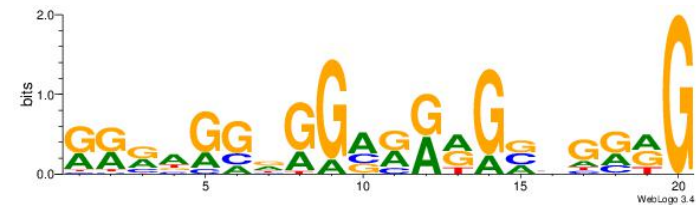
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -----CGCGBMGCCG

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
 KKKAGGDGGAKKMGBBGKMG



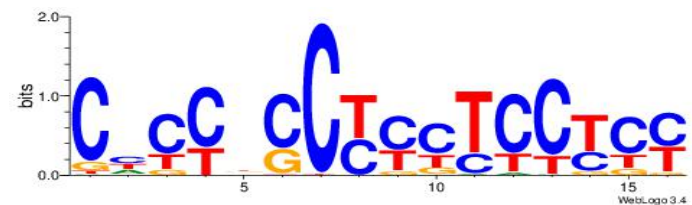
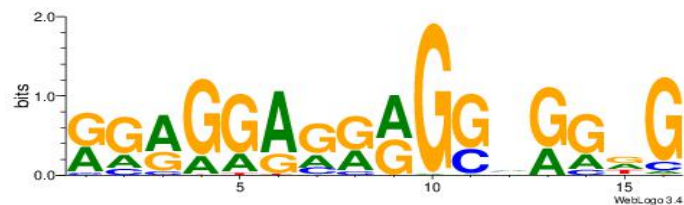
Dataset #:	1
Motif ID:	6
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0814831

Alignment:

CHCCBCKMCTCCKCM
 CGGCYBCGCG-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

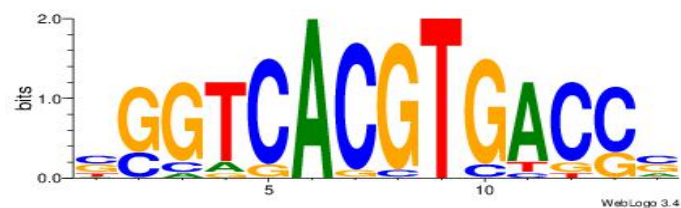
Reverse complement motif Consensus sequence:
 CHCCBCKMCTCCKCM



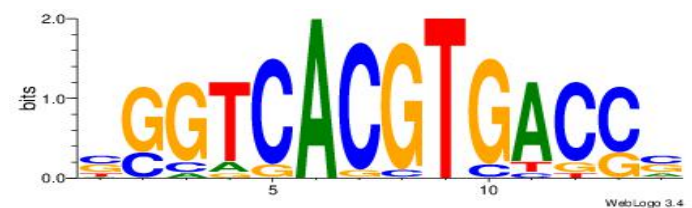
Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0895189

Alignment:
 SGGTCACGTGACCS
 ----CGCGBMGCCG

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 1
 Motif ID: 2

Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	1.09499

Alignment:

```
--CCGCGCGS
CGGCYBCGCG
```

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



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: 19** **Motif name: wsTACwGTAsw**

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTA VH



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

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:	1
Number of overlap:	11
Similarity score:	0.0199592

Alignment:
 GBTGCAGGTGB
 HVTACWGATABD

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

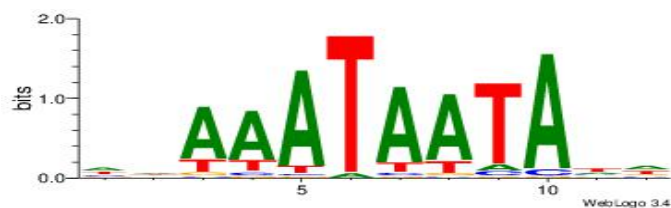


Dataset #: 2
Motif ID: 17
Motif name: wwAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0309343

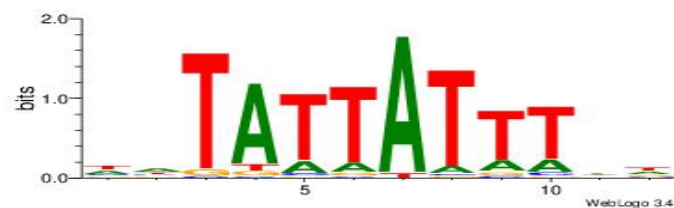
Alignment:

DDTATTATTTDH
-HVTACWGATABD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

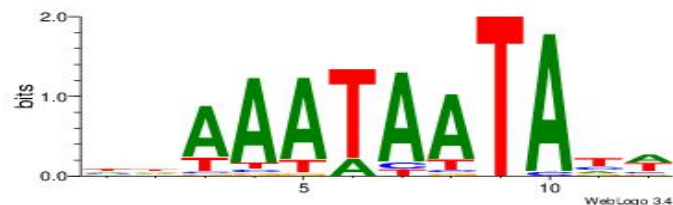


Dataset #: 2
 Motif ID: 13
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0337121

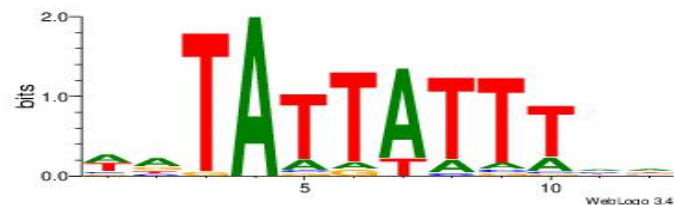
Alignment:

HDAAATAATAHW
 DBTACWGTAVH-

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH



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

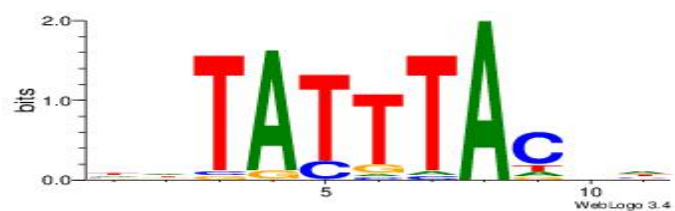
Similarity score: 0.037518

Alignment:
DBGTAAATAHD
DBTACWGTAVH

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD

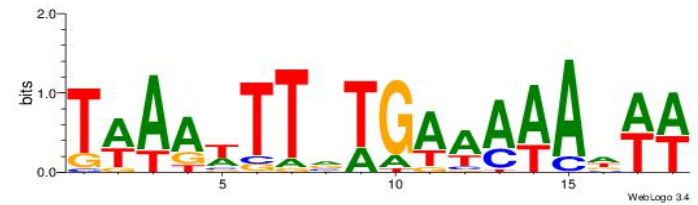
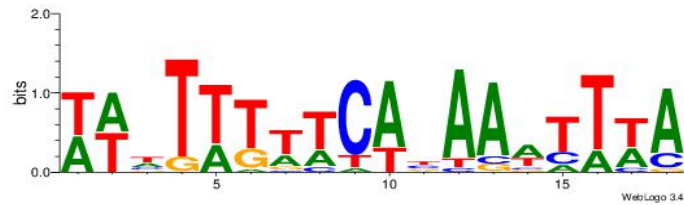


Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 11
Similarity score: 0.0413797

Alignment:
WWHTTTTTTCABAAWTTWA
---DBTACWGTAVH----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TAAAWTTVTGAAAAHWW

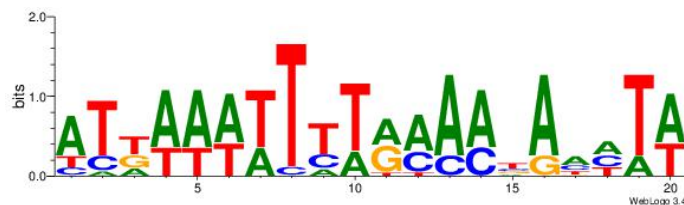


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0445707

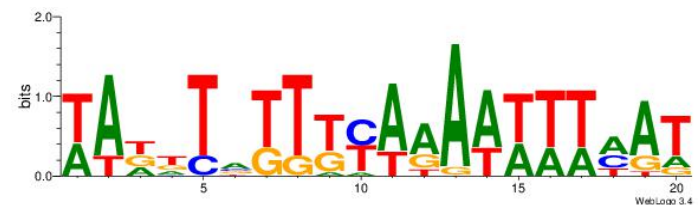
Alignment:

WAHHTVTTYKAAAATTRAT
 -----HVTACWGATABD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



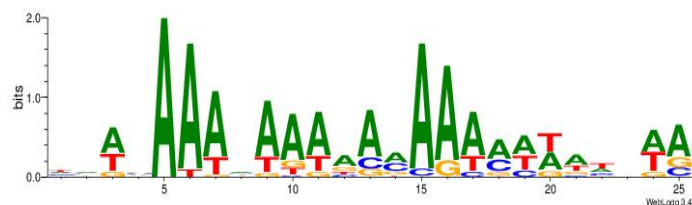
Dataset #: 1

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

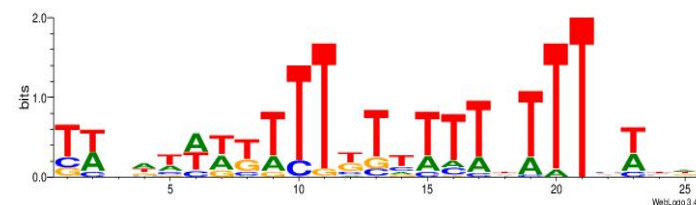
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 ---DBTACWGTAVH-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTTYTTTTHTTTVWBH



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: 2
 Number of overlap: 10

Similarity score: 0.544444

Alignment:
HCAGAATGTHD-
-HVTACWGTTABD

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

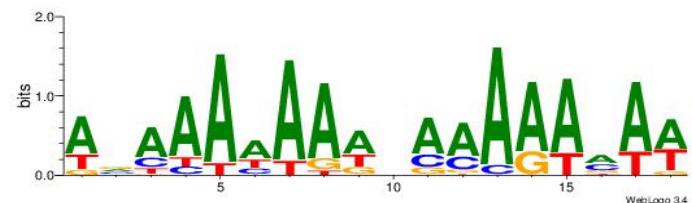
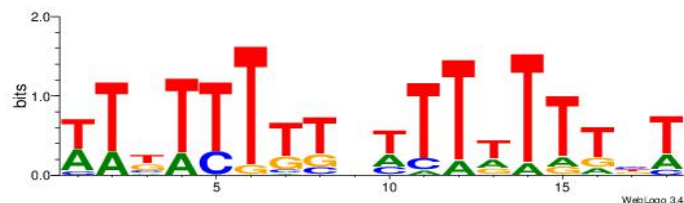


Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 9
Similarity score: 1.04742

Alignment:
WTKTTTTTHWTTTTTTBT--
-----DBTACWGTTAVH

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAWHAAAAARAW



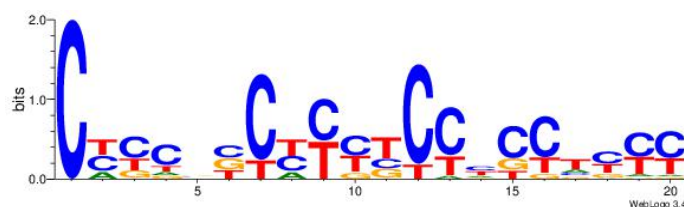
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 15
 Number of overlap: 6
 Similarity score: 2.54736

Alignment:

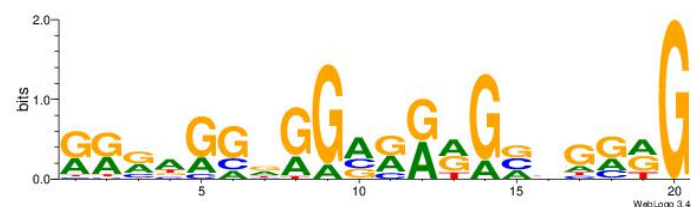
```

-----CYYCBBCYYYTCCHCCTYYY
DBTACWGTAVH-----
  
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

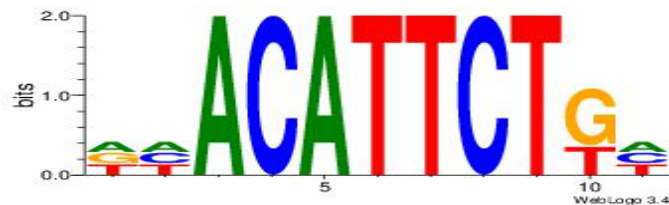


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



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

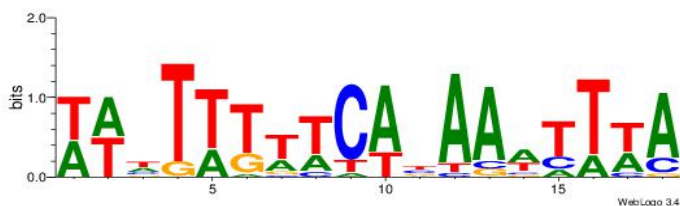
Dataset #:	1
Motif ID:	8
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	8
Number of overlap:	11
Similarity score:	0.00522383

Alignment:

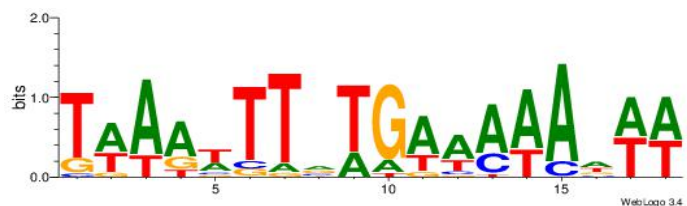
```

WWHTTTTTCABAAWTTWA
HCAGAATGTHD-----
  
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



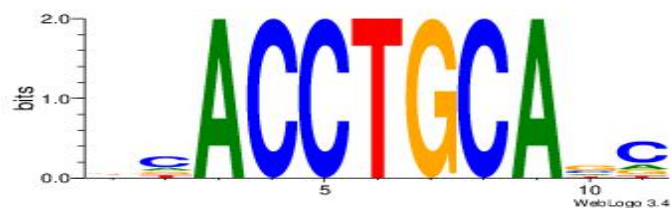
Dataset #: 2
 Motif ID: 16
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.00731643

Alignment:

BCACCTGCABC

DHACATTCTGH

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

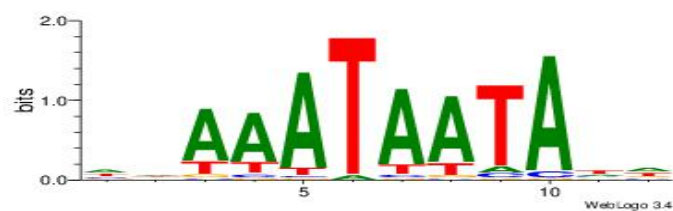


Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

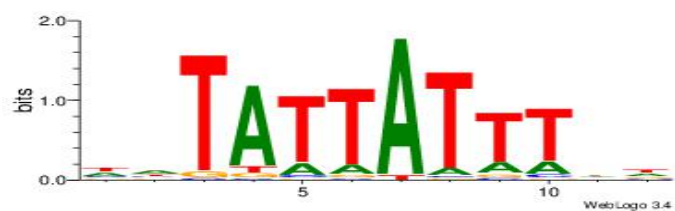
Similarity score: 0.0127231

Alignment:
DDTATTATTTDH
-HCAGAATGTHD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

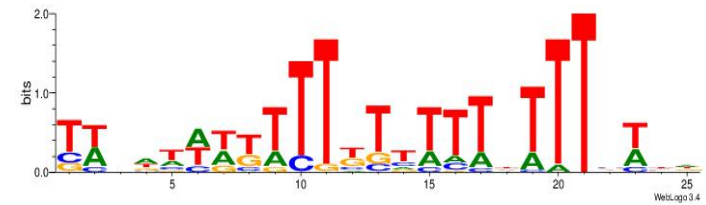
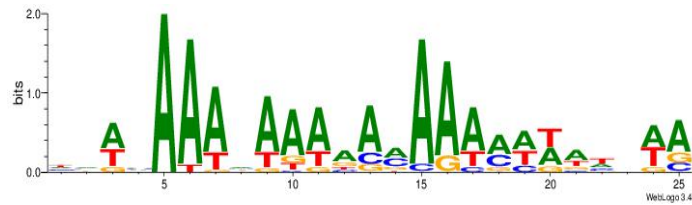


Dataset #: 1
Motif ID: 11
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 11
Number of overlap: 11
Similarity score: 0.014258

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
----HCAGAATGTHD-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTHTTTVWBH

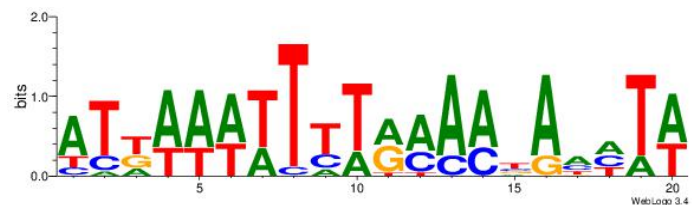


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 11
 Similarity score: 0.0192045

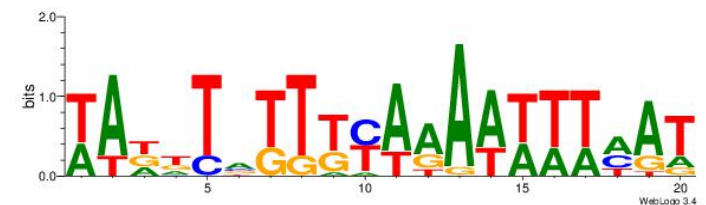
Alignment:

ATKAAWTTTTRMAABAHHTW
 -DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

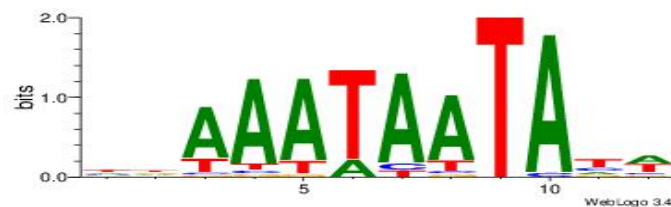


Dataset #: 2

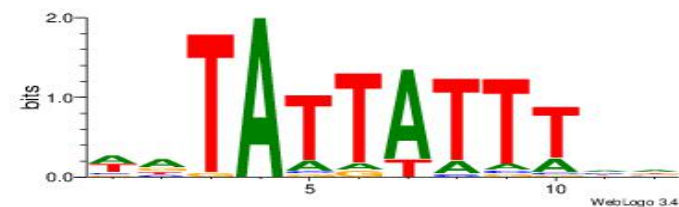
Motif ID: 13
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0199621

Alignment:
 WHTATTATTTDH
 -HCAGAAATGTHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #: 2
 Motif ID: 15
 Motif name: kCAGCCAATmr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0247304

Alignment:

MBATTGGCTGH

DHACATTCTGH

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



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

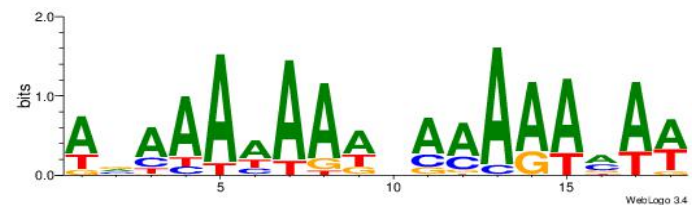
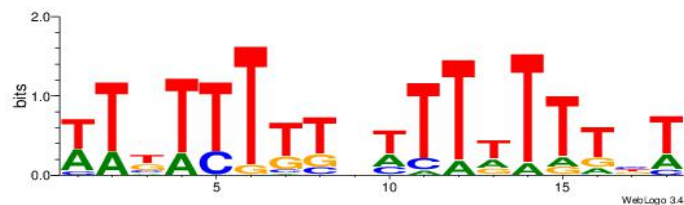
Alignment:

ABAAAAAWhAAAAARAW-

-----HCAGAATGTHD

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW



Dataset #: 2
 Motif ID: 19
 Motif name: wsTACwGTAsw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.527917

Alignment:
 -DBTACWGTAVH
 DHACATTCTGH-

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



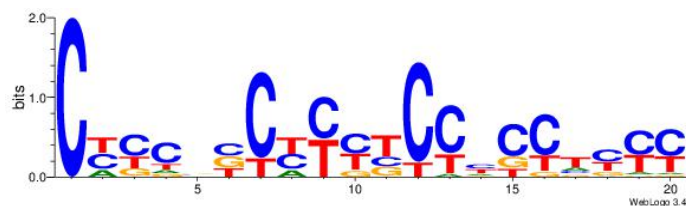
Dataset #: 1
 Motif ID: 9

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

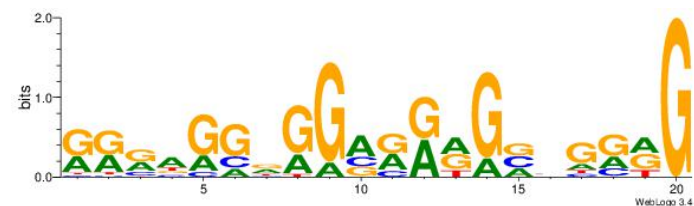
Alignment:

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

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

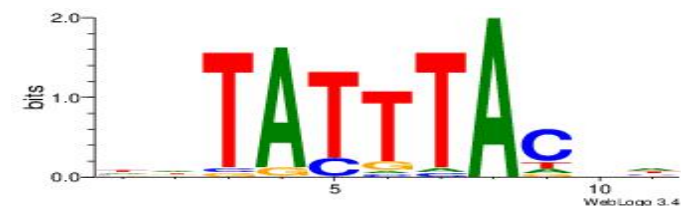


Dataset #: 2 Motif ID: 21 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



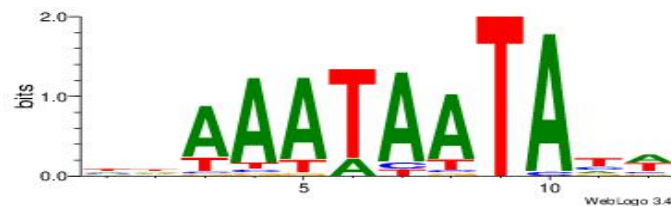
Best Matches for Significant Motif ID 21 (Highest to Lowest)

Dataset #: 2
Motif ID: 13
Motif name: tkAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0162338

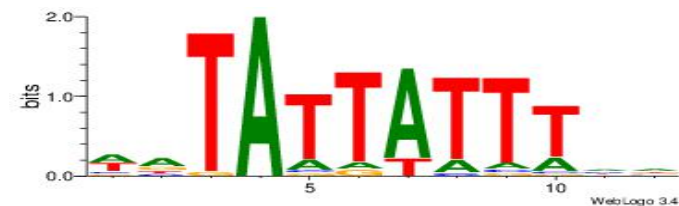
Alignment:

HDAAATAATAHW
-DBGTAATAHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

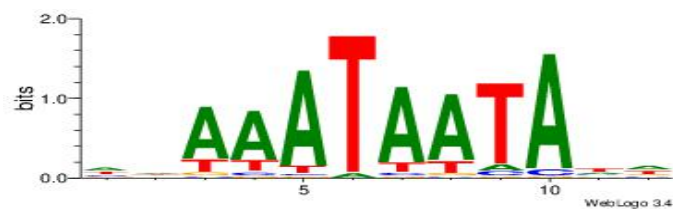


Dataset #: 2
Motif ID: 17
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

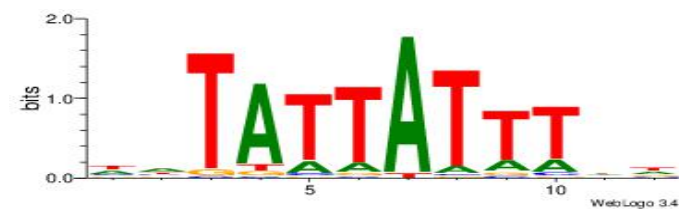
Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0164863

Alignment:
 DDTATTATTTDH
 DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



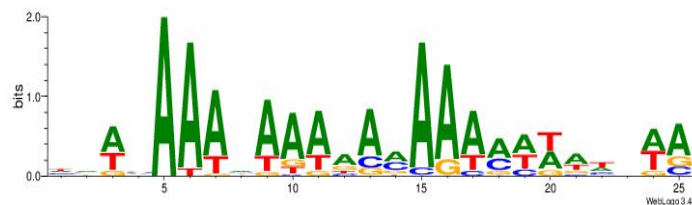
Reverse complement motif Consensus sequence: DDTATTATTTDH



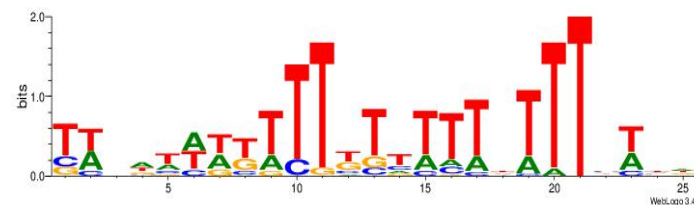
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 11
 Similarity score: 0.0192768

Alignment:
 TWVHWWYTTTYTTTTTHTTTVWBH
 -----DHTATTTACBD

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWTYYYYTTTTTHTTTVWBH

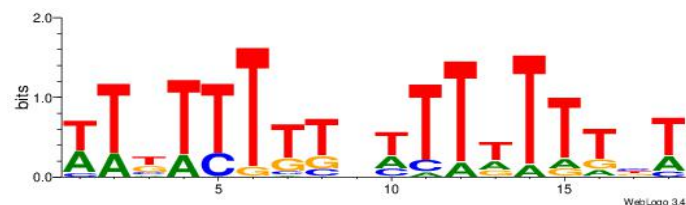


Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0283217

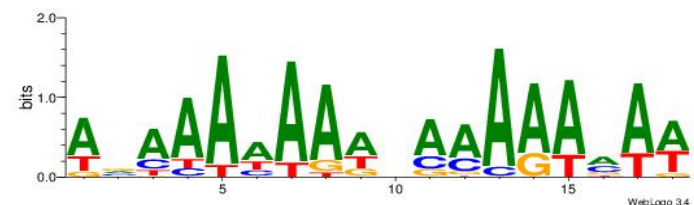
Alignment:

WTKTTTTTHWTTTTTTBT
DHTATTTACBD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW

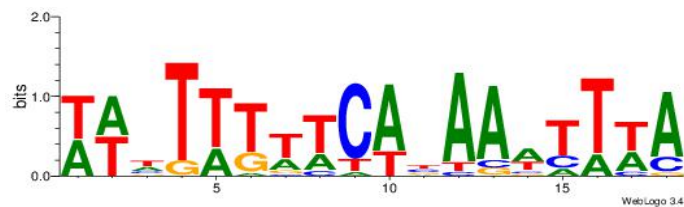


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0308097

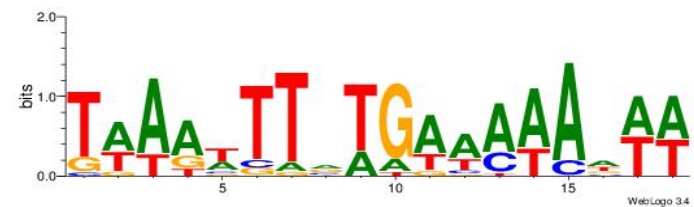
Alignment:

WWHTTTTTTCABAAWTTWA
 -----DHTATTTACBD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

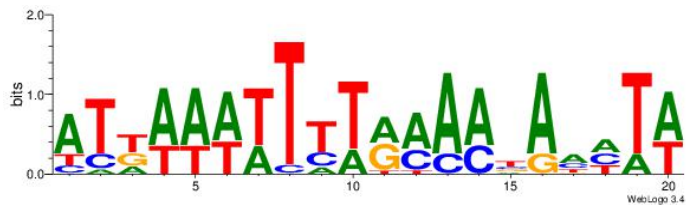


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

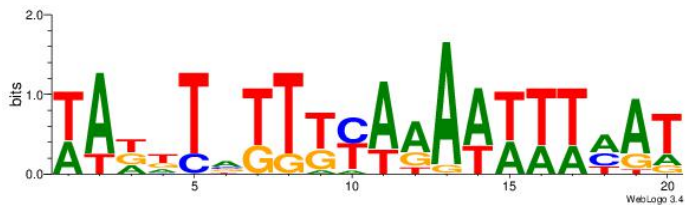
Number of overlap: 11
Similarity score: 0.0333874

Alignment:
ATKAAWTTTTRMAABAHHTW
-----DBGTAAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2
Motif ID: 19
Motif name: wsTACwGTAsw
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0472403

Alignment:
HVTACWGATABD
DHTATTTACBD

Original motif Consensus sequence: HVTACWGATABD

Reverse complement motif Consensus sequence: DBTACWGTAHVH



Dataset #: 2
 Motif ID: 15
 Motif name: kCAGCCAATmr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.554132

Alignment:
 -MBATTGGCTGH
 DHTATTTACBD-

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



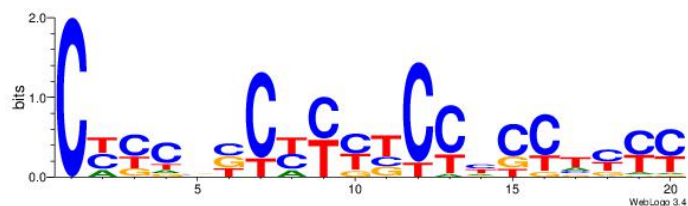
Dataset #: 1
 Motif ID: 9

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

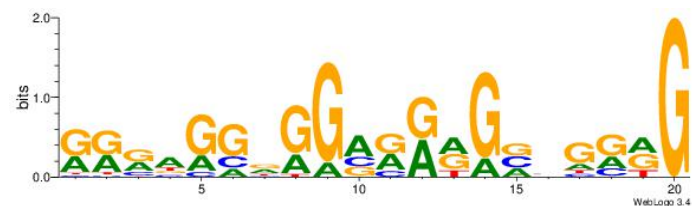
Alignment:

-----KKKAGGDGGAKKMGBBGKMG
 DHTATTTACBD-----

Original motif Consensus sequence: CYCBBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

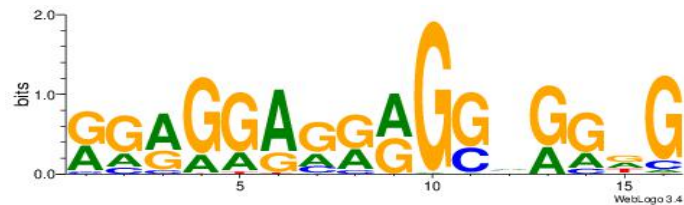


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 12
 Number of overlap: 5
 Similarity score: 3.05714

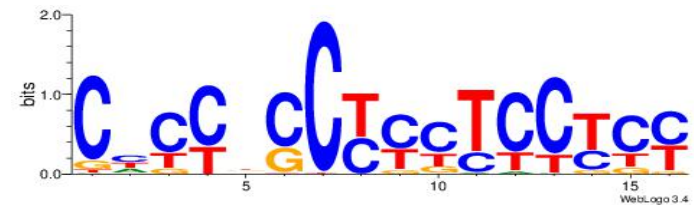
Alignment:

-----CHCCBCKMCTCCKCM
DHTATTTACBD-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

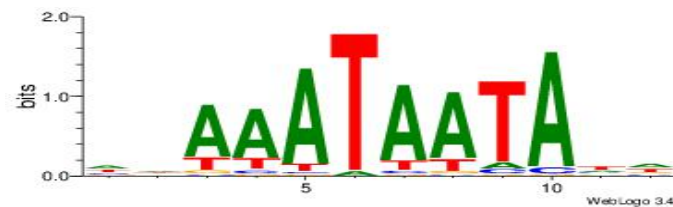


Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

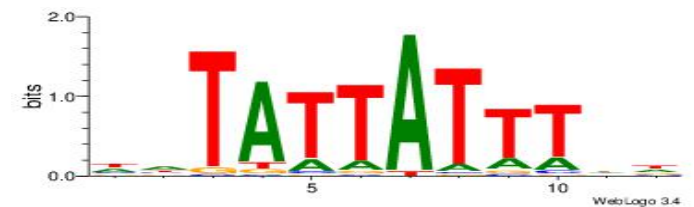


Dataset #: 2 Motif ID: 17 Motif name: wwAAATAATatw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



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

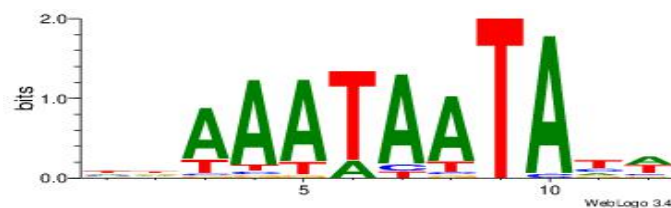
Dataset #:	2
Motif ID:	13
Motif name:	tkAAATAATatw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 1
Number of overlap: 12
Similarity score: 0

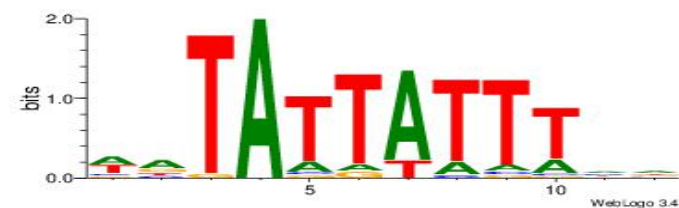
Alignment:

HDAAATAATAHW
HDAAATAATADD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH

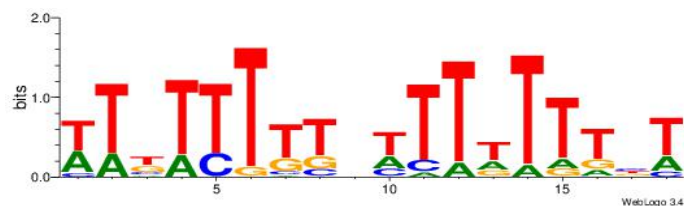


Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 12
Similarity score: 0.0565705

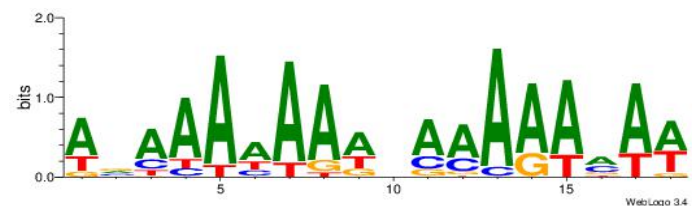
Alignment:

ABAAAAAAWHAAAAARAW
-----HDAAATAATADD

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAw

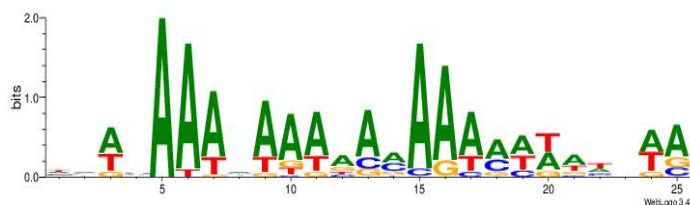


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0575935

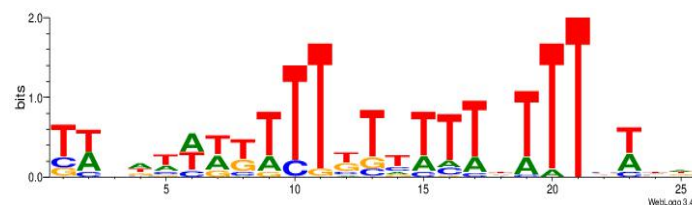
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 --HDAAATAATADD-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTTYTTTTTHTTTVWBH

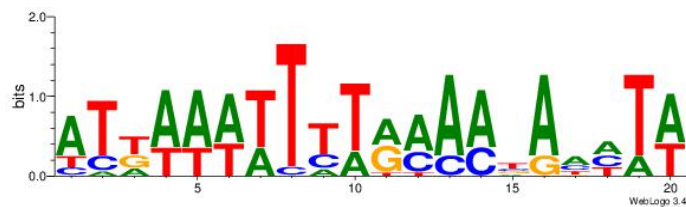


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0712963

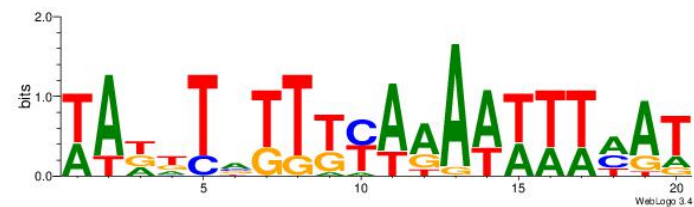
Alignment:

ATKAAWTTTTRMAABAHHTW
 -----DDTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



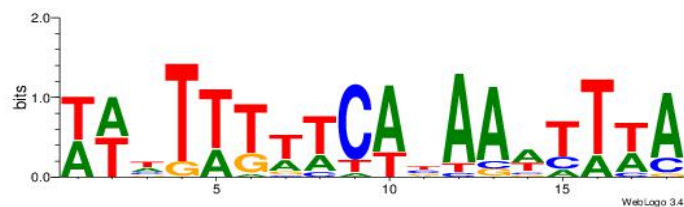
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0733516

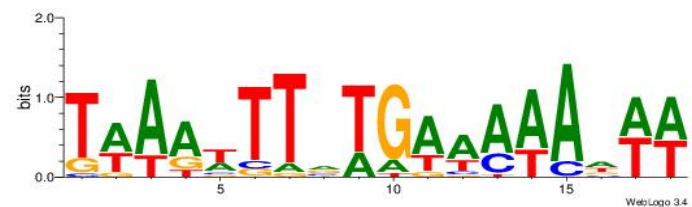
Alignment:

TWAAWTTVTGAAAAHWW
-----HDAAATAATADD

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



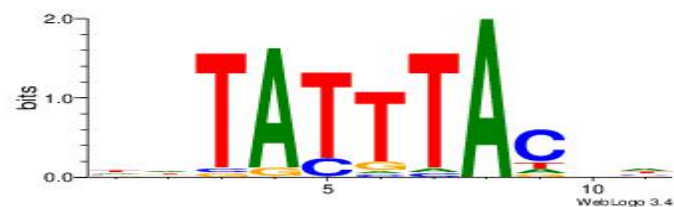
Dataset #: 2
Motif ID: 21
Motif name: wbgTAAATAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.560545

Alignment:

DHTATTTACBD-
DDTATTATTTDH

Original motif Consensus sequence: DBGTAATAHD

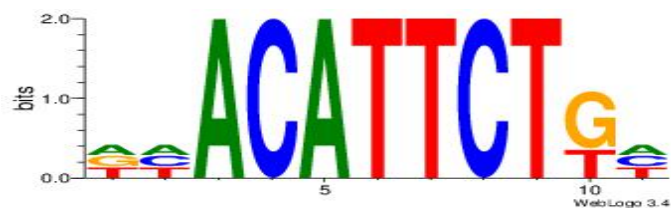
Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.583032

Alignment:
 -HCAGAAATGTHD
 DDTATTATTTDH

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAAATGTHD



Dataset #: 2
 Motif ID: 19

Motif name:	wsTACwGTAsw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.584715

Alignment:

-DBTACWGTAVH
HDAAATAATADD

Original motif Consensus sequence: HVTACWGTABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



Dataset #:	2
Motif ID:	15
Motif name:	kCAGCCAATmr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.59598

Alignment:

-MBATTGGCTGH
DDTATTATTTDH

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



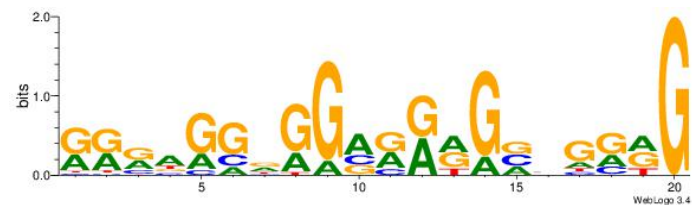
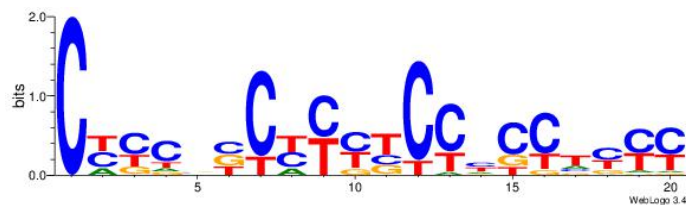
Dataset #:	1
Motif ID:	9
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	16
Number of overlap:	5
Similarity score:	3.59569

Alignment:

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

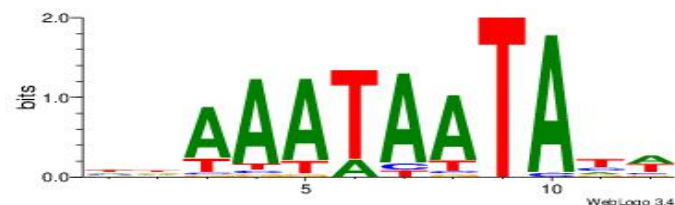
Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

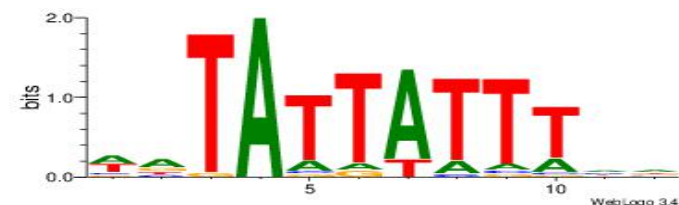


Dataset #: 2 **Motif ID: 13** **Motif name: tkAAATAATAtw**

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

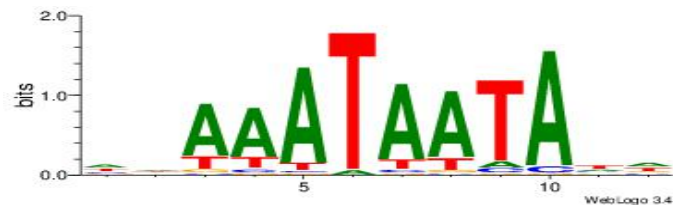


Best Matches for Significant Motif ID 13 (Highest to Lowest)

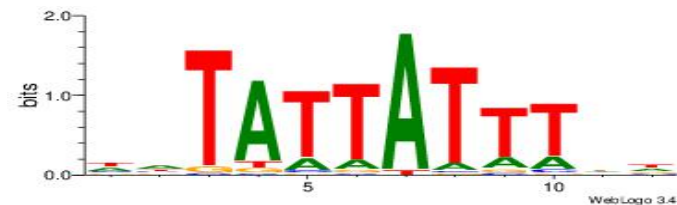
Dataset #:	2
Motif ID:	17
Motif name:	wwAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:
 HDAAATAATADD
 HDAAATAATAHW

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTDDH

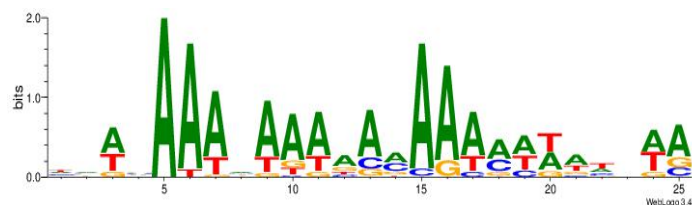


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0590505

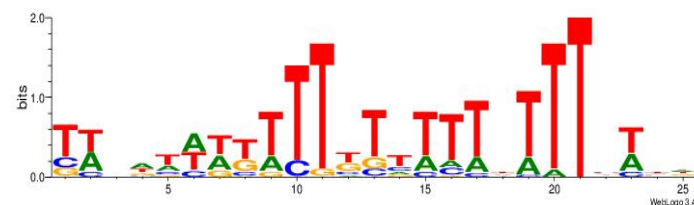
Alignment:

```
TWVHWWYTTTYYTTTTHTTTVWBH
-----WHTATTATTTDH--
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYYTTTTHTTTVWBH

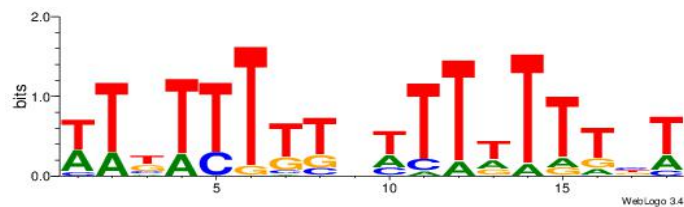


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0637702

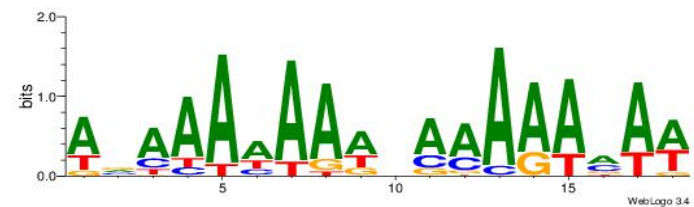
Alignment:

WKTTTTTTHWTTTTTBT
 WHTATTATTTDH-----

Original motif Consensus sequence: WKTTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

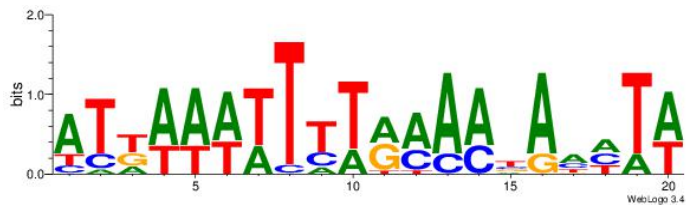


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

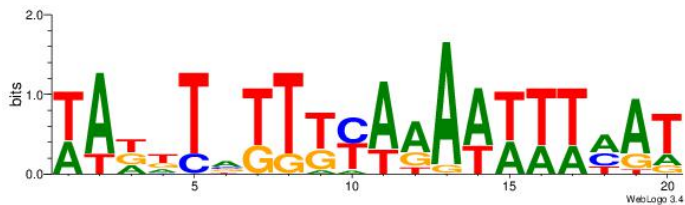
Number of overlap: 12
Similarity score: 0.0704475

Alignment:
WAHHTVTTYKAAAAWTTTRAT
HDAAATAATAHW-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



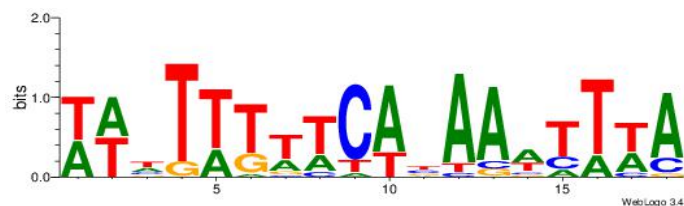
Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTTRAT



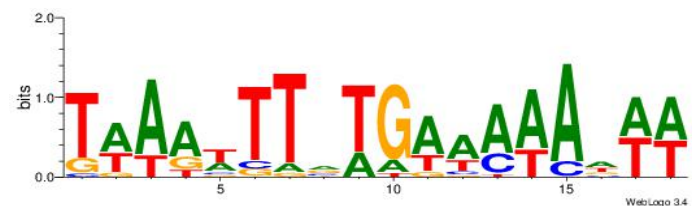
Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0763819

Alignment:
TWAAWTTVTGAAAAAHWW
-----HDAAATAATAHW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



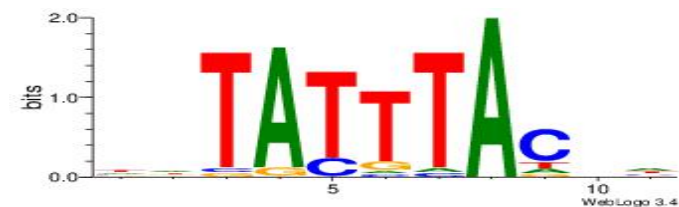
Dataset #: 2
 Motif ID: 21
 Motif name: wbgTAAATAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.560292

Alignment:
 -DBGTAAATAHD
 HDAAATAATAHW

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #: 2
 Motif ID: 19
 Motif name: wsTACwGTAsw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.587493

Alignment:

-DBTACWGTAVH
 HDAAATAATAHW

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.590271

Alignment:
-HCAGAA TGTHD
WHTATTATTTDH

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAA TGTHD



Dataset #: 2
Motif ID: 15
Motif name: kCAGCCAATmr
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.592142

Alignment:
-MBATTGGCTGH
WHTATTATTTDH

Original motif Consensus sequence: DCAGCCAATVR

Reverse complement motif Consensus sequence: MBATTGGCTGH

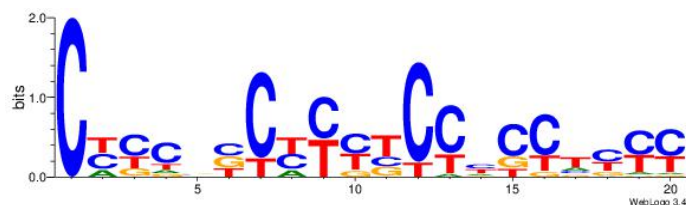


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 16
 Number of overlap: 5
 Similarity score: 3.59273

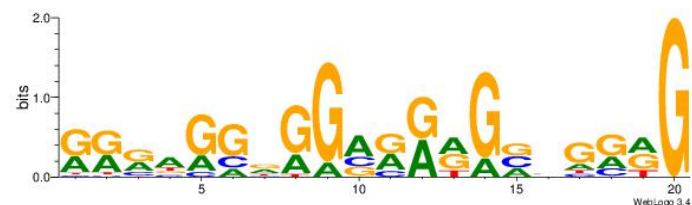
Alignment:

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

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



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

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



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

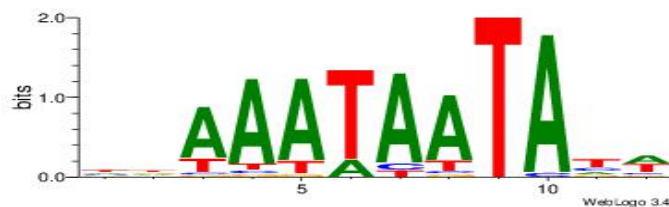
Dataset #:	2
Motif ID:	13
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0320614

Alignment:

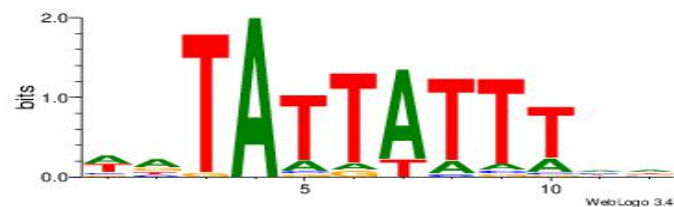
WHTATTATTTDH

-MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



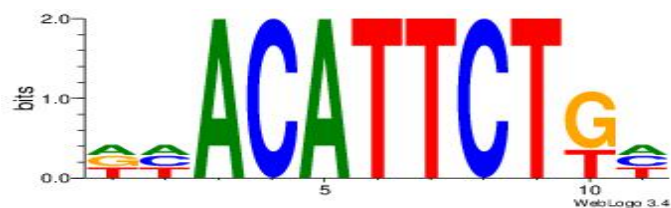
Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.034958

Alignment:

HCAGAATGTHD

DCAGCCAATVR

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

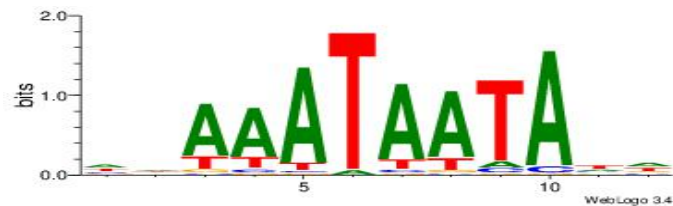


Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

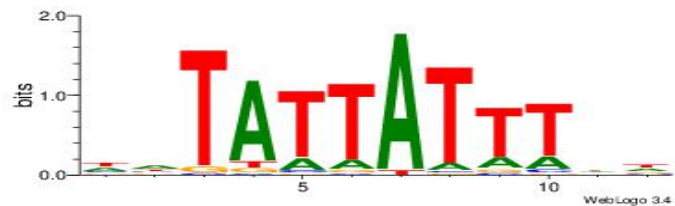
Similarity score: 0.0358988

Alignment:
DDTATTATTTDH
-MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0360892

Alignment:
BCACCTGCABC
MBATTGGCTGH

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



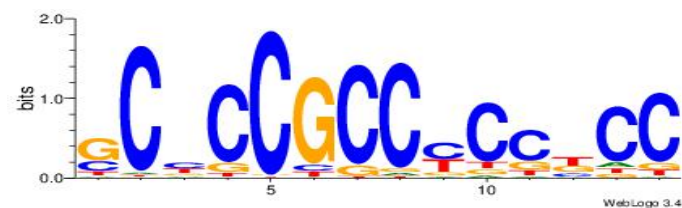
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0376063

Alignment:
 GGMGGRGGCGGVGC
 --MBATTGGCTGH--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



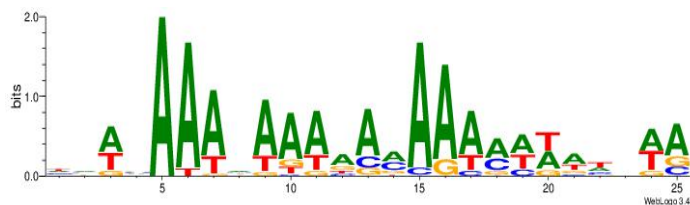
Dataset #: 1
 Motif ID: 11

Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0396371

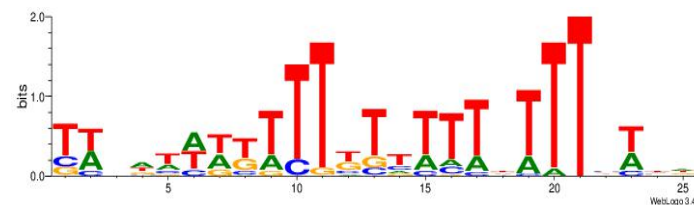
Alignment:

HDWVAAAHAAAAAAMAAAMWWWHBWA
 -----DCAGCCAATVR-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTTTTTTTHTTTVWBH



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: 2
 Number of overlap: 10
 Similarity score: 0.538109

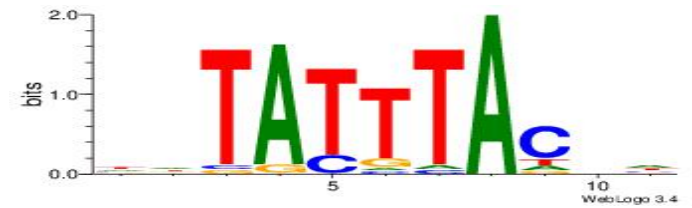
Alignment:

DHTATTTACBD-
-MBATTGGCTGH

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



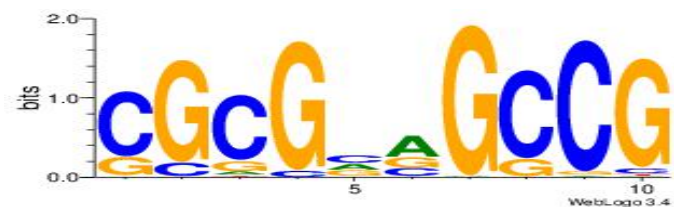
Dataset #:	1
Motif ID:	3
Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	2.01586

Alignment:

CGGCYBCGCG----
---MBATTGGCTGH

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG



Alignment:

```
RGRGGAGRRGGHGGDG-----  
-----MBATTGGCTGH
```

bits

WebLogo 3.4

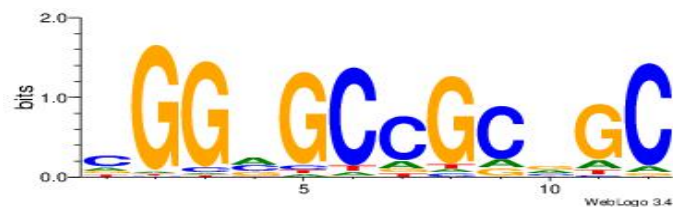
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Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 5
 Similarity score: 3

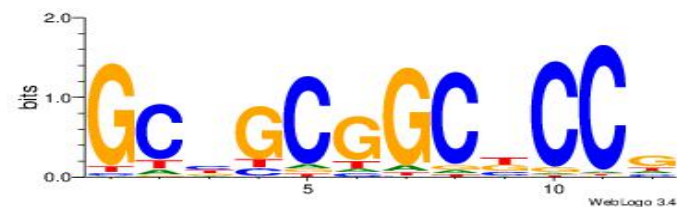
Alignment:

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

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Best Matches for Each Motif (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 Motif ID 1 (Highest to Lowest)

Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0350356

Alignment:

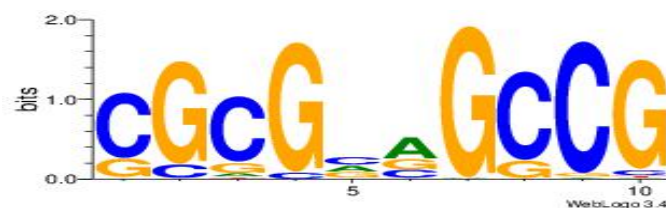
CGGCYBCGCG

----GTCGCG

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

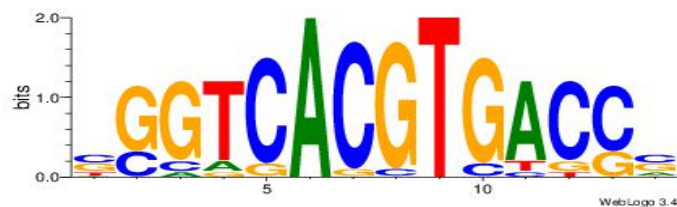


Dataset #: 2

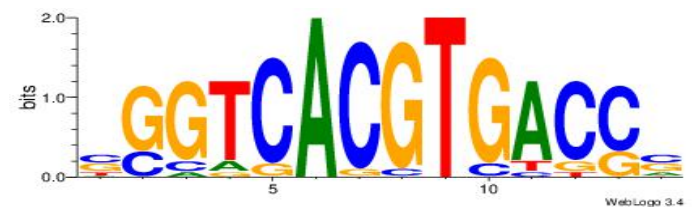
Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0375102

Alignment:
 SGGTCACGTGACCS
 --GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0381641

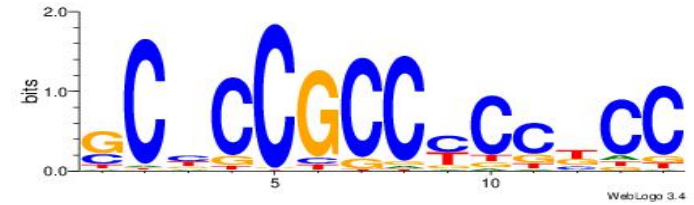
Alignment:

GCVCCGCCMCCYCC
-----CGCGAC-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



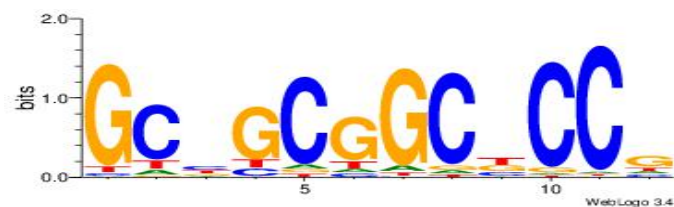
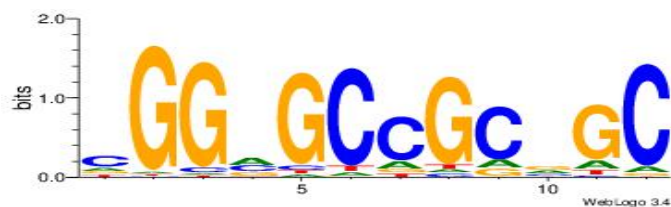
Dataset #:	1
Motif ID:	4
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0431161

Alignment:

CGGVGCCGCVGC
-----CGCGAC

Original motif Consensus sequence: CGGVGCCGCVGC

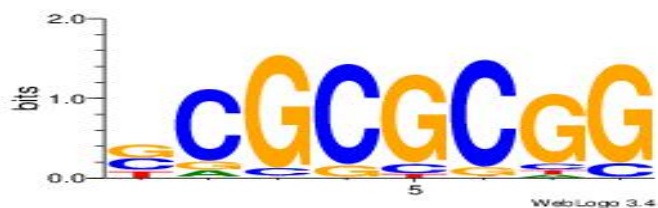
Reverse complement motif Consensus sequence: GCVGCCGCBCCG



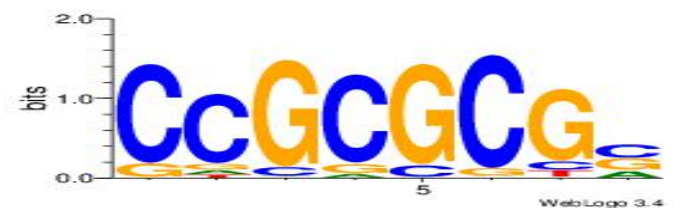
Dataset #: 1
 Motif ID: 2
 Motif name: TFW2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.052047

Alignment:
 CCGCGCGS
 -CGCGAC-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



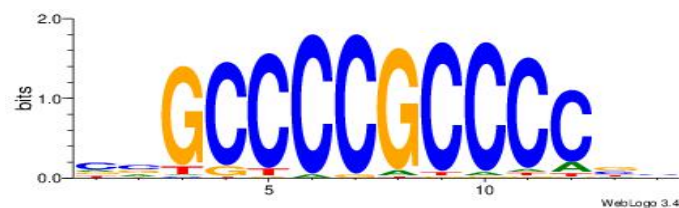
Dataset #: 2
 Motif ID: 12

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

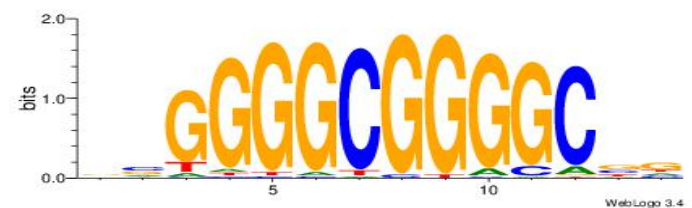
Alignment:

HVGCCCCGCCCCBB
 --GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



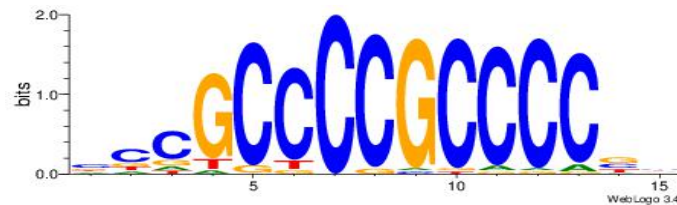
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0558733

Alignment:

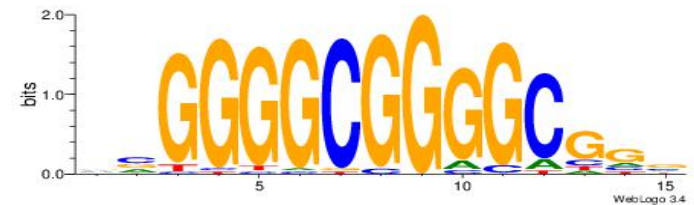
BCCGCCCCGCCCCBB

-----CGCGAC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



Dataset #:	1
Motif ID:	6
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	6
Similarity score:	0.0877631

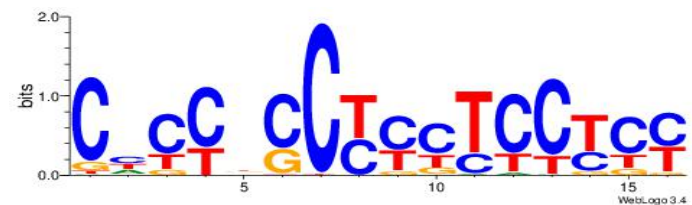
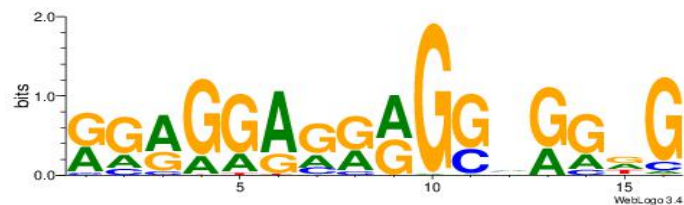
Alignment:

CHCCBCKMCTCCKCM

-----CGCGAC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM

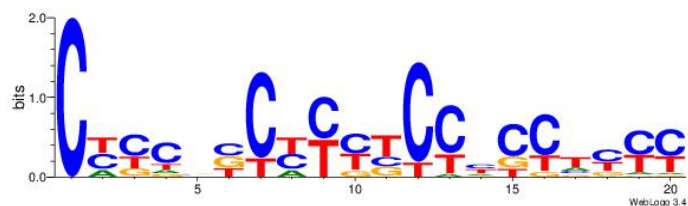


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 6
 Similarity score: 0.089121

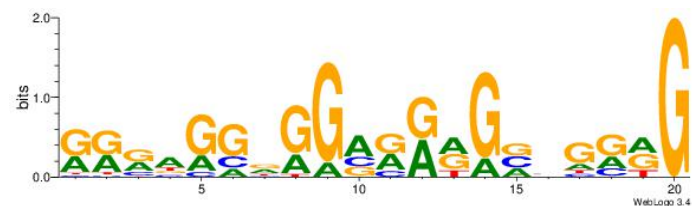
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -----GTCGCG-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



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



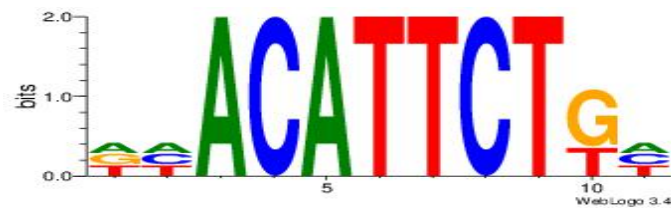
Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 4
 Similarity score: 1.09467

Alignment:

HCAGAATGTHD--

-----GTCGCG

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



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

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



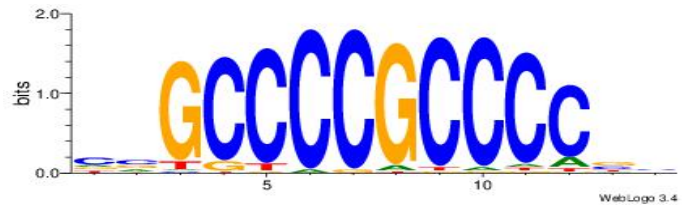
Best Matches for Motif ID 2 (Highest to Lowest)

Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6

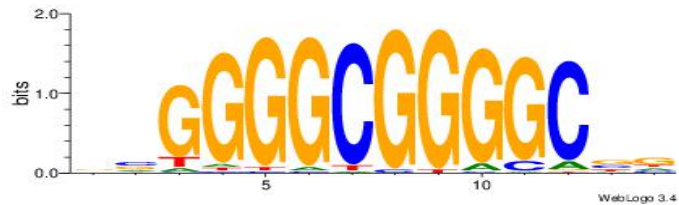
Number of overlap: 8
Similarity score: 0.0456233

Alignment:
BBGGGGCGGGGCVD
-SCGCGCGG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

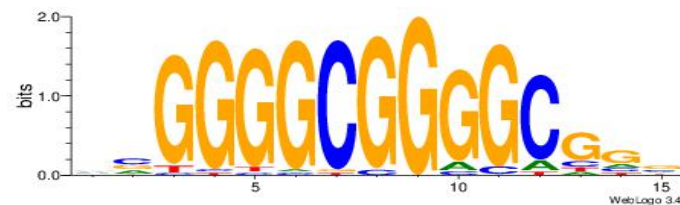
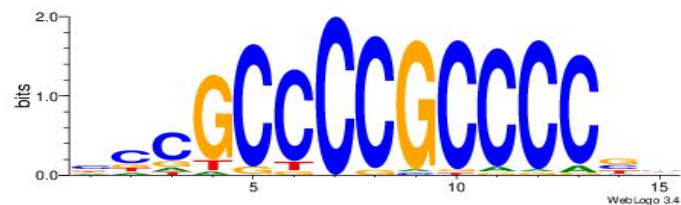


Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.045686

Alignment:
BCCGCCCCGCCCCBB
-----CCGCGCGS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB

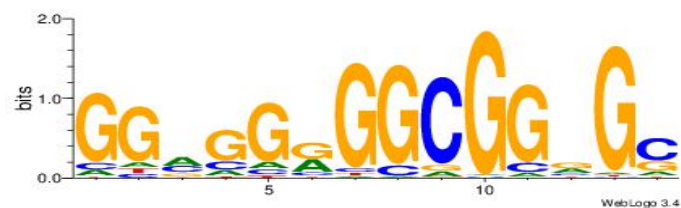
Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



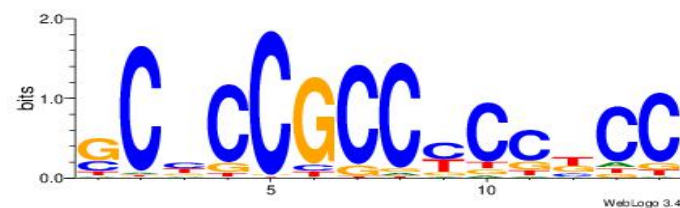
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0583967

Alignment:
 GCVCCGCCMCCYCC
 ---CCGCGCGS---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



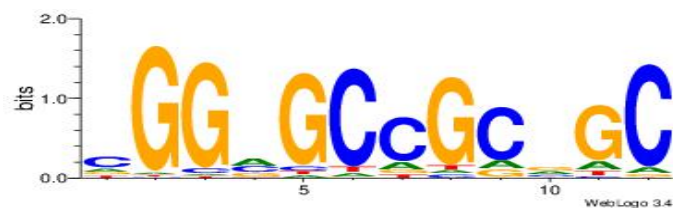
Dataset #: 1
 Motif ID: 4

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

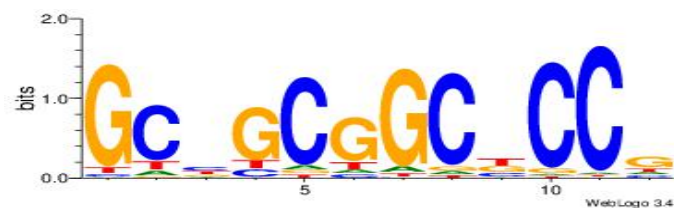
Alignment:

CGGVGCCGCVGC
 SCGCGCGG----

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #:	1
Motif ID:	3
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0906073

Alignment:

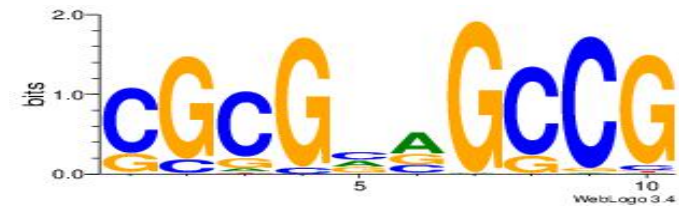
CGCGBMGCCG

--SCGCGCGG

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



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:	6
Number of overlap:	8
Similarity score:	0.0910301

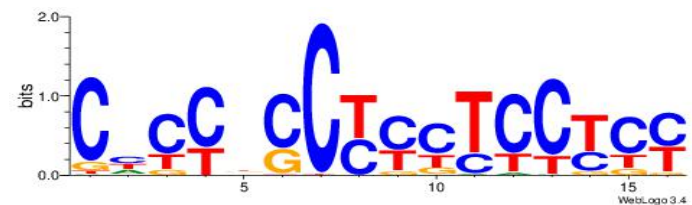
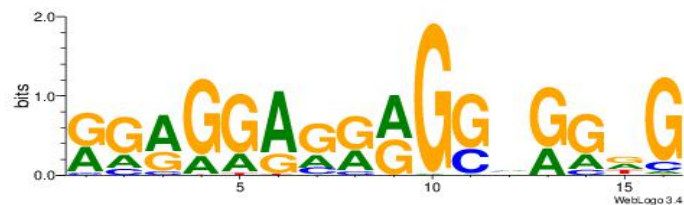
Alignment:

CHCCBCKMCTCCKCM

---CCGCGCGS-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM

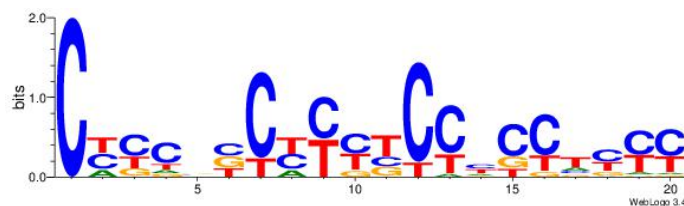


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.094473

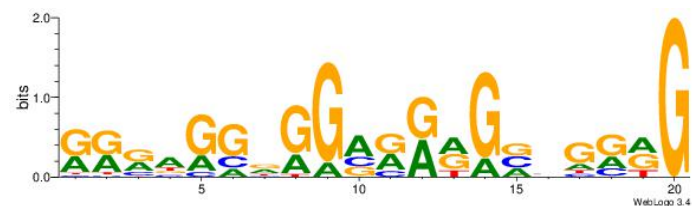
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -----SCGCGCGG----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

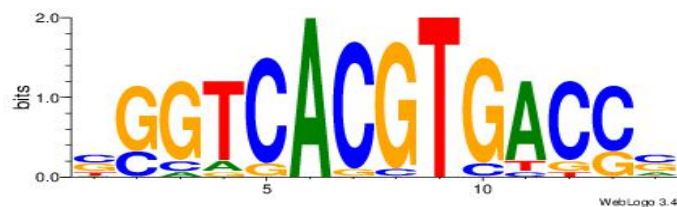


Dataset #: 2

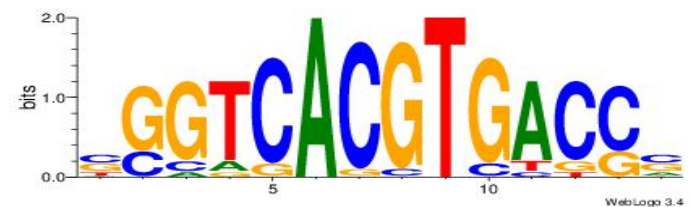
Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0988223

Alignment:
 SGGTCACGTGACCS
 ---SCGCGCGG---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 1
 Motif ID: 1
 Motif name: TFW1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 5
 Similarity score: 1.5088

Alignment:

GTCGCG---

-SCGCGCGG

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



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

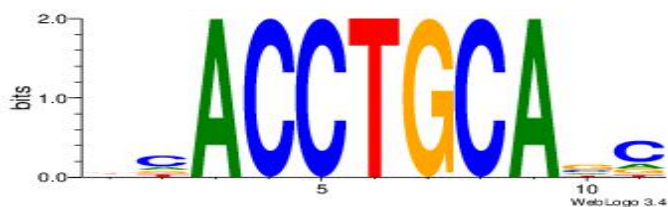
Alignment:

----GBTGCAGGTGB

SCGCGCGG-----

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



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

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

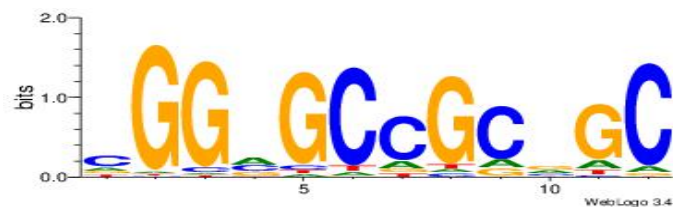


Best Matches for Motif ID 3 (Highest to Lowest)

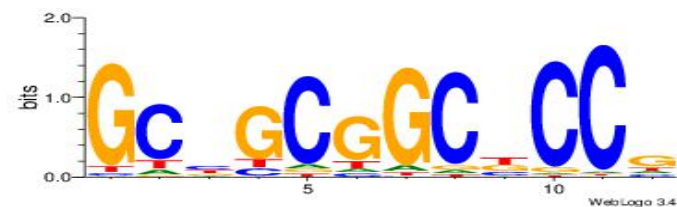
Dataset #:	1
Motif ID:	4
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0623879

Alignment:
 CGGVGCCGCVGC
 CGGCYBCGCG--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG

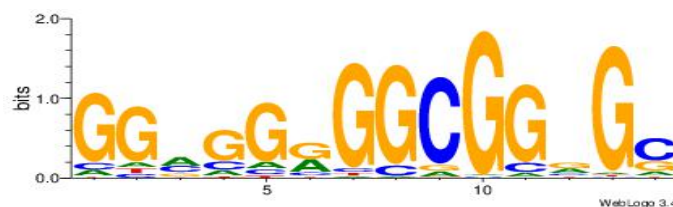


Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0645308

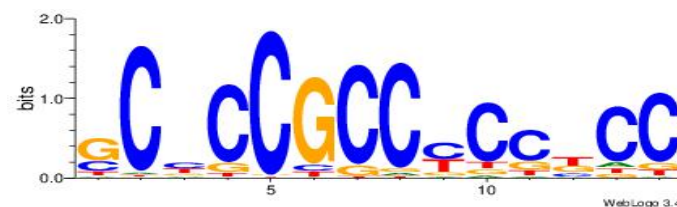
Alignment:

GGMGGRGGCGGVGC
 CGCGBMGCCG-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

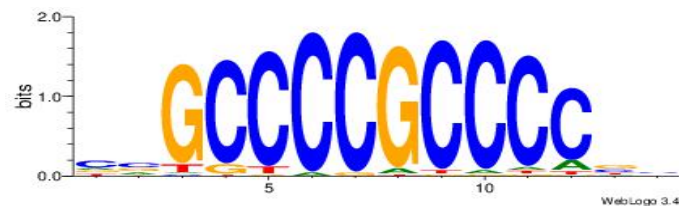


Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0718771

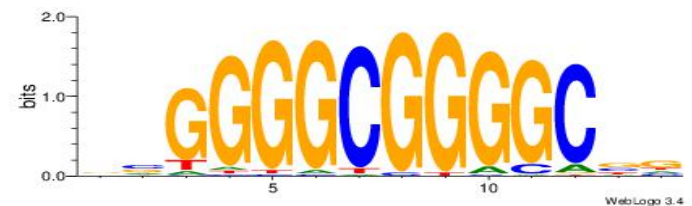
Alignment:

HVGCCCCGCCCCBB
 CGGCYBCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

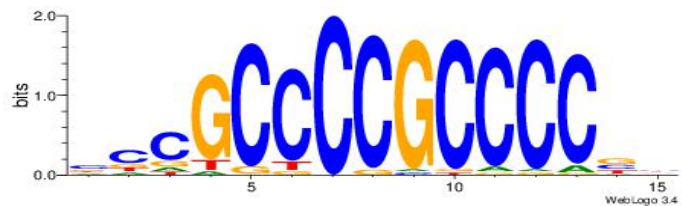


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10

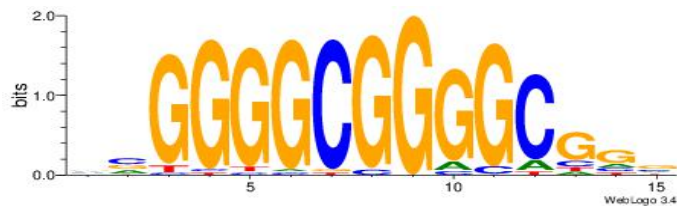
Similarity score: 0.0719604

Alignment:
BCCGCCCCGCCCCBB
-CGGCYBCGCG----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

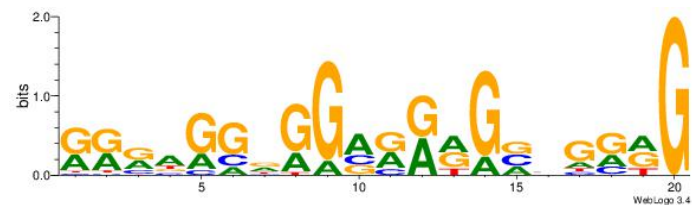
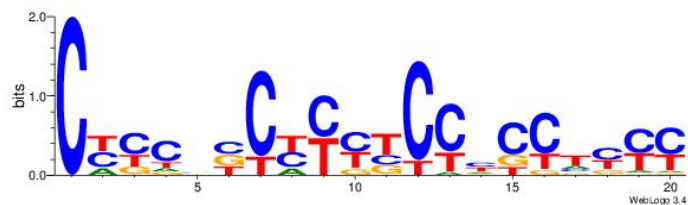


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0767689

Alignment:
KKKAGGDGGAKKMGBBGKMG
-----CGCGBMGCCG

Original motif Consensus sequence: CYCBBCYYYYTCCHCCTYYY

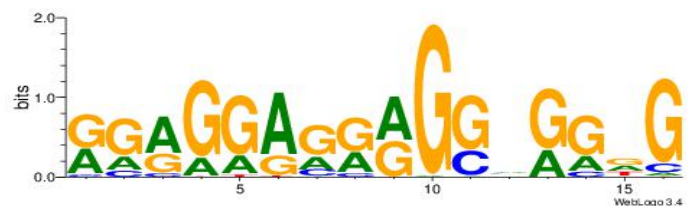
Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



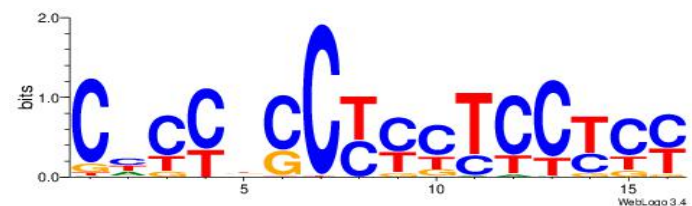
Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0814831

Alignment:
 CHCCBCCKMCTCCKCM
 CGGCYBCGCG-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



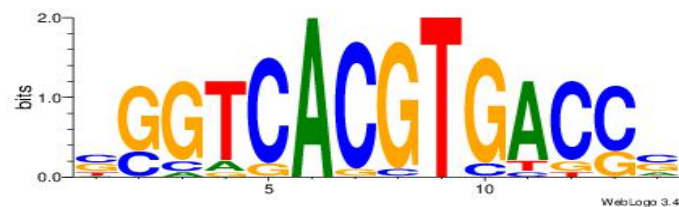
Dataset #: 2

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

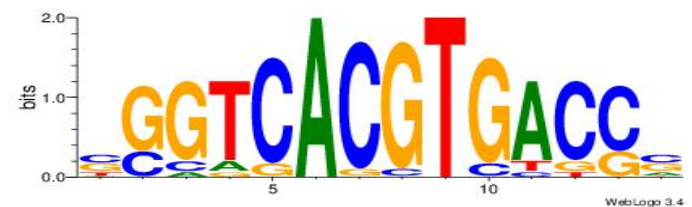
Alignment:

```
SGGTCACGTGACCS
----CGCGBMGCCG
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #:	1
Motif ID:	2
Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	1.09499

Alignment:

--CCGCGCGS
CGGCYBCGCG

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



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

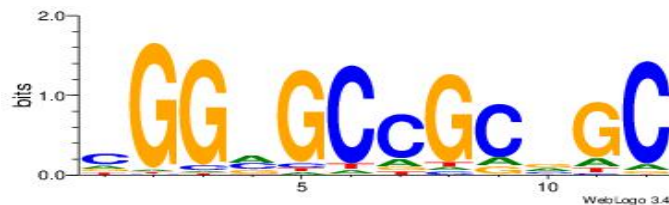


Reverse complement motif Consensus sequence: MBATTGGCTGH

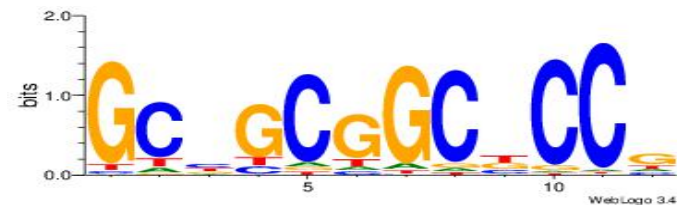


Dataset #: 1 Motif ID: 4 Motif name: TFF1

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #:	1
Motif ID:	5
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.0292081

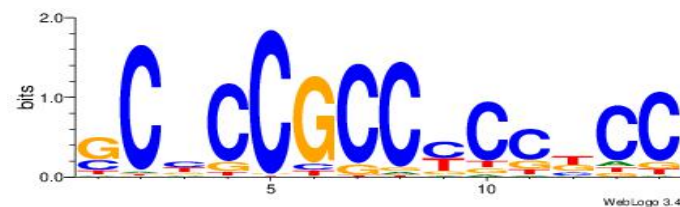
Alignment:

```
GGMGGRGGCGGVGC
--CGGVGCCGCVGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

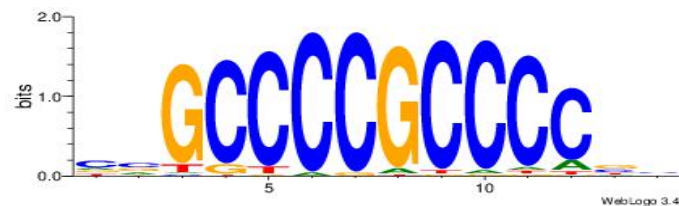


Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0542674

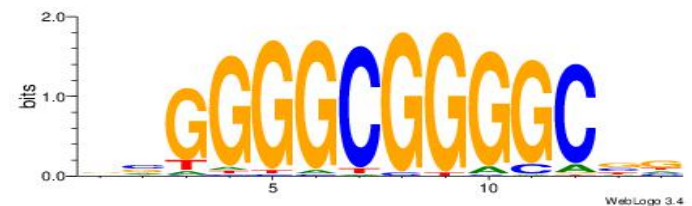
Alignment:

HVGCCCCGCCCCBB
 CGGVGCCGCVGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

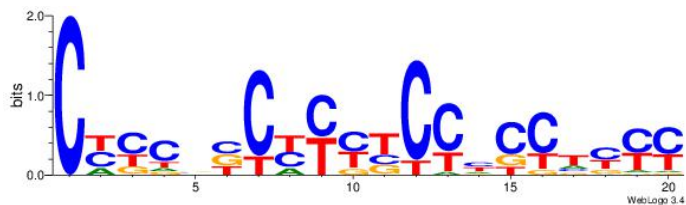


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12

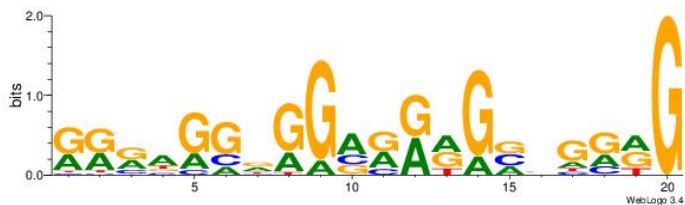
Similarity score: 0.0543272

Alignment:
KKKAGGDGGAKKMGBBGKMG
-----CGGVGCCGCVGC--

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

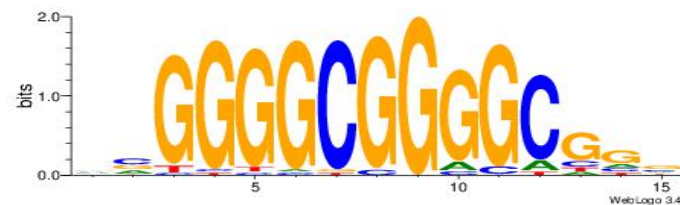
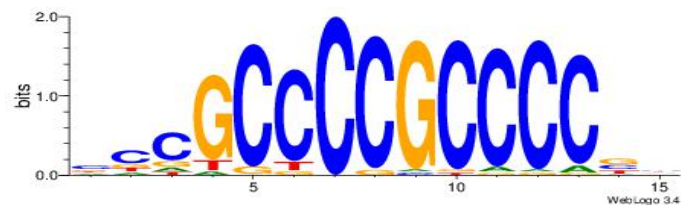


Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0548371

Alignment:
BCCGCCCCGCCCCBB
---GCVGCGGCBCCG

Original motif Consensus sequence: BCCGCCCCGCCCCBB

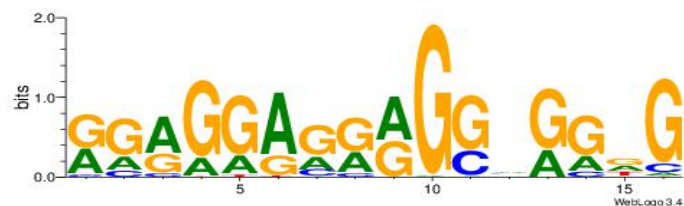
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



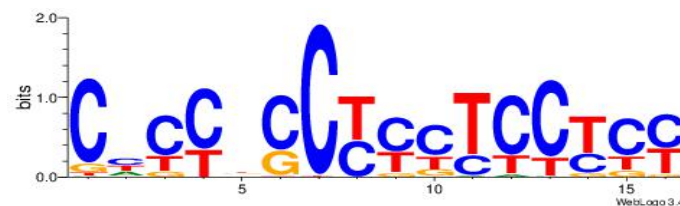
Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0594165

Alignment:
 CHCCBCKMCTCCKCM
 --GCVGCGGCBCCG--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



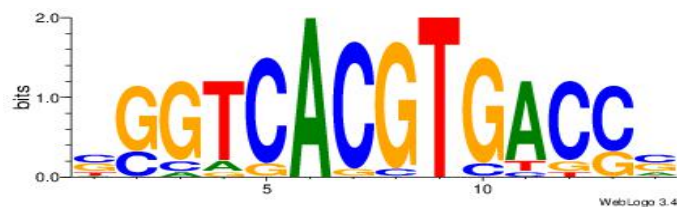
Dataset #: 2

Motif ID: 18
 Motif name: sSGTCACGTGACSS
 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

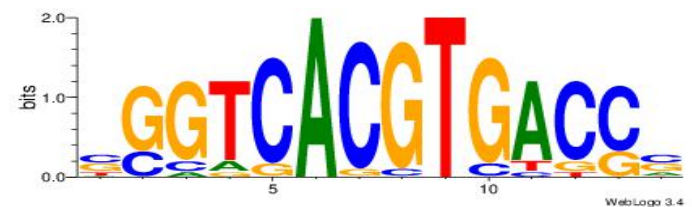
Alignment:

SGGTCACGTGACCS
 --GCVGCGGCBCCG

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 1.04219

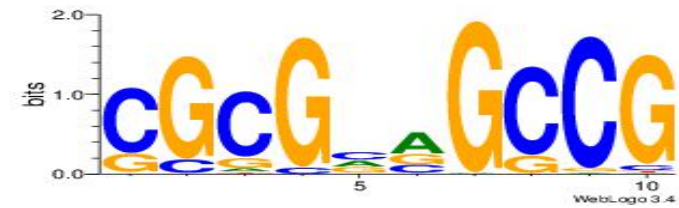
Alignment:

CGGCYBCGCG--
CGGVGCCGCVGC

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



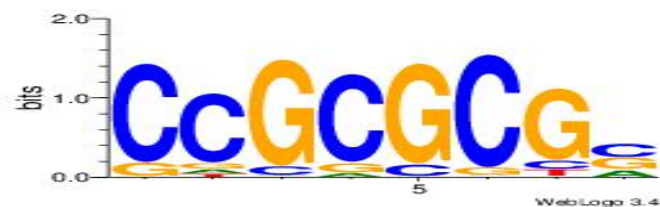
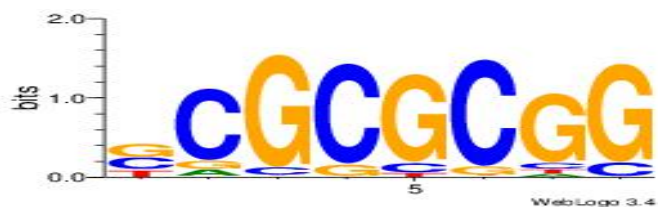
Dataset #:	1
Motif ID:	2
Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	2.04515

Alignment:

SCGCGCGG----
CGGVGCCGCVGC

Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS

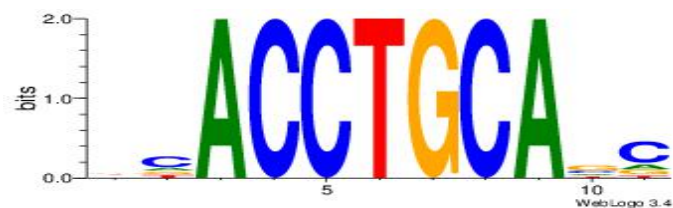


Dataset #: 2
 Motif ID: 16
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 2.08028

Alignment:

----GBTGCAGGTGB
 CGGVGCCGCVGC---

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 1
 Motif ID: 1

Motif name: TFW1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 3.02292

Alignment:

-----GTCGCG
 GCVGCGGCBCCG

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC

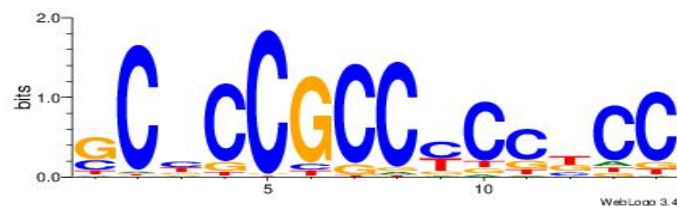


Dataset #: 1 Motif ID: 5 Motif name: TFF11

Original motif Consensus sequence: GGMGRRGGCGGVC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



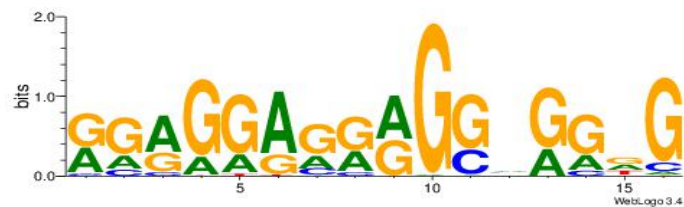
Best Matches for Motif ID 5 (Highest to Lowest)

Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.033716

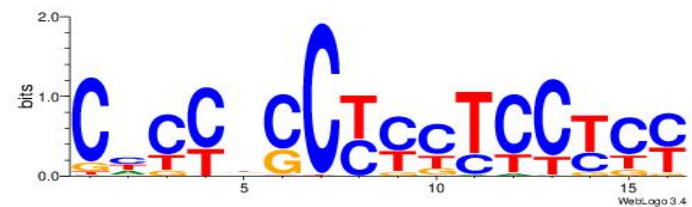
Alignment:

RGRGGAGRRGGHGGDG
 GGMGGRGGCGGVGC--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

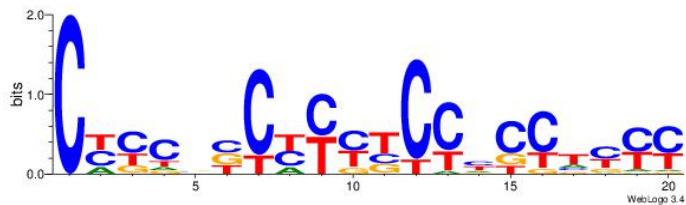


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6

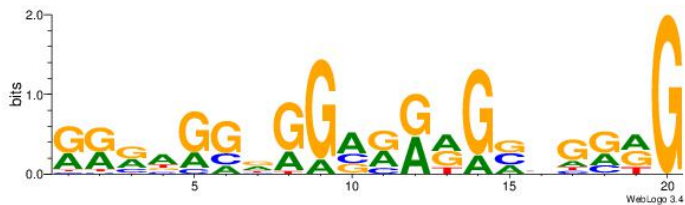
Number of overlap: 14
Similarity score: 0.0386905

Alignment:
CYYCBBCYYYYTCCHCCTYYY
-----GCVCCGCCMCCYCC-

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



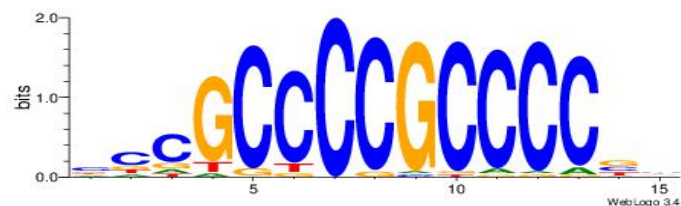
Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



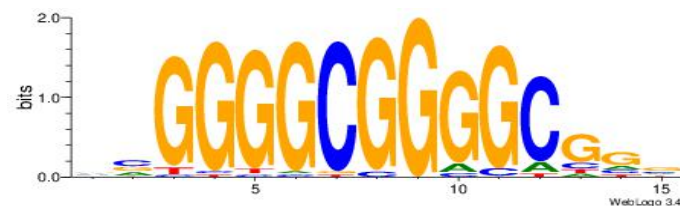
Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0548198

Alignment:
BCCGCCCCGCCCCBB
GCVCCGCCMCCYCC-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

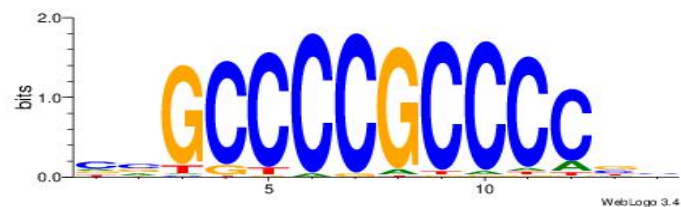


Dataset #: 2
Motif ID: 12
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0652173

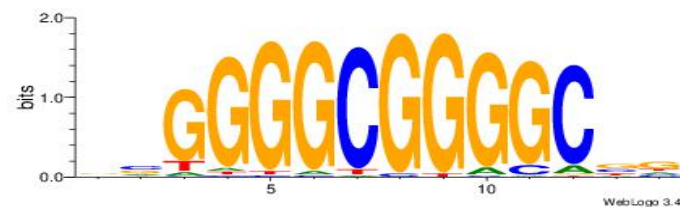
Alignment:

HVGCCCCGCCCCBB
GCVCCGCCMCCYCC

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

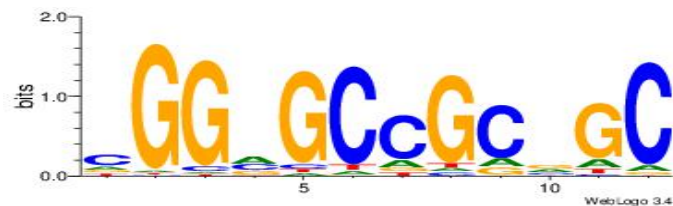


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.02659

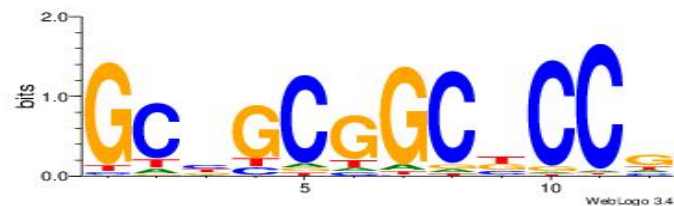
Alignment:

--CGGVGCCGCVGC
 GGMGGRGGCGGVGC

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

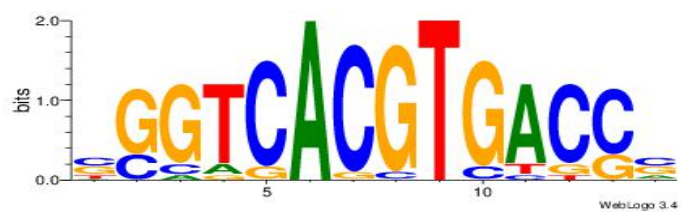


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 12

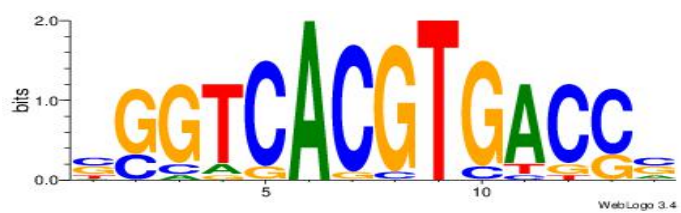
Similarity score: 1.07325

Alignment:
SGGTCACGTGACCS--
--GCVCCGCCMCCYCC

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: 1
Number of overlap: 11
Similarity score: 1.56524

Alignment:
BCACCTGCABC---
GCVCCGCCMCCYCC

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



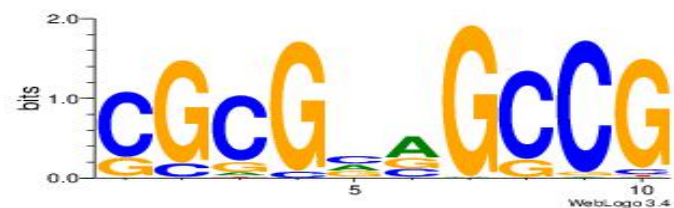
Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 2.04171

Alignment:
 CGGCYBCGCG-----
 GCVCCGCCMCCYCC

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



Dataset #: 1
 Motif ID: 2

Motif name: TFW2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 3.06679

Alignment:

-----CCGCGCGS
 GCVCCGCCMCCYCC

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



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: 4.05705

Alignment:

CGCGAC-----
GGMGGRGGCGGVGC

Original motif Consensus sequence: GTCGCG

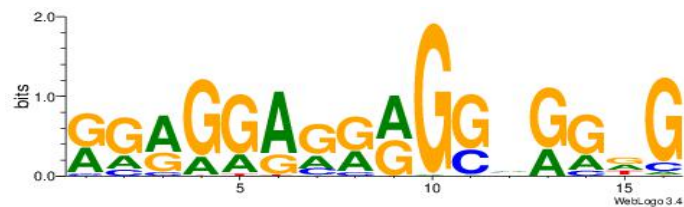


Reverse complement motif Consensus sequence: CGCGAC

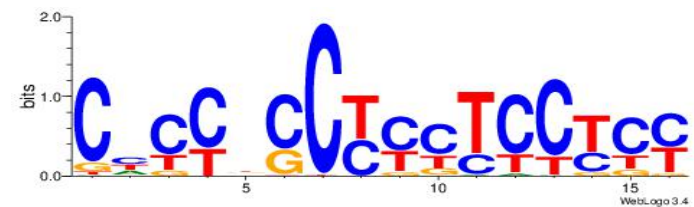


Dataset #: 1 Motif ID: 6 Motif name: TFM2

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



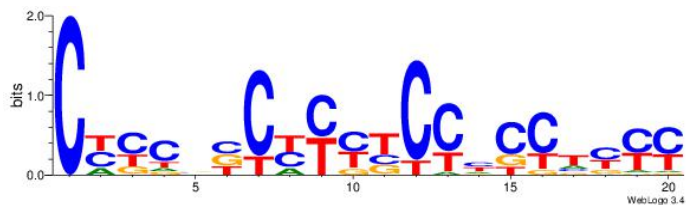
Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	1
Motif ID:	9
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward

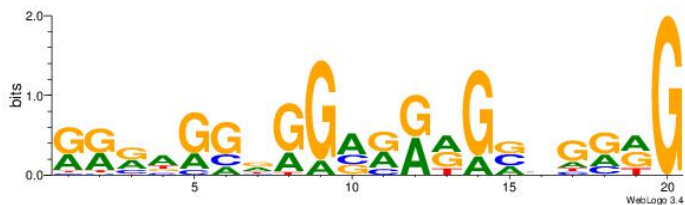
Position number: 1
Number of overlap: 16
Similarity score: 0.0331473

Alignment:
CYYCBBCYYYYTCCHCCTYYY
CHCCBCKMCTCCKCM-----

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



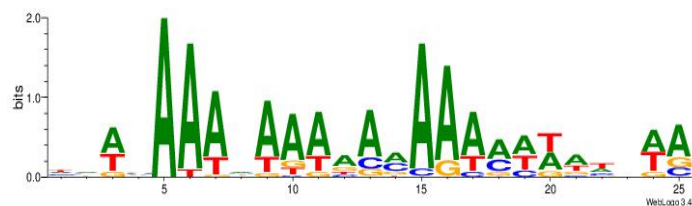
Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



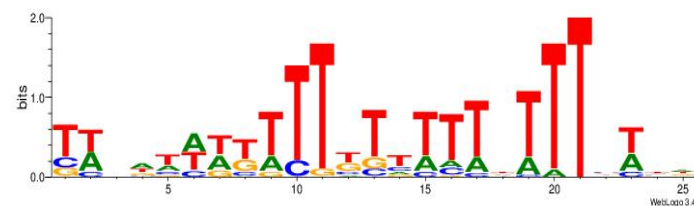
Dataset #: 1
Motif ID: 11
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 16
Similarity score: 0.0794752

Alignment:
HDWVAAAHA AAAAAMAAAMWWWHBWA
-----RGRGGAGRRGGHGGDG--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH

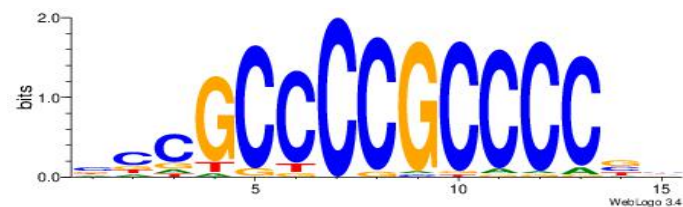


Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.558405

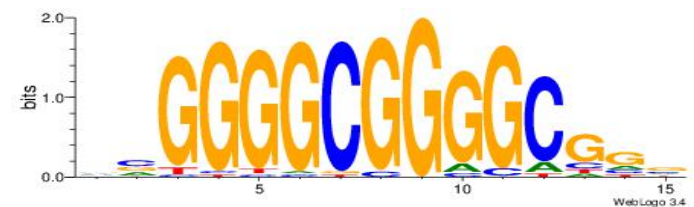
Alignment:

BBGGGGCGGGGCGGB-
RGRGGAGRRGGHGGDG

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

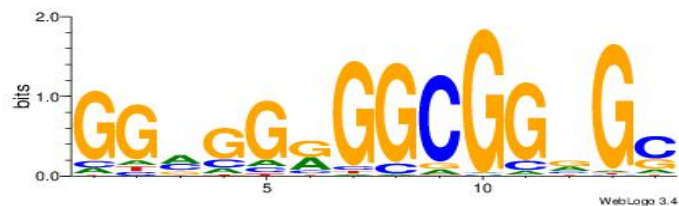


Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 1.03372

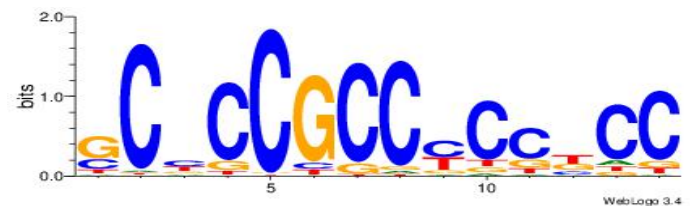
Alignment:

GGMGGRGGCGGVGC--
 RGRGGAGRRGGHGGDG

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

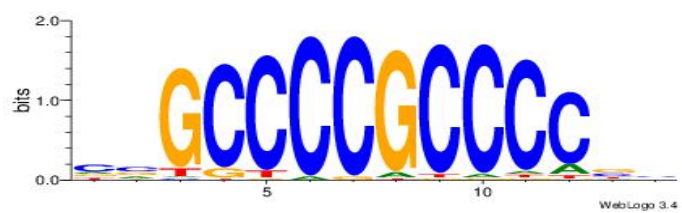


Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14

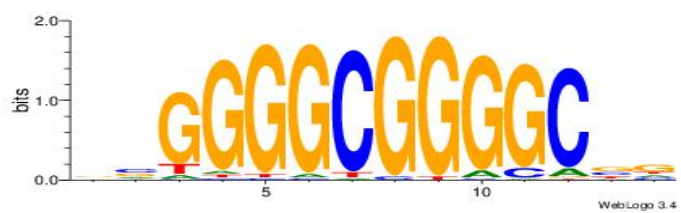
Similarity score: 1.05955

Alignment:
BBGGGGCGGGGCVD--
RGRGGAGRRGGHGGDG

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

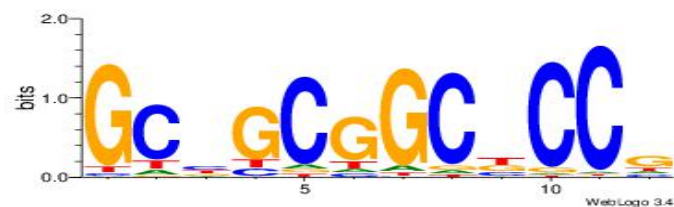
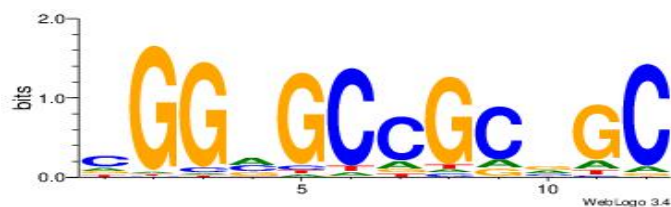


Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 2.07381

Alignment:
GCVGCGGCBCCG----
RGRGGAGRRGGHGGDG

Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 3.05867

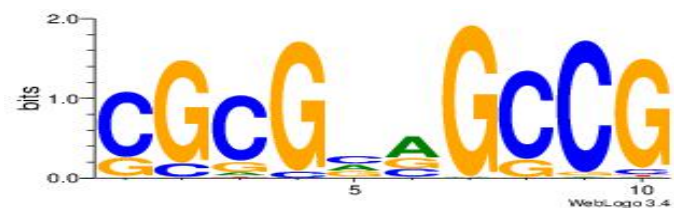
Alignment:

CGCGBMGCCG-----
 RGRGGAGRRGGHGGDG

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



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:	2
Number of overlap:	10
Similarity score:	3.07248

Alignment:

```

BCACCTGCABC-----
-CHCCBCKMCTCCKCM

```

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

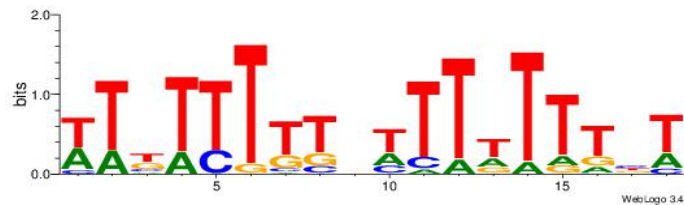


Dataset #:	1
Motif ID:	7
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	10
Number of overlap:	9
Similarity score:	3.57029

Alignment:

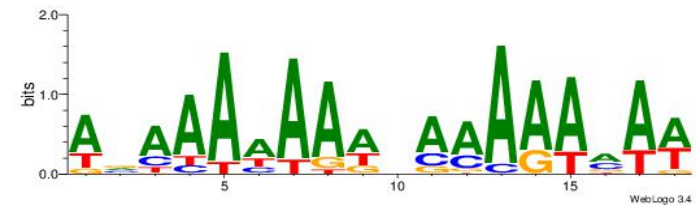
```
ABAAAAAWhAAAAARAW-----  
-----RGRGGAGRRGGHGGDG
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif
ABAAAAAWhAAAAARAW

Consensus sequence:



Dataset #:	1
Motif ID:	8
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	10
Number of overlap:	9
Similarity score:	3.57686

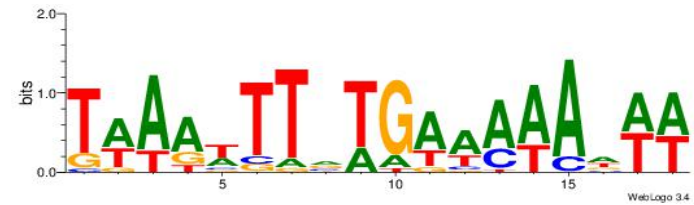
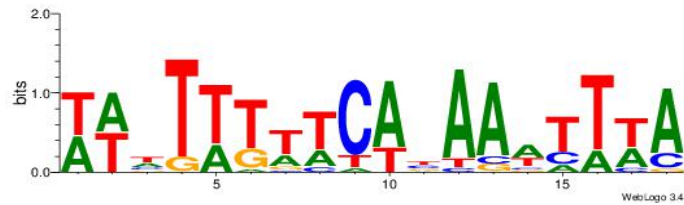
Alignment:

```
TWAAWTTVTGAAAAHWW-----  
-----RGRGGAGRRGGHGGDG
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

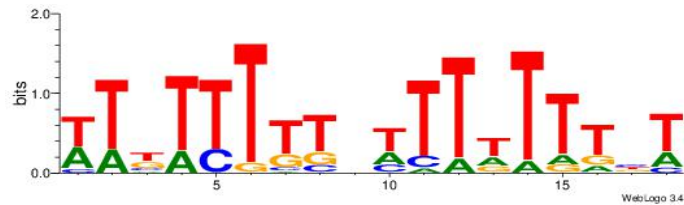
Reverse complement motif
TWAAWTTVTGAAAAHWW

Consensus sequence:

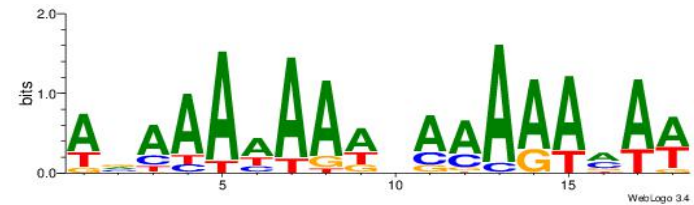


Dataset #: 1 Motif ID: 7 Motif name: TFM1

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAA WHAAAAA RAW



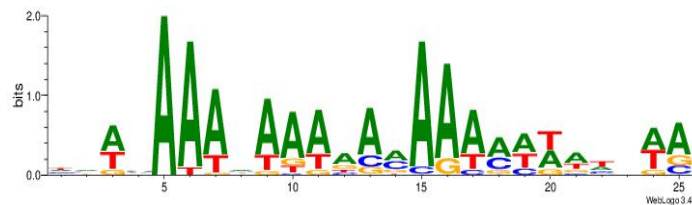
Best Matches for Motif ID 7 (Highest to Lowest)

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:	6
Number of overlap:	18
Similarity score:	0

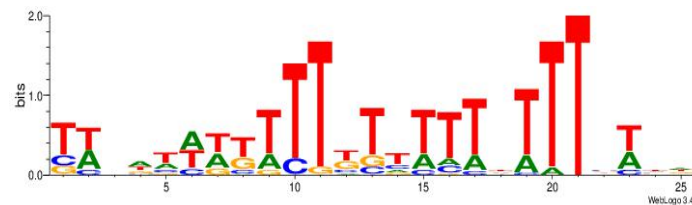
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 --ABAAAAAWHAAAAARAW-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTTYTTTTHTTTVWBH

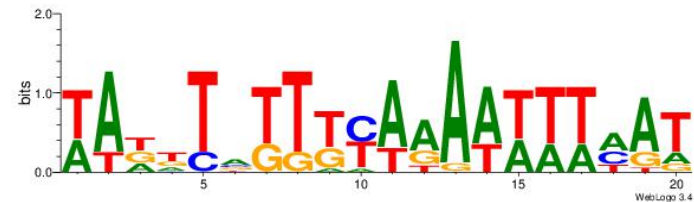
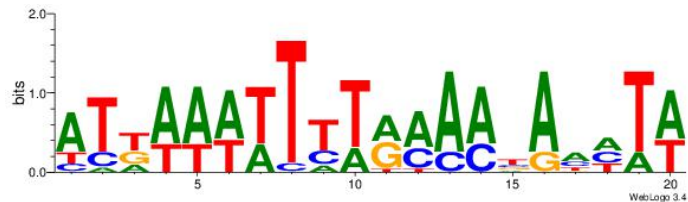


Dataset #:	1
Motif ID:	10
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	18
Similarity score:	0.0364672

Alignment:
 ATKAAWTTTTRMAABAHHTW
 ABAAAAAWHAAAAARAW--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence:
 WAHHTVTTYKAAAATTRAT

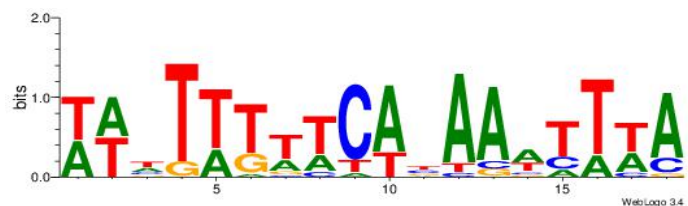


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0456974

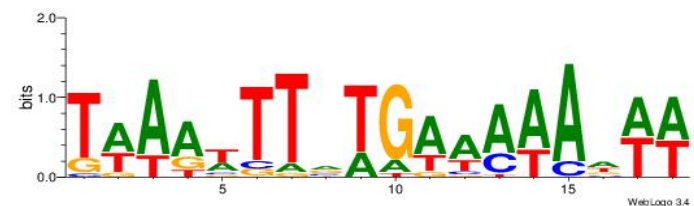
Alignment:

WWHTTTTTTCABAAWTTWA
 WTKTTTTTHWTTTTTTBT

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



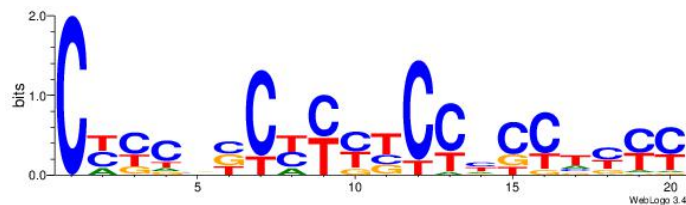
Dataset #: 1

Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.572783

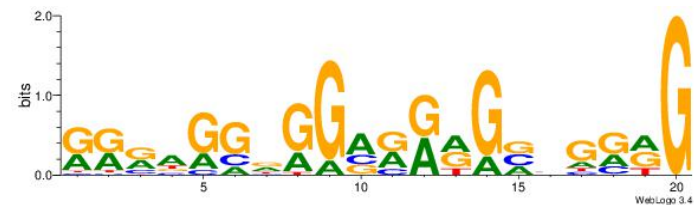
Alignment:

CYYCBBCYYYTCCHCCTYYY-
 ---WTKTTTTTTHWTTTTTBT

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

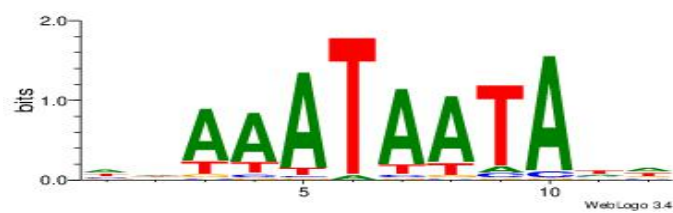


Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12

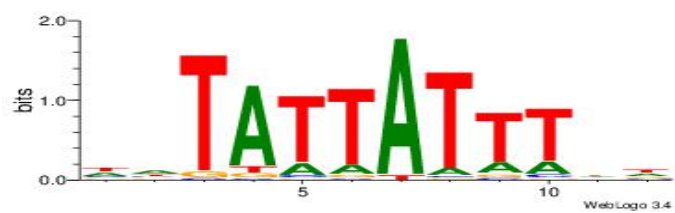
Similarity score: 3.0279

Alignment:
-----DDTATTATTTDH
WTKTTTTTHWTTTTTTBT

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

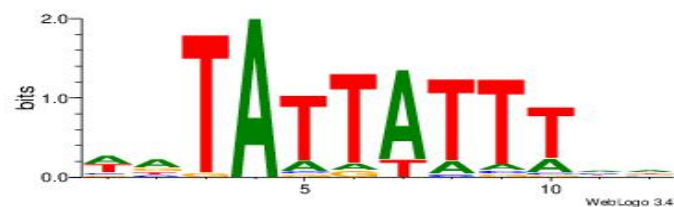
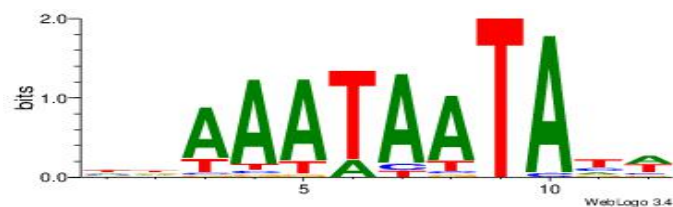


Dataset #: 2
Motif ID: 13
Motif name: tkAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 3.0351

Alignment:
HDAAATAATAHW-----
ABAAAAAWhAAAAARAW

Original motif Consensus sequence: HDAAATAATAHW

Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #: 2
 Motif ID: 21
 Motif name: wbgTAAATAww
 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: 3.54371

Alignment:

DBGTAATAHD-----
 ABAAAAAWhAAAAARAW

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #: 2
 Motif ID: 20

Motif name:	dhACATTCTkh
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	4.06154

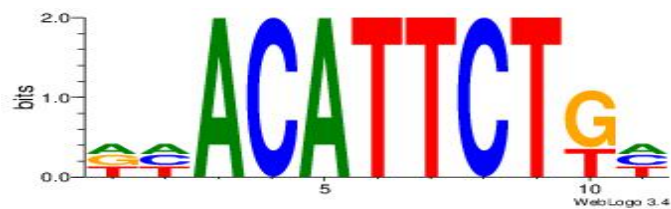
Alignment:

```

-----HCAGAATGTHD
ABAAAAAWhAAAAARAW-

```

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

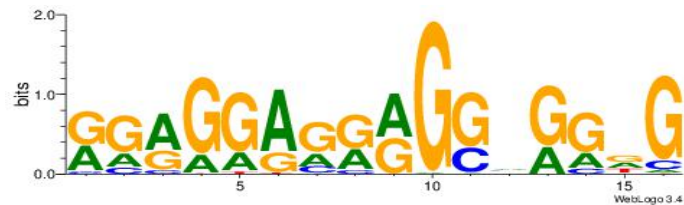


Dataset #:	1
Motif ID:	6
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	9
Similarity score:	4.56306

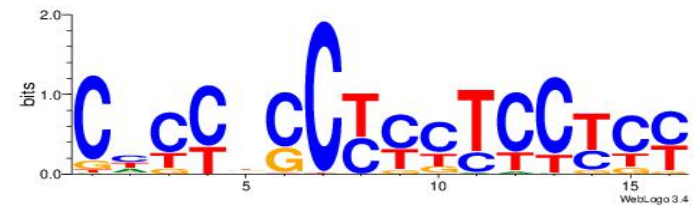
Alignment:

-----CHCCBCKMCTCCKCM
WTKTTTTTHWTTTTTTBT-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM



Dataset #:	2
Motif ID:	19
Motif name:	wsTACwGTAsw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	4.57253

Alignment:

-----HVTACWGATABD
ABAAAAAAWHAAAAARAW--

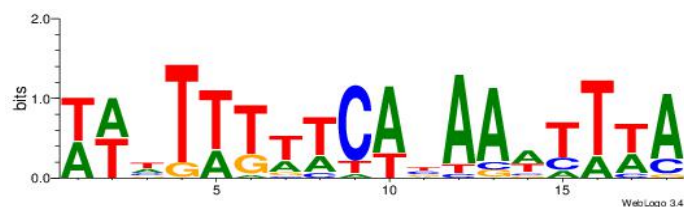
Original motif Consensus sequence: HVTACWGATABD

Reverse complement motif Consensus sequence: DBTACWGTAHVH

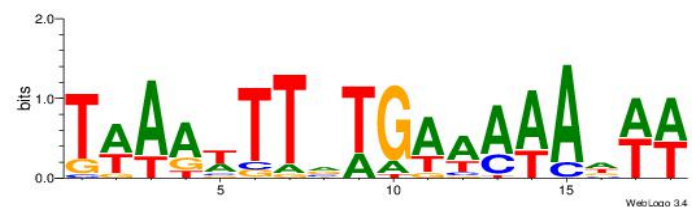


Dataset #: 1 Motif ID: 8 Motif name: TFM3

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



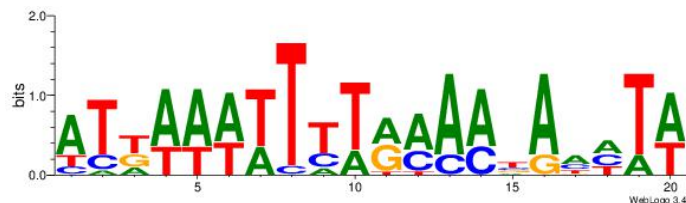
Best Matches for Motif ID 8 (Highest to Lowest)

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:	2
Number of overlap:	18
Similarity score:	0.00833981

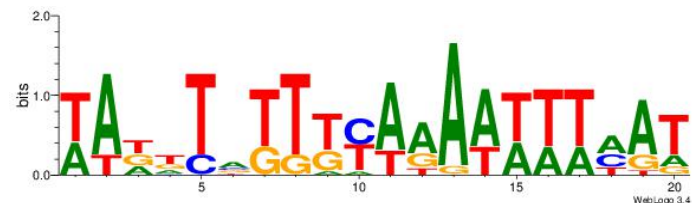
Alignment:

ATKAAWTTTTRMAABAHHTW
 -TWAAWTTVTGAAAAHWW-

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



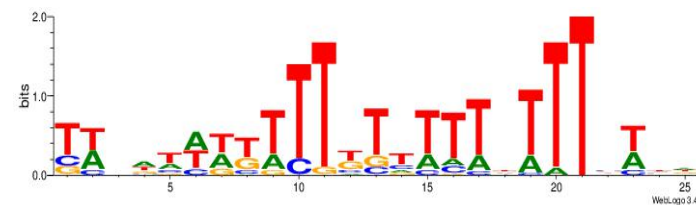
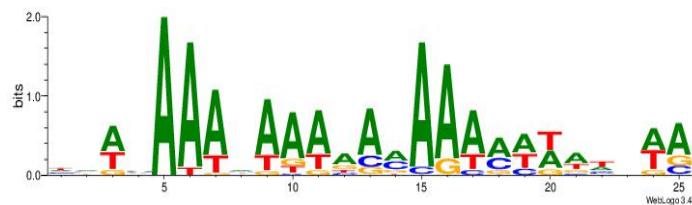
Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	18
Similarity score:	0.0346965

Alignment:

```
TWVHWWYTTTYTTTTHTTTVWBH
----WWHTTTTTCABAAWTTWA----
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTHTTTVWBH

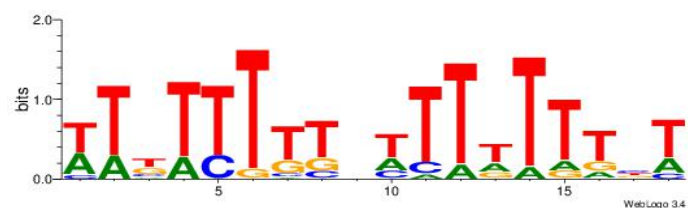


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0376845

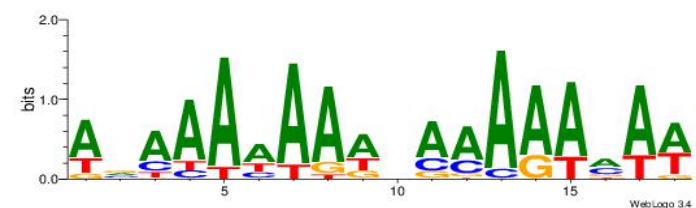
Alignment:

WTKTTTTTHWTTTTTTBT
 WWHTTTTTTCABAAWTTWA

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



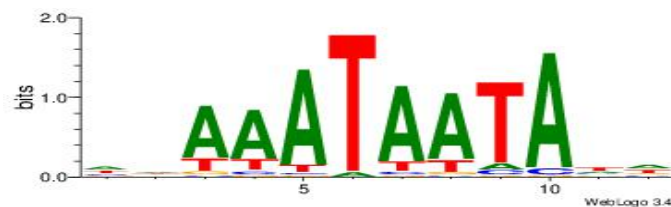
Dataset #: 2

Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 3.03666

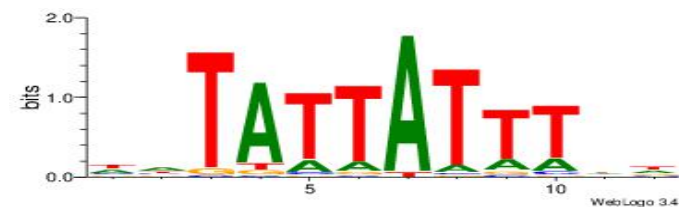
Alignment:

-----DDTATTATTDDH
 WWHTTTTTTCABAAWTTWA

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTDDH

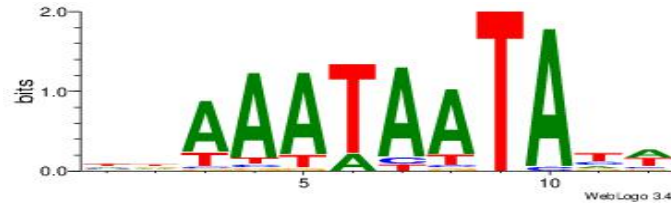


Dataset #: 2
 Motif ID: 13
 Motif name: tkAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 3.0397

Alignment:

```
-----WHTATTATTDDH
WWHTTTTTTCABAAWTTWA
```

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH



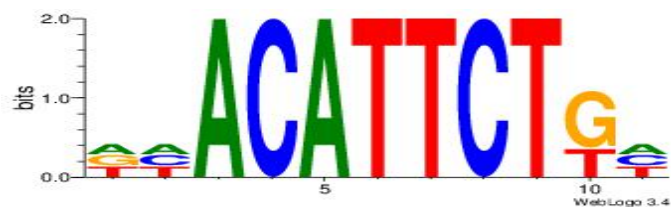
Dataset #:	2
Motif ID:	20
Motif name:	dhACATTCTkh
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	3.53885

Alignment:

```
DHACATTCTGH-----
TWAAWTTVTGAAAAHWW
```

Original motif Consensus sequence: DHACATTCTGH

Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 2
 Motif ID: 21
 Motif name: wbgTAAATAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 3.54165

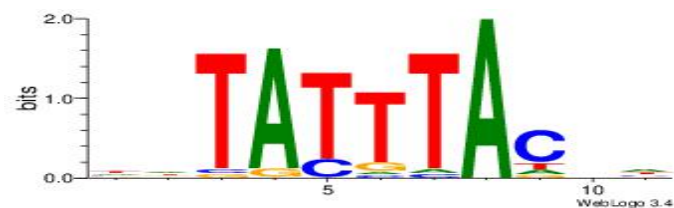
Alignment:

-----DBGTAAATAHD
 WWHTTTTTCABAAWTTWA

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #: 1
 Motif ID: 6

Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	9
Similarity score:	4.56162

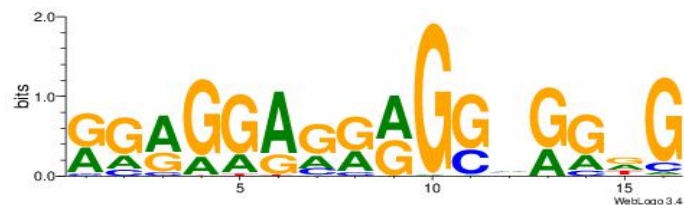
Alignment:

```

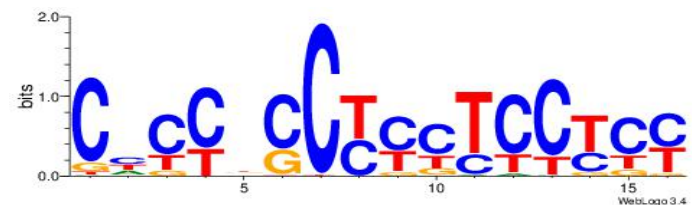
-----CHCCBCKMCTCCKCM
WWHTTTTTCABAAWTTWA-----

```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



Dataset #:	2
Motif ID:	19
Motif name:	wsTACwGTAsw
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:	5.56444

Alignment:

```
-----HVTACWGATABD
TWAAWTTVTGAAAAAHWW----
```

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAHVH



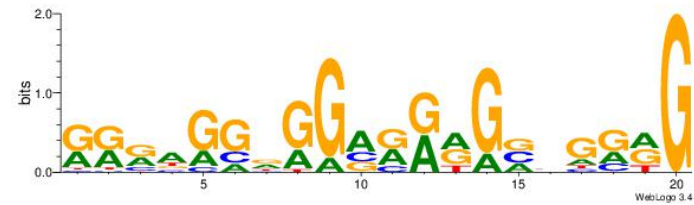
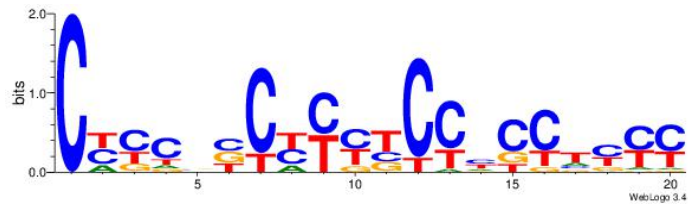
Dataset #:	1
Motif ID:	9
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	17
Number of overlap:	4
Similarity score:	7.05747

Alignment:

```
CYYCBCYYYTCCHCCTYYY-----
-----WWHTTTTTCABAAWTTWA
```

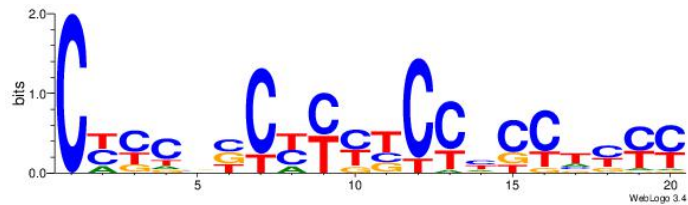
Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

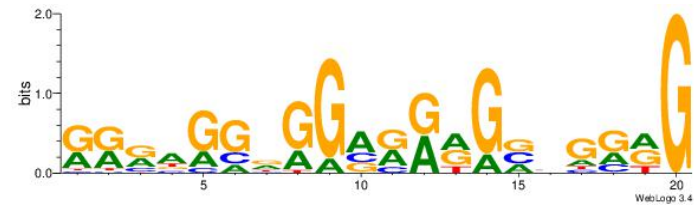


Dataset #: 1 Motif ID: 9 Motif name: TFM12

Original motif Consensus sequence: CYCBBYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



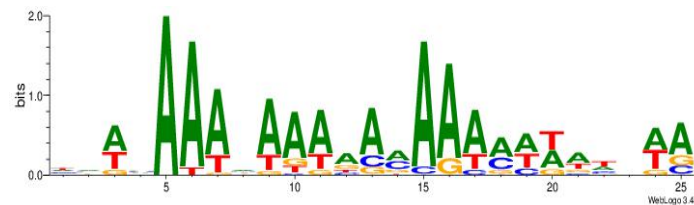
Best Matches for Motif ID 9 (Highest to Lowest)

Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	20
Similarity score:	0.0550447

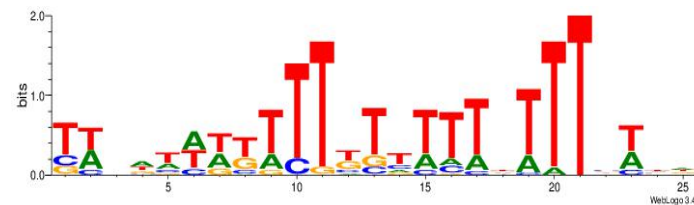
Alignment:

TWVHWWYTTTYTTTTTHTTTVWBH
 CYYCBBCYYYTCCHCCTYYY-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTTHTTTVWBH

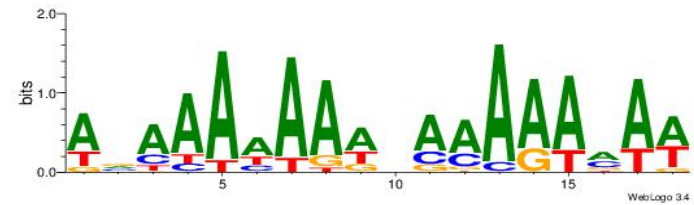
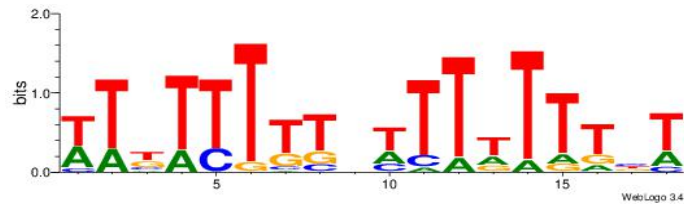


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 1.56027

Alignment:
 ---WTKTTTTTHWTTTTTTBT
 CYYCBBCYYYTCCHCCTYYY-

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence:
 ABAAAAAWHAAAAARAW

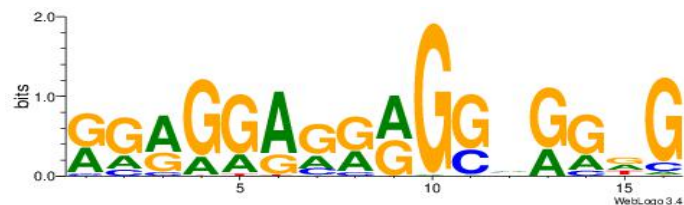


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 2.0134

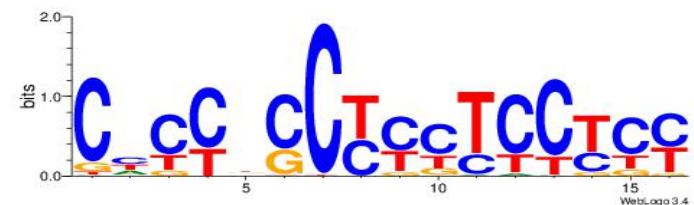
Alignment:

RGRGGAGRRGGHGGDG-----
 KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



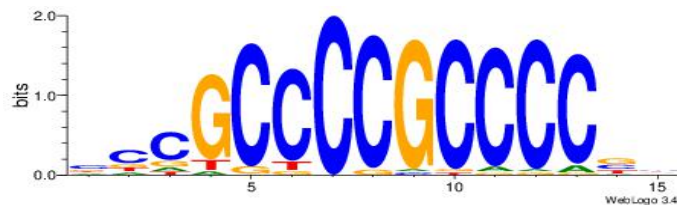
Dataset #: 2

Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 2.54994

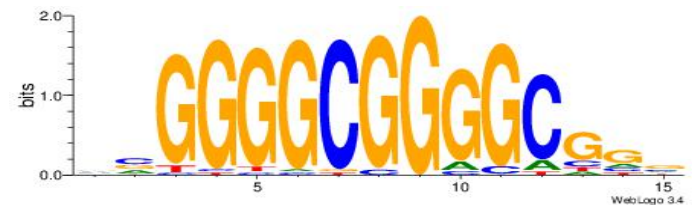
Alignment:

-----BCCGCCCCGCCCCBB
 CYYCBBCYYYTCCHCCTYYY

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

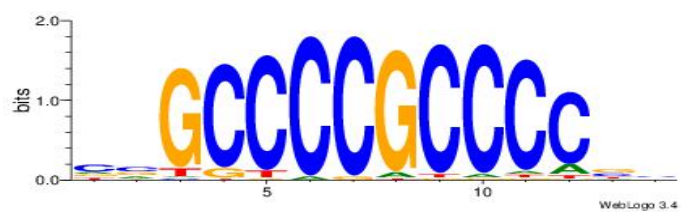


Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14

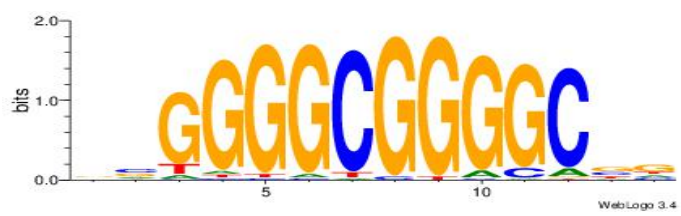
Similarity score: 3.04796

Alignment:
-----BBGGGGCGGGGCVD
KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

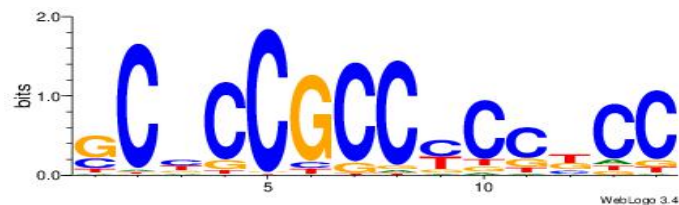
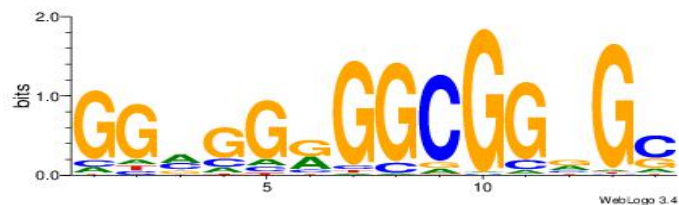


Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 3.05193

Alignment:
GGMGGRGGCGGVGC-----
KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

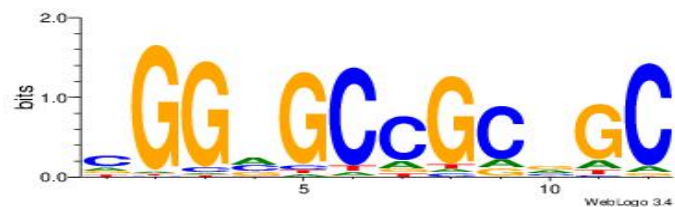


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 4.05708

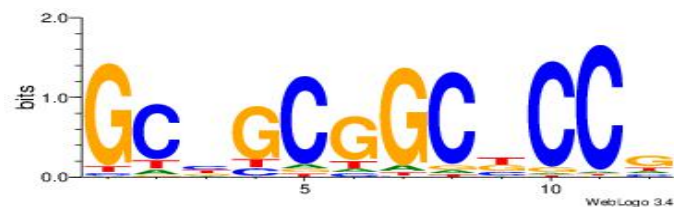
Alignment:

-----GCVGCGGCBCCG
 KKKAGGDGGAKKMGBBGKMG

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:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	5.03421

Alignment:

```

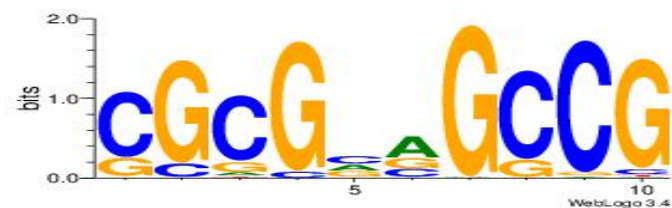
-----CGCGBMGCCG
KKKAGGDGGAKKMGBBGKMG

```

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

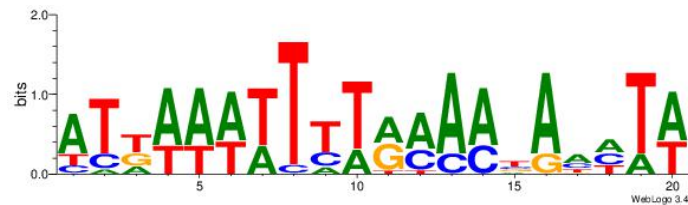


Dataset #:	1
Motif ID:	10
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	11
Number of overlap:	10
Similarity score:	5.05237

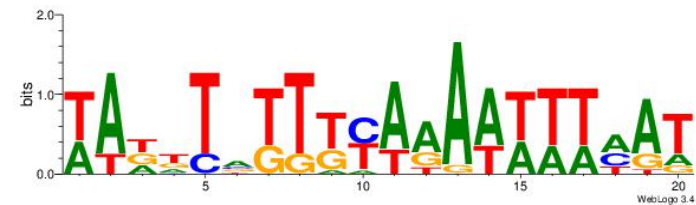
Alignment:

```
-----WAHHTVTTYKAAAATTRAT
CYYCBBCYYYTCCHCCTYYY-----
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



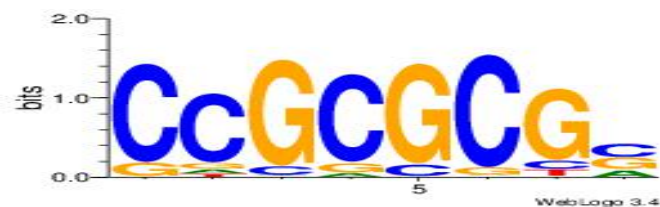
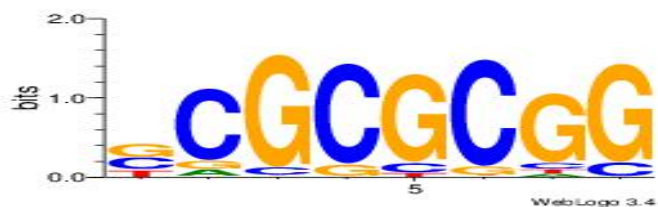
Dataset #:	1
Motif ID:	2
Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	6.06074

Alignment:

```
CCGCGCGS-----
CYYCBBCYYYTCCHCCTYYY
```

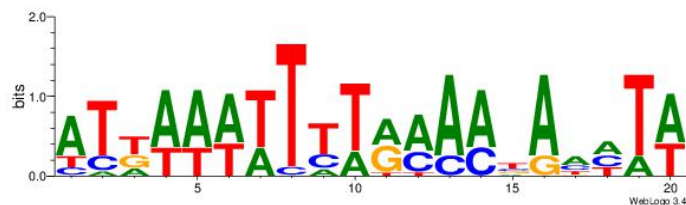
Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS

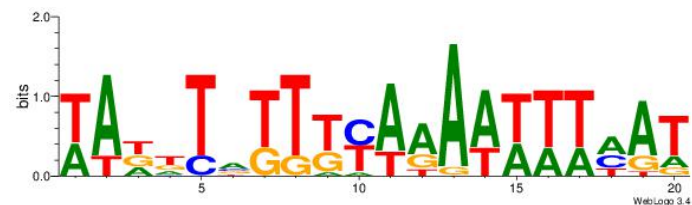


Dataset #: 1 Motif ID: 10 Motif name: TFM13

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



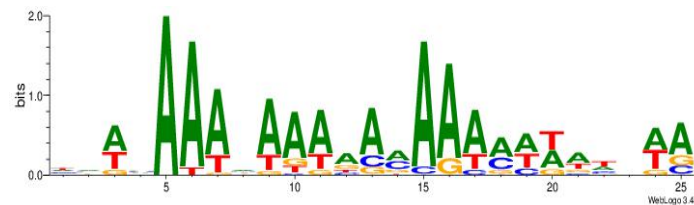
Best Matches for Motif ID 10 (Highest to Lowest)

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:	5
Number of overlap:	20
Similarity score:	0.0352451

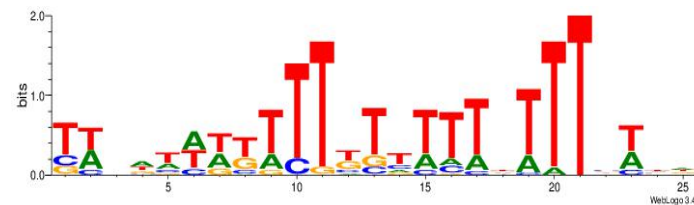
Alignment:

TWVHWWYTTTYTTTTTHTTTVWBH
 ----WAHHTVTTYKAAAAWTTRAT-

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTTHTTTVWBH

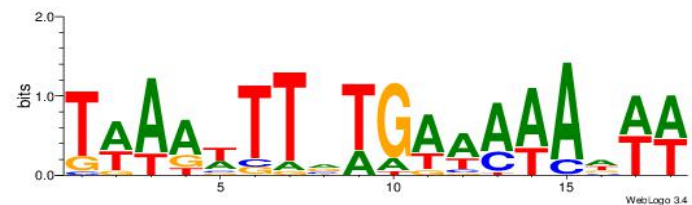
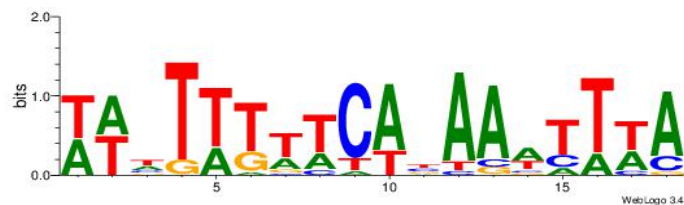


Dataset #:	1
Motif ID:	8
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	1.02254

Alignment:
 TWAAWTTVTGAAAAHWW--
 ATKAAWTTTTRMAABAHHTW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
 TWAAWTTVTGAAAAHWW

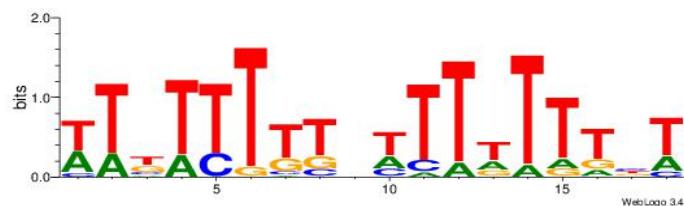


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.02868

Alignment:

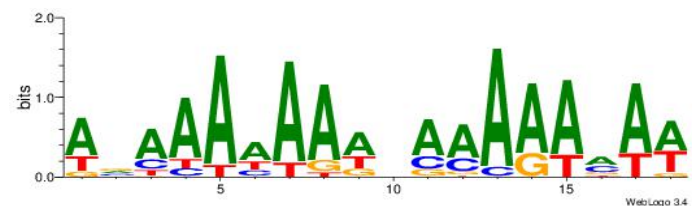
WTKTTTTTHWTTTTTBT--
 WAHHTVTTYKAAAATTRAT

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif
ABAAAAAWHAAAAARAW

Consensus sequence:



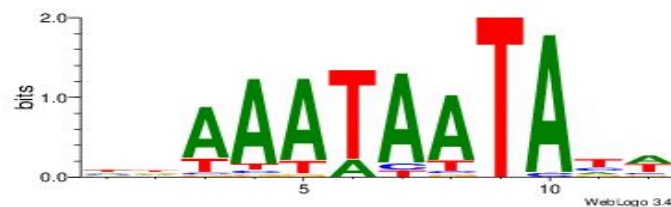
Dataset #: 2

Motif ID: 13
 Motif name: tkAAATAATAtw
 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: 4.03399

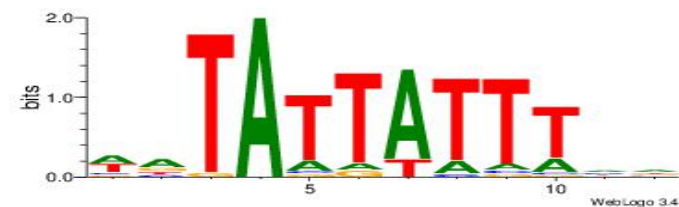
Alignment:

-----HDAAATAATAHW
 WAHHTVTTYKAAAATTRAT

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH

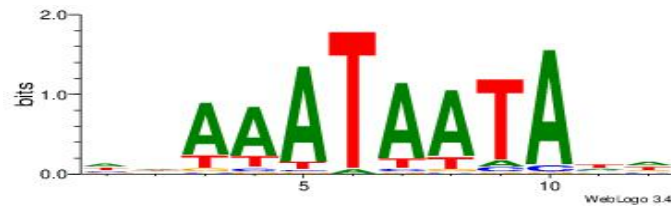


Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 4.03484

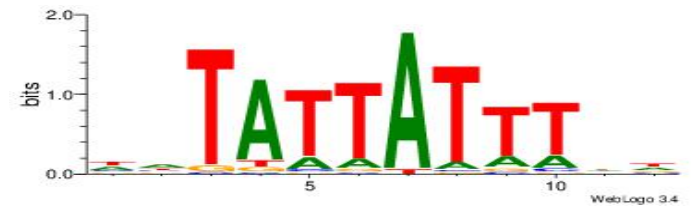
Alignment:

```
-----HDAAATAATADD
WAHHTVTTYKAAAATTRAT
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



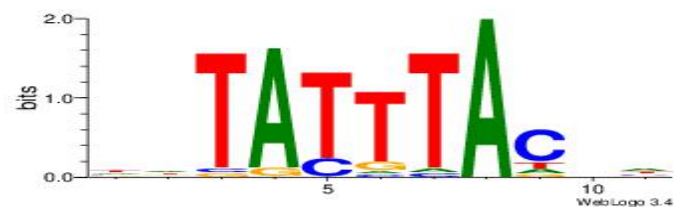
Dataset #:	2
Motif ID:	21
Motif name:	wbgTAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	4.55116

Alignment:

```
DBGTAATAHD-----
ATKAAWTTTTRMAABAHHTW
```

Original motif Consensus sequence: DBGTAATAHD

Reverse complement motif Consensus sequence: DHTATTTACBD

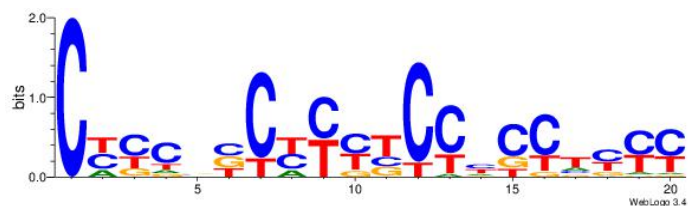


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 11
 Number of overlap: 10
 Similarity score: 5.0571

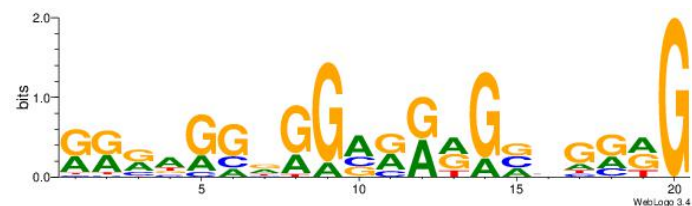
Alignment:

KKKAGGDGGAKKMGBBGKMG-----
 -----ATKAAWTTTTRMAABAHHTW

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



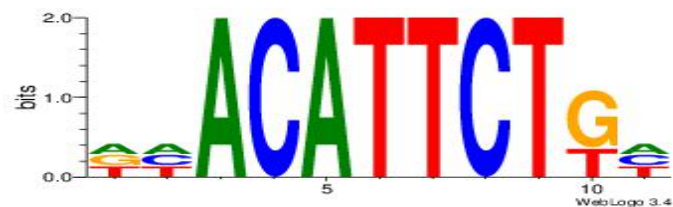
Dataset #: 2

Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 7
 Similarity score: 6.55998

Alignment:

-----DHACATTCTGH
 ATKAAWTTTTRMAABAHHTW----

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 2
 Motif ID: 15
 Motif name: kCAGCCAATmr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 5
 Similarity score: 7.55485

Alignment:

-----MBATTGGCTGH
ATKAAWTTTTRMAABAHHTW-----

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



Dataset #: 2
Motif ID: 19
Motif name: wsTACwGTAsw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 4
Similarity score: 8.01732

Alignment:

-----HVTACWGATABD
ATKAAWTTTTRMAABAHHTW-----

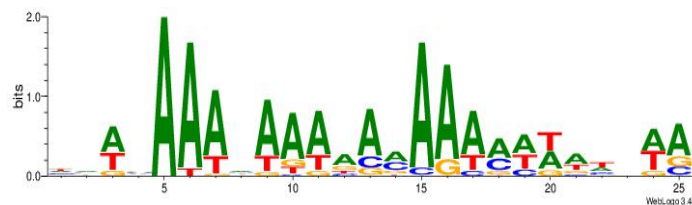
Original motif Consensus sequence: HVTACWGATABD

Reverse complement motif Consensus sequence: DBTACWGTAHV

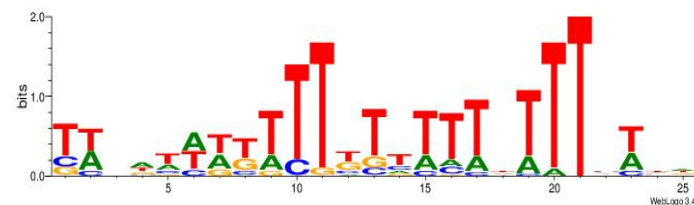


Dataset #: 1 Motif ID: 11 Motif name: TFM11

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH



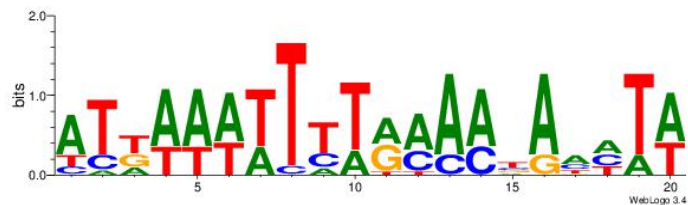
Best Matches for Motif ID 11 (Highest to Lowest)

Dataset #:	1
Motif ID:	10
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0486765

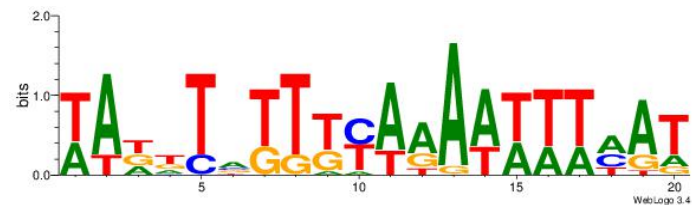
Alignment:

WAHHTVTTYKAAAATTRAT-----
 TWVHWWYTTTTYTTTTTHTTTTVWBH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



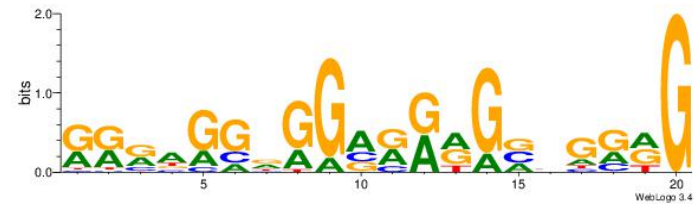
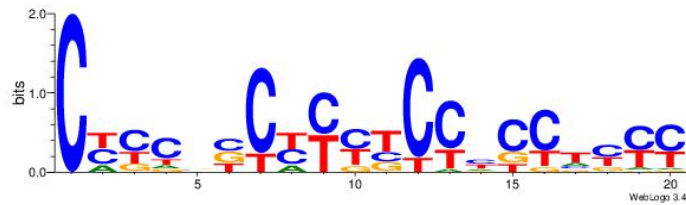
Dataset #:	1
Motif ID:	9
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0693284

Alignment:

KKKAGGDGGAKKMGBBGKMG-----
 HDWVAAAHAAAAAMAAAMWWHBWA

Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



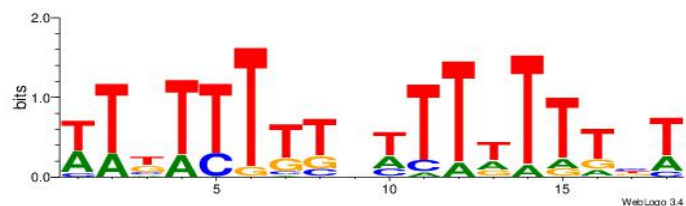
Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.0232

Alignment:

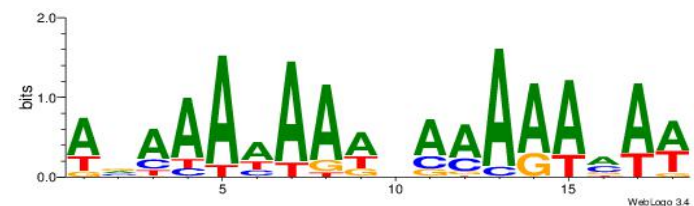
```

-----ABAAAAAWhAAAAARAW
HDWVAAAHA AAAA MAAAMWWH BWA
  
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW



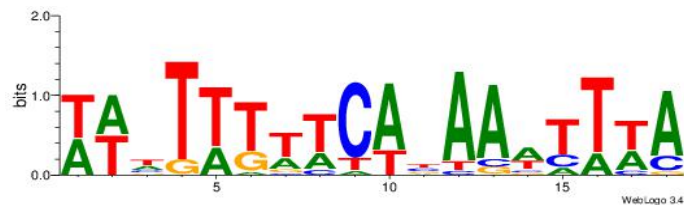
Dataset #: 1

Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.05388

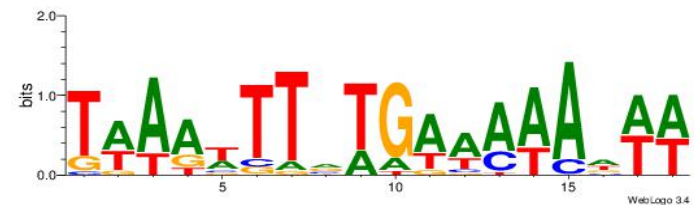
Alignment:

WWHTTTTTCABAAWTTWA-----
 TWVHWWYTTTYYTTTTTHTTTVWBH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

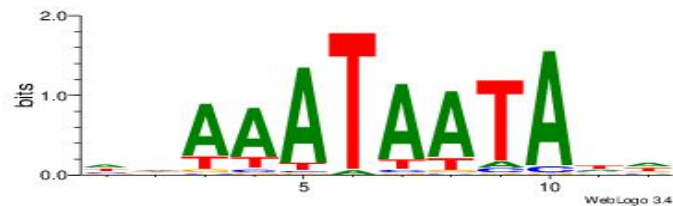


Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12

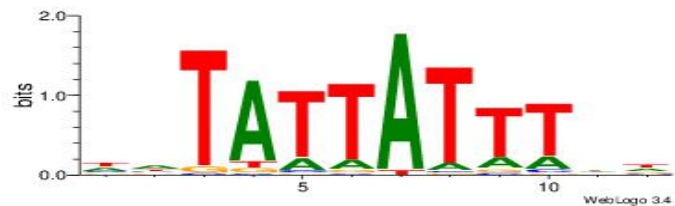
Similarity score: 4.03464

Alignment:
HDAAATAATADD-----
HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

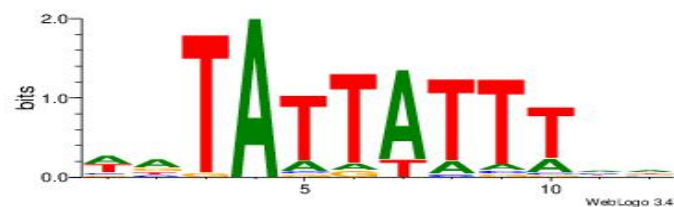
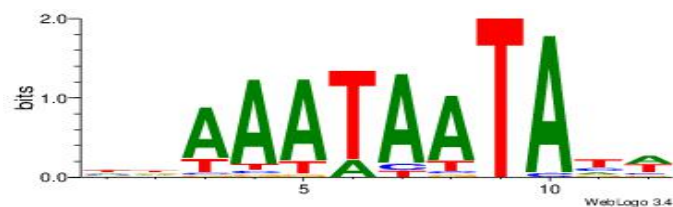


Dataset #: 2
Motif ID: 13
Motif name: tkAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 4.04436

Alignment:
HDAAATAATAHW-----
HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif Consensus sequence: HDAAATAATAHW

Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #: 2
 Motif ID: 21
 Motif name: wbgTAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 4.53643

Alignment:

```

-----DHTATTTACBD
TWVHWWYTTTYTTTTTHTTTVWBH
  
```

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #: 2
 Motif ID: 20

Motif name:	dhACATTCTkh
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	4.56457

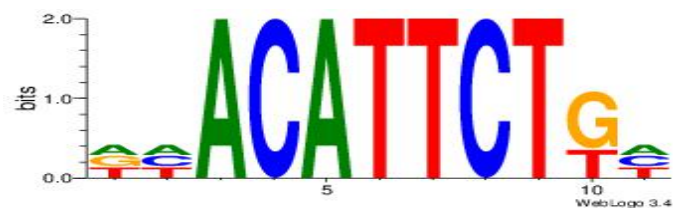
Alignment:

```

-----DHACATTCTGH
TWVHWWWYTTTYTTTTHTTTVWBH

```

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

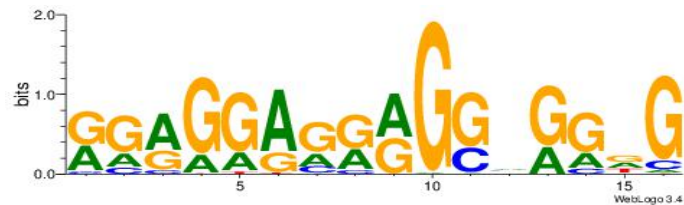


Dataset #:	1
Motif ID:	6
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	7
Similarity score:	6.57279

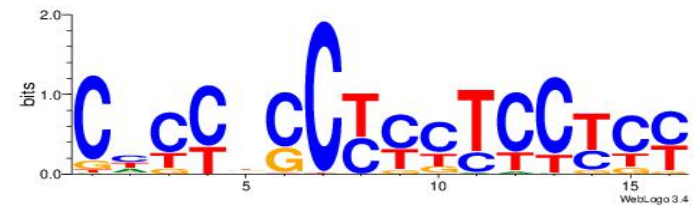
Alignment:

```
-----RGRGGAGRRGGHGGDG
HDWVAAAHA AAAA MAAAMWWWHBWA-----
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



Dataset #:	2
Motif ID:	19
Motif name:	wsTACwGTAsw
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:	8.03096

Alignment:

```
DBTACWGTAVH-----
-----TWVHWWYTTTYTTTTTHTTTVWBH
```

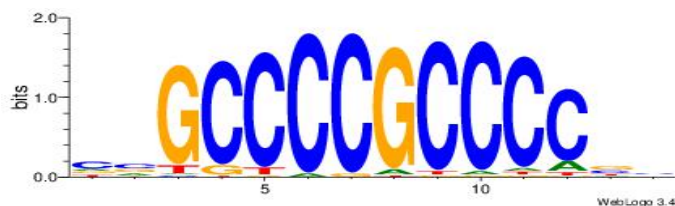
Original motif Consensus sequence: HVTACWGATABD

Reverse complement motif Consensus sequence: DBTACWGTAVH

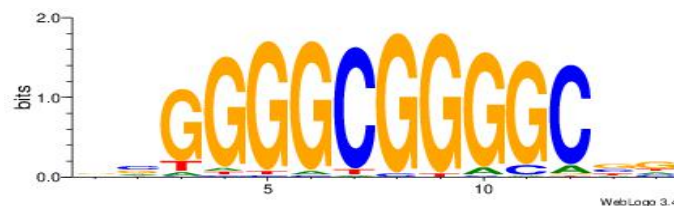


Dataset #: 2 Motif ID: 12 Motif name: csGCCCCGCCCCsc

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Best Matches for Motif ID 12 (Highest to Lowest)

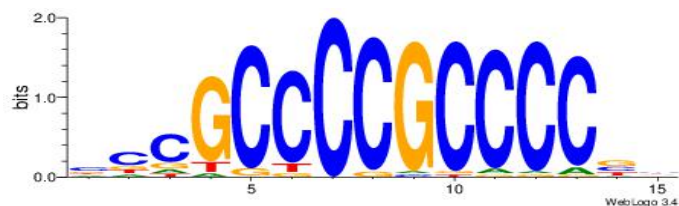
Dataset #:	2
Motif ID:	14
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0

Alignment:

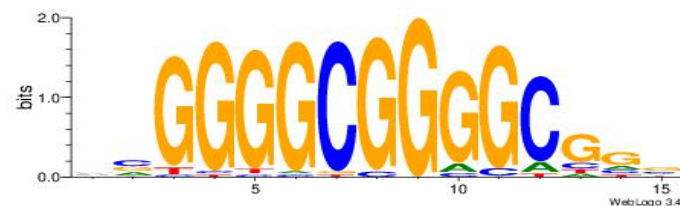
BCCGCCCCGCCCCBB

–HVGCCCCGCCCCBB

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

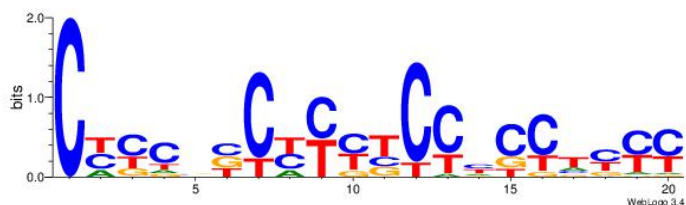


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0777991

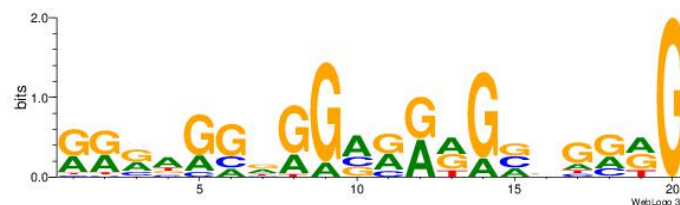
Alignment:

CYYCBBCYYYTCCHCCTYYY
---HVGCCCCGCCCCBB---

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

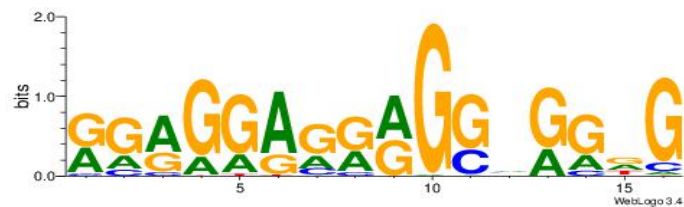


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0880609

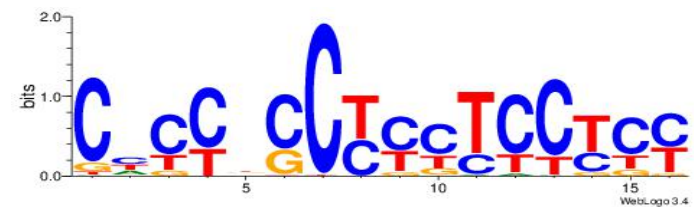
Alignment:

CHCCBCKMCTCCKCM
 HVGCCCGCCCCBB--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



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: 1

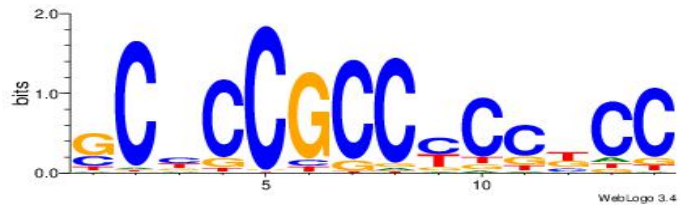
Number of overlap: 14
Similarity score: 0.0937271

Alignment:
GGMGGRGGCGGVGC
BBGGGGCGGGGCVD

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

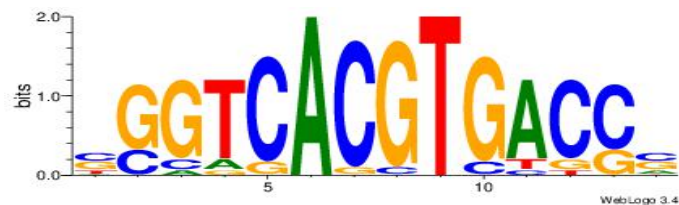
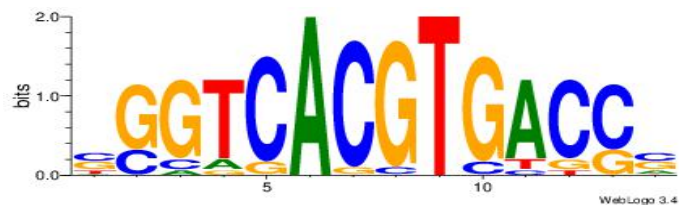


Dataset #: 2
Motif ID: 18
Motif name: sSGTCACGTGACSS
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0971132

Alignment:
SGGTCACGTGACCS
HVGCCCCGCCCCBB

Original motif Consensus sequence: SGGTCACGTGACCS

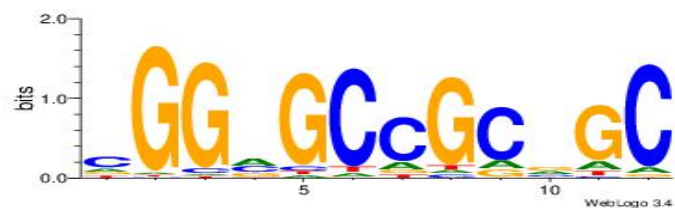
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



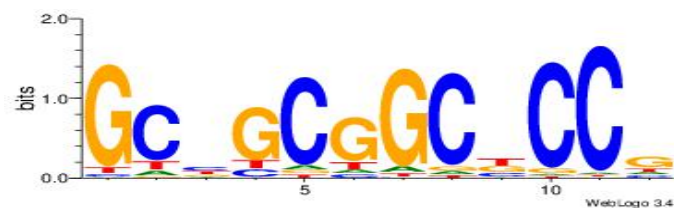
Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.08016

Alignment:
 CGGVGCCGCVGC--
 HVGCCCCGCCCCBB

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



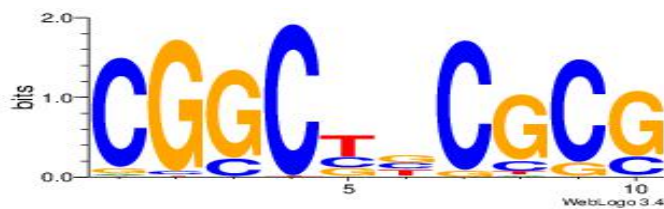
Dataset #: 1
 Motif ID: 3

Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	2.07757

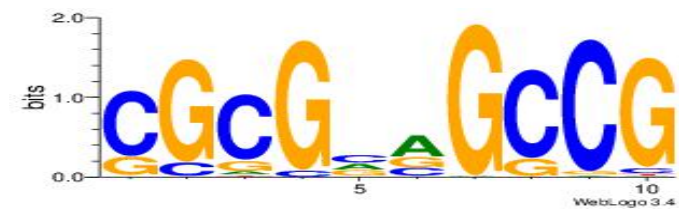
Alignment:

CGGCYBCGCG-----
HVGCCCCGCCCCBB

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



Dataset #:	1
Motif ID:	2
Motif name:	TFW2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	3.07109

Alignment:

-----CCGCGCGS
BBGGGGCGGGGCVD

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



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:	4.10276

Alignment:

CGCGAC-----
HVGCCCGCCCCBB

Original motif Consensus sequence: GTCGCG

Reverse complement motif Consensus sequence: CGCGAC

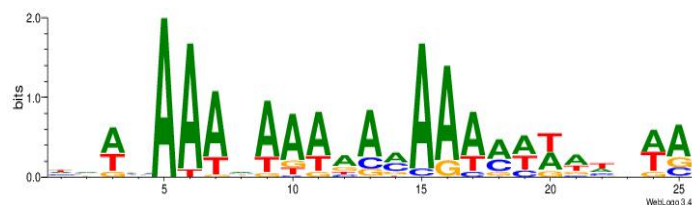


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 22
 Number of overlap: 4
 Similarity score: 5.10677

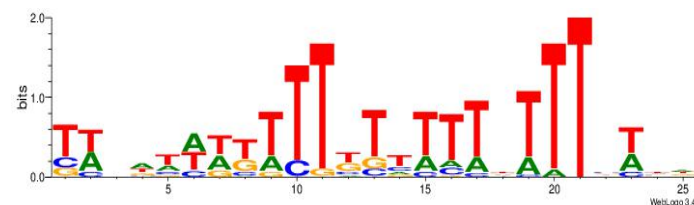
Alignment:

TWVHWWYTTTYYTTTTTHTTTVWBH-----
 -----HVGCCCCGCCCCBB

Original motif Consensus sequence:
 HDWVAAAHAAAAAAMAAAMWWWHBWA

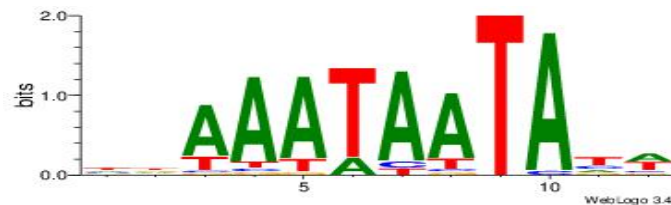


Reverse complement motif Consensus sequence:
 TWVHWWYTTTYYTTTTTHTTTVWBH

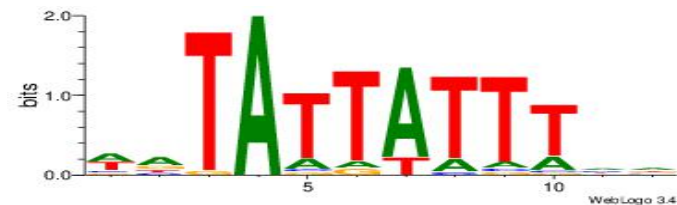


Dataset #: 2 Motif ID: 13 Motif name: tkAAATAATatw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Best Matches for Motif ID 13 (Highest to Lowest)

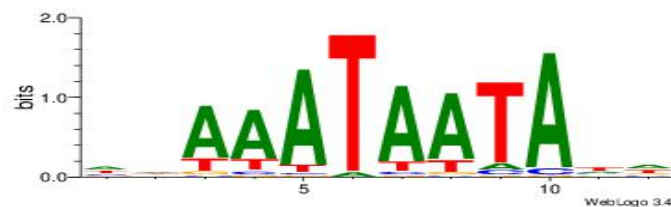
Dataset #:	2
Motif ID:	17
Motif name:	wwAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:

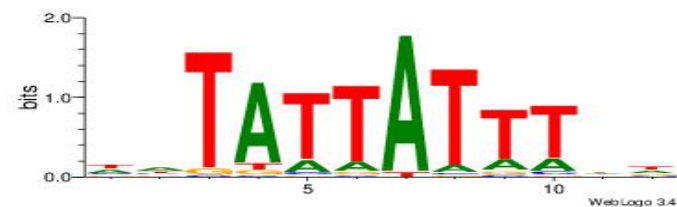
HDAAATAATADD

HDAAATAATAHW

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

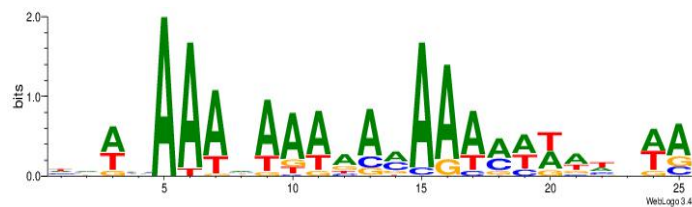


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0590505

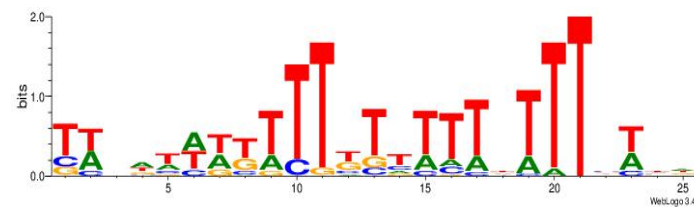
Alignment:

TWVHWWYTTTYYTTTTHTTTVWBH
 -----WHTATTATTTDH--

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYYTTTTHTTTVWBH



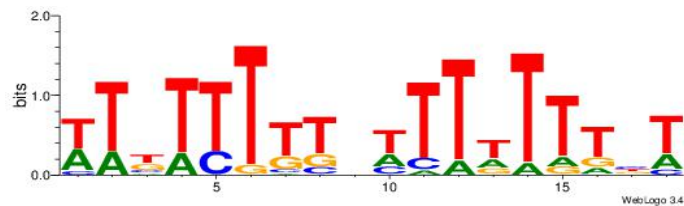
Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0637702

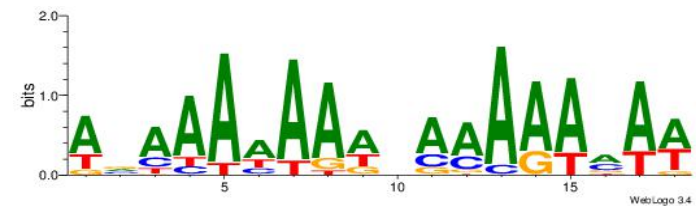
Alignment:

WTKTTTTTHWTTTTTBT
WHTATTATTTDH-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW

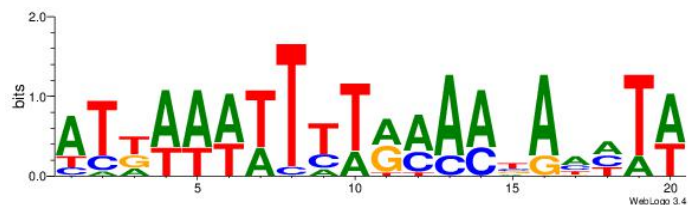


Dataset #: 1
Motif ID: 10
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0704475

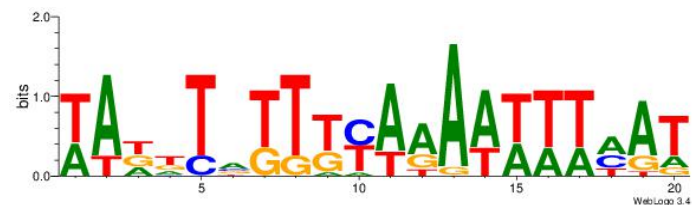
Alignment:

WAHHTVTTYKAAAWTTRAT
HDAAATAATAHW-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

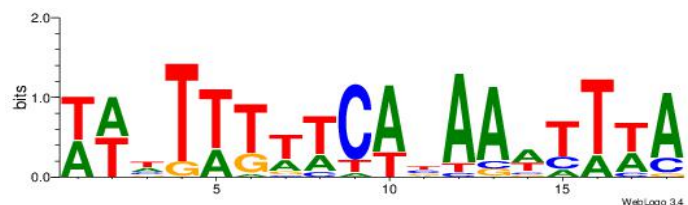


Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0763819

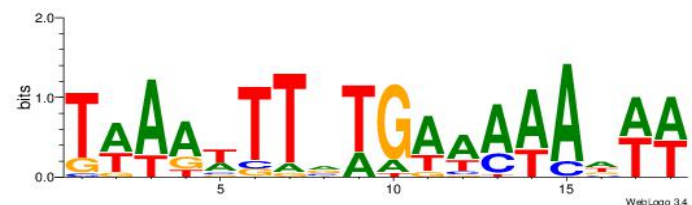
Alignment:

TWAAWTTVTGAAAAHWW
-----HDAAATAATAHW

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 2
 Motif ID: 21
 Motif name: wbgTAAATAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.560292

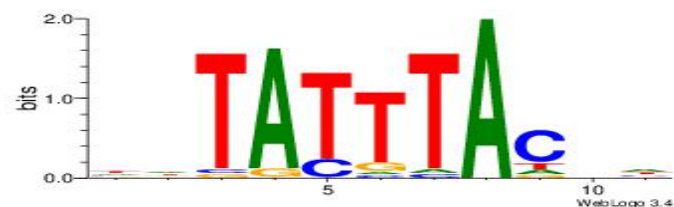
Alignment:

-DBGTAAATAHD
 HDAAATAATAHW

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #: 2
 Motif ID: 19
 Motif name: wSTACwGTAsw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.587493

Alignment:
-DBTACWGTAVH
HDAAATAATAHW

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH

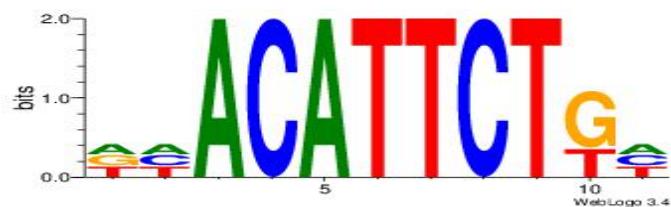


Dataset #: 2
Motif ID: 20
Motif name: dhACATTCTkh
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.590271

Alignment:
-HCAGAATGTHD
WHTATTATTTDH

Original motif Consensus sequence: DHACATTCTGH

Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 2
 Motif ID: 15
 Motif name: kCAGCCAATmr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.592142

Alignment:
 -MBATTGGCTGH
 WHTATTATTTDH

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



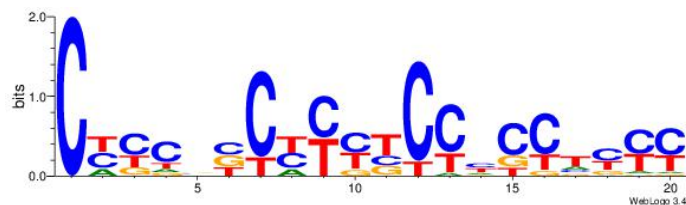
Dataset #: 1
 Motif ID: 9

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

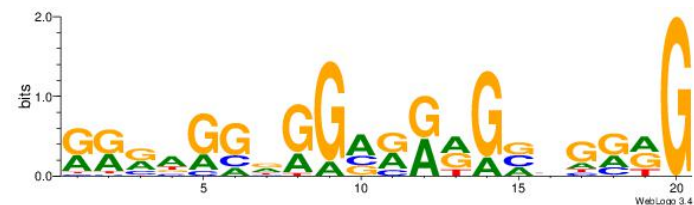
Alignment:

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

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

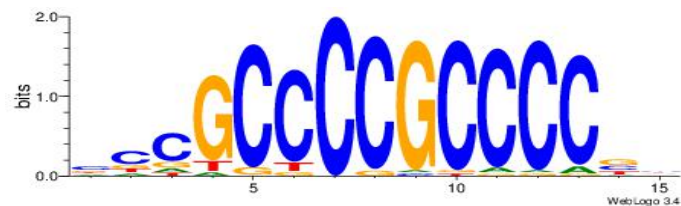


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

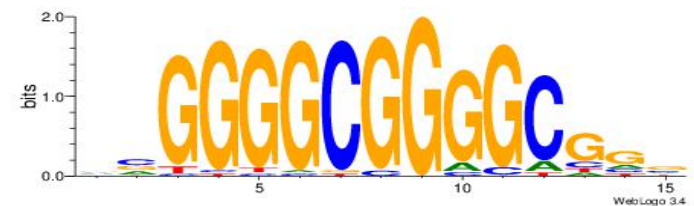


Dataset #: 2 Motif ID: 14 Motif name: cccGCCCCGCCCCsb

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



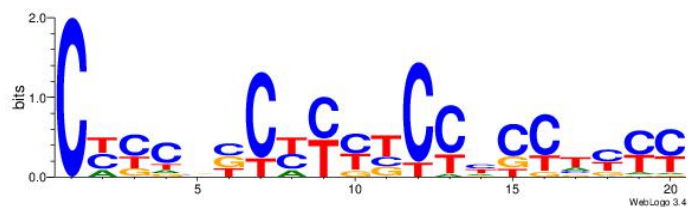
Best Matches for Motif ID 14 (Highest to Lowest)

Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 15
Similarity score: 0.0773345

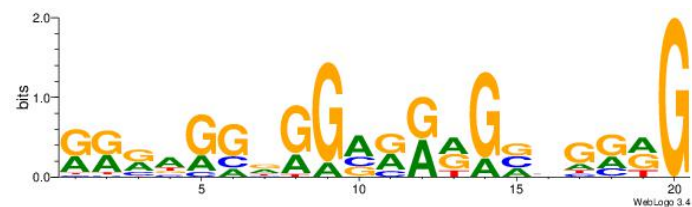
Alignment:

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

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

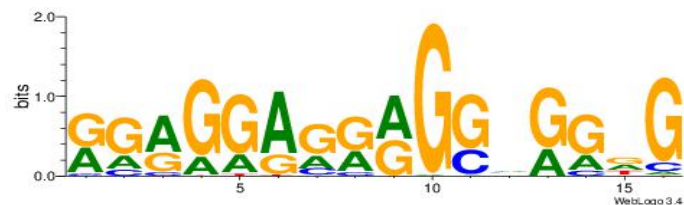


Dataset #: 1
Motif ID: 6
Motif name: TFM2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

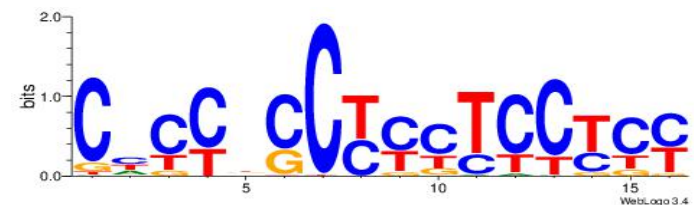
Direction: Backward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0869149

Alignment:
 CHCCBCKMCTCCKCM
 BCCGCCCCGCCCCBB-

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



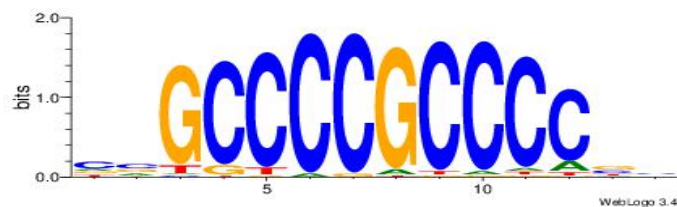
Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



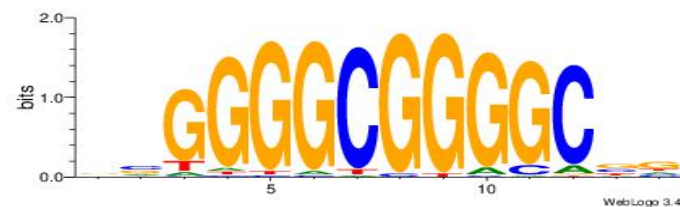
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.5

Alignment:
 -HVGCCCCGCCCCBB
 BCCGCCCCGCCCCBB

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

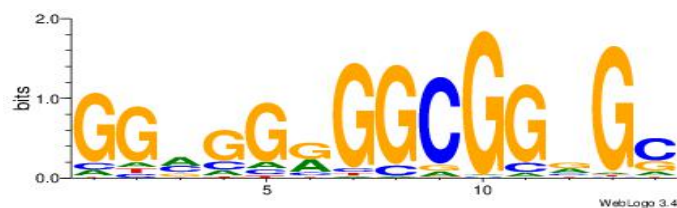


Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.58333

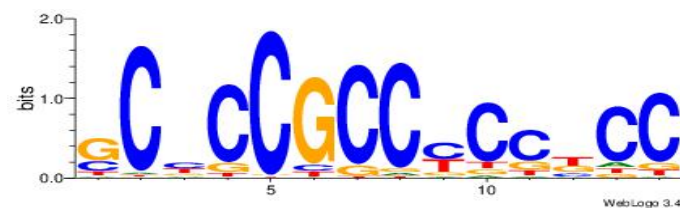
Alignment:

GGMGGRGGCGGVGC-
BBGGGGCGGGGCGB

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

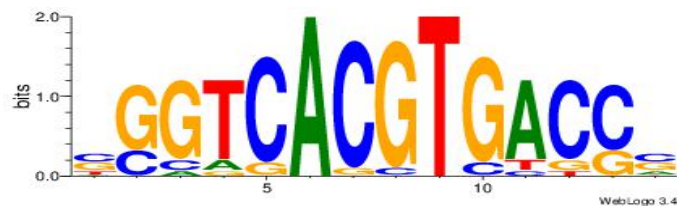


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.601399

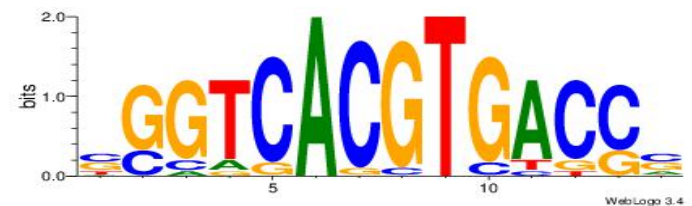
Alignment:

SGGTCACGTGACCS-
 BBGGGGCGGGGCGGB

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

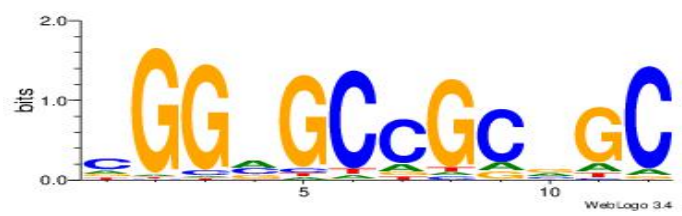


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12

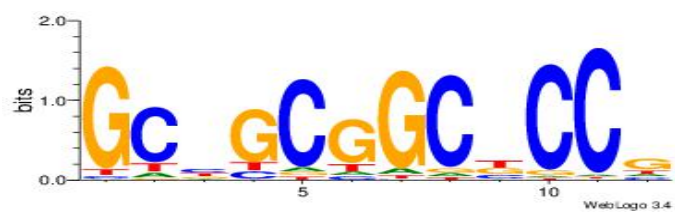
Similarity score: 1.58073

Alignment:
---CGGVGCCGCVGC
BBGGGGCGGGGCGGB

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

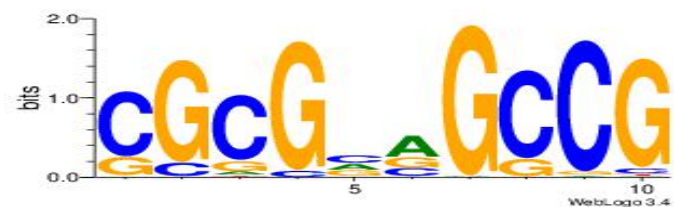
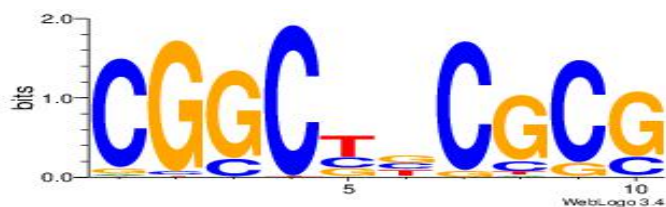


Dataset #: 1
Motif ID: 3
Motif name: TFW3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 2.6085

Alignment:
-----CGGCYBCGCG
BBGGGGCGGGGCGGB

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

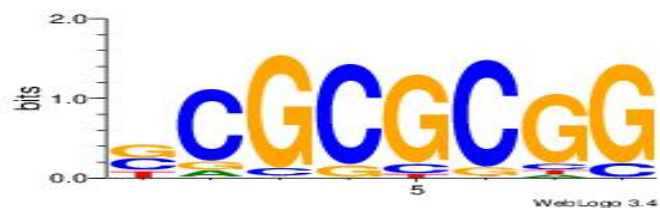


Dataset #: 1
 Motif ID: 2
 Motif name: TFW2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 3.595

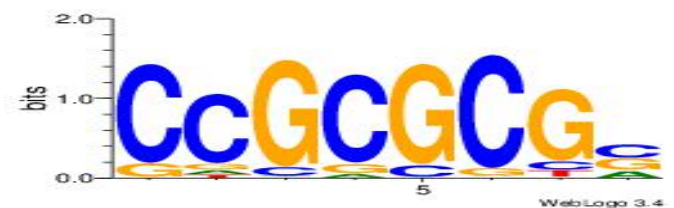
Alignment:

-----SCGCGCGG
 BBGGGGCGGGCGGB

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



Dataset #: 1
 Motif ID: 1

Motif name:	TFW1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	4.58105

Alignment:

```
GTCGCG-----
BCCGCCCCGCCCCBB
```

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC

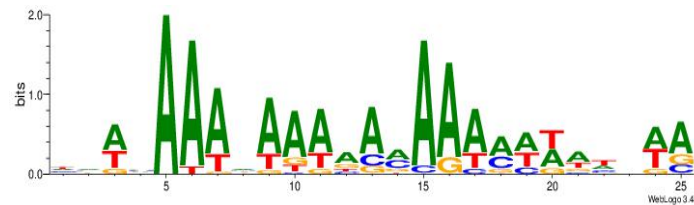


Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	22
Number of overlap:	4
Similarity score:	5.59832

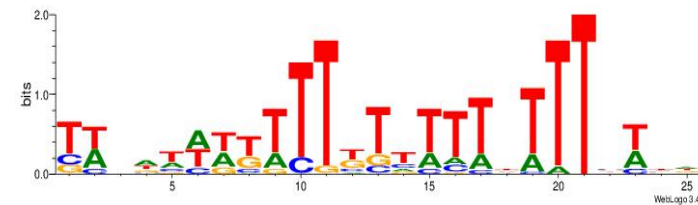
Alignment:

```
-----TWVHWWYTTTTYTTTTHTTTVWBH
BCCGCCCCGCCCCBB-----
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTHTTTVWBH



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

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



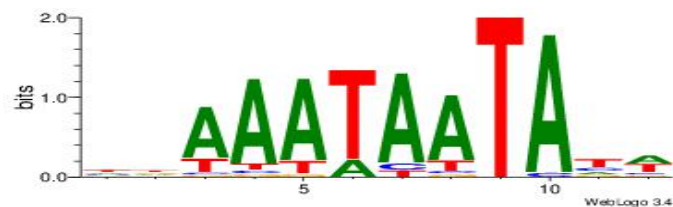
Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #:	2
Motif ID:	13
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

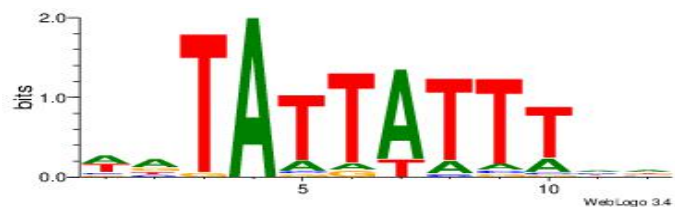
Position number: 2
Number of overlap: 11
Similarity score: 0.0320614

Alignment:
WHTATTATTTDH
-MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

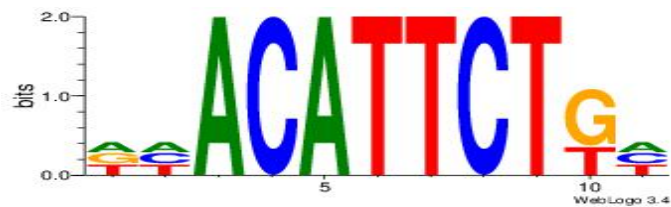


Dataset #: 2
Motif ID: 20
Motif name: dhACATTCTkh
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.034958

Alignment:
HCAGAATGTHD
DCAGCCAATVR

Original motif Consensus sequence: DHACATTCTGH

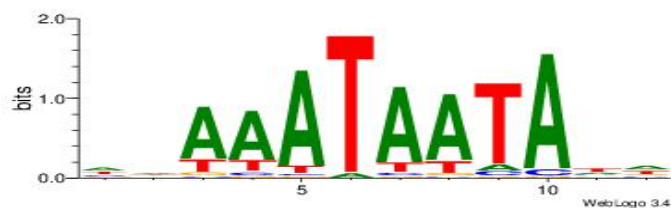
Reverse complement motif Consensus sequence: HCAGAATGTHD



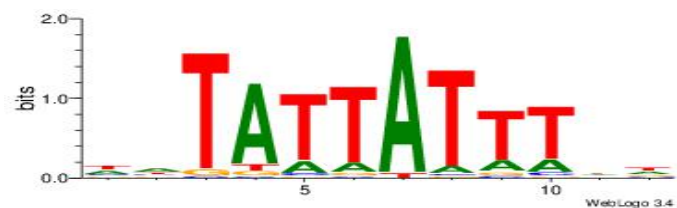
Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0358988

Alignment:
 DDTATTATTTDH
 -MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



Dataset #: 2

Motif ID: 16
 Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0360892

Alignment:

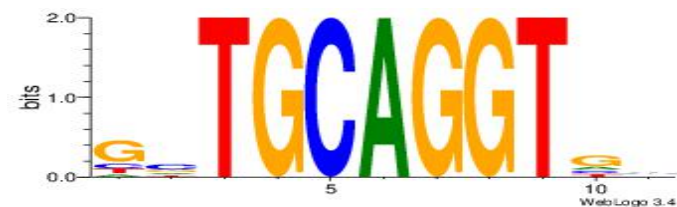
BCACCTGCABC

MBATTGGCTGH

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



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: 2
 Number of overlap: 11
 Similarity score: 0.0376063

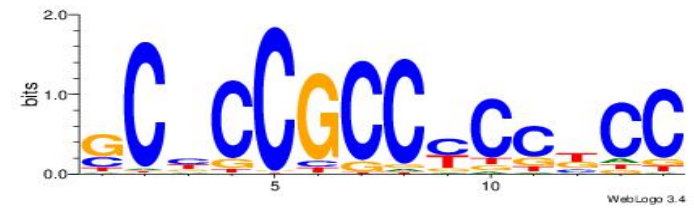
Alignment:

GGMGGRGGCGGVGC
--MBATTGGCTGH--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYGC



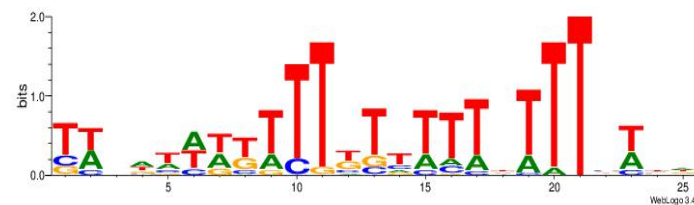
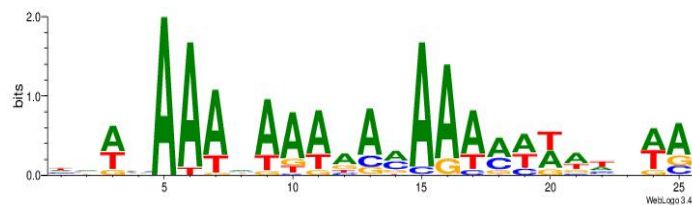
Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	11
Similarity score:	0.0396371

Alignment:

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

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
TWHVWWYTTTTYTTTTHTTTTVWBH



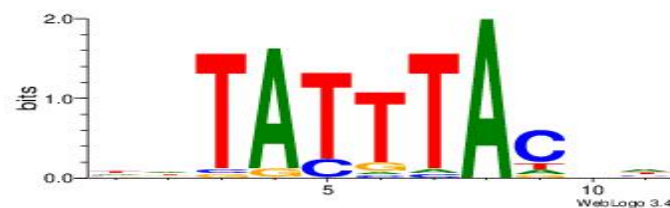
Dataset #: 2
 Motif ID: 21
 Motif name: wbgTAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.538109

Alignment:
 DHTATTTACBD-
 -MBATTGGCTGH

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #: 1
 Motif ID: 3

Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	2.01586

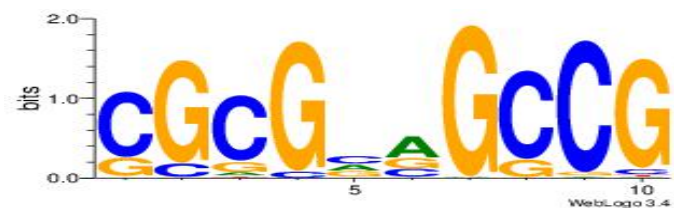
Alignment:

CGGCYBCGCG-----
 ---MBATTGGCTGH

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

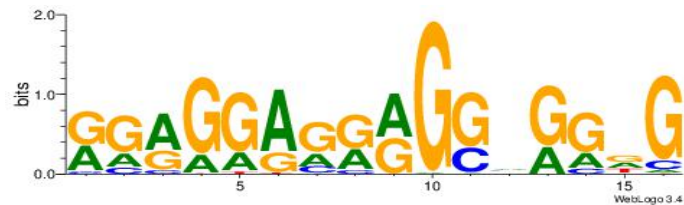


Dataset #:	1
Motif ID:	6
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	11
Number of overlap:	6
Similarity score:	2.5389

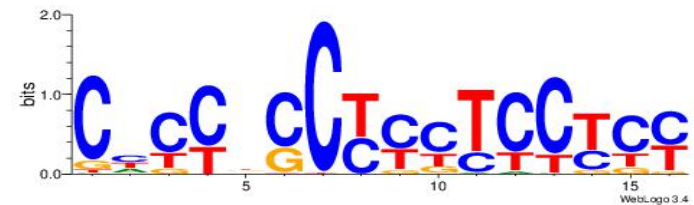
Alignment:

RGRGGAGRRGGHGGDG-----
 -----MBATTGGCTGH

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence:
 CHCCBCKMCTCCKCM



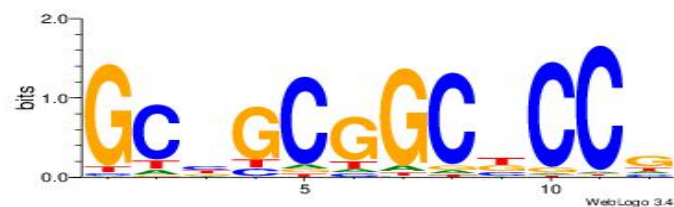
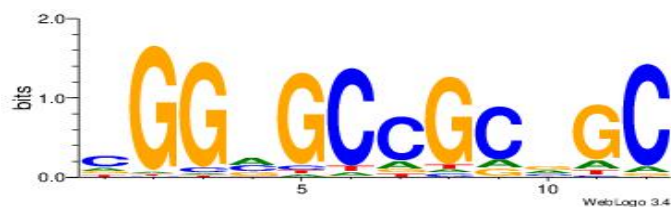
Dataset #:	1
Motif ID:	4
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	5
Similarity score:	3

Alignment:

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

Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCGGCBCCG



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

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #:	2
Motif ID:	19
Motif name:	wsTACwGTAsw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0182895

Alignment:
DBTACWGTAVH
BCACCTGCABC

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAHV



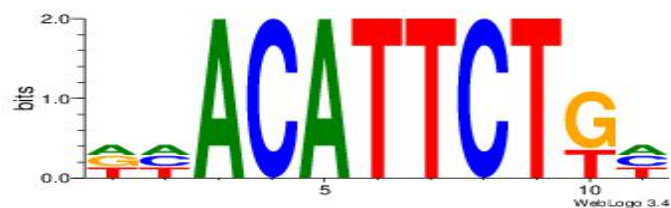
Dataset #: 2
Motif ID: 20
Motif name: dhACATTCTkh
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0221745

Alignment:

DHACATTCTGH

BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

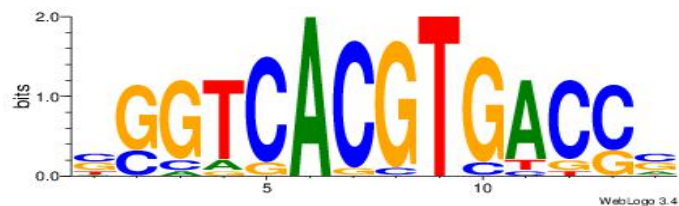


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0280991

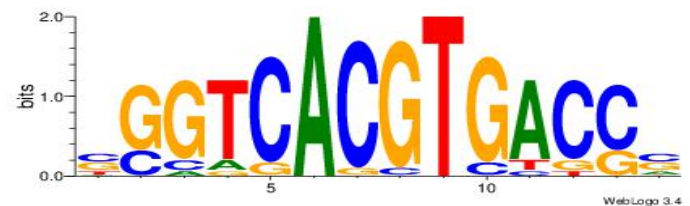
Alignment:

SGGTCACGTGACCS
 ---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

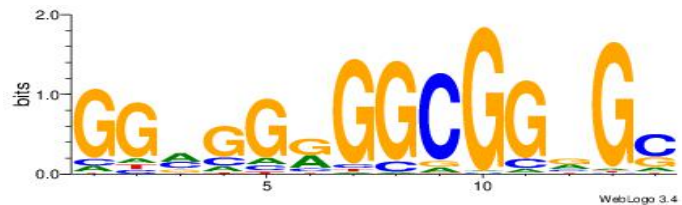


Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11

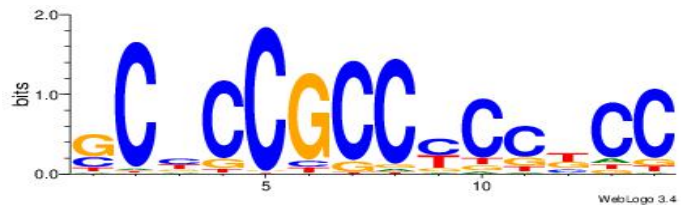
Similarity score: 0.0312321

Alignment:
GGMGGRGGCGGVGC
GBTGCAGGTGB---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

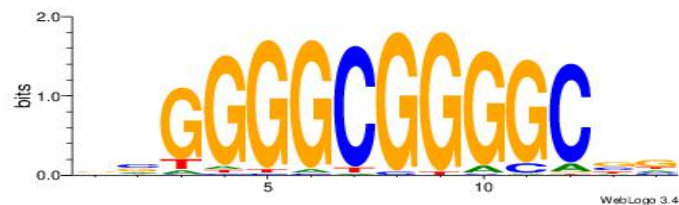
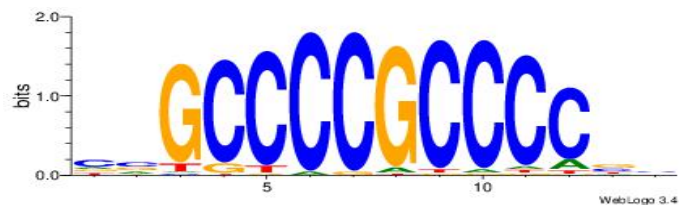


Dataset #: 2
Motif ID: 12
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0370129

Alignment:
HVGCCCCGCCCCBB
-BCACCTGCABC--

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 2
 Motif ID: 15
 Motif name: kCAGCCAATmr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0407197

Alignment:

DCAGCCAATVR

GBTGCAGGTGB

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



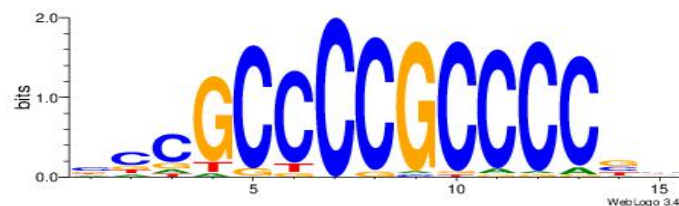
Dataset #: 2
 Motif ID: 14

Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0429055

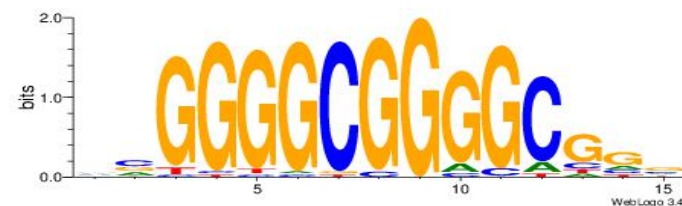
Alignment:

BCCGCCCCGCCCCBB
 --BCACCTGCABC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



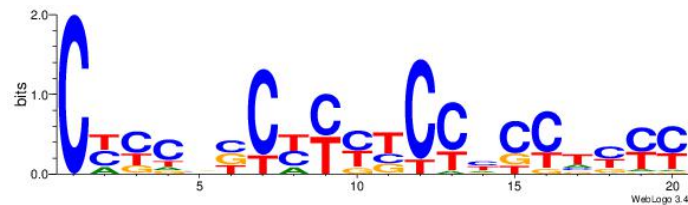
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0444938

Alignment:

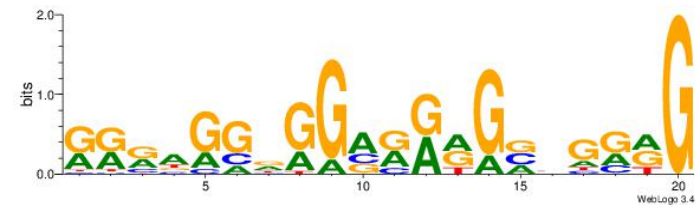
KKKAGGDGGAKKMGBBGKMG

----GBTGCAGGTGB-----

Original motif Consensus sequence: 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:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.538471

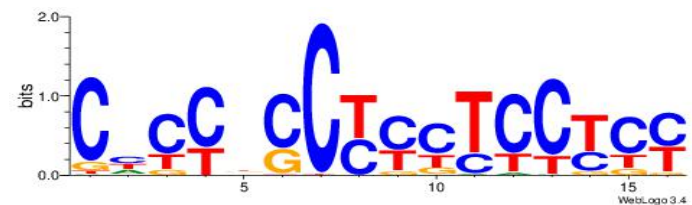
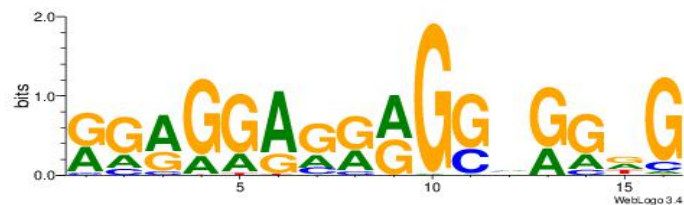
Alignment:

-RGRGGAGRRGGHGGDG

GBTGCAGGTGB-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence:
CHCCBCKMCTCKCM

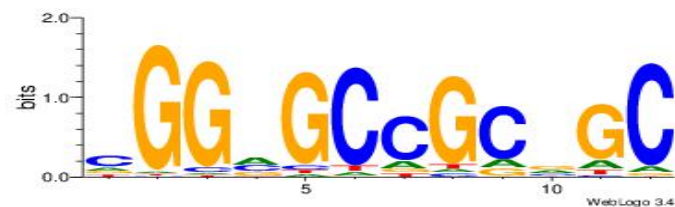


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 1.54364

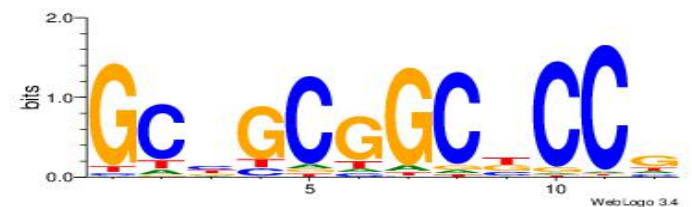
Alignment:

GCVGCGGCBCCG---
 ----BCACCTGCABC

Original motif Consensus sequence: CGGVGCCGCVGC

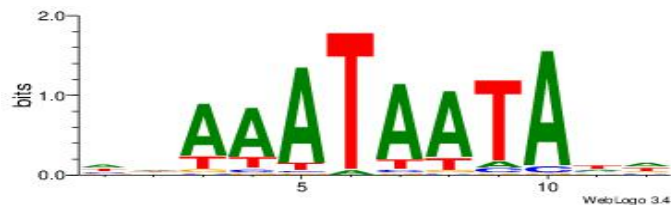


Reverse complement motif Consensus sequence: GCVGCGGCBCCG

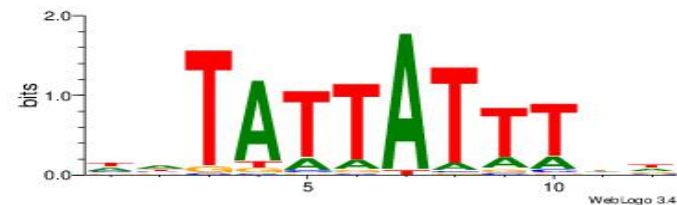


Dataset #: 2 Motif ID: 17 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTDDH



Best Matches for Motif ID 17 (Highest to Lowest)

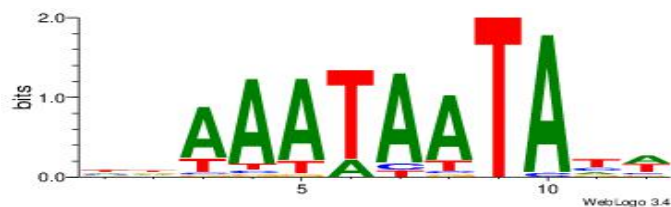
Dataset #:	2
Motif ID:	13
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:

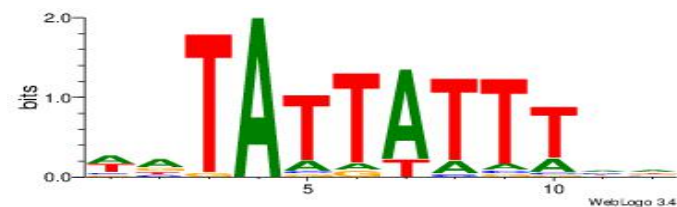
HDAAATAATAHW

HDAAATAATADD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH

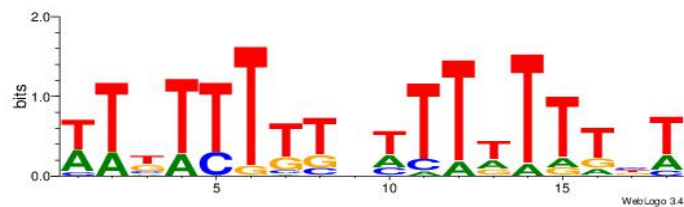


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0565705

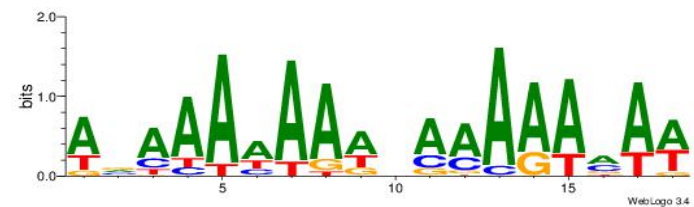
Alignment:

ABAAAAAAWHAAAAARAW
 -----HDAAATAATADD

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



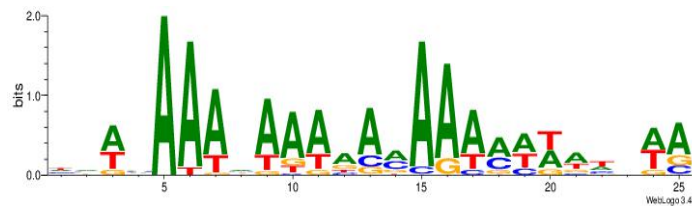
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 12
Similarity score: 0.0575935

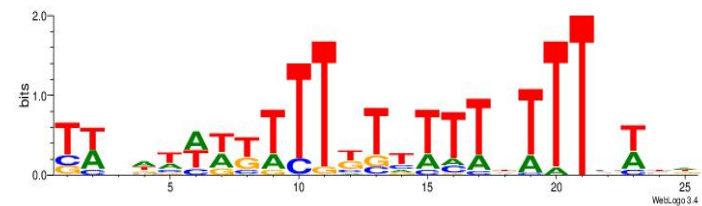
Alignment:

HDWVAAAHAAAAAAMAAAMWWWHBWA
--HDAAATAATADD-----

Original motif Consensus sequence:
HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTYYTTTTTHTTTVWBH

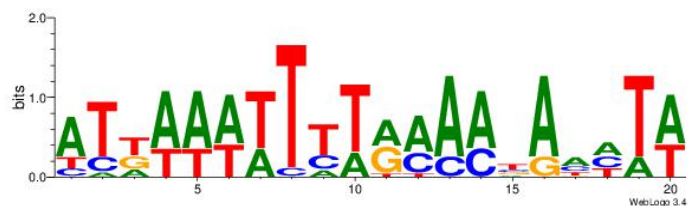


Dataset #: 1
Motif ID: 10
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0712963

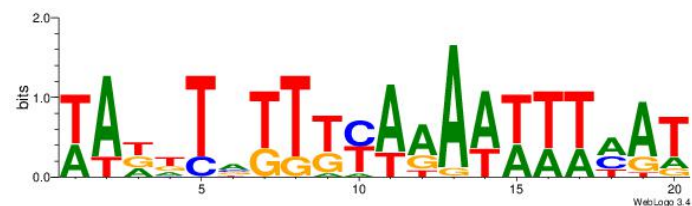
Alignment:

ATKAAWTTTTRMAABAHHTW
-----DDTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

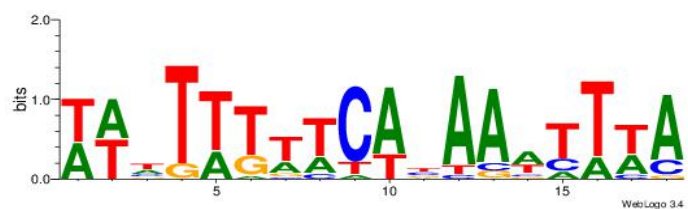


Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0733516

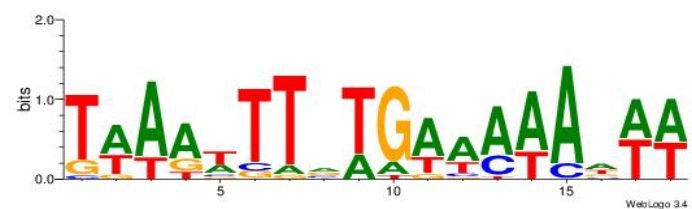
Alignment:

```
TWAAWTTVTGAAAAHWW  
-----HDAAATAATADD
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



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: 1
 Number of overlap: 11
 Similarity score: 0.560545

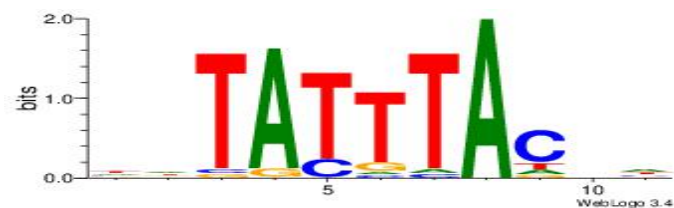
Alignment:

DHTATTTACBD-
 DDTATTATTTDH

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD

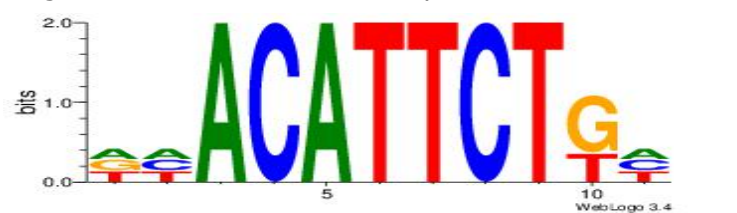


Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.583032

Alignment:
-HCAGAA TGTHD
DDTATTATTTDH

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAA TGTHD



Dataset #: 2
Motif ID: 19
Motif name: wsTACwGTAsw
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.584715

Alignment:
-DBTACWGTAVH
HDAAATAATADD

Original motif Consensus sequence: HVTACWG TABD

Reverse complement motif Consensus sequence: DBTACWGTAVH



Dataset #: 2
 Motif ID: 15
 Motif name: kCAGCCAATmr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.59598

Alignment:
 -MBATTGGCTGH
 DDTATTATTTDH

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



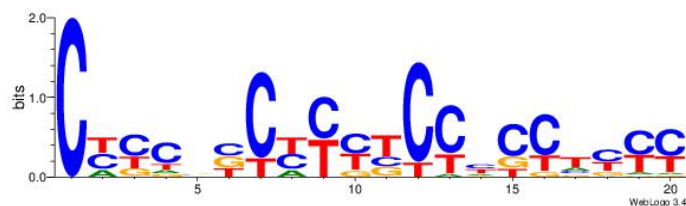
Dataset #: 1
 Motif ID: 9

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

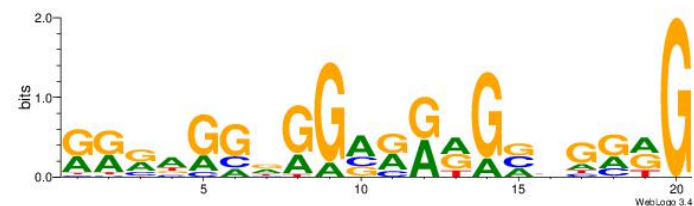
Alignment:

-----KKKAGGDGGAKKMGBBGKMG
 DDTATTATTDDH-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

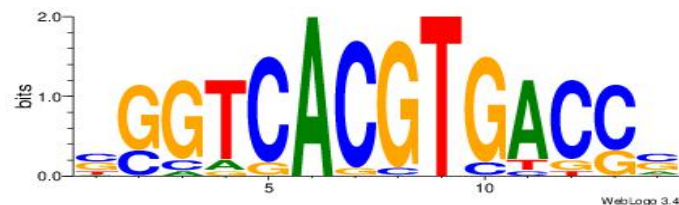


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

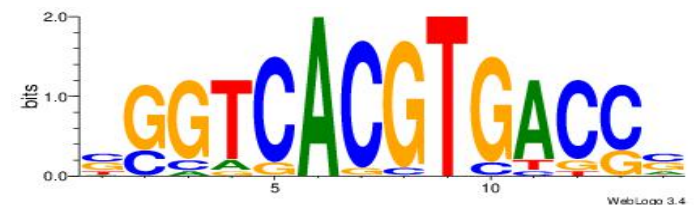


Dataset #: 2 Motif ID: 18 Motif name: sSGTCACGTGACs

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



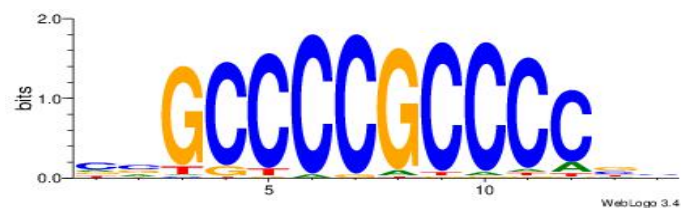
Best Matches for Motif ID 18 (Highest to Lowest)

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: 1
Number of overlap: 14
Similarity score: 0.0539097

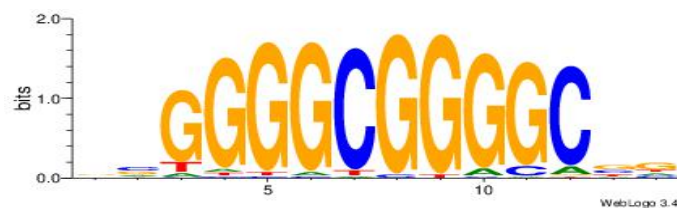
Alignment:

BBGGGGCGGGGCVD
SGGTCACGTGACCS

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

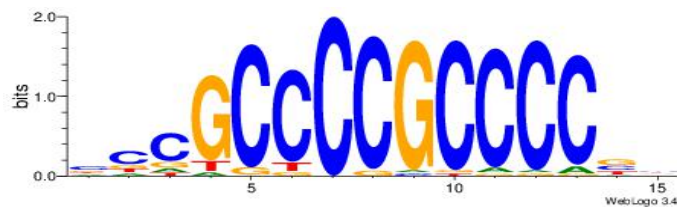


Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

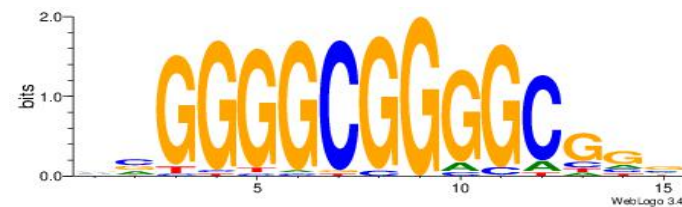
Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0581955

Alignment:
 BCCGCCCCGCCCCBB
 SGGTCACGTGACCS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



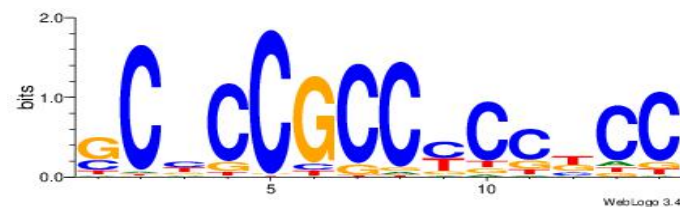
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 1.05855

Alignment:
 --GCVCCGCCMCCYCC
 SGGTCACGTGACCS--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

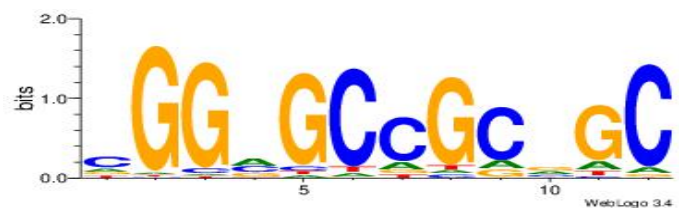


Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 1.06047

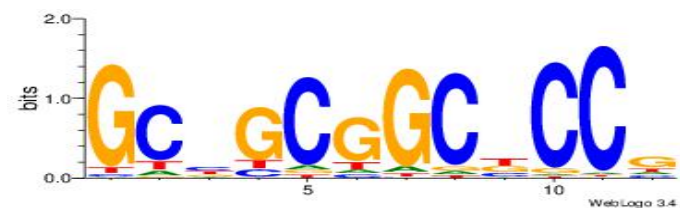
Alignment:

--CGGVGCCGCVGC
SGGTCACGTGACCS

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

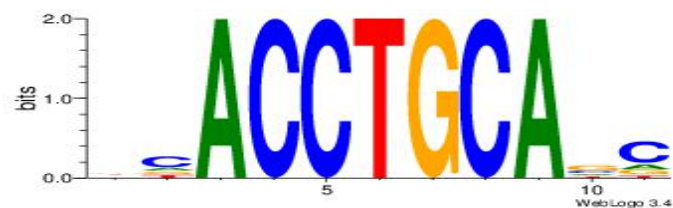


Dataset #: 2
 Motif ID: 16
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 1.54742

Alignment:

---BCACCTGCABC
 SGGTCACGTGACCS

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

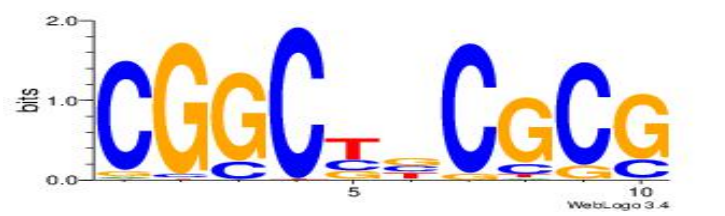


Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10

Similarity score: 2.05201

Alignment:
----CGCGBMGCCG
SGGTCACGTGACCS

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

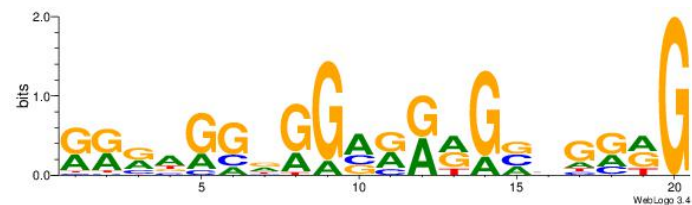
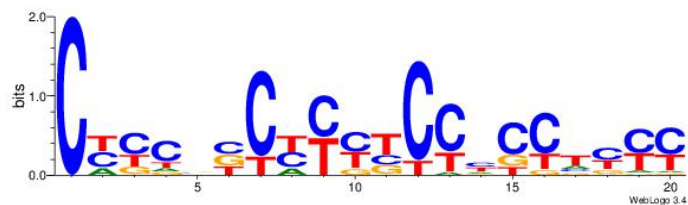


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 14
Number of overlap: 7
Similarity score: 3.55896

Alignment:
-----CYYCBCYYYTCCHCCTYYY
SGGTCACGTGACCS-----

Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



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: 2
 Number of overlap: 5
 Similarity score: 4.54286

Alignment:

-----CGCGAC
 SGGTCACGTGACCS-

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC

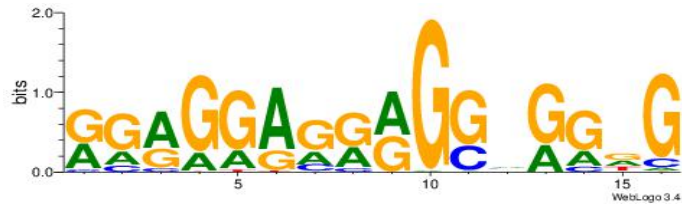


Dataset #: 1
 Motif ID: 6

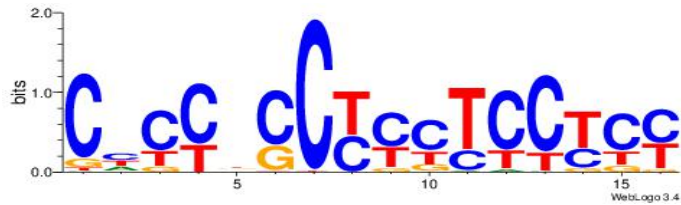
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 12
Number of overlap: 5
Similarity score: 4.549

Alignment:
-----CHCCBCKMCTCCKCM
SGGTCACGTGACCS-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



Dataset #: 1
Motif ID: 2
Motif name: TFW2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 4
Similarity score: 5.06029

Alignment:

SCGCGCGG-----
-----SGGTACAGTGACCS

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



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

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



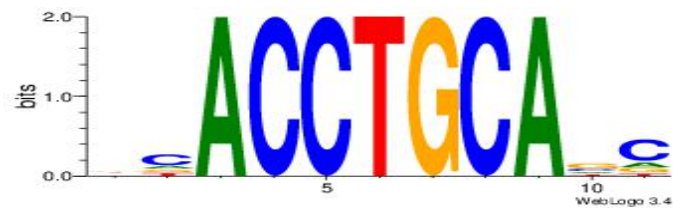
Best Matches for Motif ID 19 (Highest to Lowest)

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:	1

Number of overlap: 11
Similarity score: 0.0199592

Alignment:
GBTGCAGGTGB
HVTACWG TABD

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

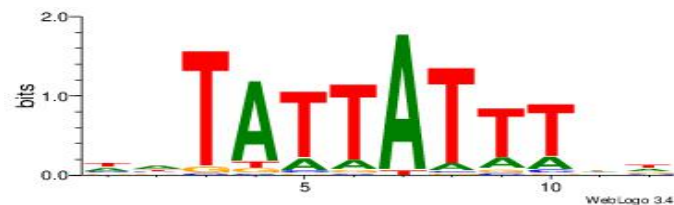
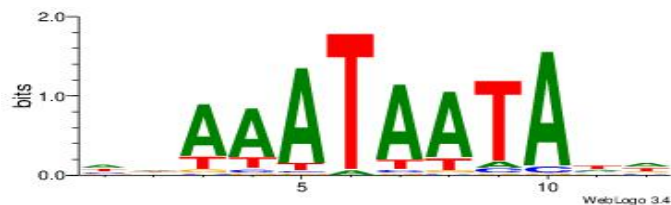


Dataset #: 2
Motif ID: 17
Motif name: wwAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0309343

Alignment:
DDTATTATTTDH
-HVTACWG TABD

Original motif Consensus sequence: HDAAATAATADD

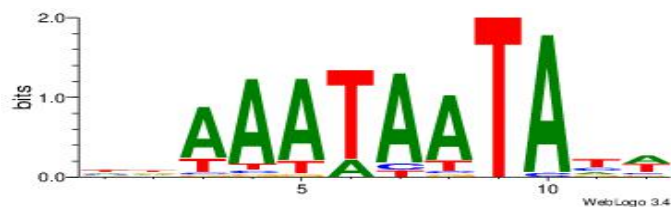
Reverse complement motif Consensus sequence: DDTATTATTTDH



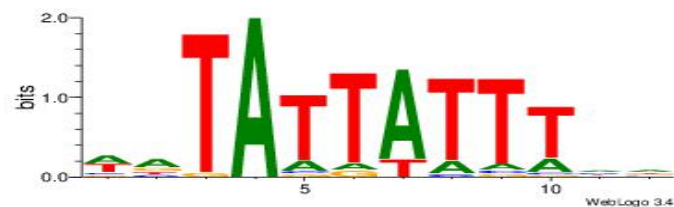
Dataset #: 2
 Motif ID: 13
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0337121

Alignment:
 HDAAATAATAHW
 DBTACWGTAVH-

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH



Dataset #: 2
 Motif ID: 21

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

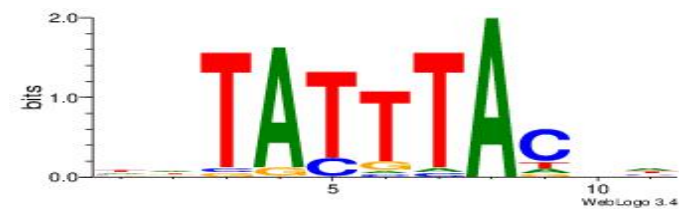
Alignment:

DBGTAAATAHD
DBTACWGTAVH

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



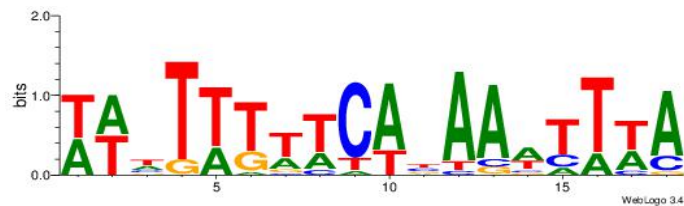
Dataset #:	1
Motif ID:	8
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	11
Similarity score:	0.0413797

Alignment:

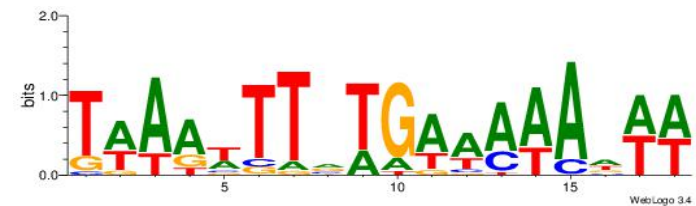
WWHTTTTTTCABAAWTTWA

---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

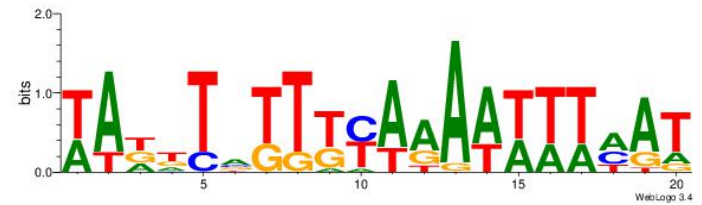
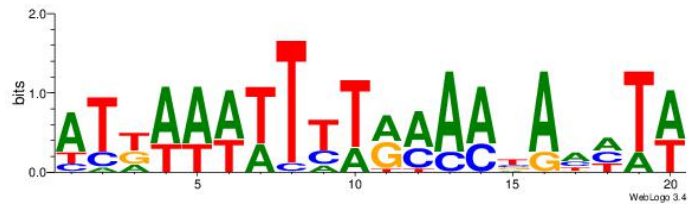
Alignment:

WAHHTVTTYKAAAATTRAT

-----HVTACWGATABD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT

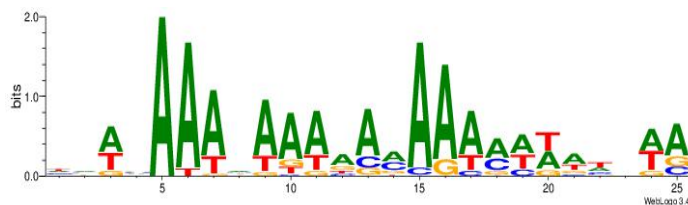


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0472742

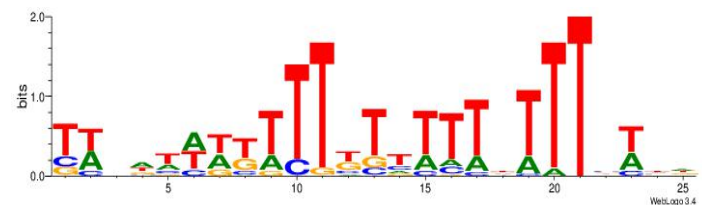
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
---DBTACWGTAVH-----
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTTTTTTTTTHTTTVWBH



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: 2
 Number of overlap: 10
 Similarity score: 0.544444

Alignment:
 HCAGAATGTHD-
 -HVTACWG TABD

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

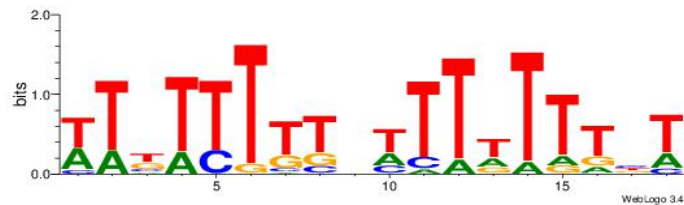


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 9
 Similarity score: 1.04742

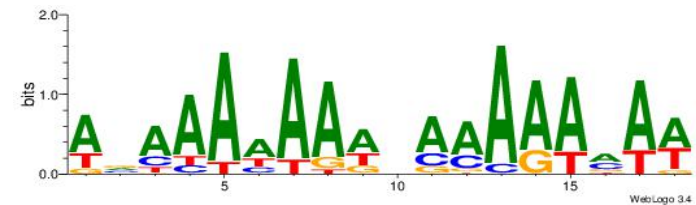
Alignment:

WKTTTTTHWTTTTTBT--
-----DBTACWGTAVH

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW



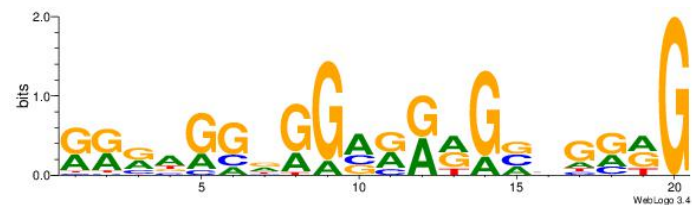
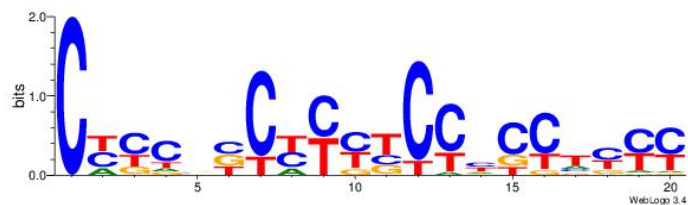
Dataset #:	1
Motif ID:	9
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	15
Number of overlap:	6
Similarity score:	2.54736

Alignment:

-----CYVCBBCYYYTCCHCCTYYY
DBTACWGTAVH-----

Original motif Consensus sequence: CYVCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



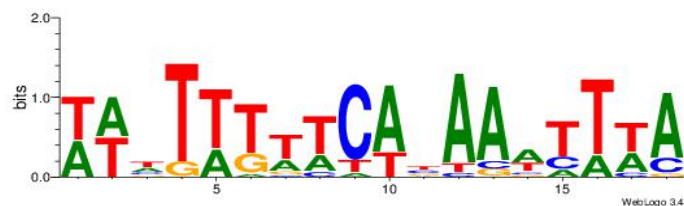
Best Matches for Motif ID 20 (Highest to Lowest)

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

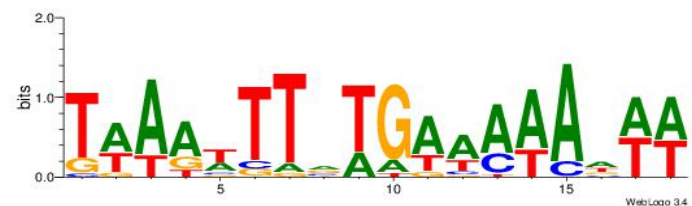
Alignment:

```
WWHTTTTTCABAAWTTWA
HCAGAATGTHD-----
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.00731643

Alignment:
BCACCTGCABC
DHACATTCTGH

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

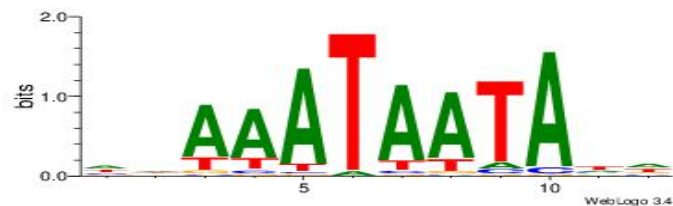


Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0127231

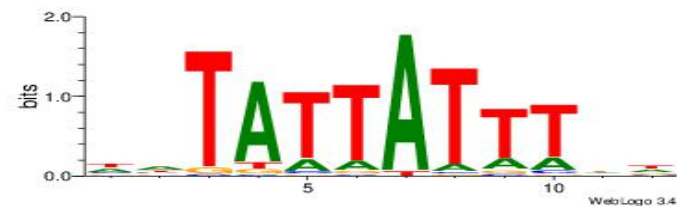
Alignment:

DDTATTATTTDH
 -HCAGAAATGTHD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

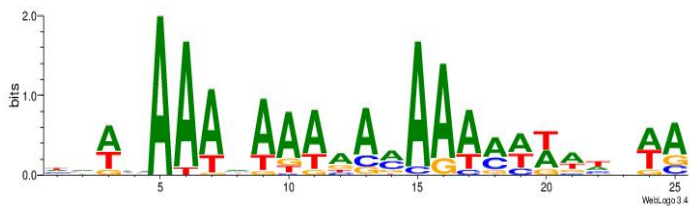


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 11

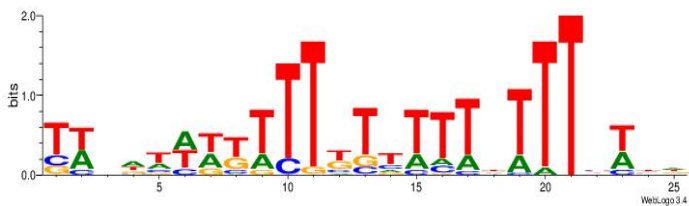
Similarity score: 0.014258

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
-----HCAGAATGTHD-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTTTTTTTHTTTVWBH

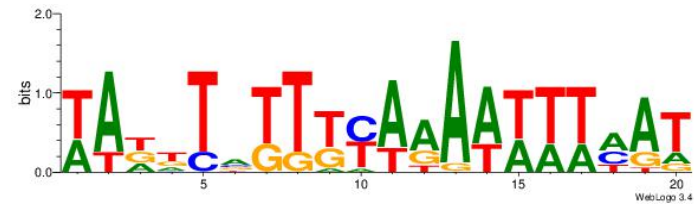
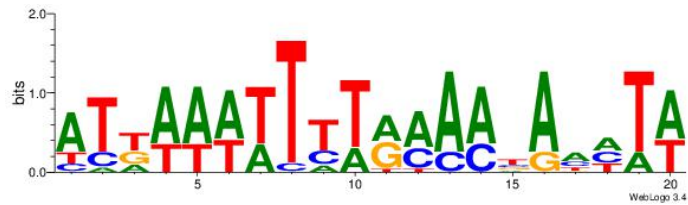


Dataset #: 1
Motif ID: 10
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 11
Similarity score: 0.0192045

Alignment:
ATKAAWTTTTTRMAABAHHTW
-DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHHTW

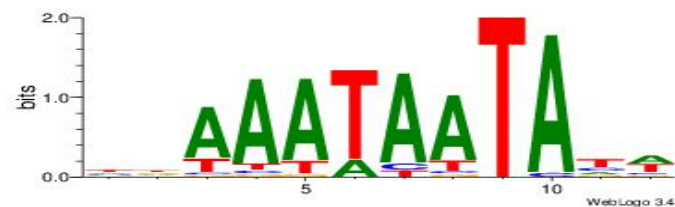
Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT



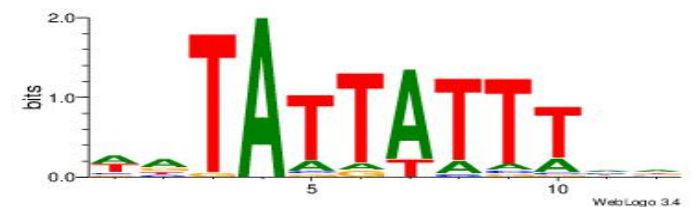
Dataset #: 2
 Motif ID: 13
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0199621

Alignment:
 WHTATTATTTDH
 -HCAGAATGTHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #: 2
 Motif ID: 15

Motif name:	kCAGCCAATmr
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0247304

Alignment:

MBATTGGCTGH
DHACATTCTGH

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH

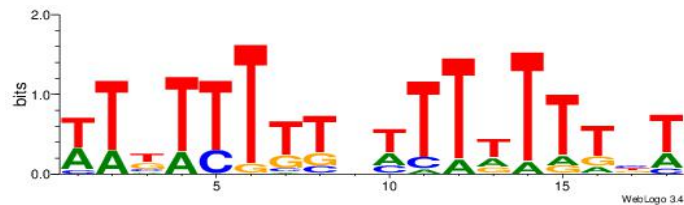


Dataset #:	1
Motif ID:	7
Motif name:	TFM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.519904

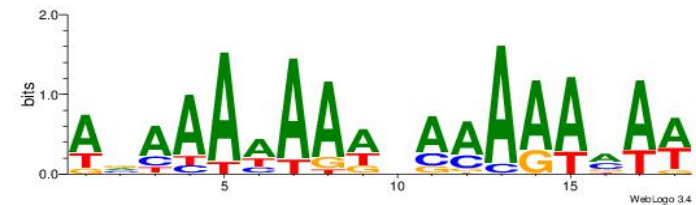
Alignment:

ABAAAAAWhAAAAARAW-
-----HCAGAATGTHD

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW



Dataset #:	2
Motif ID:	19
Motif name:	wsTACwGTAsw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.527917

Alignment:

-DBTACWGTAVH
DHACATTCTGH-

Original motif Consensus sequence: HVTACWGTabD

Reverse complement motif Consensus sequence: DBTACWGTAVH

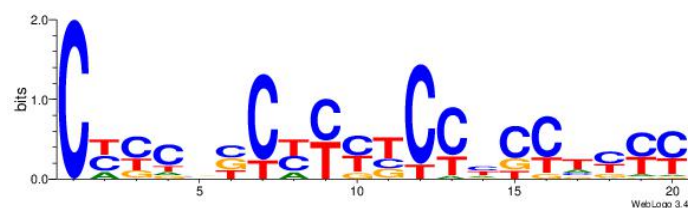


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 17
 Number of overlap: 4
 Similarity score: 3.5

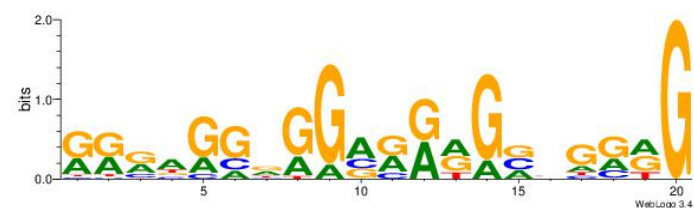
Alignment:

-----CYYCBBCYYYTCCHCCTYYY
 DHACATTCTGH-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

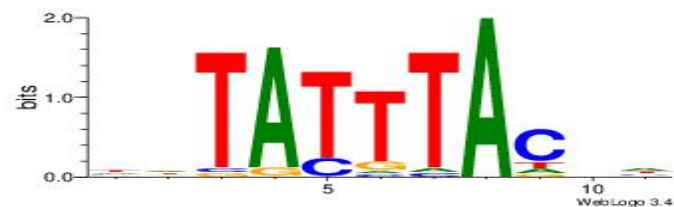


Dataset #: 2 Motif ID: 21 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Best Matches for Motif ID 21 (Highest to Lowest)

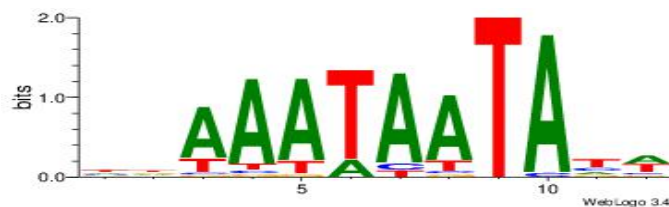
Dataset #:	2
Motif ID:	13
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0162338

Alignment:

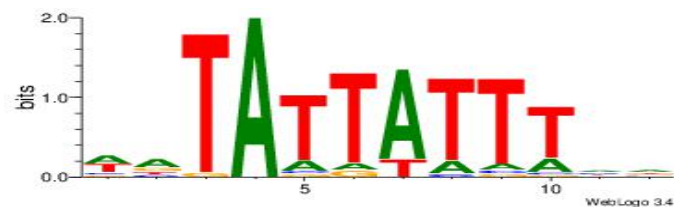
HDAAATAATAHW

-DBGTAATAHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

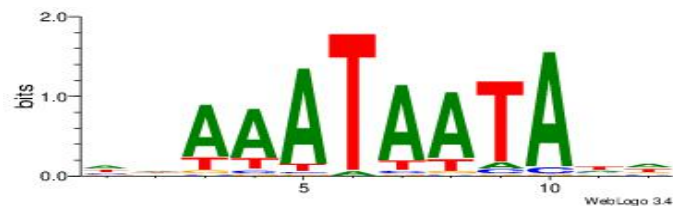


Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0164863

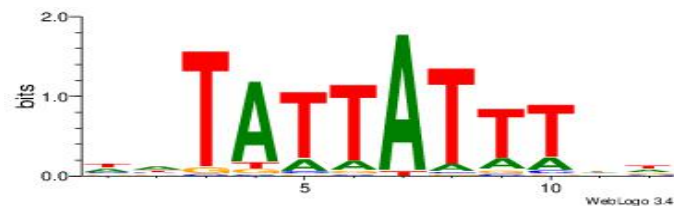
Alignment:

DDTATTATTTDH
 DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

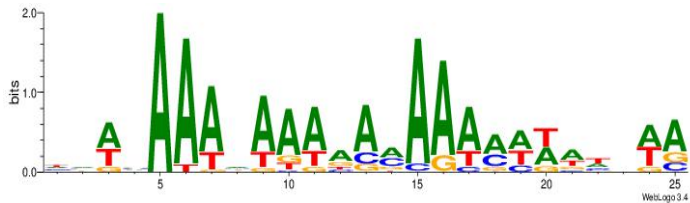


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 11

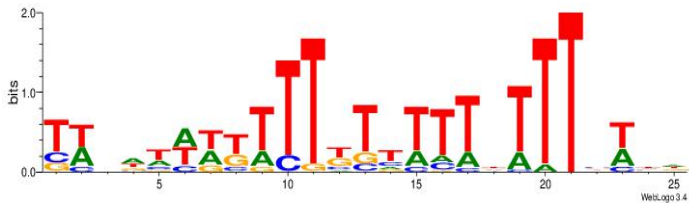
Similarity score: 0.0192768

Alignment:
TWVHWWYTTTYYTTTTHTTTVWBH
-----DHTATTTACBD

Original motif Consensus sequence:
HDWVAAAHAAAAAAMAAAMWWHBA



Reverse complement motif Consensus sequence:
TWVHWWYTTTYYTTTTHTTTVWBH

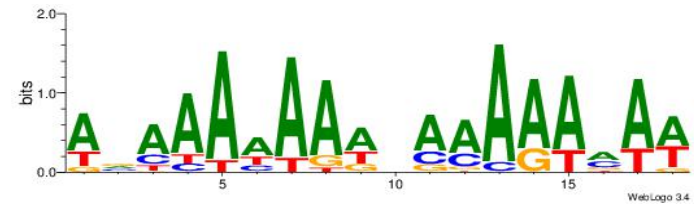
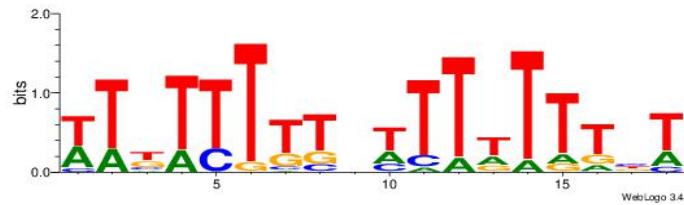


Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0283217

Alignment:
WTKTTTTTHWTTTTTTBT
DHTATTTACBD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW

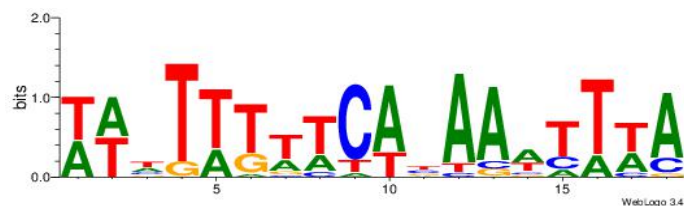


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0308097

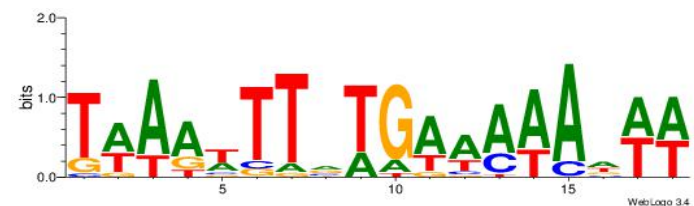
Alignment:

WWHTTTTTTCABAAWTTWA
 -----DHTATTTACBD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



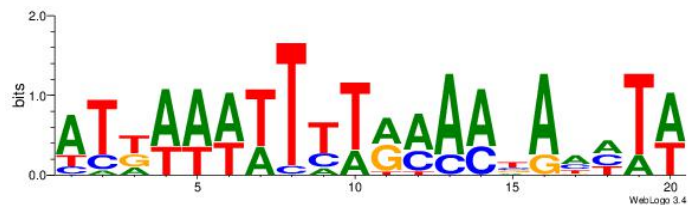
Dataset #: 1

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

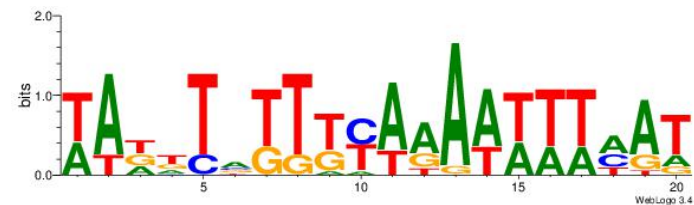
Alignment:

ATKAAWTTTTRMAABAHHTW
 -----DBGTAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2
 Motif ID: 19
 Motif name: wsTACwGTAsw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0472403

Alignment:

HVTACWG TABD

DHTATTTACBD

Original motif Consensus sequence: HVTACWG TABD



Reverse complement motif Consensus sequence: DBTACWG TAVH



Dataset #: 2
Motif ID: 15
Motif name: kCAGCCAATmr
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.554132

Alignment:

-MBATTGGCTGH

DHTATTTACBD-

Original motif Consensus sequence: DCAGCCAATVR

Reverse complement motif Consensus sequence: MBATTGGCTGH

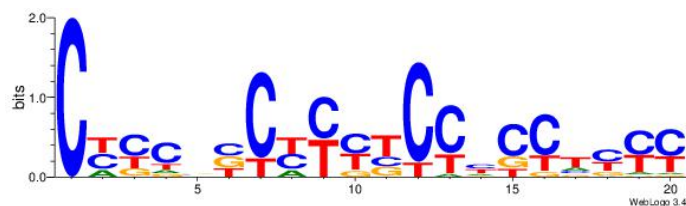


Dataset #:	1
Motif ID:	9
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	14
Number of overlap:	7
Similarity score:	2.0544

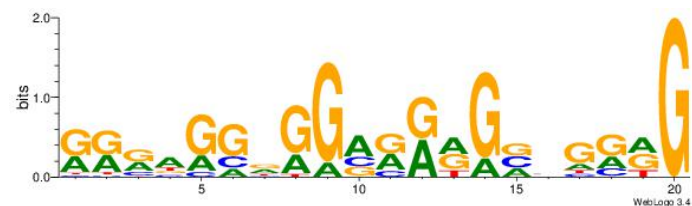
Alignment:

-----KKKAGGDGGAKKMGBBGKMG
DHTATTTACBD-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
 KKKAGGDGGAKKMGBBGKMG



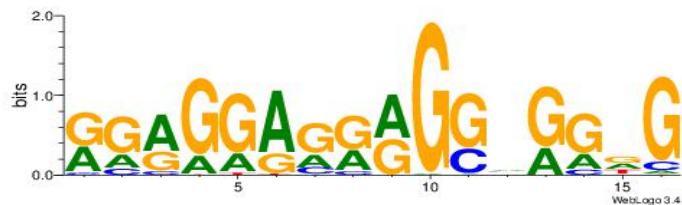
Dataset #: 1

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

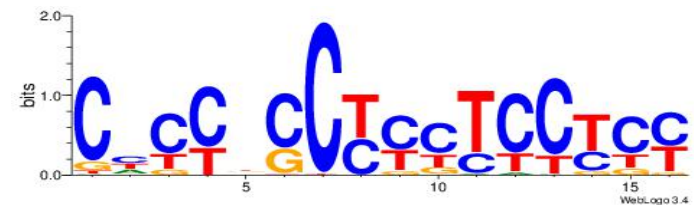
Alignment:

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

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



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

MOTIFSIM is written by Ngoc Tam L. Tran
 Motif logo generated by [weblogo](http://weblogo.threebio.com)