



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

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

Input files and motif counts

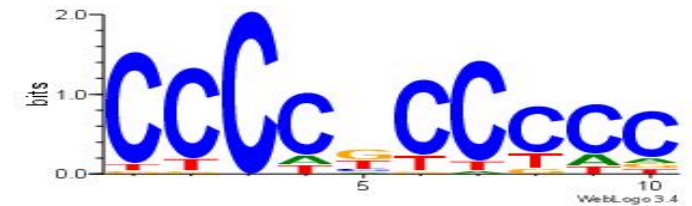
File name	Count of motifs	Dataset number
DREME_DM230.txt	1	1
MEME_DM230.txt	20	2
PScanChIP_DM230.txt	14	3
RSAT_peak-motifs_DM230.txt	10	4
W-ChIPMotifs_DM230.txt	11	5

RESULTS

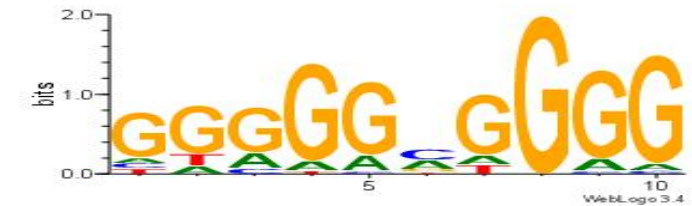
Top 5 Significant Motifs - Global Matching (Highest to Lowest)

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

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



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

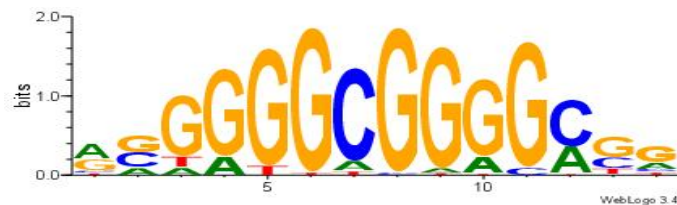
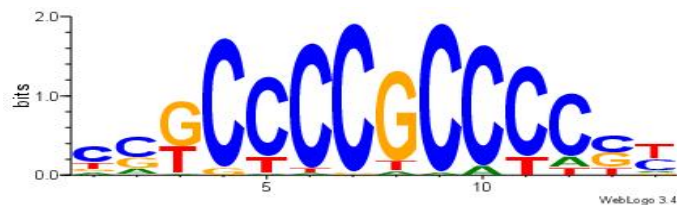
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.00451594

Alignment:

```
CSKCCCCGCCCSY
---CCCCKCCCC-
```

Original motif Consensus sequence: CSKCCCCGCCCSY

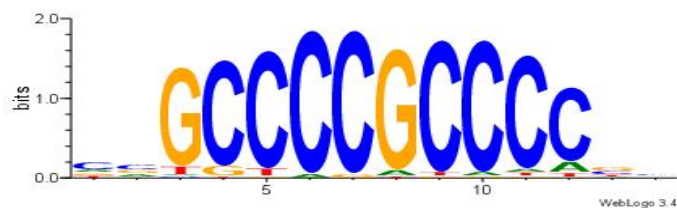
Reverse complement motif Consensus sequence: MSGGGCGGGGY



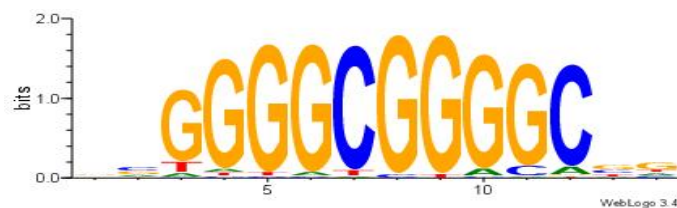
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.00965796

Alignment:
 HVGCCCCGCCCCBB
 ---CCCCKCCCC-

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGc

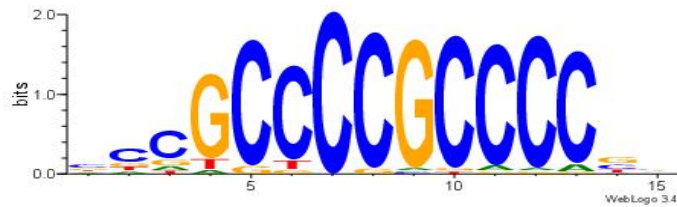


Dataset #: 4
 Motif ID: 38

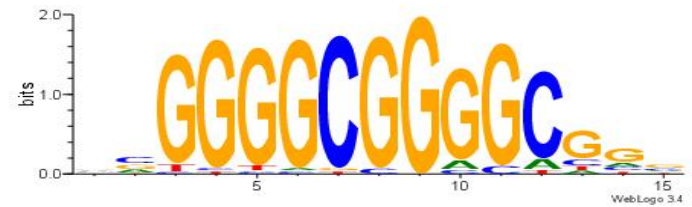
Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0127292

Alignment:
 BCCGCCCCGCCCCBB
 ----CCCCKCCCC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

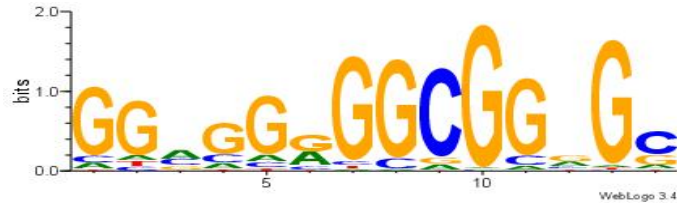


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0174405

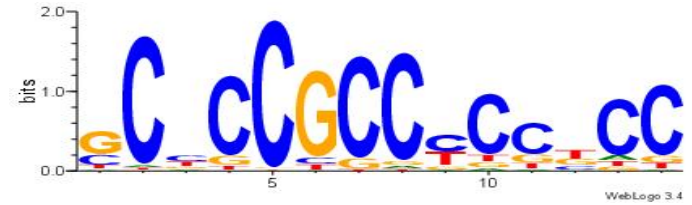
Alignment:

GGMGGRGGCGGVGC
---GGGGYGGGG---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



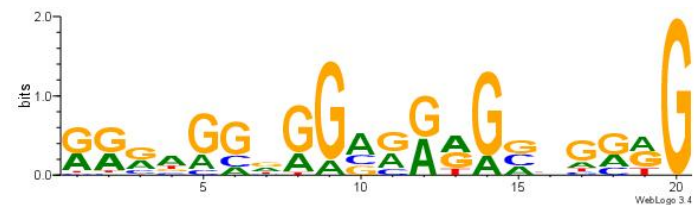
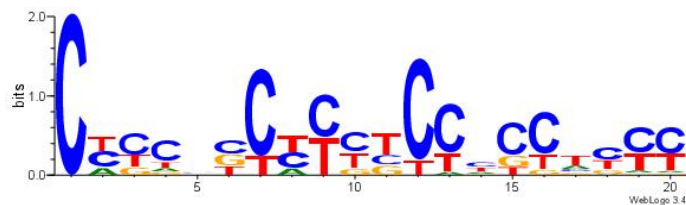
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 10
Similarity score: 0.0301548

Alignment:

CYCBBCYYYTCCHCCTYYY
-----CCCCKCCCC-----

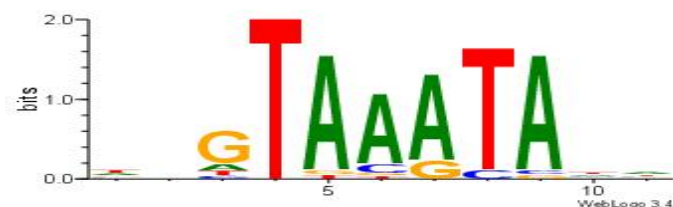
Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

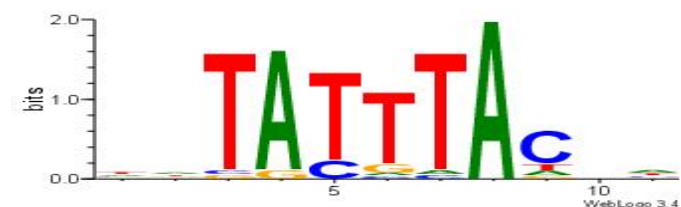


Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



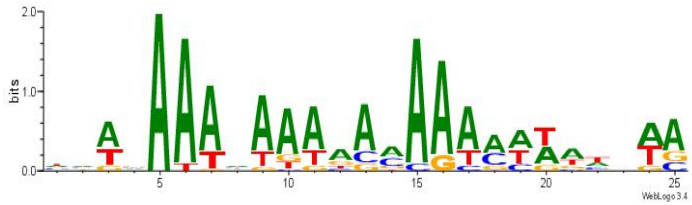
Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

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

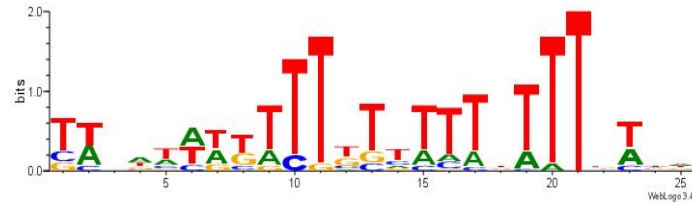
Alignment:

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

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



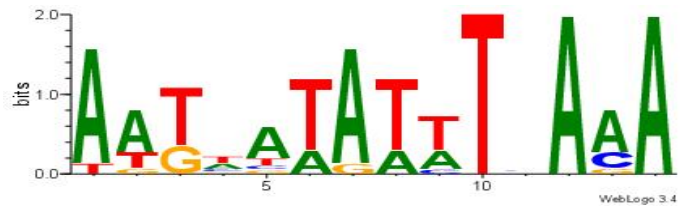
Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTHTTTTVWBH



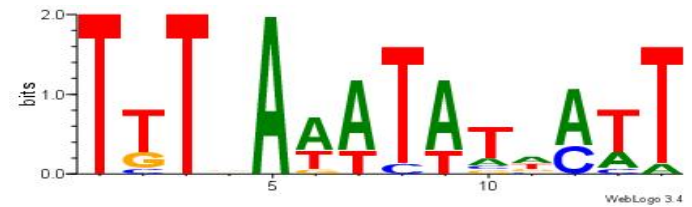
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0250541

Alignment:
 AATHATATWTHAAA
 DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



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

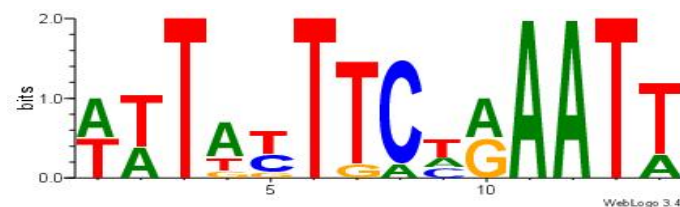
Alignment:

AATTYDGAARTAWW
 ---DBGTAAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



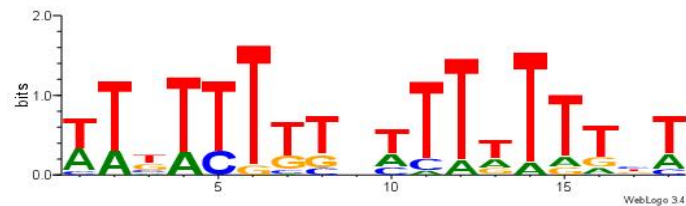
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0283217

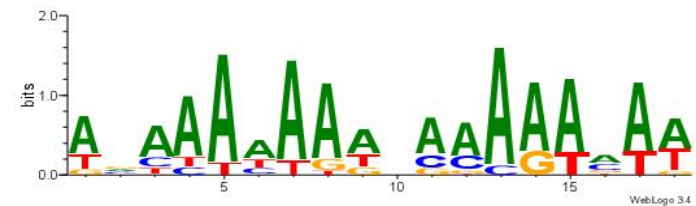
Alignment:

ABAAAAAWhAAAAARAW
DBGTAATAHD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW



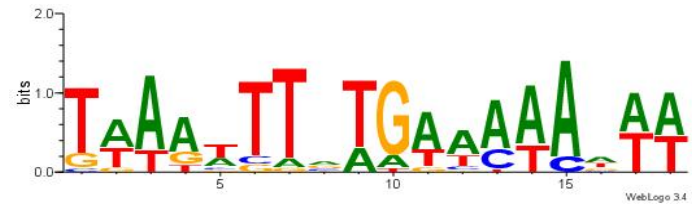
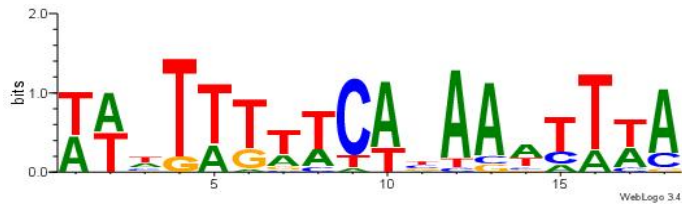
Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0308097

Alignment:

TWAAWTTVTGAAAAAHWW
-----DBGTAATAHD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TWAAWTTVTGAAAAAHWW

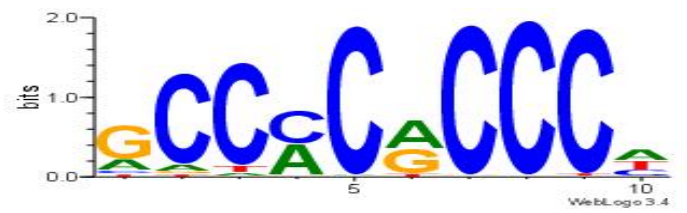


Dataset #: 3 Motif ID: 27 Motif name: Klf4

Original motif Consensus sequence: DGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

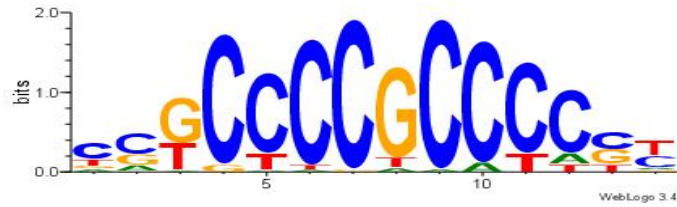


Best Matches for Top Significant Motif ID 27 (Highest to Lowest)

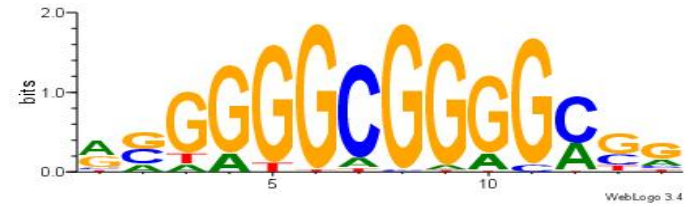
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0152457

Alignment:
 CSKCCCCGCCCSY
 --GCCYCMCCCD--

Original motif Consensus sequence: CSKCCCCGCCCSY



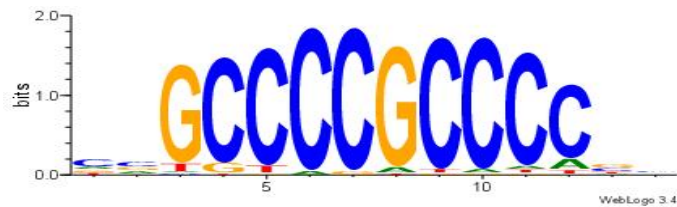
Reverse complement motif Consensus sequence: MSGGGCGGGGY



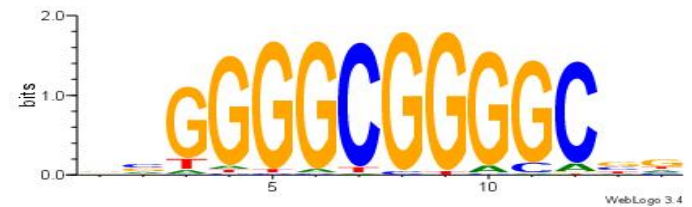
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCSc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0160185

Alignment:
BBGGGGCGGGGCVD
--DGGGYGKGGC--

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

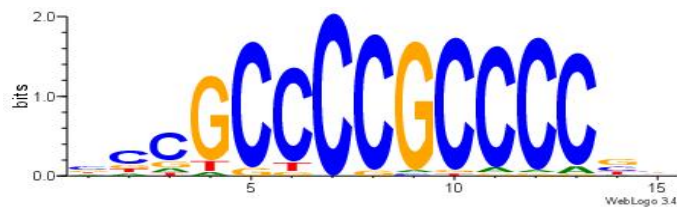


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0194893

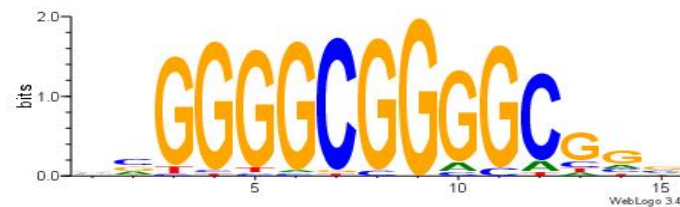
Alignment:

BBGGGGCGGGGCGGB
 --DGGGYGKGGC---

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

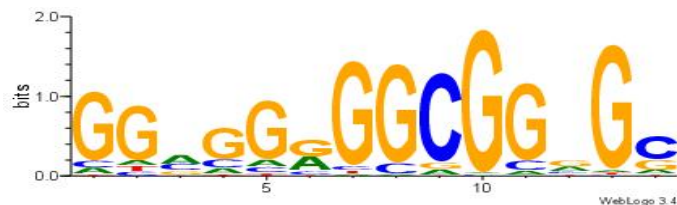


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5

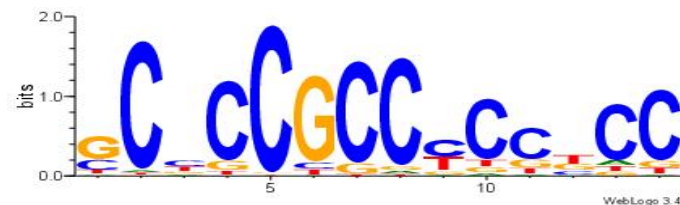
Number of overlap: 10
Similarity score: 0.0402906

Alignment:
GGMGGRGGCGGVGC
----DGGGYGKGGC

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

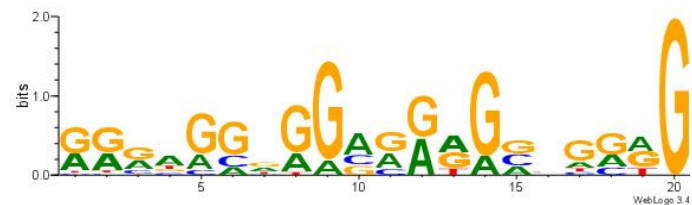
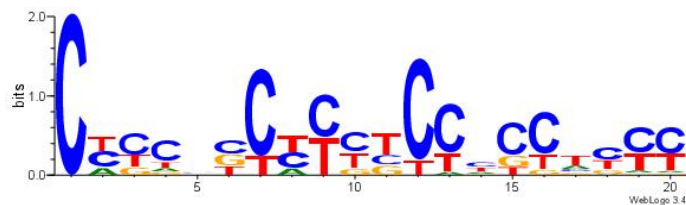


Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0556427

Alignment:
CYCBBCYYYTCCHCCTYYY
----GCCYCMCCD-----

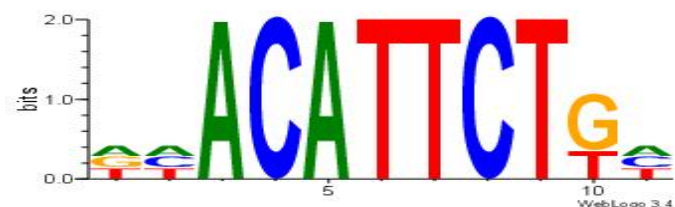
Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



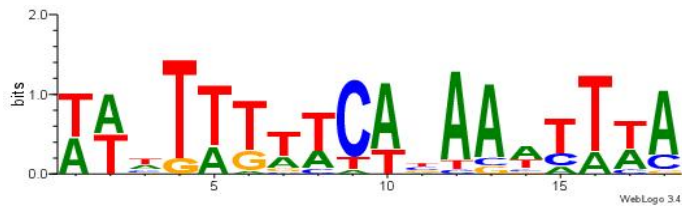
Best Matches for Top Significant Motif ID 44 (Highest to Lowest)

Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	11
Similarity score:	0.0217516

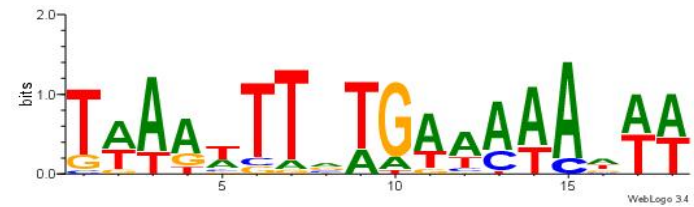
Alignment:

```
TWAAWTTVTGAAAAAHWW
DHACATTCTGH-----
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

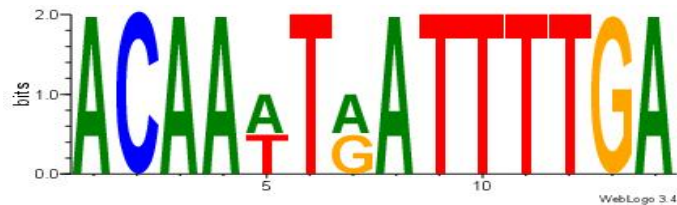


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0258838

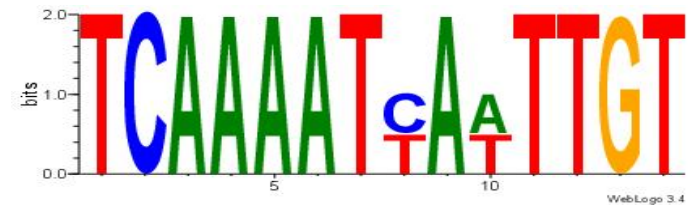
Alignment:

TCAAATKAWTTGT
HCAGAATGTHD---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAATKAWTTG

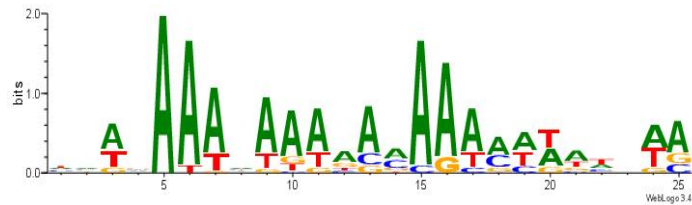


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 11
 Similarity score: 0.0307858

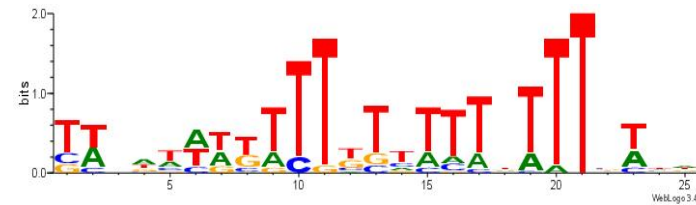
Alignment:

TWVHWWWYTTTYTTTTHTTTVWBH
 ----DHACATTCTGH-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTYTTTTHTTTVWBH



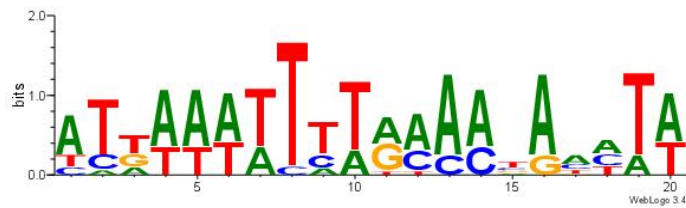
Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 11
Similarity score: 0.0357323

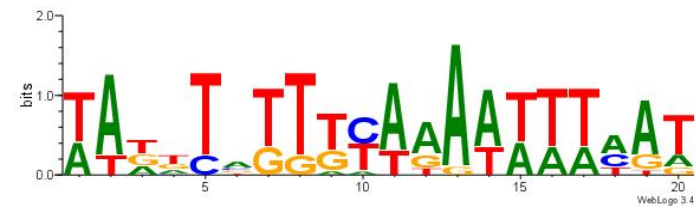
Alignment:

ATKAAWTTTTTRMAABAHTW
-DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT



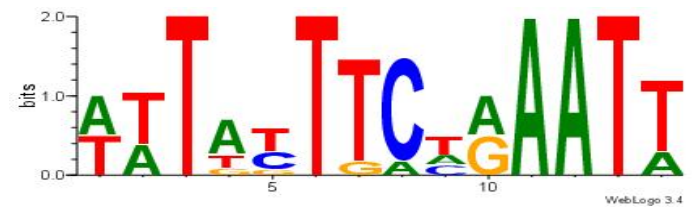
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0400884

Alignment:

AATTYDGAARTAWW
HCAGAATGTHD---

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



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

Original motif Consensus sequence: GCGGGGC



Reverse complement motif Consensus sequence: GCCCGCC

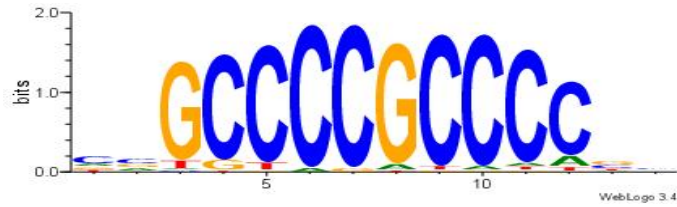


Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

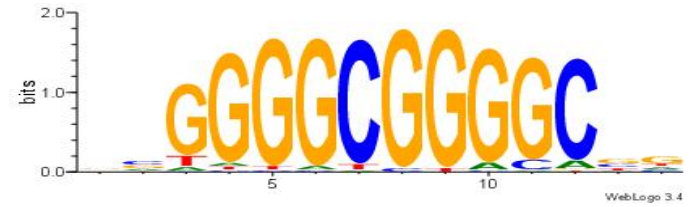
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0

Alignment:
 BBGGGGCGGGGCVD
 ----GGCGGGGC--

Original motif Consensus sequence: HVGCCCCGCCCB



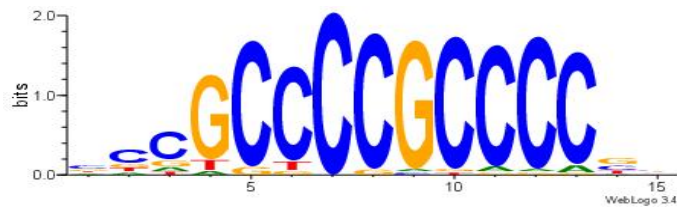
Reverse complement motif Consensus sequence: BBGGGCGGGGC



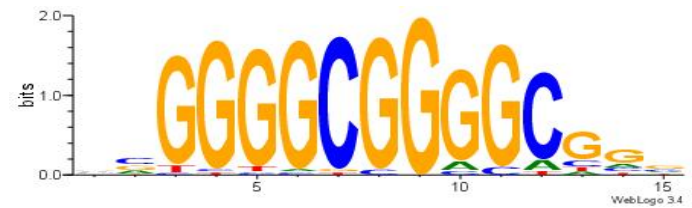
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCBsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.00250079

Alignment:
 BBGGGCGGGGCGGB
 ----GGCGGGGC----

Original motif Consensus sequence: BCCGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGCGGB

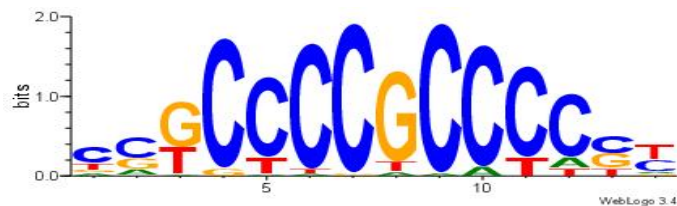


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0149958

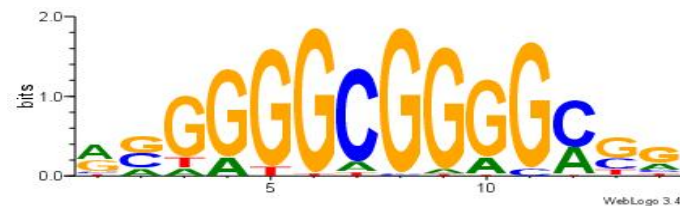
Alignment:

MSGGGGCGGGGYSG
 ----GGCGGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



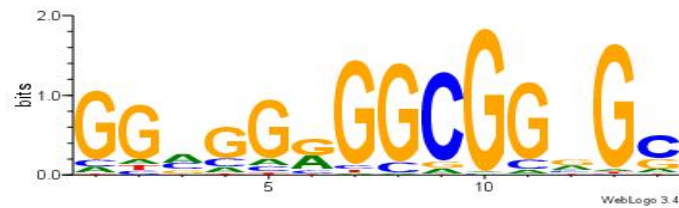
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 8

Similarity score: 0.0348969

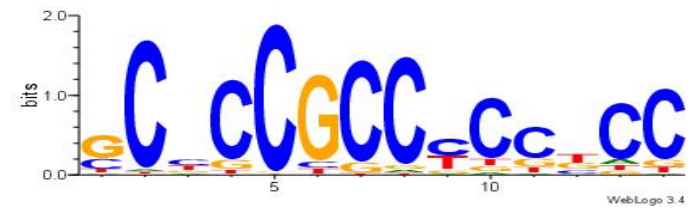
Alignment:

GCVCCGCCMCCYCC
GCCCCGCC-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



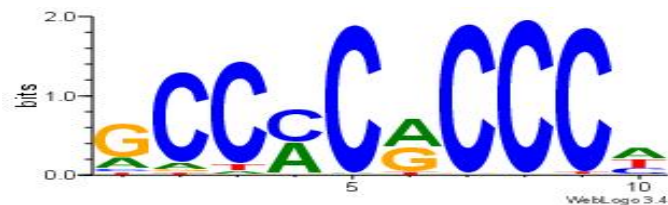
Dataset #: 3
Motif ID: 27
Motif name: Klf4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0349983

Alignment:

DGGGYGKGGC
--GGCGGGC

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

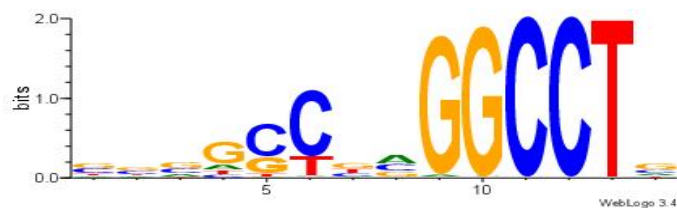


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0708224

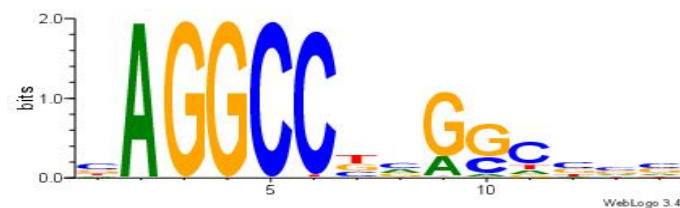
Alignment:

VAGGCCBBGGCVBB
 ---GCCCCGCC---

Original motif Consensus sequence: BBVGCCBVGCCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Results created by MOTIFSIM on 12-16-2022 12:54:26
Runtime: 365.907 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
Motif logo generated by [weblago](#)