



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

INPUT

Input Parameters

Number of files:	5
Number of top significant motifs:	10
Number of best matches:	10
Similarity cutoff \geq	0.75
Matching motif database:	UniProbe Mus Musculus
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
DREME_DM230.txt	1	1
MEME_DM230.txt	20	2
PScanChIP_DM230.txt	14	3
RSAT_peak-motifs_DM230.txt	10	4
W-ChIPMotifs_DM230.txt	11	5

RESULTS

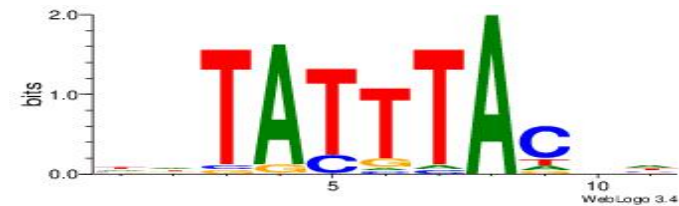
Top 10 Significant Motifs - Global Matching (Highest to Lowest)

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

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



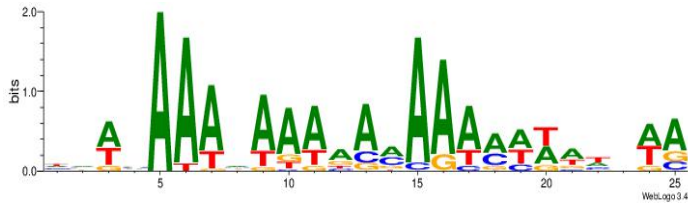
Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

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

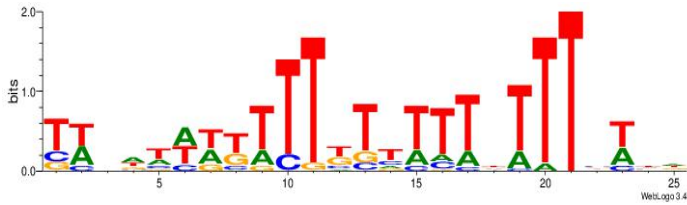
Alignment:

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

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWHBBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTHTTTVWBH



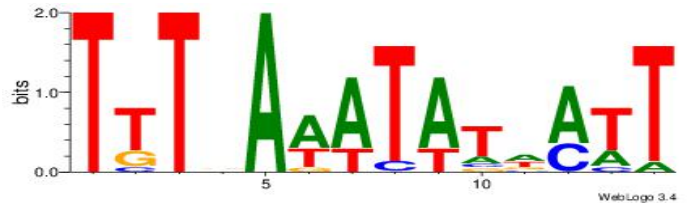
Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0250541

Alignment:
AATHATATWTHAAA
DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



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

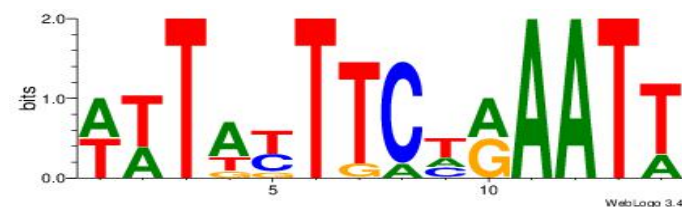
Alignment:

AATTYDGAARTAWW
 ---DBGTAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

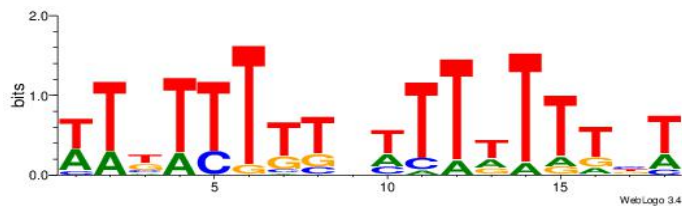


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

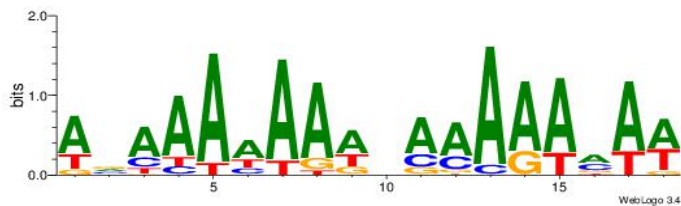
Similarity score: 0.0283217

Alignment:
ABAAAAAAWHAAAAARAW
DBGTAATAHD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW

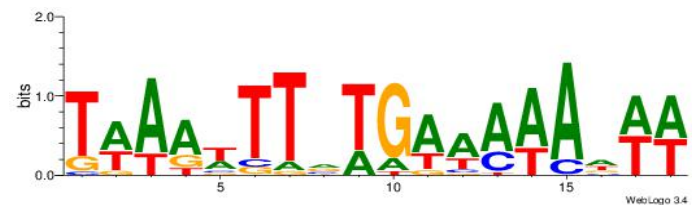
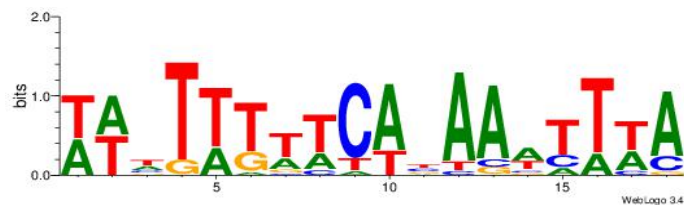


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0308097

Alignment:
TWAAWTTVTGAAAAAHWW
-----DBGTAATAHD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TWAAWTTVTGAAAAAHWW

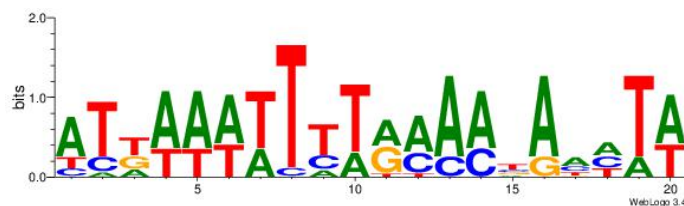


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0333874

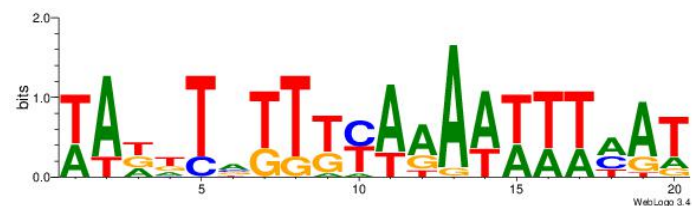
Alignment:

ATKAAWTTTTRMAABAHHTW
 -----DBGTAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2

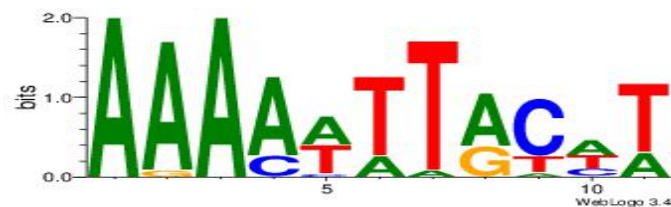
Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0361187

Alignment:

AAAWTTTCWT

DHTATTTACBD

Original motif Consensus sequence: AAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



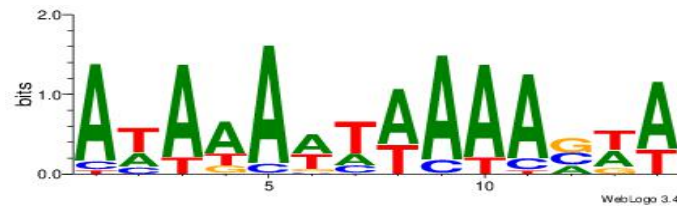
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0410381

Alignment:

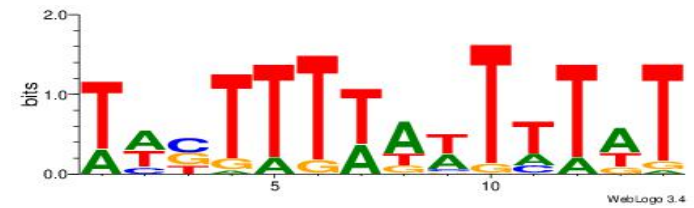
AWAAAWTWAAASWA

--DHTATTTACBD--

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV



Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0477814

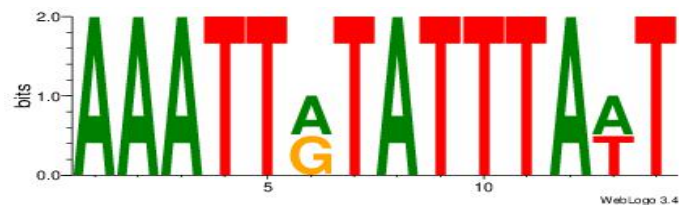
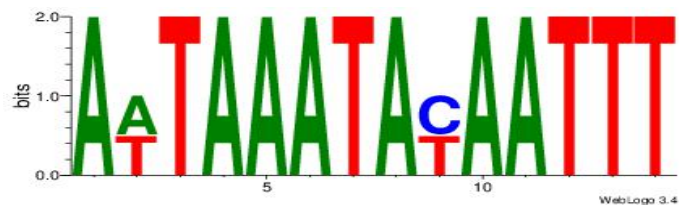
Alignment:

AWTAAATAYAATTT

---DHTATTTACBD

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW

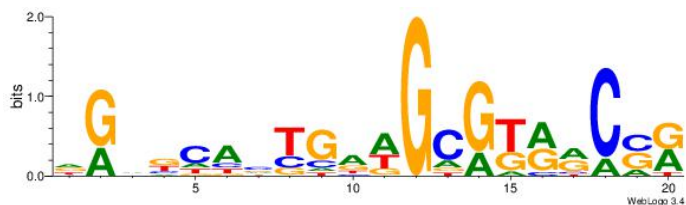


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0512987

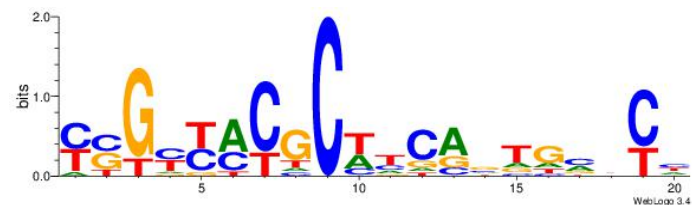
Alignment:

DGVBCABTGDWGCGRRCR
 DBGTAATAHD-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

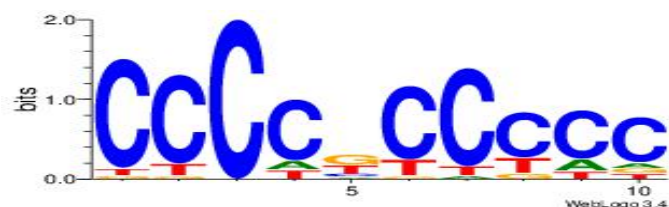


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

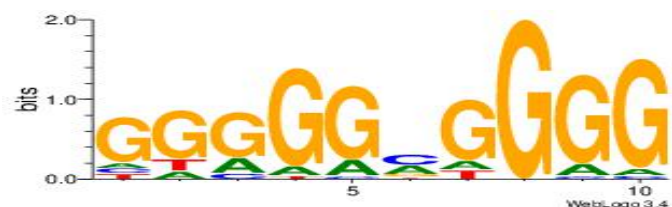


Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



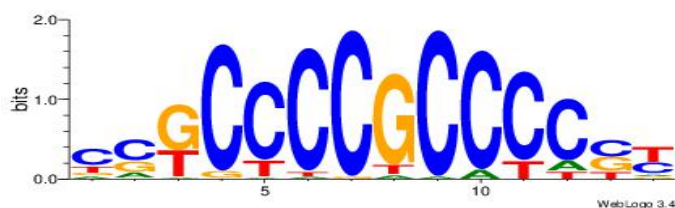
Best Matches for Top Significant Motif ID 24 (Highest to Lowest)

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

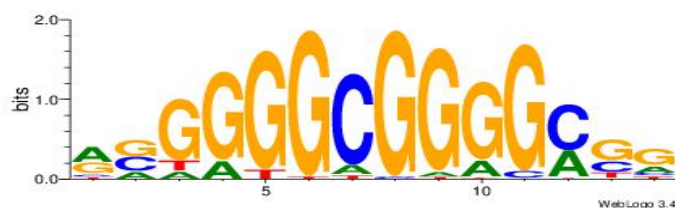
Alignment:

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

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

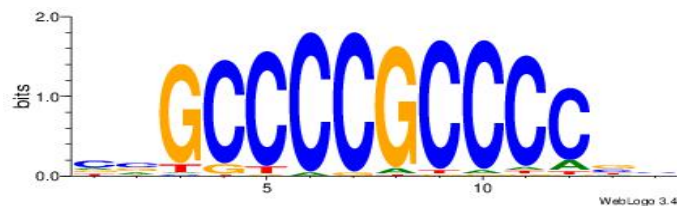


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.00965796

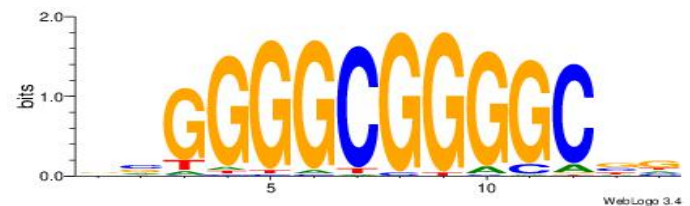
Alignment:

BBGGGGCGGGGCVD
 -GGGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

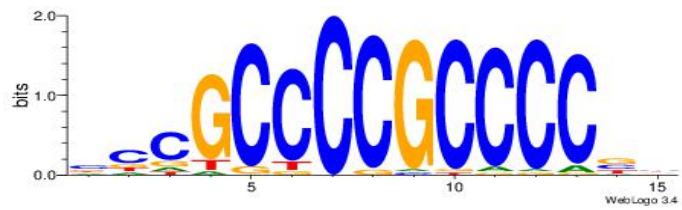


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 10

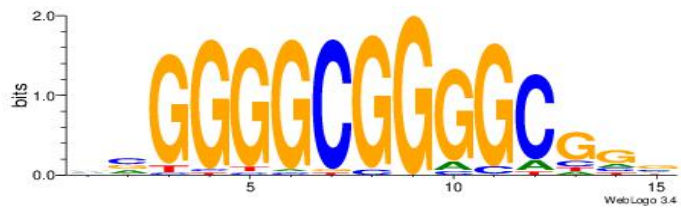
Similarity score: 0.0127292

Alignment:
BBGGGGCGGGGCGGB
-GGGGGYGGGG----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

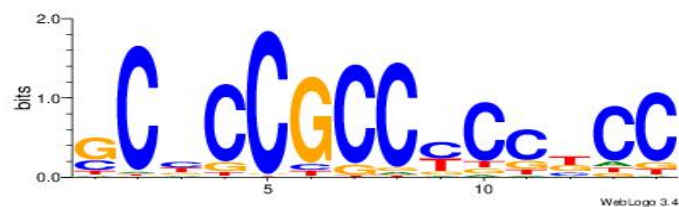


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0174405

Alignment:
GGMGGRGGCGGVGC
---GGGGGYGGGG-

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY

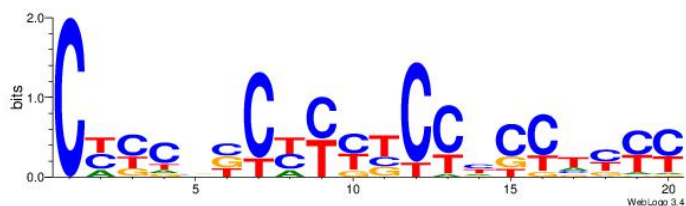


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	10
Similarity score:	0.0301548

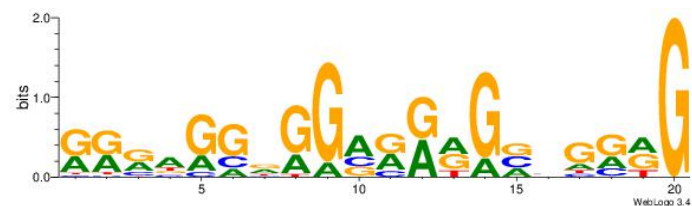
Alignment:

CYYCBBCYYYTCCHCCTYYY
-----CCCCKCCCCC-----

Original motif Consensus sequence: **CYYCBBCYYYTCCHCCTYYY**



Reverse complement motif Consensus sequence:
 KKKAGGDGGAKKMGBBGKMG



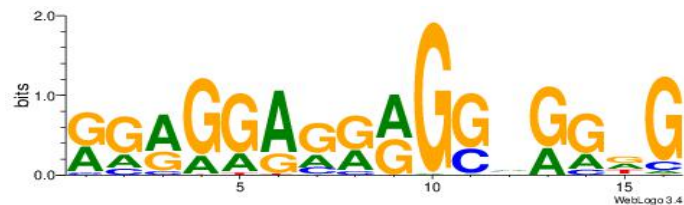
Dataset #: 5

Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0329167

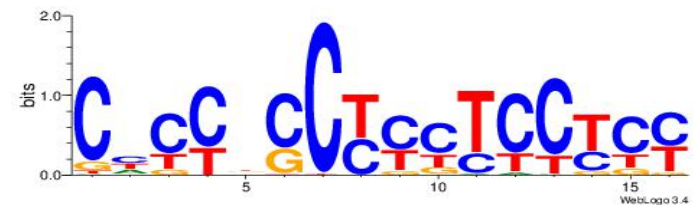
Alignment:

RGRGGAGRRGGHGGDG
 -----GGGGGYGGGG

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10

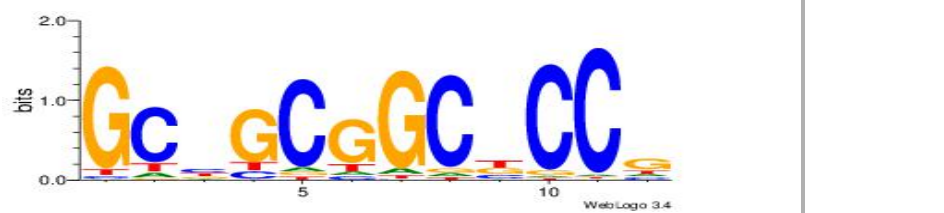
Similarity score: 0.0557738

Alignment:
GCVGCGGCBCCG
-CCCCKCCCCC-

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

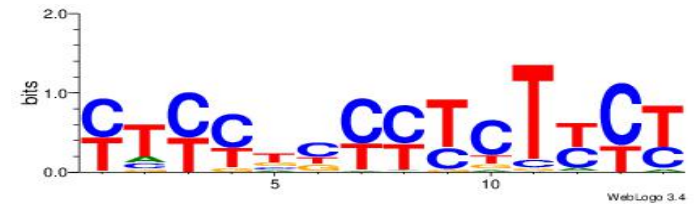
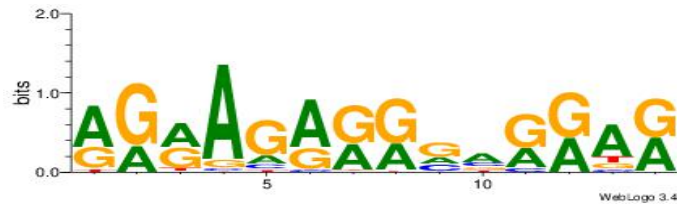


Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0648214

Alignment:
MTMMTCMMTCTKCK
----CCCCKCCCCC

Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



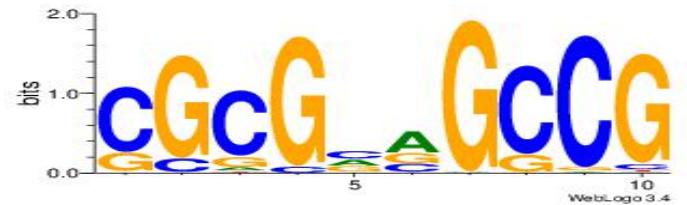
Dataset #: 5
 Motif ID: 48
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0762976

Alignment:
 CGGCYBCGCG
 CCCCCKCCCC

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



Dataset #: 4
 Motif ID: 40

Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0841987

Alignment:

GBTGCAGGTGB
 GGGGGYGGGG-

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 3 Motif ID: 32 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



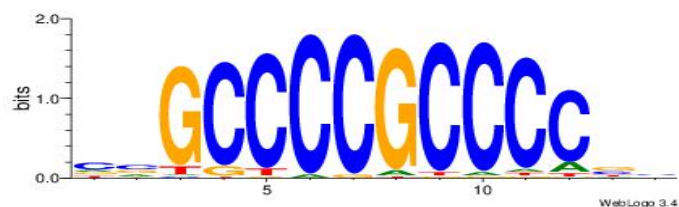
Best Matches for Top Significant Motif ID 32 (Highest to Lowest)

Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0396403

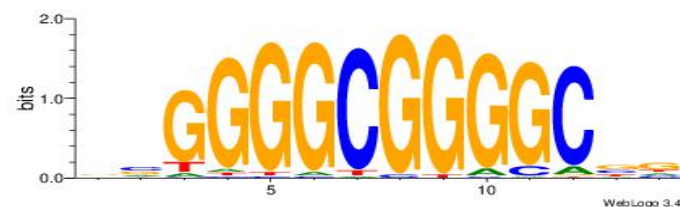
Alignment:

HVGCCCCGCCCCBB
 ----CACGCM----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 1
 Motif ID: 1
 Motif name: Motif 1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6

Similarity score: 0.040625

Alignment:
GCCCCGCC
--CACGCM

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCCGCC

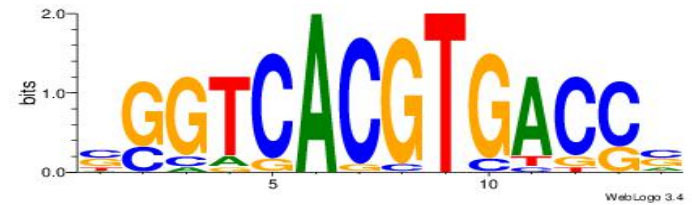
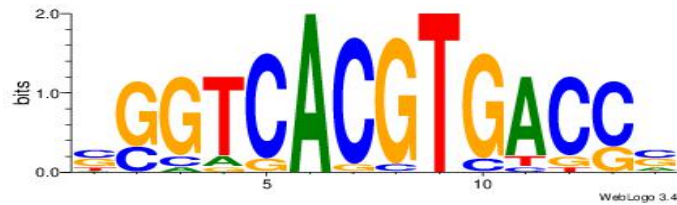


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0412037

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

Original motif Consensus sequence: SGGTCACGTGACCS

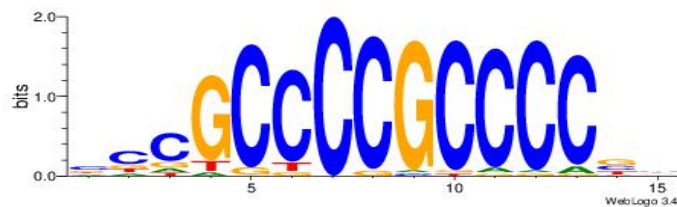
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



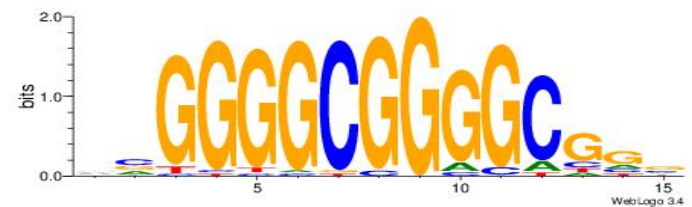
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0425089

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

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



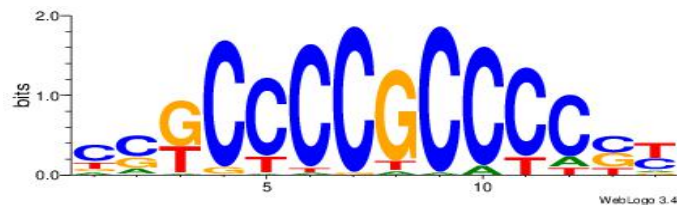
Dataset #: 2

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

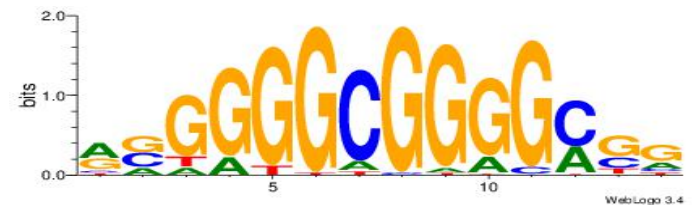
Alignment:

```
MSGGGGCGGGGYSG
----YGCGTG----
```

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #:	5
Motif ID:	47
Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0469722

Alignment:
SCGCGCGG
-YGCGTG-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS

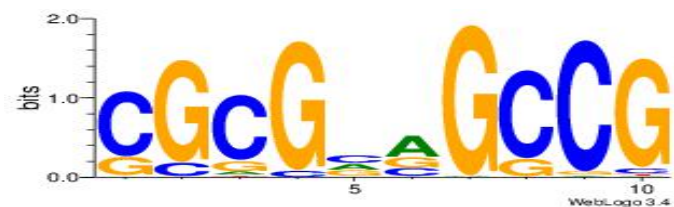


Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0586806

Alignment:
CGCGBMGCCG
CACGCM----

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG



Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0637286

Alignment:

BCACCTGCABC

-YGCGTG----

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

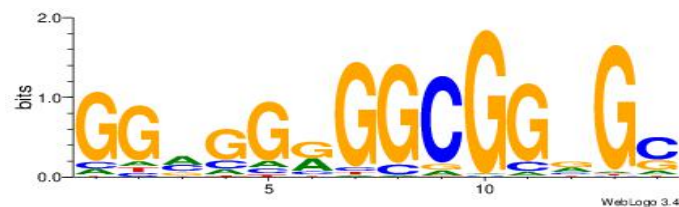


Dataset #: 5
 Motif ID: 50

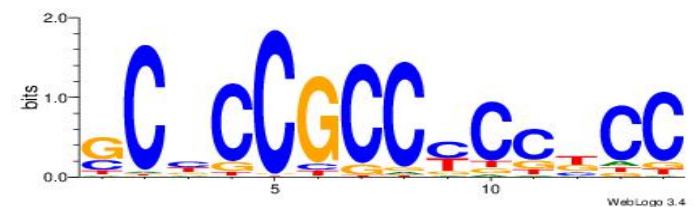
Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.066121

Alignment:
 GCVCCGCCMCCYCC
 --CACGCM-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 5
 Motif ID: 46
 Motif name: TFW1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0756826

Alignment:

CGCGAC

CACGCM

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



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

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCCGCC



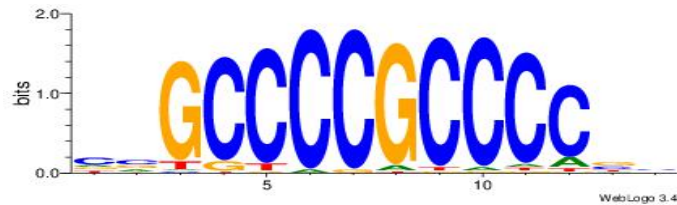
Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5

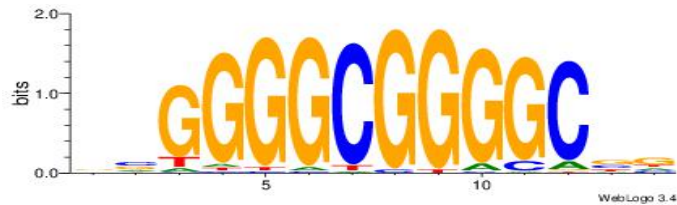
Number of overlap: 8
Similarity score: 0

Alignment:
BBGGGGCGGGGCVD
----GGCGGGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

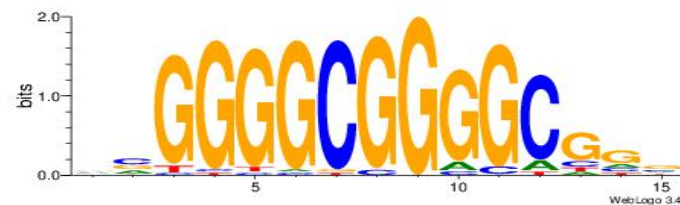
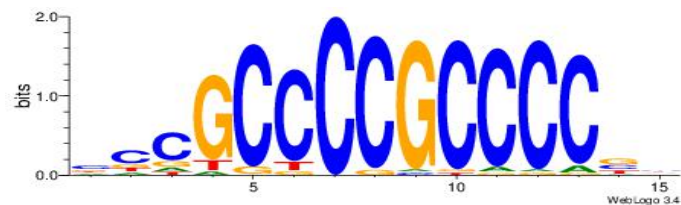


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.00250079

Alignment:
BCCGCCCCGCCCCBB
---GCCCGGCC----

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGB



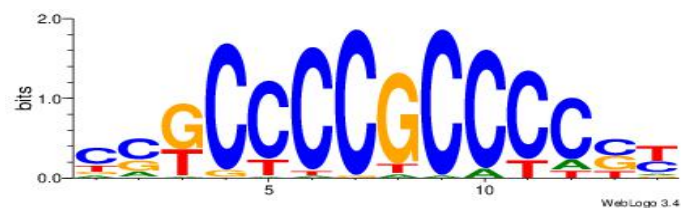
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0149958

Alignment:

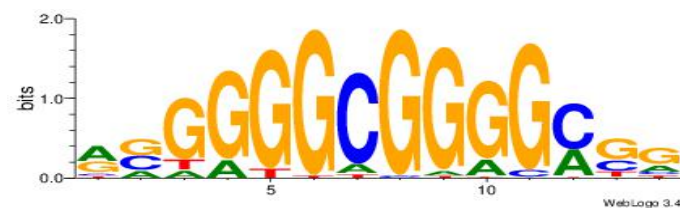
MSGGGGCGGGYSG

----GGCGGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGYSG



Dataset #: 5
 Motif ID: 50

Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	8
Similarity score:	0.0348969

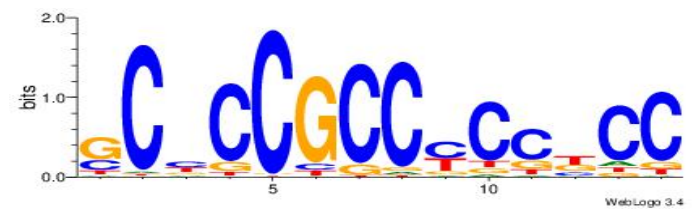
Alignment:

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

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



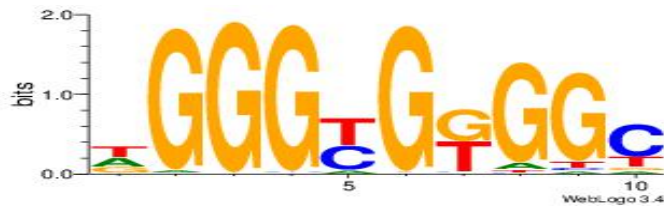
Dataset #:	3
Motif ID:	27
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0349983

Alignment:

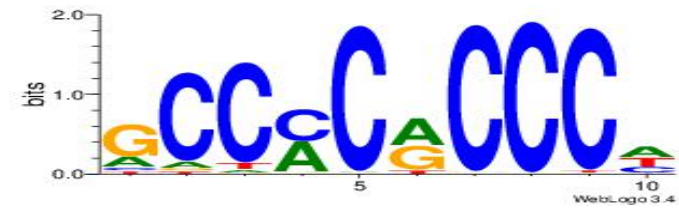
DGGGYGKGGC

--GGCGGGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



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

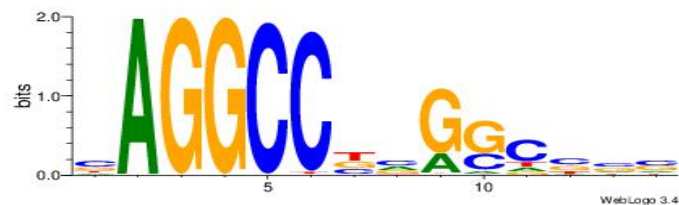
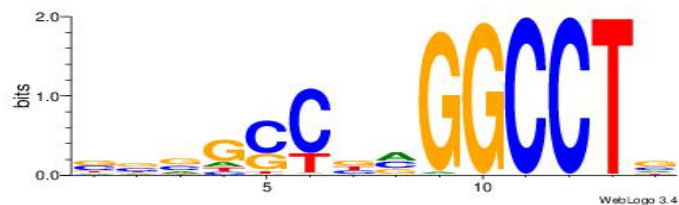
Alignment:

VAGGCCBBGGCVBB

---GCCCGGCC---

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Dataset #: 5
 Motif ID: 48
 Motif name: TFW3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.071681

Alignment:

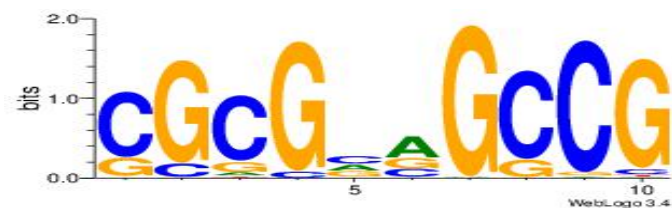
CGCGBMGCCG

–GCCCCGCC–

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



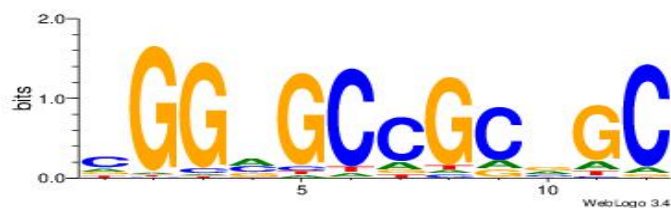
Dataset #: 5
 Motif ID: 49

Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0803996

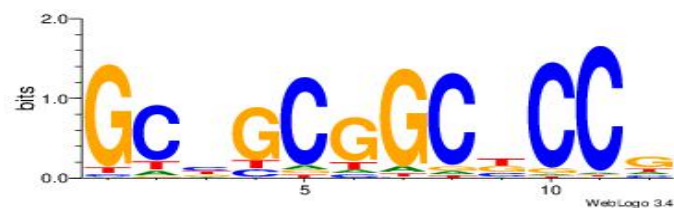
Alignment:

CGGVGCCGCVGC
 --GCCCCGCC--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



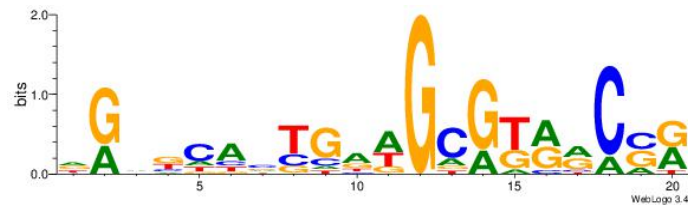
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0853847

Alignment:

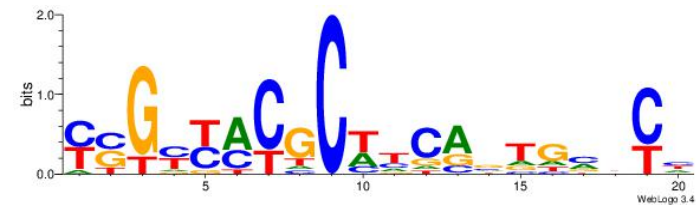
DGVBCABTGDWGCGRRCR

-----GGCGGGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



Dataset #:	3
Motif ID:	23
Motif name:	Egr1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0878731

Alignment:

YCGCCCACGCH

---GCCCGGCC

Original motif Consensus sequence: HGCGTGGGCGK

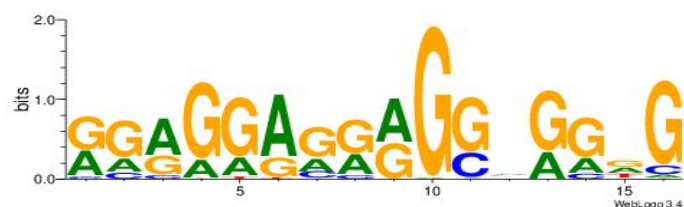
Reverse complement motif Consensus sequence: YCGCCCACGCH



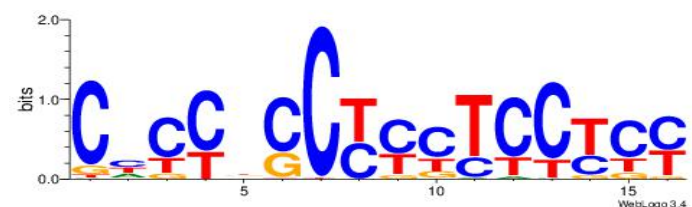
Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0928252

Alignment:
 CHCCBCKMCTCCKCM
 --GCCCCGCC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



Dataset #: 5 Motif ID: 46 Motif name: TFW1

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



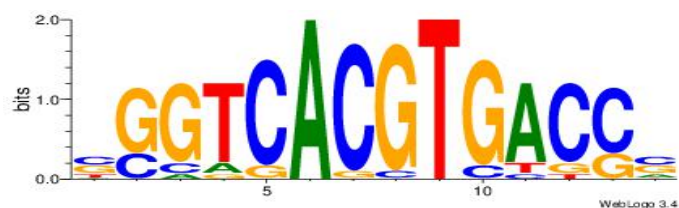
Best Matches for Top Significant Motif ID 46 (Highest to Lowest)

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

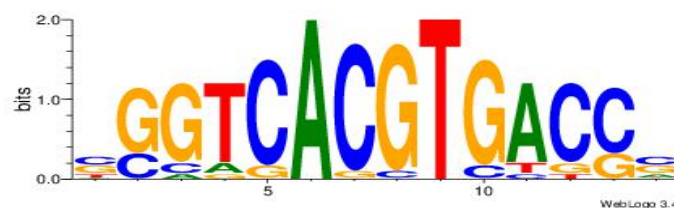
Alignment:

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

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 3
 Motif ID: 33
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0537993

Alignment:

GCCACGTGSD

----GTCGCG

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

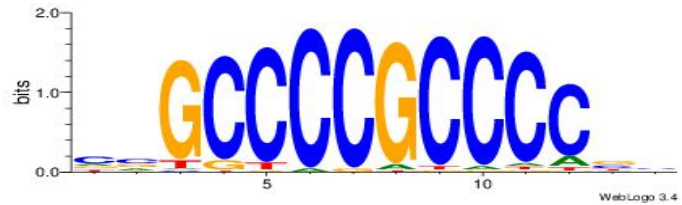


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6

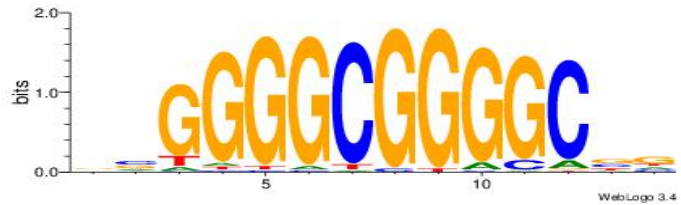
Similarity score: 0.0539

Alignment:
HVGCCCGCCCCBB
--GTCGCG-----

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 1
Motif ID: 1
Motif name: Motif 1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0554263

Alignment:
GCCCGGCC
--GTCGCG

Original motif Consensus sequence: GGCGGGGC

Reverse complement motif Consensus sequence: GCCCGGCC

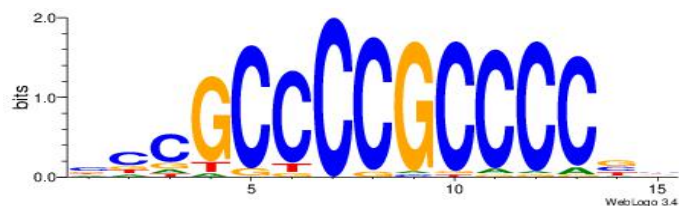


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0558733

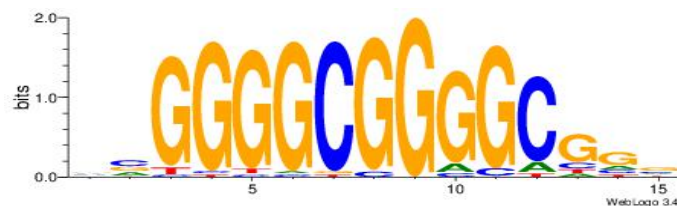
Alignment:

BBGGGGCGGGGCGGB
 -----GTCGCG--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



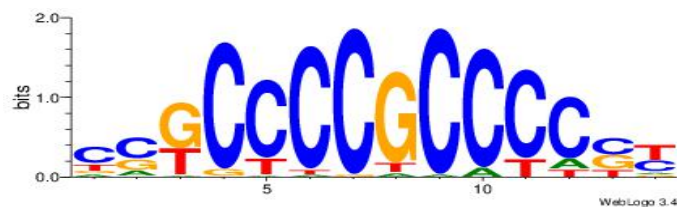
Dataset #: 2

Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0644512

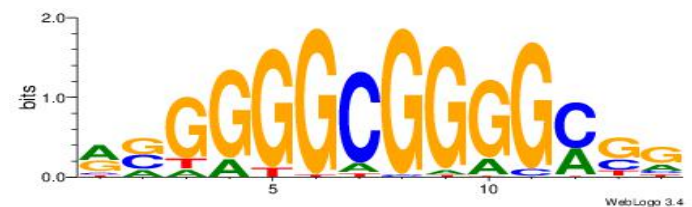
Alignment:

CSKCCCCGCCCSY
 --CGCGAC-----

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

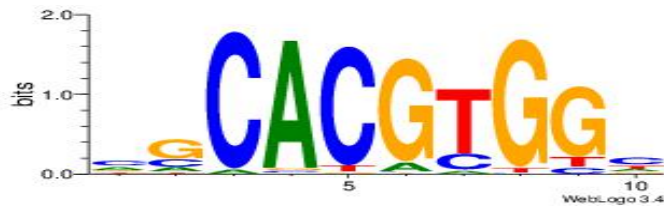


Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0664905

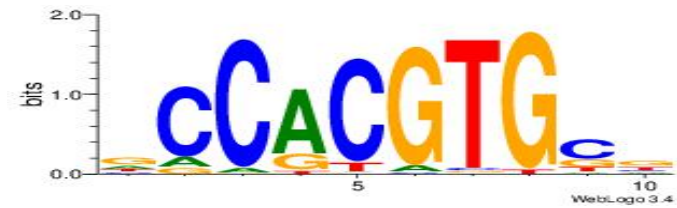
Alignment:

DCCACGTGCV
----GTCGCG

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #:	3
Motif ID:	28
Motif name:	E2F1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0698654

Alignment:

GCGCSAAA
-CGCGAC-

Original motif Consensus sequence: TTTSGCGC

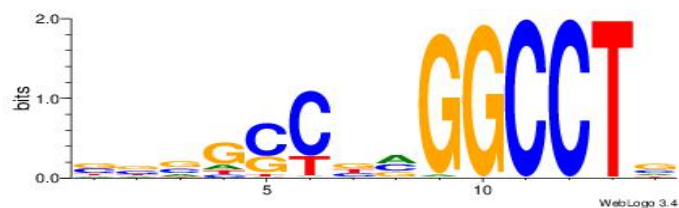
Reverse complement motif Consensus sequence: GCGCSAAA



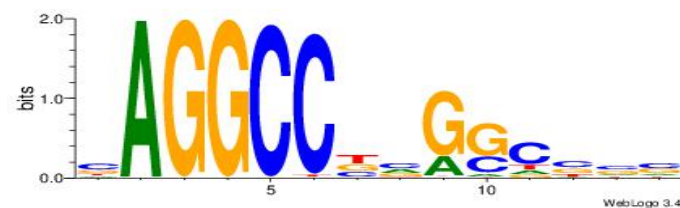
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.069909

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

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



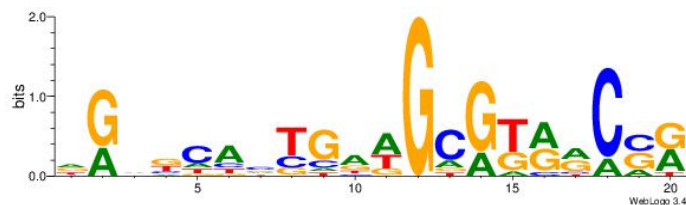
Dataset #: 3
 Motif ID: 31

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

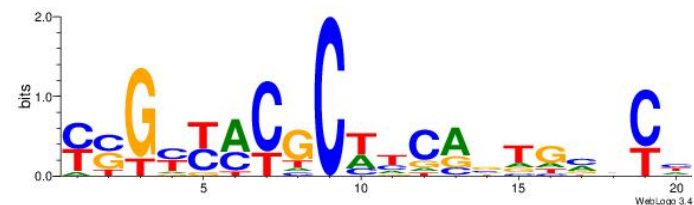
Alignment:

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

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

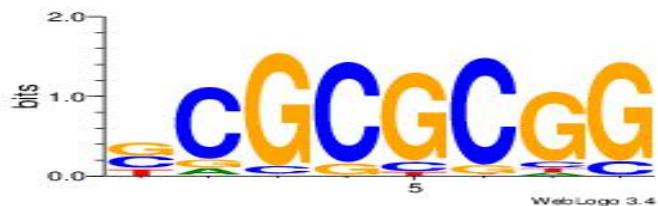


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



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

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



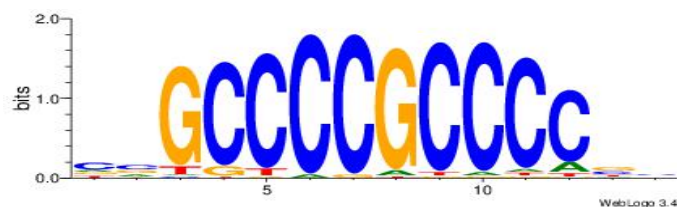
Best Matches for Top Significant Motif ID 47 (Highest to Lowest)

Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0456233

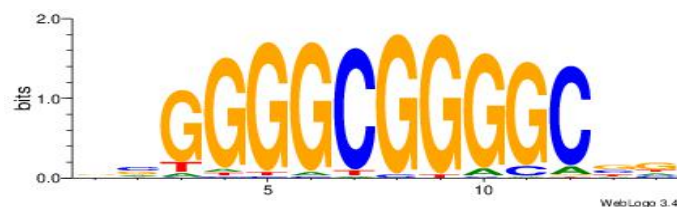
Alignment:

HVGCCCCGCCCCBB
 -CCGCGCGS-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

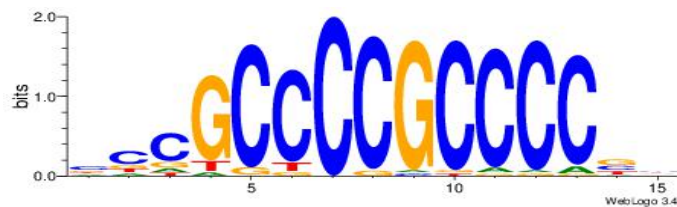


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement

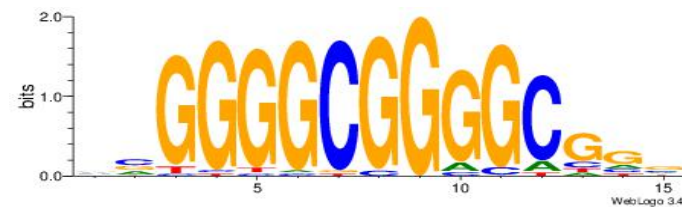
Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

Alignment:
 BBGGGGCGGGGCGGB
 -----SCGCGCGG--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



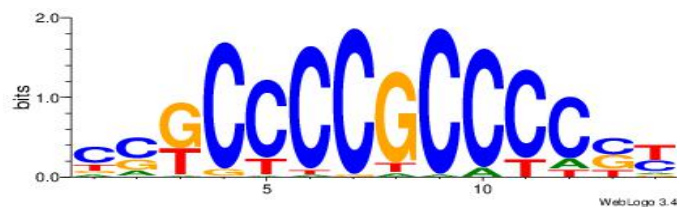
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



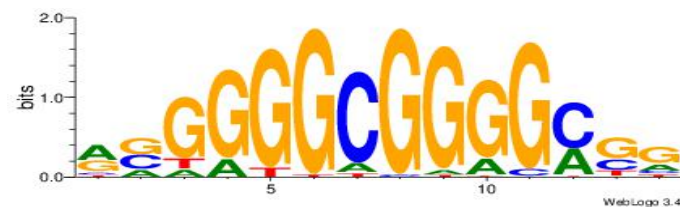
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0504058

Alignment:
 CSKCCCCGCCCCSY
 -CCGCGCGS-----

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 3
Motif ID: 33
Motif name: Mycn
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0527532

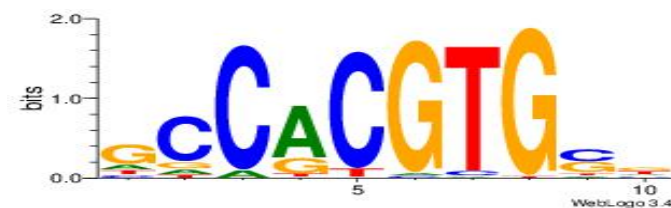
Alignment:

HSCACGTGGC
-SCGCGCGG-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



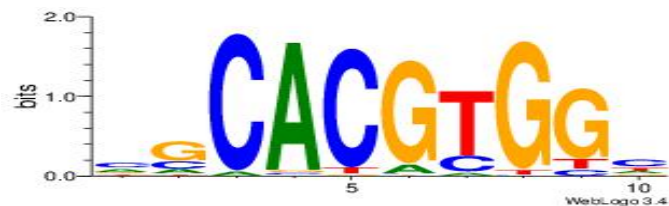
Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0574543

Alignment:

VGCACGTGGH

-SCGCGCGG-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



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

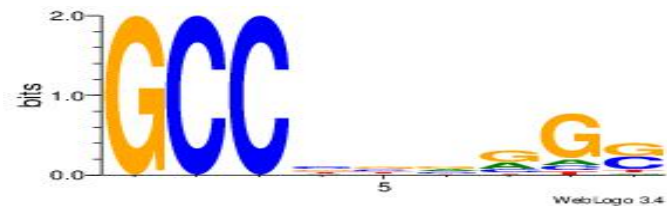
Similarity score: 0.0678925

Alignment:

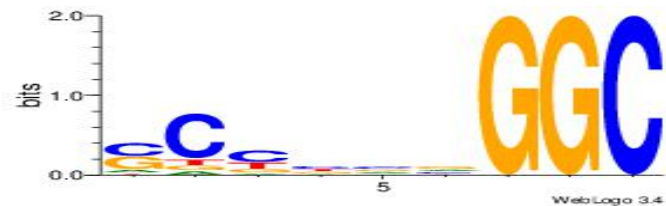
SCMVBBGGC

-SCGCGCGG

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



Dataset #: 3
Motif ID: 24
Motif name: SP1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.07018

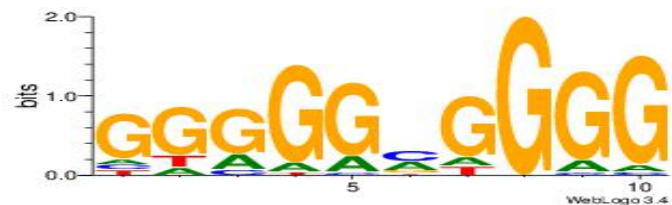
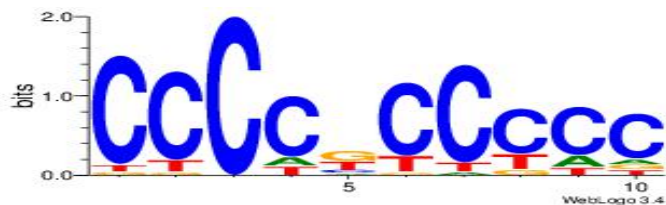
Alignment:

CCCCKCCCCC

--CCGCGCGS

Original motif Consensus sequence: CCCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG



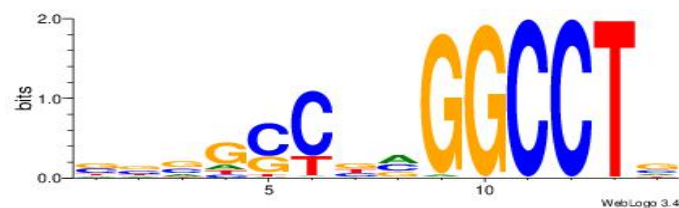
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0710499

Alignment:

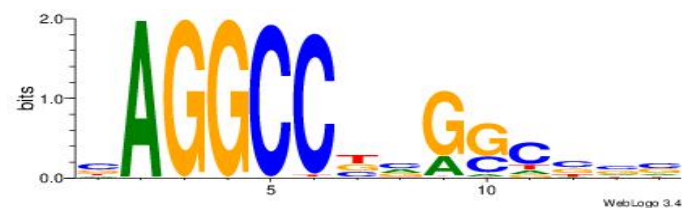
BBVGCCBVGGCCTV

--SCGCGCGG----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 3
 Motif ID: 27

Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0768965

Alignment:

DGGGYGKGGC
 -SCGCGCGG-

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



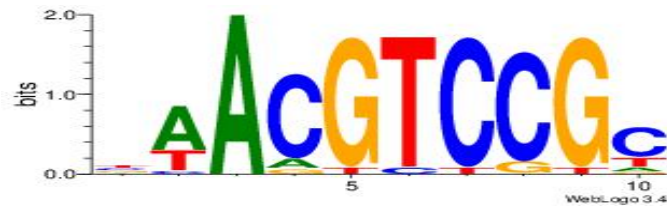
Dataset #:	3
Motif ID:	26
Motif name:	MIZF
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0837414

Alignment:

GCGGACGTTV

--SCGCGCGG

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



Dataset #: 3 Motif ID: 29 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Best Matches for Top Significant Motif ID 29 (Highest to Lowest)

Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAGc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

Number of overlap: 8
Similarity score: 0.0295473

Alignment:
GBTGCAGGTGB
---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

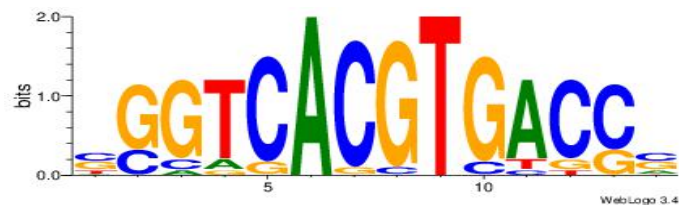
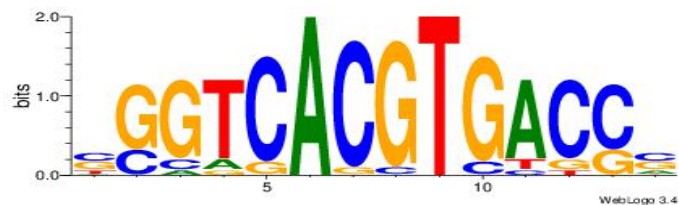


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSS
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0314837

Alignment:
SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS

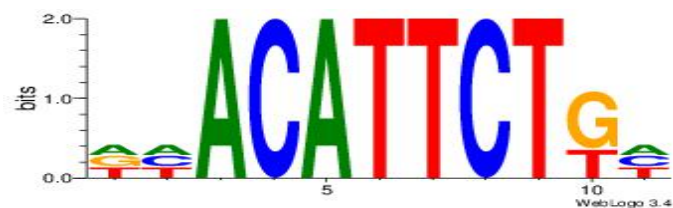
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0640024

Alignment:
 DHACATTCTGH
 VCACGTBV---

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 5
 Motif ID: 47

Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0660185

Alignment:
 CCGCGCGS
 VBACGTGV

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.067219

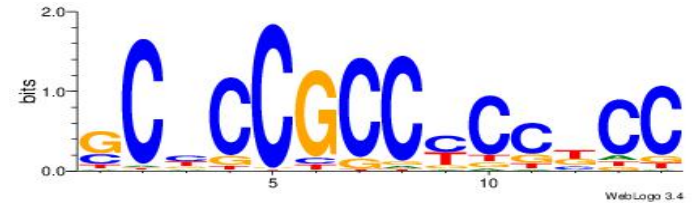
Alignment:

GCVCCGCCMCCYCC
 -----VCACGTBV

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



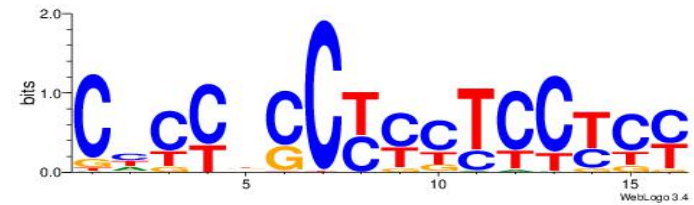
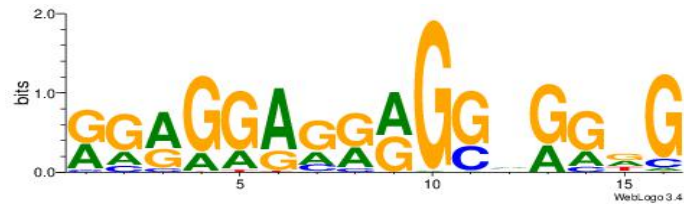
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0698117

Alignment:

RGRGGAGRRGGHGGDG
 ---VBACGTGV-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

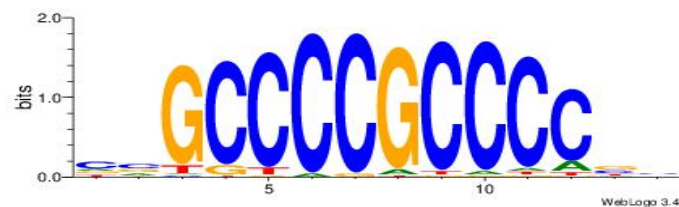
Reverse complement motif Consensus sequence:
 CHCCBCKMCTCCKCM



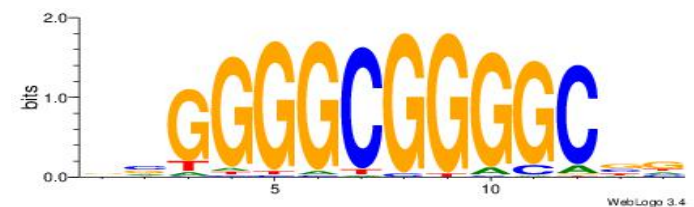
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0711168

Alignment:
 BBGGGGCGGGGCVD
 ---VBACGTGV---

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



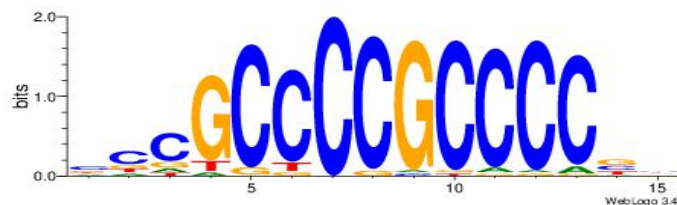
Dataset #: 4
 Motif ID: 38

Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0735453

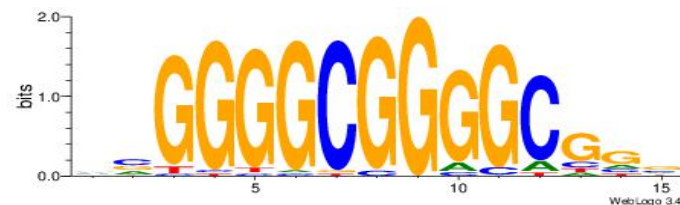
Alignment:

BBGGGGCGGGGCGGB
 ---VBACGTGV----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

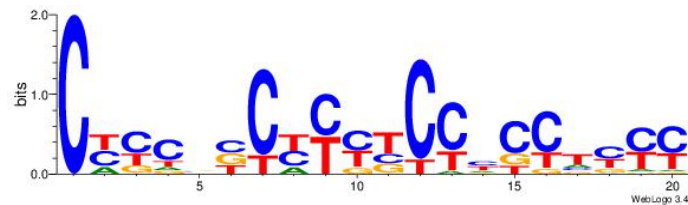


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 12
 Number of overlap: 8
 Similarity score: 0.0757612

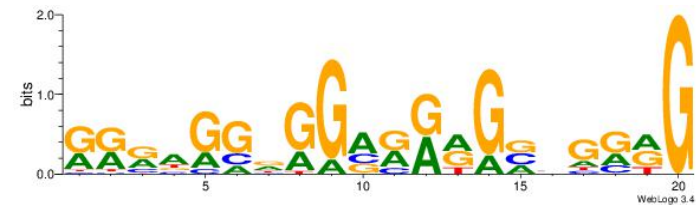
Alignment:

KKKAGGDGGAKKMGBBGKMG
-VBACGTGV-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



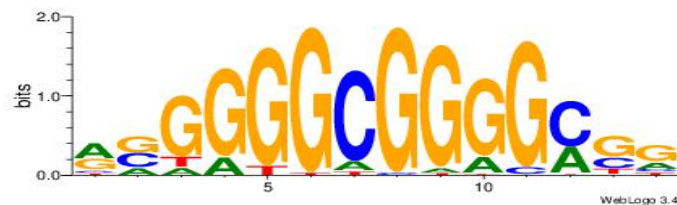
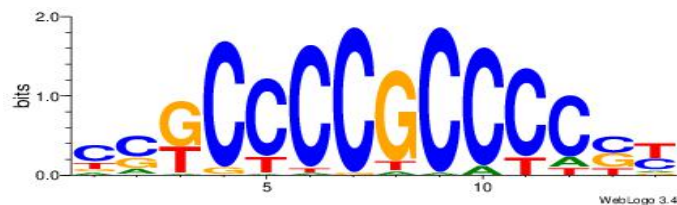
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0775335

Alignment:

CSKCCCCGCCCSY
---VCACGTBV---

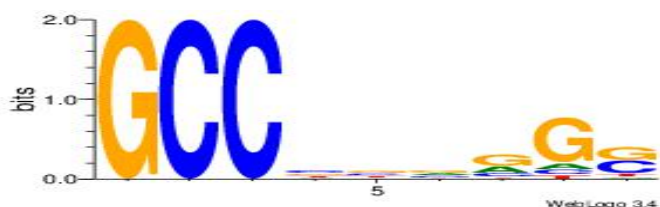
Original motif Consensus sequence: CSKCCCCGCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY

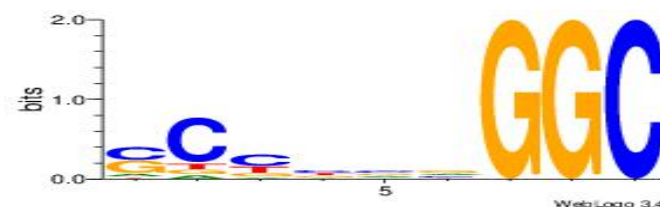


Dataset #: 3 **Motif ID: 25** **Motif name: TFAP2A**

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



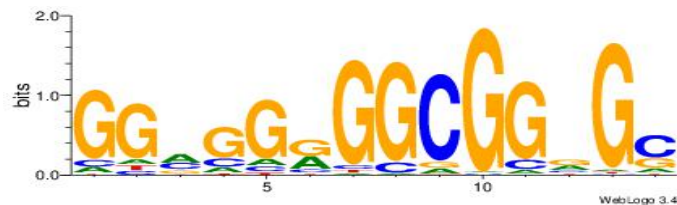
Best Matches for Top Significant Motif ID 25 (Highest to Lowest)

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

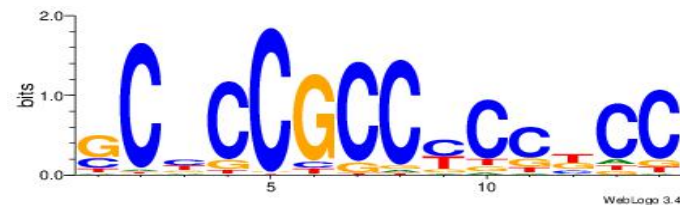
Alignment:

```
GGMGGRGGCGGVGC
SCMVBBGGC-----
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

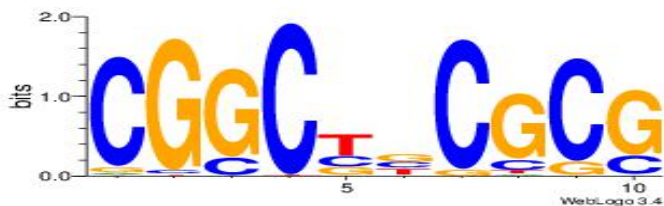


Dataset #: 5
 Motif ID: 48
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0552877

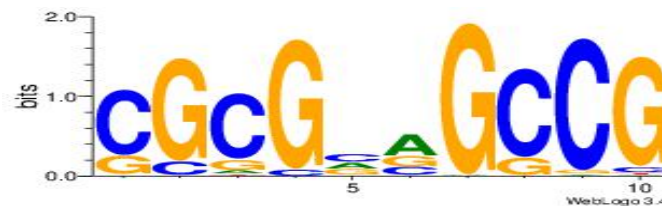
Alignment:

CGGCYBCGCG
 -GCCBBVRGS

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

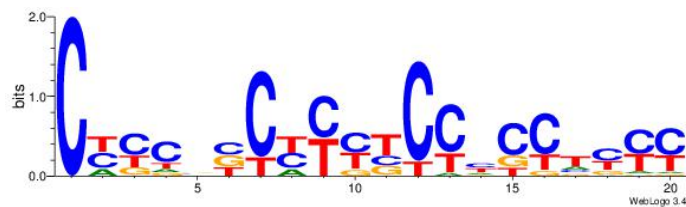


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 9
 Similarity score: 0.0630429

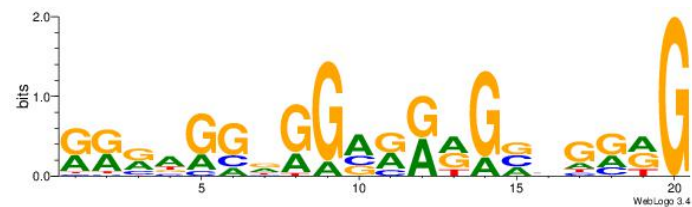
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -SCMVBBGGC-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

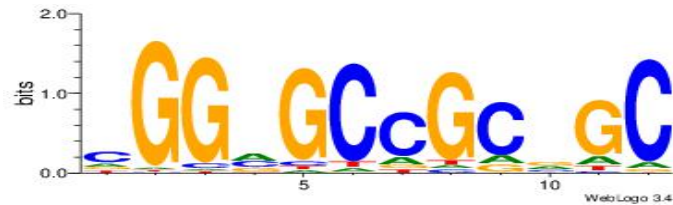


Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

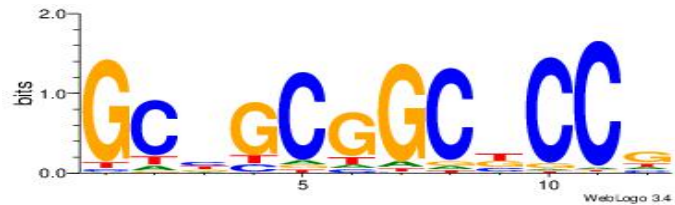
Number of overlap: 9
Similarity score: 0.0669772

Alignment:
GCVGCGGCBCCG
SCMVBBGGC---

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

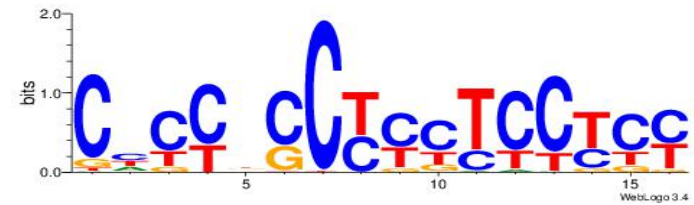
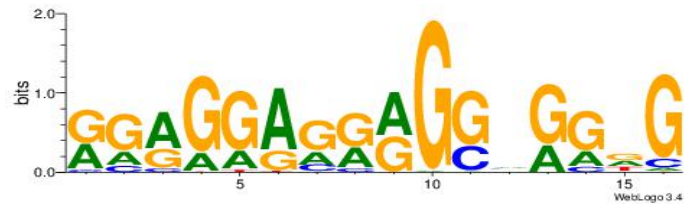


Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 9
Similarity score: 0.069755

Alignment:
CHCCBCKMCTCCKCM
SCMVBBGGC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

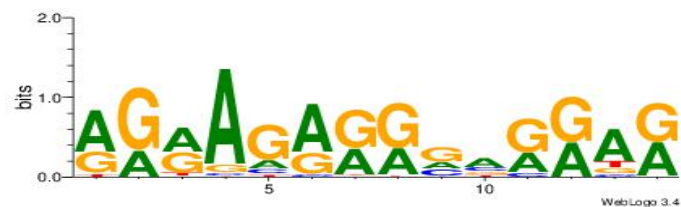
Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM



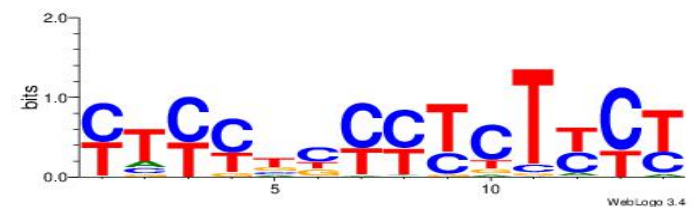
Dataset #: 2
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0715961

Alignment:
 MTMMTCMMTCTKCK
 ----SCMVBBGGC--

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



Dataset #: 4
 Motif ID: 38

Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	9
Similarity score:	0.0719489

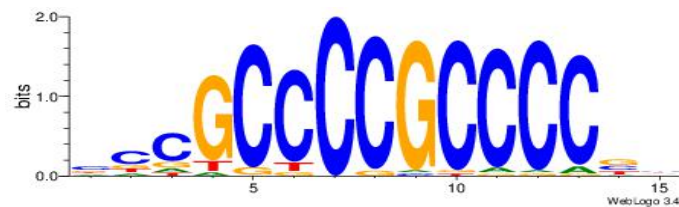
Alignment:

```

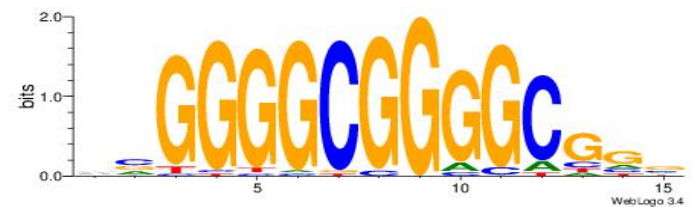
BBGGGGCGGGGCGGB
-----GCCBBVRGS-

```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

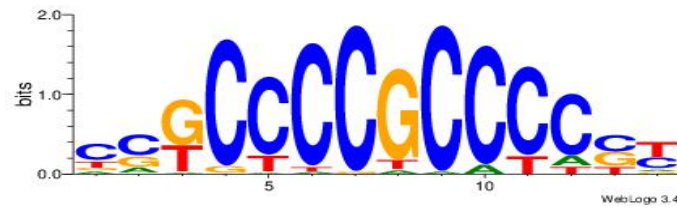


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0781606

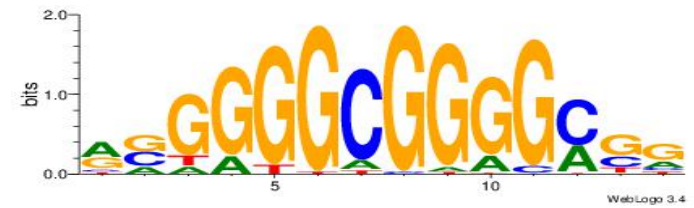
Alignment:

CSKCCCCGCCCCSY
-----SCMVBBGGC

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



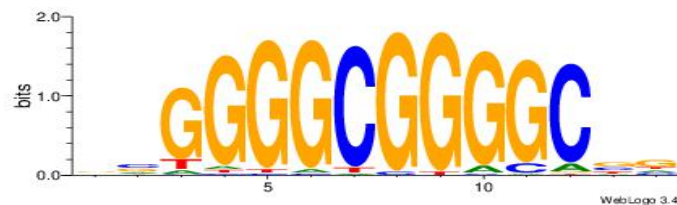
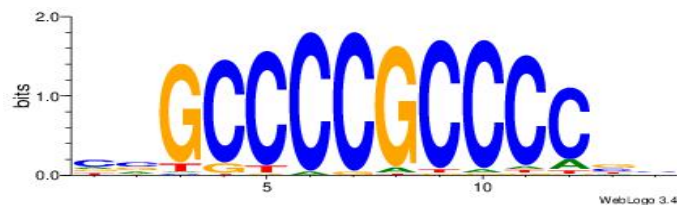
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0800026

Alignment:

BBGGGGCGGGGCVD
-----GCCBBVRGS

Original motif Consensus sequence: HVGCCCCGCCCCBB

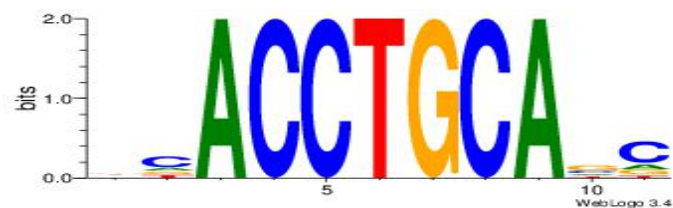
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0857416

Alignment:
 BCACCTGCABC
 --GCCBBVRGS

Original motif Consensus sequence: BCACCTGCABC

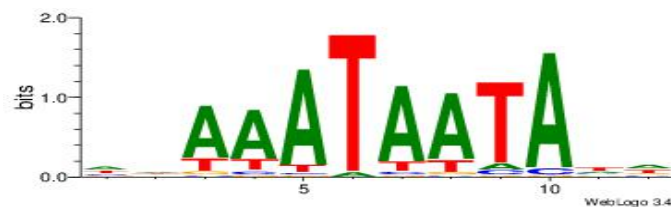


Reverse complement motif Consensus sequence: GBTGCAGGTGB

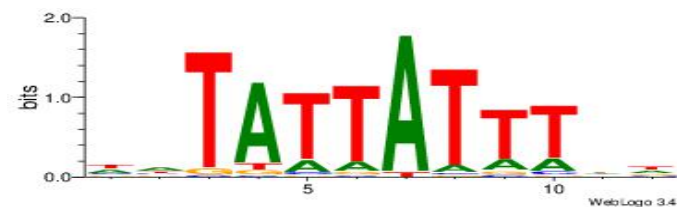


Dataset #: 4 Motif ID: 41 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTDDH



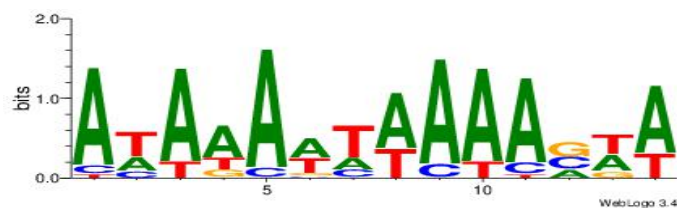
Best Matches for Top Significant Motif ID 41 (Highest to Lowest)

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

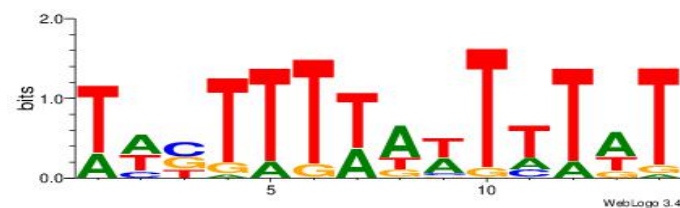
Alignment:

AWAAAWTWAAASWA
 -HDAAATAATADD-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV

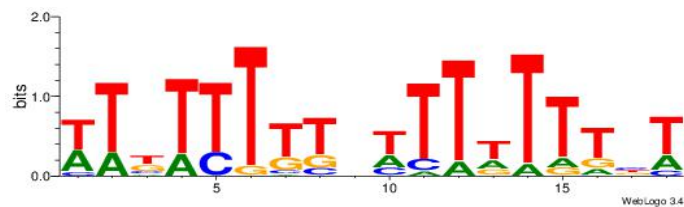


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0565705

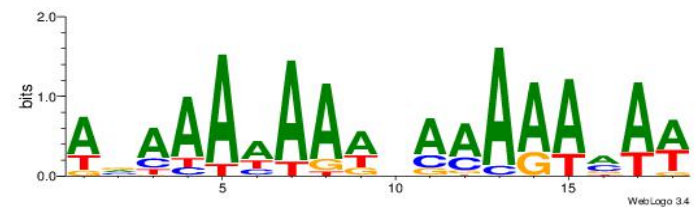
Alignment:

WTKTTTTTHWTTTTTBT
 -----DDTATTATTTDH

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

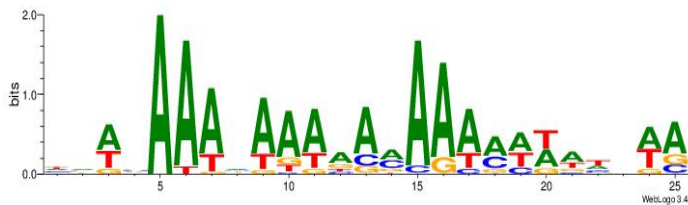


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

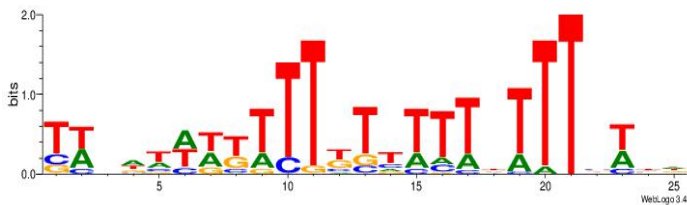
Number of overlap: 12
Similarity score: 0.0575935

Alignment:
HDWVAAAHA AAAA MAAAMWWWHBWA
--HDAAATAATADD-----

Original motif Consensus sequence:
HDWVAAAHA AAAA MAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH

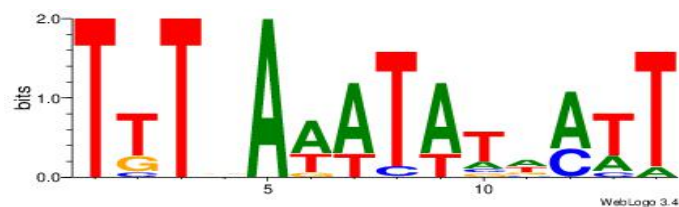


Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0591821

Alignment:
AATHATATWTHAAA
--DDTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT

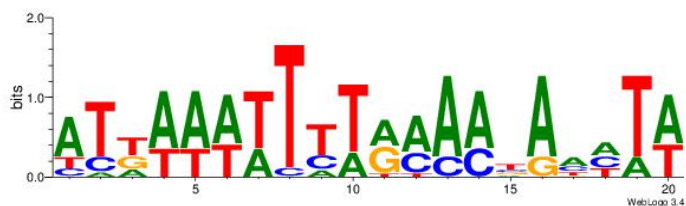


Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0712963

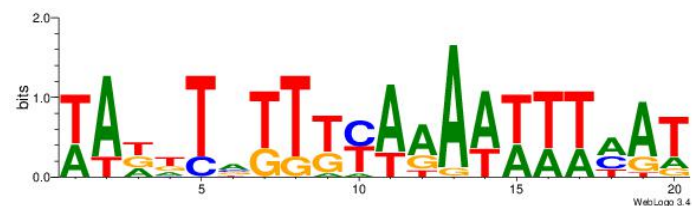
Alignment:

WAHHTVTTYKAAAWTTRAT
-----HDAAATAATADD

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT



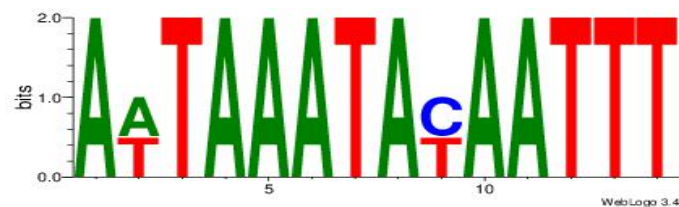
Dataset #: 2

Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0715278

Alignment:

AAATTKTATTTAWT
 -DDTATTATTTDH-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

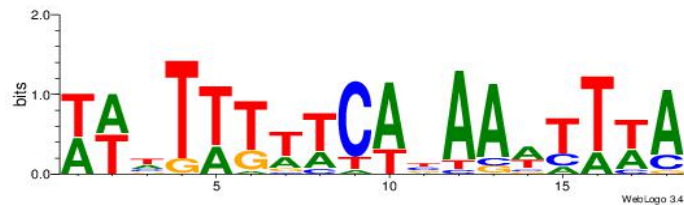


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0733516

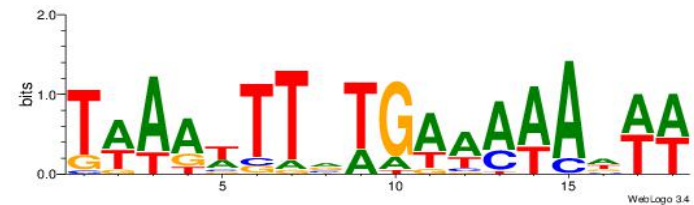
Alignment:

WWHTTTTTCABAAWTTWA
 -----DDTATTATTTDH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
 TAAWTTVTGAAAAHWW



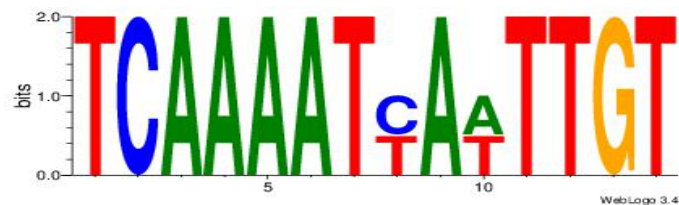
Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0912037

Alignment:

TCAAAATKAWTTGT
 --DDTATTATTTDH

Original motif Consensus sequence: ACAAWTRATTTTGA

Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0924576

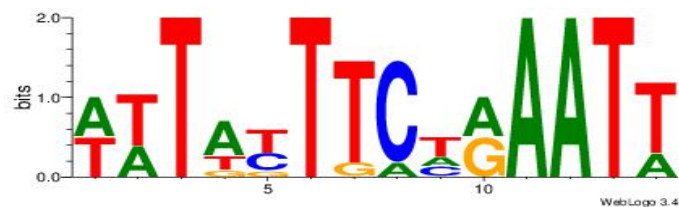
Alignment:

WWTAKTTCDKAATT
 DDTATTATTTDH--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAATT

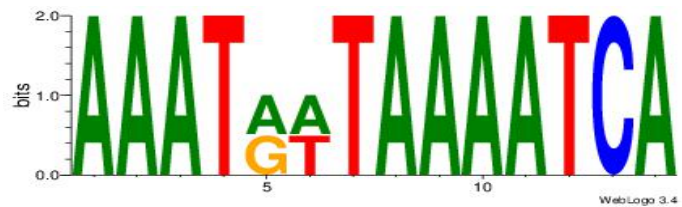


Dataset #: 2
 Motif ID: 8

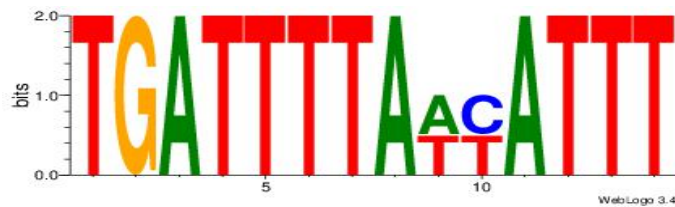
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0989198

Alignment:
TGATTTTAWKATTT
-DDTATTATTDDH-

Original motif Consensus sequence: AAATRWTAATCA

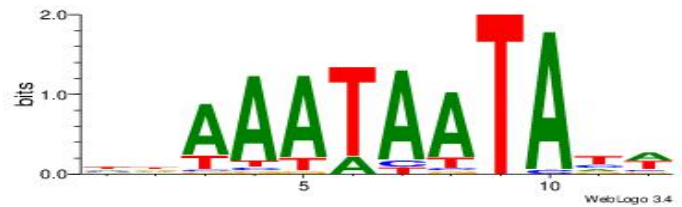


Reverse complement motif Consensus sequence: TGATTTTAWKATTT

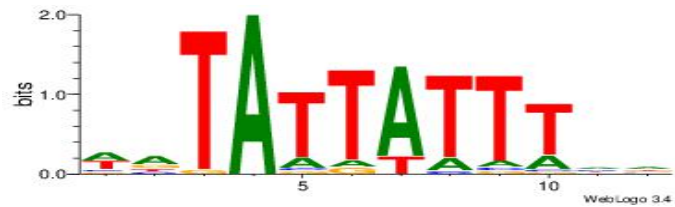


Dataset #: 4 Motif ID: 37 Motif name: tkAAATAATAtw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



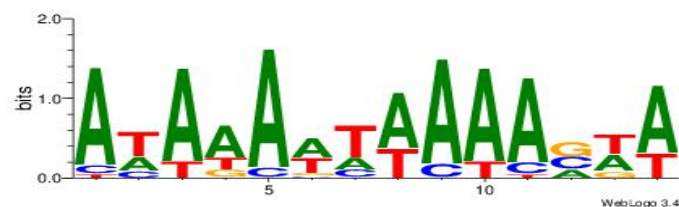
Best Matches for Top Significant Motif ID 37 (Highest to Lowest)

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

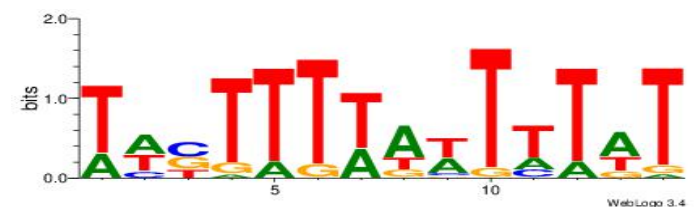
Alignment:

TWSTTTWAWTTTWT
 -WHTATTATTTDH-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

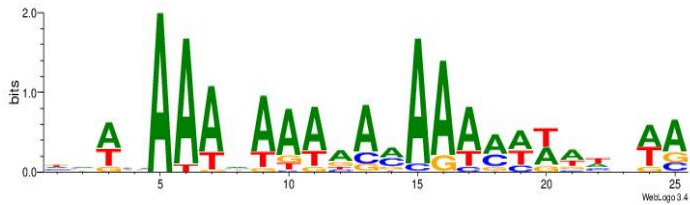


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 12

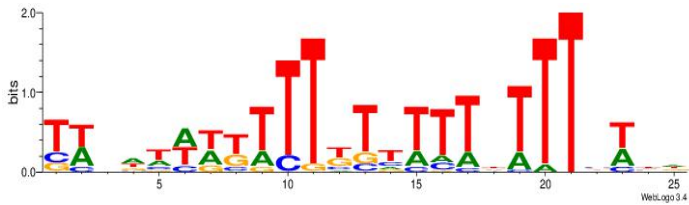
Similarity score: 0.0590505

Alignment:
TWVHWWWYTTTYTTTTTHTTTVWBH
-----WHTATTATTTDH--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH

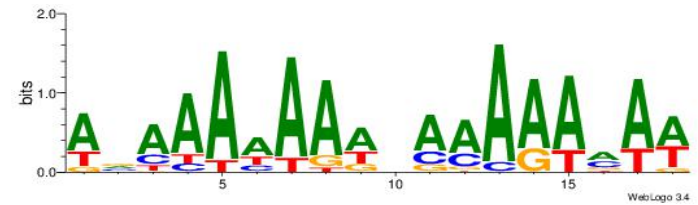
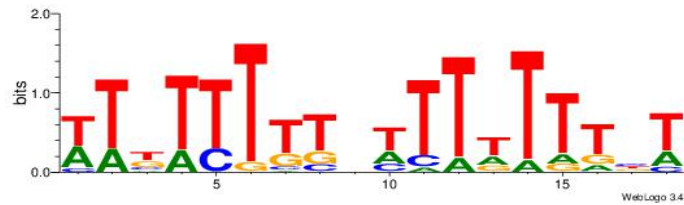


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0637702

Alignment:
ABAAAAAWhAAAAARAW
HDAAATAATAHW-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW

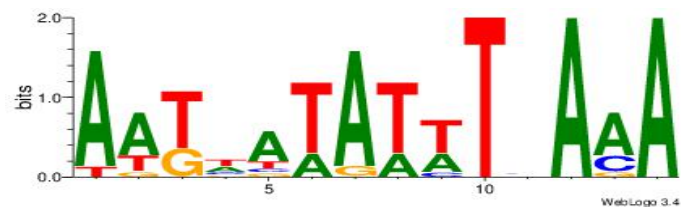


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0641975

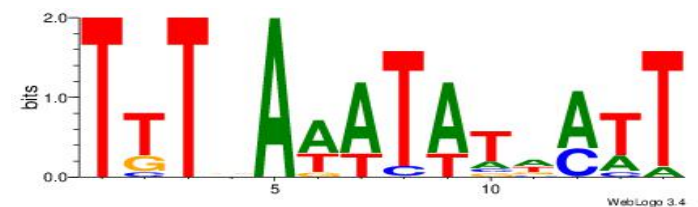
Alignment:

AATHATATWTHAAA
 --WHTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



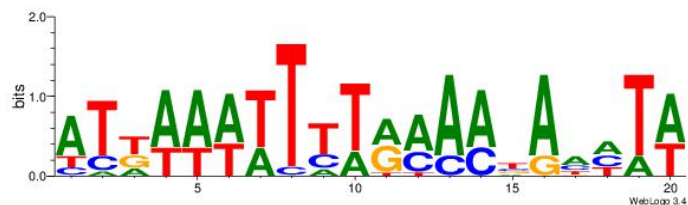
Dataset #: 5
 Motif ID: 55

Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 12
 Similarity score: 0.0704475

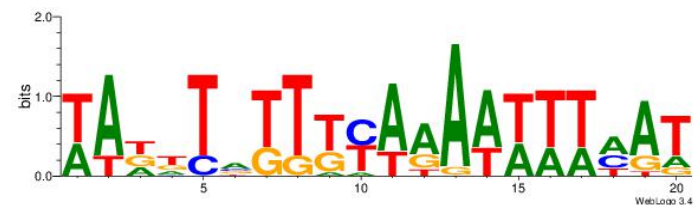
Alignment:

WAHHTVTTYKAAAATTRAT
 -----HDAAATAATAHW

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



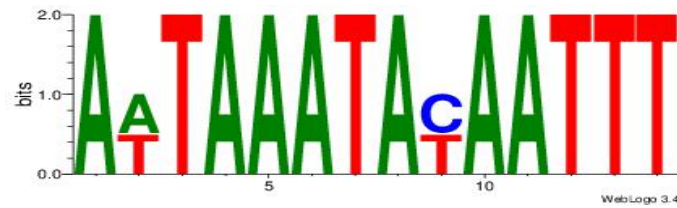
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0704475

Alignment:

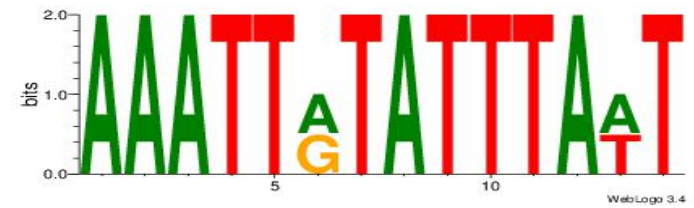
AAATTKTATTTAWT

-WHTATTATTTDH-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0763819

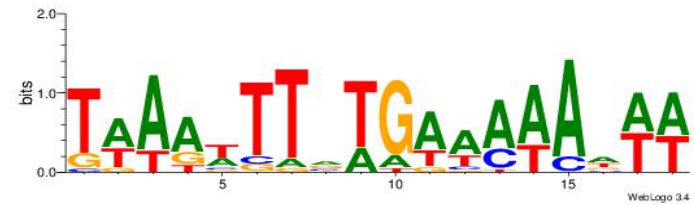
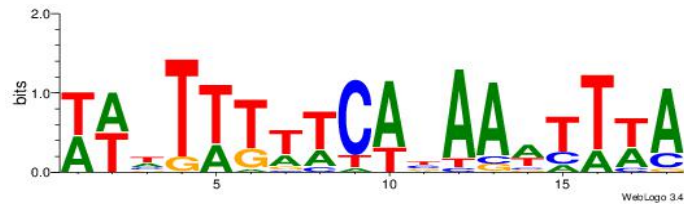
Alignment:

WWHTTTTTCABAAWTTWA

-----WHTATTATTTDH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

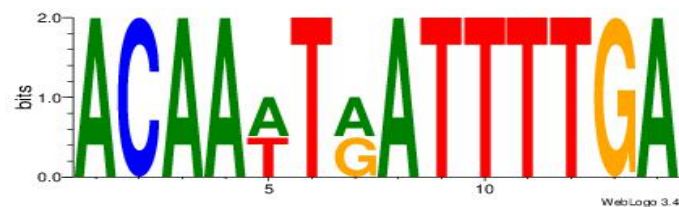
Reverse complement motif Consensus sequence:
TAAWTTVTGAAAAHWW



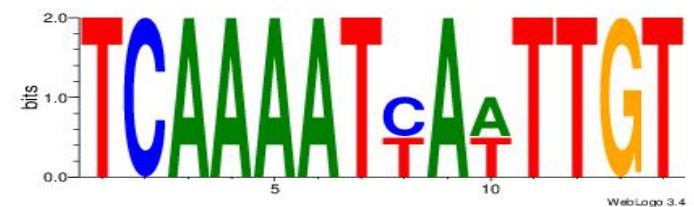
Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0864198

Alignment:
 TCAAAATKAWTTGT
 --WHTATTATTTDH

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTGT



Dataset #: 2
 Motif ID: 6

Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.09076

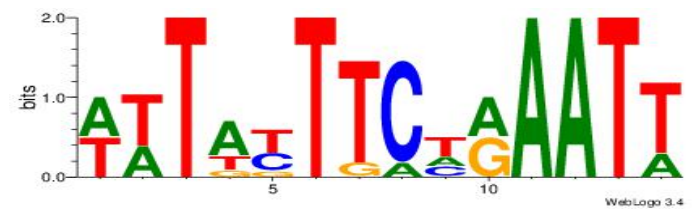
Alignment:

WWTAKTTCDKAATT
WHTATTATTTDH--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



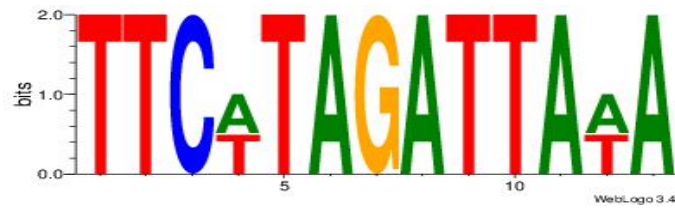
Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.096142

Alignment:

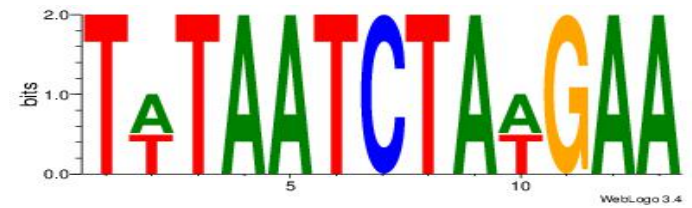
TWTAATCTAWGAA

WHTATTATTTDH-

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAATCTAWGAA



Results created by MOTIFSIM on 11-20-2016 22:10:51

Runtime: 822.546 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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