



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.0

INPUT

Input Parameters

Number of files:	5
Number of top significant motifs:	10
Number of best matches:	10
Similarity cutoff \geq	0.75
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
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Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



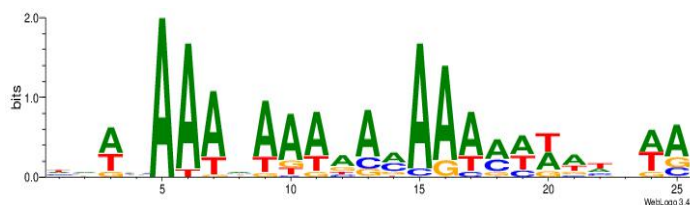
Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

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

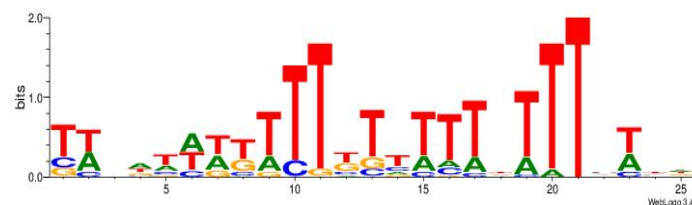
Alignment:

```
TWVHWWWYTTTTYTTTTHTTTVWBH
-----DHTATTTACBD
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTHTTTVWBH



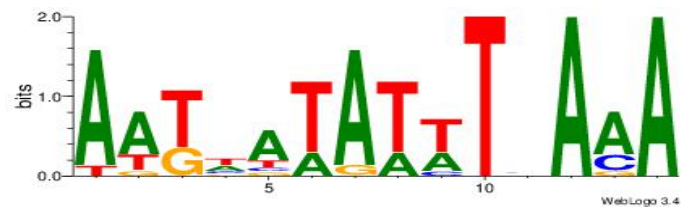
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0250541

Alignment:

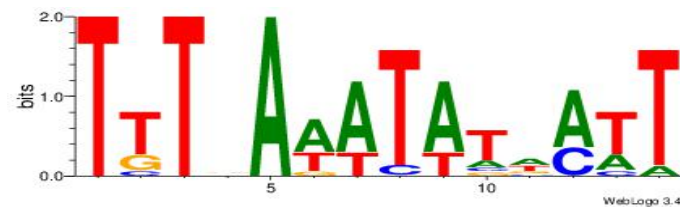
AATHATATWTHAAA

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

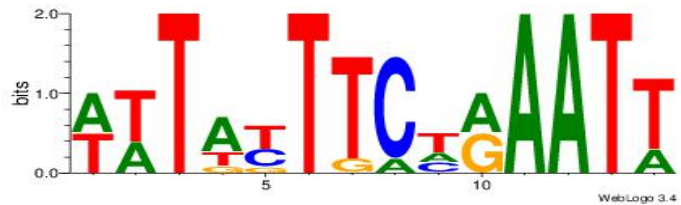
Number of overlap: 11
Similarity score: 0.027895

Alignment:
AATTYDGAARTAWW
---DBGTAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

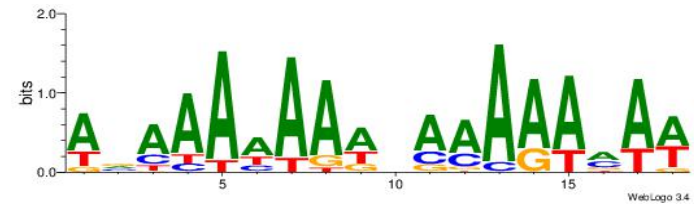
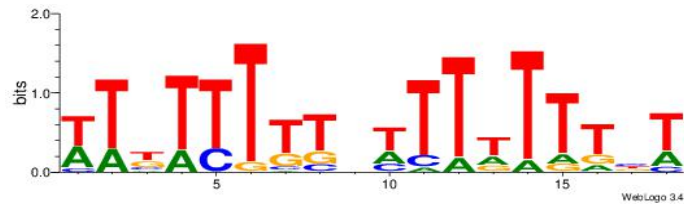


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0283217

Alignment:
ABAAAAAAWHAAAAARAW
DBGTAATAHD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW

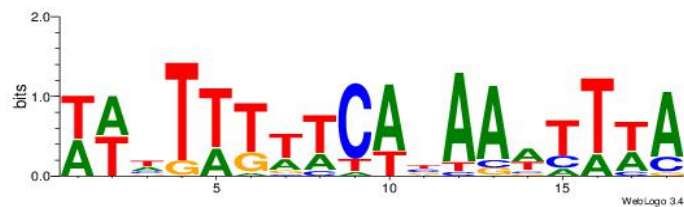


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0308097

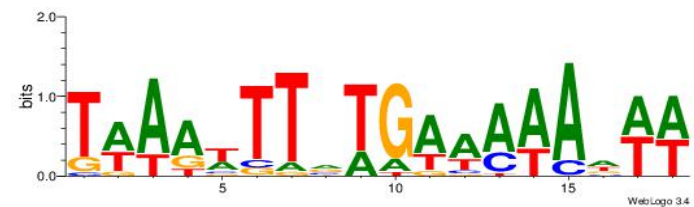
Alignment:

TWAAWTTVTGAAAAHWW
 -----DBGTAAATAHD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



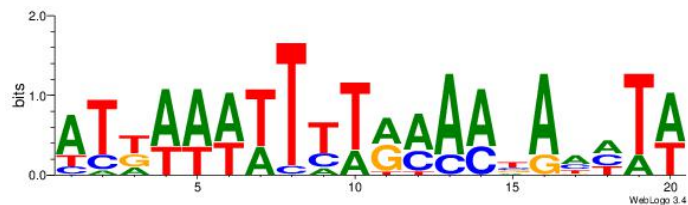
Dataset #: 5

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

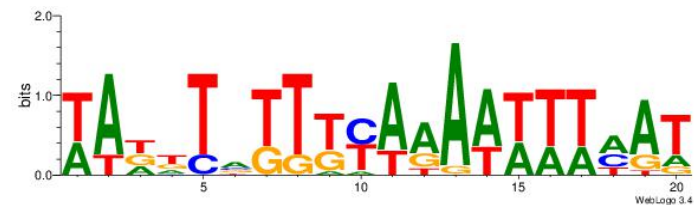
Alignment:

ATKAAWTTTTRMAABAHHTW
 -----DBGTAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

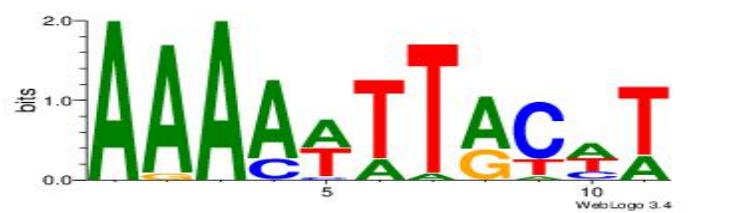


Dataset #: 2
 Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0361187

Alignment:
AAAAWTTTCWT
DHTATTTACBD

Original motif Consensus sequence: AAAAWTTTCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT

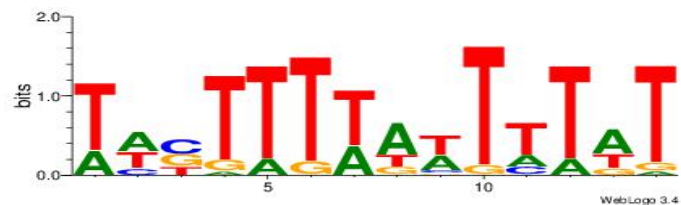
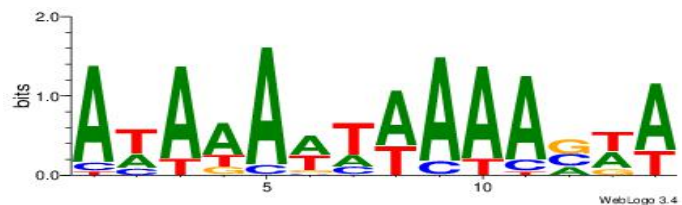


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0410381

Alignment:
AWAAAWTWAAASWA
--DHTATTTACBD--

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTT

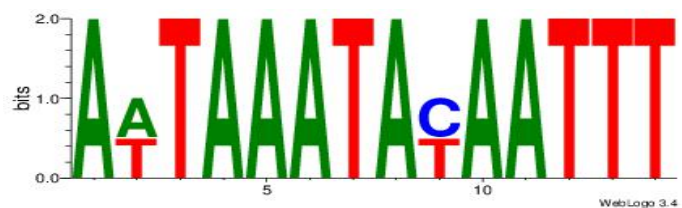


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0477814

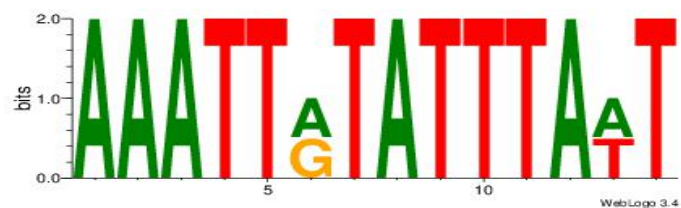
Alignment:

AWTAAATAYAATTT
 ---DHTATTTACBD

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



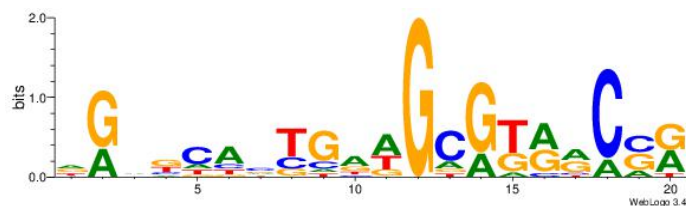
Dataset #: 3
 Motif ID: 31

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

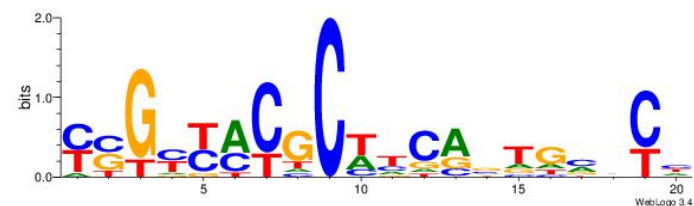
Alignment:

DGVBCABTGDWGCGRRCR
 DBGTAATAHD-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

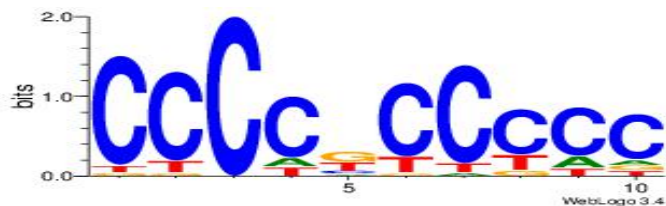


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



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

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



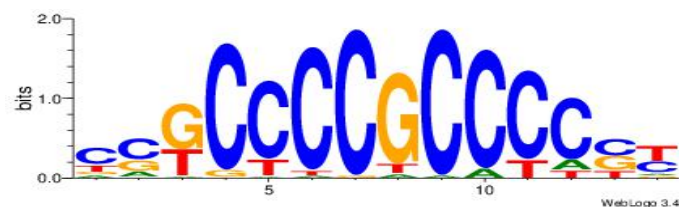
Best Matches for Top Significant Motif ID 24 (Highest to Lowest)

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

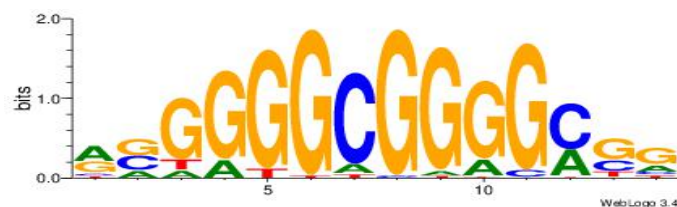
Alignment:

CSKCCCCGCCCCSY
 ---CCCKCCCC-

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

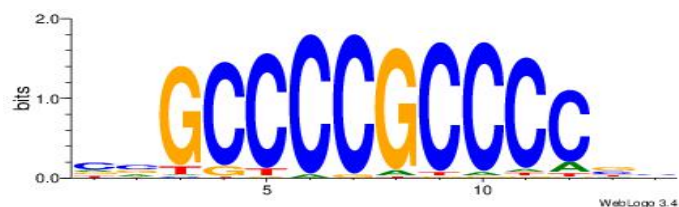


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement

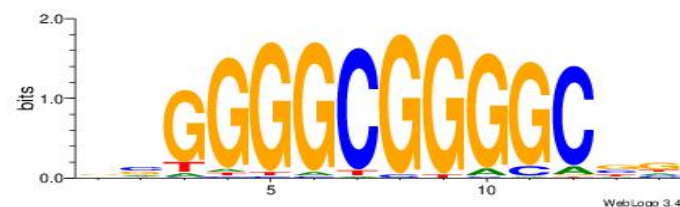
Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.00965796

Alignment:
 BBGGGGCGGGGCVD
 -GGGGGYGGGG---

Original motif Consensus sequence: HVGCCCGCCCCBB



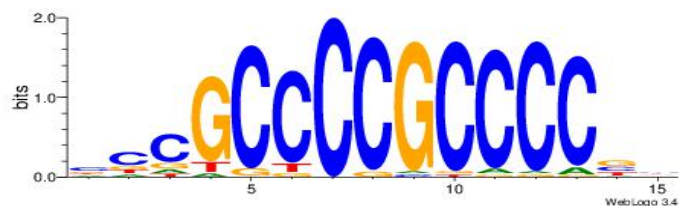
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



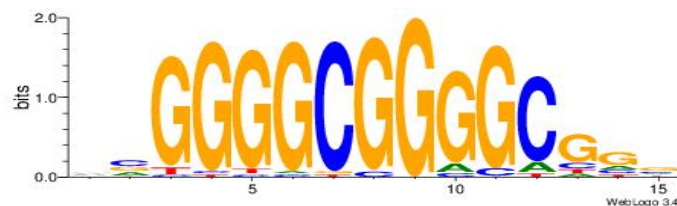
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0127292

Alignment:
 BBGGGGCGGGGCGGB
 -GGGGGYGGGG----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



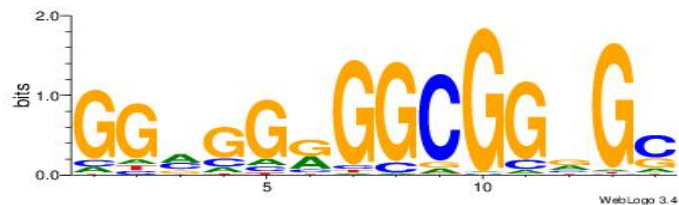
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0174405

Alignment:

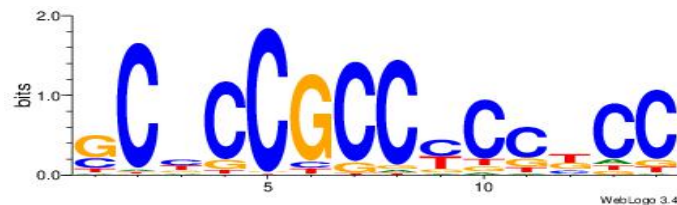
GGMGGRGGCGGVGC

---GGGGYGGGG--

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCY

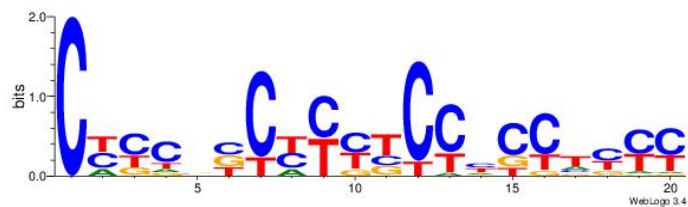


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0301548

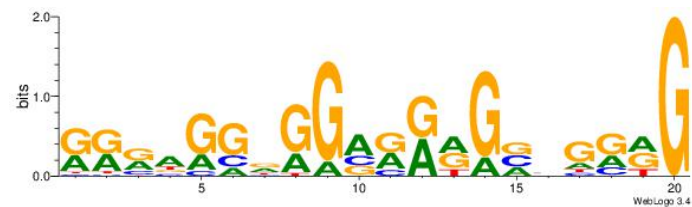
Alignment:

CYYCBBCYYYTCCHCCTYYY
 -----CCCCKCCCC-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

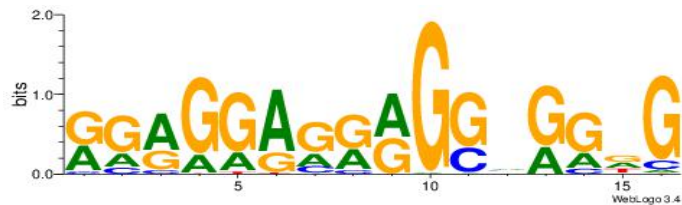


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

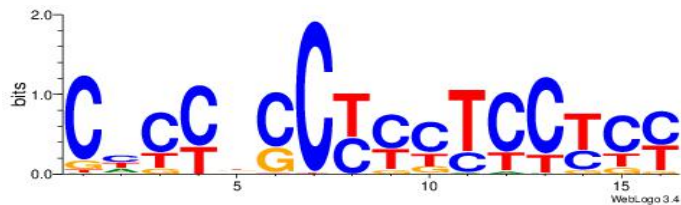
Number of overlap: 10
Similarity score: 0.0329167

Alignment:
RGRGGAGRRGGHGGDG
-----GGGGGYGGGG

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence:
CHCCBCKMCTCCKCM

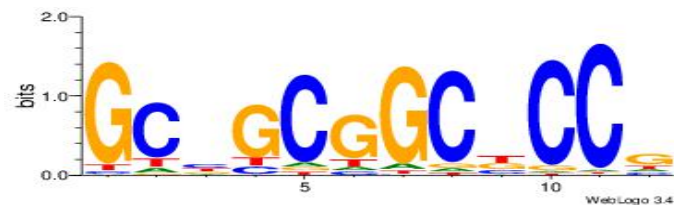
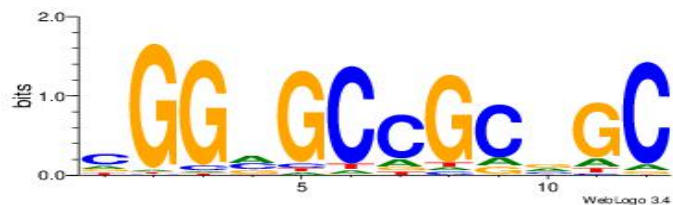


Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0557738

Alignment:
GCVGCCGCBCCG
-CCCCKCCCC-

Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCCGCBCCG

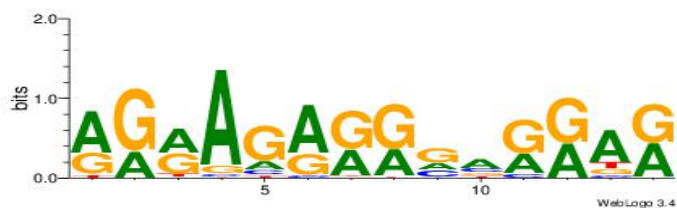


Dataset #: 2
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0648214

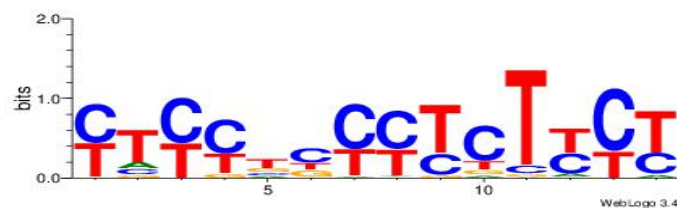
Alignment:

MTMMTCMMTCTKCK
 ----CCCCCKCCCCC

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



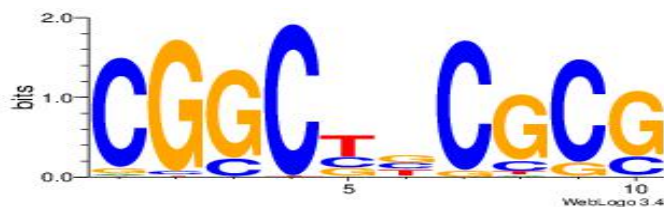
Dataset #: 5
 Motif ID: 48

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

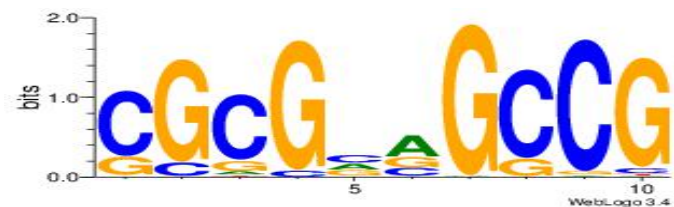
Alignment:

CGGCYBCGCG
 CCCCKCCCCC

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



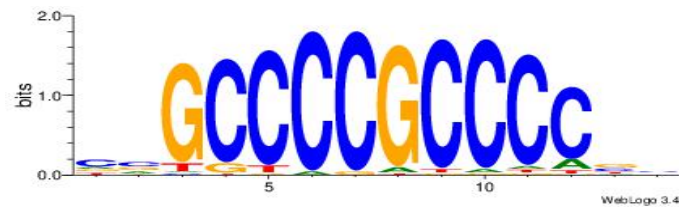
Best Matches for Top Significant Motif ID 32 (Highest to Lowest)

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

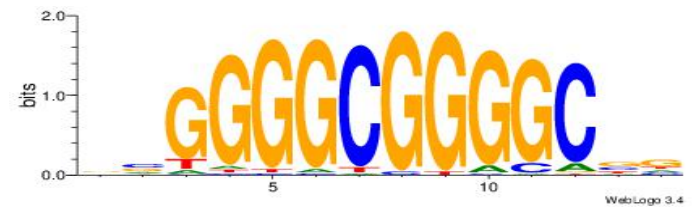
Number of overlap: 6
Similarity score: 0.0396403

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: GCGGGGC

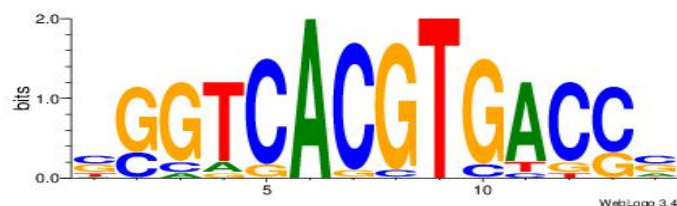
Reverse complement motif Consensus sequence: GCCCCGCC



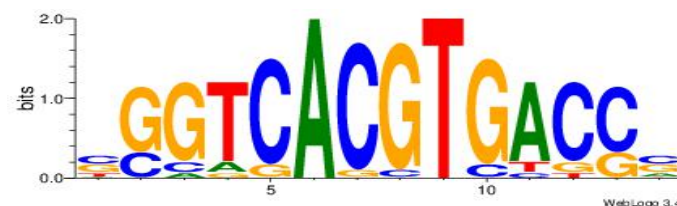
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0412037

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

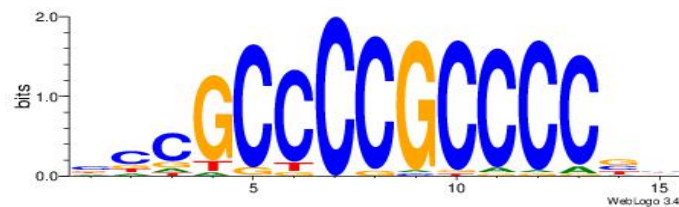
Alignment:

```

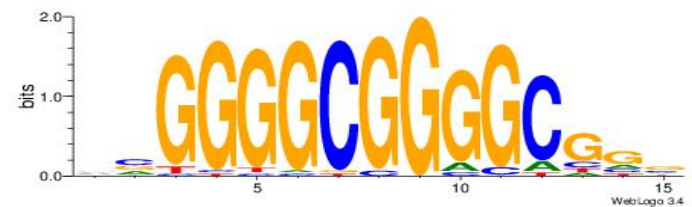
BCCGCCCCGCCCCBB
-----CACGCM-----

```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGCGGB



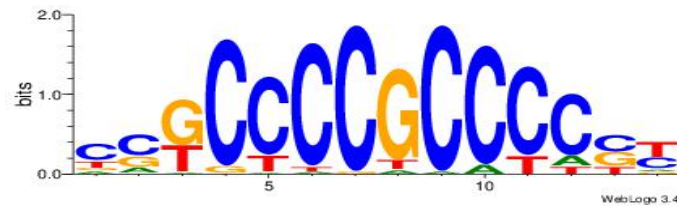
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0465867

Alignment:

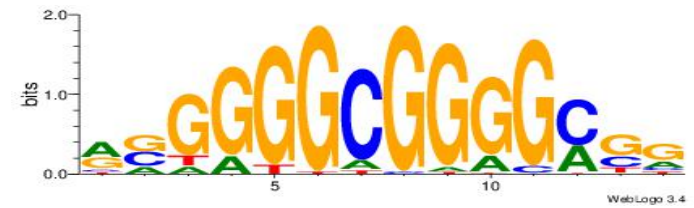
MSGGGGCGGGYSG

-----YGCGTG-----

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY



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

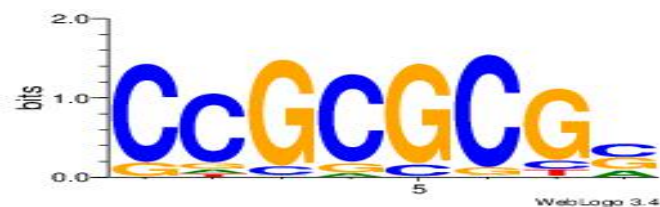
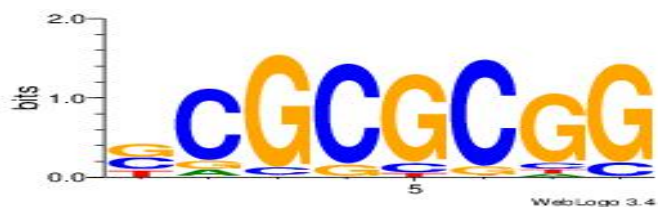
Alignment:

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:

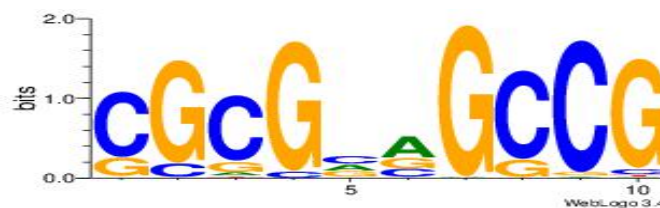
CGCGBMGCCG

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

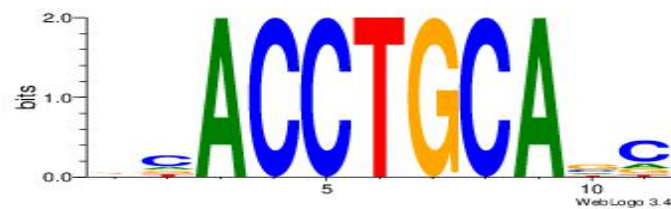
Alignment:

```

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:

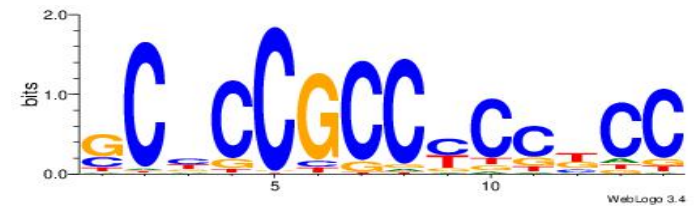
GCVCCGCCMCCYCC

--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)

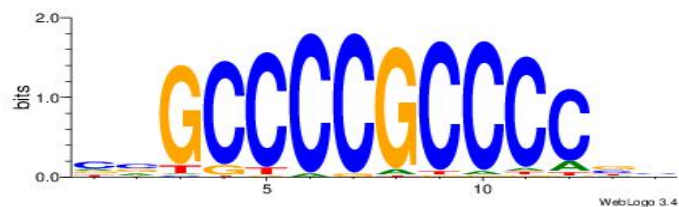
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0

Alignment:

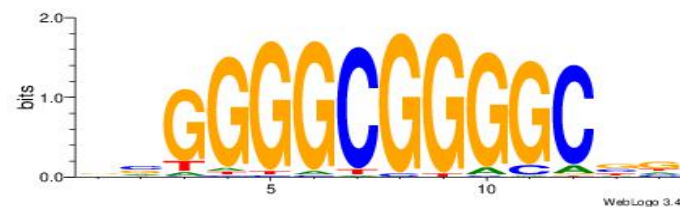
BBGGGGCGGGGCVD

----GGCGGGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

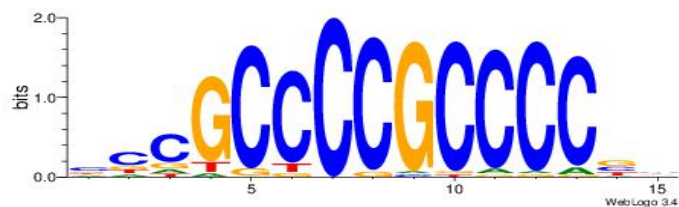


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.00250079

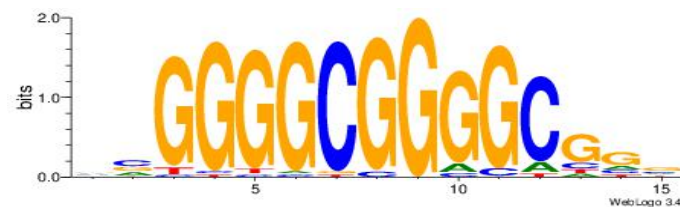
Alignment:

BCCGCCCCGCCCCBB
---GCCCCGCC----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGB

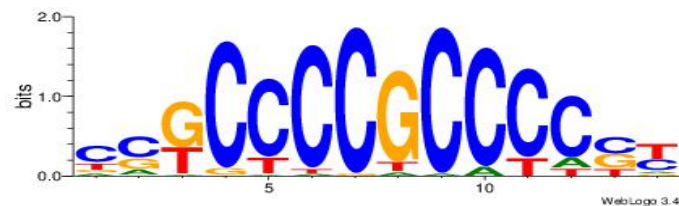


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0149958

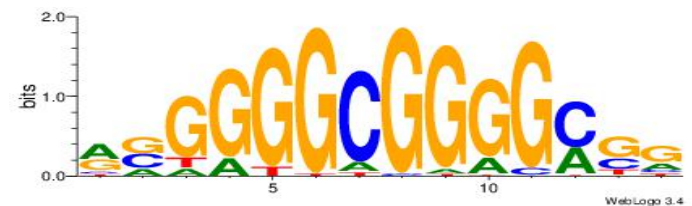
Alignment:

MSGGGGCGGGYSG
 ----GGCGGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGYSG

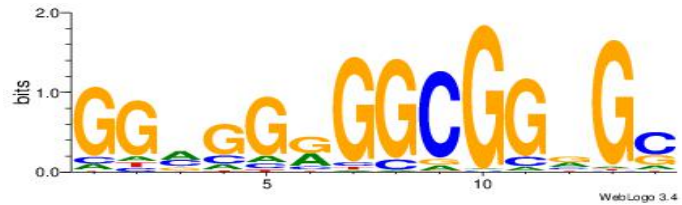


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8

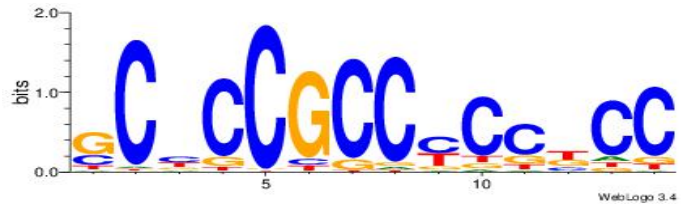
Similarity score: 0.0348969

Alignment:
GGMGGRGGCGGVGC
-----GGCGGGGC

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

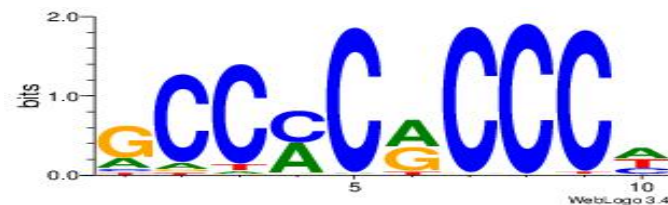


Dataset #: 3
Motif ID: 27
Motif name: Klf4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0349983

Alignment:
DGGGYGKGGC
--GGCGGGGC

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD



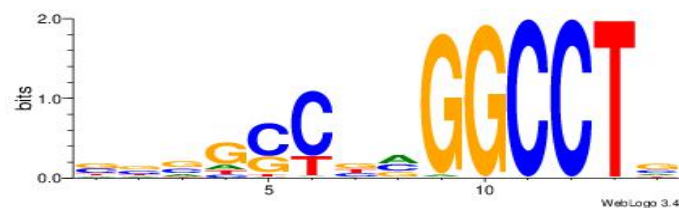
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0708224

Alignment:

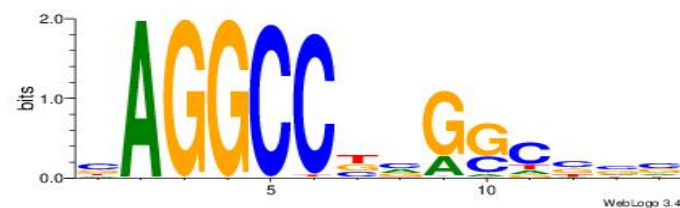
VAGGCCBBGGCVBB

---GCCCCGCC---

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

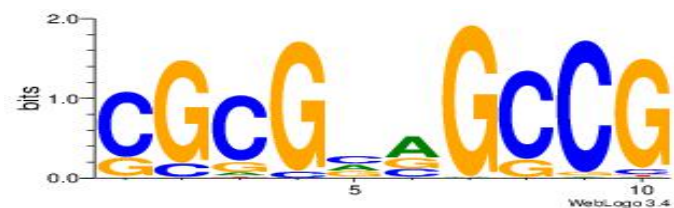
Alignment:

CGCGBMGCCG
 -GCCCCGCC-

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

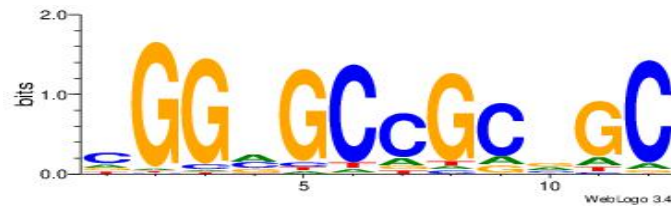


Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0803996

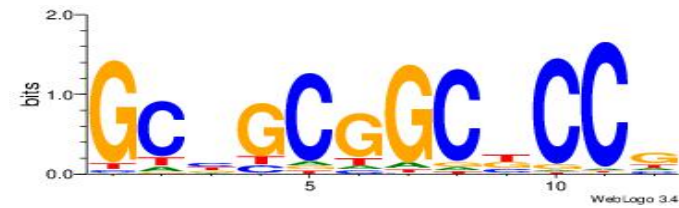
Alignment:

CGGVGCCGCVGC
--GCCCCGCC--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



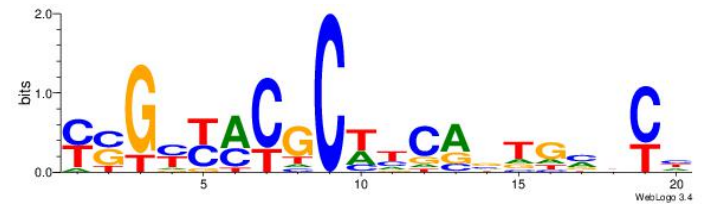
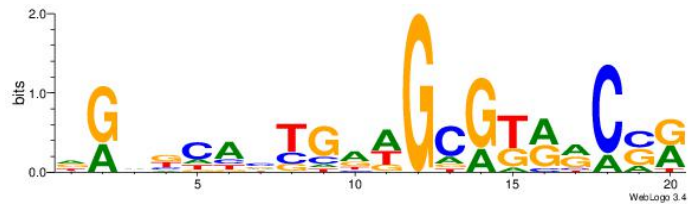
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0853847

Alignment:

DGVBCABTGDWCGKRRCSR
-----GCGGGGC--

Original motif Consensus sequence: DGVBCABTGDWCGKRRCSR

Reverse complement motif Consensus sequence:
MSGKKRCGCWDCA BTGBBCD



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:

YGCCCCACGCH
 ---GCCCGGCC

Original motif Consensus sequence: HCGTGCGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH



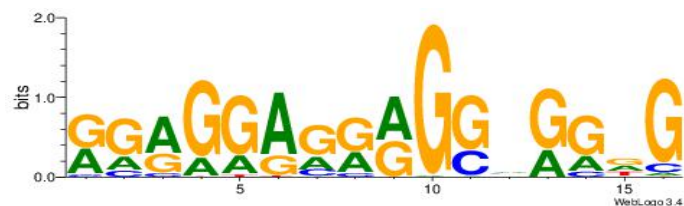
Dataset #: 5
 Motif ID: 51

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

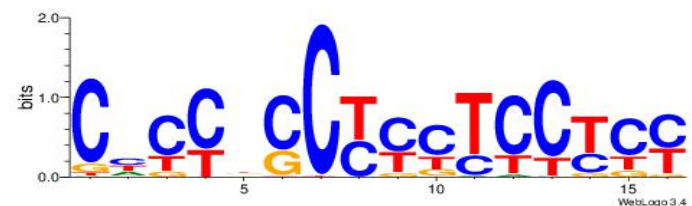
Alignment:

CHCCBCCCKMCTCCKCM
 --GCCCCGCC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCCKMCTCCKCM



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)

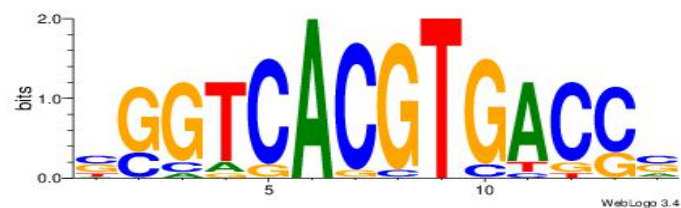
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACsS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0375102

Alignment:

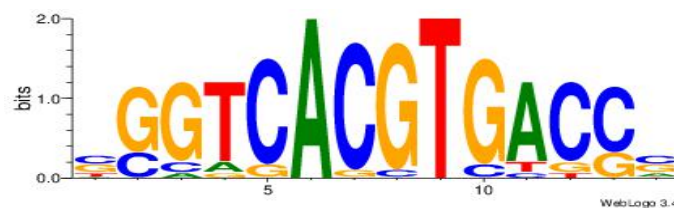
SGGTCACGTGACCS

--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



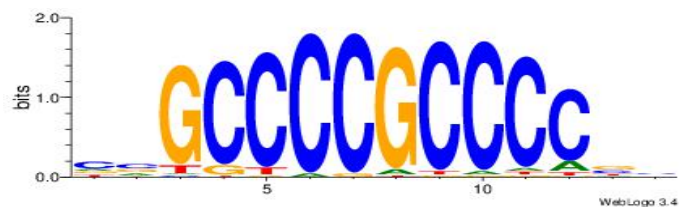
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0539

Alignment:

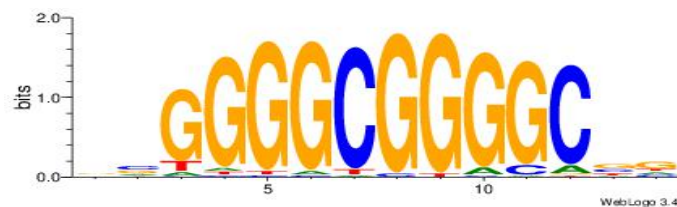
HVGCCCCGCCCCBB

--GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCB



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:
 GCCCCGCC
 --GTCGCG

Original motif Consensus sequence: GGC GG GGC



Reverse complement motif Consensus sequence: GCCCCGCC

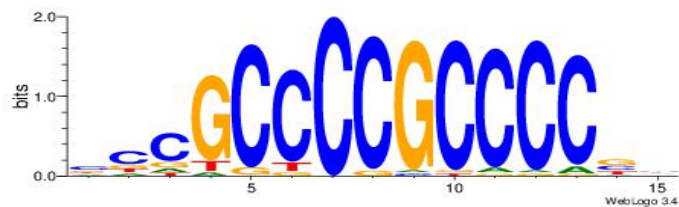


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0558733

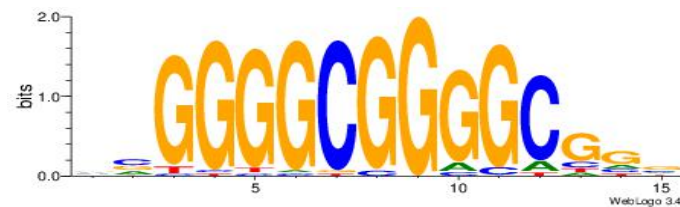
Alignment:

BBGGGGCGGGGCGGB
 -----GTCGCG--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

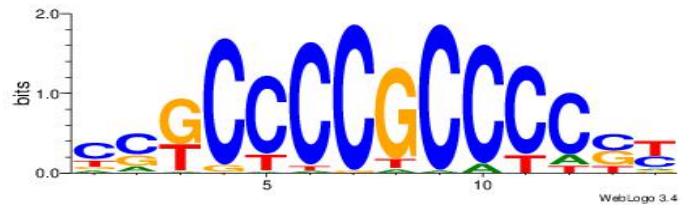


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7

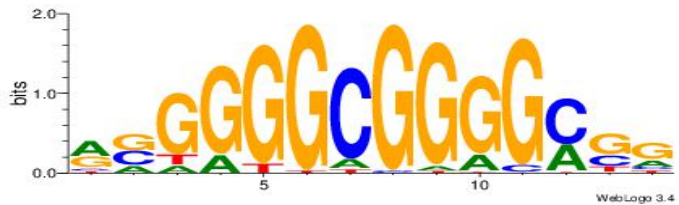
Number of overlap: 6
Similarity score: 0.0644512

Alignment:
CSKCCCCGCCCCSY
--CGCGAC-----

Original motif Consensus sequence: CSKCCCCGCCCCSY



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



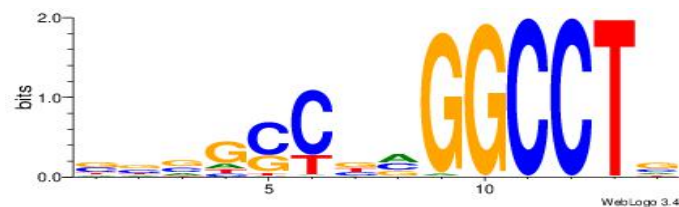
Dataset #: 3
 Motif ID: 22

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

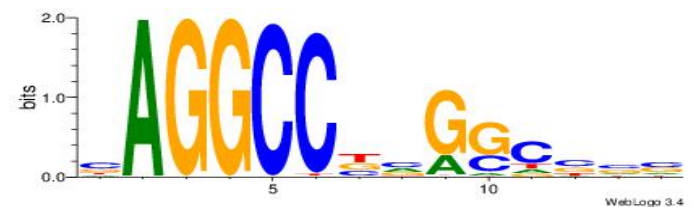
Alignment:

```
BBVGCCBVGGCCTV
---GTCGCG-----
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



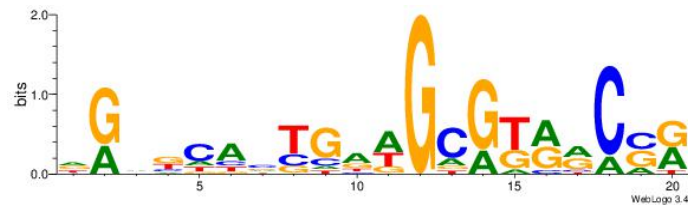
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	6
Similarity score:	0.072456

Alignment:

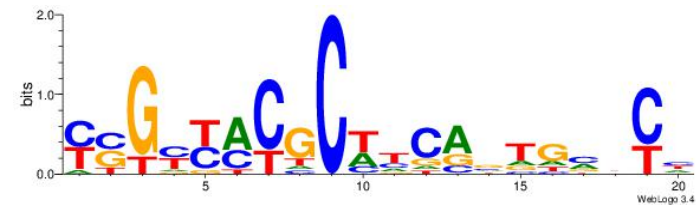
MSGKKRCGCWDCABTGBB CD

-----CGCGAC-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRC SR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTG BB CD



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

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



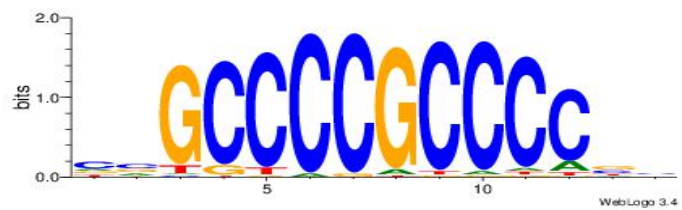
Best Matches for Top Significant Motif ID 47 (Highest to Lowest)

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

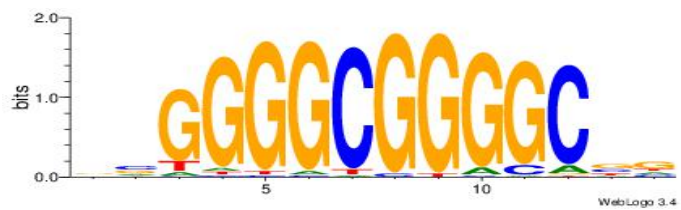
Position number: 2
Number of overlap: 8
Similarity score: 0.0456233

Alignment:
HVGCCCCGCCCCBB
-CCGCGCGS-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



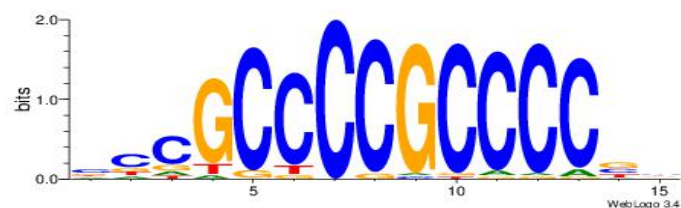
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



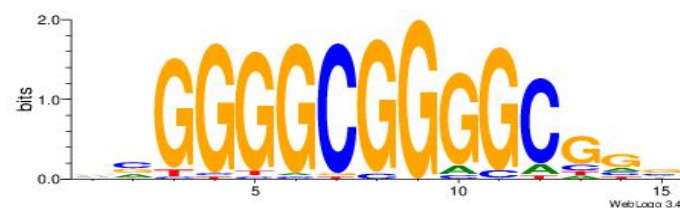
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.045686

Alignment:
BBGGGGCGGGCGGB
-----SCGCGCGG-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

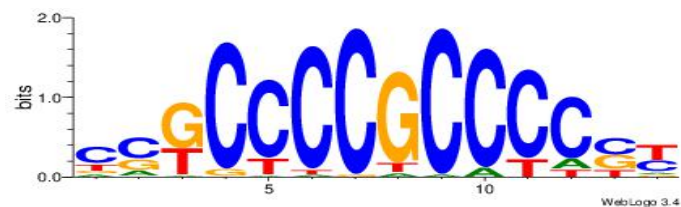


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 8
Similarity score: 0.0504058

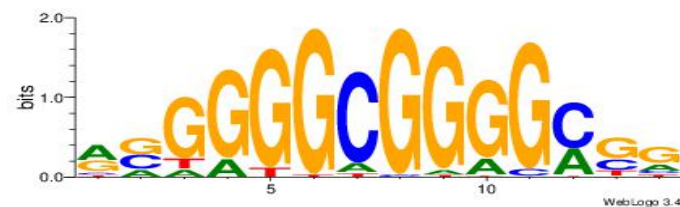
Alignment:

CSKCCCCGCCCCSY
-CCGCGCGS-----

Original motif Consensus sequence: CSKCCCCGCCCCSY



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

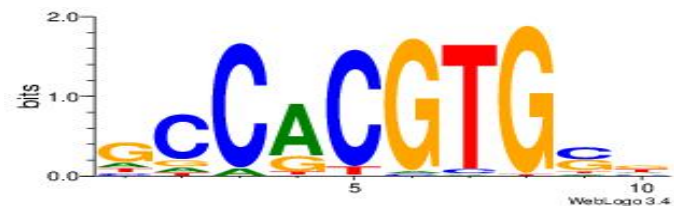
Alignment:

HSCACGTGGC
 -SCGCGCGG-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

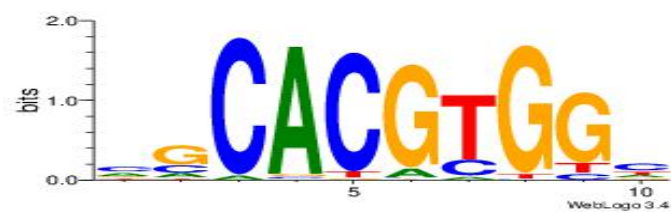


Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8

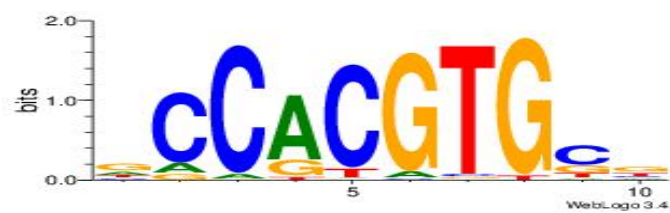
Similarity score: 0.0574543

Alignment:
VGCACGTGGH
-SCGCGCGG-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

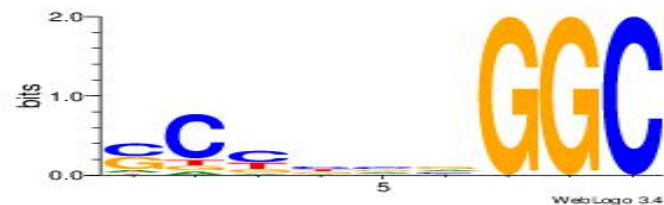
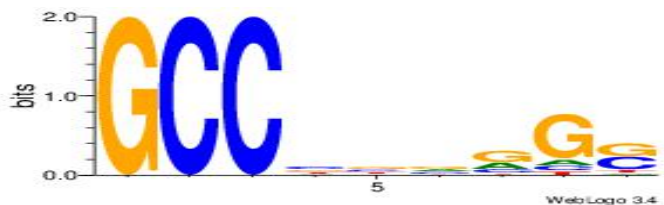


Dataset #: 3
Motif ID: 25
Motif name: TFAP2A
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0678925

Alignment:
SCMVBBGGC
-SCGCGCGG-

Original motif Consensus sequence: GCCBBVRGS

Reverse complement motif Consensus sequence: SCMVBBGGC



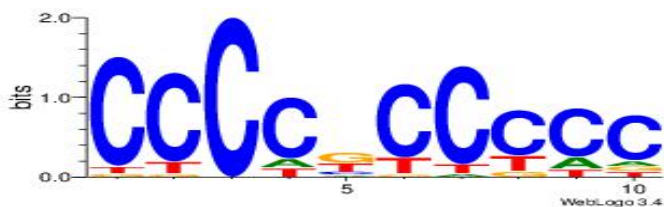
Dataset #: 3
 Motif ID: 24
 Motif name: SP1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.07018

Alignment:

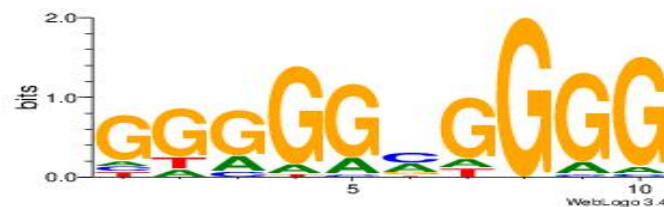
CCCCKCCCCC

--CCGCGCGS

Original motif Consensus sequence: CCCCCCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



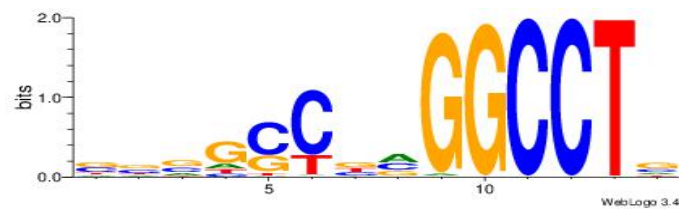
Dataset #: 3
 Motif ID: 22

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

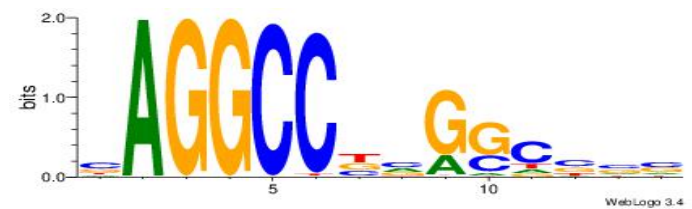
Alignment:

BBVGCCBVGGCCTV
 --SCGCGCGG----

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



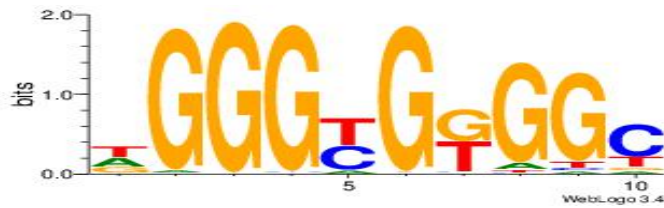
Dataset #:	3
Motif ID:	27
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0768965

Alignment:

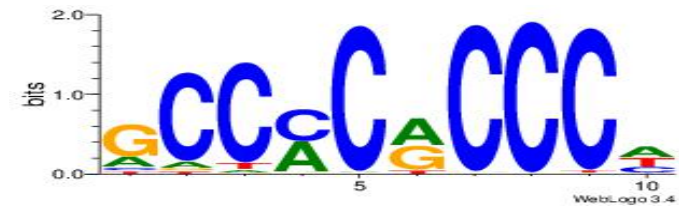
DGGGYGKGGC

-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)

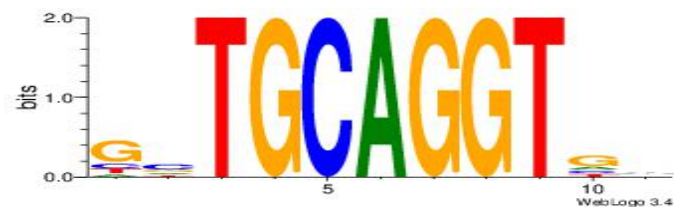
Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAGc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0295473

Alignment:
 GBTGCAGGTGB
 ---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



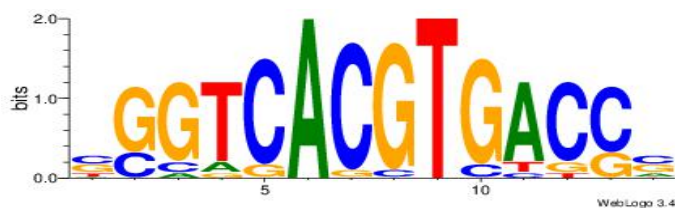
Reverse complement motif Consensus sequence: GBTGCAGGTGB



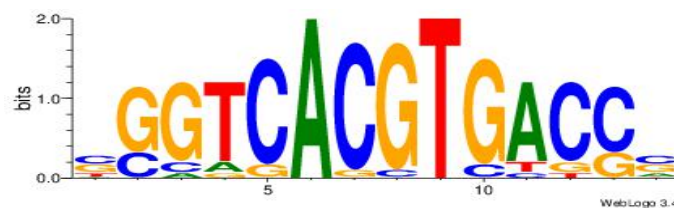
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0314837

Alignment:
 SGGTCACGTGACCS
 ---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

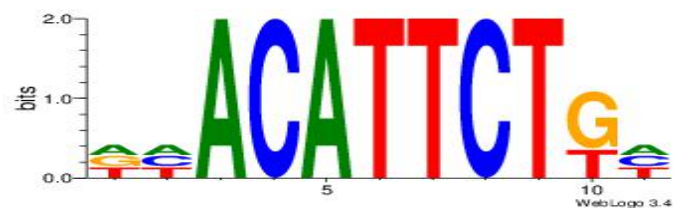


Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0640024

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

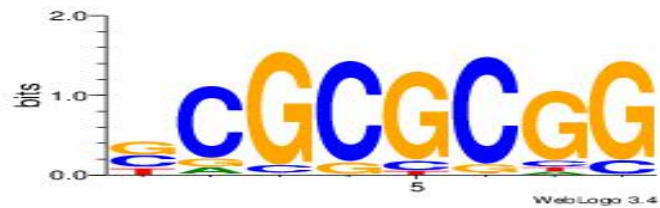
Similarity score: 0.0660185

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

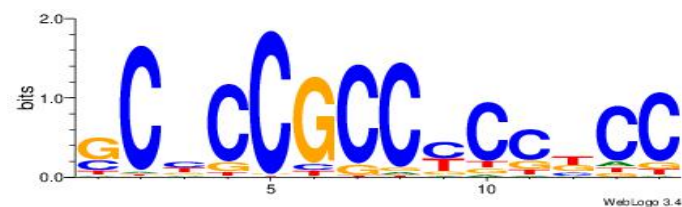
Alignment:

GCVCCGCCMCCYCC

-----VCACGTBV

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Alignment:

```
RGRGGAGRRGGHGGDG
---VBACGTGV-----
```

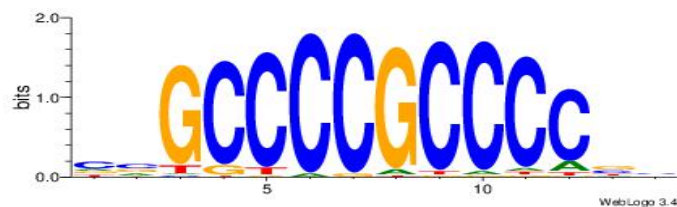
Dataset #: 4

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

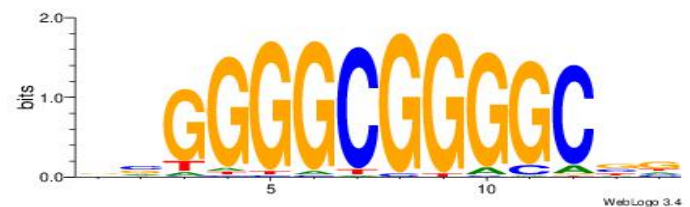
Alignment:

BBGGGGCGGGGCVD
 ---VBACGTGV---

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



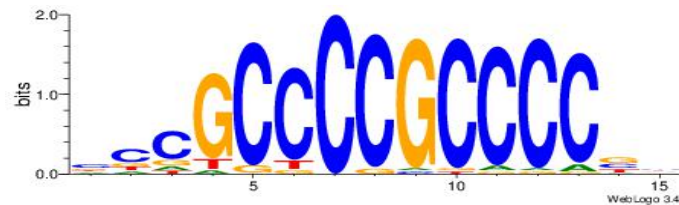
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0735453

Alignment:

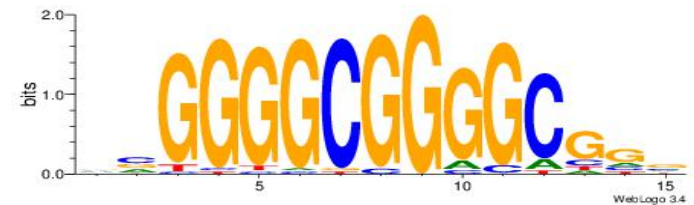
BBGGGGCGGGGCGGB

---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

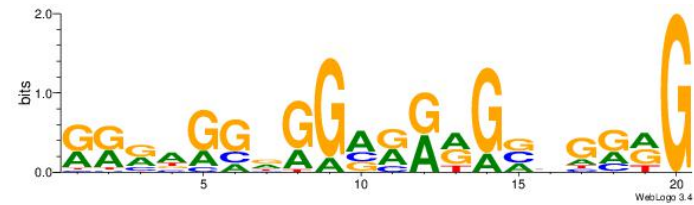
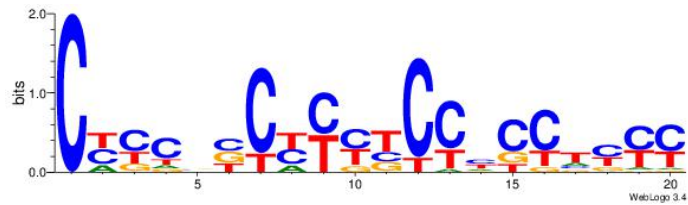
Alignment:

KKKAGGDGGAKKMGBBGKMG

-VBACGTGV-----

Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY

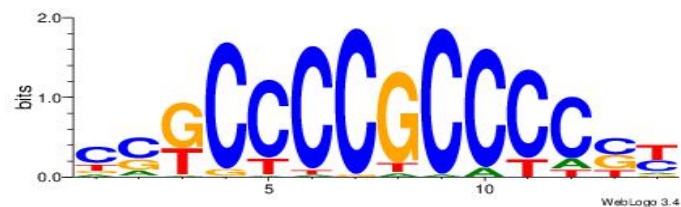
Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



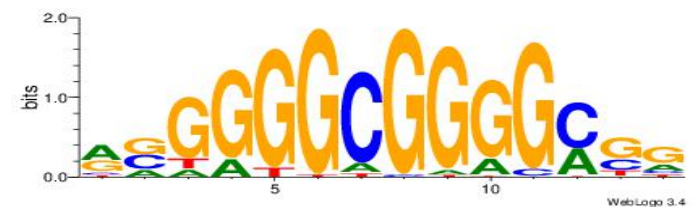
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0775335

Alignment:
 CSKCCCCGCCCCSY
 ---VCACGTBV---

Original motif Consensus sequence: CSKCCCCGCCCCSY

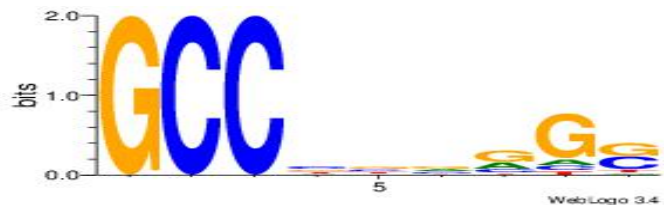


Reverse complement motif Consensus sequence: MSGGGGCGGGGY

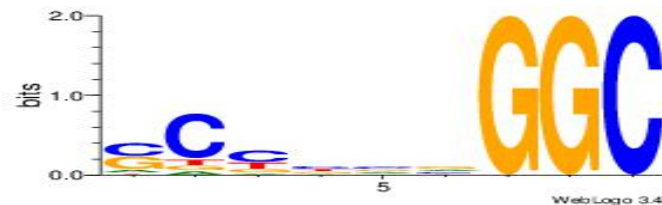


Dataset #: 3 Motif ID: 25 Motif name: TFAP2A

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



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

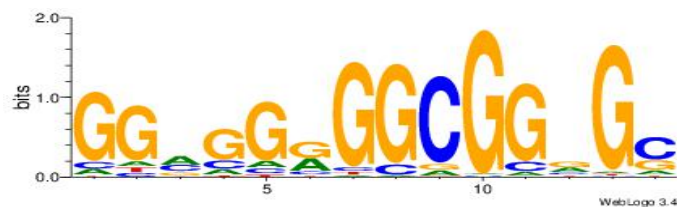
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.0415732

Alignment:

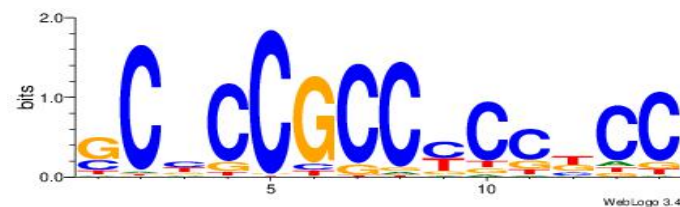
GGMGGRGGCGGVGC

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

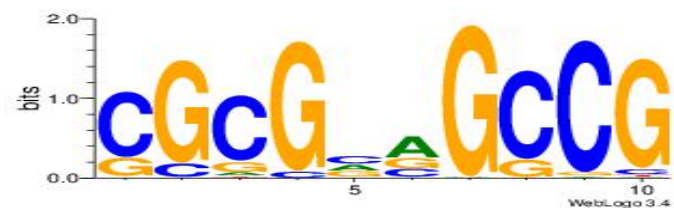
Alignment:

CGGCYBCGCG
 -GCCBBVRGS

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

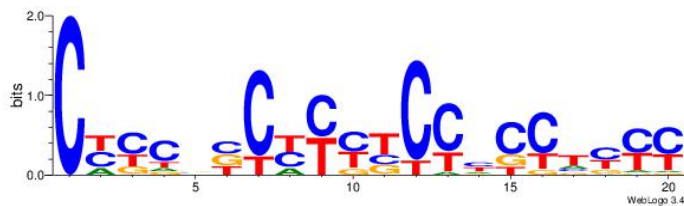


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 9

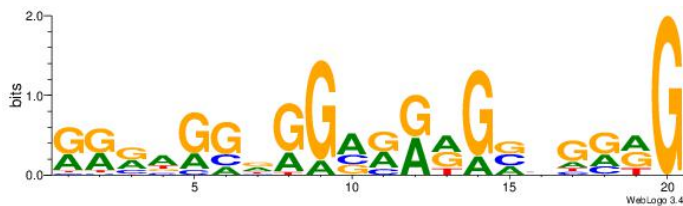
Similarity score: 0.0630429

Alignment:
KKKAGGDGGAKKMGBBGKMG
-SCMVBBGGC-----

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

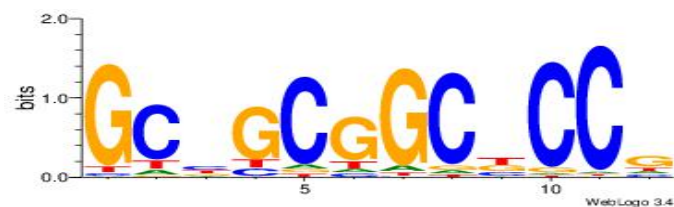
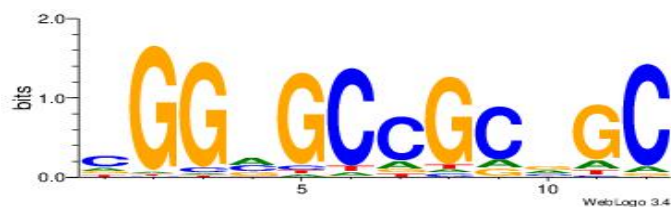


Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 9
Similarity score: 0.0669772

Alignment:
GCVGCGGCBCCG
SCMVBBGGC---

Original motif Consensus sequence: CGGVGCCGCVGC

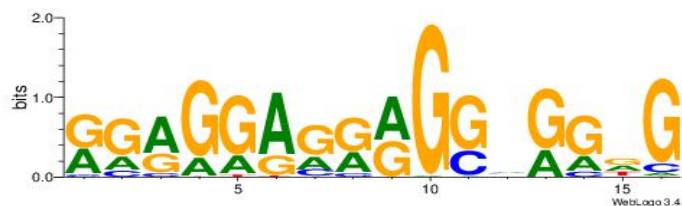
Reverse complement motif Consensus sequence: GCVGCGGCBCCG



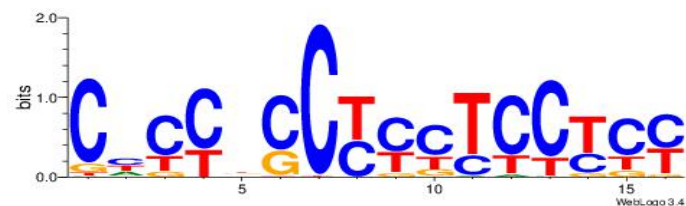
Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 9
 Similarity score: 0.069755

Alignment:
 CHCCBCKMCTCCKCM
 SCMVBBGGC-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

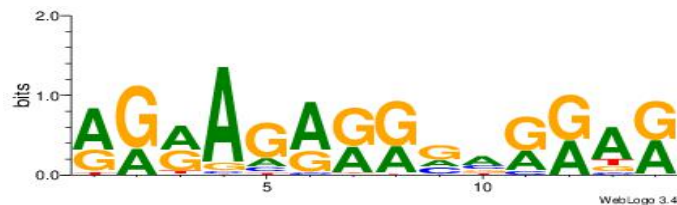


Dataset #: 2

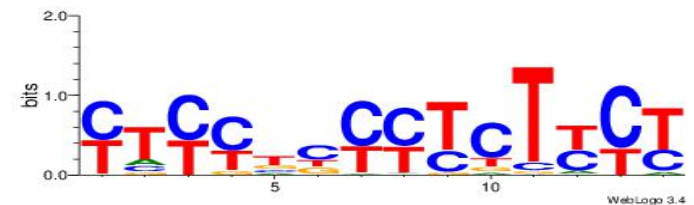
Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0715961

Alignment:
 MTMMTCMMTCTKCK
 ----SCMVBBGGC-

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



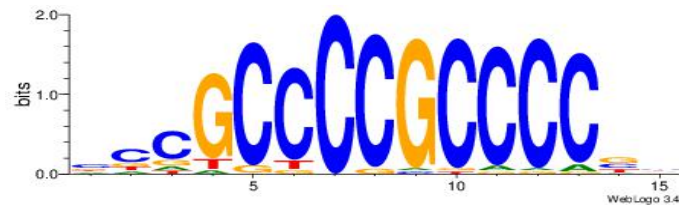
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0719489

Alignment:

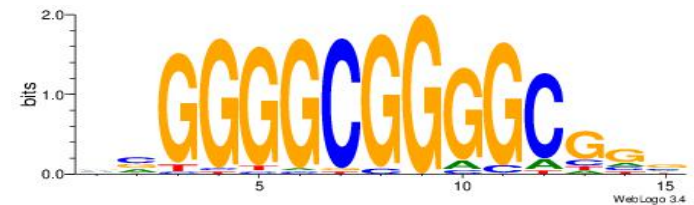
BBGGGGCGGGGCGGB

-----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

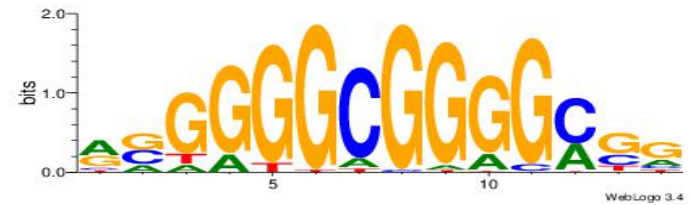
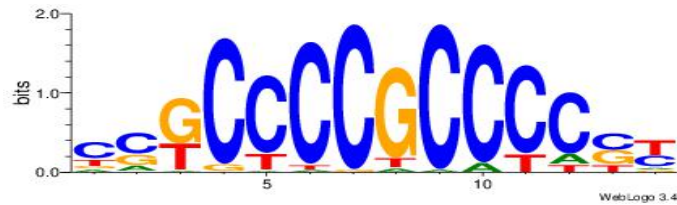
Alignment:

CSKCCCCGCCCCSY

-----SCMVBBGGC

Original motif Consensus sequence: CSKCCCCGCCCCSY

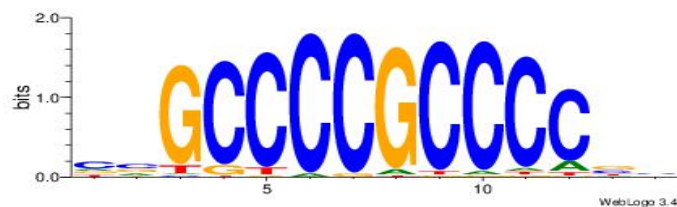
Reverse complement motif Consensus sequence: MSGGGGCGGGGY



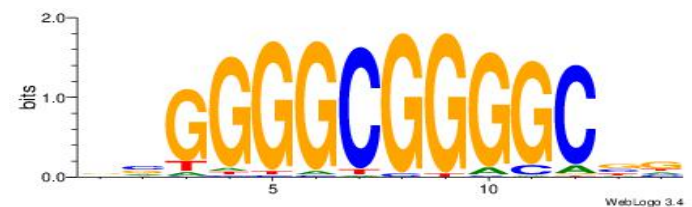
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0800026

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

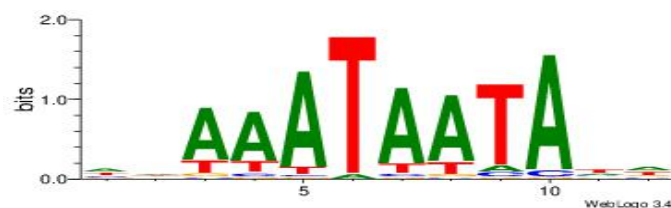


Reverse complement motif Consensus sequence: GBTGCAGGTGB

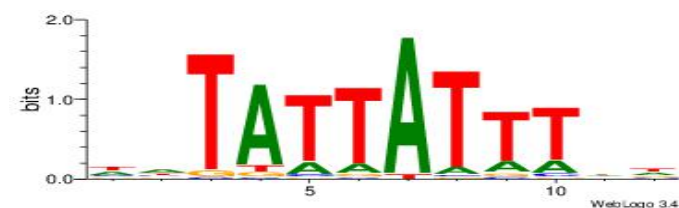


Dataset #: 4 Motif ID: 41 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTDDH



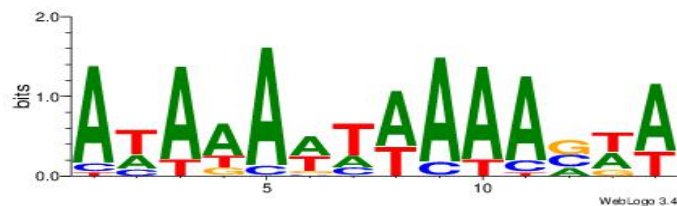
Best Matches for Top Significant Motif ID 41 (Highest to Lowest)

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

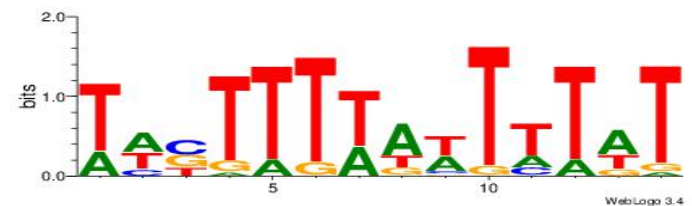
Alignment:

AWAAAWTWAAASWA
 -HDAAATAATADD-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV



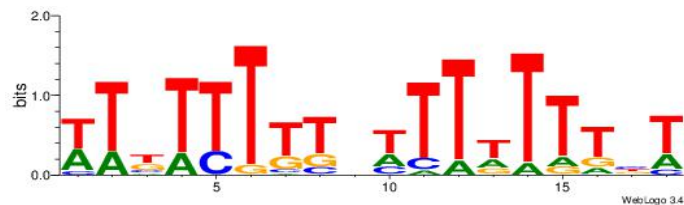
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 12

Similarity score: 0.0565705

Alignment:

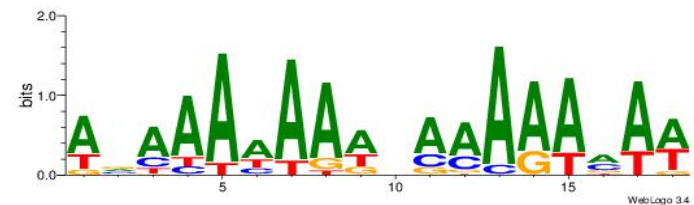
WTKTTTTTHWTTTTTBT
-----DDTATTATTTDH

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif
ABAAAAAWhAAAAARAW

Consensus sequence:



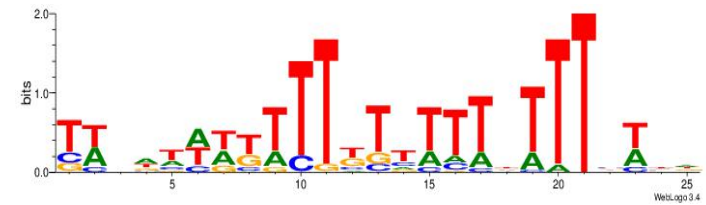
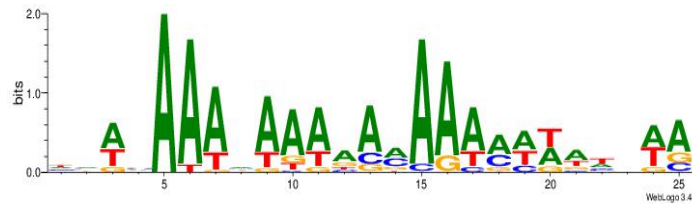
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0575935

Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
--HDAAATAATADD-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

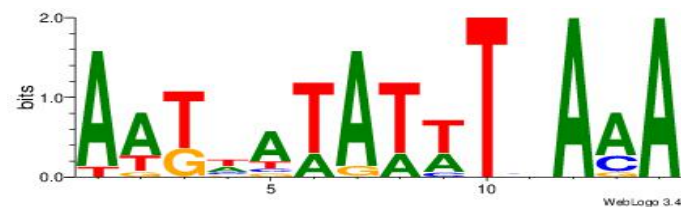
Reverse complement motif Consensus sequence:
TWVHWWWYTTTTYTTTTTHTTTVWBH



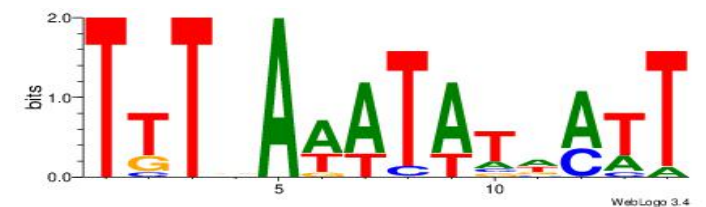
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0591821

Alignment:
 AATHATATWTHAAA
 --DDTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



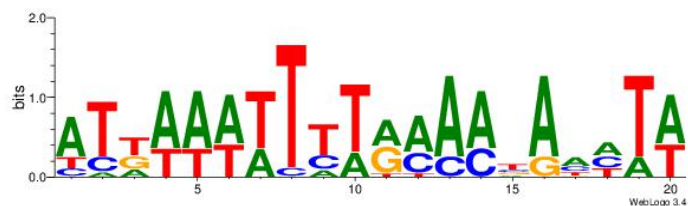
Dataset #: 5
 Motif ID: 55

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

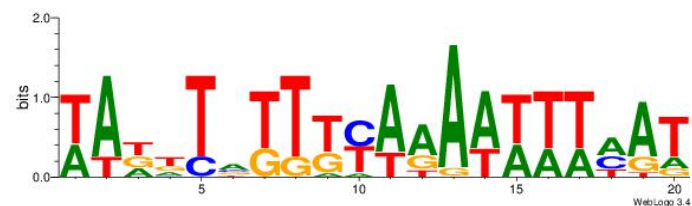
Alignment:

WAHHTVTTYKAAAWTTRAT
 -----HDAAATAATADD

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAWTTRAT



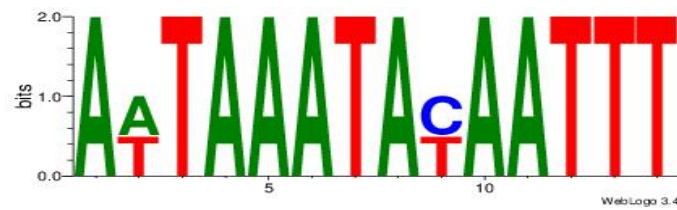
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0715278

Alignment:

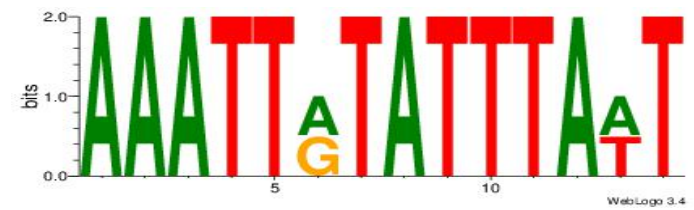
AAATTKTATTTAWT

-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

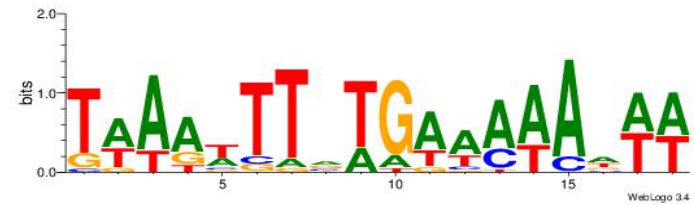
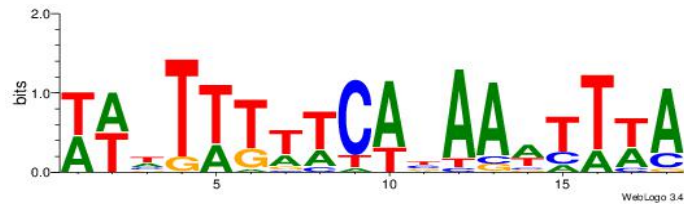
Alignment:

WWHTTTTTCABAAWTTWA

-----DDTATTATTTDH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TAAWTTVTGAAAAHWW

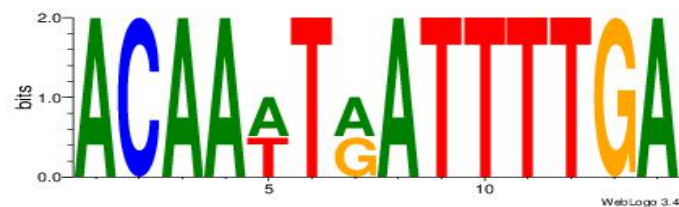


Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0912037

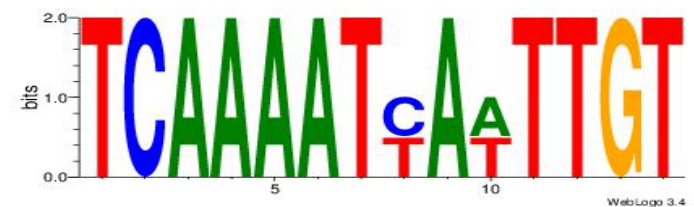
Alignment:

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:

```

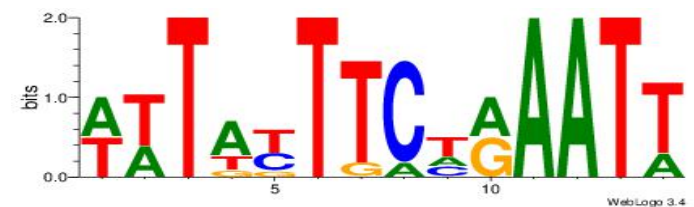
WWTAKTTCDKAATT
DDTATTATTDDH--

```

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAATT



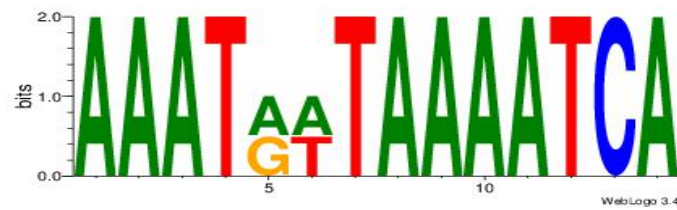
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0989198

Alignment:

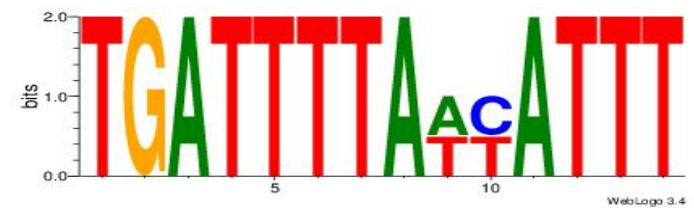
TGATTTTAWKATTT

-DDTATTATTDDH-

Original motif Consensus sequence: AAATRWTAATCA

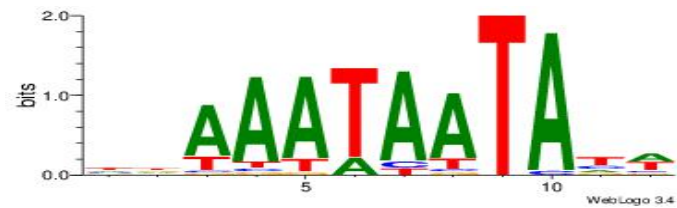


Reverse complement motif Consensus sequence: TGATTTTAWKATTT

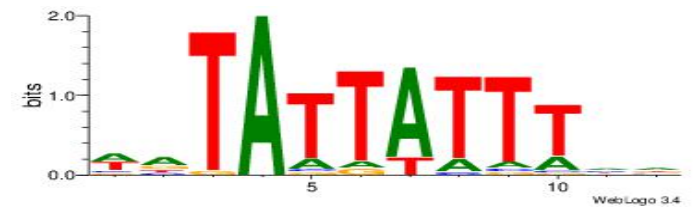


Dataset #: 4 Motif ID: 37 Motif name: tkAAATAATAtw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTDDH



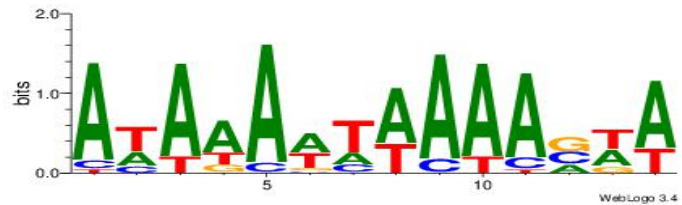
Best Matches for Top Significant Motif ID 37 (Highest to Lowest)

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

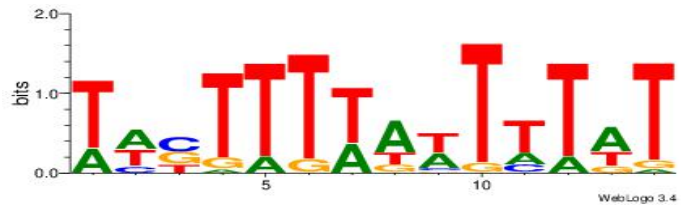
Number of overlap: 12
Similarity score: 0.0522317

Alignment:
TWSTTTWAWTTTWT
-WHTATTATTDDH-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

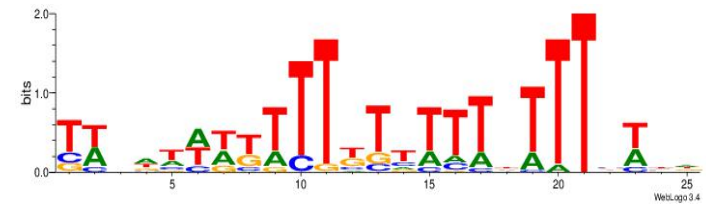
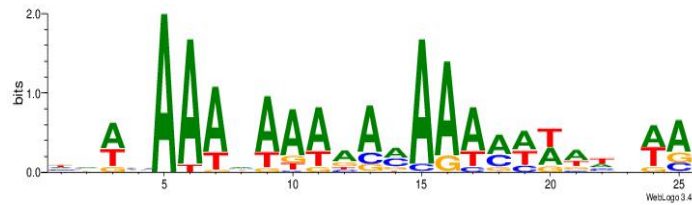


Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 12
Number of overlap: 12
Similarity score: 0.0590505

Alignment:
TWVHWWYTTTTYTTTTHTTTVWBH
-----WHTATTATTDDH--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
TWVHWWYTTTTYTTTTHTTTVWBH

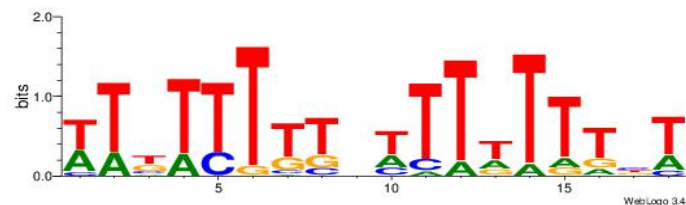


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0637702

Alignment:

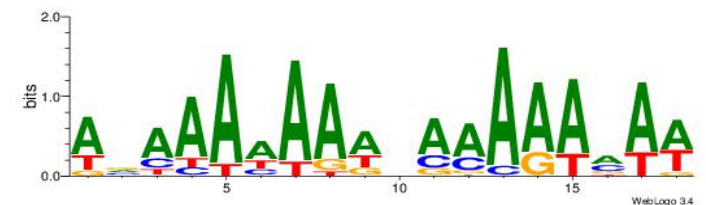
ABAAAAAAWHAAAAARAW
 HDAAATAATAHW-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif
ABAAAAAAWHAAAAARAW

Consensus sequence:



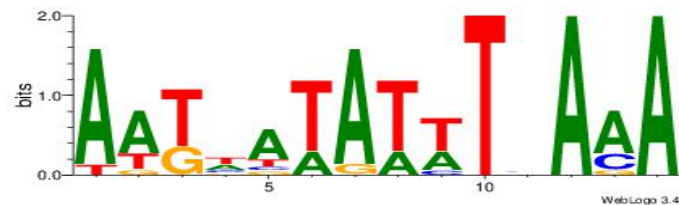
Dataset #: 2

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

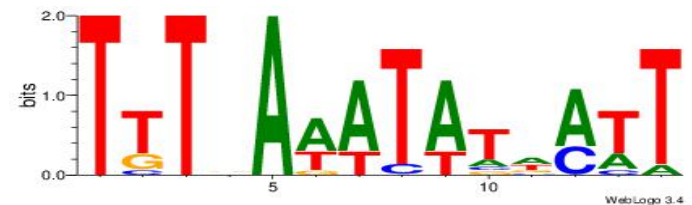
Alignment:

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

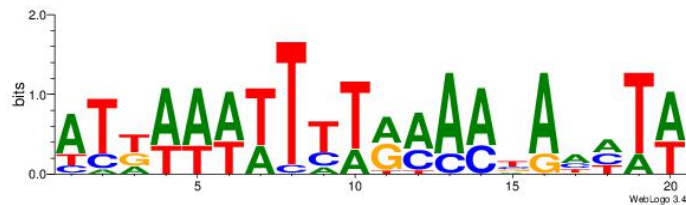
Alignment:

```

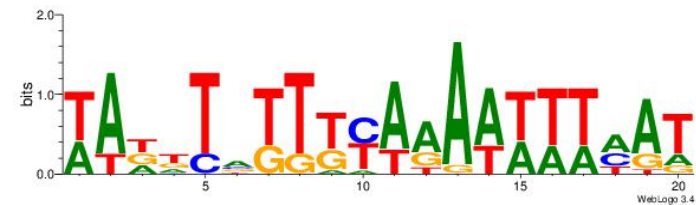
WAHHTVTTYKAAAATTRAT
-----HDAAATAATAHW

```

Original motif Consensus sequence: 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:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0704475

Alignment:

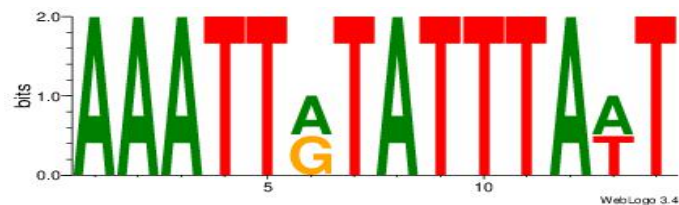
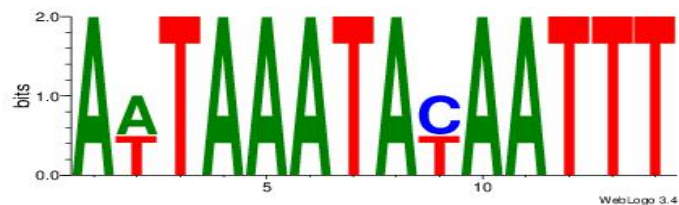
```

AAATTKTATTTAWT
-WHTATTATTTDH-

```

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAWT

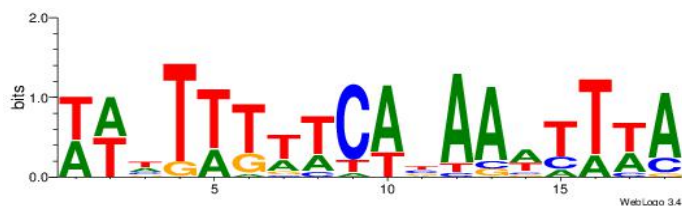


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0763819

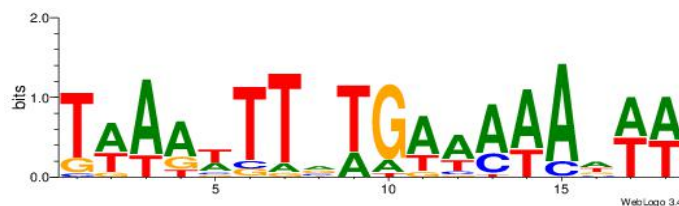
Alignment:

WWHTTTTTCABAAWTTWA
 -----WHTATTATTTDH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



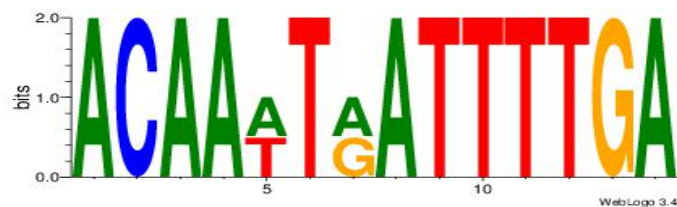
Dataset #: 2

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

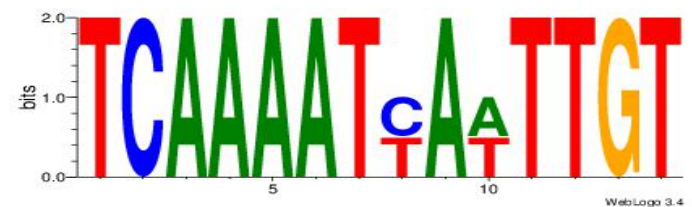
Alignment:

TCAAATKAWTTGT
 --WHTATTATTTDH

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAATKAWTTG



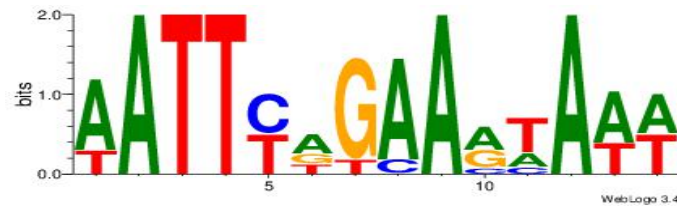
Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.09076

Alignment:

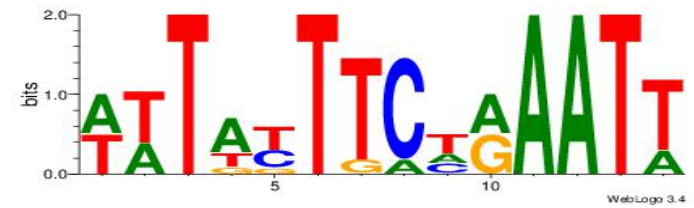
WWTAKTTCDKAATT

WHTATTATTTDH--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAATT



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

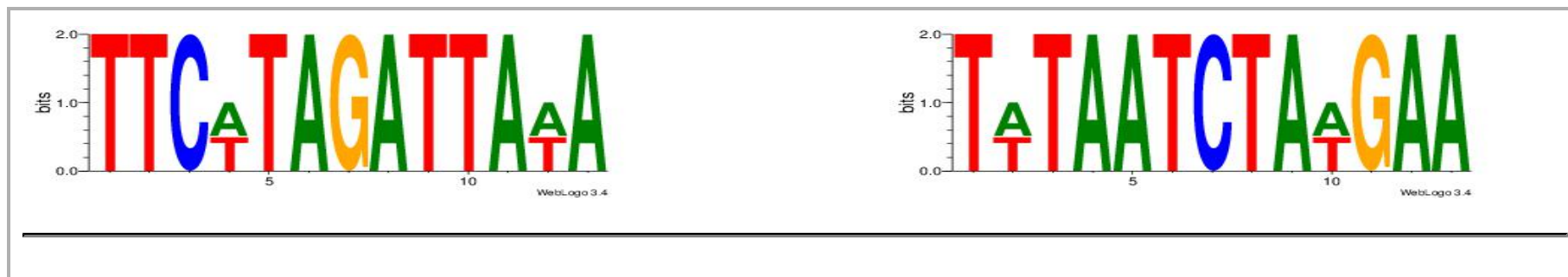
Alignment:

TWTAATCTAWGAA

WHTATTATTTDH-

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA



Results created by MOTIFSIM on 09-23-2015 12:50:42
Runtime: 75.0307 seconds.

MOTIFSIM is written by Ngoc Tam L. Tran
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