



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

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
Motif tree:	Yes
Combined similar motifs:	Yes
Output file type:	All
Output file format:	All

Input files and motif counts

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

RESULTS

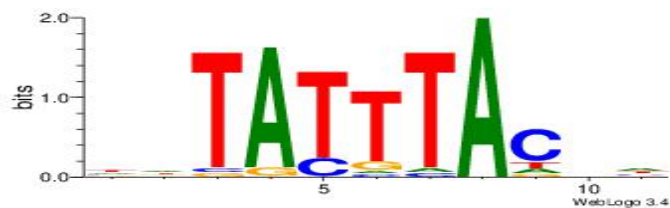
Top 10 Significant Motifs - Global Matching (Highest to Lowest)

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

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



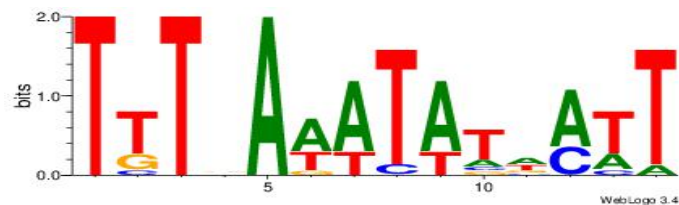
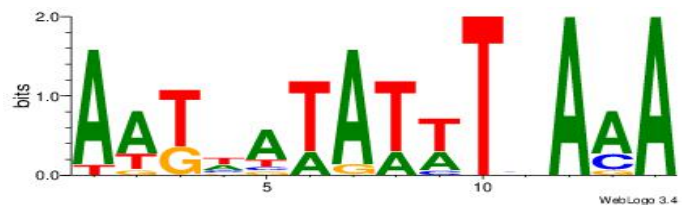
Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

Dataset #:	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:	0.0177412

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: 0.0205821

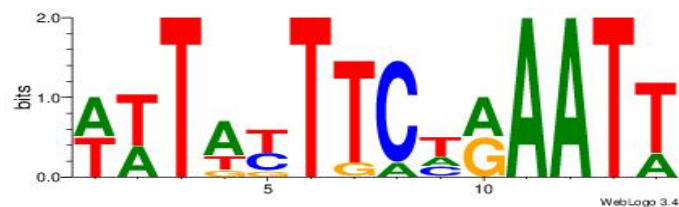
Alignment:

AATTYDGAARTAWW
 ---DBGTAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



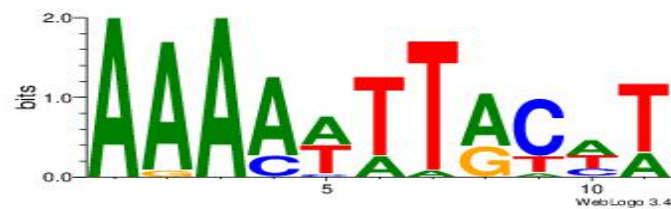
Dataset #: 2
 Motif ID: 4

Motif name:	Motif 4
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0288058

Alignment:

AWGKAAWTTTT
DBGTAATAHD

Original motif Consensus sequence: AAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



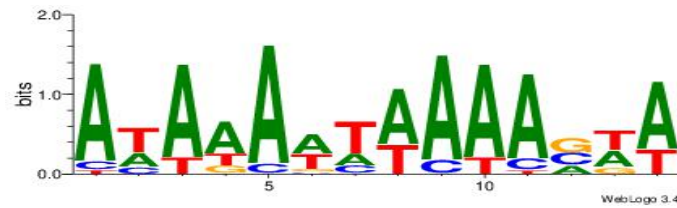
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0337252

Alignment:

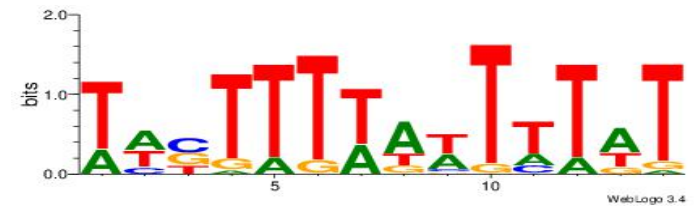
AWAAAWTWAAASWA

--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:	0.0404685

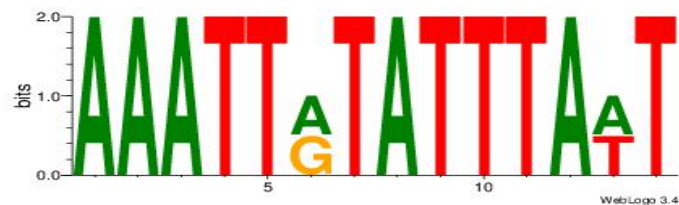
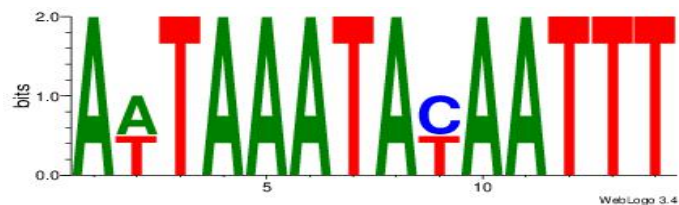
Alignment:

AWTAAATAYAATTT

---DHTATTTACBD

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW

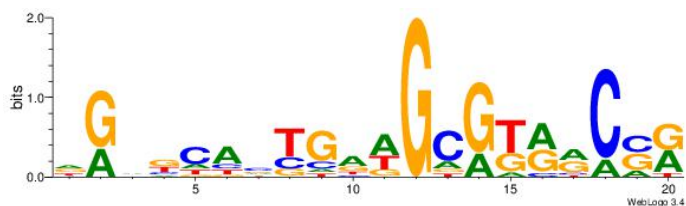


Dataset #: 5
 Motif ID: 55
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.0439858

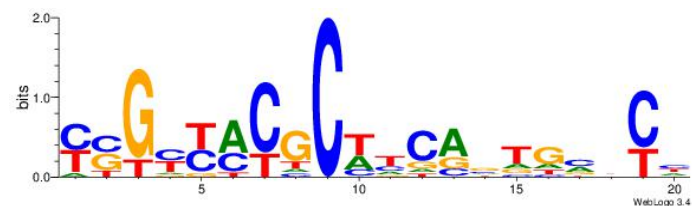
Alignment:

DGVBCABTGDWGCGRRCR
 DBGTAATAHD-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



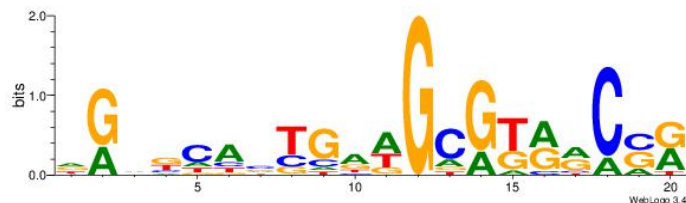
Dataset #: 3

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: 0.0439858

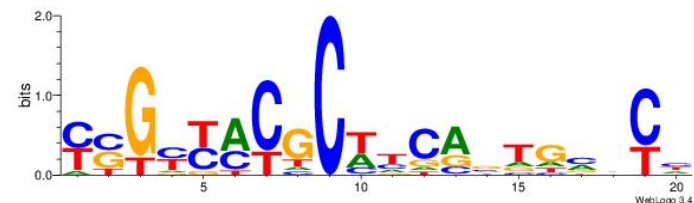
Alignment:

DGVBCABTGDWGCGRRCR
 DBGTAATAHD-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBB CD



Dataset #: 5
 Motif ID: 59
 Motif name: GABPA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11

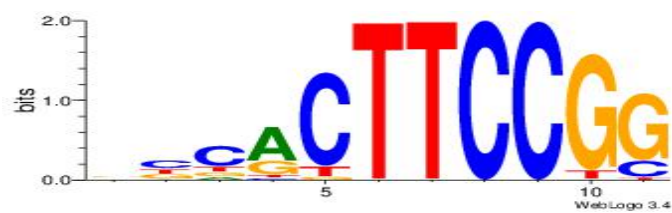
Similarity score: 0.0439962

Alignment:
CCGGAAGTGVV
DBGTAATAHD

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG

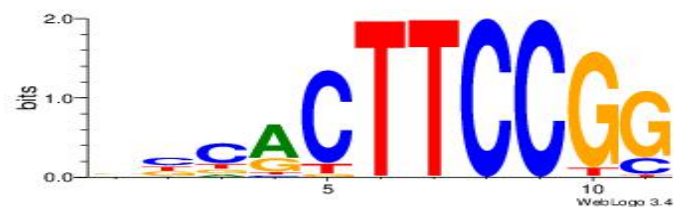


Dataset #: 3
Motif ID: 35
Motif name: GABPA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0439962

Alignment:
CCGGAAGTGVV
DBGTAATAHD

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



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: 11
 Similarity score: 0.0477737

Alignment:

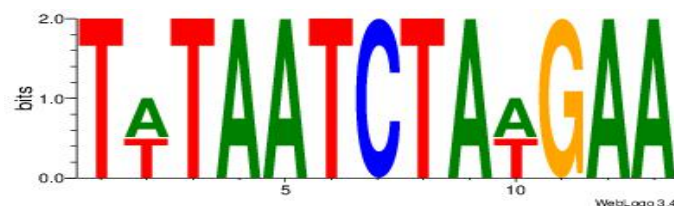
TWTAATCTAWGAA

-DHTATTTACBD-

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAATCTAWGAA



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

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCGGCC



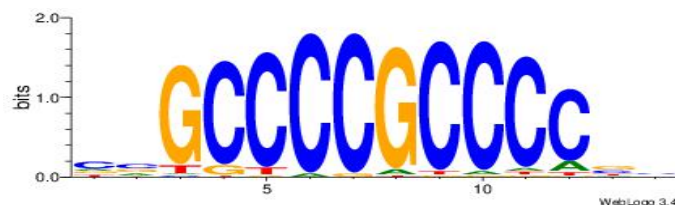
Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

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:	8
Similarity score:	0

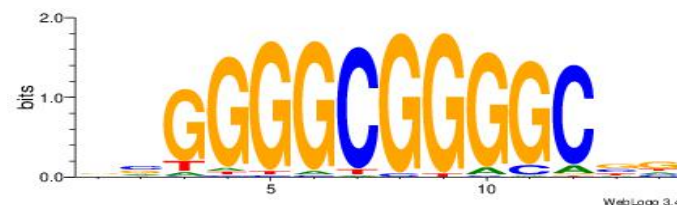
Alignment:

```
HVGCCCCGCCCCBB
--GCCCCGCC----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

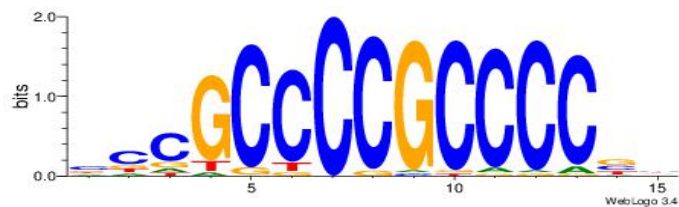


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.00250079

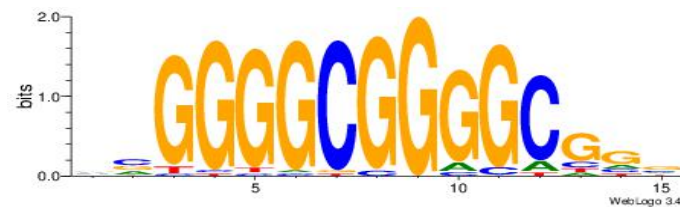
Alignment:

BCCGCCCCGCCCCBB
 ---GCCCCGCC----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

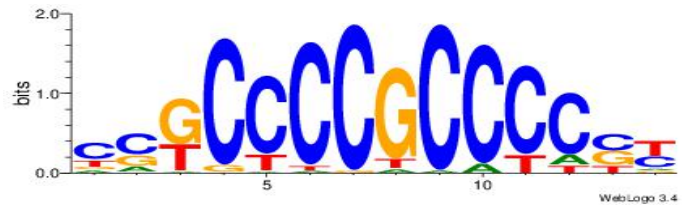


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

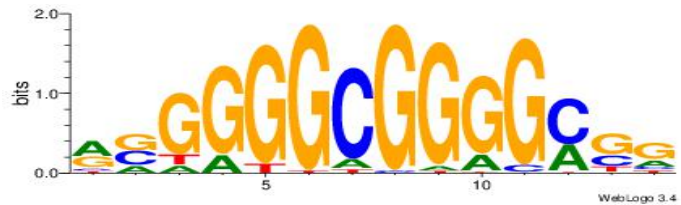
Number of overlap: 8
Similarity score: 0.0149958

Alignment:
MSGGGGCGGGYSG
----GGCGGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY

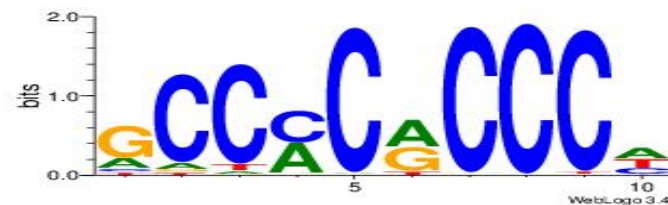


Dataset #: 5
Motif ID: 51
Motif name: Klf4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0349983

Alignment:
DGGGYGKGGC
--GGCGGGGC

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD



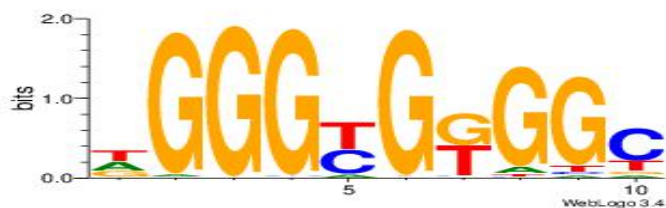
Dataset #: 3
 Motif ID: 27
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0349983

Alignment:

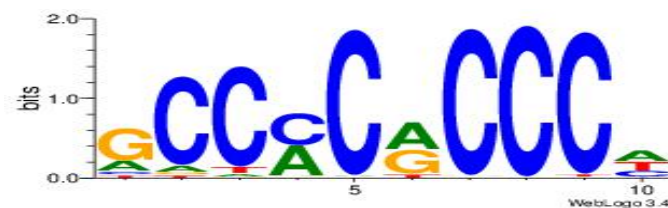
DGGGYGKGGC

--GGCGGGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



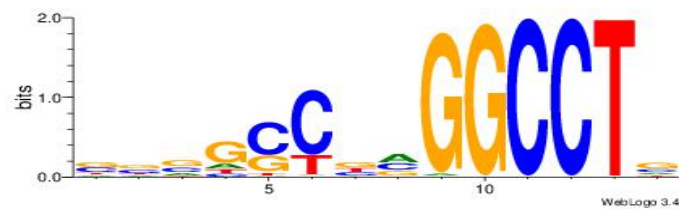
Dataset #: 3
 Motif ID: 22

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

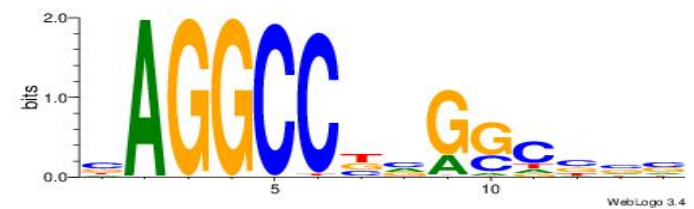
Alignment:

VAGGCCBBGGCVBB
 ---GCCCGGCC---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



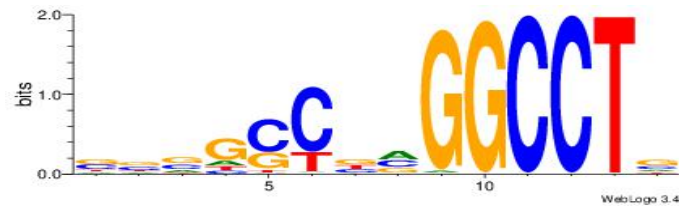
Dataset #: 5
 Motif ID: 46
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0708224

Alignment:

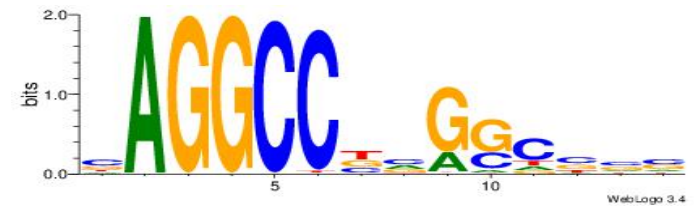
VAGGCCBBGGCVBB

---GCCCGGCC---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



Dataset #:	5
Motif ID:	55
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

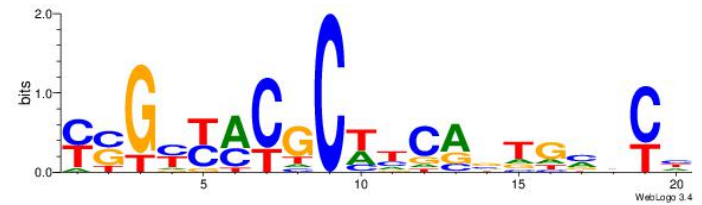
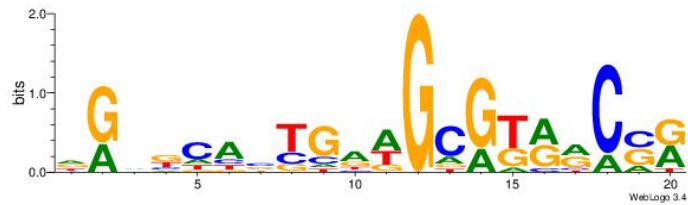
Alignment:

DGVBCABTGDWGCGRRCR

-----GCCGGGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif Consensus sequence:
MSGKKRCGCWDCA BTGBBCD

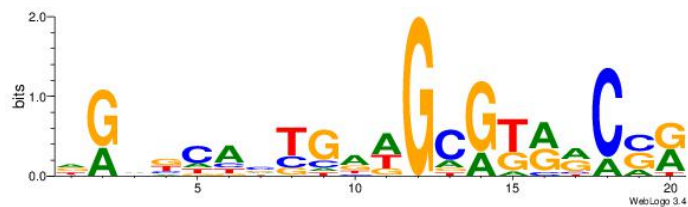


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0853847

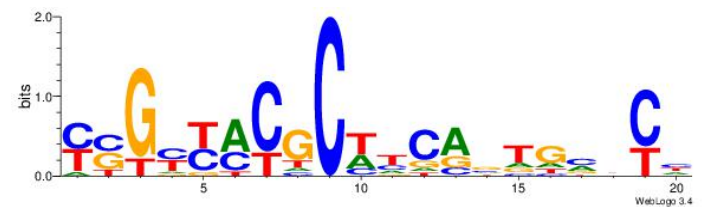
Alignment:

DGVBCABTGDWGCGRRCR
 -----GCGGGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3

Motif ID: 23
 Motif name: Egr1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0878731

Alignment:

HGCGTGGGCGK

GGCGGGGC---

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH



Dataset #: 5
 Motif ID: 47
 Motif name: Egr1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0878731

Alignment:

HGCGTGGGCGK

GGCGGGGC---

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



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 #:	5
Motif ID:	56
Motif name:	ArntAhr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

Number of overlap: 6
Similarity score: 0

Alignment:

YGCGTG

YGCGTG

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Dataset #: 5
Motif ID: 47
Motif name: Egr1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.0340278

Alignment:

HGCGTGGGCGK

YGCGTG-----

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YGCCCCACGCH



Dataset #: 5
 Motif ID: 53
 Motif name: HIF1AARNT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0452724

Alignment:
 VBACGTGV
 -YGCGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Dataset #: 5
 Motif ID: 57

Motif name:	Mycn
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:	0.0718227

Alignment:

GCCACGTGSD

--YGCGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



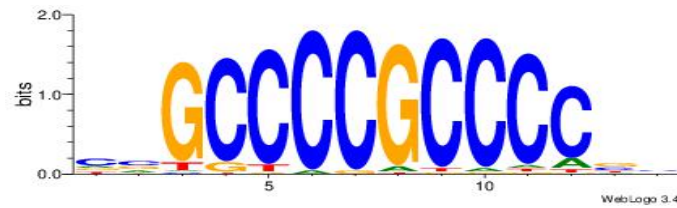
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0736681

Alignment:

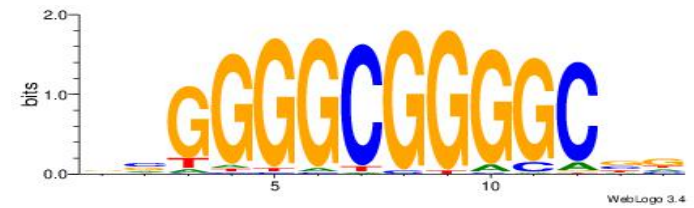
HVGCCCGCCCCBB

-----CACGCM-----

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #:	5
Motif ID:	58
Motif name:	Myc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0739492

Alignment:

DCCACGTGCV

--YGCGTG--

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



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: 0.0746528

Alignment:
 GCCCGCC
 --CACGCM

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCGGCC

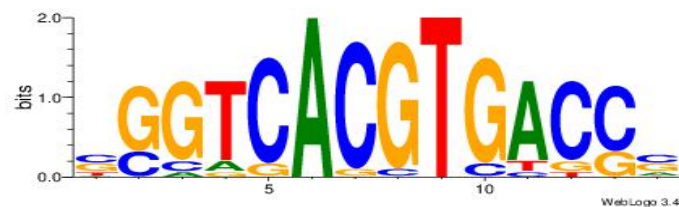


Dataset #: 4
 Motif ID: 42

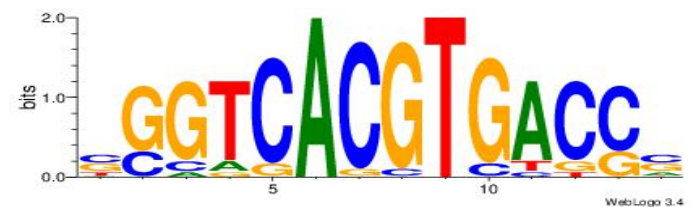
Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0752315

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

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



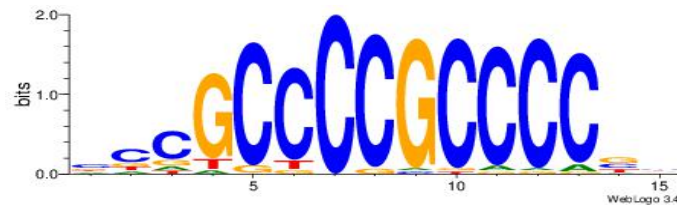
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0765366

Alignment:

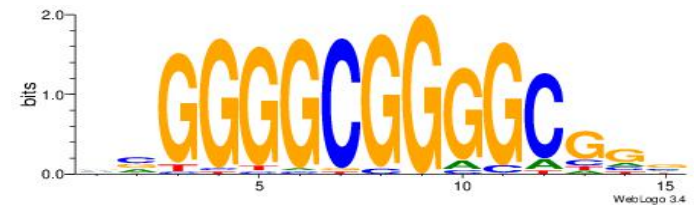
BCCGCCCCGCCCCBB

-----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:	0.0806145

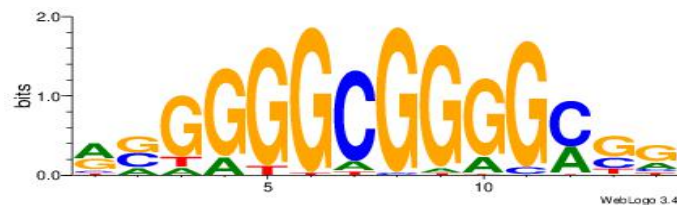
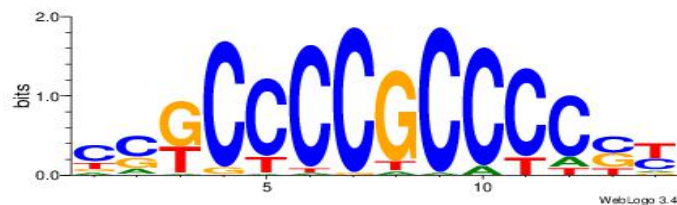
Alignment:

MSGGGGCGGGGYSG

-----YGCGTG-----

Original motif Consensus sequence: CSKCCCCGCCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 5 **Motif ID: 56** **Motif name: ArntAhr**

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Best Matches for Top Significant Motif ID 56 (Highest to Lowest)

Dataset #:	3
Motif ID:	32
Motif name:	ArntAhr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

YGCGTG

YGCGTG

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



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: 6
Similarity score: 0.0340278

Alignment:

YGCCCCACGCH
-----CACGCM

Original motif Consensus sequence: HGC GTGGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH



Dataset #: 3
 Motif ID: 29
 Motif name: HIF1AARNT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0452724

Alignment:
 VBACGTGV
 -YGCGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV

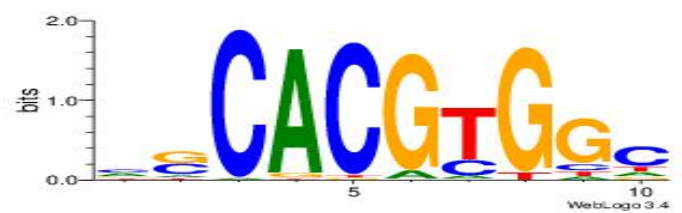


Dataset #: 3
 Motif ID: 33
 Motif name: Mycn
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6

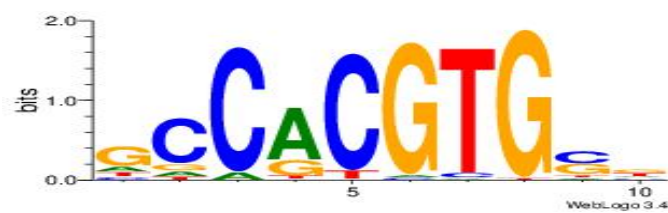
Similarity score: 0.0718227

Alignment:
HSCACGTGGC
--CACGCM--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

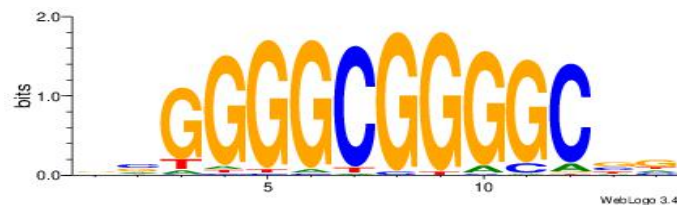
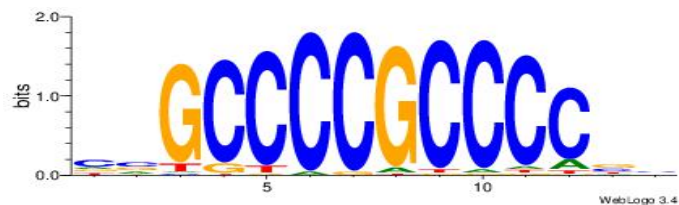


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0736681

Alignment:
BBGGGGCGGGGCVD
----YGCGTG----

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0739492

Alignment:

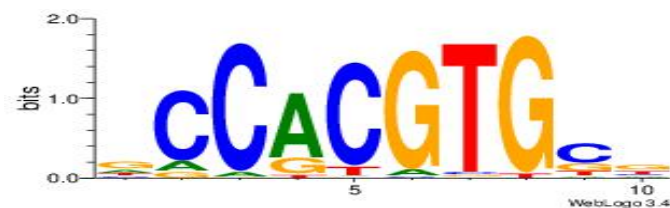
VGCACGTGGH

--CACGCM--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



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:	0.0746528

Alignment:
GCCCCGCC
--CACGCM

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCCGCC



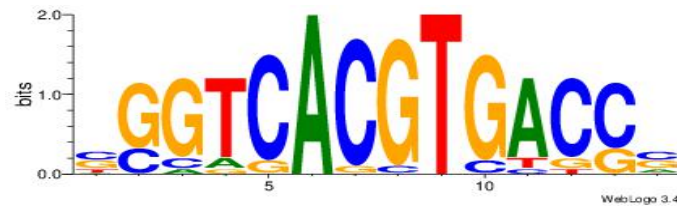
Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSS
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0752315

Alignment:

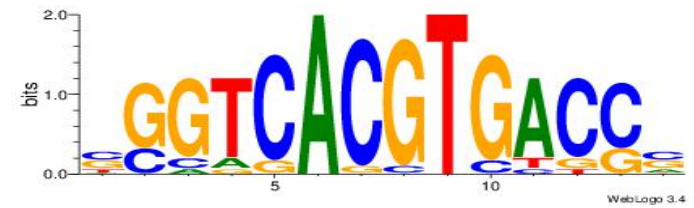
SGGTCACGTGACCS

-----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:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.0765366

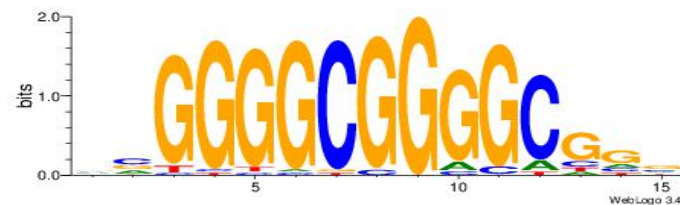
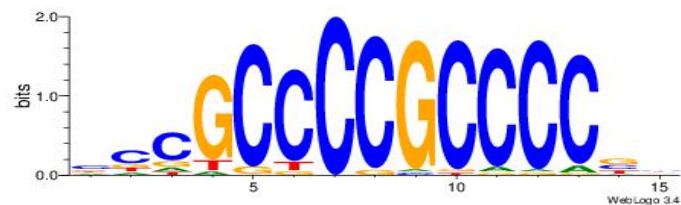
Alignment:

BBGGGGCGGGGCGGB

-----YGCGTG-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



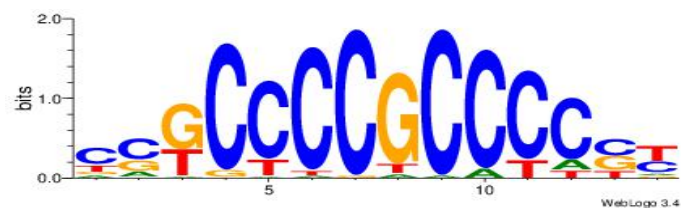
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0806145

Alignment:

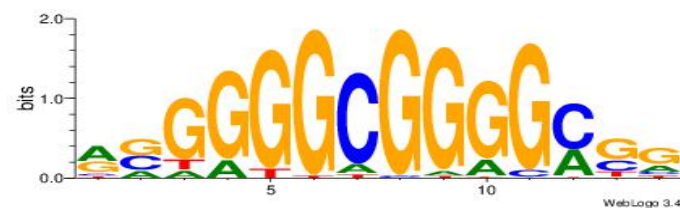
MSGGGGCGGGYSG

----YGCGTG----

Original motif Consensus sequence: CSKCCCCGCCCSY

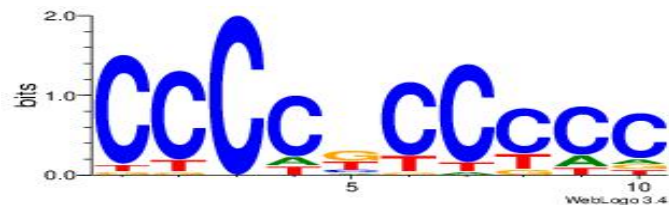


Reverse complement motif Consensus sequence: MSGGGGCGGGY

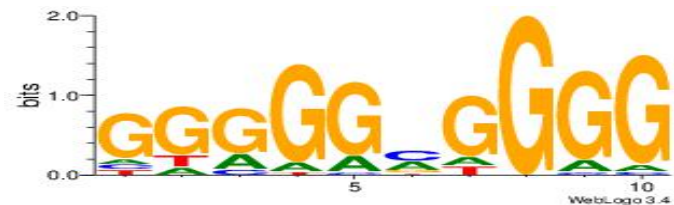


Dataset #: 3 **Motif ID: 24** **Motif name: SP1**

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



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

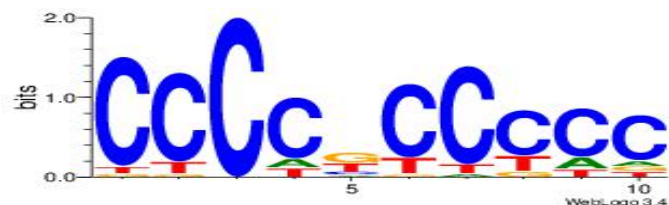
Dataset #:	5
Motif ID:	48
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0

Alignment:

CCCCKCCCCC

CCCCKCCCCC

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

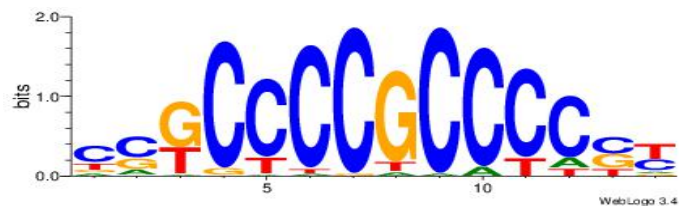


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.043504

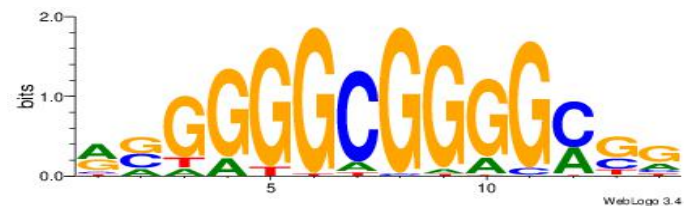
Alignment:

CSKCCCCGCCCCSY
 ---CCCKCCCC-

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

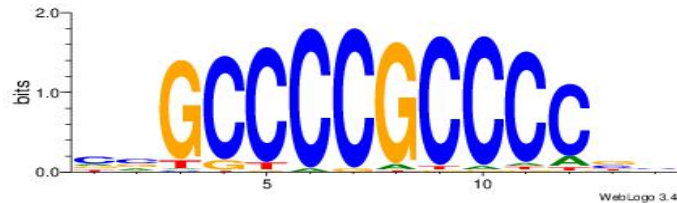


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10

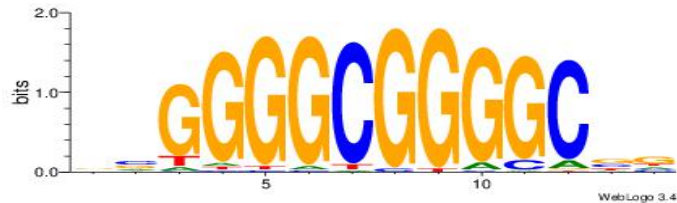
Similarity score: 0.0486461

Alignment:
BBGGGGCGGGGCVD
-GGGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

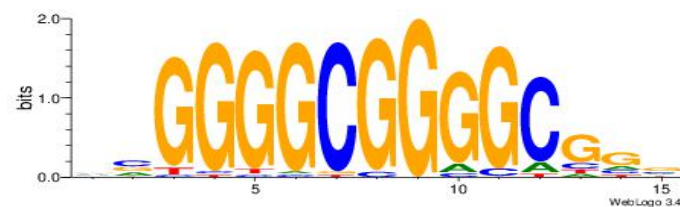
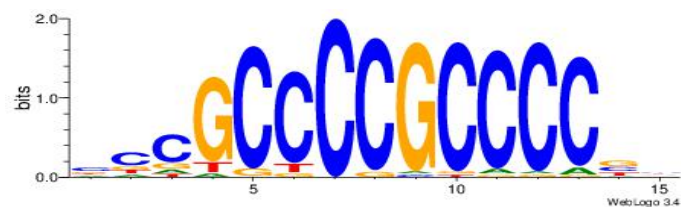


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCB
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0517173

Alignment:
BCCGCCCCGCCCB
----CCCCKCCCC-

Original motif Consensus sequence: BCCGCCCCGCCCB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGB

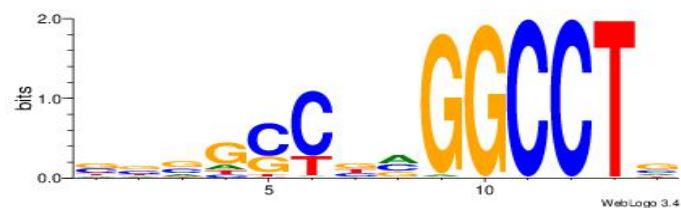


Dataset #: 5
 Motif ID: 46
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0930706

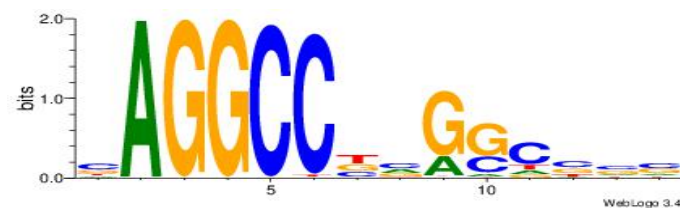
Alignment:

VAGGCCBBGGCVBB
 ----CCCCCKCCCC

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



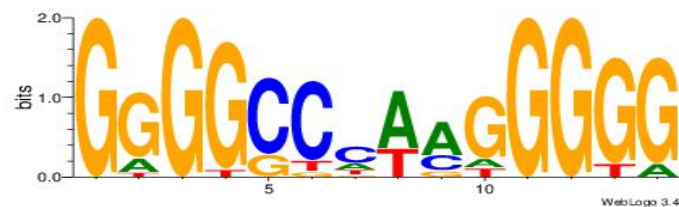
Dataset #: 5
 Motif ID: 54

Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0990873

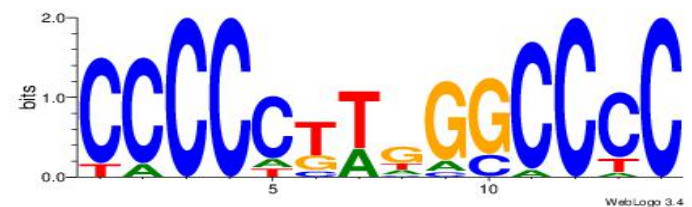
Alignment:

```
CCCCCTTGGGCCCC
-CCCCKCCCCC---
```

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC



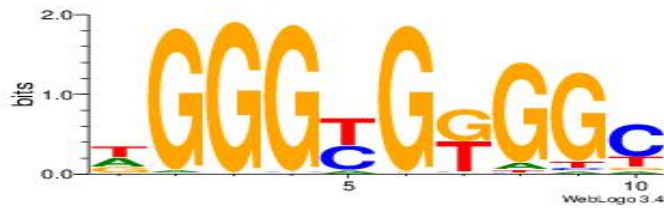
Dataset #:	5
Motif ID:	51
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.102706

Alignment:

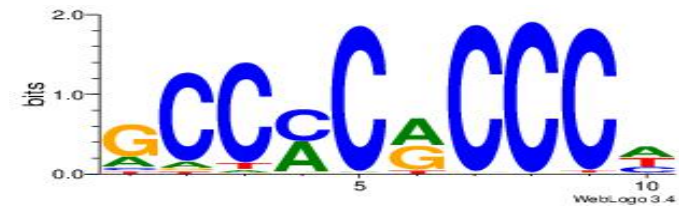
GCCYCMCCCD

CCCCKCCCCC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



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:	0.103809

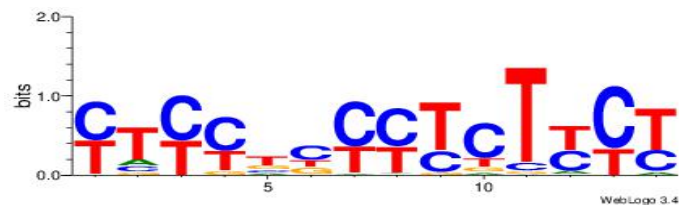
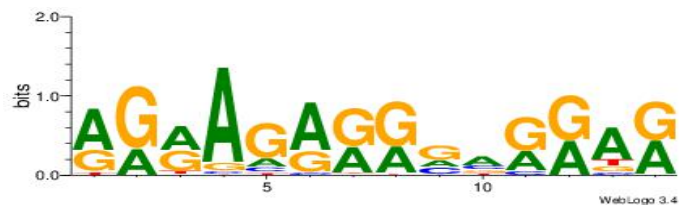
Alignment:

MTMMTCMMTCTKCK

----CCCCKCCCCC

Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



Dataset #: 5
 Motif ID: 47
 Motif name: Egr1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.106429

Alignment:

HGCGTGGGCGK

GGGGYGGGG-

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



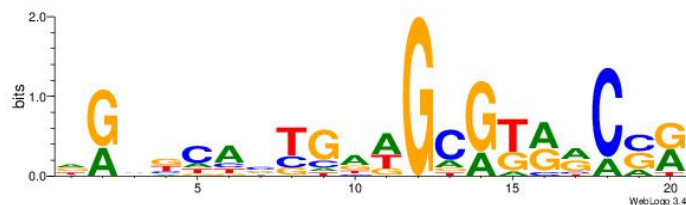
Dataset #: 5
 Motif ID: 55

Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	10
Similarity score:	0.11125

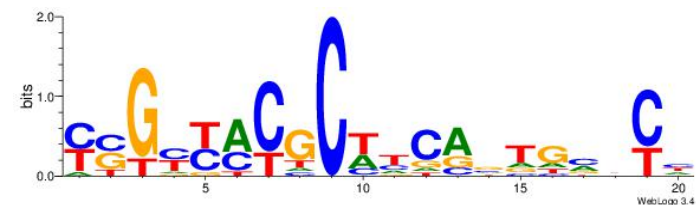
Alignment:

```
DGVBCABTGDWGCGRRCR
-----GGGGYGGG----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

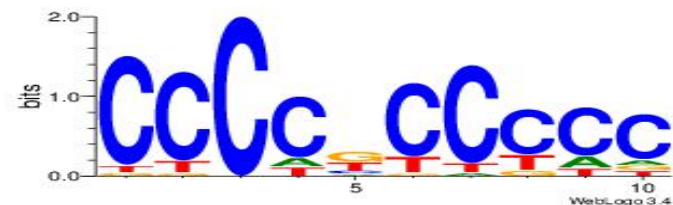


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

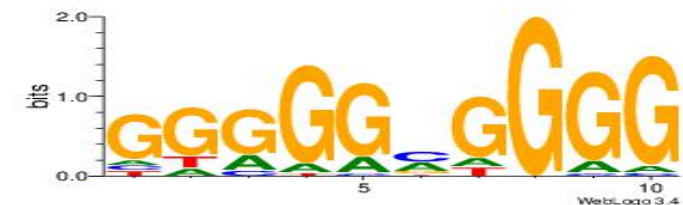


Dataset #: 5 Motif ID: 48 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



Best Matches for Top Significant Motif ID 48 (Highest to Lowest)

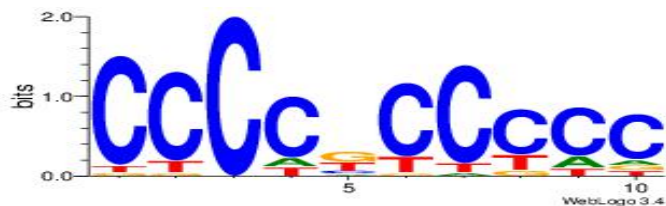
Dataset #: 3
 Motif ID: 24
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0

Alignment:

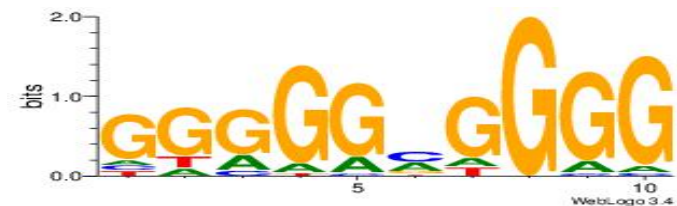
CCCCKCCCCC

CCCCKCCCCC

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

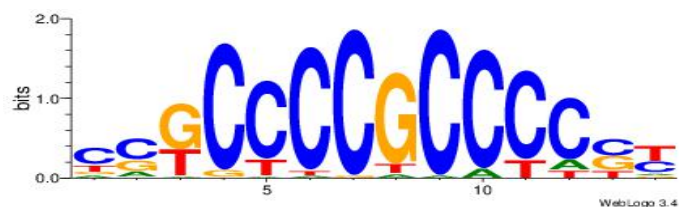


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif

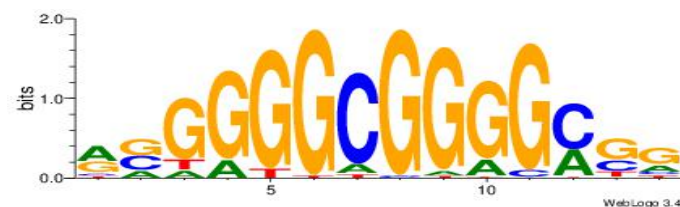
Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.043504

Alignment:
 CSKCCCCGCCCCSY
 ---CCCCKCCCC--

Original motif Consensus sequence: CSKCCCCGCCCCSY



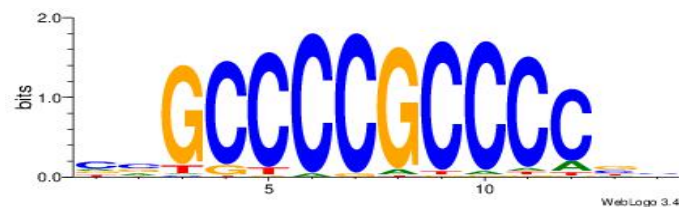
Reverse complement motif Consensus sequence: MSGGGGCGGGGY



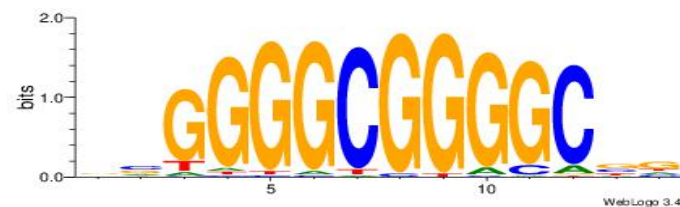
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0486461

Alignment:
 BBGGGGCGGGGCVD
 -GGGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

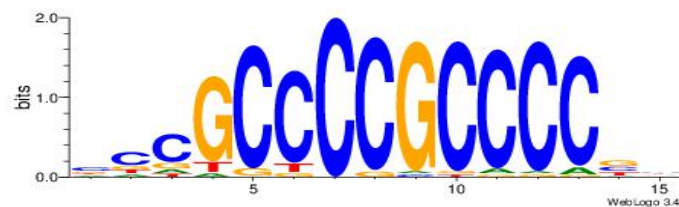


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0517173

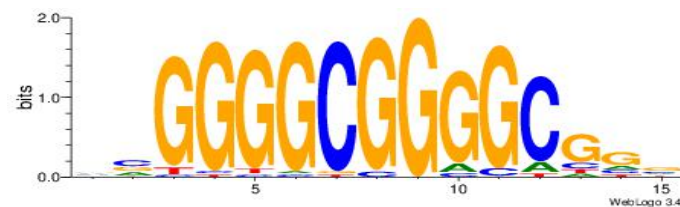
Alignment:

BCCGCCCCGCCCCBB
 ----CCCCKCCCC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

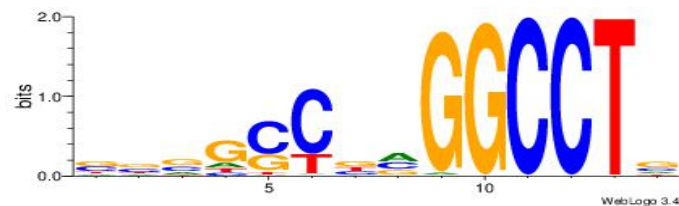


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0930706

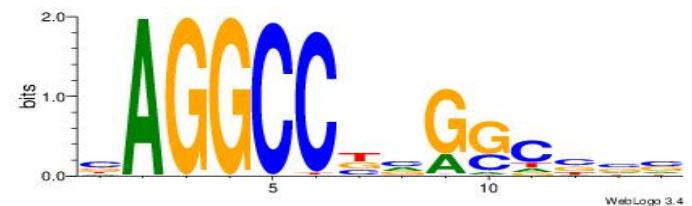
Alignment:

BBVGCCBVGGCCTV
 ----GGGGGYGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV

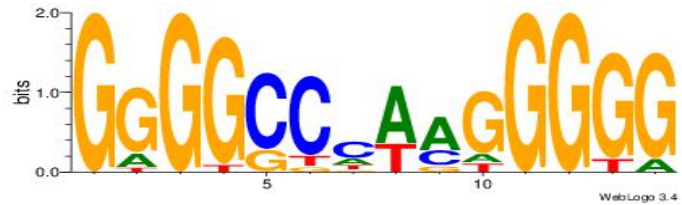


Dataset #: 3
 Motif ID: 30
 Motif name: PLAG1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10

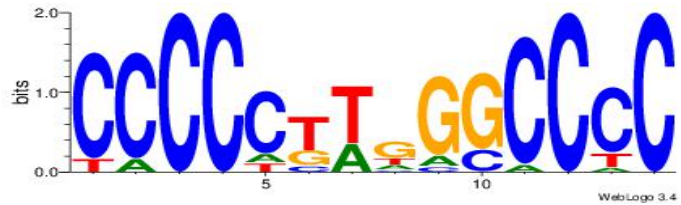
Similarity score: 0.0990873

Alignment:
GGGGCCCAAGGGG
-GGGGYGGGG---

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCC

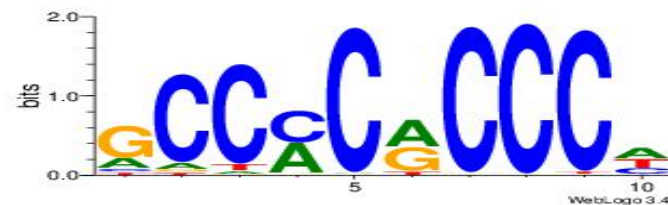


Dataset #: 3
Motif ID: 27
Motif name: Klf4
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.102706

Alignment:
DGGGYGKGGC
GGGGYGGGG

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

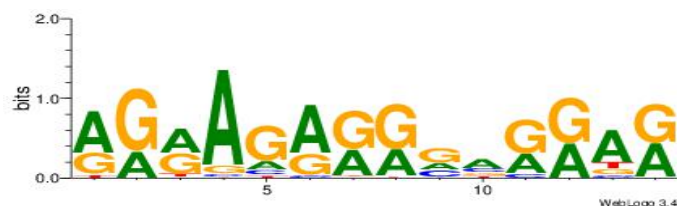


Dataset #: 2
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.103809

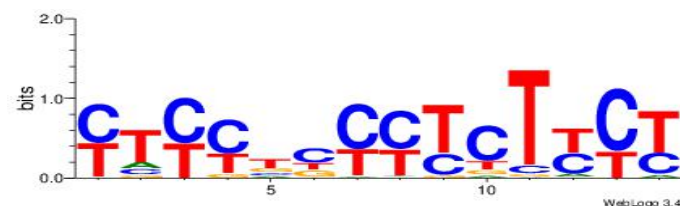
Alignment:

MTMMTCMMTCTKCK
 ----CCCCCKCCCC

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



Dataset #: 3
 Motif ID: 23

Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.106429

Alignment:

YCGCCCACGCH
 CCCCKCCCCC-

Original motif Consensus sequence: HCGTG GGGCGK



Reverse complement motif Consensus sequence: YCGCCCACGCH



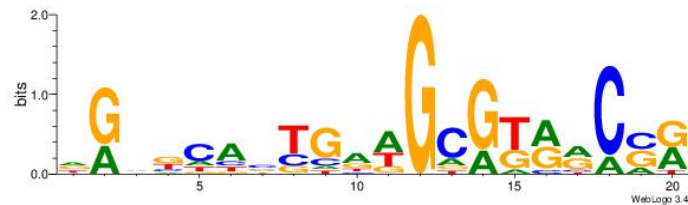
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	10
Similarity score:	0.11125

Alignment:

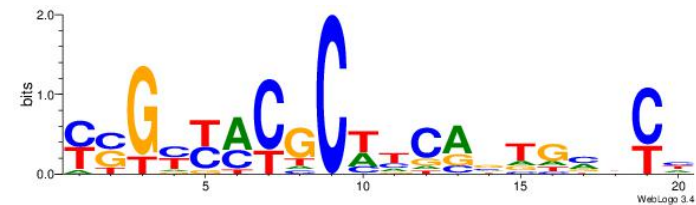
MSGKKRCGCWDCABTGBBCD

-----CCCCKCCCCC----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 5 Motif ID: 53 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Best Matches for Top Significant Motif ID 53 (Highest to Lowest)

Dataset #:	3
Motif ID:	29
Motif name:	HIF1AARNT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 1
Number of overlap: 8
Similarity score: 0

Alignment:
VBACGTGV
VBACGTGV

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV

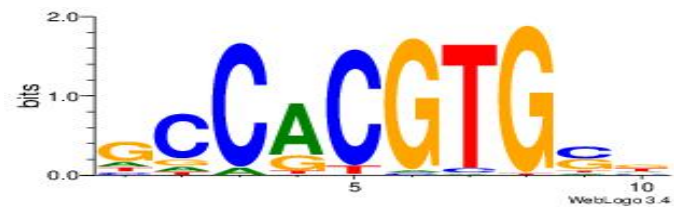


Dataset #: 3
Motif ID: 33
Motif name: Mycn
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0575825

Alignment:
GCCACGTGSD
-VBACGTGV-

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



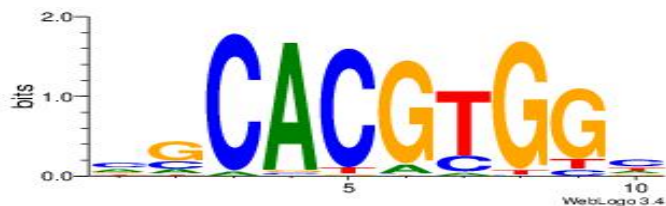
Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0597215

Alignment:

DCCACGTGCV

-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



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: 0.0748197

Alignment:

GBTGCAGGTGB
 ---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



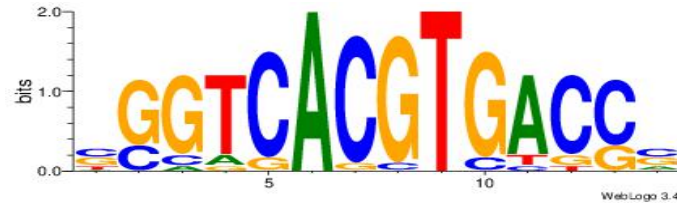
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0767561

Alignment:

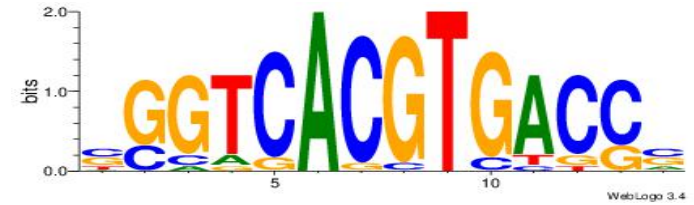
SGGTCACGTGACCS

---VBACGTGV---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #:	3
Motif ID:	26
Motif name:	MIZF
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:	0.0829928

Alignment:

GCGGACGTTV

--VCACGTBV

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

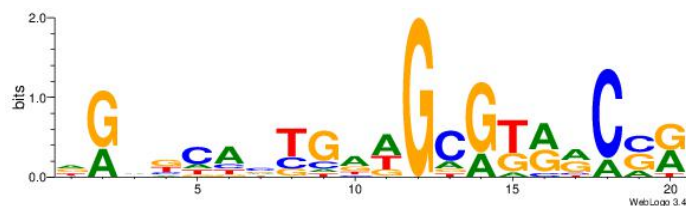


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 8
 Similarity score: 0.100962

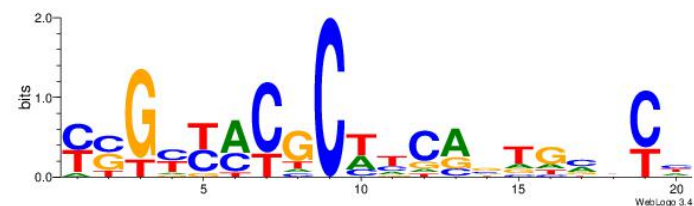
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----VCACGTBV-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 4

Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.109275

Alignment:
 HCAGAATGTHD
 VBACGTGV---

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.110088

Alignment:

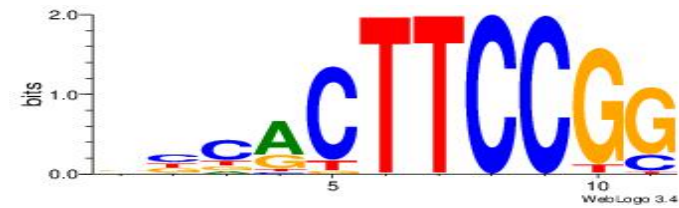
VVCACTTCCGG

--VBACGTGV--

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



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:	4
Number of overlap:	8
Similarity score:	0.116389

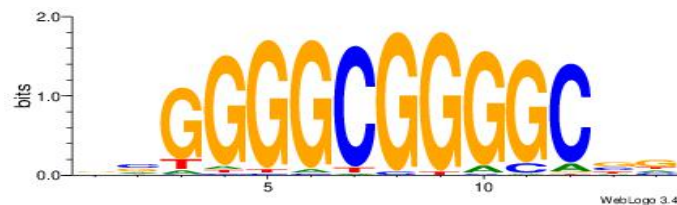
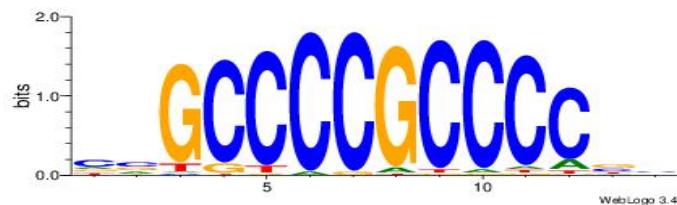
Alignment:

HVGCCCCGCCCCBB

---VCACGTBV---

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



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 #:	5
Motif ID:	53
Motif name:	HIF1AARNT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:
VBACGTGV
VBACGTGV

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Dataset #: 5
 Motif ID: 57
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0575825

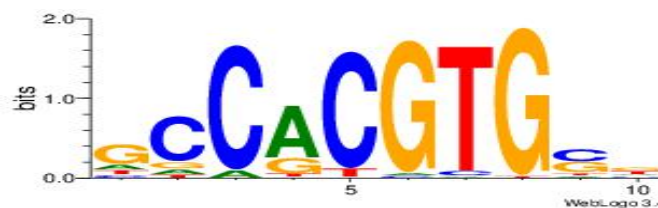
Alignment:

GCCACGTGSD
 -VBACGTGV-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 5
 Motif ID: 58
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0597215

Alignment:

DCCACGTGCV

-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

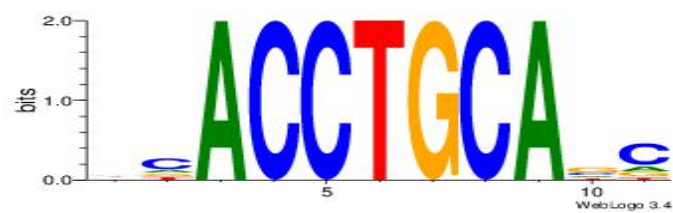


Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAgc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0748197

Alignment:
GBTGCAGGTGB
---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

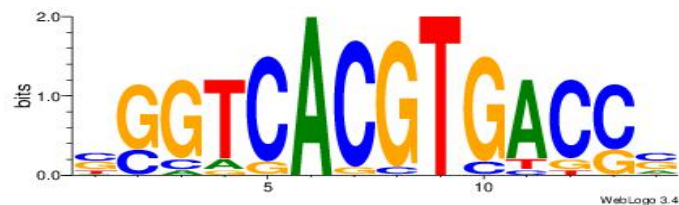
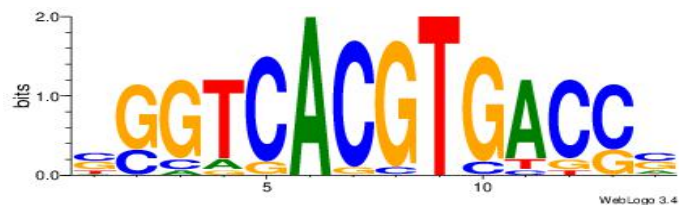


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACs
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0767561

Alignment:
SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACCS



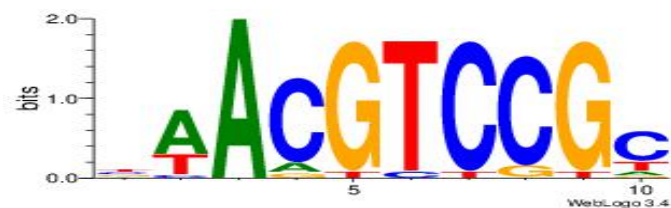
Dataset #: 5
 Motif ID: 50
 Motif name: MIZF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0829928

Alignment:

GCGGACGTTV

--VCACGTBV

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



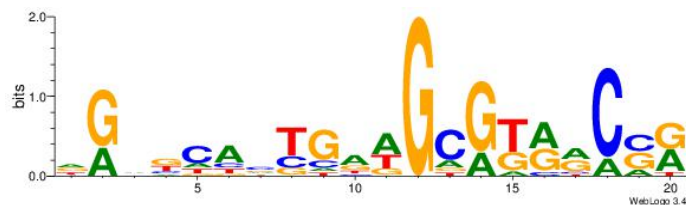
Dataset #: 5
 Motif ID: 55

Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	8
Similarity score:	0.100962

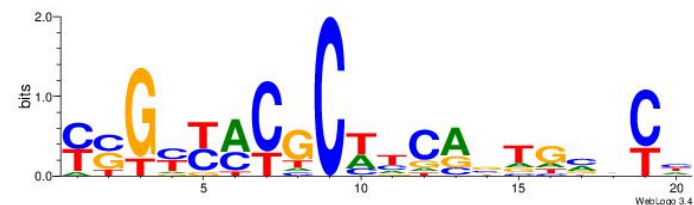
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----VCACGTBV-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #:	4
Motif ID:	44
Motif name:	dhACATTCTkh
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:	0.109275

Alignment:

DHACATTCTGH

VCACGTBV---

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #:	5
Motif ID:	59
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.110088

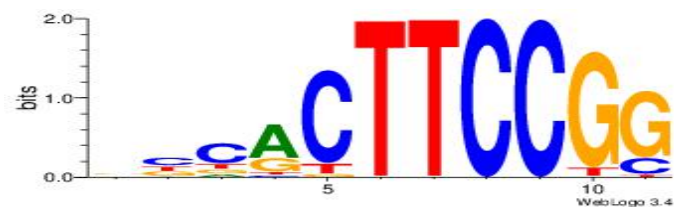
Alignment:

CCGGAAGTGVV

--VCACGTBV-

Original motif Consensus sequence: CCGGAAGTGVV

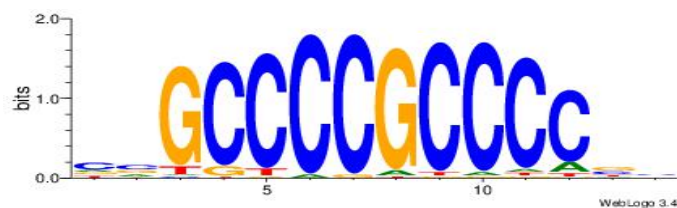
Reverse complement motif Consensus sequence: VVCACTTCCGG



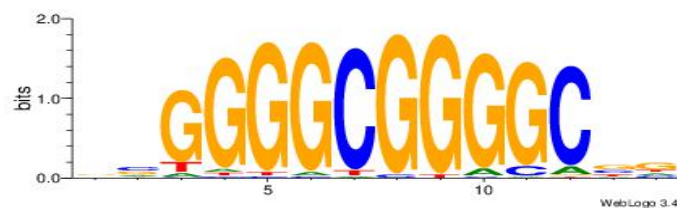
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.116389

Alignment:
 BBGGGGCGGGGCVD
 ---VBACGTGV---

Original motif Consensus sequence: HVGCCCCGCCCCBB

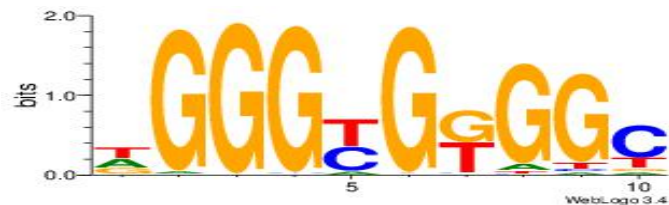


Reverse complement motif Consensus sequence: BBGGGGCGGGGC

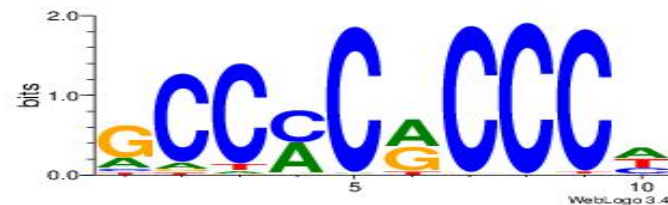


Dataset #: 5 Motif ID: 51 Motif name: Klf4

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Best Matches for Top Significant Motif ID 51 (Highest to Lowest)

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

Alignment:

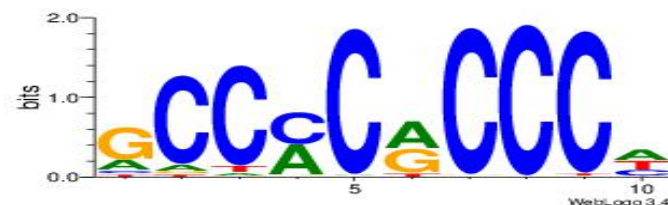
DGGGYGKGGC

DGGGYGKGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

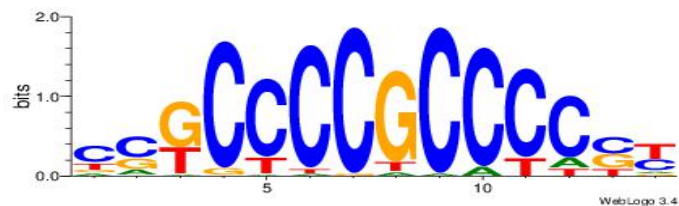


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0516385

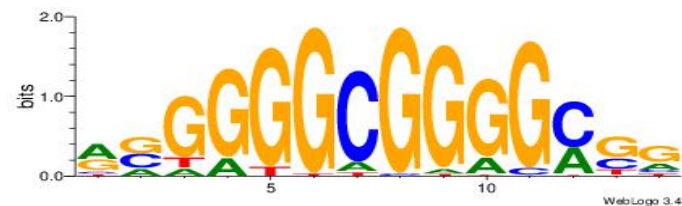
Alignment:

CSKCCCCGCCCSY
 --GCCYCMCCCD--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

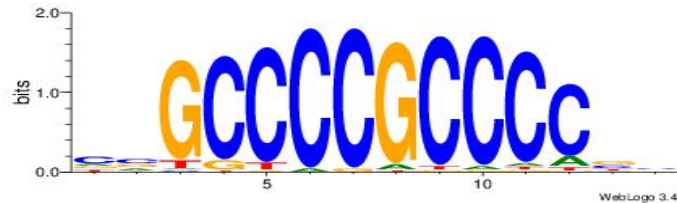


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCSY
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10

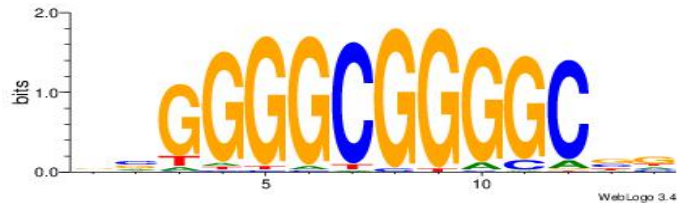
Similarity score: 0.0524114

Alignment:
HVGCCCGCCCCBB
--GCCYCMCCCD--

Original motif Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

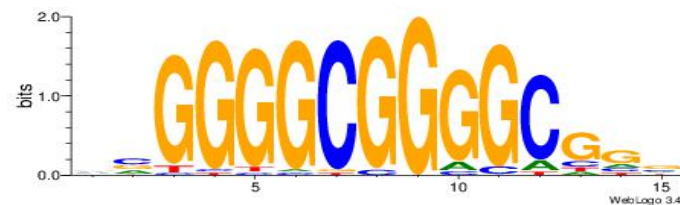
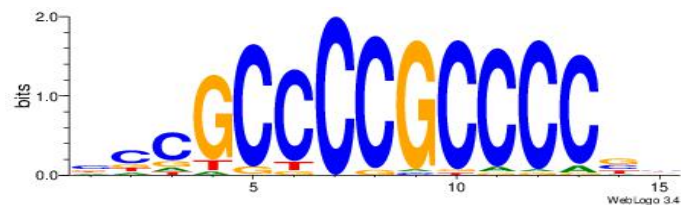


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0558821

Alignment:
BCCGCCCCGCCCCBB
--GCCYCMCCCD---

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

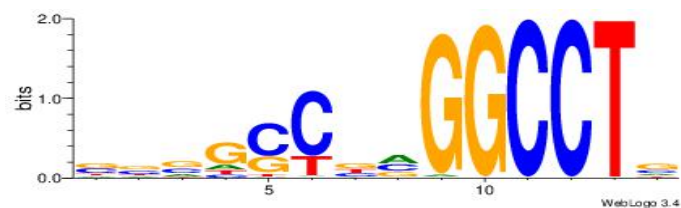


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0987519

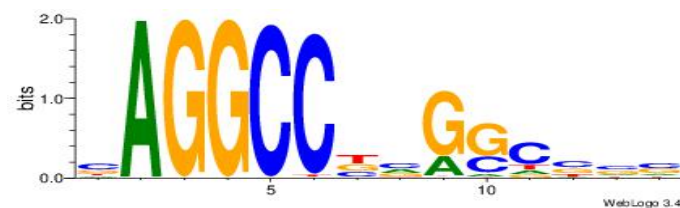
Alignment:

BBVGCCBVGGCCTV
 -GCCYCMCCCD---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 3
 Motif ID: 24

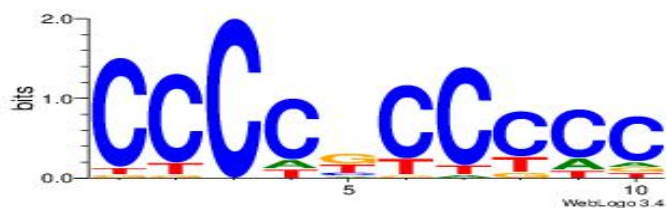
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.102706

Alignment:

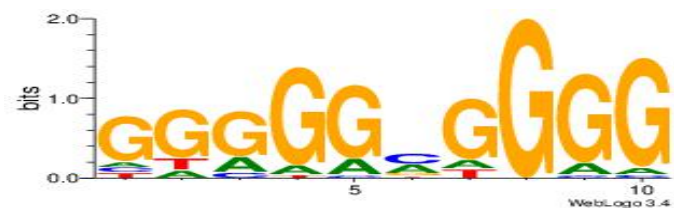
GGGGGYGGGG

DGGGYGKGGC

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

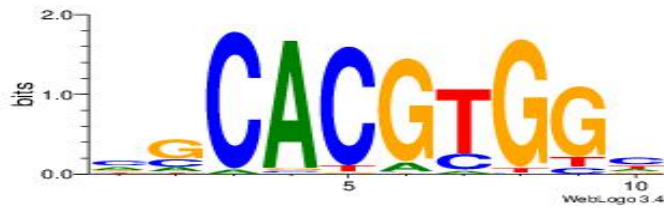


Dataset #:	3
Motif ID:	34
Motif name:	Myc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.105078

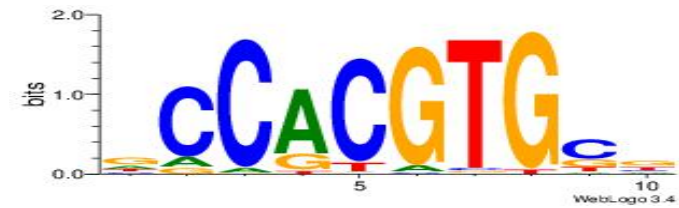
Alignment:

VGCACGTGGH
DGGGYGKGGC

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



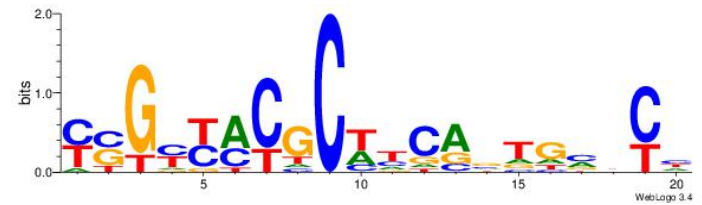
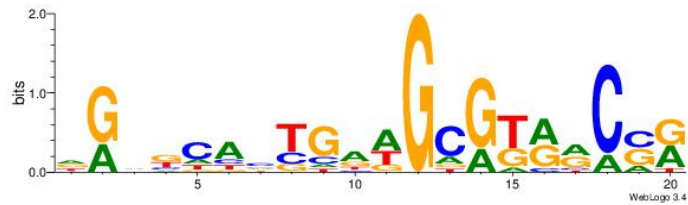
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.105953

Alignment:

DGVBCABTGDWCGKRRCSR
-----DGGGYGKGGC--

Original motif Consensus sequence: DGVBCABTGDWCGKRRCSR

Reverse complement motif Consensus sequence:
MSGKKRCGCWD CABTGBBCD



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: 1
 Number of overlap: 10
 Similarity score: 0.10603

Alignment:

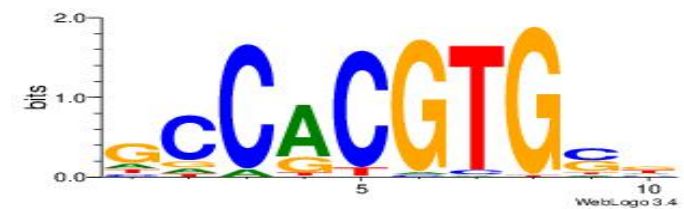
HSCACGTGGC

DGGYGKGGC

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



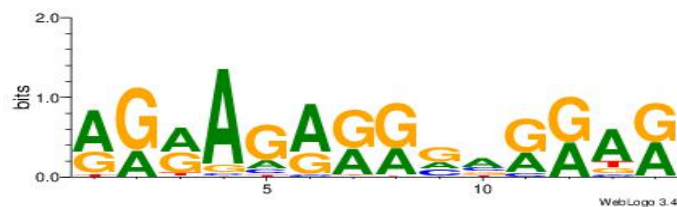
Dataset #: 2
 Motif ID: 2

Motif name:	Motif 2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.110488

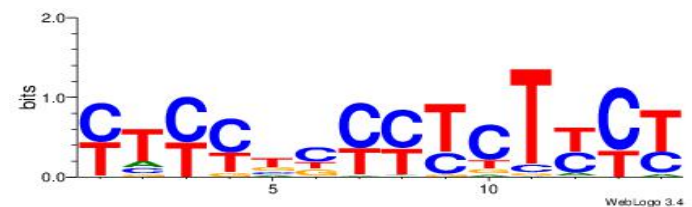
Alignment:

```
MTMMTCMMTCTKCK
-GCCYCMCCCD---
```

Original motif Consensus sequence: RGRAGARRGARRAR

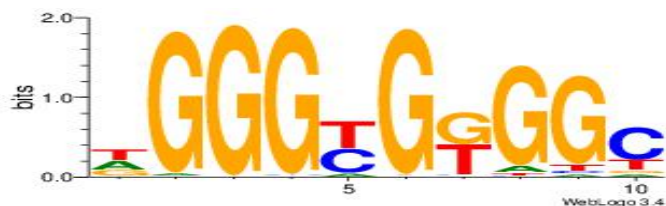


Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK

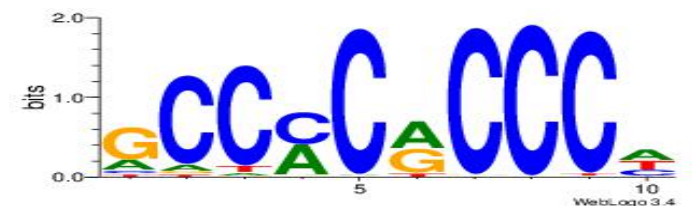


Dataset #: 3 Motif ID: 27 Motif name: Klf4

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



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

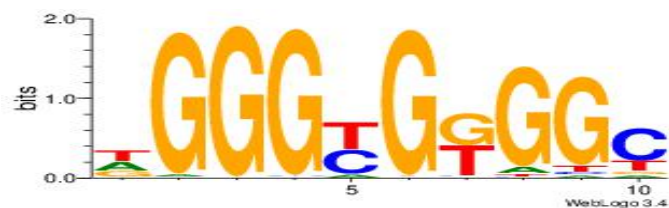
Dataset #: 5
 Motif ID: 51
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0

Alignment:

DGGGYGKGGC

DGGGYGKGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

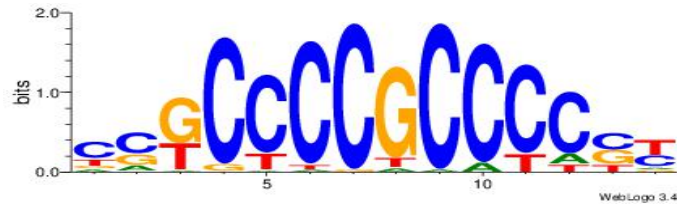


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10

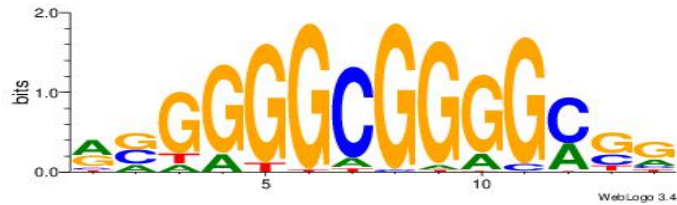
Similarity score: 0.0516385

Alignment:
CSKCCCCGCCCCSY
--GCCYCMCCCD--

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

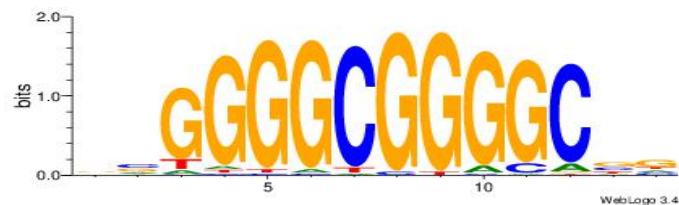
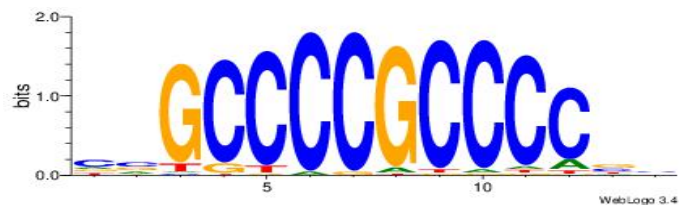


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0524114

Alignment:
BBGGGGCGGGGCVD
--DGGGYGKGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC

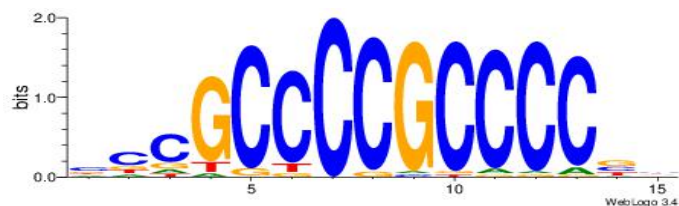


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0558821

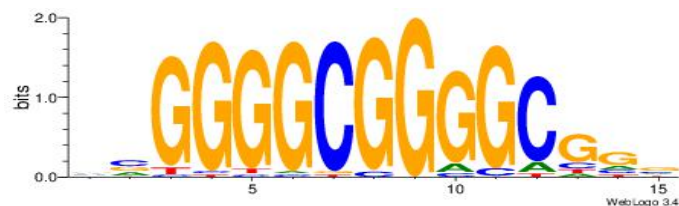
Alignment:

BBGGGGCGGGGCGGB
 --DGGGYGKGGC---

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



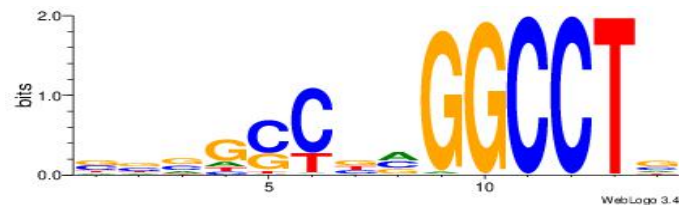
Dataset #: 5

Motif ID: 46
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0987519

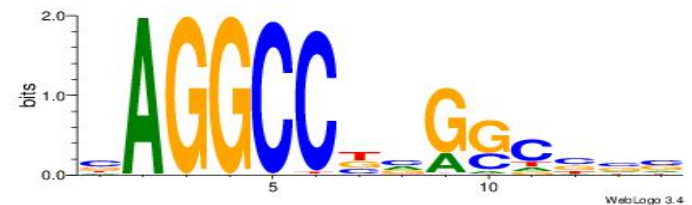
Alignment:

VAGGCCBBGGCVBB
 -DGGGYGKGGC---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



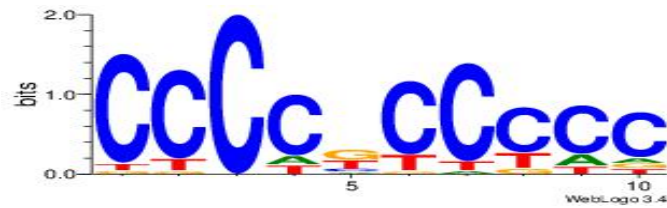
Dataset #: 5
 Motif ID: 48
 Motif name: SP1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.102706

Alignment:

CCCCKCCCCC

GCCYCMCCCD

Original motif Consensus sequence: CCCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



Dataset #:	5
Motif ID:	58
Motif name:	Myc
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:	0.105078

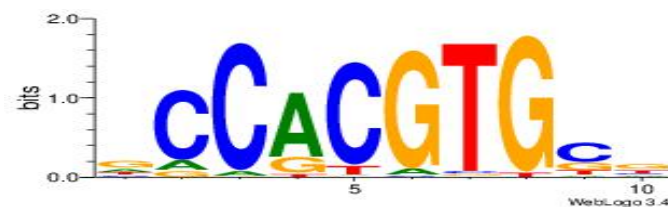
Alignment:

VGCACGTGGH

DGGGYGKGGC

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

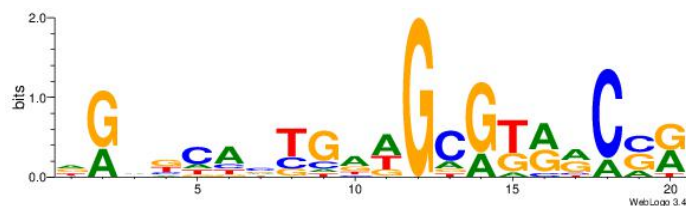


Dataset #: 5
 Motif ID: 55
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.105953

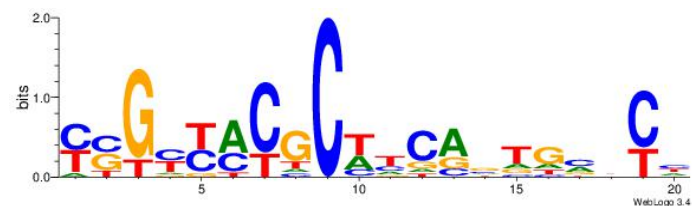
Alignment:

DGVBCABTGDWGCGRRCR
 -----DGGYGKGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 5

Motif ID: 57
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.10603

Alignment:

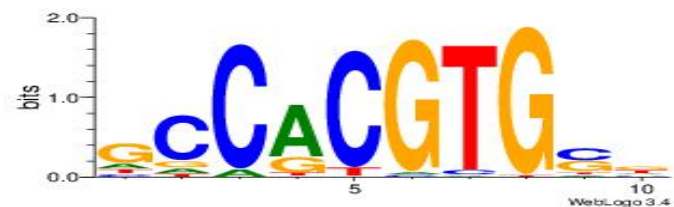
HSCACGTGGC

DGGYGKGGC

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



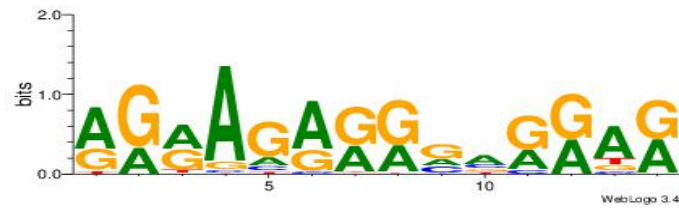
Dataset #: 2
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.110488

Alignment:

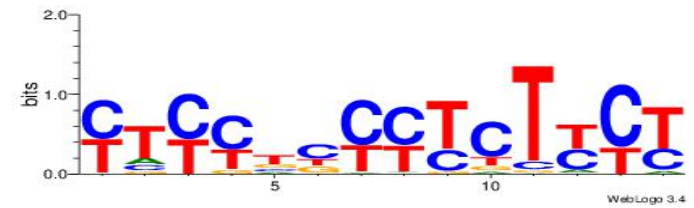
MTMMTCMMTCTKCK

-GCCYCMCCCD---

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK



Results created by MOTIFSIM on 06-18-2018 14:32:36

Runtime: 695.758 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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