



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

Number of files:	1
Number of top significant motifs:	4
Number of best matches:	4
Similarity cutoff >=	0.5
Matching motif database:	Jaspar Core
Motif tree:	Yes
Combined similar motifs:	No
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
U20240419_R_04-19-24_1712_InsertFile1.txt	3	1

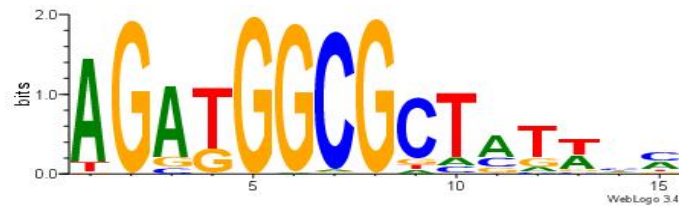
RESULTS

Best Matches in Database for Each Motif (Highest to Lowest)

Dataset #: 1	Motif ID: 1	Motif name: Motif 1
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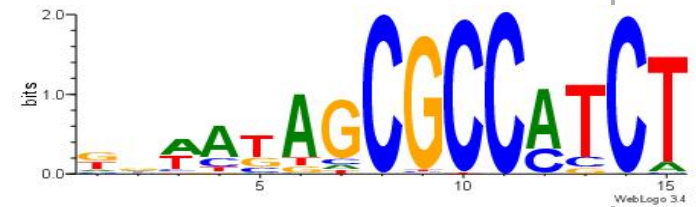
Original motif

Consensus sequence: AGATGGCGCTATWHM



Reverse complement motif

Consensus sequence: RDWATAGCGCCATCT



Best Matches for Motif ID 1 (Highest to Lowest)

Motif ID: [MA0469.2](#)
Motif name: E2F3
Taxon: Vertebrates
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 15
Similarity score: 0.038099

Alignment:

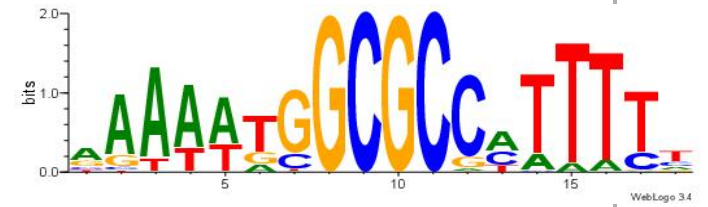
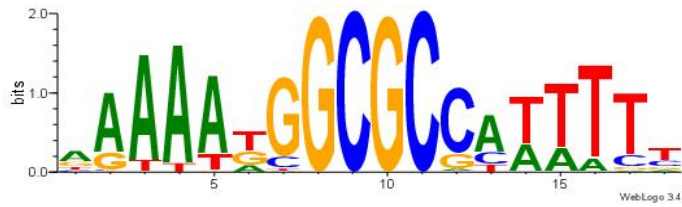
```
AAAAWTGGCGCCRTTTTT  
-RDWATAGCGCCATCT--
```

Original motif

Consensus sequence: AAAAAKGGCGCCA WTTTT

Reverse complement motif

Consensus sequence: AAAAWTGGCGCCRTTTTT

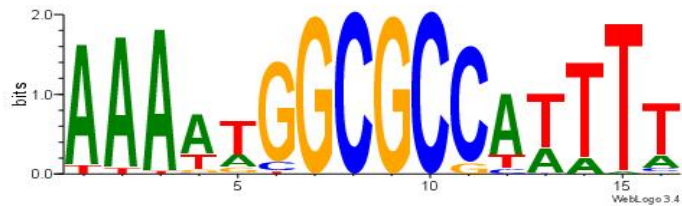


Motif ID: [MA0864.1](#)
 Motif name: E2F2
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0458125

Alignment:
 AAAATGGCGCCATTTT
 RDWATAGCGCCATCT-

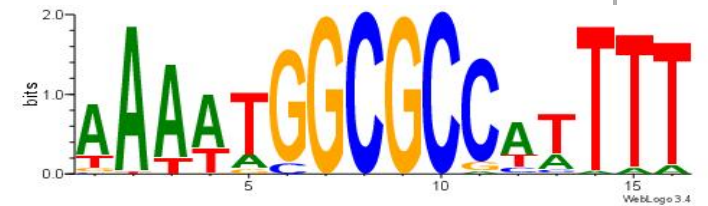
Original motif

Consensus sequence: AAAATGGCGCCATTTT



Reverse complement motif

Consensus sequence: AAAATGGCGCCATTTT



Motif ID: [MA0395.1](#)
 Motif name: STP2

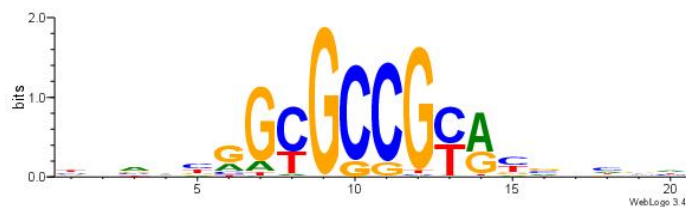
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	15
Similarity score:	0.0557025

Alignment:

```
HVVHBGGCGCCGYRYVHHBH
RDWATAGCGCCATCT-----
```

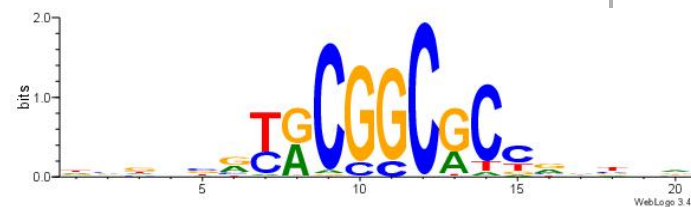
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



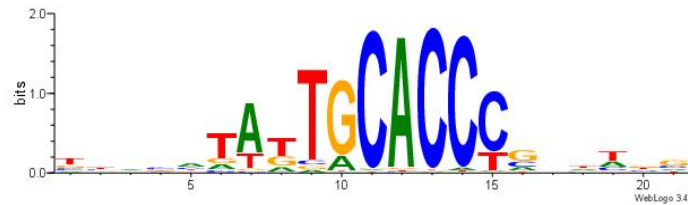
Motif ID:	MA0269.1
Motif name:	AFT1
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	15
Similarity score:	0.0580634

Alignment:

```
VBWDBSGGGTGCARTAHBDVV  
---AGATGGCGCTATWHM---
```

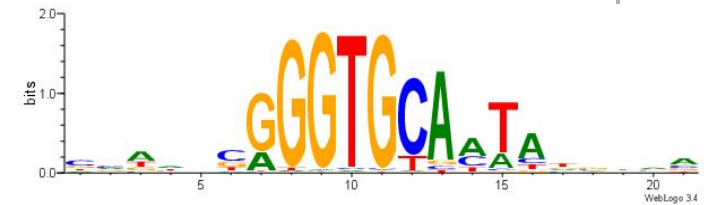
Original motif

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif

Consensus sequence: VBWDBSGGGTGCARTAHBDVV



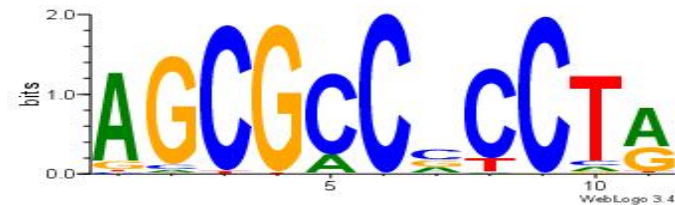
Dataset #: 1

Motif ID: 2

Motif name: Motif 2

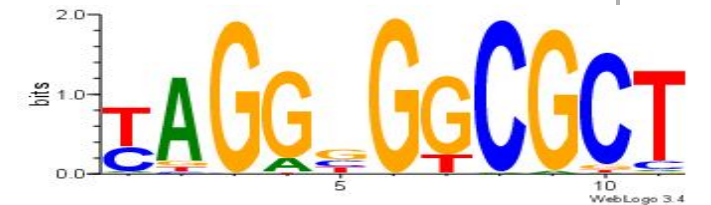
Original motif

Consensus sequence: AGCGCCVCCTR



Reverse complement motif

Consensus sequence: KAGGVGGCGCT



Best Matches for Motif ID 2 (Highest to Lowest)

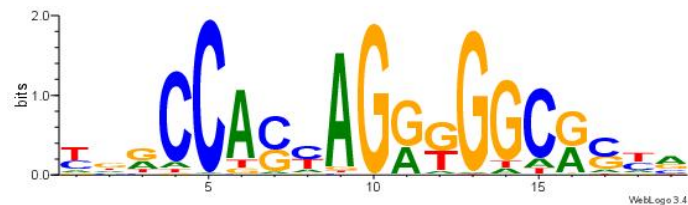
Motif ID:	MA0139.1
Motif name:	CTCF
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0371543

Alignment:
BMSGCCYMCTKSTGGMHM
-AGCGCCVCCTR-----

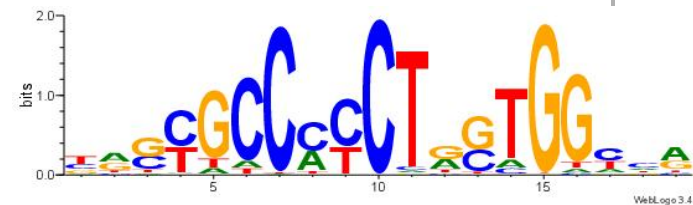
Original motif

Consensus sequence: YDRCCASYAGRKGGCRSYV



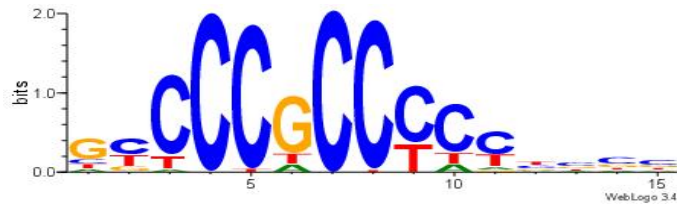
Reverse complement motif

Consensus sequence: BMSGCCYMCTKSTGGMHM



Motif ID: [MA0685.1](#)
Motif name: SP4
Taxon: Vertebrates
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 11
Similarity score: 0.0623319

Alignment:

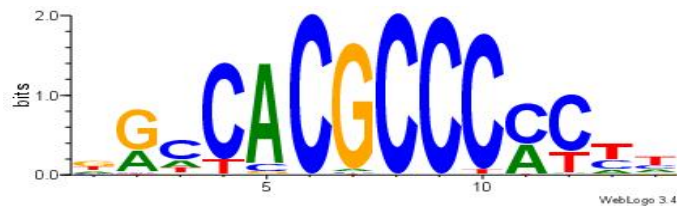


Motif ID: [MA0740.1](#)
 Motif name: KLF14
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0647375

Alignment:
 HMGRGGGCGTGGMH
 KAGGVGGCGCT---

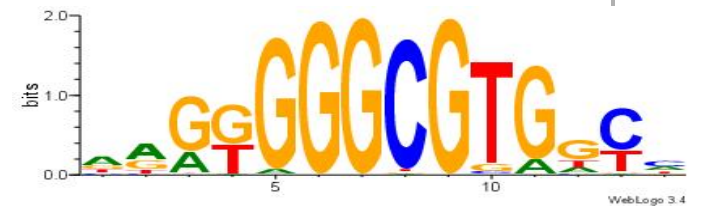
Original motif

Consensus sequence: DRCCACGCCCMCYH



Reverse complement motif

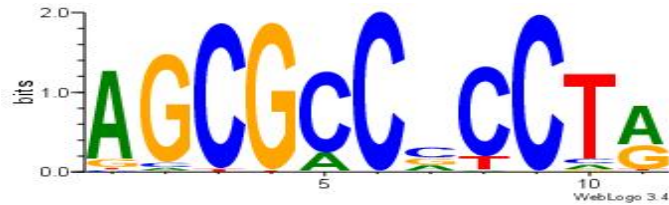
Consensus sequence: HMGRGGGCGTGGMH



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

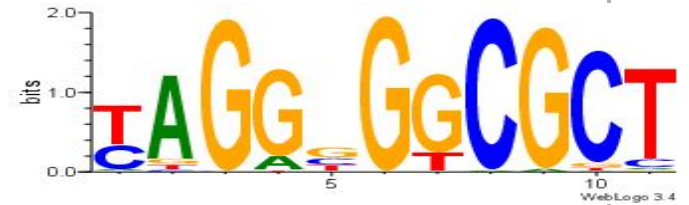
Original motif

Consensus sequence: AGCGCCVCCTR



Reverse complement motif

Consensus sequence: KAGGVGGCGCT



Best Matches for Motif ID 3 (Highest to Lowest)

Motif ID: [MA0139.1](#)
Motif name: CTCF
Taxon: Vertebrates
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0371543

Alignment:

BMSMGCCYMCTKSTGGMHM

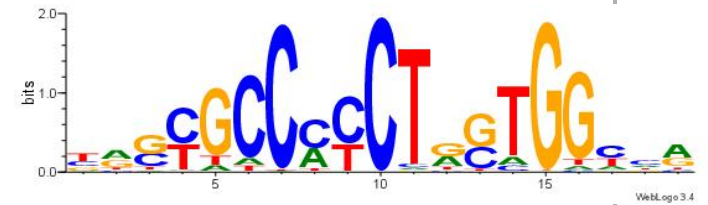
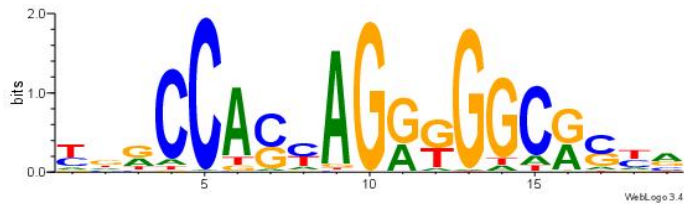
-AGCGCCVCCTR-----

Original motif

Consensus sequence: YDRCCASYAGRKGGCRSYV

Reverse complement motif

Consensus sequence: BMSMGCCYMCTKSTGGMHM

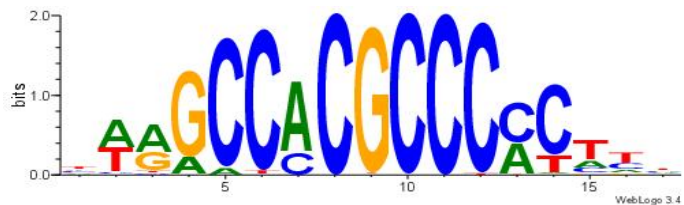


Motif ID: [MA0685.1](#)
 Motif name: SP4
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0623319

Alignment:
 HMAGRGGGCGTGGCKWV
 -KAGGVGGCGCT-----

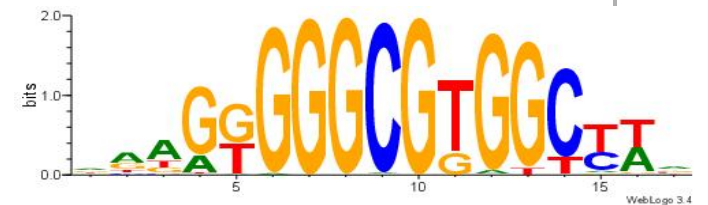
Original motif

Consensus sequence: BWRGCCACGCCCMCTYH



Reverse complement motif

Consensus sequence: HMAGRGGGCGTGGCKWV



Motif ID: [MA0516.1](#)

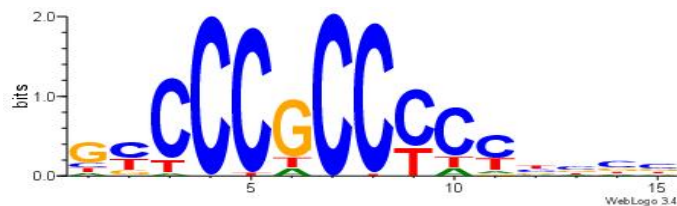
Motif name: SP2
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0637624

Alignment:

BBBVKGGCGGGKC
 --KAGGVGGCGCT--

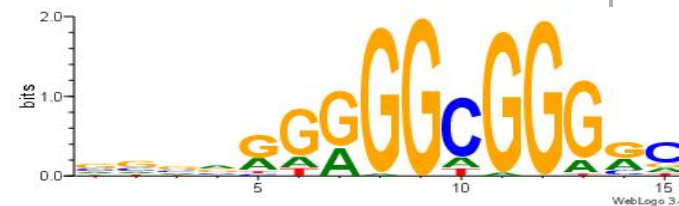
Original motif

Consensus sequence: GYCCCGCCYCYBBBB



Reverse complement motif

Consensus sequence: BBBVKGGCGGGKC



Motif ID: [MA0740.1](#)
 Motif name: KLF14
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score:

0.0647375

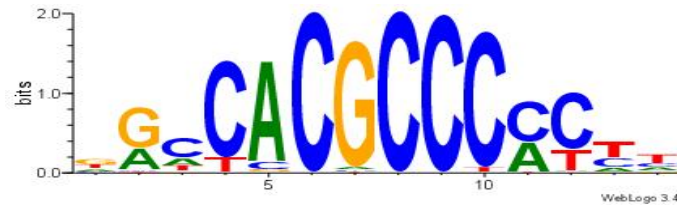
Alignment:

HMGRGGGCGTGGMH

KAGGVGGCGCT---

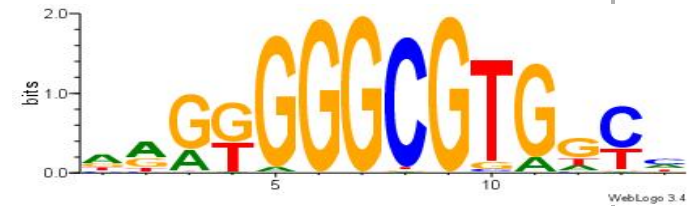
Original motif

Consensus sequence: DRCCACGCCCMCYH



Reverse complement motif

Consensus sequence: HMGRGGGCGTGGMH



Results created by MOTIFSIM on 04-19-2024 14:13:07

Runtime: 532.394 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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