



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

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

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_DM05.txt	11	5

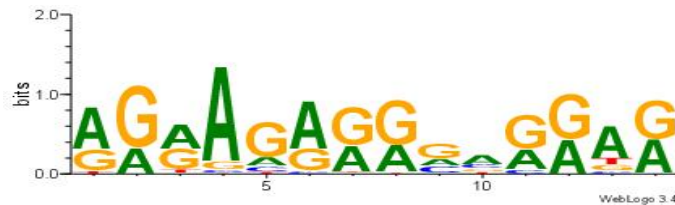
RESULTS

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

Dataset #: 2 Motif ID: 2 Motif name: Motif 2

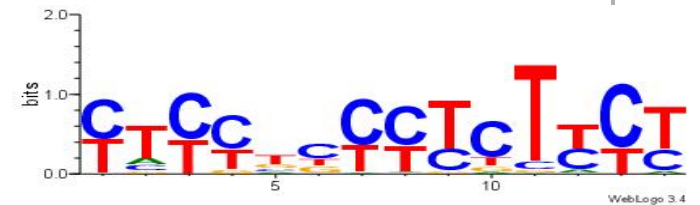
Original motif

Consensus sequence: RGRAGARRGARRAR



Reverse complement motif

Consensus sequence: MTMMTCMMTCTKCK



Best Matches for Motif ID 2 (Highest to Lowest)

Motif ID: [UP00611](#)
Motif name: PAX6
Species: Homo sapiens
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0234155

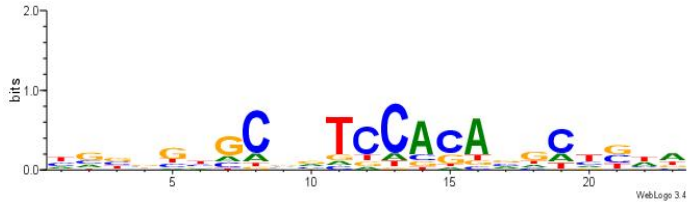
Alignment:

```
DHBHGCVTGTGGAVVGCVCBBVH  
-----MTMMTCMMTCTKCK
```

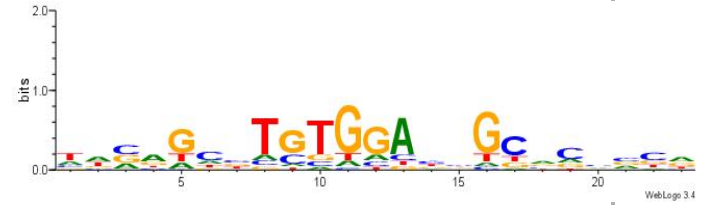
Original motif

Reverse complement motif

Consensus sequence: HVBBGBGCVVTCACAVGCHBHD



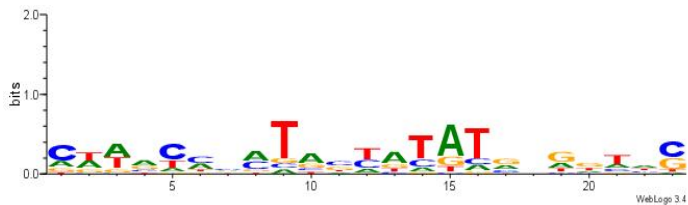
Consensus sequence: DHBHGCVTGTGGAVVGCVCBBVH



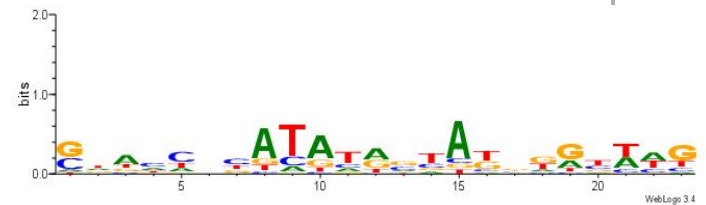
Motif ID: [UP00624](#)
Motif name: VENTX_R143C_R1
Species: Homo sapiens
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0262931

Alignment:
SHAHHHVATATMBTAYVRGBWWG
MTMMTCMMTCTKCK-----

Original motif
Consensus sequence: CWWVCMVMTABYATATVHDDTHS



Reverse complement motif
Consensus sequence: SHAHHHVATATMBTAYVRGBWWG



Motif ID: [UP00629](#)

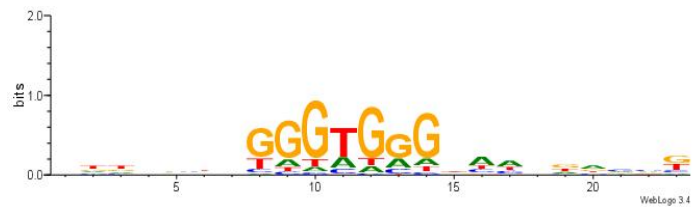
Motif name: ZNF200_H322Y_R1
 Species: Homo sapiens
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0268132

Alignment:

DDDDDHDGGGTGGGHHHDDDVVK
 -----RGRAGARRGARRAR--

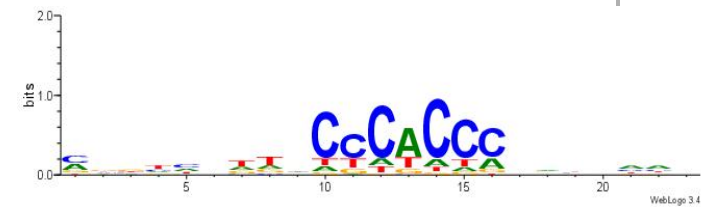
Original motif

Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



Reverse complement motif

Consensus sequence: YVVDHDHHHCCCACCCHHDDDDD



Motif ID: [UP00594](#)
 Motif name: HESX1
 Species: Homo sapiens
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 14

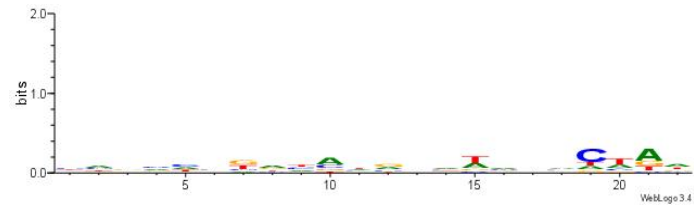
Similarity score: 0.03053

Alignment:

DTHGBBBWHDVHBHDBVDVBHB
----MTMMTCMMTCTKCK----

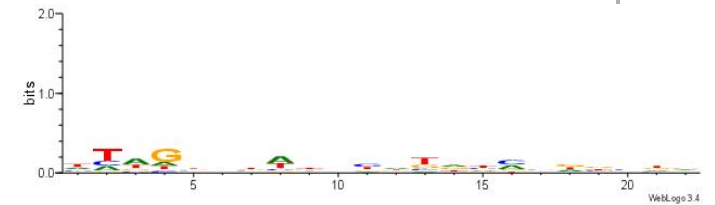
Original motif

Consensus sequence: BHBVHVBDHVHVDHWVBVCHAD



Reverse complement motif

Consensus sequence: DTHGBBBWHDVHBHDBVDVBHB



Motif ID: [UP00629](#)
Motif name: ZNF200_S265Y_R1
Species: Homo sapiens
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 9
Number of overlap: 14
Similarity score: 0.0308188

Alignment:

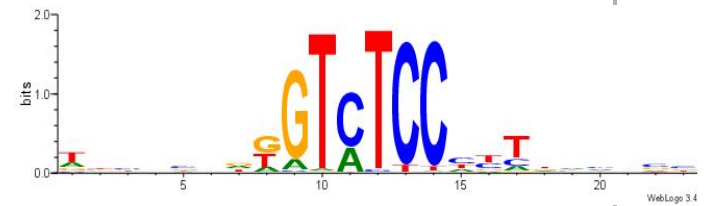
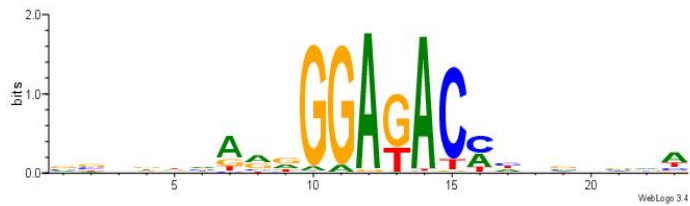
VBHDDHARDGGAGACMHDVDVVA
-----RGRAGARRGARRAR-

Original motif

Consensus sequence: VBHDDHARDGGAGACMHDVDVVA

Reverse complement motif

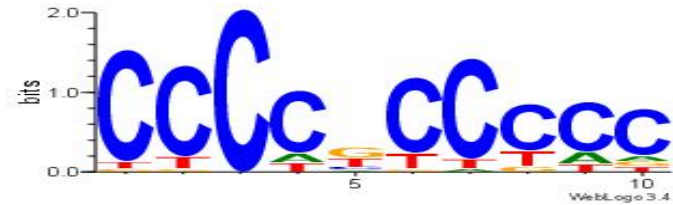
Consensus sequence: TBVDVDDRGTCCTCCHKTHDHHBV



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

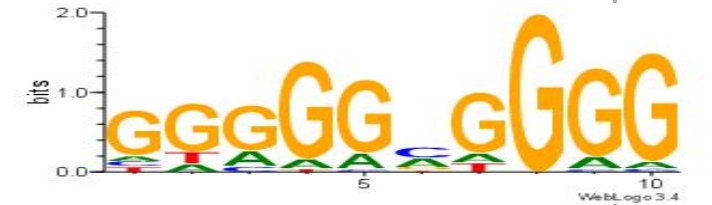
Original motif

Consensus sequence: CCCCKCCCC



Reverse complement motif

Consensus sequence: GGGGYGGGG



Best Matches for Motif ID 24 (Highest to Lowest)

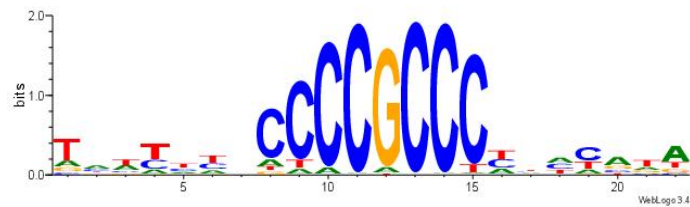
Motif ID:	UP00587
Motif name:	EGR2
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	10
Similarity score:	0

Alignment:

THWYHHDCCCCGCCCHHHYADA
-----CCCCKCCCC-----

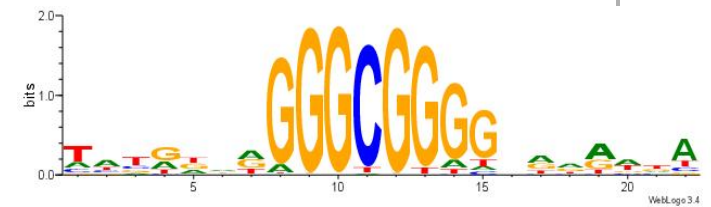
Original motif

Consensus sequence: THWYHHDCCCCGCCCHHHYADA



Reverse complement motif

Consensus sequence: TDTKHHHGGGCGGGGDHHMWHA



Motif ID: [UP00627](#)
Motif name: WT1_REF_R1
Species: Homo sapiens
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0153751

Alignment:

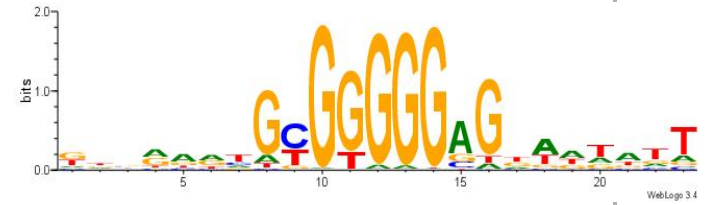
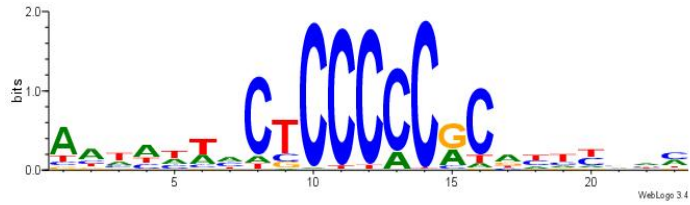
AAHAHWHCTCCCCRCDDHHYVHM
-----CCCCKCCCC-----

Original motif

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM

Reverse complement motif

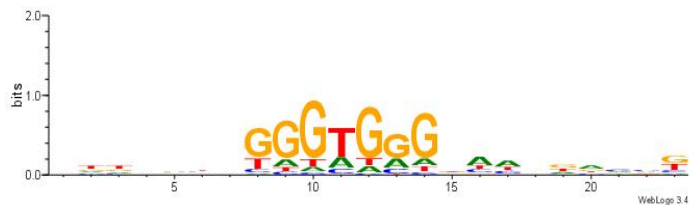
Consensus sequence: RHVMHHDGMGGGGAGHWHHTHT



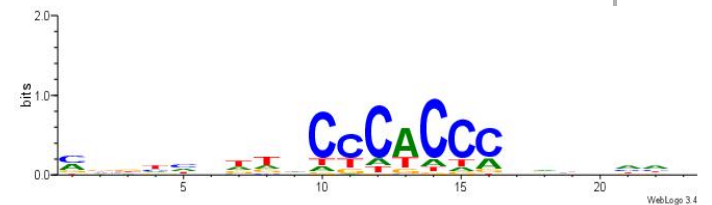
Motif ID: [UP00629](#)
 Motif name: ZNF200_H322Y_R1
 Species: Homo sapiens
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0162022

Alignment:
 YVVDHDHHHCCCACCCHHDDDDD
 -----CCCCKCCCC-----

Original motif
 Consensus sequence: DDDDDHDGGGTGGGHHHDDDDVVK



Reverse complement motif
 Consensus sequence: YVVDHDHHHCCCACCCHHDDDDD



Motif ID: [UP00600](#)

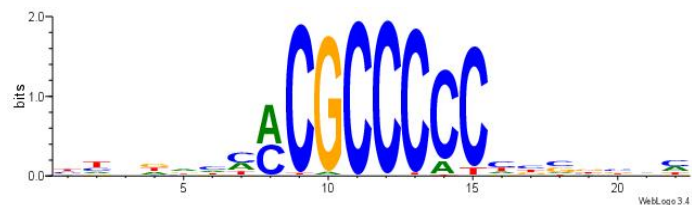
Motif name: KLF11
 Species: Homo sapiens
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 13
 Number of overlap: 10
 Similarity score: 0.0178026

Alignment:

DBBBSBDGGGGGCGYRDDHHHV
 GGGGGYGGGG-----

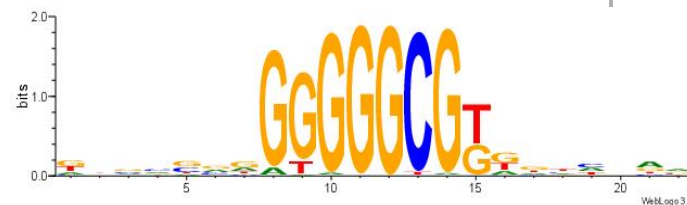
Original motif

Consensus sequence: BHHDDHMMCGCCCCCHBSBBVH



Reverse complement motif

Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV



Motif ID: [UP00627](#)
 Motif name: WT1_R366C_R1
 Species: Homo sapiens
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 10

Similarity score:

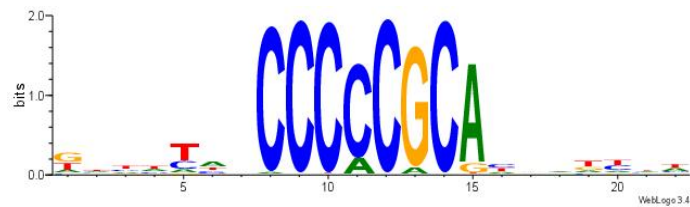
0.0274038

Alignment:

HHHDHHD TGCGGGGGHHAHHY
----GGGGYGGG-----

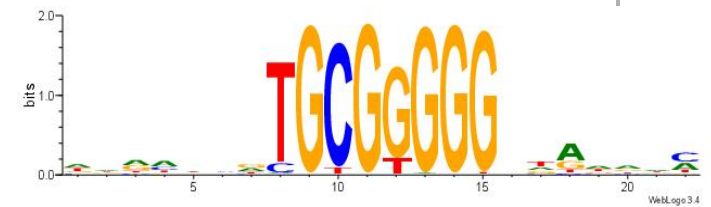
Original motif

Consensus sequence: KHHHTHHCCCCCGCAHDHDH



Reverse complement motif

Consensus sequence: HHHDHHD TGCGGGGGHHAHHY



Dataset #: 4

Motif ID: 40

Motif name: kcACCTGCAGc

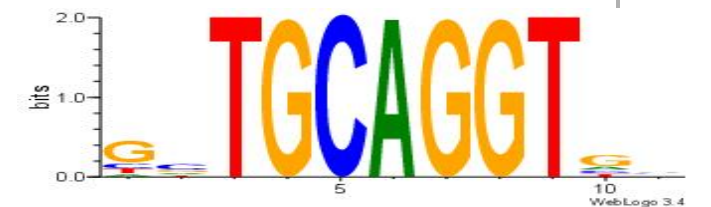
Original motif

Consensus sequence: BCACCTGCABC



Reverse complement motif

Consensus sequence: GBTGCAGGTGB



Best Matches for Motif ID 40 (Highest to Lowest)

Motif ID:

[UP00621](#)

Motif name:

SNAI2_T234I_R1

Species:

Homo sapiens

Matching format of first motif:

Reverse Complement

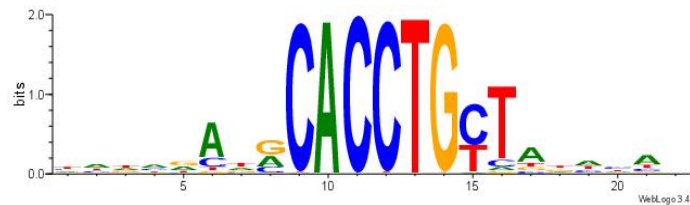
Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0

Alignment:

DTDHDTAKCAGGTGMDTHHDHH
 ----GBTGCAGGTGB-----

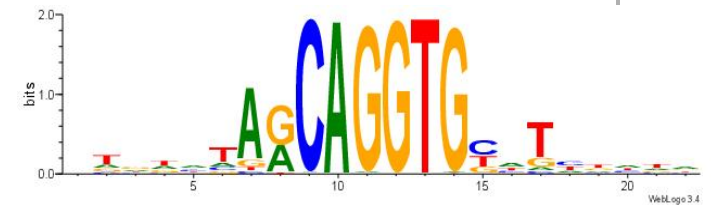
Original motif

Consensus sequence: HHDHDADRCACCTGYTADHHAD



Reverse complement motif

Consensus sequence: DTDHDTAKCAGGTGMDTHHDHH



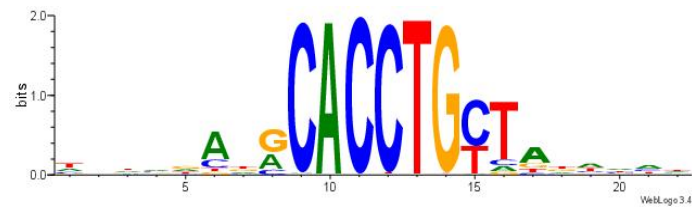
Motif ID: [UP00621](#)
 Motif name: SNAI2_D119E_R1
 Species: Homo sapiens
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.000881825

Alignment:

HHHHDTAKCAGGTGMDTHBDDH
----GBTGCAGGTGB-----

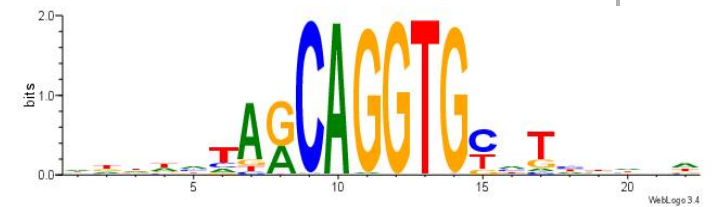
Original motif

Consensus sequence: HDDVDADRCACCTGYTADHHHH



Reverse complement motif

Consensus sequence: HHHHDTAKCAGGTGMDTHBDDH



Motif ID: [UP00621](#)
Motif name: SNAI2_REF_R1
Species: Homo sapiens
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 11
Similarity score: 0.0013625

Alignment:

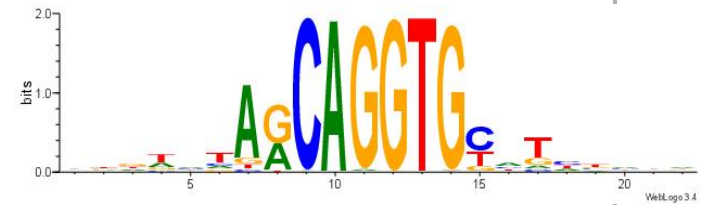
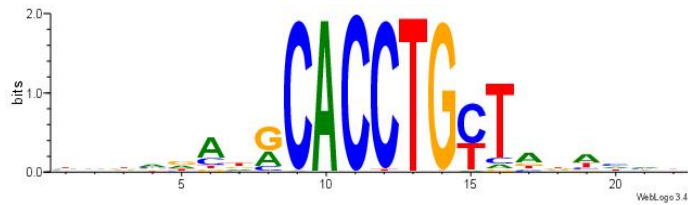
DHDHDTAKCAGGTGMDTHBDHH
----GBTGCAGGTGB-----

Original motif

Consensus sequence: HDDVDADRCACCTGYTADHHHD

Reverse complement motif

Consensus sequence: HHHHDTAKCAGGTGMDTHBDDH

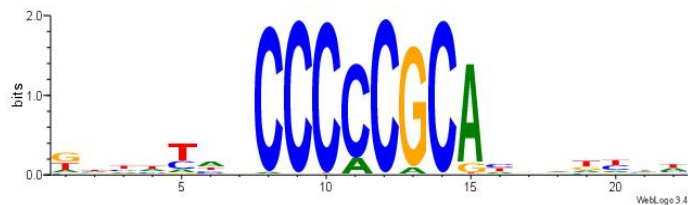


Motif ID: [UP00627](#)
 Motif name: WT1_R366C_R1
 Species: Homo sapiens
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0178142

Alignment:
 KHHHTHHCCCCCGCAHDHDH
 -----BCACCTGCABC-----

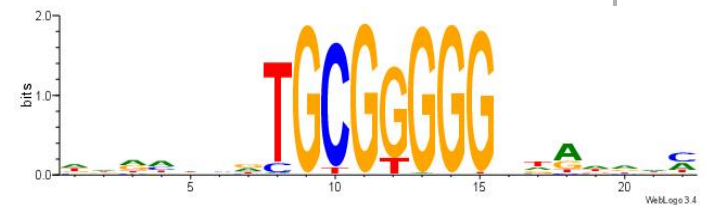
Original motif

Consensus sequence: KHHHTHHCCCCCGCAHDHDH



Reverse complement motif

Consensus sequence: HHHDHDTGCGGGGGHHAHHY



Motif ID: [UP00627](#)

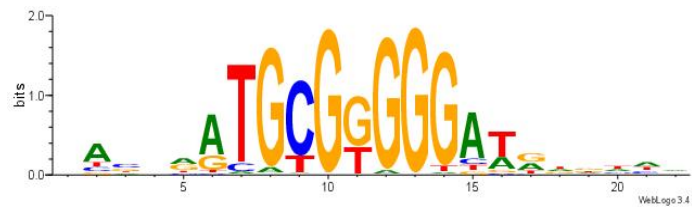
Motif name: WT1_R366L_R1
 Species: Homo sapiens
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0381181

Alignment:

VABVRATGCGKGGGATRDDHHH
 ----GBTGCAGGTGB-----

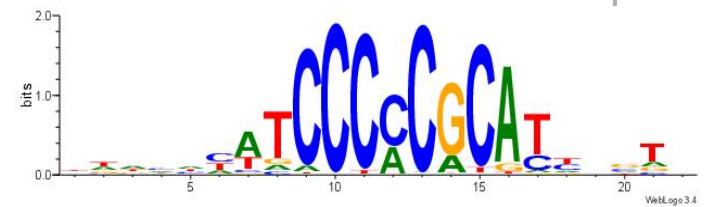
Original motif

Consensus sequence: VABVRATGCGKGGGATRDDHHH



Reverse complement motif

Consensus sequence: HHHHDMATCCCYCGCATKVBTV



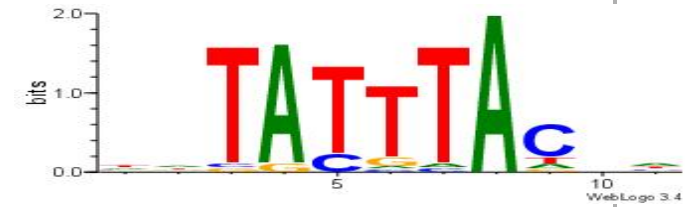
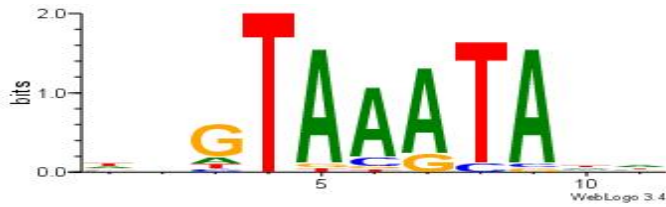
Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif

Consensus sequence: DBGTAAATAHD

Reverse complement motif

Consensus sequence: DHTATTTACBD



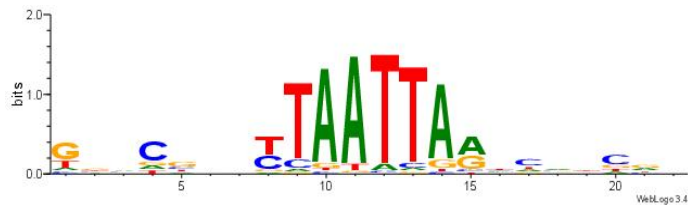
Best Matches for Motif ID 45 (Highest to Lowest)

Motif ID: [UP00616](#)
 Motif name: POU3F4
 Species: Homo sapiens
 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

Alignment:
 BHGDBDHKTAATTAMBBBGHBC
 -----DHTATTTACBD-----

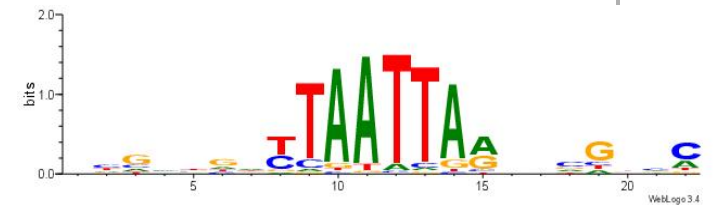
Original motif

Consensus sequence: GBHCBBBYTAATTARHHVDCDB



Reverse complement motif

Consensus sequence: BHGDBDHKTAATTAMBBBGHBC



Motif ID: [UP00585](#)
 Motif name: BCL6
 Species: Homo sapiens
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.00546358

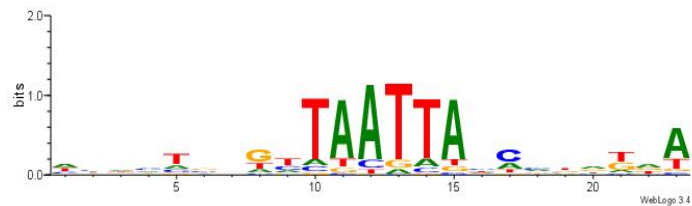
Alignment:

```

TDRDVVGDTAATTAHCDBADDDH
-----DHTATTTACBD-----
  
```

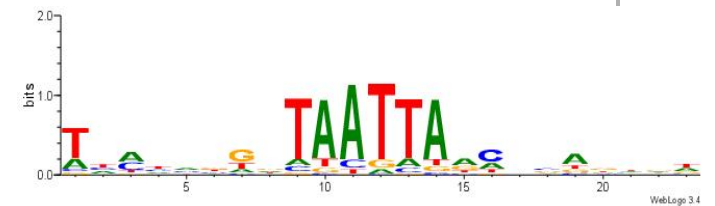
Original motif

Consensus sequence: HHDHTBDGHTAATTAHCVBDKDA



Reverse complement motif

Consensus sequence: TDRDVVGDTAATTAHCVBDKDA



Motif ID: [UP00596](#)
 Motif name: HOXC4_R158L_R1
 Species: Homo sapiens
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8

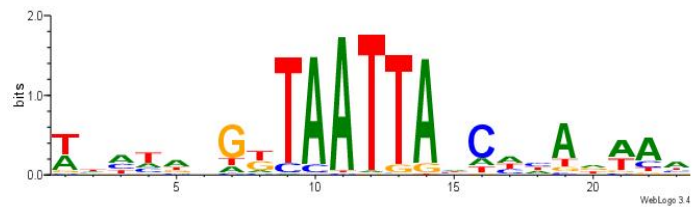
Number of overlap: 11
Similarity score: 0.00584685

Alignment:

WHHHDDGKTAATTAHCHHADWAH
-----DBGTAATAHD-----

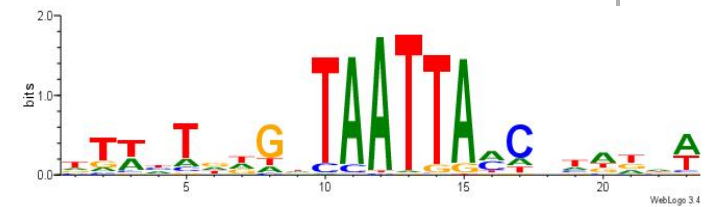
Original motif

Consensus sequence: WHHHDDGKTAATTAHCHHADWAH



Reverse complement motif

Consensus sequence: HTWDTDHGHTAATTARCDDHHHH



Motif ID: [UP00589](#)
Motif name: FOXC1
Species: Homo sapiens
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 11
Similarity score: 0.00675467

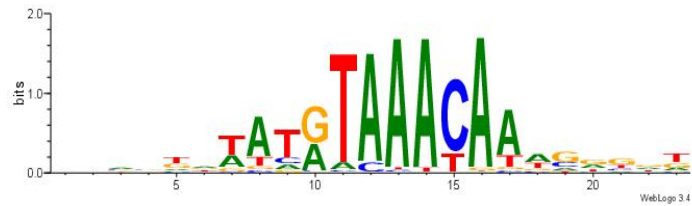
Alignment:

BHVVDWATR TAAACAAWSDBDD
-----DBGTAATAHD-----

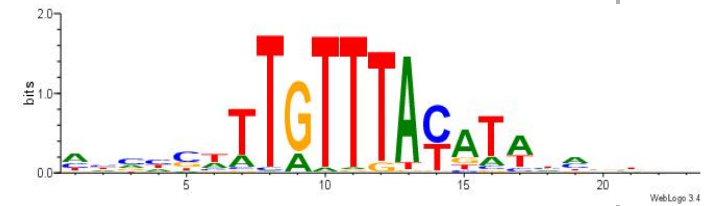
Original motif

Reverse complement motif

Consensus sequence: BHVDDWATRTAAACAWSDBDD



Consensus sequence: DHBHSWTTGTTTAMATWDDVBDB



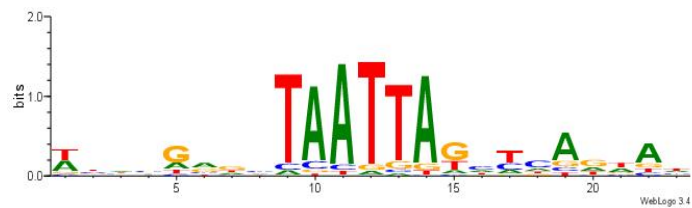
Motif ID: [UP00618](#)
Motif name: POU6F2_E639K_R1
Species: Homo sapiens
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 11
Similarity score: 0.00679091

Alignment:

```
HTDHTDMDYTAATTAVHBCBHVV  
-----DHTATTTACBD-----
```

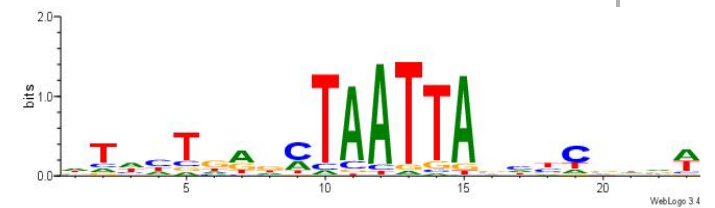
Original motif

Consensus sequence: WBHBGVDVTAATTAKHYHADDAAH



Reverse complement motif

Consensus sequence: HTDHTDMDYTAATTAVHBCBHVV



Dataset #: 5 **Motif ID: 46** **Motif name: TFW3**

Original motif

Consensus sequence: GCACTG



Reverse complement motif

Consensus sequence: CAGTGC



Best Matches for Motif ID 46 (Highest to Lowest)

Motif ID: [UP00605](#)
Motif name: NKX2-8
Species: Homo sapiens
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 6
Similarity score: 0

Alignment:

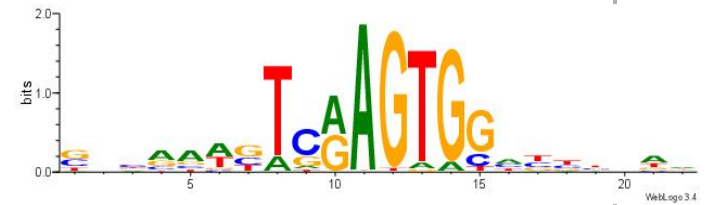
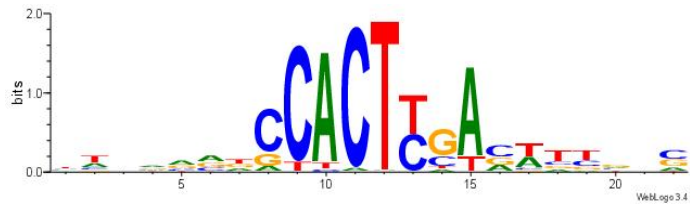
```
SBVMAWVTCMAGTGGDBBDHH  
-----CAGTGC-----
```

Original motif

Consensus sequence: HHDVVVDCCACTYGAVWTYVBS

Reverse complement motif

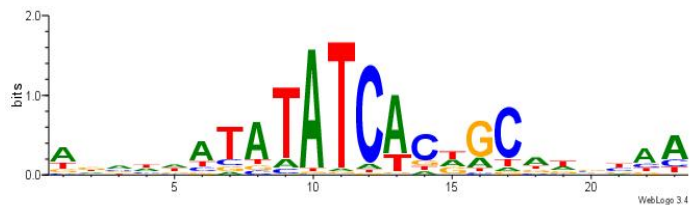
Consensus sequence: SBVMAWVTCMAGTGGDBBDHH



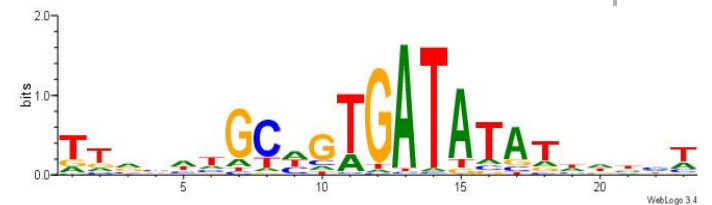
Motif ID: [UP00591](#)
 Motif name: GFI1
 Species: Homo sapiens
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0161376

Alignment:
 TTVBDDGCDGTGATATATDHBHT
 -----GCACTG-----

Original motif
 Consensus sequence: ADVHDATAATACACDGCDDBBAA



Reverse complement motif
 Consensus sequence: TTVBDDGCDGTGATATATDHBHT



Motif ID: [UP00592](#)

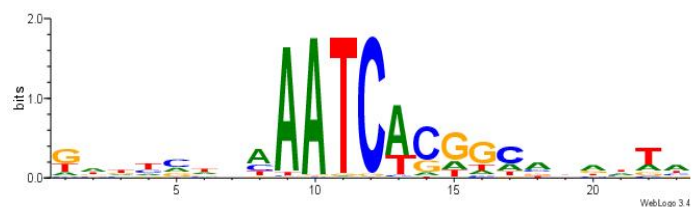
Motif name: GFI1B_A204T_R1
 Species: Homo sapiens
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0198609

Alignment:

HAHDDBGCCGTGATTTTHDVHDDY
 -----GCACTG-----

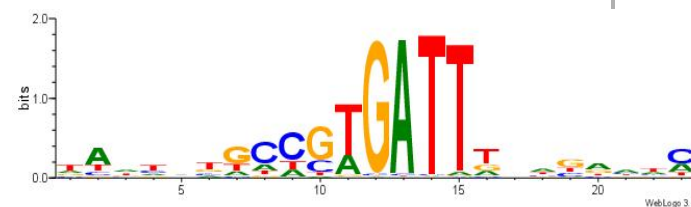
Original motif

Consensus sequence: KDDHVDDAAATCACGGCVDDHHTH



Reverse complement motif

Consensus sequence: HAHDDBGCCGTGATTTTHDVHDDY



Motif ID: [UP00592](#)
 Motif name: GFI1B_A204T_R2
 Species: Homo sapiens
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 12
 Number of overlap: 6

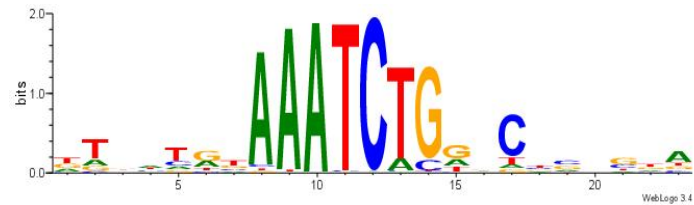
Similarity score: 0.0232927

Alignment:

TDBHVVGVMCAGATTTVMAHHAD
-----GCACTG-----

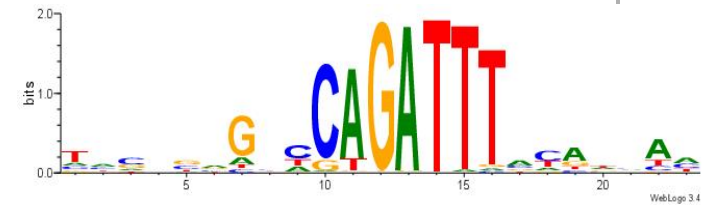
Original motif

Consensus sequence: DTDHTRBAAATCTGRVCBVHBD A



Reverse complement motif

Consensus sequence: TDBHVVGVMCAGATTTVMAHHAD



Motif ID: [UP00620](#)
Motif name: SIX6_REF_R1
Species: Homo sapiens
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 6
Similarity score: 0.0327593

Alignment:

VBCGKVTYAWTGATACBTKHDB
-----GCACTG-----

Original motif

Consensus sequence: VDDRABGTATCAWTKABYCGVV

Reverse complement motif

Consensus sequence: VBCGKVTYAWTGATACBTKHDB



Results created by MOTIFSIM on 06-24-2023 16:08:01

Runtime: 118.467 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

Motif logo generated by [weblogo](#)