



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

Original motif

Consensus sequence: GGCGGGGC



Reverse complement motif

Consensus sequence: GCCCGGCC



### Best Matches for Motif ID 1 (Highest to Lowest)

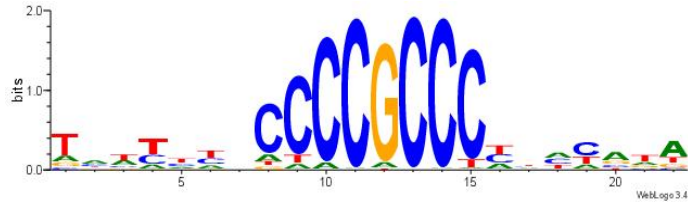
Motif ID:	<a href="#">UP00587</a>
Motif name:	EGR2
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	8
Similarity score:	0

Alignment:

```
THWYHHDCCCCGCCCHHHYADA  
-----GCCCGCC-----
```

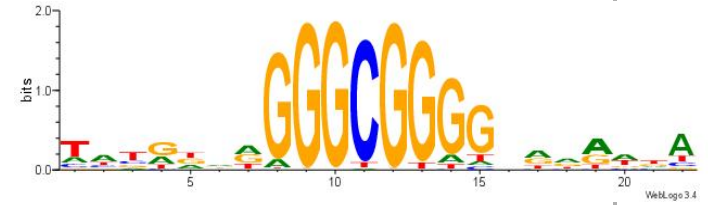
Original motif

Consensus sequence: THWYHHDCCCCGCCCHHYYADA



Reverse complement motif

Consensus sequence: TDTKHHHGGGCGGGGDHHMWHA



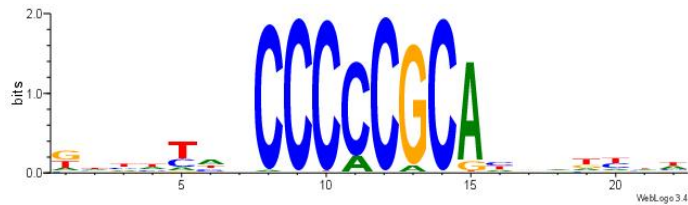
Motif ID: [UP00627](#)  
 Motif name: WT1\_R366C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 8  
 Similarity score: 0.0340362

Alignment:

```
HHHDHHD TGCGGGGGHHAHHHY
-----GGCGGGGC-----
```

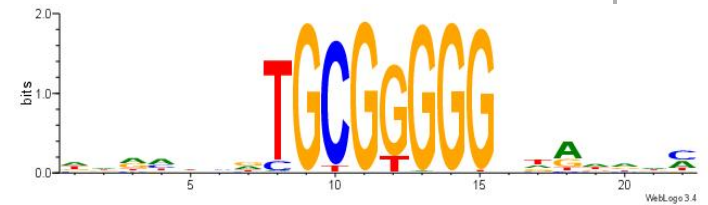
Original motif

Consensus sequence: KHHHTHHCCCCGCAHDHDH



Reverse complement motif

Consensus sequence: HHHDHHD TGCGGGGGHHAHHHY



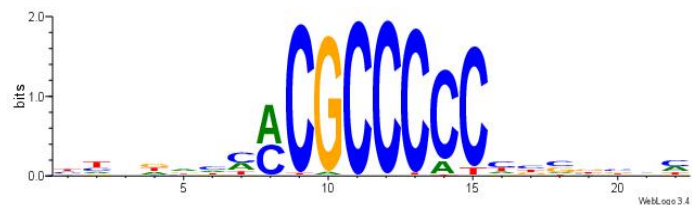
Motif ID: [UP00600](#)  
 Motif name: KLF11  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 8  
 Similarity score: 0.0368821

Alignment:

BHHDDHMMCGCCCCCHBSBBVH  
 ----GCCCCGCC-----

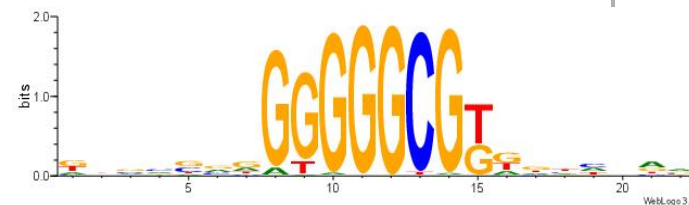
Original motif

Consensus sequence: BHHDDHMMCGCCCCCHBSBBVH



Reverse complement motif

Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV



Motif ID: [UP00627](#)  
 Motif name: WT1\_R366L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward

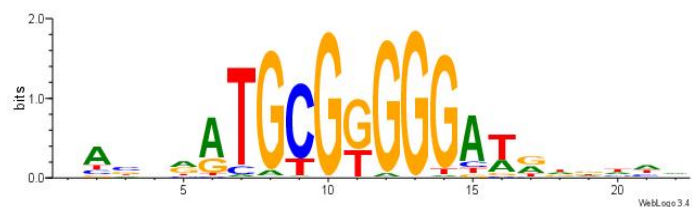
Position number: 7  
Number of overlap: 8  
Similarity score: 0.0478168

Alignment:

HHHDMATCCCYCGCATKVBTV  
-----GCCCGCC-----

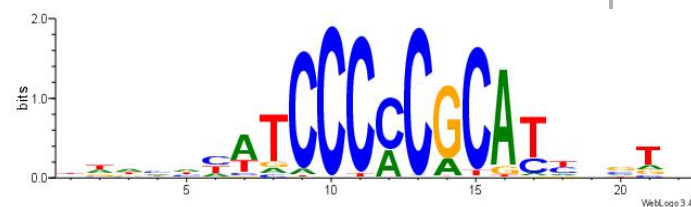
Original motif

Consensus sequence: VABVRATGCGKGGGATRDDHHH



Reverse complement motif

Consensus sequence: HHHHDMATCCCYCGCATKVBTV



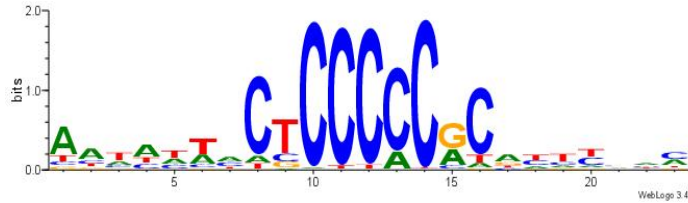
Motif ID: [UP00627](#)  
Motif name: WT1\_REF\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 7  
Number of overlap: 8  
Similarity score: 0.0498717

Alignment:

RHVMHHDGMGGGGGAGHWHHTTT  
-----GGCGGGGC-----

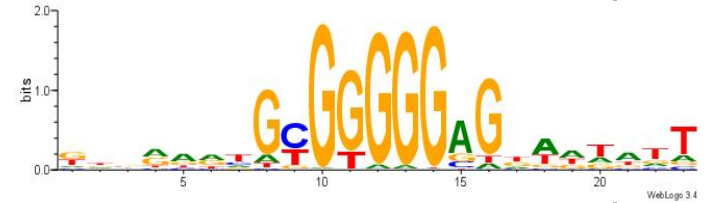
Original motif

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



Reverse complement motif

Consensus sequence: RHVMHHDGMGGGGGAGHWHHTHT



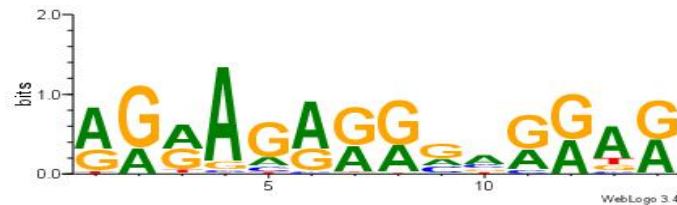
**Dataset #: 2**

**Motif ID: 2**

**Motif name: Motif 2**

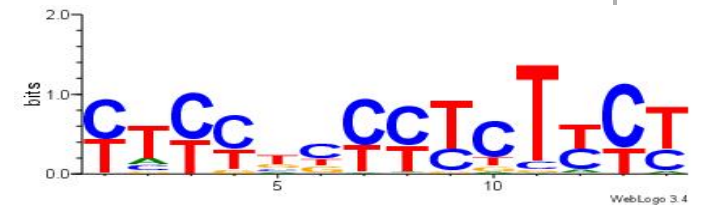
Original motif

Consensus sequence: RGRAGARRGARRAR



Reverse complement motif

Consensus sequence: MTMMTCMMTCTKCK



### Best Matches for Motif ID 2 (Highest to Lowest)

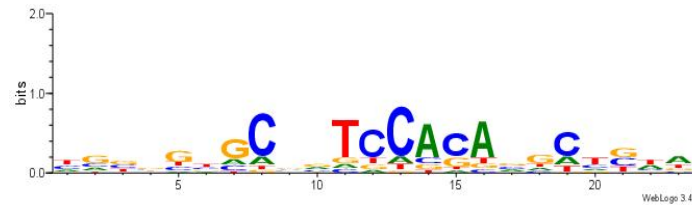
Motif ID:	<a href="#">UP00611</a>
Motif name:	PAX6
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0234155

Alignment:

DHBHGCVTGTGGAVVGCVCBBVH  
-----MTMMTCMMTCTKCK

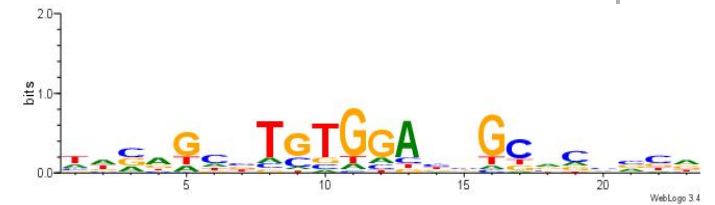
Original motif

Consensus sequence: HVBBGBGCVVTCCACAVGCHBHD



Reverse complement motif

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:

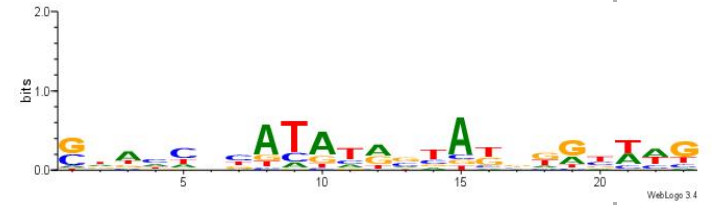
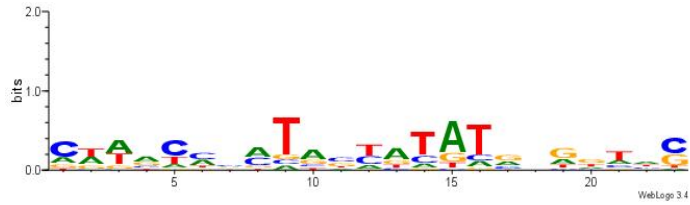
SHAHHHVATATMBTAYVRGBWWG  
MTMMTCMMTCTKCK-----

Original motif

Consensus sequence: CWWVCMVMTABYATATVHDDTHS

Reverse complement motif

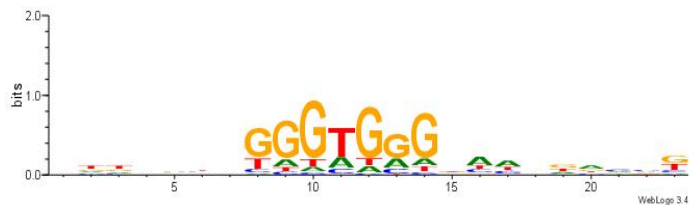
Consensus sequence: SHAHHHVATATMBTAYVRGBWWG



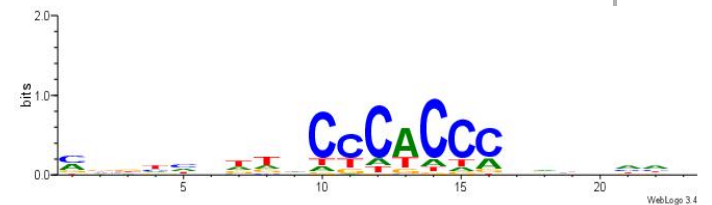
Motif ID: [UP00629](#)  
 Motif name: ZNF200\_H322Y\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0268132

Alignment:  
 DDDDDHDGGGTGGGHHHDDDVVK  
 -----RGRAGARRGARRAR--

Original motif  
 Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



Reverse complement motif  
 Consensus sequence: YVVDHDHHHCCCACCCHHDDDDD



Motif ID: [UP00594](#)



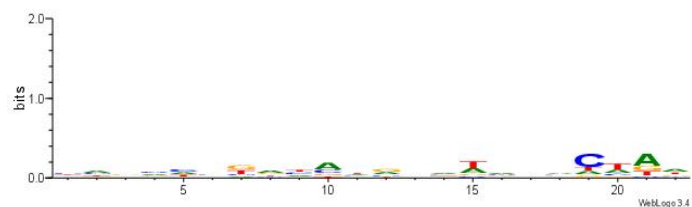
Motif name: HESX1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.03053

**Alignment:**

DTHGBBBWHDVHBHDBVDVBHB  
 ----MTMMTCMMTCTKCK----

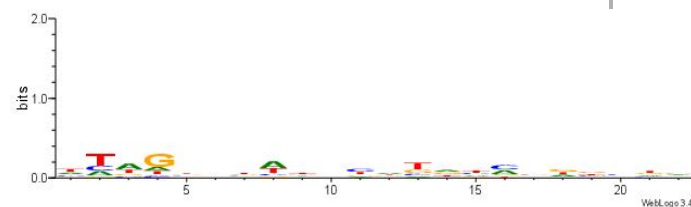
**Original motif**

Consensus sequence: BHBVHVBDHVHVDHWVBVCHAD



**Reverse complement motif**

Consensus sequence: DTHGBBBWHDVHBHDBVDVBHB



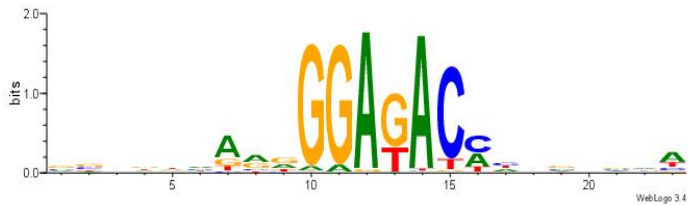

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Motif ID: [UP00629](#)  
 Motif name: ZNF200\_S265Y\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 9  
 Number of overlap: 14

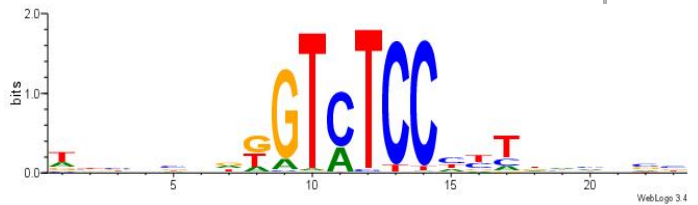
Similarity score: 0.0308188

Alignment:  
VBHDDHARDGGAGACMHDVDVVA  
-----RGRAGARRGARRAR-

Original motif  
Consensus sequence: VBHDDHARDGGAGACMHDVDVVA

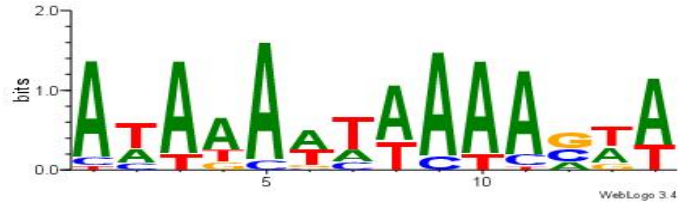


Reverse complement motif  
Consensus sequence: TBVDVDDRGTCTCCHKTHDHHBV

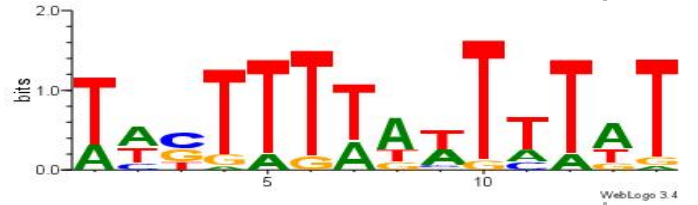


**Dataset #: 2      Motif ID: 3      Motif name: Motif 3**

Original motif  
Consensus sequence: AWAAAWTWAASWA



Reverse complement motif  
Consensus sequence: TWSTTTWAWTTTWT



**Best Matches for Motif ID 3 (Highest to Lowest)**

Motif ID: [UP00627](#)  
Motif name: WT1\_R394L\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif

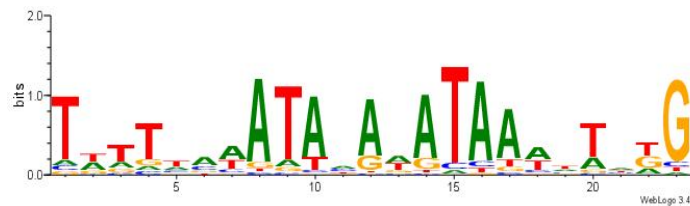
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 14  
 Similarity score: 0.00761781

Alignment:

TWTTTHVWATAHAWATAAWHTHKG  
 -----AWAAAWTWAAASWA--

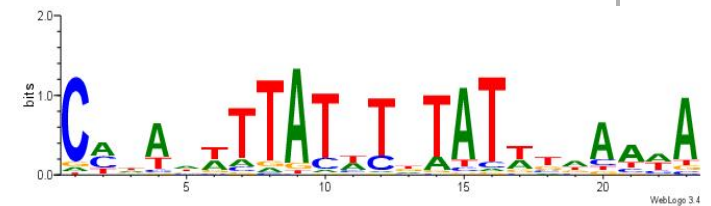
Original motif

Consensus sequence: TWTTTHVWATAHAWATAAWHTHKG



Reverse complement motif

Consensus sequence: CRHAHWTTATWHTATWBHAAWA




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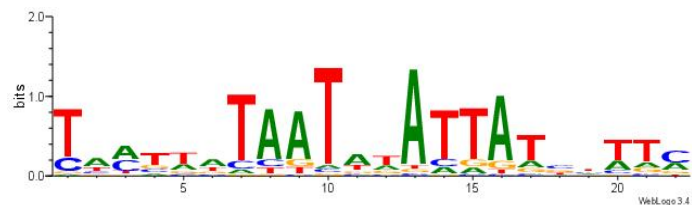
Motif ID: [UP00599](#)  
 Motif name: KLF1\_R328H\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 14  
 Similarity score: 0.00934745

Alignment:

THMTWDTAATADATTATBHATTM  
TWSTTTWAWTTTWT-----

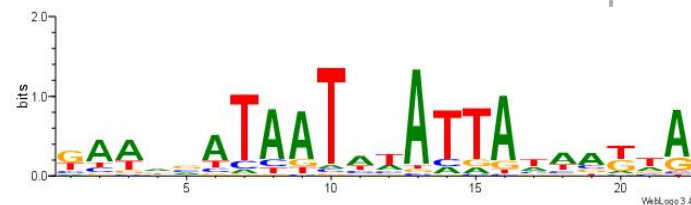
Original motif

Consensus sequence: THMTWDTAATADATTATBHATTM



Reverse complement motif

Consensus sequence: RAAHBATAATDTATTADWAYHA



Motif ID: [UP00627](#)  
Motif name: WT1\_H373Y\_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: 0.00935632

Alignment:

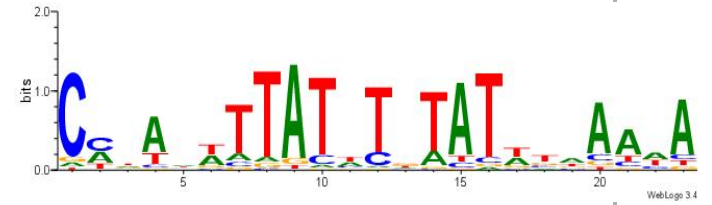
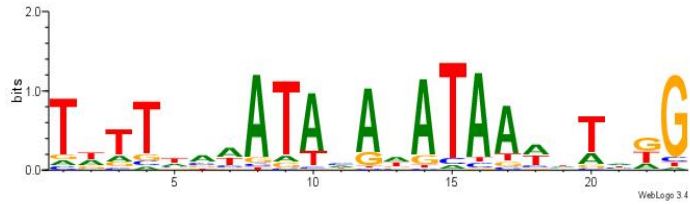
TDTTHVWATAHADATAAWHTHKG  
-----AWAAAWTWAAASWA--

Original motif

Consensus sequence: TDTTHVWATAHADATAAWHTHKG

Reverse complement motif

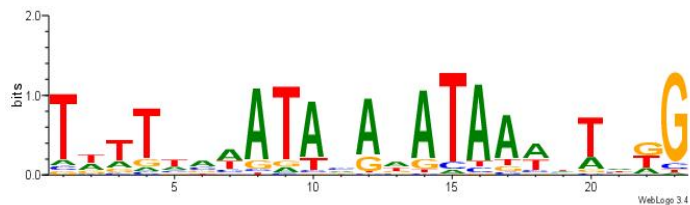
Consensus sequence: CYHAHWTTATDTDTATWBHAADA



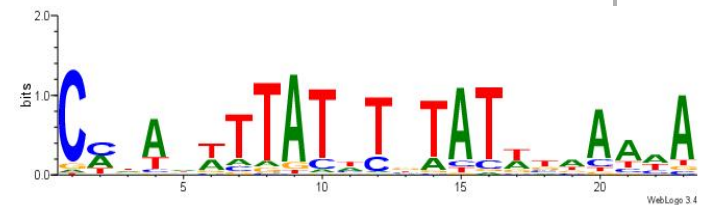
Motif ID: [UP00627](#)  
 Motif name: WT1\_F392L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 14  
 Similarity score: 0.0117725

Alignment:  
 TWTHVWATAVADATAAWHTHKG  
 -----AWAAAWTWAAASWA--

Original motif  
 Consensus sequence: TWTHVWATAVADATAAWHTHKG



Reverse complement motif  
 Consensus sequence: CYHAHWTTATDTVTATWBHAAWA



Motif ID: [UP00606](#)

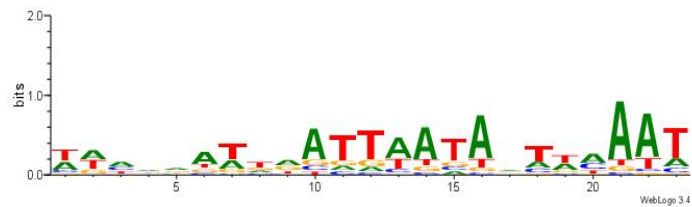
Motif name: NR1H4  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.0125288

**Alignment:**

WWHVDAWDDATTWATAVTWMAAT  
 -----AWAAAWTWAAASWA-----

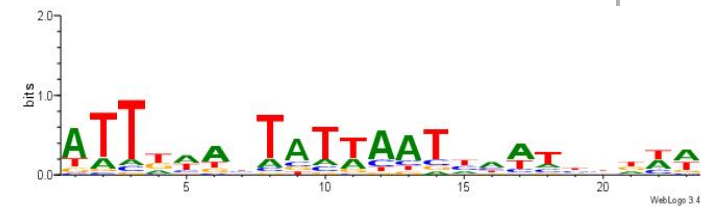
**Original motif**

Consensus sequence: WWHVDAWDDATTWATAVTWMAAT



**Reverse complement motif**

Consensus sequence: ATTYWABTATWAATDDWTDBHWW



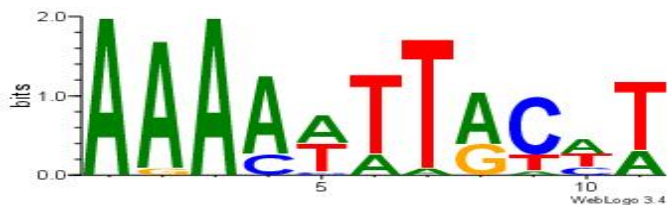
**Dataset #: 2      Motif ID: 4      Motif name: Motif 4**

**Original motif**

Consensus sequence: AAAAWTTRCWT

**Reverse complement motif**

Consensus sequence: AWGKAAWTTTT

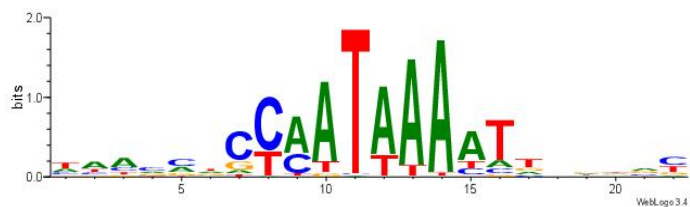


**Best Matches for Motif ID 4 (Highest to Lowest)**

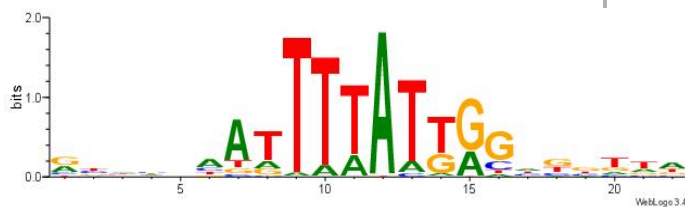
Motif ID: [UP00597](#)  
 Motif name: HOXD13\_S316C\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0171027

Alignment:  
 HHAVVDCCMATAAAAATDBDDVY  
 -----AAAATTRCWT

Original motif  
 Consensus sequence: HHAVVDCCMATAAAAATDBDDVY



Reverse complement motif  
 Consensus sequence: KBDHVDATTTTATYGGDVVTHH



Motif ID: [UP00627](#)

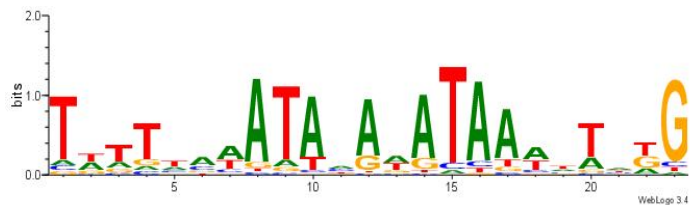
Motif name: WT1\_R394L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 12  
 Number of overlap: 11  
 Similarity score: 0.0174438

**Alignment:**

CRHAHWTTATWTHATWBHAAWA  
 -AAAWTTRCWT-----

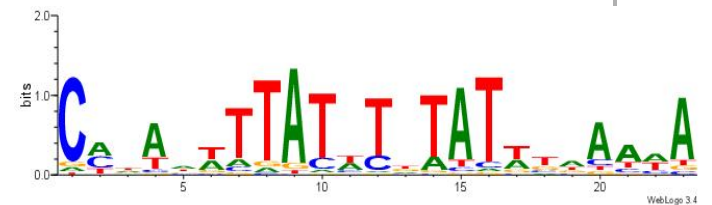
**Original motif**

Consensus sequence: TWTHVWATAHAWATAAWHHTHGK



**Reverse complement motif**

Consensus sequence: CRHAHWTTATWTHATWBHAAWA




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Motif ID: [UP00627](#)  
 Motif name: WT1\_R394W\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11



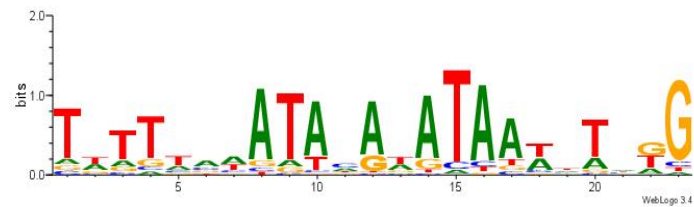
Similarity score: 0.0198047

Alignment:

```
TWTHVWATAHAWATAAWHTHKG  
-----AWGKAAWTTTT-
```

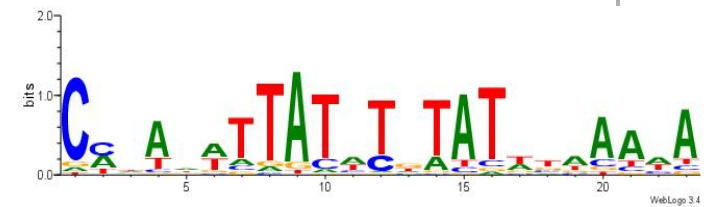
Original motif

Consensus sequence: TWTHVWATAHAWATAAWHTHKG



Reverse complement motif

Consensus sequence: CYHAHWTTATWTDATWBHAAWA



Motif ID: [UP00627](#)  
Motif name: WT1\_F392L\_R1  
Species: Homo sapiens  
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: 0.0206321

Alignment:

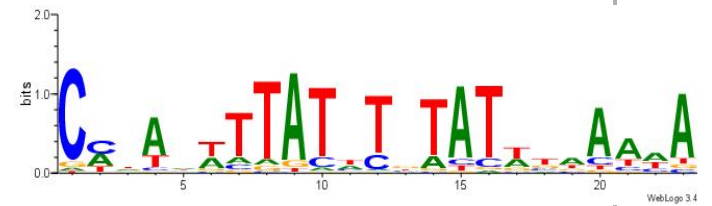
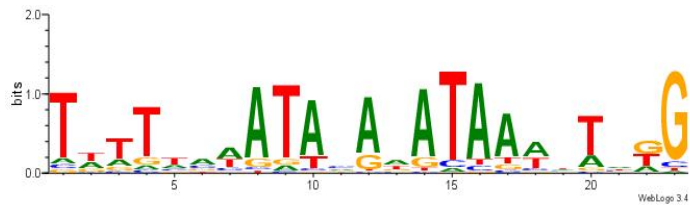
```
TWTHVWATAVADATAAWHTHKG  
-----AWGKAAWTTTT-
```

Original motif

Consensus sequence: TWTHVWATAVADATAAWHTHKG

Reverse complement motif

Consensus sequence: CYHAHWTTATDTVTATWBHAAWA



Motif ID: [UP00523](#)  
 Motif name: FOXR1\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0206685

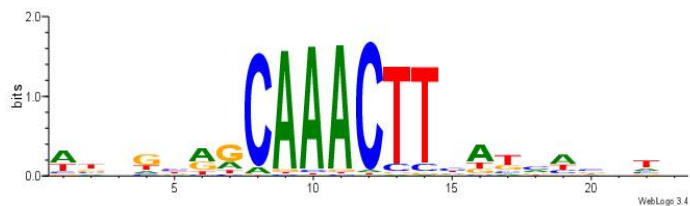
**Alignment:**

```

WBHGBRGCAAAC TTHAKVHBHHD
-----AAAAWTTRCWT-----
  
```

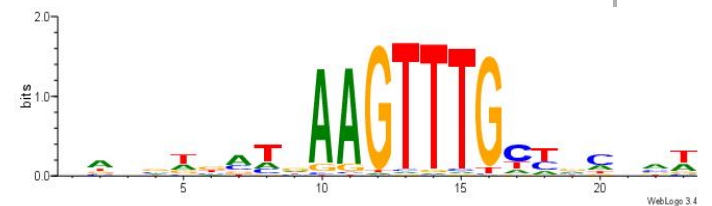
**Original motif**

Consensus sequence: WBHGBRGCAAAC TTHAKVHBHHD



**Reverse complement motif**

Consensus sequence: DHHBHVRTDAAGTTTGCKBCHVW



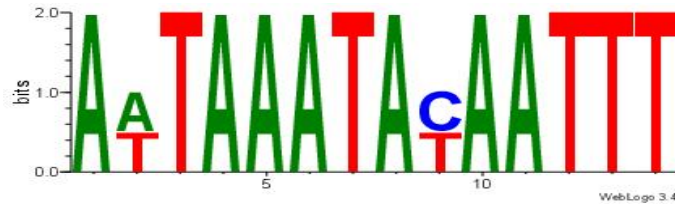
**Dataset #: 2**

**Motif ID: 5**

**Motif name: Motif 5**

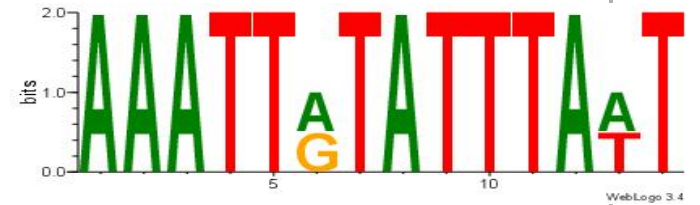
Original motif

Consensus sequence: AWTAATAYAATTT



Reverse complement motif

Consensus sequence: AAATTKTATTTAWT



**Best Matches for Motif ID 5 (Highest to Lowest)**

Motif ID: [UP00627](#)  
 Motif name: WT1\_R394L\_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: 14  
 Similarity score: 0.0123886

Alignment:

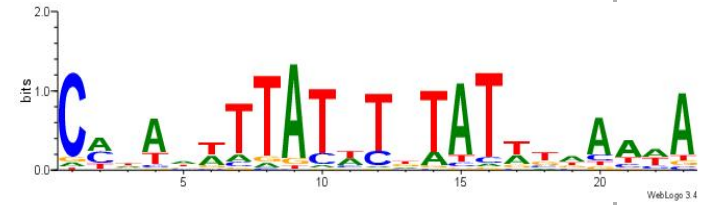
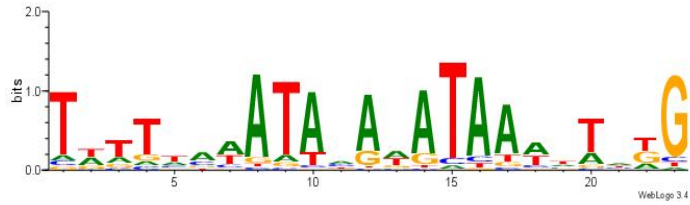
```
TWTHVWATAHAWATAAWHTHKG
-----AWTAAATAYAATTT----
```

Original motif

Consensus sequence: TWTHVWATAHAWATAAWHTHKG

Reverse complement motif

Consensus sequence: CRHAHWTTATWHTATWBHAAWA

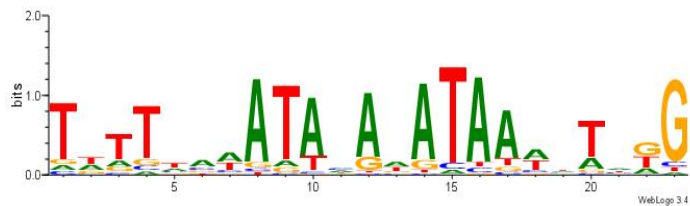


Motif ID: [UP00627](#)  
 Motif name: WT1\_H373Y\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.013075

Alignment:  
 TDTTHVWATAHADATAAWHTHKG  
 -----AWTAAATAYAATTT----

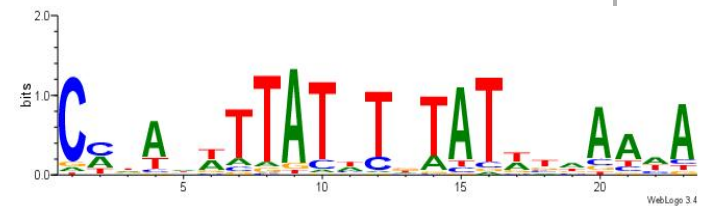
Original motif

Consensus sequence: TDTTHVWATAHADATAAWHTHKG



Reverse complement motif

Consensus sequence: CYHAHWTTATDTDTATWBHAADA



Motif ID: [UP00627](#)

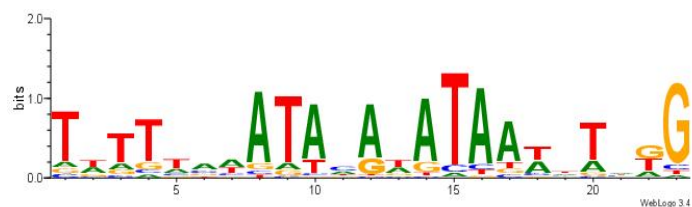
Motif name: WT1\_R394W\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.013818

**Alignment:**

TWTTTHVWATAHAWATAAWHHTKGG  
 -----AWTAAATAYAATTT----

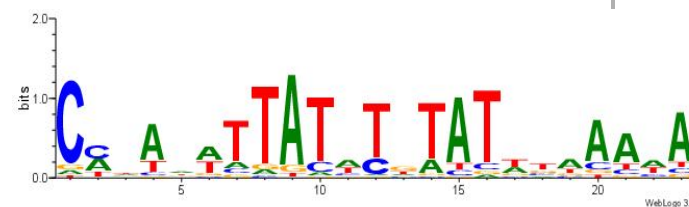
**Original motif**

Consensus sequence: TWTTTHVWATAHAWATAAWHHTKGG



**Reverse complement motif**

Consensus sequence: CYHAHWTTATWTDATWBHAAWA




---

Motif ID: [UP00627](#)  
 Motif name: WT1\_F392L\_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: 14

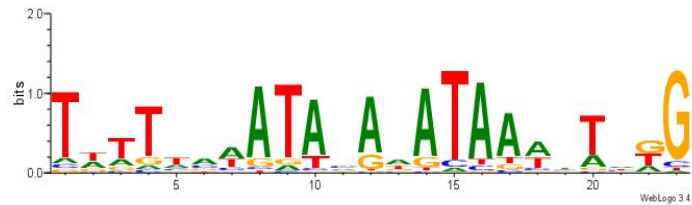
Similarity score: 0.0165843

Alignment:

```
TWTHVWATAVADATAAWHTHKG  
-----AWTAAATAYAATTT---
```

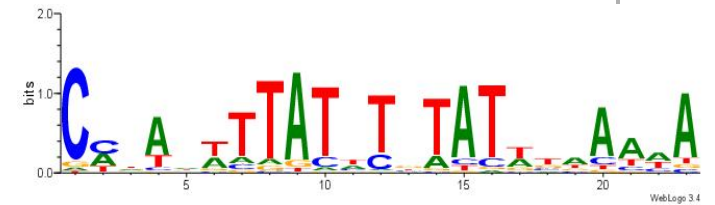
Original motif

Consensus sequence: TWTHVWATAVADATAAWHTHKG



Reverse complement motif

Consensus sequence: CYHAHWTTATDTVTATWBHAAWA



Motif ID: [UP00619](#)  
Motif name: PROP1\_R99Q\_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: 14  
Similarity score: 0.0167999

Alignment:

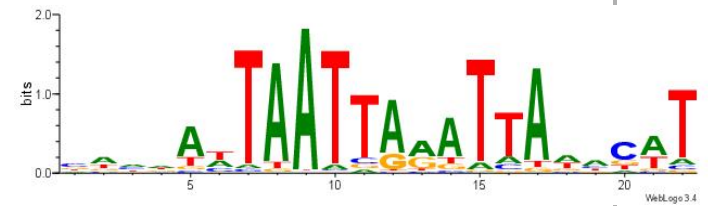
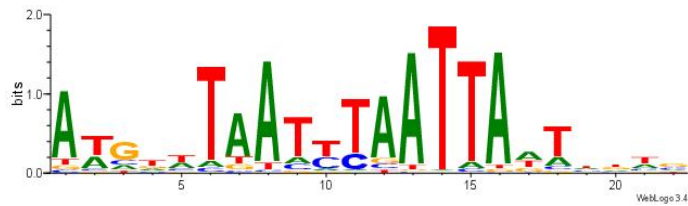
```
AWGDWTAATYTAATTADTHDHV  
----AAATTKTATTTAWT----
```

Original motif

Consensus sequence: AWGDWTAATYTAATTADTHDHV

Reverse complement motif

Consensus sequence: VHDHADTAATTAMATTAWDCWT



**Dataset #: 2      Motif ID: 6      Motif name: Motif 6**

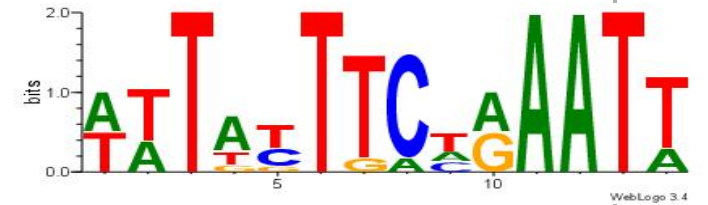
Original motif

Consensus sequence: AATTYDGAARTAWW



Reverse complement motif

Consensus sequence: WWTAKTTCDKAATT



**Best Matches for Motif ID 6 (Highest to Lowest)**

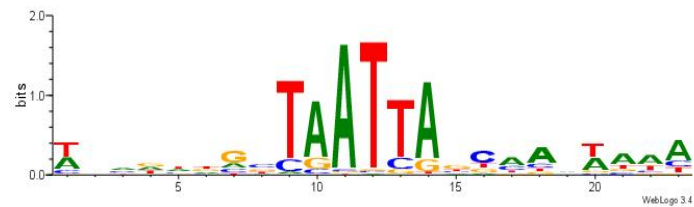
Motif ID:	<a href="#">UP00624</a>
Motif name:	VENTX_REF_R1
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0255961

Alignment:

TWTWDTHGBTAATTABCDHHBDW  
WWTAKTTCDKAATT-----

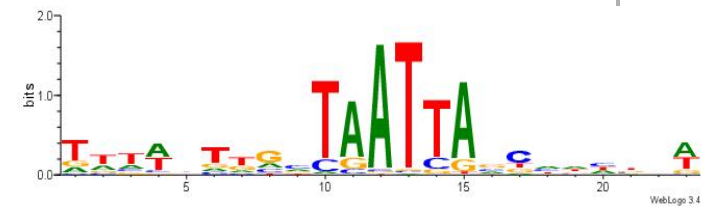
Original motif

Consensus sequence: WDVDHDGBTAATTABCHADWAWA



Reverse complement motif

Consensus sequence: TWTWDTHGBTAATTABCDHHBDW



Motif ID: [UP00596](#)  
Motif name: HOXC4\_R158L\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 14  
Similarity score: 0.0332804

Alignment:

HTWDTDHGHTAATTARCDDHHHW  
WWTAKTTCDKAATT-----

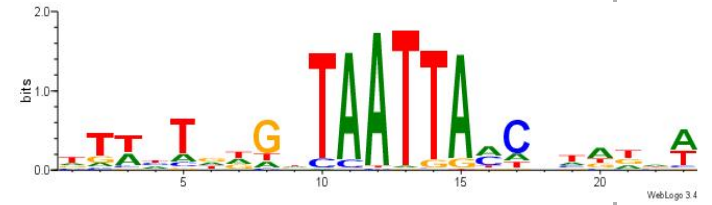
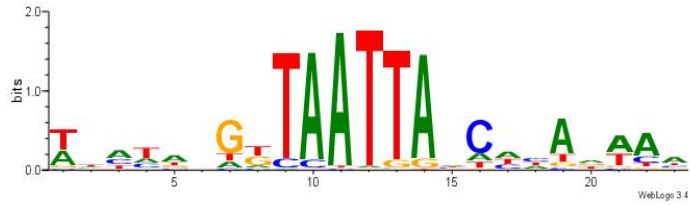
Original motif

Consensus sequence: WHHHDDGKTAATTAHCHHADWAH

Reverse complement motif

Consensus sequence: HTWDTDHGHTAATTARCDDHHHW



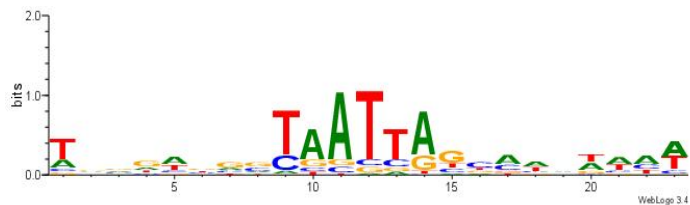


Motif ID: [UP00624](#)  
 Motif name: VENTX\_E101K\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 14  
 Similarity score: 0.0354322

Alignment:  
 WHWWDHYBCTAATTAVVBWHVHA  
 WWTAKTTCDKAATT-----

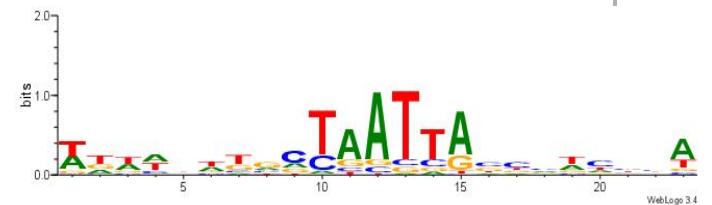
Original motif

Consensus sequence: TDVDWBVTAATTAGBMHDWWHW



Reverse complement motif

Consensus sequence: WHWWDHYBCTAATTAVVBWHVHA



Motif ID: [UP00625](#)

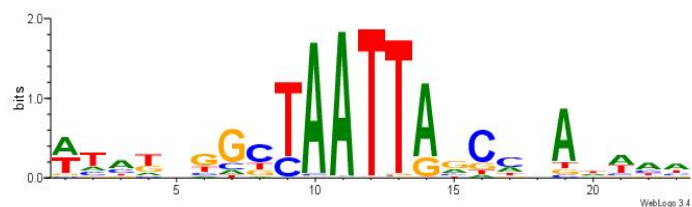
Motif name: VSX1\_Q175H\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 14  
 Similarity score: 0.0359429

**Alignment:**

HHWDTHRGVTAATTAGCCHRHAW  
 WWTAKTTCDKAATT-----

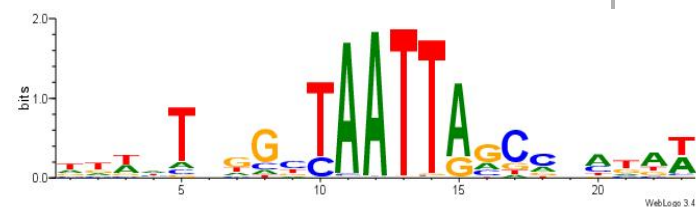
**Original motif**

Consensus sequence: WTHKHGGCTAATTAVCMHADWHH



**Reverse complement motif**

Consensus sequence: HHWDTHRGVTAATTAGCCHRHAW




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Motif ID: [UP00588](#)  
 Motif name: ESX1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 14

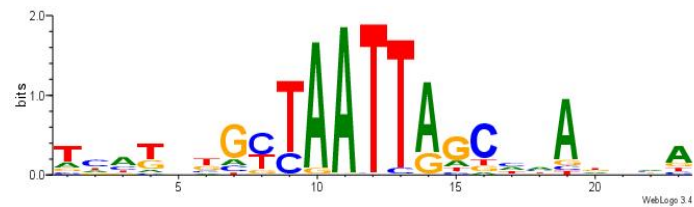
Similarity score: 0.0398477

Alignment:

THDDTHDGCTAATTAKCVRHDA  
WWTAKTTCDKAATT-----

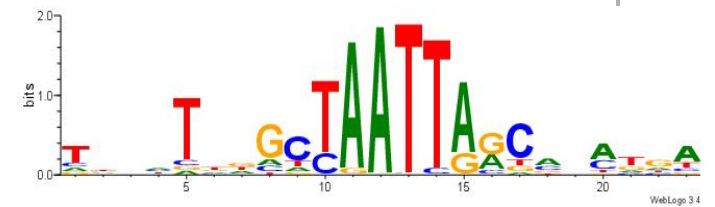
Original motif

Consensus sequence: THHKVBGYTAATTAGCHHADDHA



Reverse complement motif

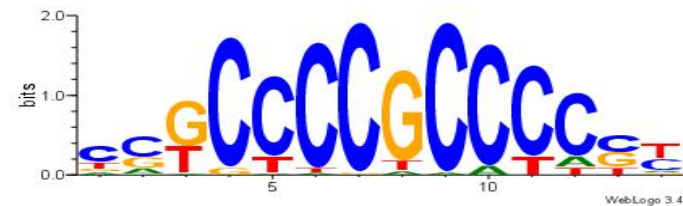
Consensus sequence: THDDTHDGCTAATTAKCVRHDA



**Dataset #: 2      Motif ID: 7      Motif name: Motif 7**

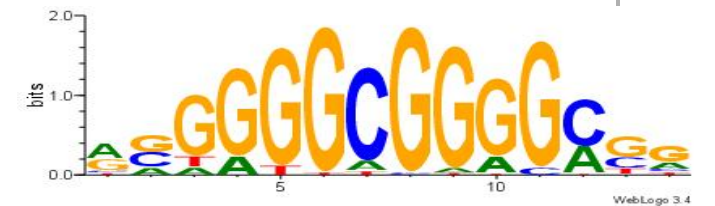
Original motif

Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif

Consensus sequence: MSGGGGCGGGYSG



**Best Matches for Motif ID 7 (Highest to Lowest)**

Motif ID: [UP00587](#)  
Motif name: EGR2  
Species: Homo sapiens  
Matching format of first motif: Original Motif

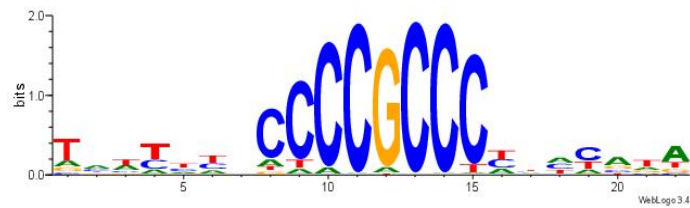
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0

Alignment:

THWYHHDCCCCGCCCHHHYADA  
 ----CSKCCCCGCCCSY----

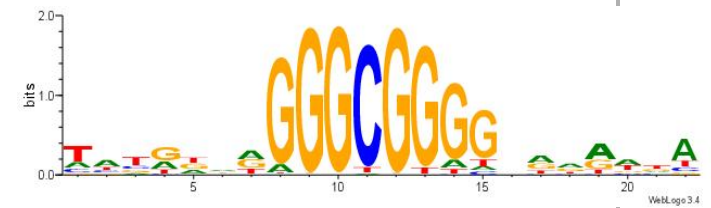
Original motif

Consensus sequence: THWYHHDCCCCGCCCHHHYADA



Reverse complement motif

Consensus sequence: TDTKHHHGGGCGGGGDHHMWHA



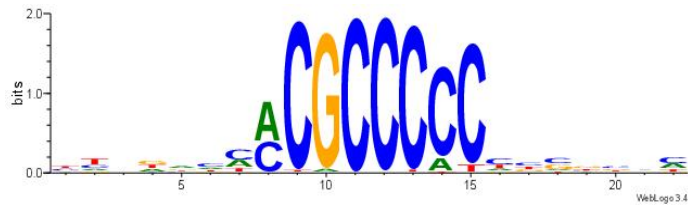
Motif ID: [UP00600](#)  
 Motif name: KLF11  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0205365

Alignment:

BHHDDHMMCGCCCCCHBSBBVH  
--CSKCCCCGCCCSY-----

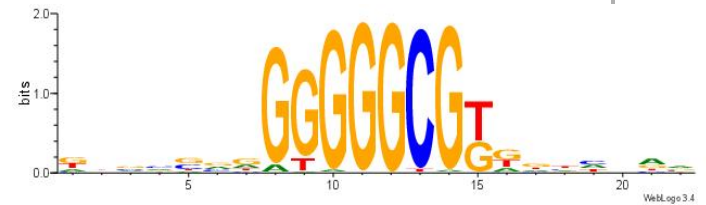
Original motif

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: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 6  
Number of overlap: 14  
Similarity score: 0.0376028

Alignment:

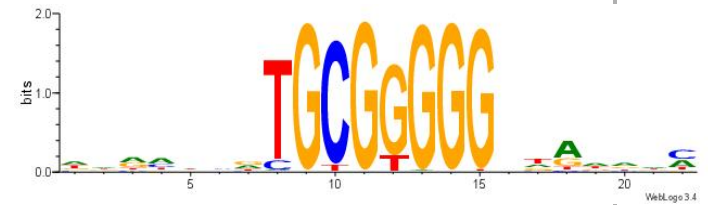
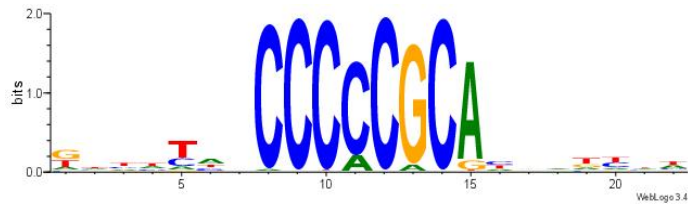
KHHHTHHCCCCCGCAHDHDHHH  
-----CSKCCCCGCCCSY----

Original motif

Consensus sequence: KHHHTHHCCCCCGCAHDHDHHH

Reverse complement motif

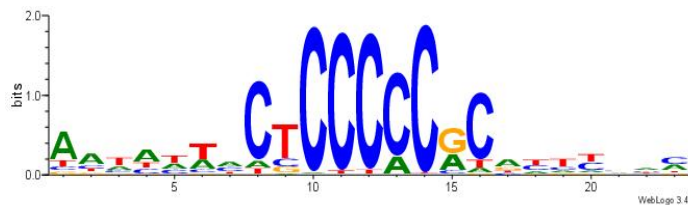
Consensus sequence: HHHDHHTGCGGGGGHHAHHHY



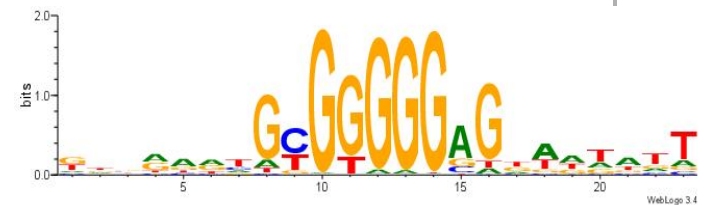
Motif ID: [UP00627](#)  
 Motif name: WT1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.043376

Alignment:  
 RHVMHHDGMGGGGGAGHWHHTTT  
 -----MSGGGGCGGGGYSG-----

Original motif  
 Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



Reverse complement motif  
 Consensus sequence: RHVMHHDGMGGGGGAGHWHHTTT



Motif ID: [UP00629](#)

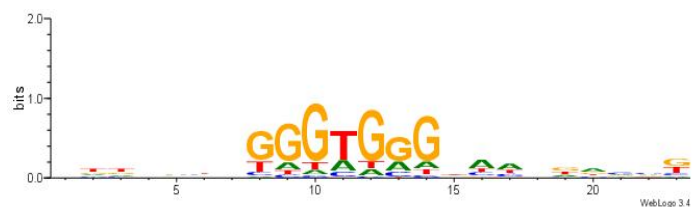
Motif name: ZNF200\_H322Y\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0476064

**Alignment:**

DDDDDHDGGGTGGGHHHDDDVVK  
 ----MSGGGGCGGGYSG-----

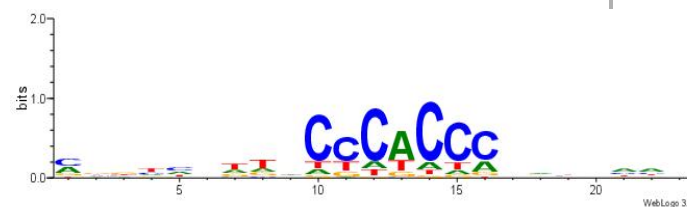
**Original motif**

Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



**Reverse complement motif**

Consensus sequence: YVVDHDHHHCCCACCCHHDDDDD




---

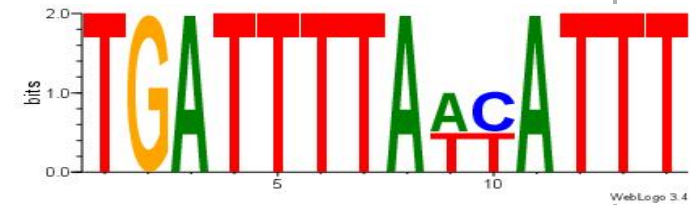
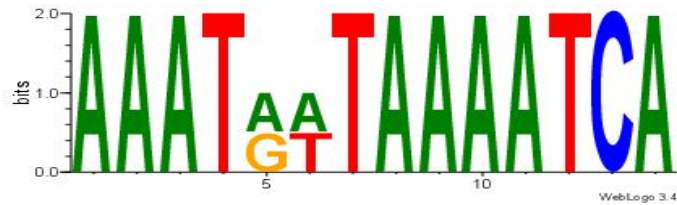
**Dataset #: 2      Motif ID: 8      Motif name: Motif 8**

**Original motif**

Consensus sequence: AAATRWATAAATCA

**Reverse complement motif**

Consensus sequence: TGATTTTAWKATTT



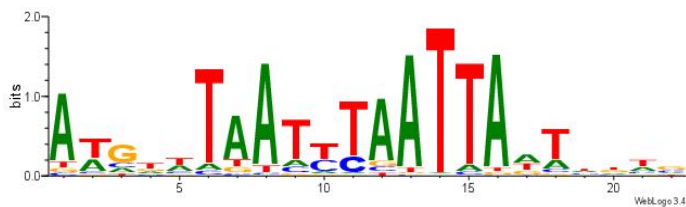
**Best Matches for Motif ID 8 (Highest to Lowest)**

Motif ID: [UP00619](#)  
 Motif name: PROP1\_R99Q\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.0194922

Alignment:  
 AWGDWTAATYTAATTADTHDHV  
 -----TGATTTTAWKATTT----

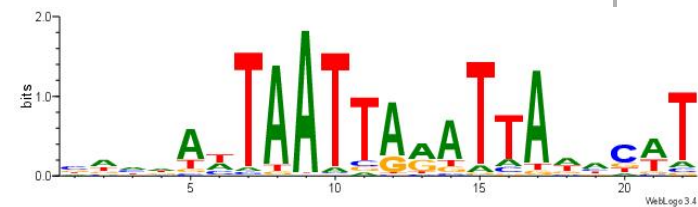
**Original motif**

Consensus sequence: AWGDWTAATYTAATTADTHDHV



**Reverse complement motif**

Consensus sequence: VHDHADTAATTAMATTAWDCWT





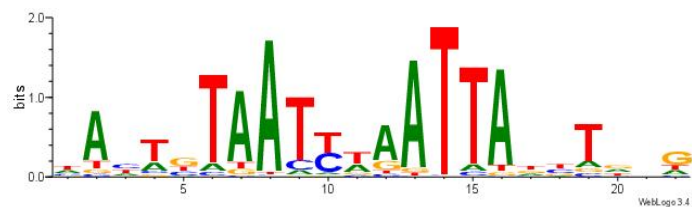
Motif ID: [UP00619](#)  
 Motif name: PROP1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.0209962

**Alignment:**

HAHTBTAATYWAATTADBTDVG  
 -----TGATTTTAWKATTT----

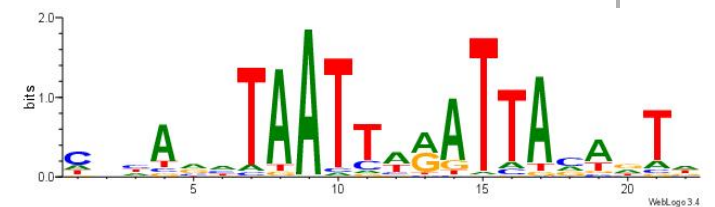
**Original motif**

Consensus sequence: HAHTBTAATYWAATTADBTDVG



**Reverse complement motif**

Consensus sequence: CBHAVDTAATTWMATTABADTH



Motif ID: [UP00597](#)  
 Motif name: HOXD13\_S316C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6

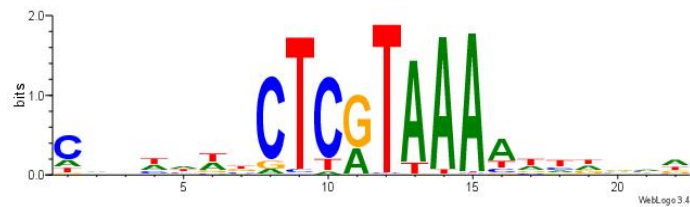
Number of overlap: 14  
Similarity score: 0.0258194

Alignment:

DHVDHDTTTTACGAGVWHHDDG  
---TGATTTTAWKATTT-----

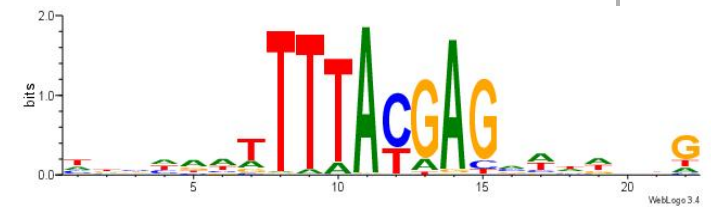
Original motif

Consensus sequence: CDDHHWBCTCGTAAAADHDVHD



Reverse complement motif

Consensus sequence: DHVDHDTTTTACGAGVWHHDDG



Motif ID: [UP00607](#)  
Motif name: NR2E3  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 8  
Number of overlap: 14  
Similarity score: 0.0263894

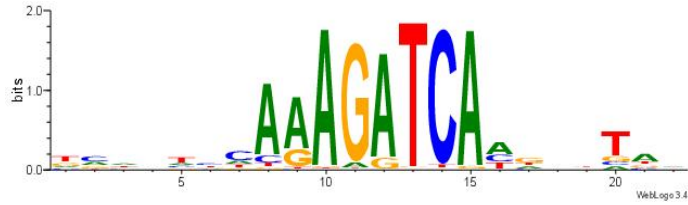
Alignment:

DDADHHHTGATCTTTGBHVDVD  
-----TGATTTTAWKATTT-

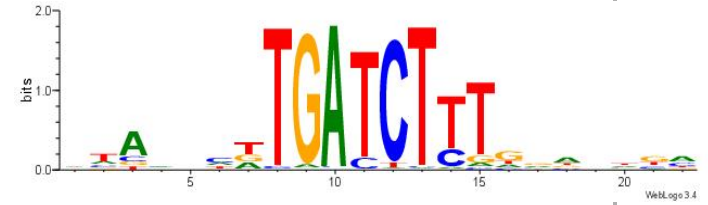
Original motif

Reverse complement motif

Consensus sequence: DVDBHBCAAAGATCAHDHDTDD



Consensus sequence: DDADHHHTGATCTTTGBHVDVD



Motif ID: [UP00597](#)  
 Motif name: HOXD13\_S316C\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.031562

Alignment:

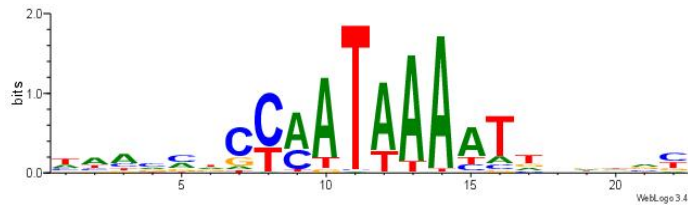
```

HHAVVDCCMATAAAATDBDDVY
-----AAATRWTAAAATCA-----

```

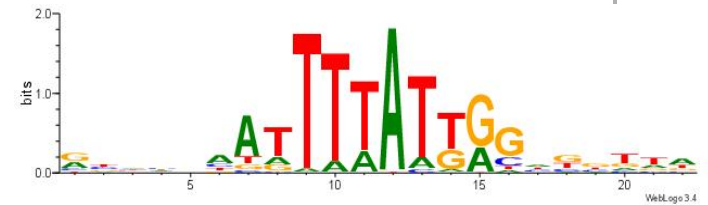
Original motif

Consensus sequence: HHAVVDCCMATAAAATDBDDVY



Reverse complement motif

Consensus sequence: KBDHVDATTTTATYGGDVVTHH



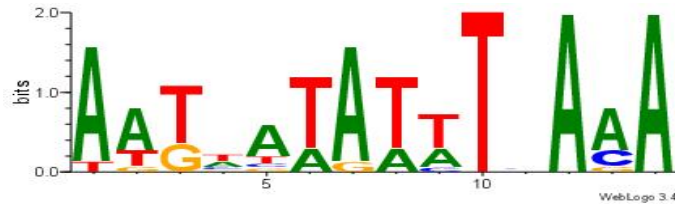
**Dataset #: 2**

**Motif ID: 9**

**Motif name: Motif 9**

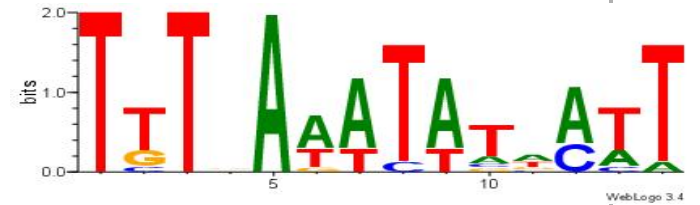
Original motif

Consensus sequence: AATHATATWTHAAA



Reverse complement motif

Consensus sequence: TTTDAWATATHATT



### Best Matches for Motif ID 9 (Highest to Lowest)

Motif ID:	<a href="#">UP00627</a>
Motif name:	WT1_H373Y_R1
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0084574

Alignment:

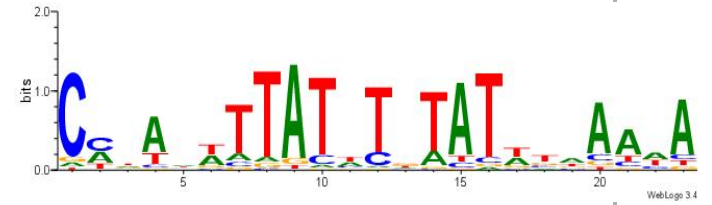
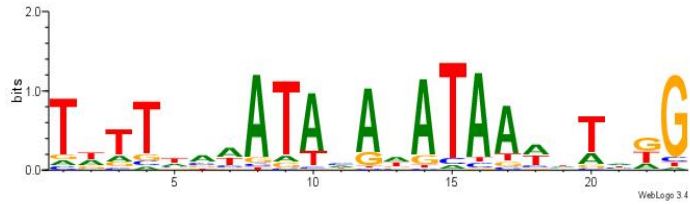
```
CYHAHWTTATD TDTATWBHAADA  
-----AATHATATWTHAAA-
```

Original motif

Consensus sequence: TDTTHVWATAHADATAAWHTHKG

Reverse complement motif

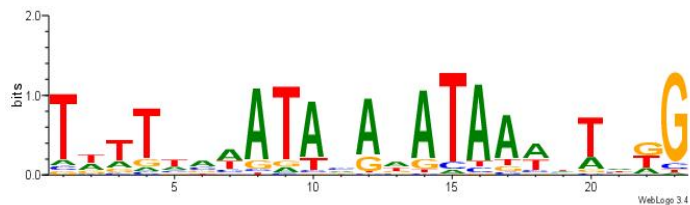
Consensus sequence: CYHAHWTTATD TDTATWBHAADA



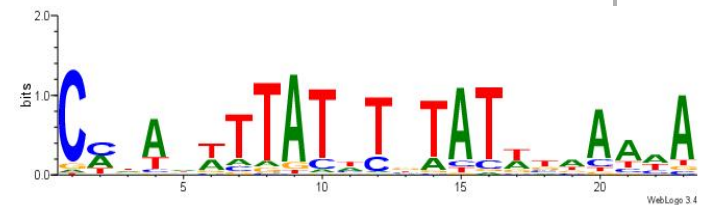
Motif ID: [UP00627](#)  
 Motif name: WT1\_F392L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 9  
 Number of overlap: 14  
 Similarity score: 0.0100981

Alignment:  
 CYHAHWTTATDTVTATWBHAAWA  
 -----AATHATATWTHAAA-

Original motif  
 Consensus sequence: TWTHVWATAVADATAAWHTHKG



Reverse complement motif  
 Consensus sequence: CYHAHWTTATDTVTATWBHAAWA



Motif ID: [UP00627](#)

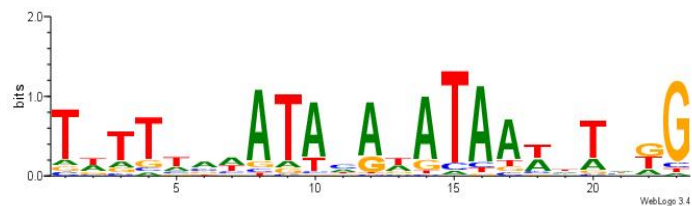
Motif name: WT1\_R394W\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0118845

**Alignment:**

CYHAHWTTATWTDATWBHAAWA  
 -----AATHATATWTHAAA-

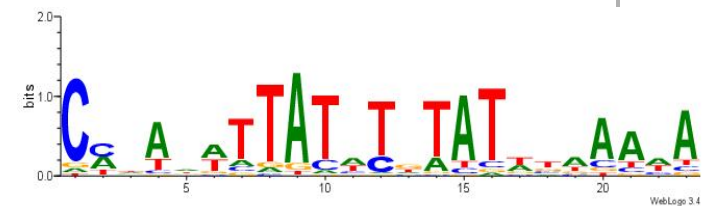
**Original motif**

Consensus sequence: TWTHVWATAHAWATAAWHHTHGK



**Reverse complement motif**

Consensus sequence: CYHAHWTTATWTDATWBHAAWA




---

Motif ID: [UP00606](#)  
 Motif name: NR1H4  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14

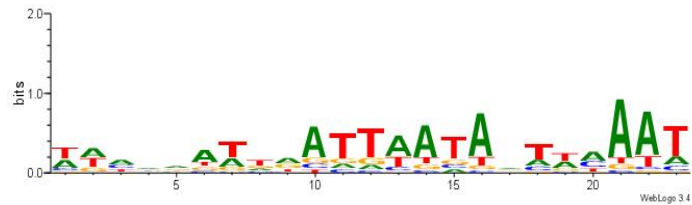
Similarity score: 0.012666

Alignment:

```
WWHVDAWDDATTWATAVTWMAAT  
-----AATHATATWTHAAA
```

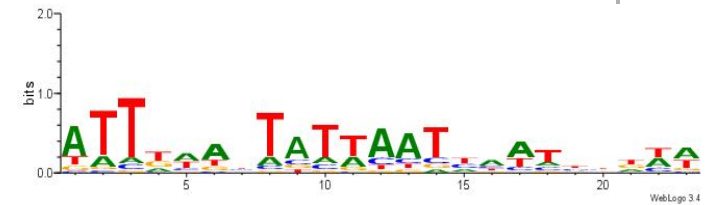
Original motif

Consensus sequence: WWHVDAWDDATTWATAVTWMAAT



Reverse complement motif

Consensus sequence: ATTYWABTATWAATDDWTDBHWW



Motif ID: [UP00627](#)  
Motif name: WT1\_R394L\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 14  
Similarity score: 0.0128993

Alignment:

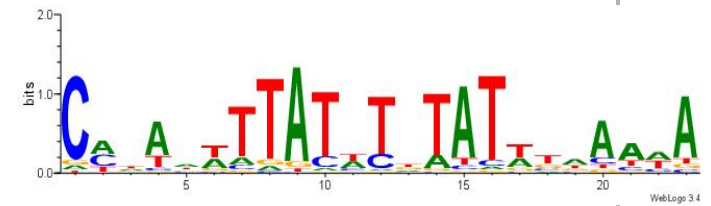
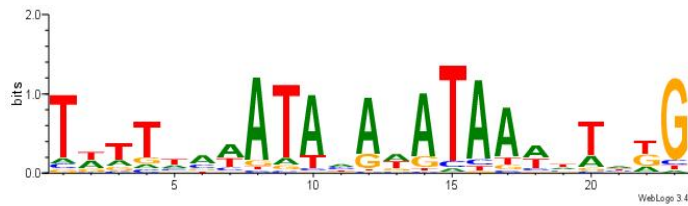
```
CRHAHWTTATWHTATWBHAAWA  
-----AATHATATWTHAAA-
```

Original motif

Consensus sequence: TWTHVWATAHAWATAAWHHTKGG

Reverse complement motif

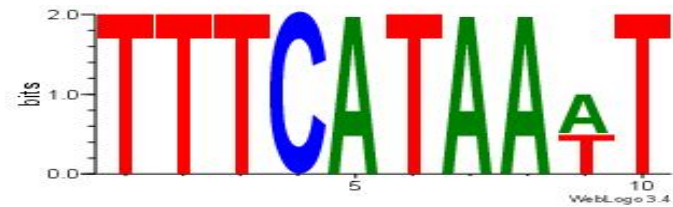
Consensus sequence: CRHAHWTTATWHTATWBHAAWA



**Dataset #: 2      Motif ID: 10      Motif name: Motif 10**

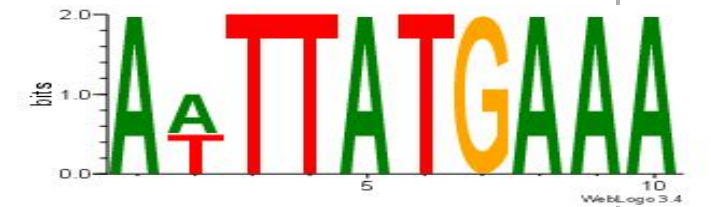
Original motif

Consensus sequence: TTTTCATAAAT



Reverse complement motif

Consensus sequence: AWTTATGAAA



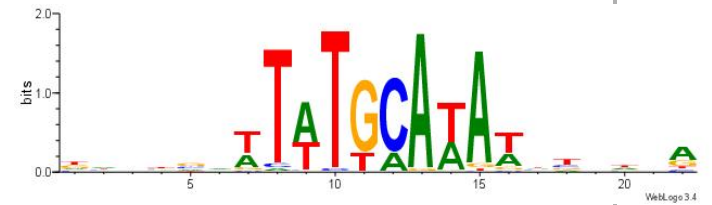
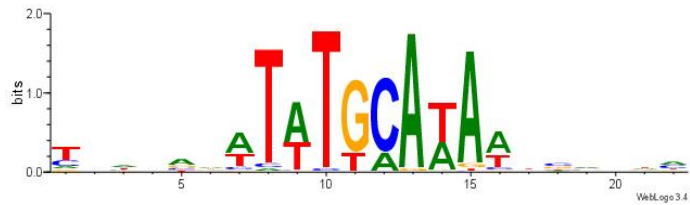
**Best Matches for Motif ID 10 (Highest to Lowest)**

Motif ID:	<a href="#">UP00619</a>
Motif name:	PROP1_R99Q_R1
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	10
Similarity score:	0

Alignment:





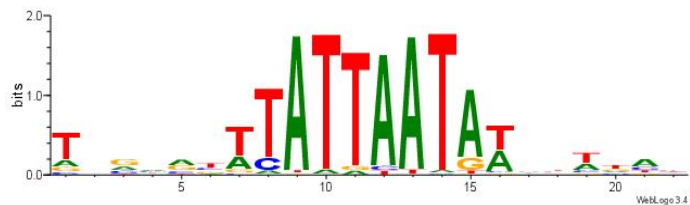


Motif ID: [UP00617](#)  
 Motif name: POU4F3  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 10  
 Similarity score: 0.0024968

Alignment:  
 THVHVBTTATTAATAWHBWDHB  
 ----AWTTATGAAA-----

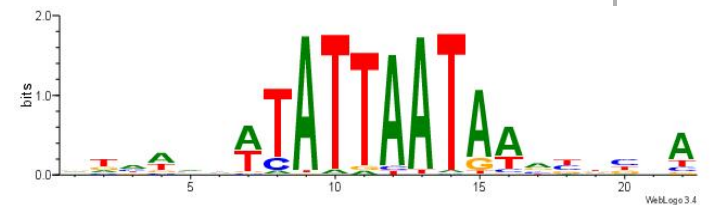
Original motif

Consensus sequence: THVHVBTTATTAATAWHBWDHB



Reverse complement motif

Consensus sequence: BHDWVHWTATTAATAAVBHVHA



Motif ID: [UP00597](#)

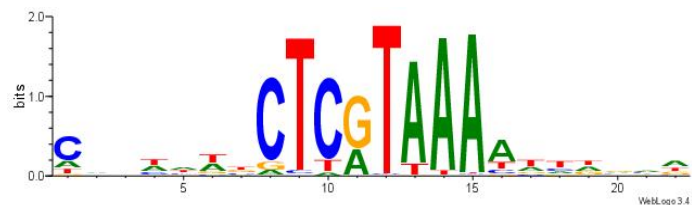
Motif name: HOXD13\_S316C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.00671131

**Alignment:**

CDDHHWBCTCGTAAAADHDVHD  
 -----TTTCATAAWT-----

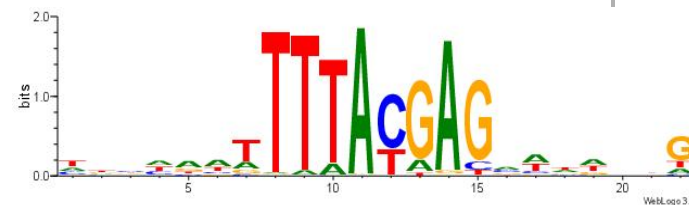
**Original motif**

Consensus sequence: CDDHHWBCTCGTAAAADHDVHD



**Reverse complement motif**

Consensus sequence: DHVDHDTTTTACGAGVWHHDDG




---

Motif ID: [UP00588](#)  
 Motif name: ESX1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 10

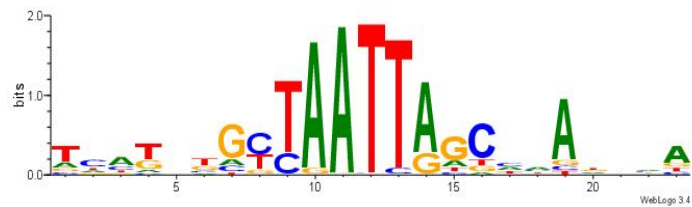
Similarity score: 0.00948327

Alignment:

THDDTHDGCTAATTAKCVVRHDA  
----TTCATAAWT-----

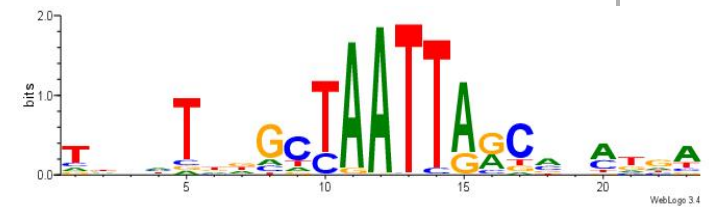
Original motif

Consensus sequence: THHKVBGYTAATTAGCHHADDHA



Reverse complement motif

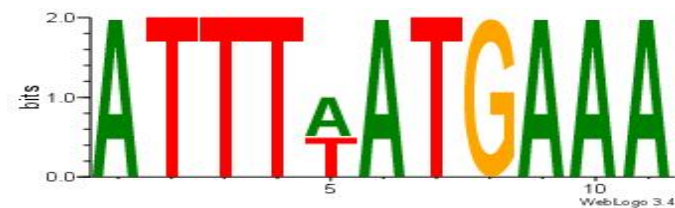
Consensus sequence: THDDTHDGCTAATTAKCVVRHDA



**Dataset #: 2      Motif ID: 11      Motif name: Motif 11**

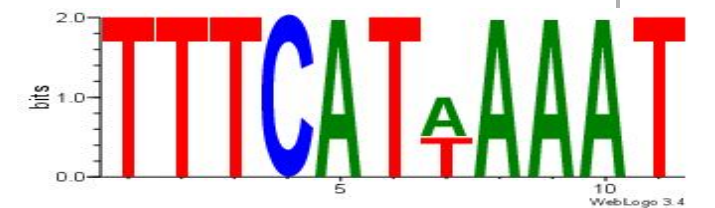
Original motif

Consensus sequence: ATTTWATGAAA



Reverse complement motif

Consensus sequence: TTTCATWAAAT



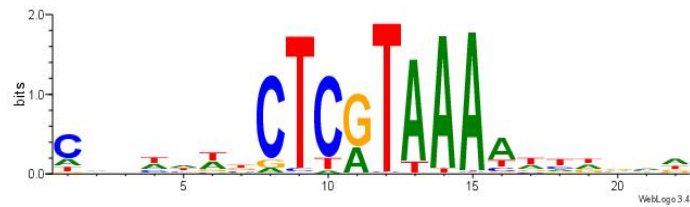
**Best Matches for Motif ID 11 (Highest to Lowest)**

Motif ID: [UP00597](#)  
Motif name: HOXD13\_S316C\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement

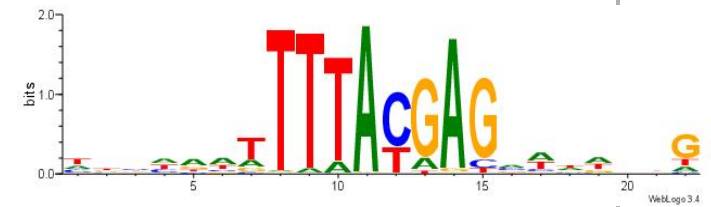
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0

Alignment:  
 CDDHHWBCTCGTAAAADHDVHD  
 -----TTTCATWAAAT-----

Original motif  
 Consensus sequence: CDDHHWBCTCGTAAAADHDVHD



Reverse complement motif  
 Consensus sequence: DHVDHDTTTTACGAGVWHHDDG



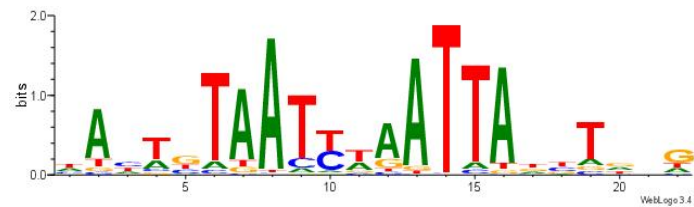
Motif ID: [UP00619](#)  
 Motif name: PROP1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0031995

Alignment:

HAHTBTAATYWAATTADBTDVG  
---TTTCATWAAAT-----

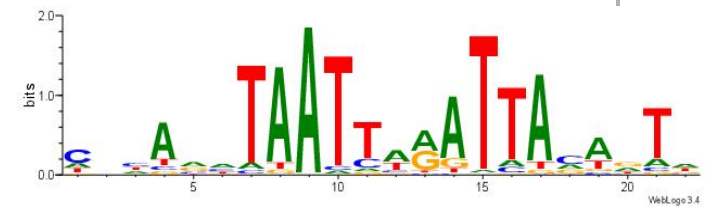
Original motif

Consensus sequence: HAHTBTAATYWAATTADBTDVG



Reverse complement motif

Consensus sequence: CBHAVDTAATTWMATTABADTH



Motif ID: [UP00619](#)  
Motif name: PROP1\_R99Q\_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: 0.0047045

Alignment:

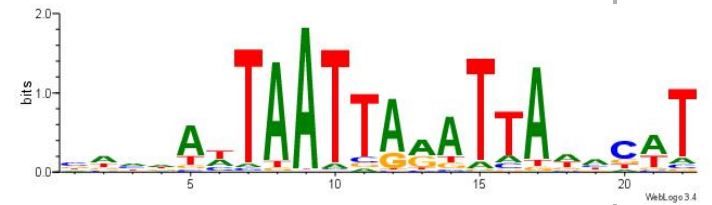
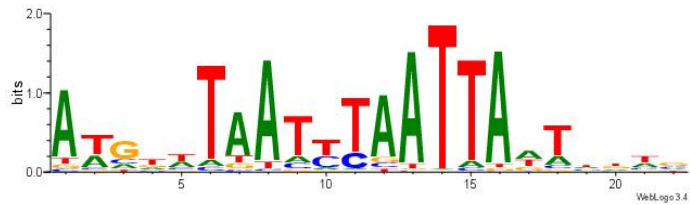
VHDHADTAATTAMATTAWDCWT  
----TTTCATWAAAT-----

Original motif

Consensus sequence: AWGDWTAATYTAATTADTHDHV

Reverse complement motif

Consensus sequence: VHDHADTAATTAMATTAWDCWT

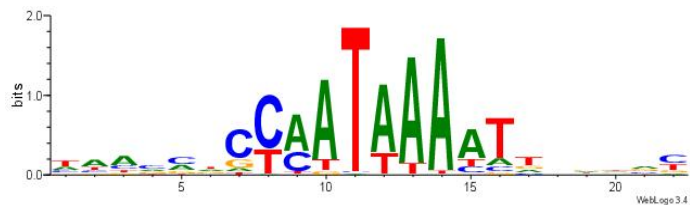


Motif ID: [UP00597](#)  
 Motif name: HOXD13\_S316C\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.00591402

Alignment:  
 HHAVVDCCMATAAAAATDBDDVY  
 -----TTCATWAAAT-----

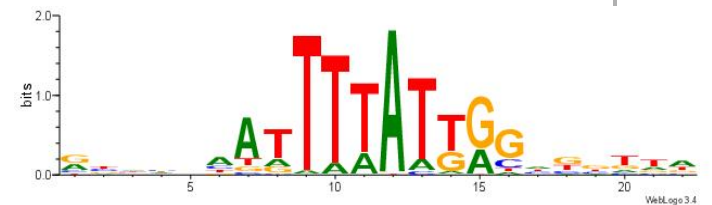
Original motif

Consensus sequence: HHAVVDCCMATAAAAATDBDDVY



Reverse complement motif

Consensus sequence: KBDHVDATTTTATYGGDVVTHH



Motif ID: [UP00626](#)

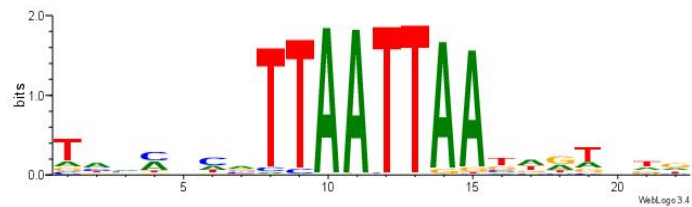
Motif name: VSX2\_R200Q\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.00705472

**Alignment:**

THVMDHVTTAATTAABDRTHDD  
 -----TTTCATWAAAT-----

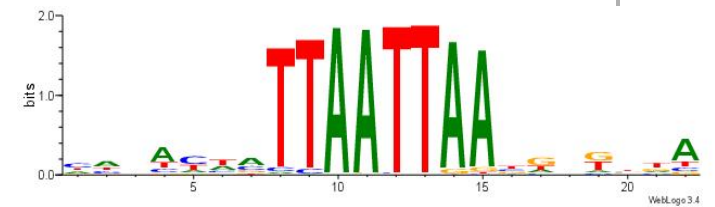
**Original motif**

Consensus sequence: THVMDHVTTAATTAABDRTHDD



**Reverse complement motif**

Consensus sequence: HDHAMDVTTAATTAABDRBHA




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**Dataset #: 2      Motif ID: 12      Motif name: Motif 12**

**Original motif**

Consensus sequence: AAAACAAA

**Reverse complement motif**

Consensus sequence: TTTGTTTT





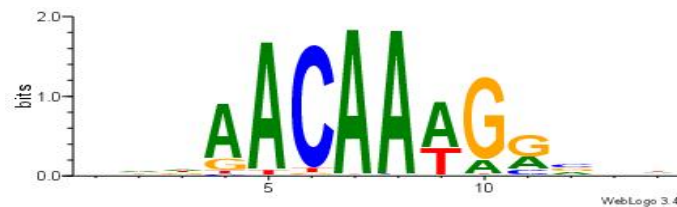
### Best Matches for Motif ID 12 (Highest to Lowest)

Motif ID: [UP00401](#)  
 Motif name: Sox4  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 8  
 Similarity score: 0

Alignment:  
 HBVMCWTGTGTTDDD  
 -----TTTGTTTT-

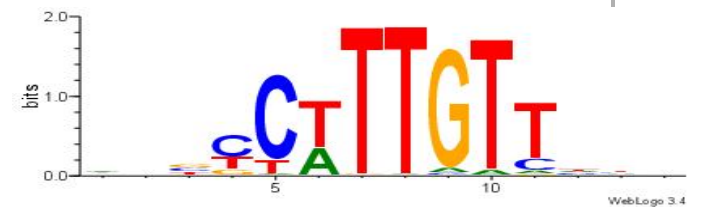
#### Original motif

Consensus sequence: DDDAACAAWGRVVH



#### Reverse complement motif

Consensus sequence: HBVMCWTGTGTTDDD



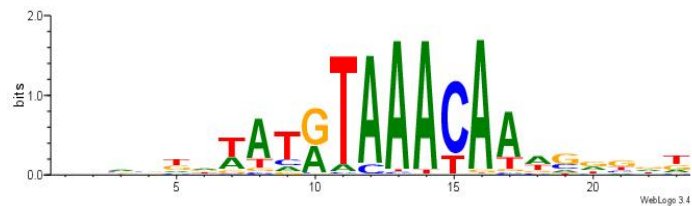
Motif ID: [UP00589](#)  
 Motif name: FOXC1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 11  
 Number of overlap: 8  
 Similarity score: 0.00359317

**Alignment:**

BHVVDDWATRTAAACAAWSDBDD  
 -----AAAACAAA-----

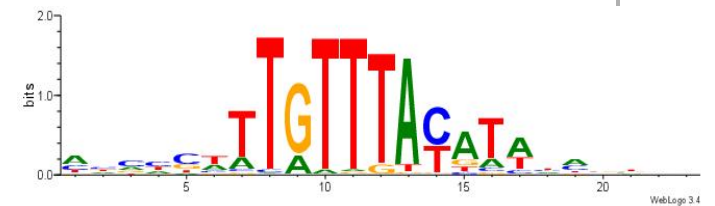
**Original motif**

Consensus sequence: BHVVDDWATRTAAACAAWSDBDD



**Reverse complement motif**

Consensus sequence: DHBHSWTTGTTTAMATWDDVBDB



Motif ID: [UP00523](#)  
 Motif name: FOXR1\_primary  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10

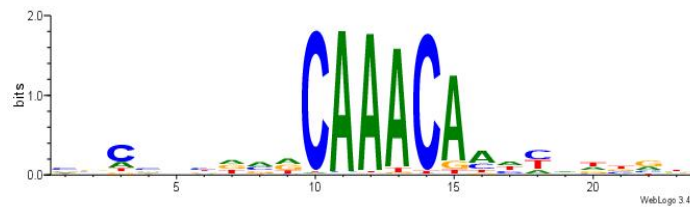
Number of overlap: 8  
Similarity score: 0.0103105

Alignment:

DVVD BKHTT GTTT GDBDBHVG VV  
-----TTTGTTT-----

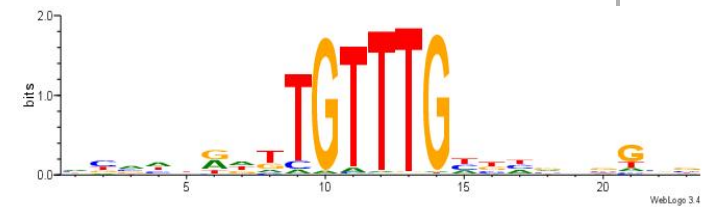
Original motif

Consensus sequence: VVCVHBDVDCAAACAAHYVDBVD



Reverse complement motif

Consensus sequence: DVVD BKHTT GTTT GDBDBHVG VV



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Motif ID: [UP00523](#)  
Motif name: FOXR1\_secondary  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 8  
Similarity score: 0.0310557

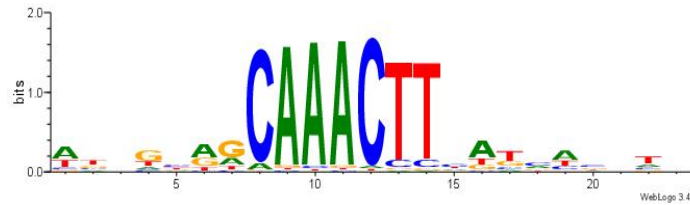
Alignment:

DHHBHV RTDAAGTTTGCKBCHVW  
-----TTTGTTT-----

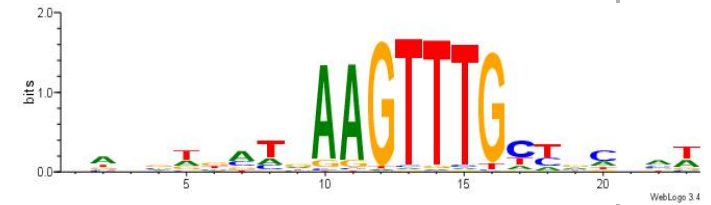
Original motif

Reverse complement motif

Consensus sequence: WBHGBRGCAAACCTTHAKVHBHHD



Consensus sequence: DHHBHVRTDAAGTTTGCKBCHVW



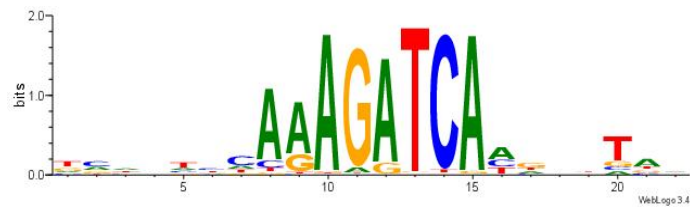
Motif ID: [UP00607](#)  
Motif name: NR2E3  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 10  
Number of overlap: 8  
Similarity score: 0.0433693

Alignment:

```
DVDBHBCAAAGATCAHDHDTDD  
-----AAAACAAA-----
```

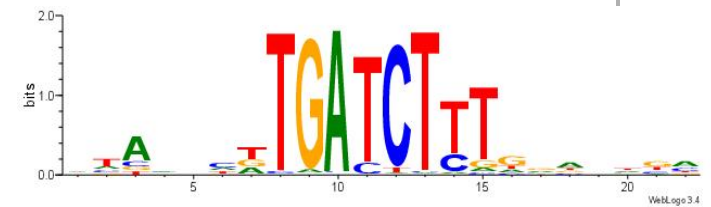
Original motif

Consensus sequence: DVDBHBCAAAGATCAHDHDTDD



Reverse complement motif

Consensus sequence: DDADHHHTGATCTTTGBHVDVD



**Dataset #: 2      Motif ID: 13      Motif name: Motif 13**

Original motif

Consensus sequence: AAAGATTT



Reverse complement motif

Consensus sequence: AAATCTTT



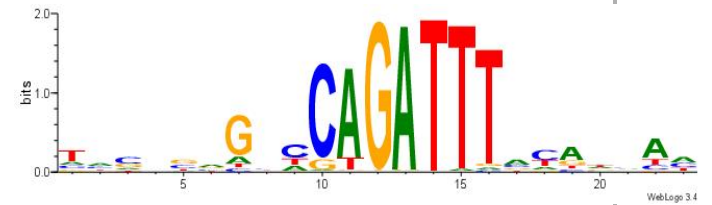
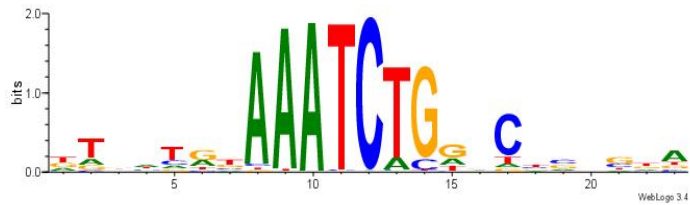
**Best Matches for Motif ID 13 (Highest to Lowest)**

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: Forward  
Position number: 9  
Number of overlap: 8  
Similarity score: 0

Alignment:  
TDBHVVGVMCAGATTTVMAHHAD  
-----AAAGATTT-----

Original motif  
Consensus sequence: DTDHTRBAAATCTGRVCBVBDA

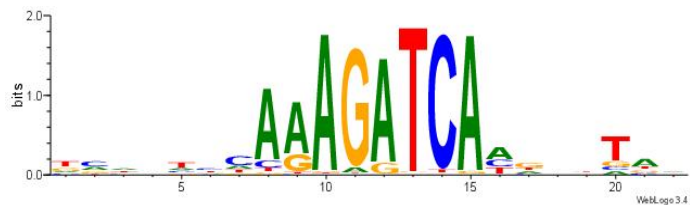
Reverse complement motif  
Consensus sequence: TDBHVVGVMCAGATTTVMAHHAD



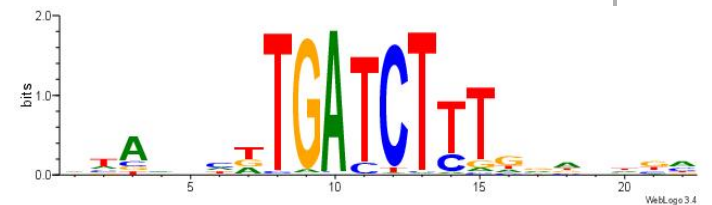
Motif ID: [UP00607](#)  
 Motif name: NR2E3  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 8  
 Similarity score: 0.0198394

Alignment:  
 DVDBHBCAAAGATCAHDHDTDD  
 -----AAAGATTT-----

Original motif  
 Consensus sequence: DVDBHBCAAAGATCAHDHDTDD



Reverse complement motif  
 Consensus sequence: DDADHHHTGATCTTTGBHVVDV



Motif ID: [UP00523](#)

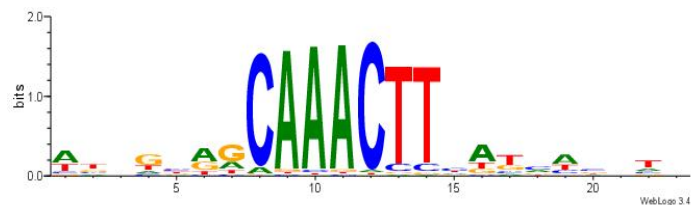
Motif name: FOXR1\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 8  
 Similarity score: 0.033006

**Alignment:**

WBHGBRGCAAACCTTHAKVHBHHD  
 -----AAATCTTT-----

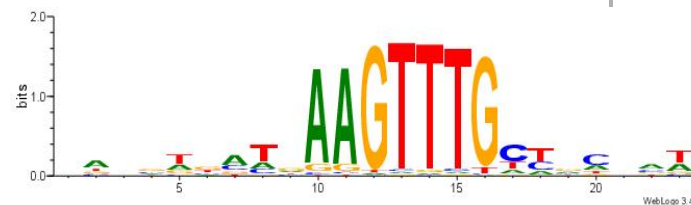
**Original motif**

Consensus sequence: WBHGBRGCAAACCTTHAKVHBHHD



**Reverse complement motif**

Consensus sequence: DHHBHVRTDAAGTTTGCKBCHVW




---

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: 9  
 Number of overlap: 8

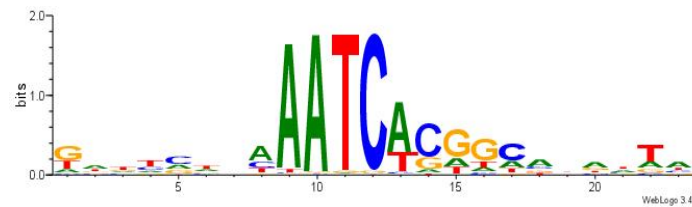
Similarity score: 0.0331884

Alignment:

HAHDDBGCCGTGATTTHDVHDDY  
-----AAAGATTT-----

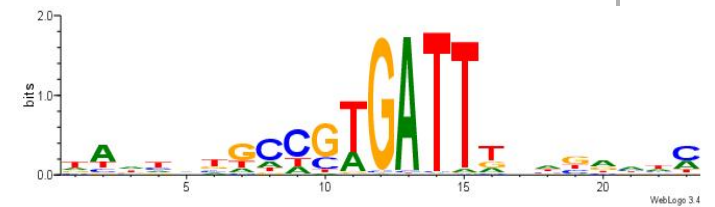
Original motif

Consensus sequence: KDDHVDDAAATCACGGCVDDHTH



Reverse complement motif

Consensus sequence: HAHDDBGCCGTGATTTHDVHDDY



Motif ID: [UP00609](#)  
Motif name: PAX3  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 7  
Number of overlap: 8  
Similarity score: 0.0367542

Alignment:

HBBHDVTAATCGATTADBHDDB  
-----AAAGATTT-----

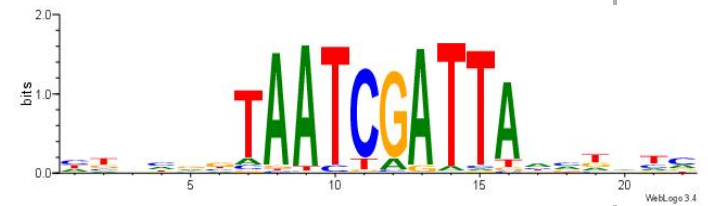
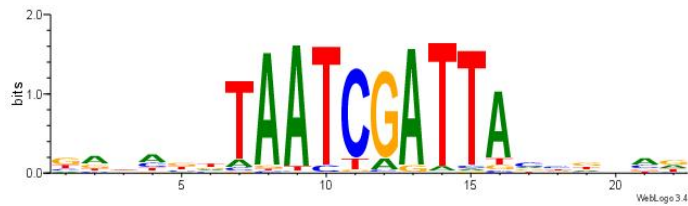
Original motif

Consensus sequence: BDDHBDTAATCGATTAVHDBVD

Reverse complement motif

Consensus sequence: HBBHDVTAATCGATTADBHDDB





**Dataset #: 2      Motif ID: 14      Motif name: Motif 14**

Original motif

Consensus sequence: AWAATAA



Reverse complement motif

Consensus sequence: TTATTTWT



### Best Matches for Motif ID 14 (Highest to Lowest)

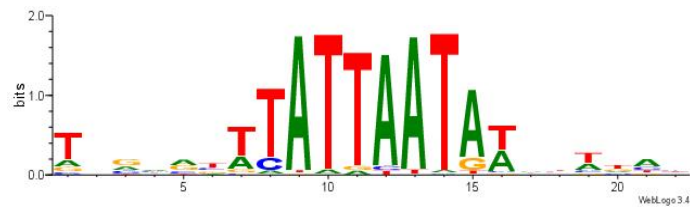
Motif ID:	<a href="#">UP00617</a>
Motif name:	POU4F3
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	8
Similarity score:	0

Alignment:

BHDWVHWTATTAATAAVBHVHA  
-----AWAAATAA-----

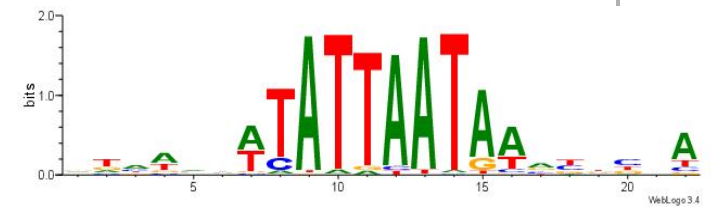
Original motif

Consensus sequence: THVHVBTTATTAATAWHBWDHB



Reverse complement motif

Consensus sequence: BHDWVHWTATTAATAAVBHVHA



Motif ID: [UP00627](#)  
Motif name: WT1\_H373Y\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 8  
Similarity score: 0.000449511

Alignment:

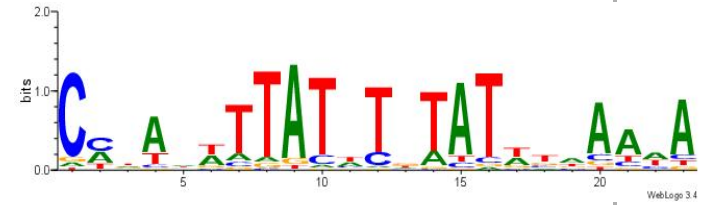
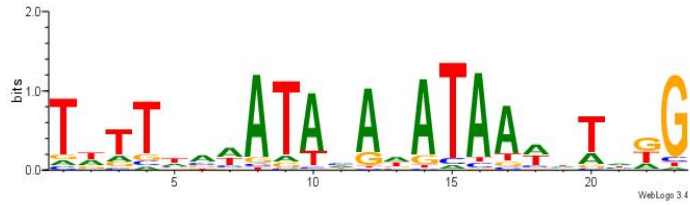
CYHAHWTTATD TDTATWBHAADA  
-----TTATTTWT-----

Original motif

Consensus sequence: TDTTHVWATAHADATAAWHHTKGG

Reverse complement motif

Consensus sequence: CYHAHWTTATD TDTATWBHAADA

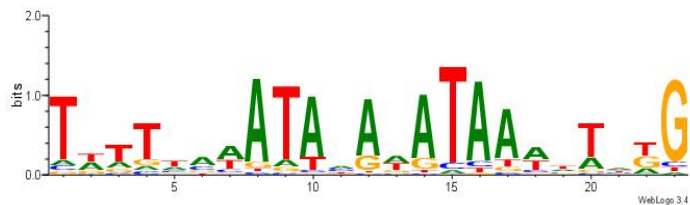


Motif ID: [UP00627](#)  
 Motif name: WT1\_R394L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 8  
 Similarity score: 0.000763656

Alignment:  
 CRHAHWTTATWTHTATWBHAAWA  
 -----TTATTTWT-----

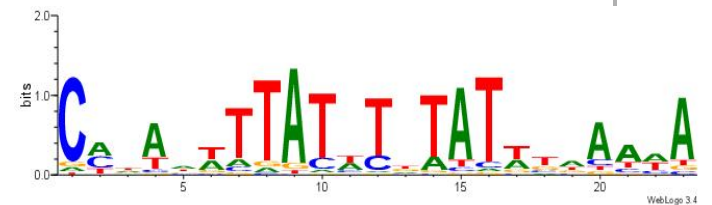
Original motif

Consensus sequence: TWTHVWATAHAWATAAWHTHKG



Reverse complement motif

Consensus sequence: CRHAHWTTATWTHTATWBHAAWA



Motif ID: [UP00589](#)

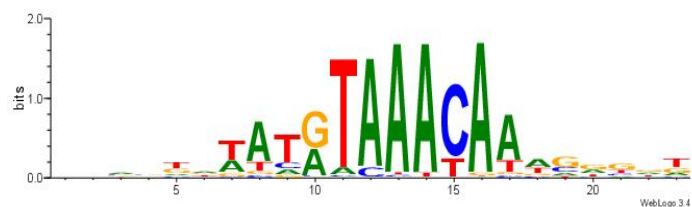
Motif name: FOXC1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 8  
 Similarity score: 0.00312951

**Alignment:**

BHVVDDWATRTAAACAAWSDBDD  
 -----AWAAATAA-----

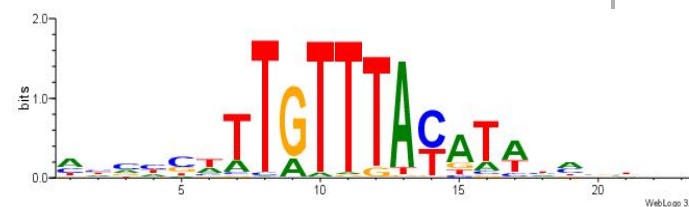
**Original motif**

Consensus sequence: BHVVDDWATRTAAACAAWSDBDD



**Reverse complement motif**

Consensus sequence: DHBHSWTTGTTTAMATWDDVBDB




---

Motif ID: [UP00627](#)  
 Motif name: WT1\_F392L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 8

Similarity score:

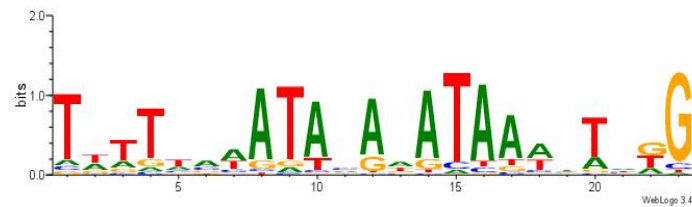
0.0065948

Alignment:

TWTHVWATAVADATAAWHTHKG  
-----AWAAATAA-----

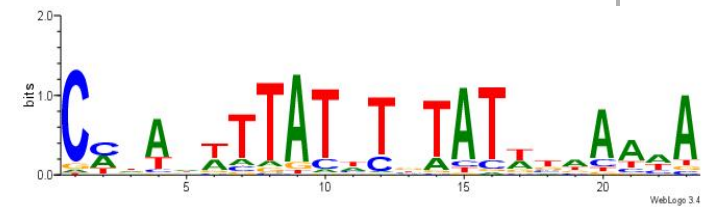
Original motif

Consensus sequence: TWTHVWATAVADATAAWHTHKG



Reverse complement motif

Consensus sequence: CYHAHWTTATDTVTATWBHAAWA



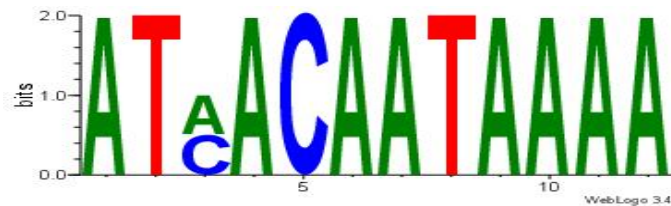
**Dataset #: 2**

**Motif ID: 15**

**Motif name: Motif 15**

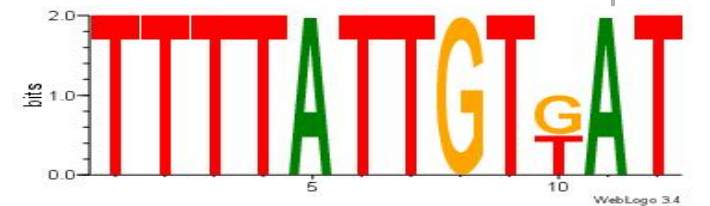
Original motif

Consensus sequence: ATMACAATAAAA



Reverse complement motif

Consensus sequence: TTTTATTGTAT



### Best Matches for Motif ID 15 (Highest to Lowest)

Motif ID:

[UP00597](#)

Motif name:

HOXD13\_S316C\_R2

Species:

Homo sapiens

Matching format of first motif:

Reverse Complement

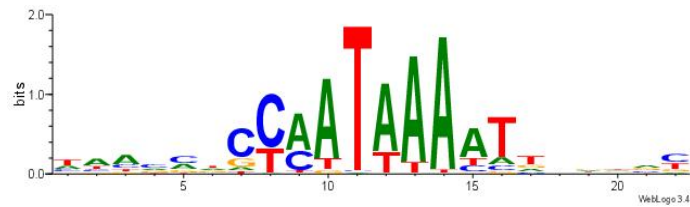
Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 12  
 Similarity score: 0

Alignment:

KBDHVDATTTTATYGGDVVTHH  
 -----TTTTATTGTAT----

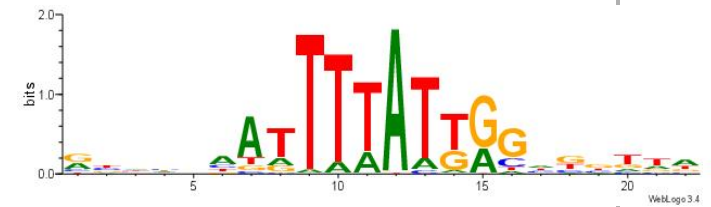
Original motif

Consensus sequence: HHAVVDCCMATAAAATDBDDVY



Reverse complement motif

Consensus sequence: KBDHVDATTTTATYGGDVVTHH



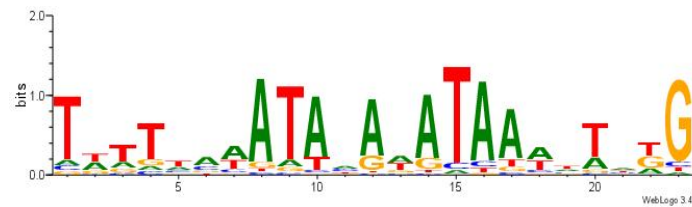
Motif ID: [UP00627](#)  
 Motif name: WT1\_R394L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 12  
 Similarity score: 0.00155138

Alignment:

CRHAHWTTATWTHTATWBHAAWA  
----TTTTATTGTYAT-----

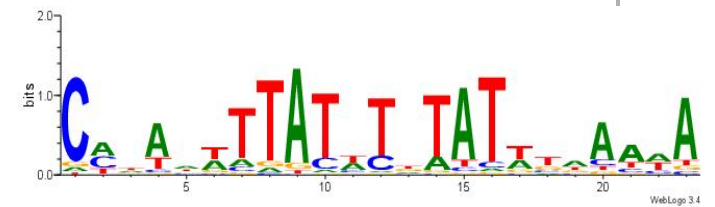
Original motif

Consensus sequence: TWTHVWATAHAWATAAWHCHKG



Reverse complement motif

Consensus sequence: CRHAHWTTATWTHTATWBHAAWA



Motif ID: [UP00627](#)  
Motif name: WT1\_H373Y\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 5  
Number of overlap: 12  
Similarity score: 0.00507302

Alignment:

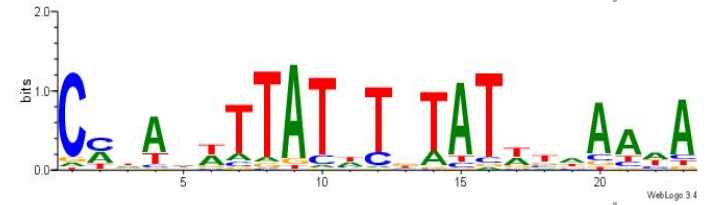
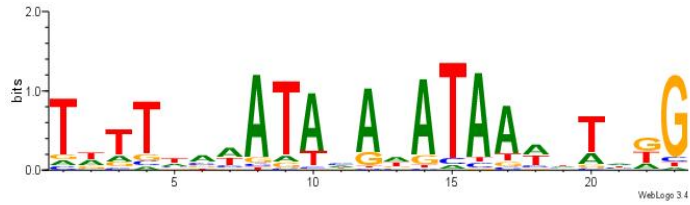
TDTTHVWATAHADATAAWHCHKG  
-----ATMACAATAAAA-----

Original motif

Consensus sequence: TDTTHVWATAHADATAAWHCHKG

Reverse complement motif

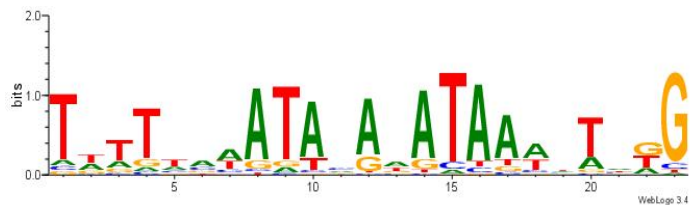
Consensus sequence: CYHAHWTTATDTDTATWBHAADA



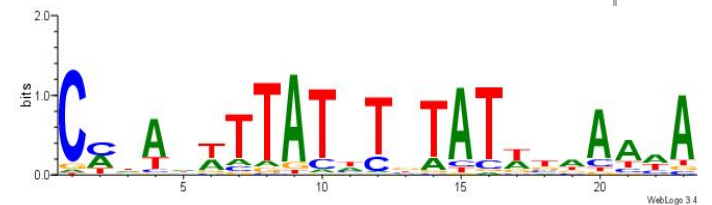
Motif ID: [UP00627](#)  
 Motif name: WT1\_F392L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 12  
 Similarity score: 0.00621945

Alignment:  
 CYHAHWTTATDVTATWBHAAWA  
 ----TTTTATTGTYAT-----

Original motif  
 Consensus sequence: TWTHVWATAVADATAAWHTHKG



Reverse complement motif  
 Consensus sequence: CYHAHWTTATDVTATWBHAAWA



Motif ID: [UP00627](#)



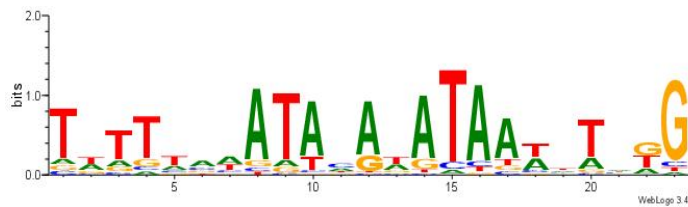
Motif name: WT1\_R394W\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 12  
 Similarity score: 0.010042

**Alignment:**

CYHAHWTTATWTDATWBHAAWA  
 ----TTTTATTGTYAT-----

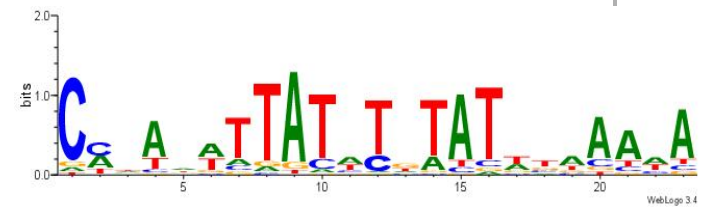
**Original motif**

Consensus sequence: TWTHVWATAHAWATAAWHHTKGG



**Reverse complement motif**

Consensus sequence: CYHAHWTTATWTDATWBHAAWA



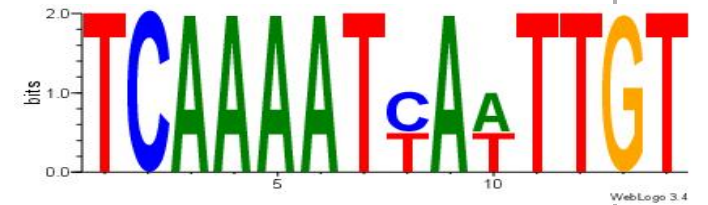
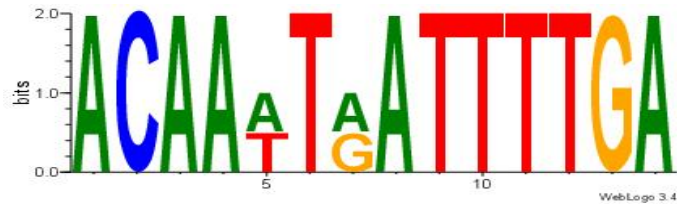
**Dataset #: 2      Motif ID: 16      Motif name: Motif 16**

**Original motif**

Consensus sequence: ACAAWTRATTTTGA

**Reverse complement motif**

Consensus sequence: TCAAAATKAWTTGT



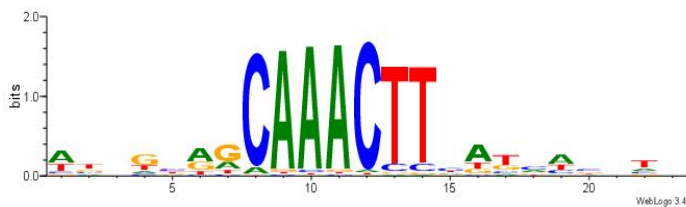
**Best Matches for Motif ID 16 (Highest to Lowest)**

Motif ID: [UP00523](#)  
 Motif name: FOXR1\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.0239714

Alignment:  
 DHHBHVRTDAAGTTTGCKBCHVW  
 ---ACAAWTRATTTTGA-----

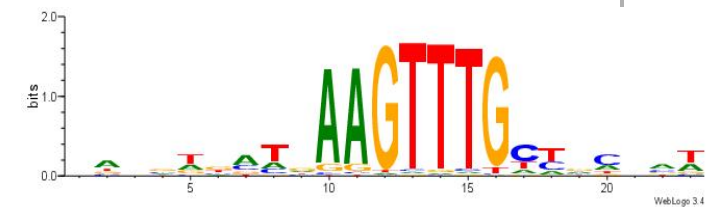
**Original motif**

Consensus sequence: WBHGBRGCAAACTTHAKVHBHHD



**Reverse complement motif**

Consensus sequence: DHHBHVRTDAAGTTTGCKBCHVW



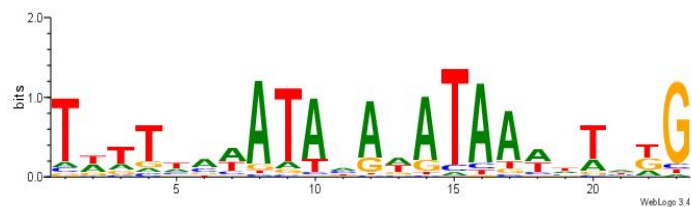
Motif ID: [UP00627](#)  
 Motif name: WT1\_R394L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0257984

**Alignment:**

CRHAHWTTATWTHTATWBHAAWA  
 -ACAAWTRATTTTGA-----

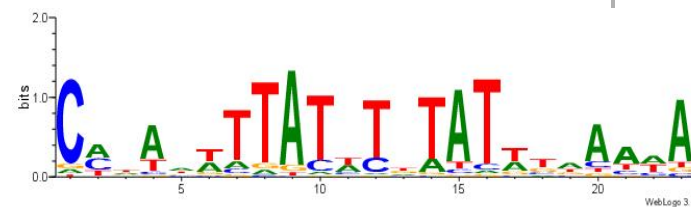
**Original motif**

Consensus sequence: TWTHVWATAHAWATAAWHCHKG



**Reverse complement motif**

Consensus sequence: CRHAHWTTATWTHTATWBHAAWA



Motif ID: [UP00619](#)  
 Motif name: PROP1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4

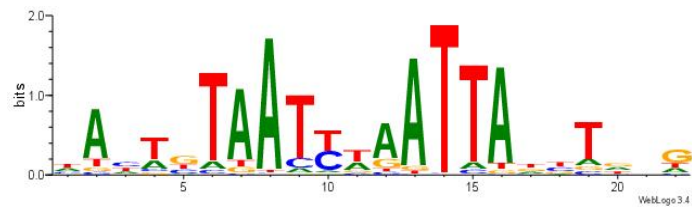
Number of overlap: 14  
Similarity score: 0.0270326

Alignment:

HAHTBTAATYWAATTADBTDVG  
---TCAAAATKAWTTGT-----

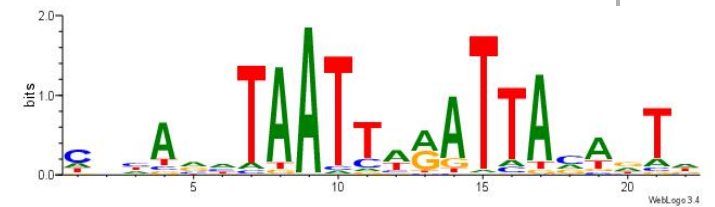
Original motif

Consensus sequence: HAHTBTAATYWAATTADBTDVG



Reverse complement motif

Consensus sequence: CBHAVDTAATTWMATTABADTH



Motif ID: [UP00626](#)  
Motif name: VSX2\_R200Q\_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: 14  
Similarity score: 0.0282702

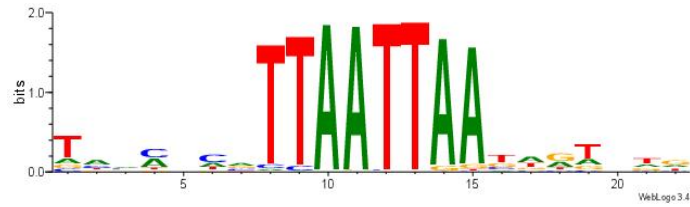
Alignment:

HDHAMDVTTAATTAABDDRBHA  
---ACAAWTRATTTTGA-----

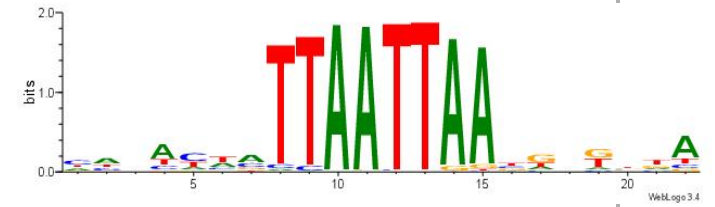
Original motif

Reverse complement motif

Consensus sequence: THVMDHVTTAATTAABDRTHDD



Consensus sequence: HDHAMDVTTAATTAABDDRHBHA



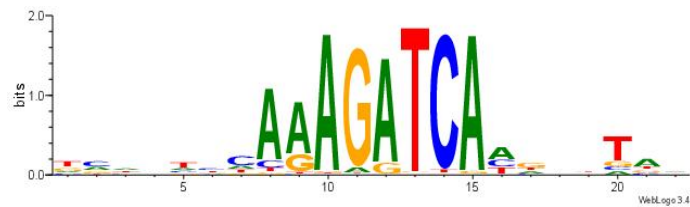
Motif ID: [UP00607](#)  
Motif name: NR2E3  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 7  
Number of overlap: 14  
Similarity score: 0.0288801

Alignment:

```
DDADHHHTGATCTTTGBHVDVD  
--ACAATRATTTTGA-----
```

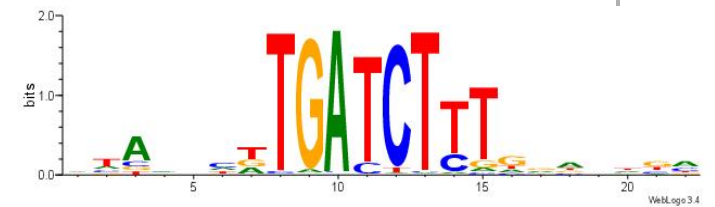
Original motif

Consensus sequence: DVDBHBCAAAGATCAHDHDTDD



Reverse complement motif

Consensus sequence: DDADHHHTGATCTTTGBHVDVD



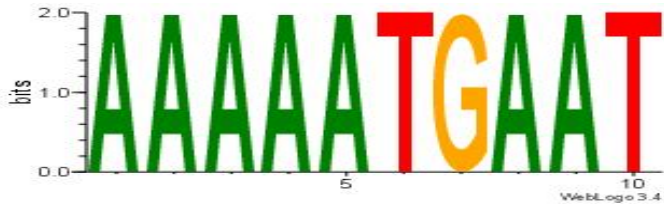
**Dataset #: 2**

**Motif ID: 17**

**Motif name: Motif 17**

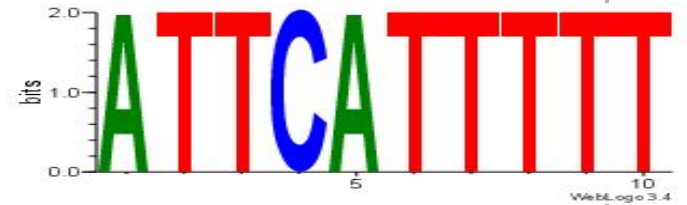
Original motif

Consensus sequence: AAAAAATGAAT



Reverse complement motif

Consensus sequence: ATTCATTTTT



### Best Matches for Motif ID 17 (Highest to Lowest)

Motif ID: [UP00607](#)  
Motif name: NR2E3  
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: 10  
Similarity score: 0.00963039

Alignment:

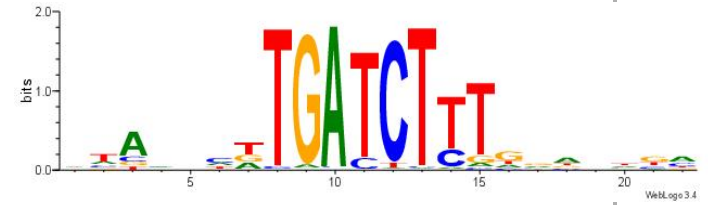
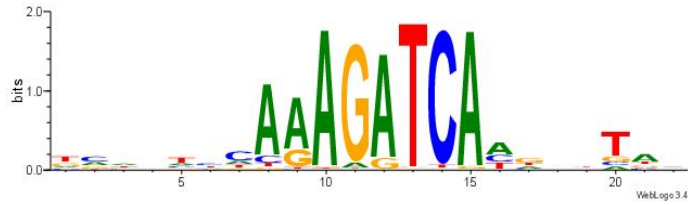
```
DVDBHBCAAAGATCAHDHDTDD  
-----AAAAATGAAT-----
```

Original motif

Consensus sequence: DVDBHBCAAAGATCAHDHDTDD

Reverse complement motif

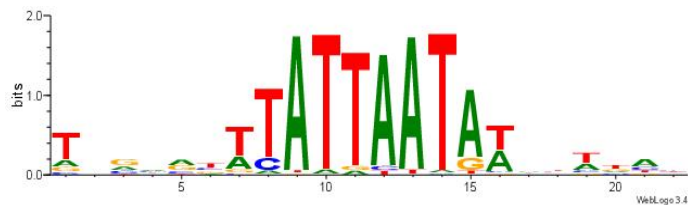
Consensus sequence: DDADHHHTGATCTTTGBHVDVD



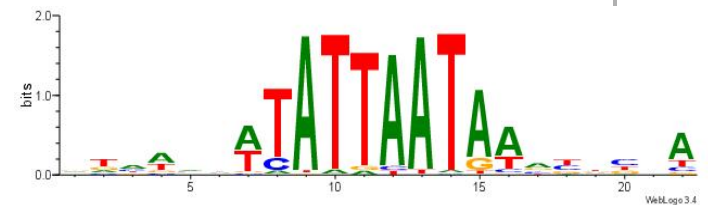
Motif ID: [UP00617](#)  
 Motif name: POU4F3  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 9  
 Number of overlap: 10  
 Similarity score: 0.0124223

Alignment:  
 THVHVBTTATTAATAWHBWDHB  
 -----ATTCATTTTT-----

Original motif  
 Consensus sequence: THVHVBTTATTAATAWHBWDHB



Reverse complement motif  
 Consensus sequence: BHDWVHWTATTAATAAVBHVHA



Motif ID: [UP00626](#)

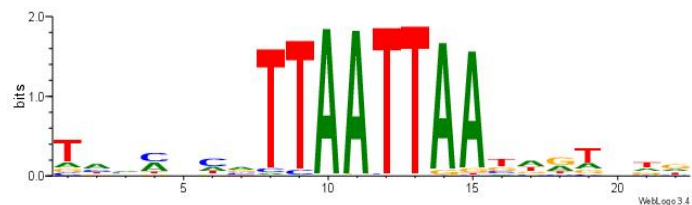
Motif name: VSX2\_R200Q\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 10  
 Similarity score: 0.0175439

**Alignment:**

HDHAMDVTTAATTAABDDRBHA  
 --AAAAATGAAT-----

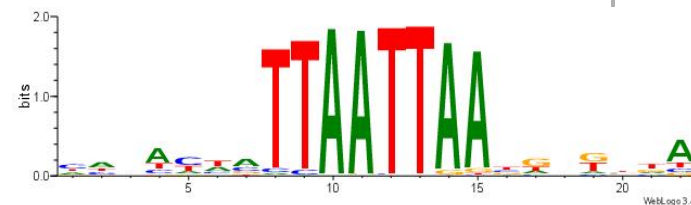
**Original motif**

Consensus sequence: THVMDHVTTAATTAABDRTHDD



**Reverse complement motif**

Consensus sequence: HDHAMDVTTAATTAABDDRBHA




---

Motif ID: [UP00603](#)  
 Motif name: MSX2\_R172H\_R2  
 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: 10



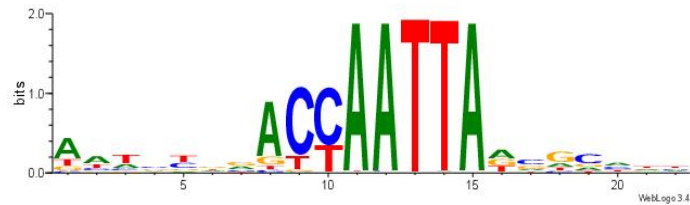
Similarity score: 0.0180636

Alignment:

```
HDHGCVDTAATTGGTVHMHHT  
-----ATTCATTTTT-----
```

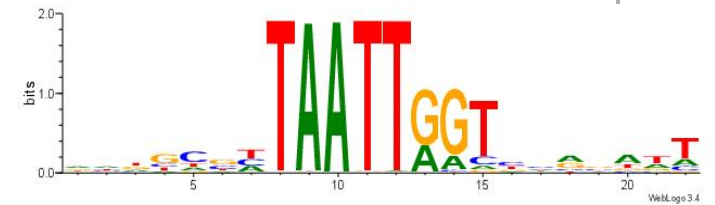
Original motif

Consensus sequence: AHHVYDVACCAATTADVGCHDH



Reverse complement motif

Consensus sequence: HDHGCVDTAATTGGTVHMHHT



Motif ID: [UP00401](#)  
Motif name: Sox4  
Species: Homo sapiens  
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: 0.0214899

Alignment:

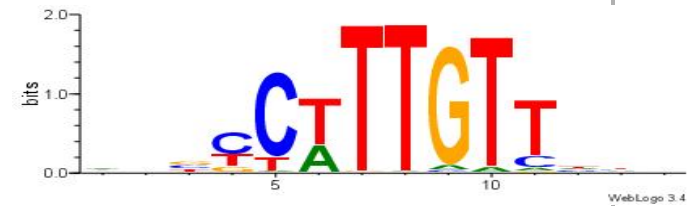
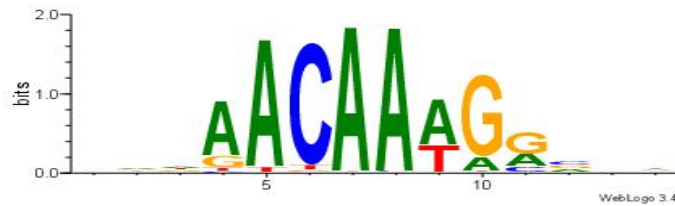
```
DDDAACAAWGRVVH  
---AAAATGAAT---
```

Original motif

Consensus sequence: DDDAACAAWGRVVH

Reverse complement motif

Consensus sequence: HBVMCWTTGTTDDD



**Dataset #: 2      Motif ID: 18      Motif name: Motif 18**

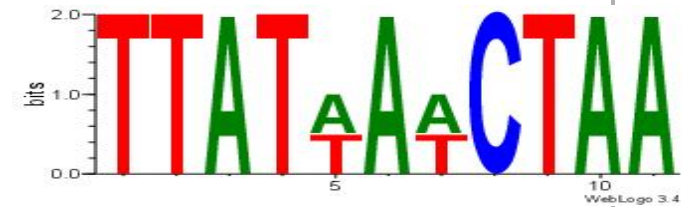
Original motif

Consensus sequence: TTAGWTWATAA



Reverse complement motif

Consensus sequence: TTATWAWCTAA



**Best Matches for Motif ID 18 (Highest to Lowest)**

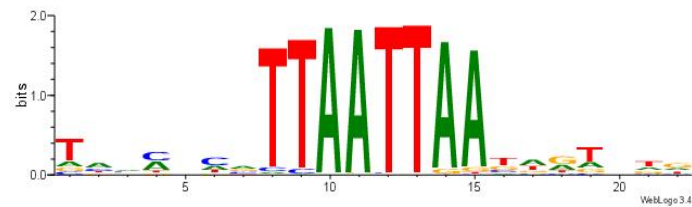
Motif ID:	<a href="#">UP00626</a>
Motif name:	VSX2_R200Q_R1
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	11
Similarity score:	0

Alignment:

THVMDHVTTAATTAABDRTHDD  
-----TTAGWTWATAA-----

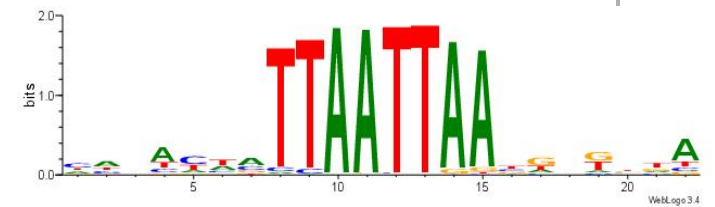
Original motif

Consensus sequence: THVMDHVTTAATTAABDRTHDD



Reverse complement motif

Consensus sequence: HDHAMDVTTAATTAABDDRHBHA



Motif ID: [UP00604](#)  
Motif name: NKX2-5  
Species: Homo sapiens  
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: 0.00381186

Alignment:

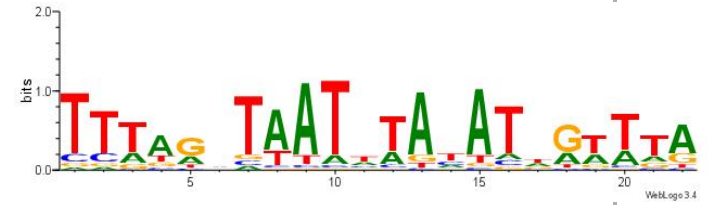
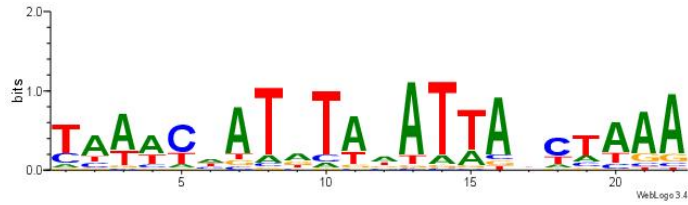
TTTAGHTAATDTADATHGWTTA  
-TTAGWTWATAA-----

Original motif

Consensus sequence: TAAWCHATDTADATTAHCTAAA

Reverse complement motif

Consensus sequence: TTTAGHTAATDTADATHGWTTA

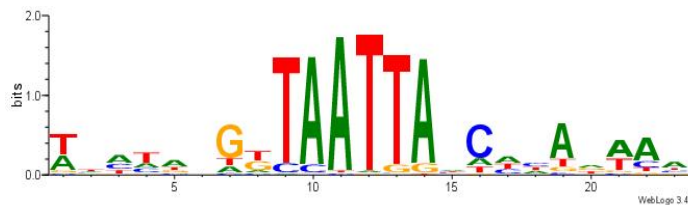


Motif ID: [UP00596](#)  
 Motif name: HOXC4\_R158L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 11  
 Similarity score: 0.00443857

Alignment:  
 HTWDTDHGHTAATTARCDDHHHW  
 ----TTAGWTWATAA-----

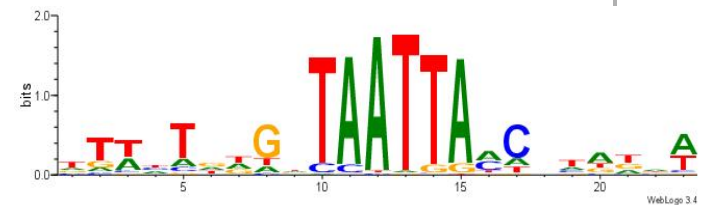
Original motif

Consensus sequence: WHHHDDGKTAATTAHCHHADWAH



Reverse complement motif

Consensus sequence: HTWDTDHGHTAATTARCDDHHHW



Motif ID: [UP00620](#)

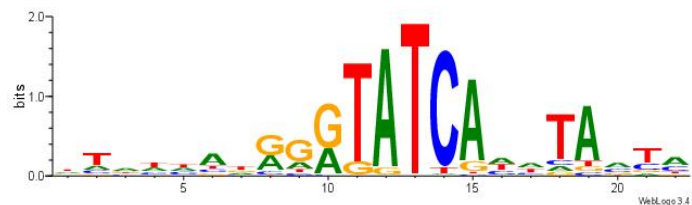
Motif name: SIX6\_H141N\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.00509375

**Alignment:**

YABTAHHTGATAMCMDTHHDAD  
 --TTAGWTWATAA-----

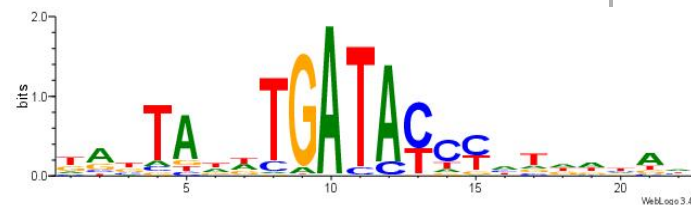
**Original motif**

Consensus sequence: DTDHHADRGRTATCAHHTAVTM



**Reverse complement motif**

Consensus sequence: YABTAHHTGATAMCMDTHHDAD




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Motif ID: [UP00619](#)  
 Motif name: PROP1\_R99Q\_R1  
 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

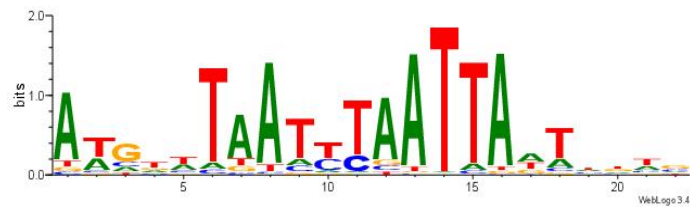
Similarity score: 0.00541381

Alignment:

VHDHADTAATTAMATTAWDCWT  
-----TTATWAWCTAA-----

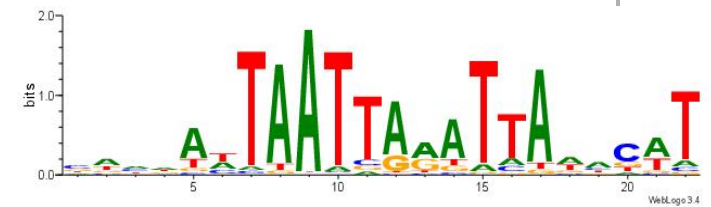
Original motif

Consensus sequence: AWGDWTAATYTAATTADTHDHV



Reverse complement motif

Consensus sequence: VHDHADTAATTAMATTAWDCWT



**Dataset #: 2 Motif ID: 19 Motif name: Motif 19**

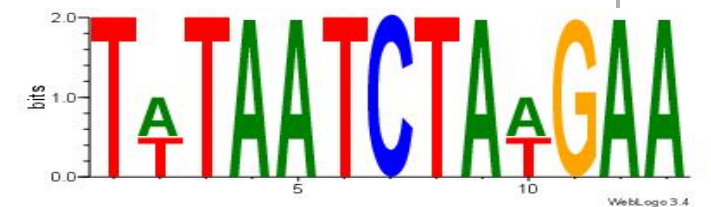
Original motif

Consensus sequence: TTCWTAGATTAWA



Reverse complement motif

Consensus sequence: TWTAACTAWGAA



**Best Matches for Motif ID 19 (Highest to Lowest)**

Motif ID: [UP00609](#)  
Motif name: PAX3  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement

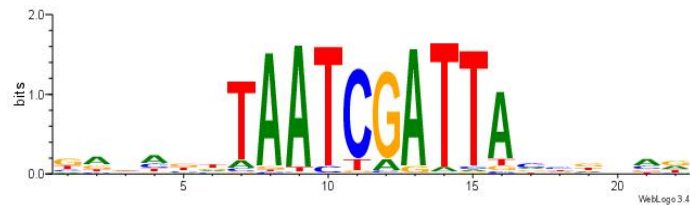
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 6  
Number of overlap: 13  
Similarity score: 0.00606198

Alignment:

HBBHDVTAATCGATTADBHDDB  
-----TWTAATCTAWGAA-----

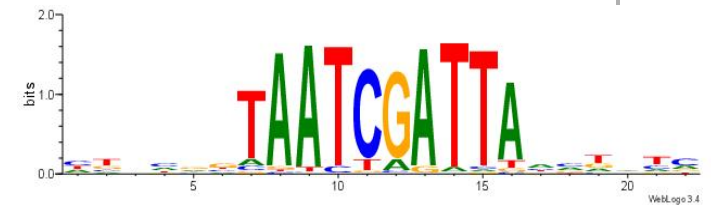
Original motif

Consensus sequence: BDDHBDTAATCGATTAVHDBVD



Reverse complement motif

Consensus sequence: HBBHDVTAATCGATTADBHDDB



---

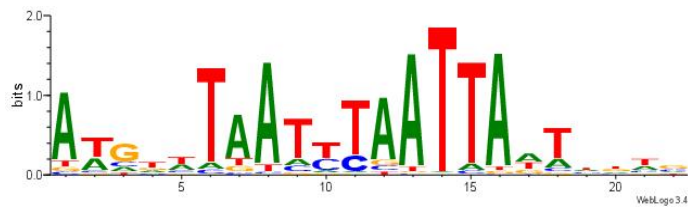
Motif ID: [UP00619](#)  
Motif name: PROP1\_R99Q\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 13  
Similarity score: 0.00857347

Alignment:

AWGDWTAATYTAATTADTHDHV  
---TWTAATCTAWGAA-----

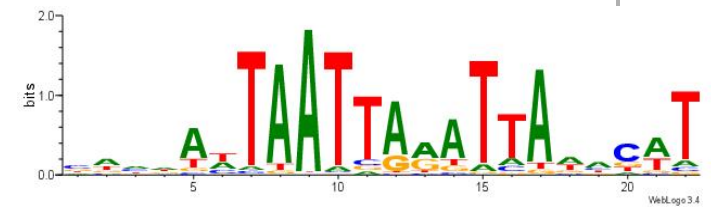
Original motif

Consensus sequence: AWGDWTAATYTAATTADTHDHV



Reverse complement motif

Consensus sequence: VHDHADTAATTAMATTAWDCWT



Motif ID: [UP00599](#)  
Motif name: KLF1\_R328H\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 6  
Number of overlap: 13  
Similarity score: 0.0131396

Alignment:

THMTWDTAATADATTATBHATTM  
----TWTAATCTAWGAA-----

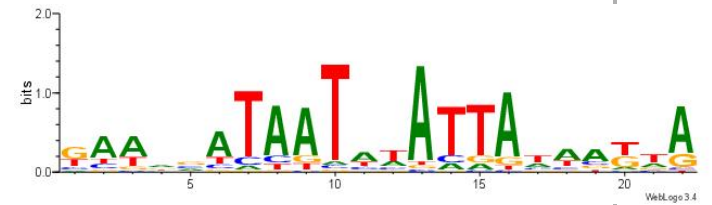
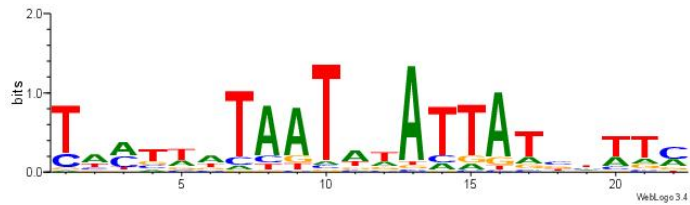
Original motif

Consensus sequence: THMTWDTAATADATTATBHATTM

Reverse complement motif

Consensus sequence: RAAHBATAATDTATTADWAYHA

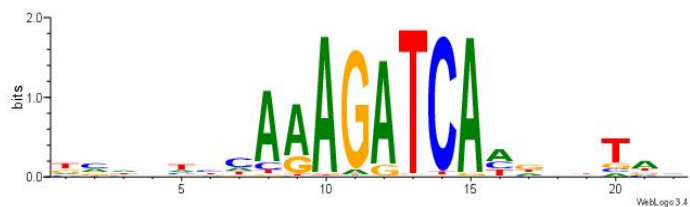




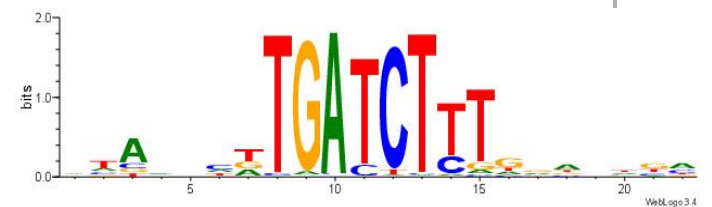
Motif ID: [UP00607](#)  
 Motif name: NR2E3  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 13  
 Similarity score: 0.0148096

Alignment:  
 DVDBHBCAAAGATCAHDHDTDD  
 ----TTCWTAGATTAWA-----

Original motif  
 Consensus sequence: DVDBHBCAAAGATCAHDHDTDD



Reverse complement motif  
 Consensus sequence: DDADHHHTGATCTTTGBHVDVD



Motif ID: [UP00615](#)

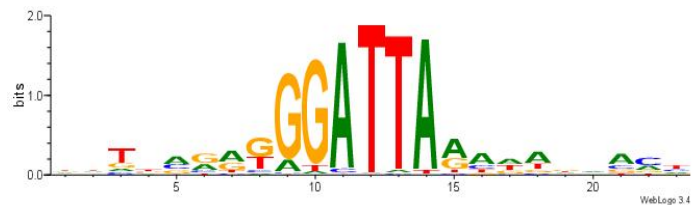
Motif name: PITX2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 13  
 Similarity score: 0.0156306

**Alignment:**

DDTBVRRKGGATTARADWDHAVH  
 ---TTCWTAGATTAWA-----

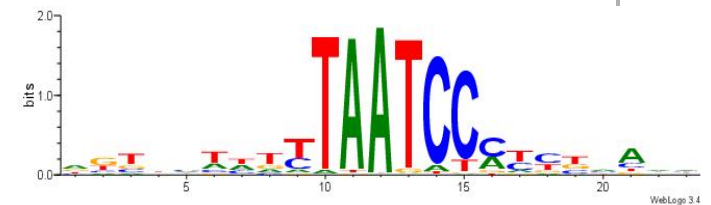
**Original motif**

Consensus sequence: DDTBVRRKGGATTARADWDHAVH



**Reverse complement motif**

Consensus sequence: HVTTHWDTKTAATCCYKMBVADD




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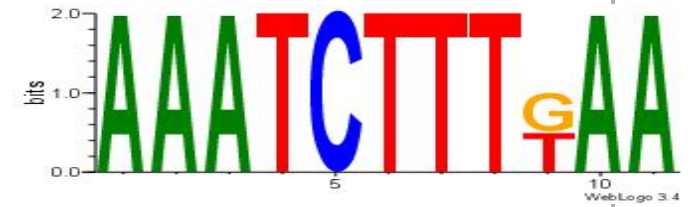
**Dataset #: 2      Motif ID: 20      Motif name: Motif 20**

**Original motif**

Consensus sequence: TTMAAAGATTT

**Reverse complement motif**

Consensus sequence: AAATCTTTYAA



### Best Matches for Motif ID 20 (Highest to Lowest)

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: 8  
 Number of overlap: 11  
 Similarity score: 0.00709542

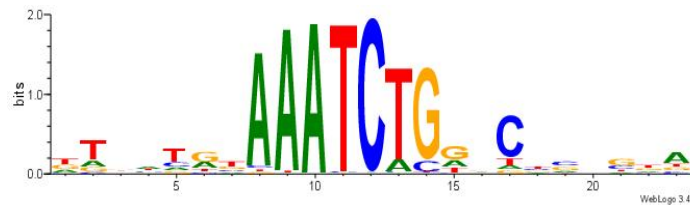
#### Alignment:

```

TDBHVVGVMCAGATTTVMAHHD
-----TTMAAAGATTT-----
  
```

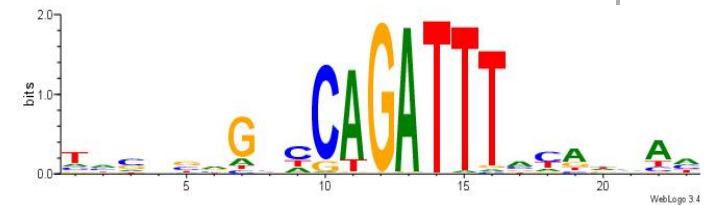
#### Original motif

Consensus sequence: DTDHTRBAAATCTGRVCBVBDA



#### Reverse complement motif

Consensus sequence: TDBHVVGVMCAGATTTVMAHHD



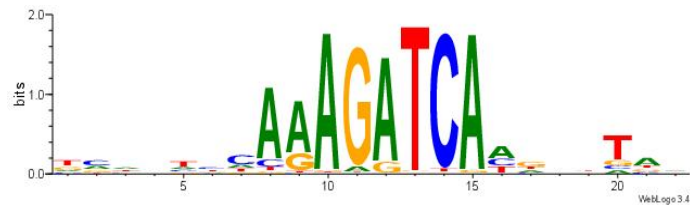
Motif ID: [UP00607](#)  
 Motif name: NR2E3  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.00890281

**Alignment:**

DVDBHBCAAAGATCAHDHDTDD  
 ----TTMAAAGATTT-----

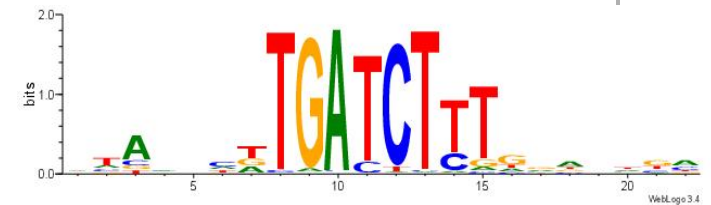
**Original motif**

Consensus sequence: DVDBHBCAAAGATCAHDHDTDD



**Reverse complement motif**

Consensus sequence: DDADHHHTGATCTTTGBHVDVD



Motif ID: [UP00609](#)  
 Motif name: PAX3  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6

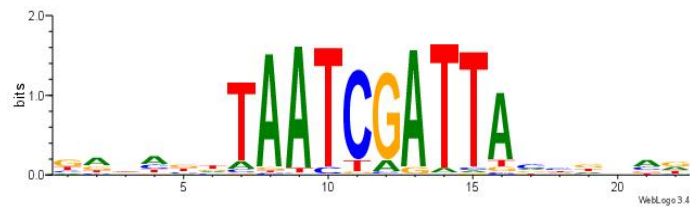
Number of overlap: 11  
Similarity score: 0.0138471

Alignment:

HBBHDVTAATCGATTADBHDDB  
-----AAATCTTTYAA-----

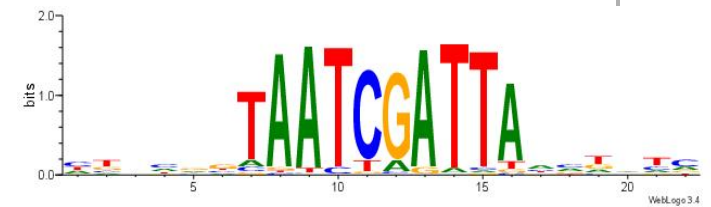
Original motif

Consensus sequence: BDDHBDTAATCGATTAVHDBVD



Reverse complement motif

Consensus sequence: HBBHDVTAATCGATTADBHDDB



---

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: Backward  
Position number: 8  
Number of overlap: 11  
Similarity score: 0.0230866

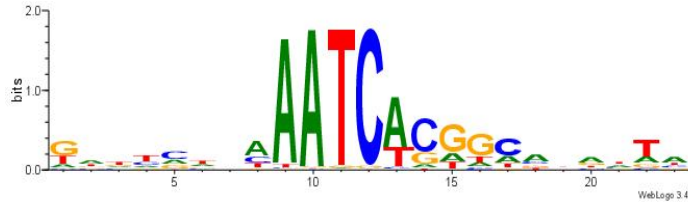
Alignment:

HAHDDBGCCGTGATTTTHDVHDDY  
-----TTMAAAGATTT-----

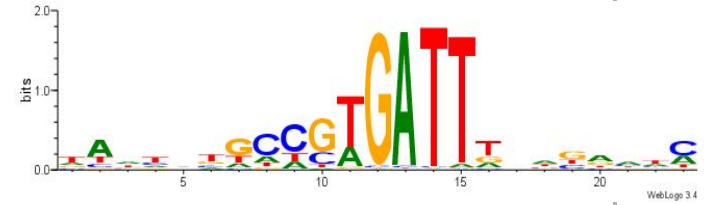
Original motif

Reverse complement motif

Consensus sequence: KDDHVDDAAATCACGGCVDDHHTH



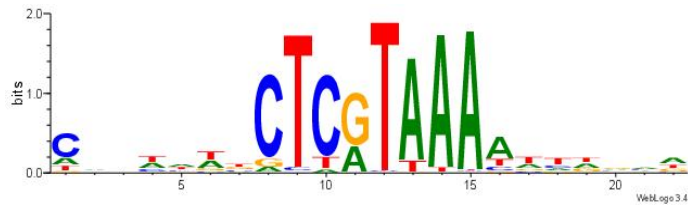
Consensus sequence: HAHDDBGCCGTGATTTHDVHDDY



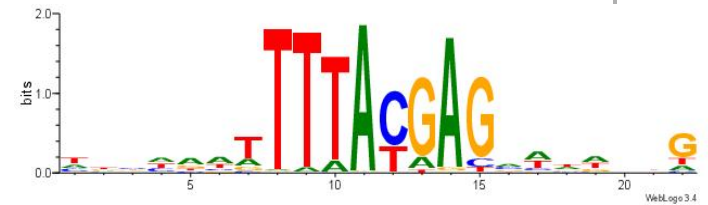
Motif ID: [UP00597](#)  
Motif name: HOXD13\_S316C\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 9  
Number of overlap: 11  
Similarity score: 0.0281874

Alignment:  
DHVDHDTTTTACGAGVWHHDDG  
-----TTMAAAGATT-----

Original motif  
Consensus sequence: CDDHHWBCTCGTAAADHDVHD



Reverse complement motif  
Consensus sequence: DHVDHDTTTTACGAGVWHHDDG



**Dataset #: 2**

**Motif ID: 21**

**Motif name: Motif 21**

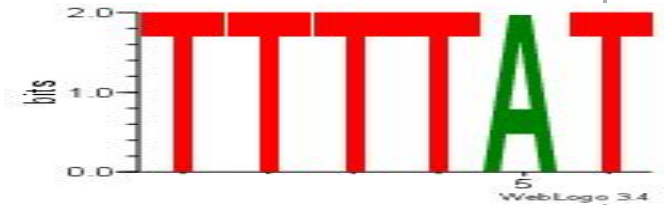
Original motif

Consensus sequence: ATAAAA



Reverse complement motif

Consensus sequence: TTTTAT



### Best Matches for Motif ID 21 (Highest to Lowest)

Motif ID: [UP00597](#)  
Motif name: HOXD13\_S316C\_R2  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 6  
Similarity score: 0

Alignment:

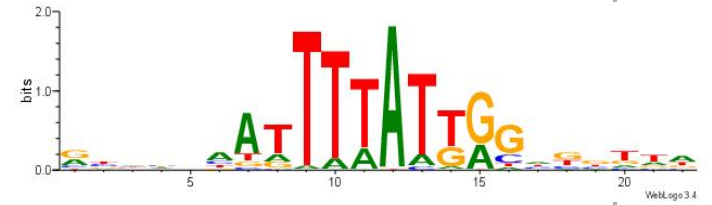
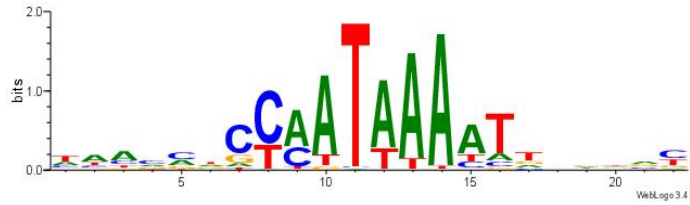
```
KBDHVDATTTTATYGGDVVTHH  
-----TTTAT-----
```

Original motif

Consensus sequence: HHAVVDCCMATAAAAATDBDDVY

Reverse complement motif

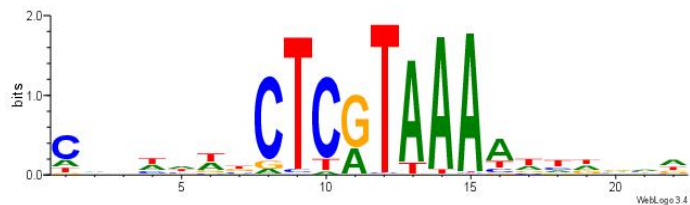
Consensus sequence: KBDHVDATTTTATYGGDVVTHH



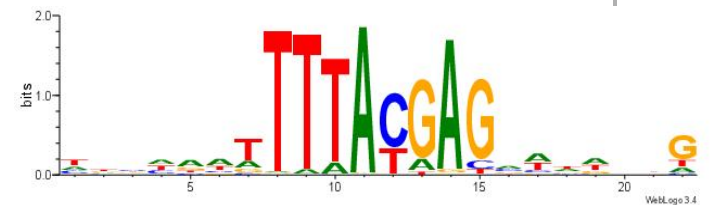
Motif ID: [UP00597](#)  
 Motif name: HOXD13\_S316C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 6  
 Similarity score: 0.0141667

Alignment:  
 CDDHHWBCTCGTAAAADHDVHD  
 -----ATAAAA-----

Original motif  
 Consensus sequence: CDDHHWBCTCGTAAAADHDVHD



Reverse complement motif  
 Consensus sequence: DHVDHTTTTACGAGVWHHDDG



Motif ID: [UP00589](#)



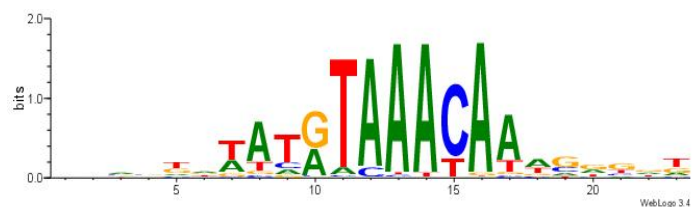
Motif name: FOXC1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 6  
 Similarity score: 0.0387267

**Alignment:**

BHVVDDWATRTAAACAAWSDBDD  
 -----ATAAAA-----

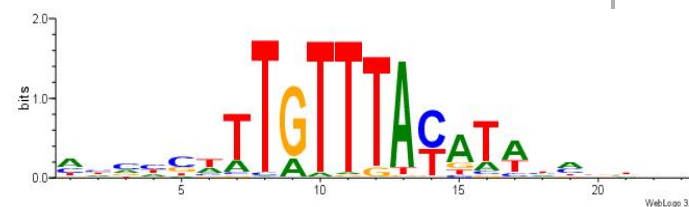
**Original motif**

Consensus sequence: BHVVDDWATRTAAACAAWSDBDD



**Reverse complement motif**

Consensus sequence: DHBHSWTTGTTTAMATWDDVBDB



Motif ID: [UP00627](#)  
 Motif name: WT1\_H373Y\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 14  
 Number of overlap: 6

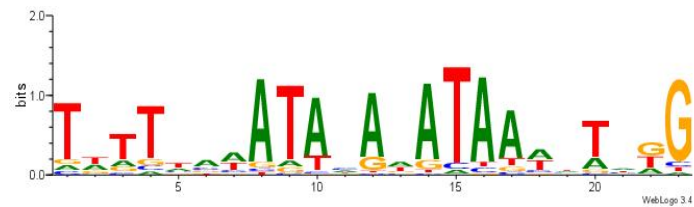
Similarity score: 0.0420082

Alignment:

CYHAHWTTATD TDTATWBHAADA  
----TTTTAT-----

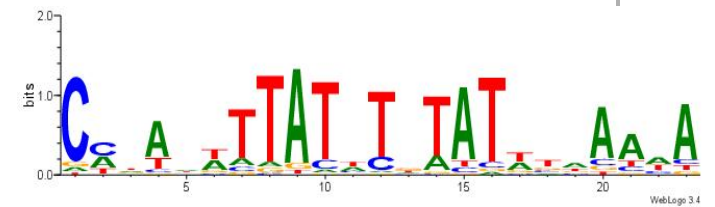
Original motif

Consensus sequence: TDTTHVWATAHADATAAWHCHKG



Reverse complement motif

Consensus sequence: CYHAHWTTATD TDTATWBHAADA



Motif ID: [UP00627](#)  
Motif name: WT1\_R394L\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 14  
Number of overlap: 6  
Similarity score: 0.0438866

Alignment:

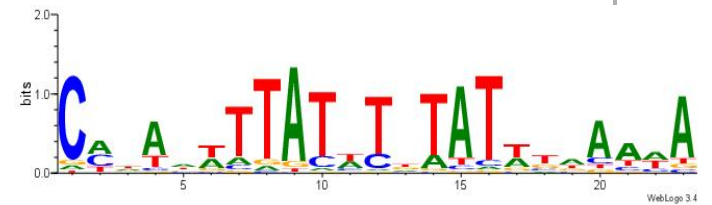
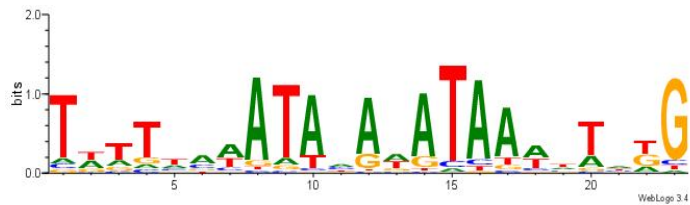
CRHAHWTTATW THTATWBHAAWA  
----TTTTAT-----

Original motif

Consensus sequence: TWTHVWATAHAWATAAWHCHKG

Reverse complement motif

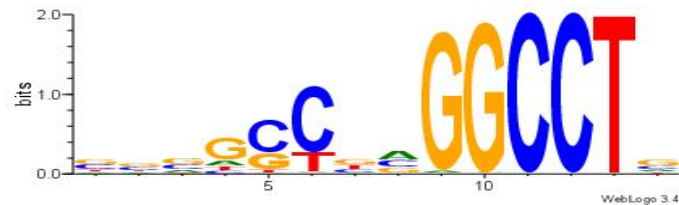
Consensus sequence: CRHAHWTTATW THTATWBHAAWA



**Dataset #: 3      Motif ID: 22      Motif name: Zfx**

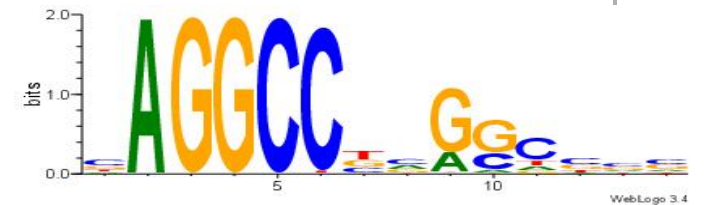
Original motif

Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif

Consensus sequence: VAGGCCBBGGCVBB



**Best Matches for Motif ID 22 (Highest to Lowest)**

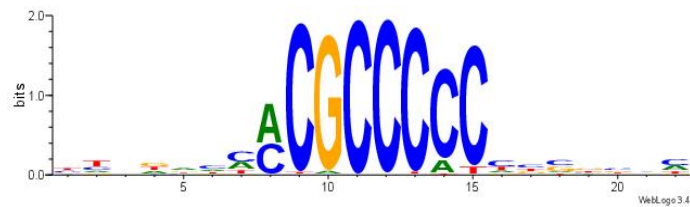
Motif ID:	<a href="#">UP00600</a>
Motif name:	KLF11
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	14
Similarity score:	0.0479447

Alignment:

BHHDDHMMCGCCCCCHBSBBVH  
-----VAGGCCBBGGCVBB--

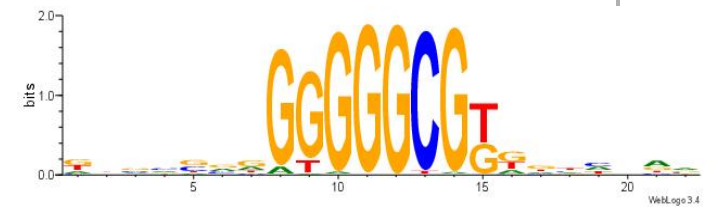
Original motif

Consensus sequence: BHHDDHMMCGCCCCCHBSBBVH



Reverse complement motif

Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV



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: 14  
Similarity score: 0.0513

Alignment:

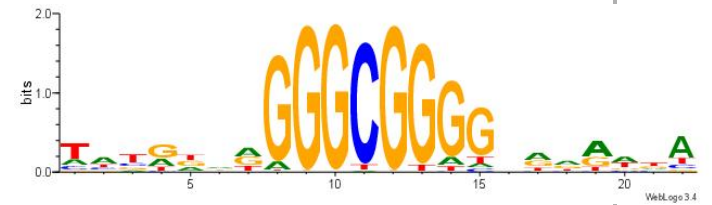
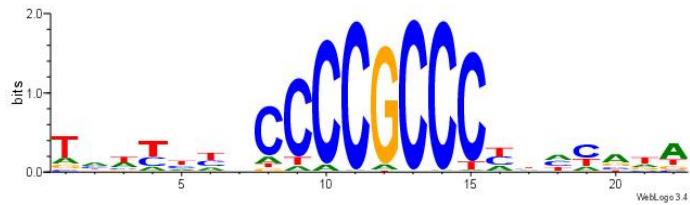
THWYHHDCCCCGCCCHHHYADA  
---BBVGCCBVGGCCTV-----

Original motif

Consensus sequence: THWYHHDCCCCGCCCHHHYADA

Reverse complement motif

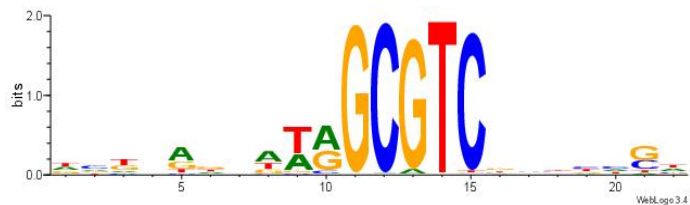
Consensus sequence: TDTKHHHGGGCGGGGDHHMWHA



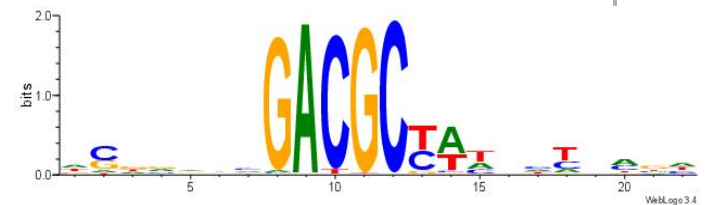
Motif ID: [UP00521](#)  
 Motif name: FOXN2\_primary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 14  
 Similarity score: 0.0532525

Alignment:  
 DVKHRDHDWRGCGTCBHHBHSH  
 -BBVGCCBVGCCCTV-----

Original motif  
 Consensus sequence: DVKHRDHDWRGCGTCBHHBHSH



Reverse complement motif  
 Consensus sequence: HSDBHHBGACGCKWDHHKHRVD



Motif ID: [UP00522](#)

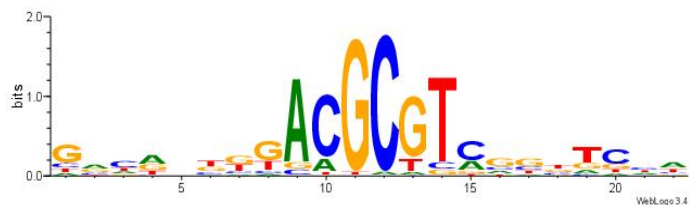
Motif name: FOXN4\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 14  
 Similarity score: 0.0534632

**Alignment:**

HDGAVBVGACGCGTCYVBDDBC  
 -BBVGCCBVGGCCTV-----

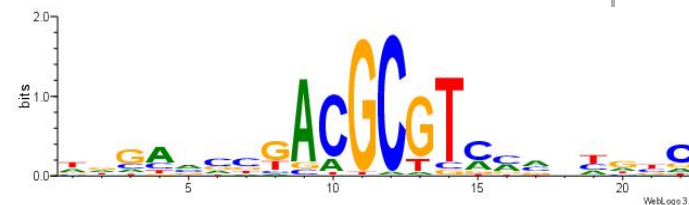
**Original motif**

Consensus sequence: GVHDBBK**GACGCGTC**VBBTCHH



**Reverse complement motif**

Consensus sequence: HDGAVBVGACGCGTCYVBDDBC




---

Motif ID: [UP00521](#)  
 Motif name: FOXN2\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 14

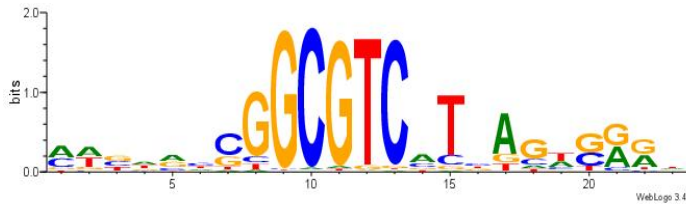
Similarity score: 0.0583839

Alignment:

MWBDVHCGGCGTCVTBAGWSRRD  
--BBVGCCBVGGCCTV-----

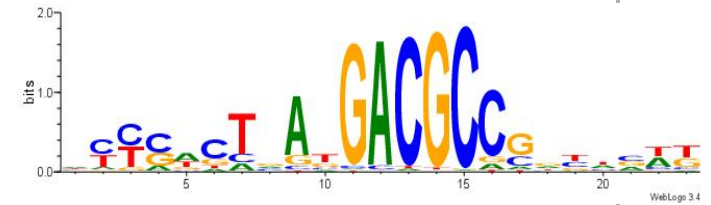
Original motif

Consensus sequence: MWBDVHCGGCGTCVTBAGWSRRD



Reverse complement motif

Consensus sequence: DMMSWCTBABGACGCCGDBDBWY



**Dataset #: 3      Motif ID: 23      Motif name: Egr1**

Original motif

Consensus sequence: HGCGTGGGCGK



Reverse complement motif

Consensus sequence: YCGCCCACGCH



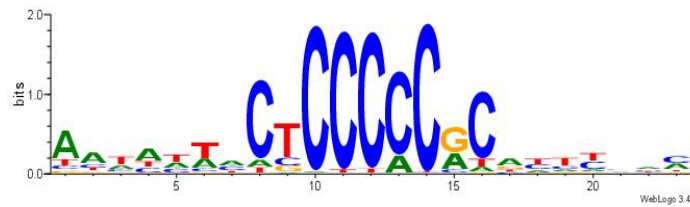
**Best Matches for Motif ID 23 (Highest to Lowest)**

Motif ID: [UP00627](#)  
Motif name: WT1\_REF\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement

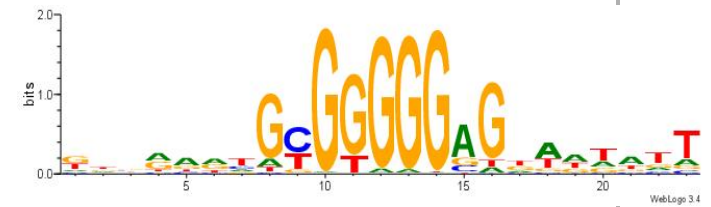
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0

Alignment:  
 AAHAHWHCTCCCCRCDDHHYVHM  
 -----YCGCCACGCH-----

Original motif  
 Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



Reverse complement motif  
 Consensus sequence: RHMHHDDGMGGGGGAGHWHHTT




---

Motif ID: [UP00627](#)  
 Motif name: WT1\_R366L\_R1  
 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: 11  
 Similarity score: 0.00681456

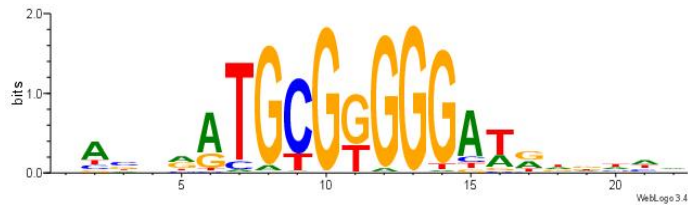
Alignment:



VABVRATGCGKGGGATRDDHHH  
-----HCGGTGGGCGK-----

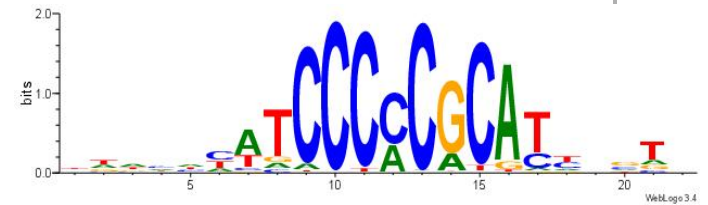
Original motif

Consensus sequence: VABVRATGCGKGGGATRDDHHH



Reverse complement motif

Consensus sequence: HHHHDMATCCCYCGCATKVBT



Motif ID: [UP00627](#)  
Motif name: WT1\_R366C\_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: 0.0070197

Alignment:

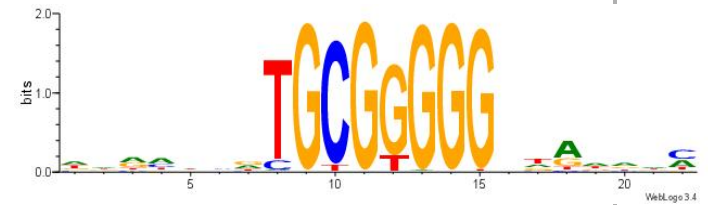
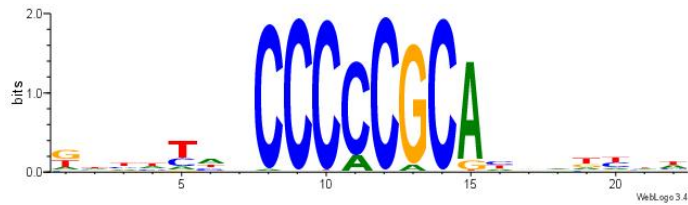
KHHHTHHCCCCCGCAHDHDHHH  
----YCGCCACGCH-----

Original motif

Consensus sequence: KHHHTHHCCCCCGCAHDHDHHH

Reverse complement motif

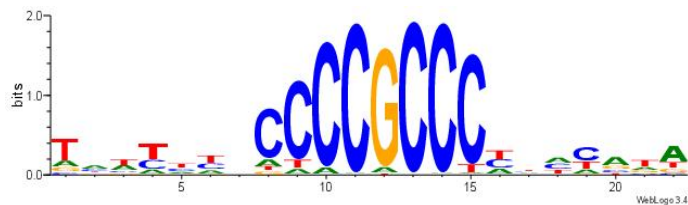
Consensus sequence: HHHHHDHTGCGGGGGHHAHHHY



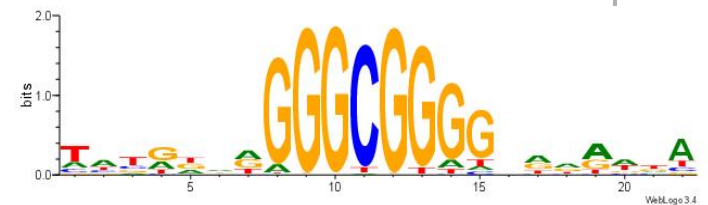
Motif ID: [UP00587](#)  
 Motif name: EGR2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 11  
 Similarity score: 0.0126311

Alignment:  
 TDTKHHHGGGCGGGGDHMMWHA  
 --HGCGTGGGCGK-----

Original motif  
 Consensus sequence: THWYHHDCCCCGCCCHHHYADA



Reverse complement motif  
 Consensus sequence: TDTKHHHGGGCGGGGDHMMWHA



Motif ID: [UP00600](#)

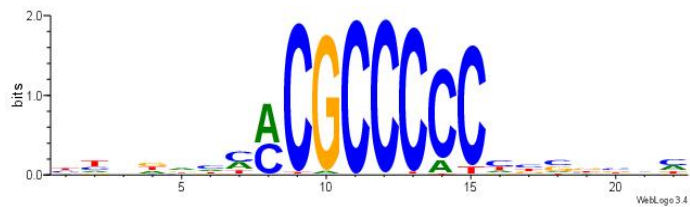
Motif name: KLF11  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.0135196

Alignment:

DBBBSBDGGGGGCGYRDDHHHV  
 ----HGCGTGGGCGK-----

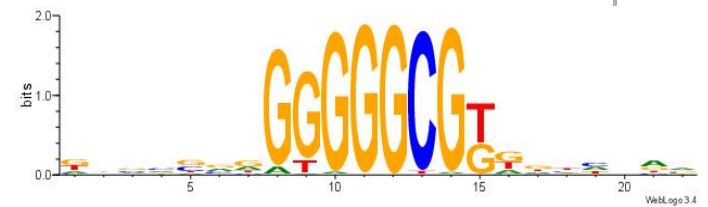
Original motif

Consensus sequence: BHHDDHMMCGCCCCCHBSBBVH



Reverse complement motif

Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV



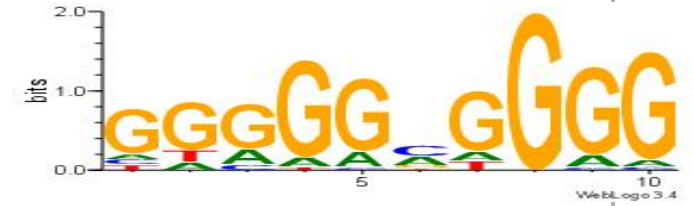
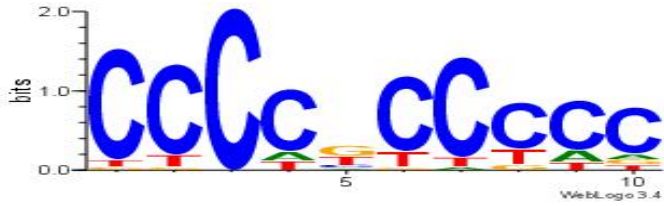
**Dataset #: 3      Motif ID: 24      Motif name: SP1**

Original motif

Consensus sequence: CCCCKCCCCC

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

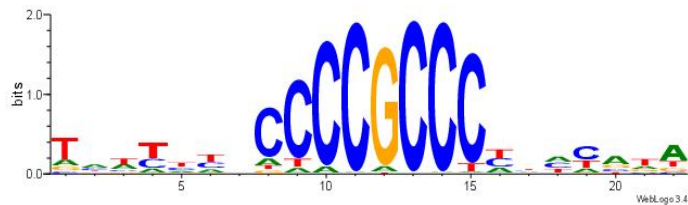
#### Alignment:

```

THWYHHDCCCCGCCCHHHYADA
-----CCCCKCCCC-----
  
```

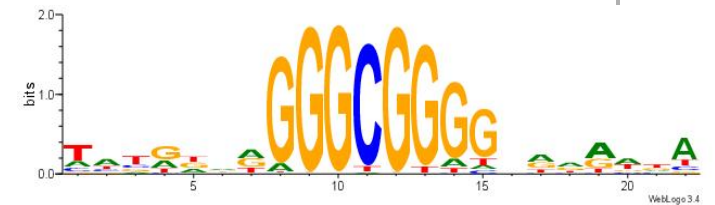
#### Original motif

Consensus sequence: THWYHHDCCCCGCCCHHHYADA



#### Reverse complement motif

Consensus sequence: TDTKHHHGGGCGGGGDHHMWHA



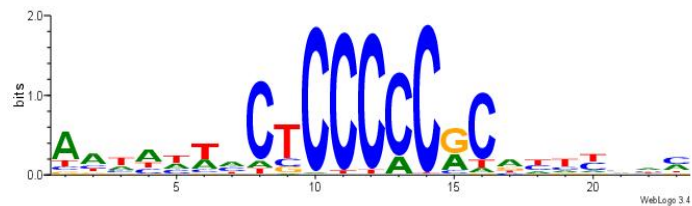
Motif ID: [UP00627](#)  
 Motif name: WT1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.0153751

Alignment:

AAHAHWHCTCCCCRCDDHHYVHM  
 -----CCCKCCCC-----

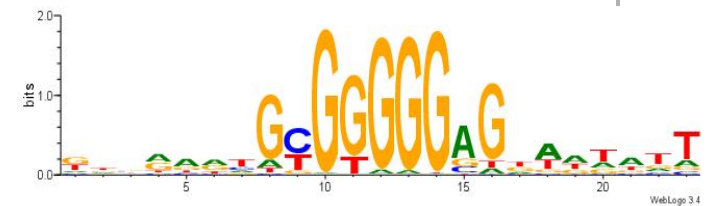
Original motif

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



Reverse complement motif

Consensus sequence: RHVMHHDGMGGGGGAGHWHHTHT



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: Forward  
 Position number: 9

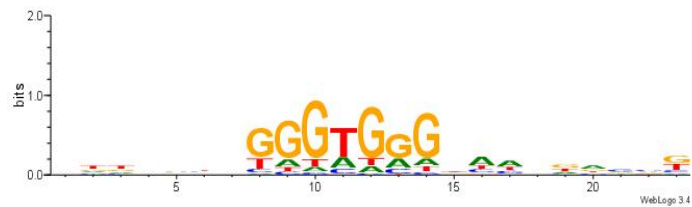
Number of overlap: 10  
Similarity score: 0.0162022

Alignment:

YVVDHDDHHCCCACCCCHHDDDDD  
-----CCCCKCCCC-----

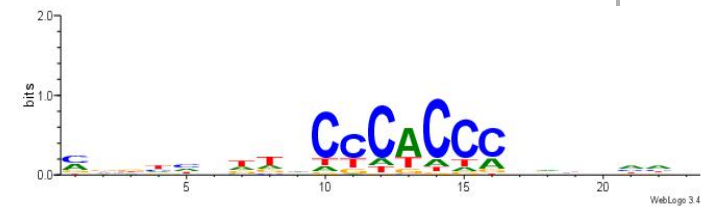
Original motif

Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



Reverse complement motif

Consensus sequence: YVVDHDDHHCCCACCCCHHDDDDD



Motif ID: [UP00600](#)  
Motif name: KLF11  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 10  
Similarity score: 0.0178026

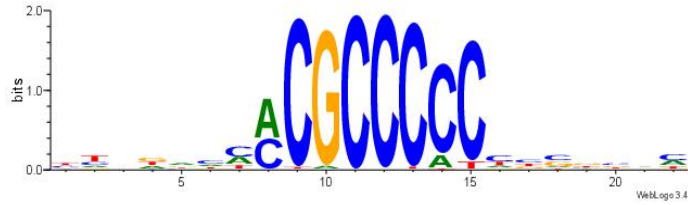
Alignment:

DBBBSBDGGGGGCGYRDDHHHV  
GGGGGYGGGG-----

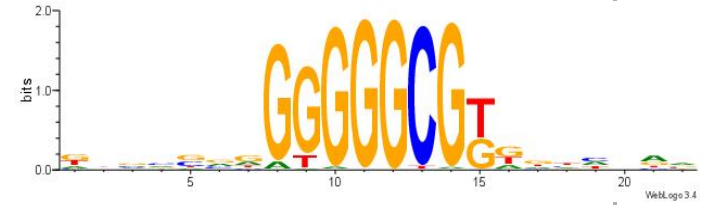
Original motif

Reverse complement motif

Consensus sequence: BHHDDHMMCGCCCCCHBSBBVH



Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV



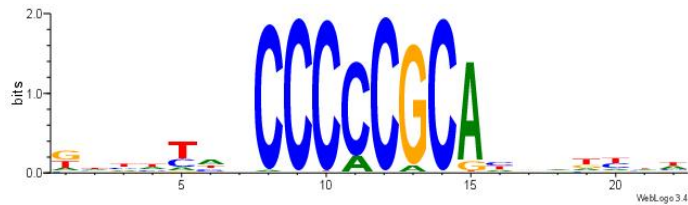
Motif ID: [UP00627](#)  
Motif name: WT1\_R366C\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 9  
Number of overlap: 10  
Similarity score: 0.0274038

Alignment:

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

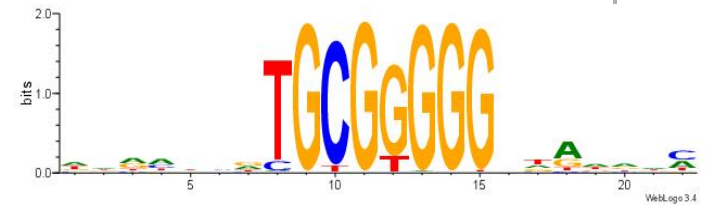
Original motif

Consensus sequence: KHHHTHHCCCCGCAHDHDH



Reverse complement motif

Consensus sequence: HHHDHHD TGCGGGGGHHAHHY



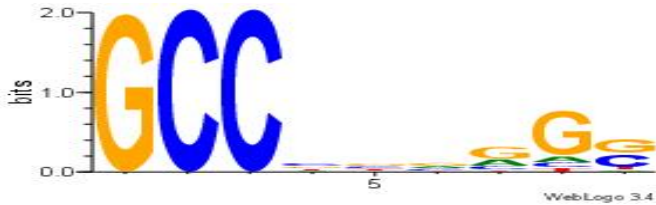
**Dataset #: 3**

**Motif ID: 25**

**Motif name: TFAP2A**

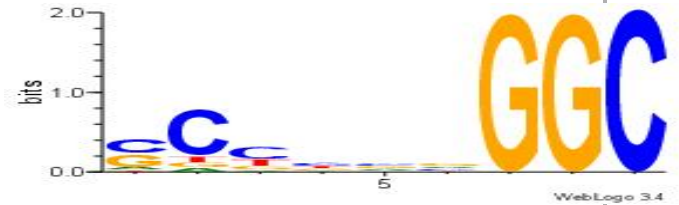
Original motif

Consensus sequence: GCCBBVRGS



Reverse complement motif

Consensus sequence: SCMVBBGGC



### Best Matches for Motif ID 25 (Highest to Lowest)

Motif ID:	<a href="#">UP00521</a>
Motif name:	FOXN2_secondary
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	14
Number of overlap:	9
Similarity score:	0.0115283

Alignment:

```
MWBDVHCGGCGTCVTBAGWSRRD  
-SCMVBBGGC-----
```

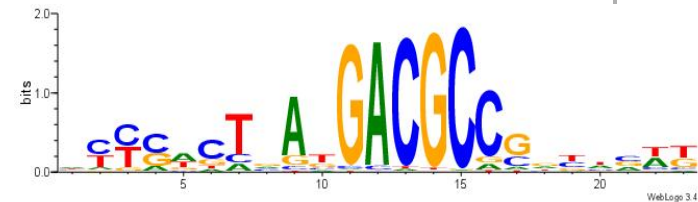
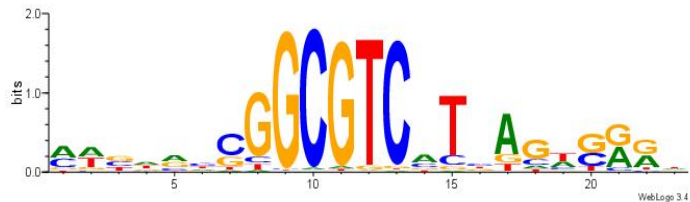
Original motif

Consensus sequence: MWBDVHCGGCGTCVTBAGWSRRD

Reverse complement motif

Consensus sequence: DMMSWCTBAGACGCCGDBDBW

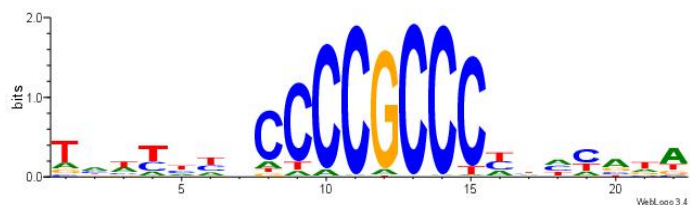




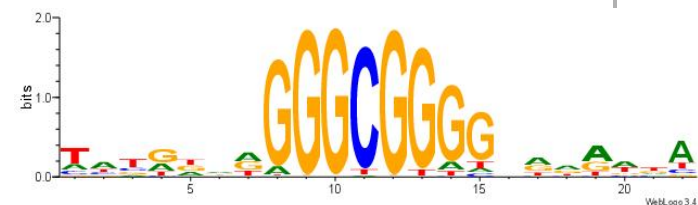
Motif ID: [UP00587](#)  
 Motif name: EGR2  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 9  
 Similarity score: 0.0158432

Alignment:  
 TDTKHHHGGGCGGGGDHMMWHA  
 --SCMVBBGGC-----

Original motif  
 Consensus sequence: THWYHHDCCCCGCCCHHHYADA



Reverse complement motif  
 Consensus sequence: TDTKHHHGGGCGGGGDHMMWHA



Motif ID: [UP00523](#)

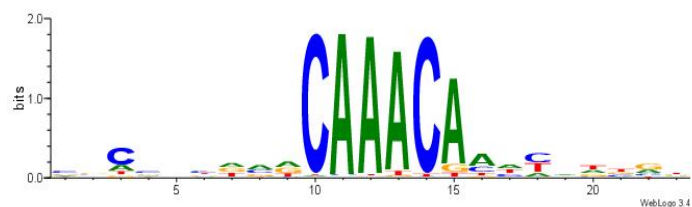
Motif name: FOXR1\_primary  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 14  
 Number of overlap: 9  
 Similarity score: 0.0171317

**Alignment:**

VVCVHBDVDCAAACAAHYVDBVD  
 -SCMVBBGGC-----

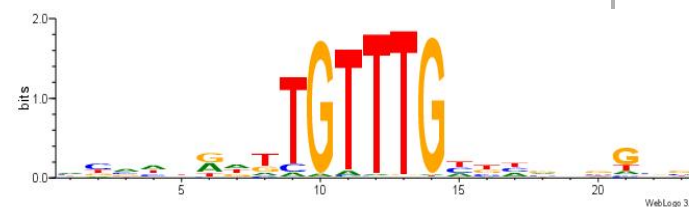
**Original motif**

Consensus sequence: VVCVHBDVDCAAACAAHYVDBVD



**Reverse complement motif**

Consensus sequence: DVVDBKHHTTGTTTGDBDBHVGWV




---

Motif ID: [UP00600](#)  
 Motif name: KLF11  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 13  
 Number of overlap: 9

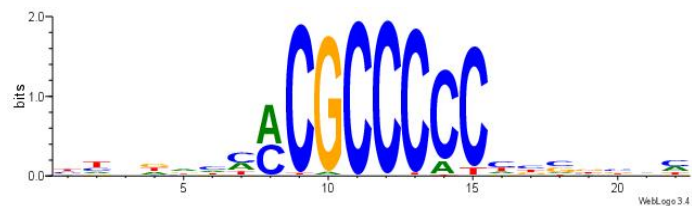
Similarity score: 0.0181013

Alignment:

BHHDDHMMCGCCCCCHBSBBVH  
-----GCCBBVRGS-

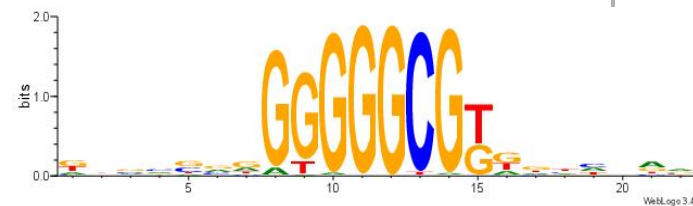
Original motif

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: 2  
Number of overlap: 9  
Similarity score: 0.0214094

Alignment:

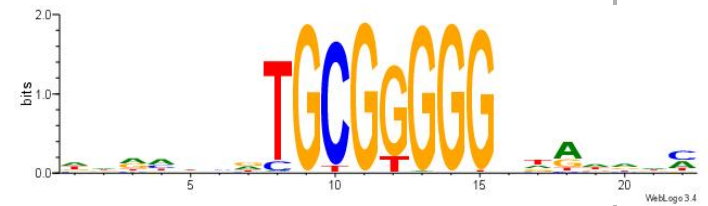
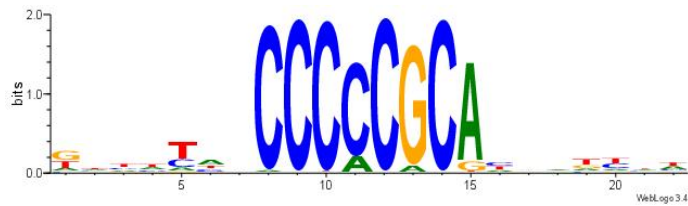
HHHDHHD TGCGGGGGHHAHHHY  
-SCMVBBGGC-----

Original motif

Consensus sequence: KHHHTHCCCCGCAHDHDH

Reverse complement motif

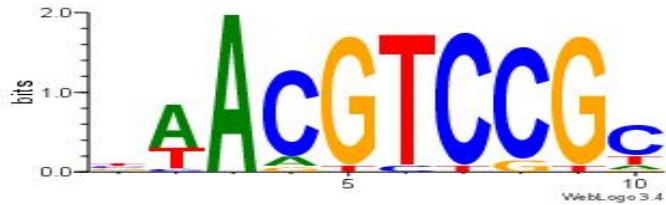
Consensus sequence: HHHDHHD TGCGGGGGHHAHHHY



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

Original motif

Consensus sequence: BAACGTCCGC



Reverse complement motif

Consensus sequence: GCGGACGTTT



### Best Matches for Motif ID 26 (Highest to Lowest)

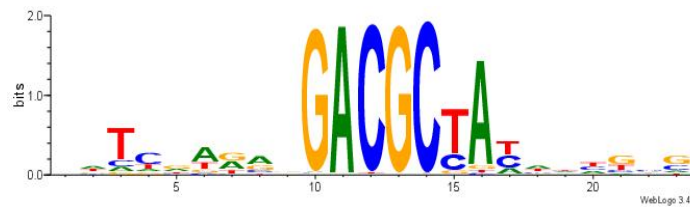
Motif ID:	<a href="#">UP00522</a>
Motif name:	FOXN4_primary
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	10
Similarity score:	0.007999

Alignment:

SDYHHHMTAGCGTCBBMTHGADH  
-----BAACGTCCGC-----

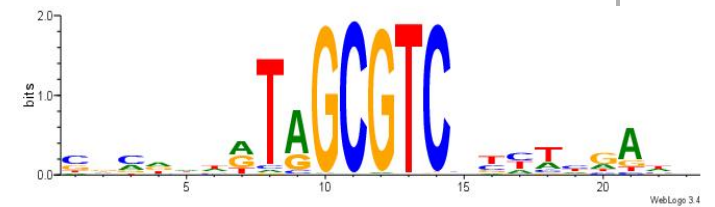
Original motif

Consensus sequence: HDTCDARVBGACGCTAYHHHKHS



Reverse complement motif

Consensus sequence: SDYHHHMTAGCGTCBBMTHGADH



Motif ID: [UP00600](#)  
Motif name: KLF11  
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: 10  
Similarity score: 0.0100757

Alignment:

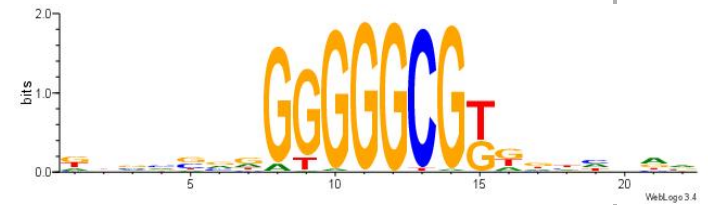
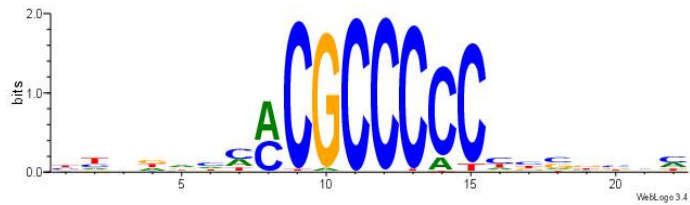
BHDDHMMCGCCCCCHBSBBVH  
-----BAACGTCCGC-----

Original motif

Consensus sequence: BHDDHMMCGCCCCCHBSBBVH

Reverse complement motif

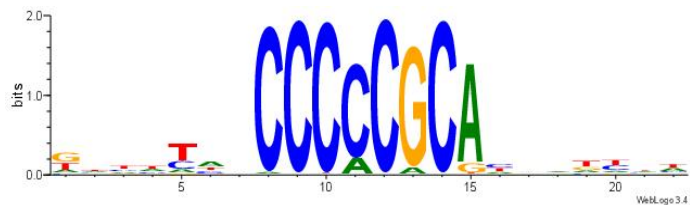
Consensus sequence: DBBBSBDGGGGCGYRDDHHHV



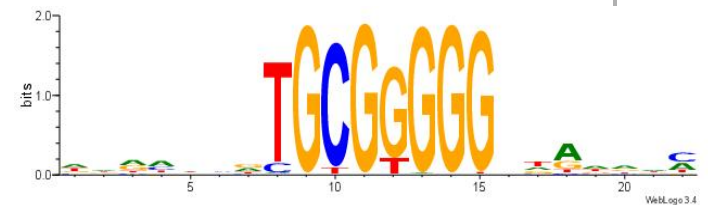
Motif ID: [UP00627](#)  
 Motif name: WT1\_R366C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 10  
 Similarity score: 0.0152921

Alignment:  
 KHHHTHHCCCCCGCAHDHDH  
 ---BAACGTCCGC-----

Original motif  
 Consensus sequence: KHHHTHHCCCCCGCAHDHDH



Reverse complement motif  
 Consensus sequence: HHHDHDTGCGGGGGHHAHHY



Motif ID: [UP00523](#)

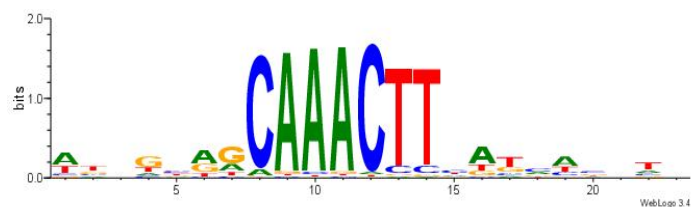
Motif name: FOXR1\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 10  
 Similarity score: 0.0161684

**Alignment:**

DHHBHVRTDAAGTTTGCKBCHVW  
 -----BAACGTCCGC-----

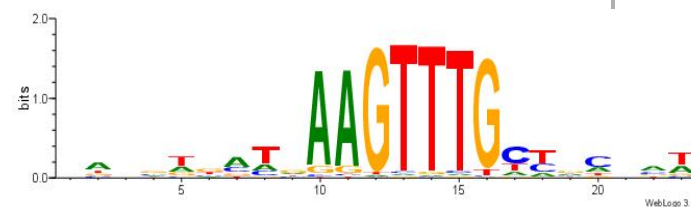
**Original motif**

Consensus sequence: WBHGBRGCAAACCTTHAKVHBHHD



**Reverse complement motif**

Consensus sequence: DHHBHVRTDAAGTTTGCKBCHVW




---

Motif ID: [UP00521](#)  
 Motif name: FOXN2\_primary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 10

Similarity score:

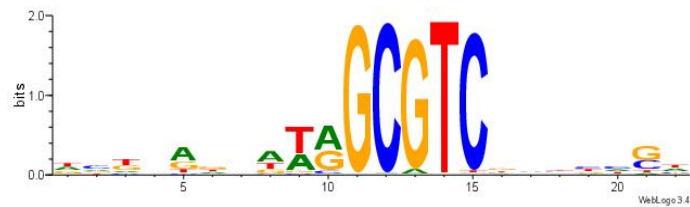
0.0163494

Alignment:

DVKHRDHDWRGCGTCBHHBHS  
-----BAACGTCCGC-----

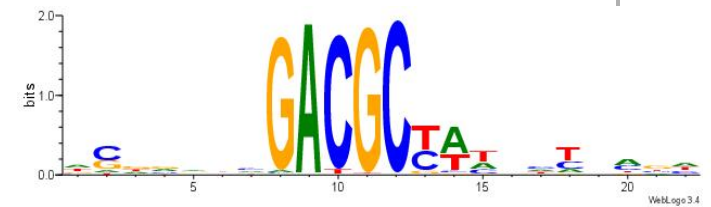
Original motif

Consensus sequence: DVKHRDHDWRGCGTCBHHBHS



Reverse complement motif

Consensus sequence: HSDBHBBGACGCKWDHKKHRVD



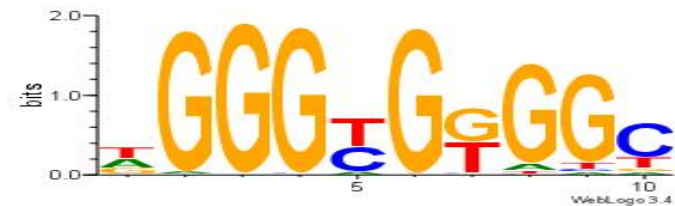
**Dataset #: 3**

**Motif ID: 27**

**Motif name: Klf4**

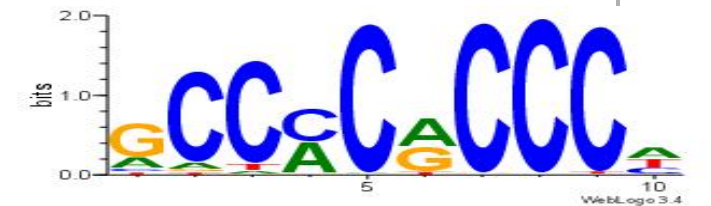
Original motif

Consensus sequence: DGGGYGKGGC



Reverse complement motif

Consensus sequence: GCCYCMCCCD



### Best Matches for Motif ID 27 (Highest to Lowest)

Motif ID: [UP00587](#)  
Motif name: EGR2  
Species: Homo sapiens  
Matching format of first motif: Original Motif



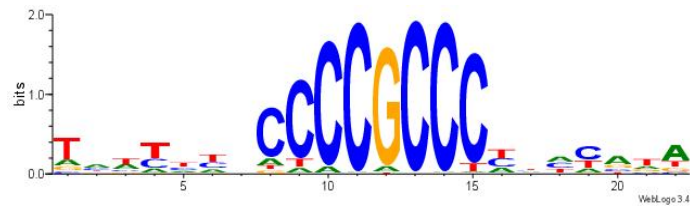
Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0

Alignment:

TDTKHHHGGGCGGGGDHMMWHA  
 -----DGGGYGKGGC-----

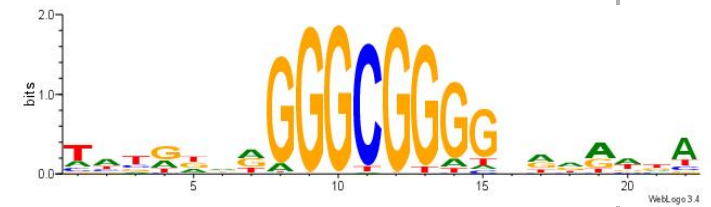
Original motif

Consensus sequence: THWYHHDCCCCGCCCHHYADA



Reverse complement motif

Consensus sequence: TDTKHHHGGGCGGGGDHMMWHA



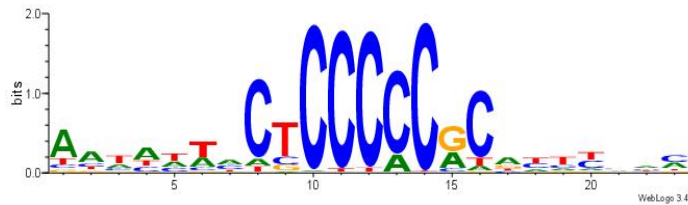
Motif ID: [UP00627](#)  
 Motif name: WT1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0140563

Alignment:

AAHAHWHCTCCCCRCDDHHYVHM  
-----GCCYCMCCCD-----

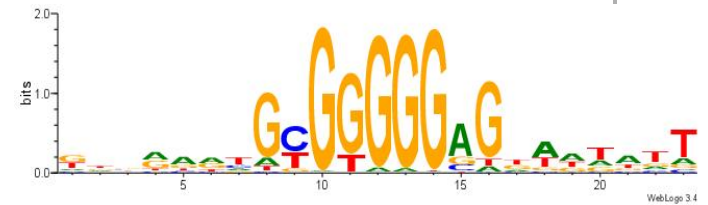
Original motif

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



Reverse complement motif

Consensus sequence: RHMVHHDGMGGGGGAGHWHTHT



Motif ID: [UP00600](#)  
Motif name: KLF11  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 9  
Number of overlap: 10  
Similarity score: 0.0236259

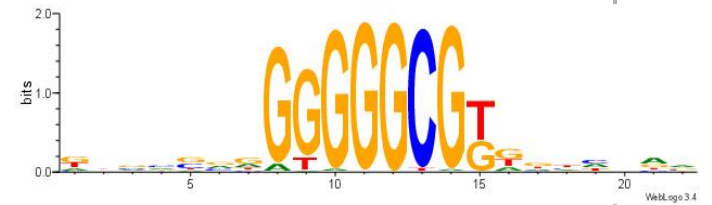
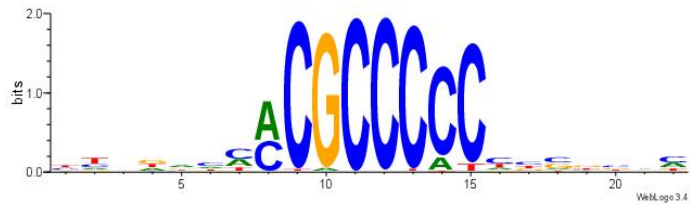
Alignment:  
DBBBSBDGGGGGCGYRDDHHHV  
-----DGGGYGKGGC-----

Original motif

Consensus sequence: BHDDHMMCGCCCCCHBSBBVH

Reverse complement motif

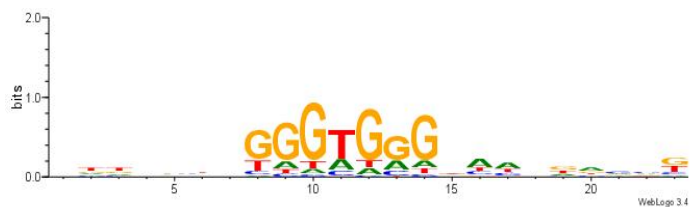
Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV



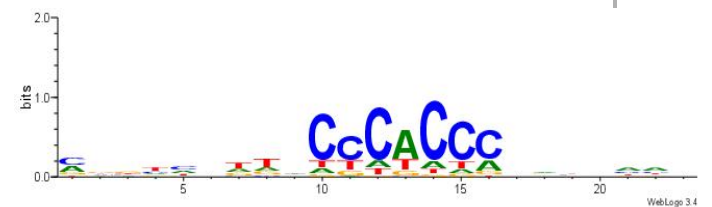
Motif ID: [UP00629](#)  
 Motif name: ZNF200\_H322Y\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.0319872

Alignment:  
 DDDDDHDGGGTGGGHHHDDDVVK  
 -----DGGGYGKGGC-----

Original motif  
 Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



Reverse complement motif  
 Consensus sequence: YVVDHDHHHCCCACCCHHDDDDD



Motif ID: [UP00627](#)

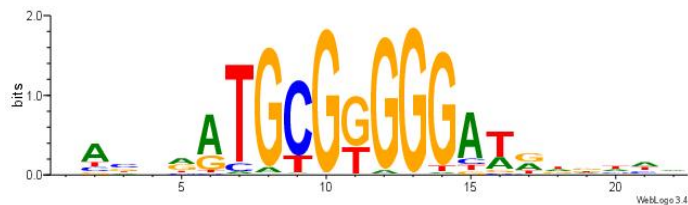
Motif name: WT1\_R366L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 10  
 Similarity score: 0.0363573

Alignment:

VABVRATGCGKGGGATRDDHHH  
 ----DGGGYGKGGC-----

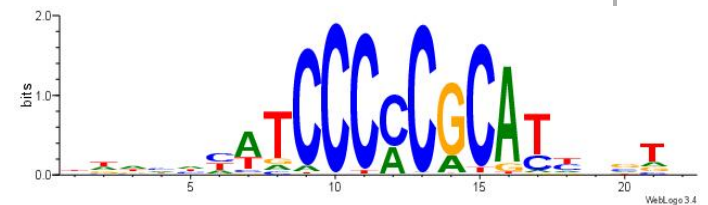
Original motif

Consensus sequence: VABVRATGCGKGGGATRDDHHH



Reverse complement motif

Consensus sequence: HHHHDMATCCCYCGCATKVBTV



**Dataset #: 3      Motif ID: 28      Motif name: E2F1**

Original motif

Consensus sequence: TTTSGCGC

Reverse complement motif

Consensus sequence: GCGCSAAA

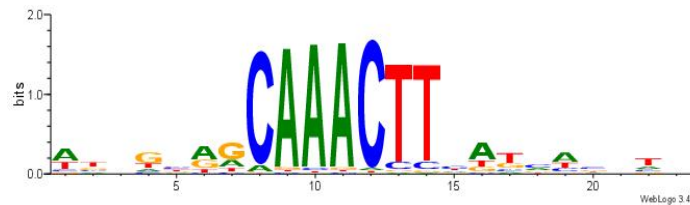


### Best Matches for Motif ID 28 (Highest to Lowest)

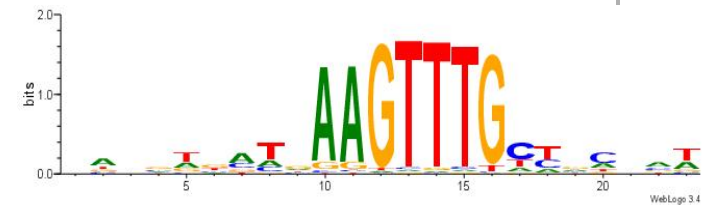
Motif ID: [UP00523](#)  
 Motif name: FOXR1\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 8  
 Similarity score: 0

Alignment:  
 WBHG  
B  
R  
G  
C  
A  
A  
A  
C  
T  
T  
H  
A  
K  
V  
H  
B  
H  
H  
D  
 ---G  
C  
G  
C  
S  
A  
A  
A  
-----

Original motif  
 Consensus sequence: WBHG  
B  
R  
G  
C  
A  
A  
A  
C  
T  
T  
H  
A  
K  
V  
H  
B  
H  
H  
D



Reverse complement motif  
 Consensus sequence: DHH  
B  
H  
V  
R  
T  
D  
A  
A  
G  
T  
T  
T  
G  
C  
K  
B  
C  
H  
V  
W



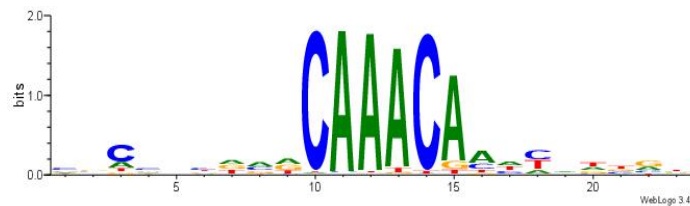
Motif ID: [UP00523](#)  
 Motif name: FOXR1\_primary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 8  
 Similarity score: 0.00633054

**Alignment:**

DVVDBKHHTTGTGGDBDBHVGVV  
 -----TTTSGCGC-----

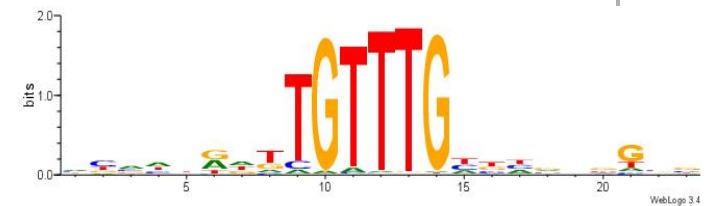
**Original motif**

Consensus sequence: VVCVHBDVDCAAACAAHYVDBVD



**Reverse complement motif**

Consensus sequence: DVVDBKHHTTGTGGDBDBHVGVV



Motif ID: [UP00522](#)  
 Motif name: FOXN4\_primary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6

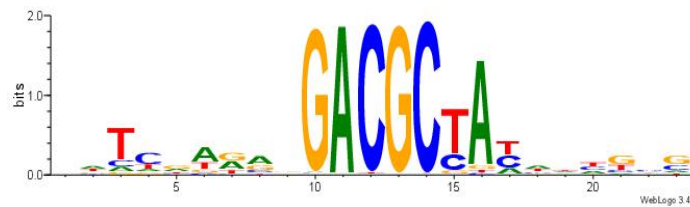
Number of overlap: 8  
Similarity score: 0.0144303

Alignment:

SDYHHHMTAGCGTCBBMTHGADH  
-----TTTSGCGC-----

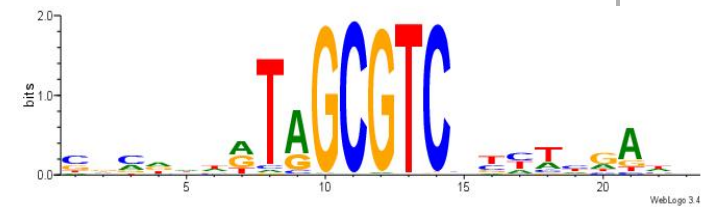
Original motif

Consensus sequence: HDTCDARVBGACGCTAYHHHKHS



Reverse complement motif

Consensus sequence: SDYHHHMTAGCGTCBBMTHGADH



Motif ID: [UP00522](#)  
Motif name: FOXN4\_secondary  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 8  
Similarity score: 0.0178986

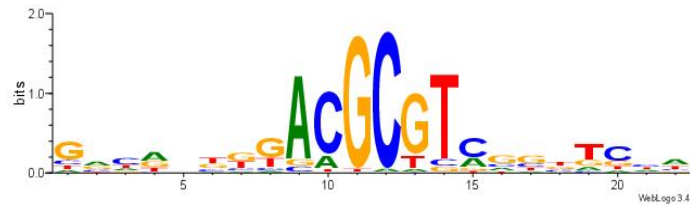
Alignment:

GVHDBBKGACCGTCVBBTCHH  
-----TTTSGCGC-----

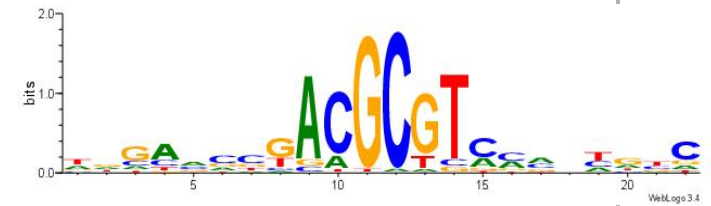
Original motif

Reverse complement motif

Consensus sequence: GVHDBBKGACGCGTCVBBTCHH



Consensus sequence: HDGAVBVGACGCGTCYVBDDBC



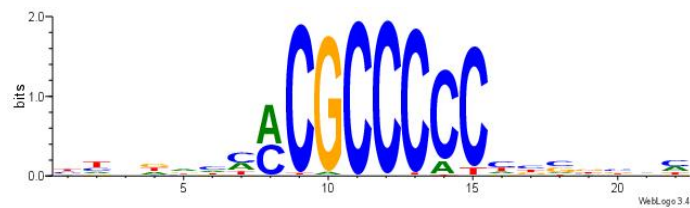
Motif ID: [UP00600](#)  
Motif name: KLF11  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 8  
Similarity score: 0.0184566

Alignment:

```
DBBBSBDGGGGGCGYRDDHHHV  
-----GCGCSAAA----
```

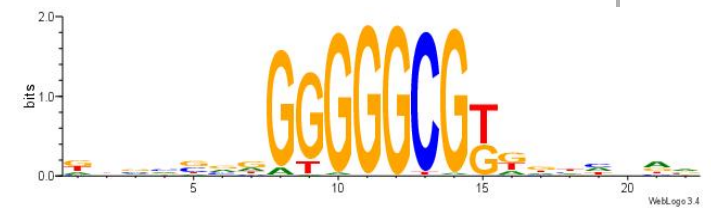
Original motif

Consensus sequence: BHHDDHMMCGCCCCCHBSBBVH



Reverse complement motif

Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV





**Dataset #: 3**

**Motif ID: 29**

**Motif name: HIF1AARNT**

Original motif

Consensus sequence: VBACGTGV



Reverse complement motif

Consensus sequence: VCACGTBV



### Best Matches for Motif ID 29 (Highest to Lowest)

Motif ID: [UP00621](#)  
Motif name: SNAI2\_T234I\_R1  
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: 8  
Similarity score: 0.00630757

Alignment:

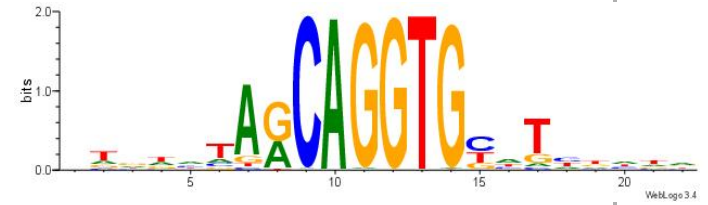
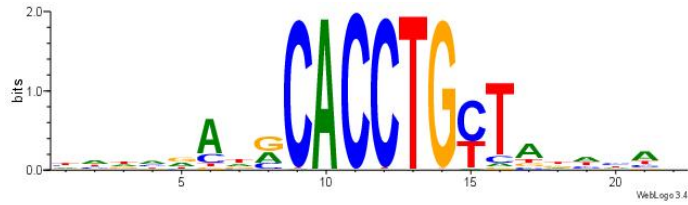
```
HHDHDADRCACCTGYTADHHAD  
-----VBACGTGV-----
```

Original motif

Consensus sequence: HHDHDADRCACCTGYTADHHAD

Reverse complement motif

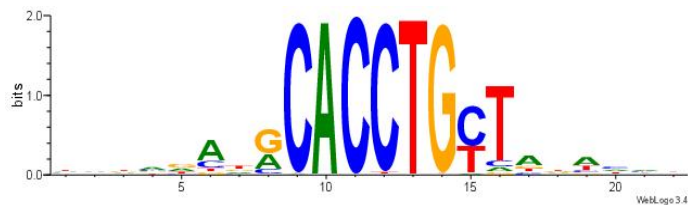
Consensus sequence: DTDHDTAKCAGGTGMDTHHDHH



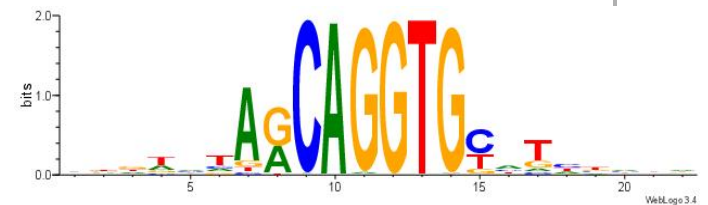
Motif ID: [UP00621](#)  
 Motif name: SNAI2\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 8  
 Similarity score: 0.00804833

Alignment:  
 HHDVDADRCACCTGYTADHHHD  
 -----VBACGTGV-----

Original motif  
 Consensus sequence: HHDVDADRCACCTGYTADHHHD



Reverse complement motif  
 Consensus sequence: DHDHTAKCAGGTGMDTHBDHH



Motif ID: [UP00621](#)

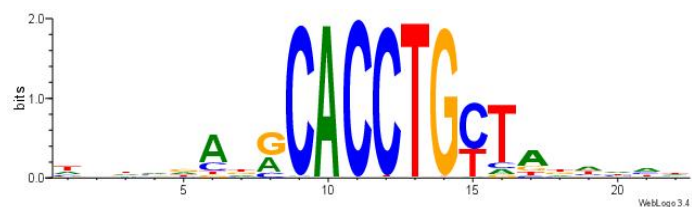
Motif name: SNAI2\_D119E\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 8  
 Similarity score: 0.0083564

**Alignment:**

HHHHDTAKCAGGTGMDTHBDDH  
 -----VCACGTBV-----

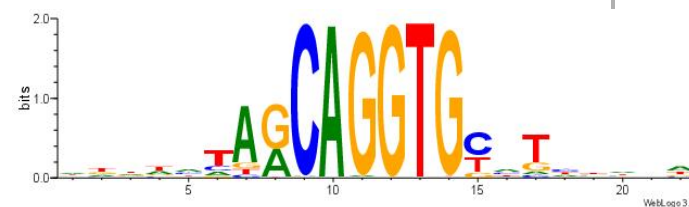
**Original motif**

Consensus sequence: HDDVDADRCACCTGYTADHHHH



**Reverse complement motif**

Consensus sequence: HHHHDTAKCAGGTGMDTHBDDH




---

Motif ID: [UP00612](#)  
 Motif name: PAX7  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 9  
 Number of overlap: 8

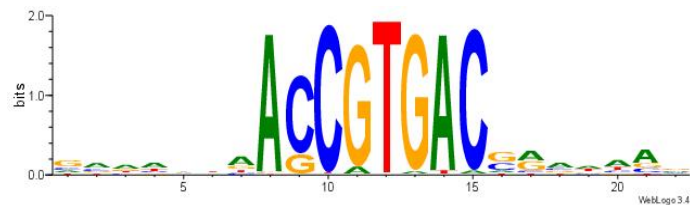
Similarity score: 0.0210813

Alignment:

VTHDBKSGTCACGGTTHDHDBV  
-----VCACGTBV-----

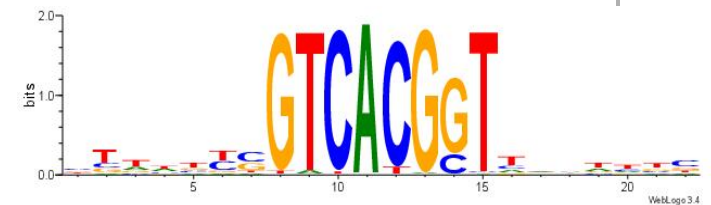
Original motif

Consensus sequence: VVDHDHAACCGTGACSRVDHAV



Reverse complement motif

Consensus sequence: VTHDBKSGTCACGGTTHDHDBV



Motif ID: [UP00522](#)  
Motif name: FOXN4\_secondary  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 7  
Number of overlap: 8  
Similarity score: 0.0215974

Alignment:

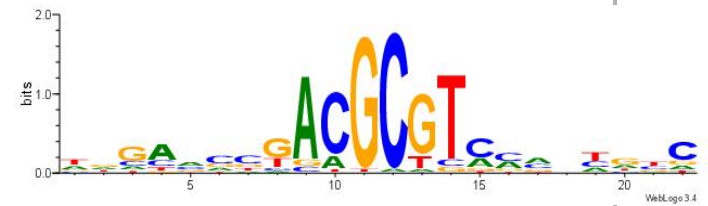
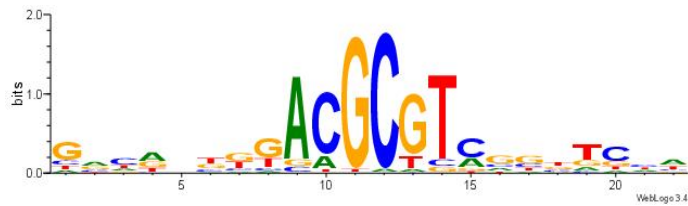
HDGAVBVGACGCGTCYVBDDBC  
-----VCACGTBV-----

Original motif

Consensus sequence: GVHDBBKACGCGTCVBBTCHH

Reverse complement motif

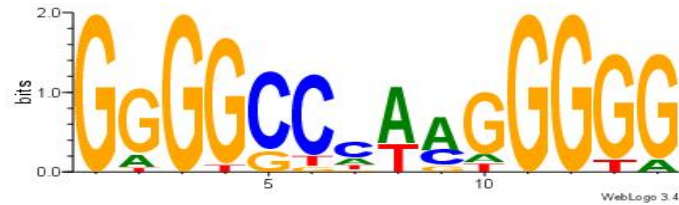
Consensus sequence: HDGAVBVGACGCGTCYVBDDBC



**Dataset #: 3      Motif ID: 30      Motif name: PLAG1**

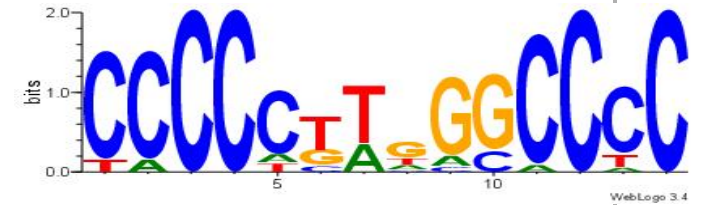
Original motif

Consensus sequence: GGGCCCAAGGGG



Reverse complement motif

Consensus sequence: CCCCTTGGCCCC



**Best Matches for Motif ID 30 (Highest to Lowest)**

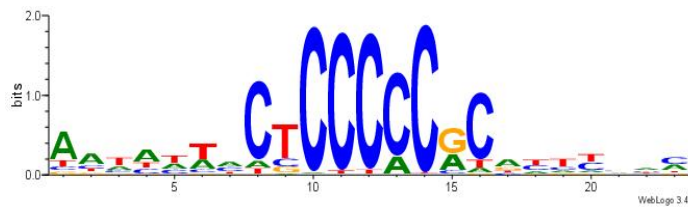
Motif ID:	<a href="#">UP00627</a>
Motif name:	WT1_REF_R1
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0264444

Alignment:

RHVMHHDGMGGGGGAGHWHHTTT  
GGGGCCCAAGGGG-----

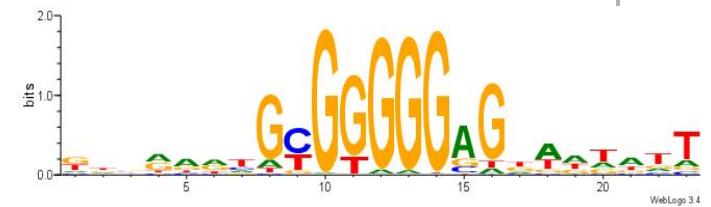
Original motif

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



Reverse complement motif

Consensus sequence: RHVMHHDGMGGGGGAGHWHHTTT



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: 10  
Number of overlap: 14  
Similarity score: 0.0354436

Alignment:

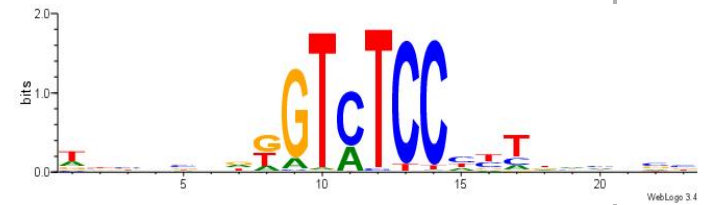
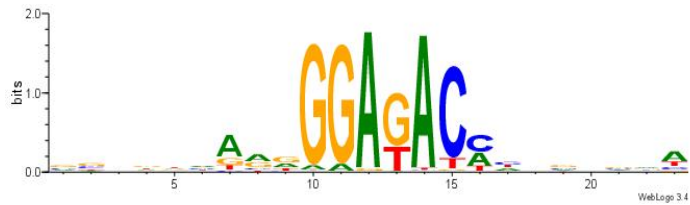
VBHDDHARDGGGAGACMHDVDVVA  
-----GGGGCCCAAGGGG

Original motif

Consensus sequence: VBHDDHARDGGGAGACMHDVDVVA

Reverse complement motif

Consensus sequence: TBVDVDDRGTCCTCHKTHDHHBV

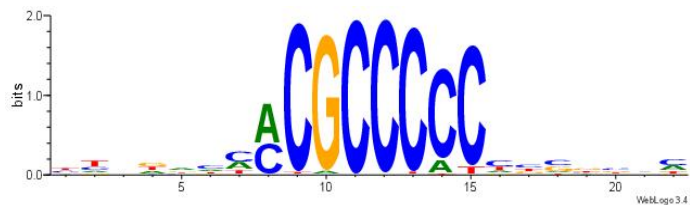


Motif ID: [UP00600](#)  
 Motif name: KLF11  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0356408

Alignment:  
 BHHDDHMMCGCCCCCHBSBBVH  
 -CCCCCTTGGGCCCC-----

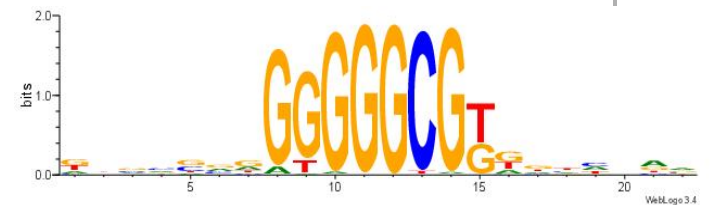
Original motif

Consensus sequence: BHHDDHMMCGCCCCCHBSBBVH



Reverse complement motif

Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV



Motif ID: [UP00629](#)

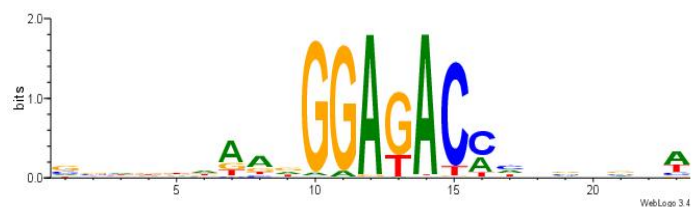
Motif name: ZNF200\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 14  
 Similarity score: 0.0363329

**Alignment:**

VBHDDDAADGGAGACMHHVDVDW  
 -----GGGGCCCAAGGGGG

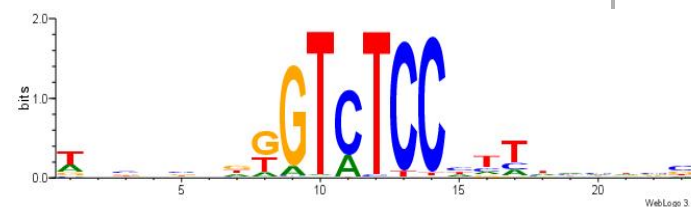
**Original motif**

Consensus sequence: VBHDDDAADGGAGACMHHVDVDW



**Reverse complement motif**

Consensus sequence: WDVDVHDRGTCTCCHTTDDHHBV




---

Motif ID: [UP00521](#)  
 Motif name: FOXN2\_secondary  
 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:

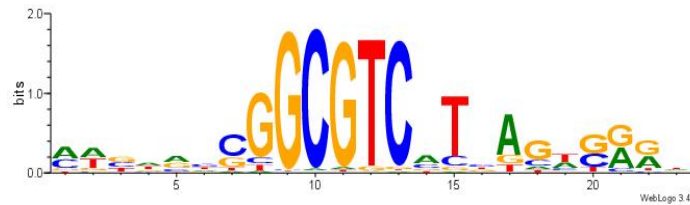
0.0372132

Alignment:

MWBDVHCGGCGTCVTBAGWSRRD  
-----GGGGCCCAAGGGGG--

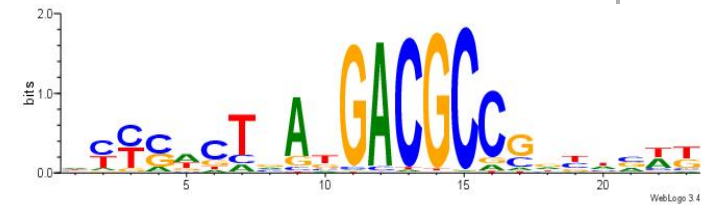
Original motif

Consensus sequence: MWBDVHCGGCGTCVTBAGWSRRD



Reverse complement motif

Consensus sequence: DMMSWCTBABGACGCCGDBDBWY



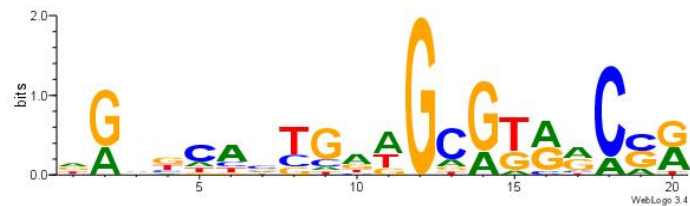
**Dataset #: 3**

**Motif ID: 31**

**Motif name: Pax5**

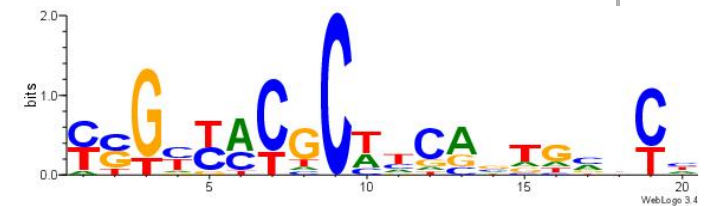
Original motif

Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif

Consensus sequence: MSGKKRCGCWDCABTGBBCD



### Best Matches for Motif ID 31 (Highest to Lowest)

Motif ID: [UP00629](#)  
Motif name: ZNF200\_H322Y\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif

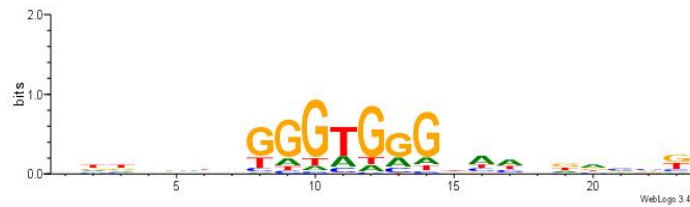
Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 20  
 Similarity score: 0.0431517

Alignment:

DDDDDHDGGGTGGGHHHDDDVVK  
 DGVBCABTGDWCGKRRCSR---

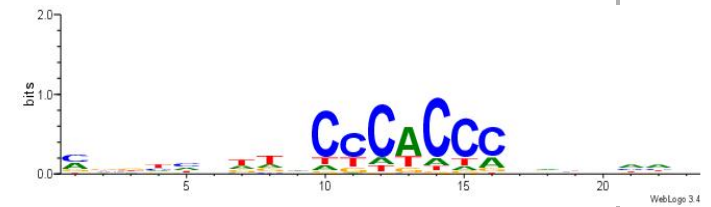
Original motif

Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



Reverse complement motif

Consensus sequence: YVVDHDHHHCCCACCCCHHDDDDD




---

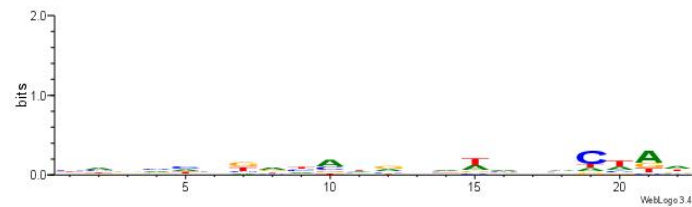
Motif ID: [UP00594](#)  
 Motif name: HESX1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0480075

Alignment:

DTHGBBBWHDVHBHDBVDVBHB  
--DGVBCABTGDWGCCGKRCSR

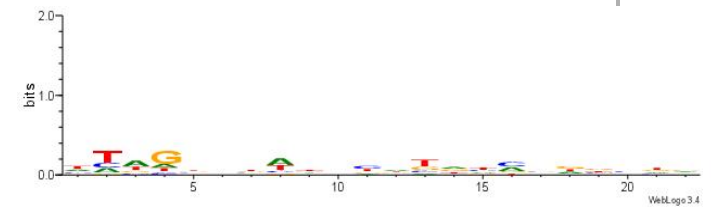
Original motif

Consensus sequence: BHBVHVBDHVHVDHWVBVCHAD



Reverse complement motif

Consensus sequence: DTHGBBBWHDVHBHDBVDVBHB



Motif ID: [UP00611](#)  
Motif name: PAX6  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 20  
Similarity score: 0.0504226

Alignment:

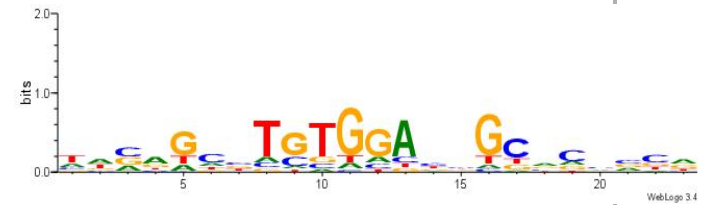
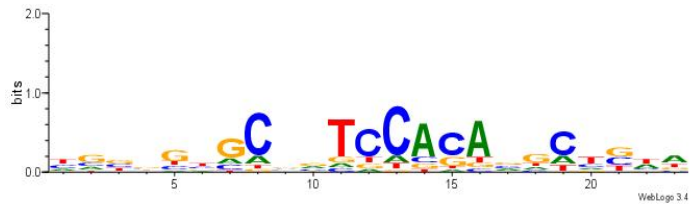
HVBBGBGCVVTCCACAVGCHBHD  
-MSGKKRCGCWDCABTGBCD--

Original motif

Consensus sequence: HVBBGBGCVVTCCACAVGCHBHD

Reverse complement motif

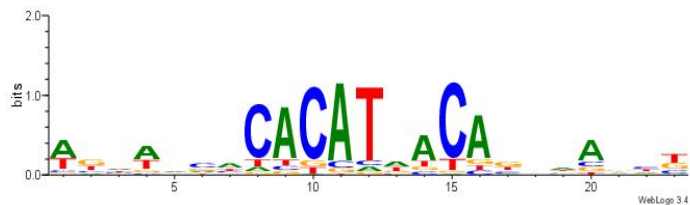
Consensus sequence: DHBHGCVTGTGGAVVGCVCBBVH



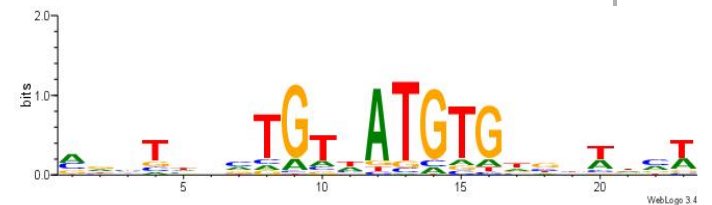
Motif ID: [UP00599](#)  
 Motif name: KLF1\_R328H\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.050775

Alignment:  
 RDHTDDBTGTDATGTGHVDWHBW  
 DGVCABTGDWCGKRRCSR---

Original motif  
 Consensus sequence: WBHWDVHCACATDACABDDADHK



Reverse complement motif  
 Consensus sequence: RDHTDDBTGTDATGTGHVDWHBW



Motif ID: [UP00600](#)

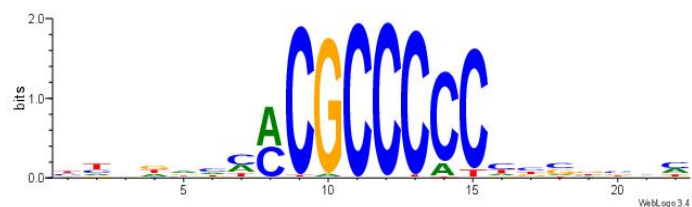
Motif name: KLF11  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 20  
 Similarity score: 0.0513444

**Alignment:**

DBBBSBDGGGGGCGYRDDHHHV  
 DGVBCABTGDWCGCKRRCR--

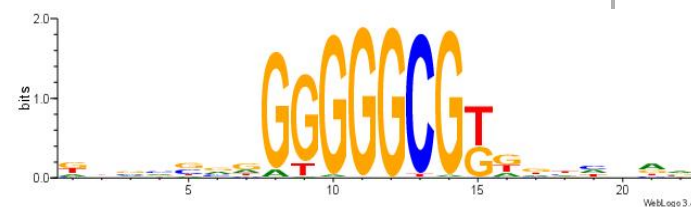
**Original motif**

Consensus sequence: BHHDDHMMCGCCCCCHBSBBVH



**Reverse complement motif**

Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV



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

**Original motif**

Consensus sequence: YGCGTG

**Reverse complement motif**

Consensus sequence: CACGCM



### Best Matches for Motif ID 32 (Highest to Lowest)

Motif ID: [UP00627](#)  
 Motif name: WT1\_R366L\_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: 6  
 Similarity score: 0

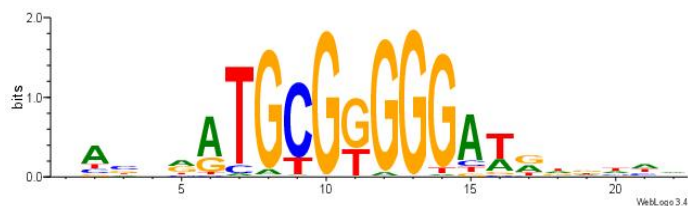
#### Alignment:

```

VABVRATGCGKGGGATRDDHHH
-----YCGTG-----
  
```

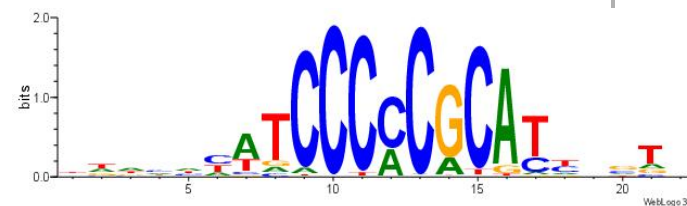
#### Original motif

Consensus sequence: VABVRATGCGKGGGATRDDHHH



#### Reverse complement motif

Consensus sequence: HHHHDMATCCCcCGCATKVBT



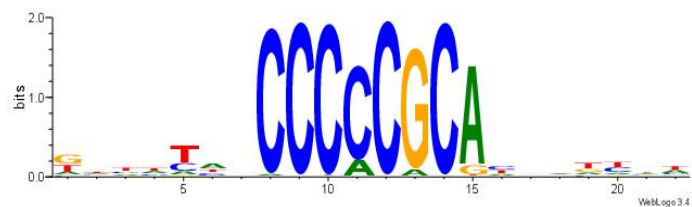
Motif ID: [UP00627](#)  
 Motif name: WT1\_R366C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 6  
 Similarity score: 0.00272949

**Alignment:**

KHHHTHHCCCCGCAHDHDH  
 -----CACGCM-----

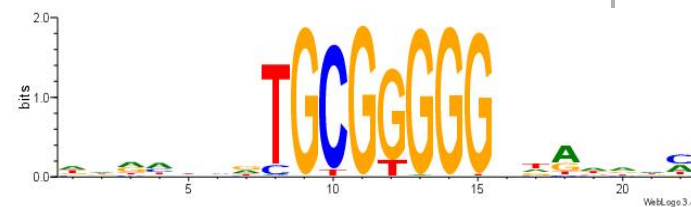
**Original motif**

Consensus sequence: KHHHTHHCCCCGCAHDHDH



**Reverse complement motif**

Consensus sequence: HHHDHDTGCGGGGGHHAHHY



Motif ID: [UP00521](#)  
 Motif name: FOXN2\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 11

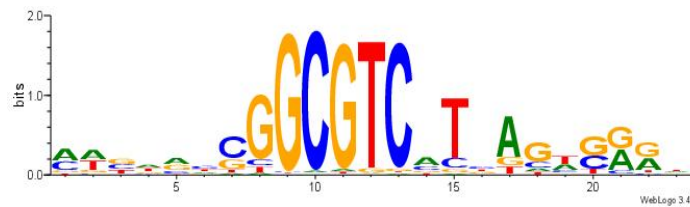
Number of overlap: 6  
Similarity score: 0.00939422

Alignment:

DMMSWCTBABGACGCCGDBDBWY  
-----CACGCM-----

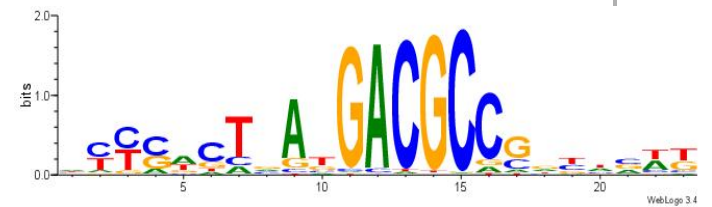
Original motif

Consensus sequence: MWBDVHCGGCGTCVTBAGWSRRD



Reverse complement motif

Consensus sequence: DMMSWCTBABGACGCCGDBDBWY



Motif ID: [UP00522](#)  
Motif name: FOXN4\_primary  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 6  
Similarity score: 0.0119829

Alignment:

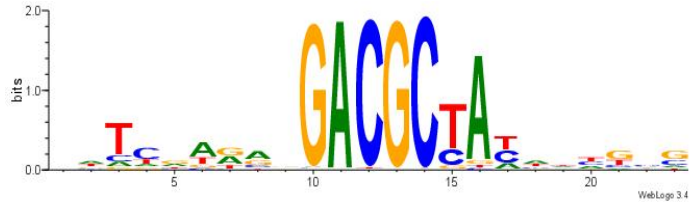
SDYHHHMTAGCGTCBBMTHGADH  
-----YCGTG-----

Original motif

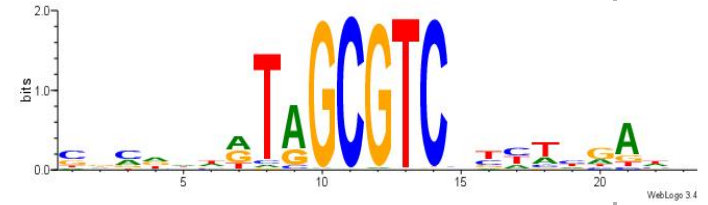
Reverse complement motif



Consensus sequence: HDTCDARVBGACGCTAYHHHKHS



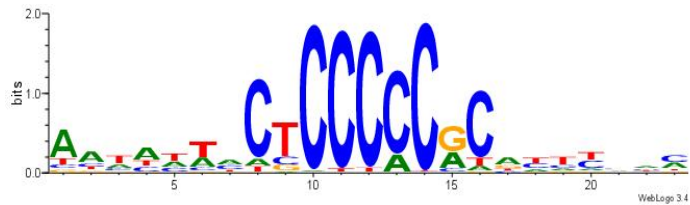
Consensus sequence: SDYHHHMTAGCGTCBBMTHGADH



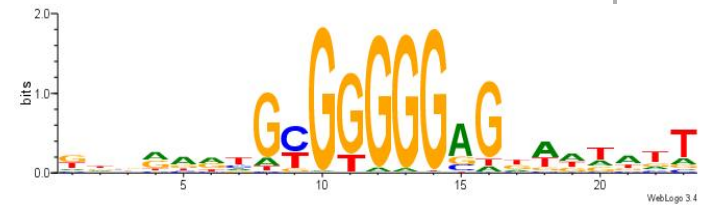
Motif ID: [UP00627](#)  
Motif name: WT1\_REF\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 7  
Number of overlap: 6  
Similarity score: 0.0121968

Alignment:  
AAHAHWHCTCCCCRCDDHHYVHM  
-----CACGCM-----

Original motif  
Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



Reverse complement motif  
Consensus sequence: RHVMHHDGMGGGGGAGHWHTHT



**Dataset #: 3**      **Motif ID: 33**      **Motif name: Mycn**

Original motif

Consensus sequence: HSCACGTGGC



Reverse complement motif

Consensus sequence: GCCACGTGSD



### Best Matches for Motif ID 33 (Highest to Lowest)

Motif ID:	<a href="#">UP00605</a>
Motif name:	NKX2-8
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:	10
Similarity score:	0

Alignment:

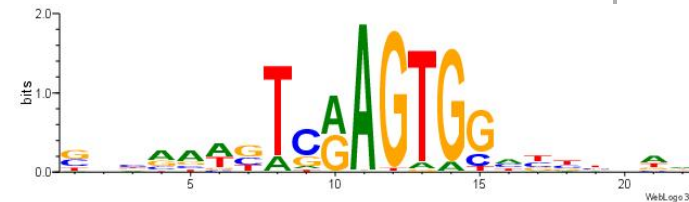
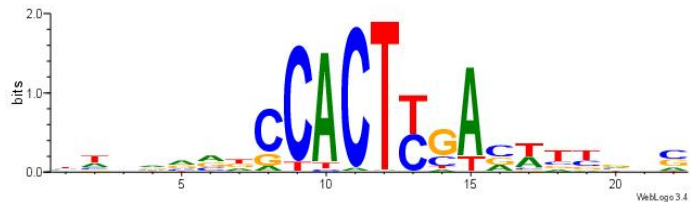
```
SBVMAWVTCMAGTGGDBBBDHH  
-----GCCACGTGSD-----
```

Original motif

Consensus sequence: HHDVVVDCCACTYGAVWTYVBS

Reverse complement motif

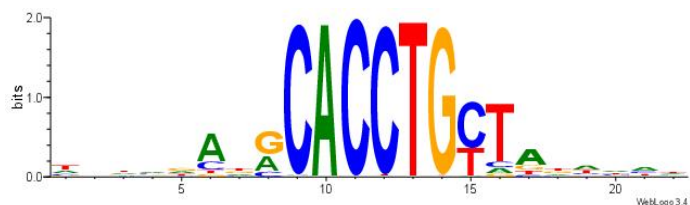
Consensus sequence: SBVMAWVTCMAGTGGDBBBDHH



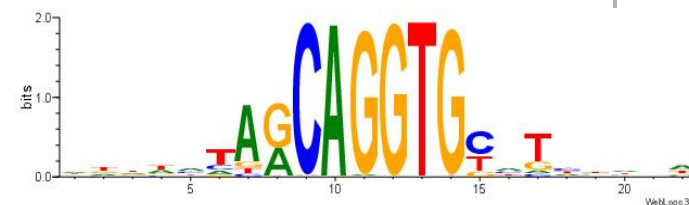
Motif ID: [UP00621](#)  
 Motif name: SNAI2\_D119E\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.00142642

Alignment:  
 HHHHDTAKCAGGTGMDTHBDDH  
 -----GCCACGTGSD-----

Original motif  
 Consensus sequence: HDDVDADRCACCTGYTADHHHH



Reverse complement motif  
 Consensus sequence: HHHHDTAKCAGGTGMDTHBDDH



Motif ID: [UP00621](#)

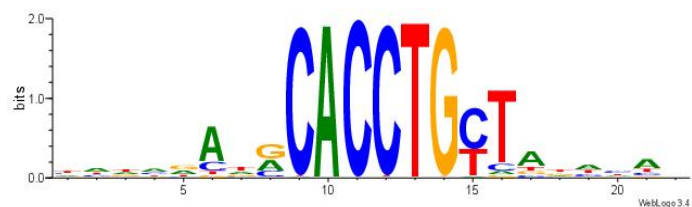
Motif name: SNAI2\_T234I\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.00196758

**Alignment:**

DTDHDTAKCAGGTGMDTHHDHH  
 -----GCCACGTGSD-----

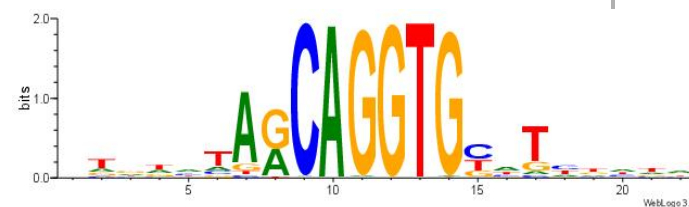
**Original motif**

Consensus sequence: HHDHDADRCACCTGYTADHHAD



**Reverse complement motif**

Consensus sequence: DTDHDTAKCAGGTGMDTHHDHH




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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: Forward  
 Position number: 7  
 Number of overlap: 10

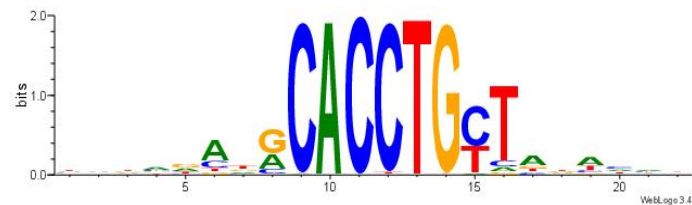
Similarity score: 0.00337084

Alignment:

DHDHDTAKCAGGTGMDTHBDHH  
-----GCCACGTGSD-----

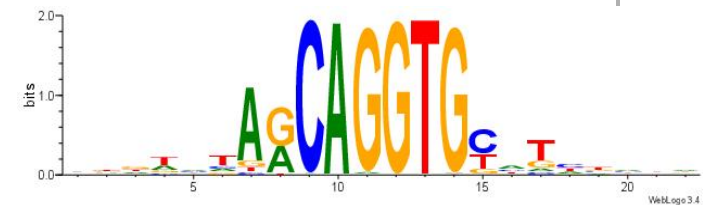
Original motif

Consensus sequence: HHDVDADRCACCTGYTADHHHD



Reverse complement motif

Consensus sequence: DHDHDTAKCAGGTGMDTHBDHH



Motif ID: [UP00522](#)  
Motif name: FOXN4\_secondary  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 8  
Number of overlap: 10  
Similarity score: 0.00795147

Alignment:

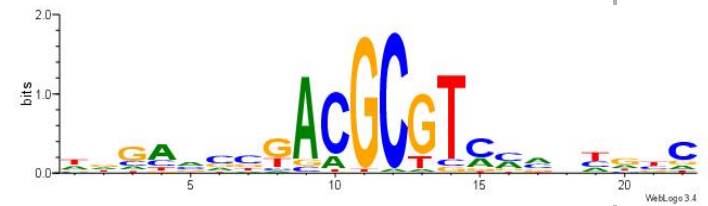
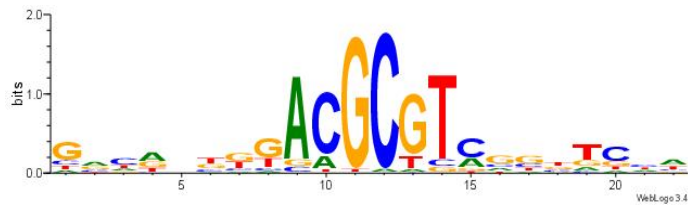
HDGAVBVGACGCGTCYVBDDBC  
-----HSCACGTGGC-----

Original motif

Consensus sequence: GVHDBBKACGCGTCVBBTCHH

Reverse complement motif

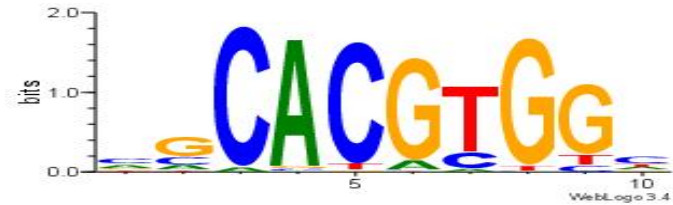
Consensus sequence: HDGAVBVGACGCGTCYVBDDBC



**Dataset #: 3      Motif ID: 34      Motif name: Myc**

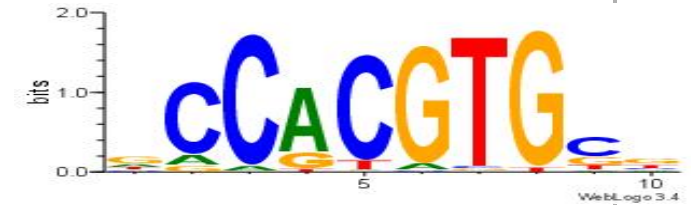
Original motif

Consensus sequence: VGCACGTGGH



Reverse complement motif

Consensus sequence: DCCACGTGCV



**Best Matches for Motif ID 34 (Highest to Lowest)**

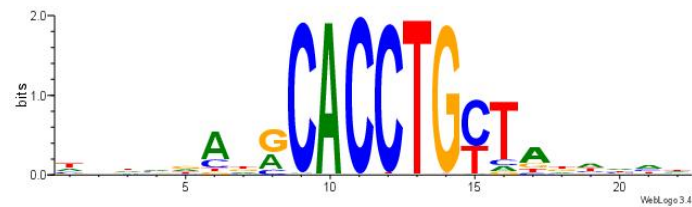
Motif ID:	<a href="#">UP00621</a>
Motif name:	SNAI2_D119E_R1
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	10
Similarity score:	0

Alignment:

HHHHDTAKCAGGTGMDTHBDDH  
-----DCCACGTGCV-----

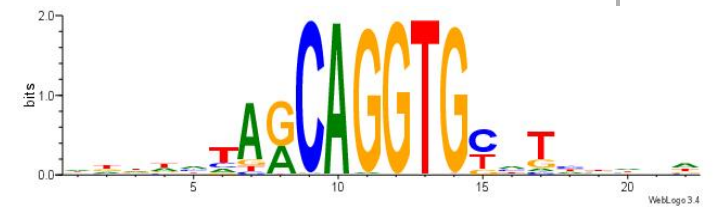
Original motif

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: Forward  
Position number: 7  
Number of overlap: 10  
Similarity score: 0.00177738

Alignment:

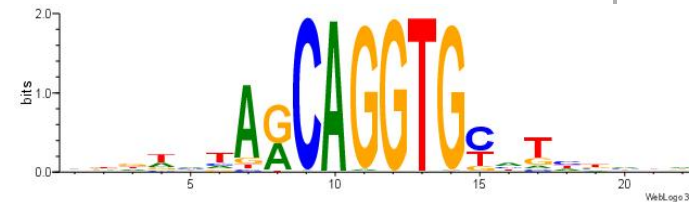
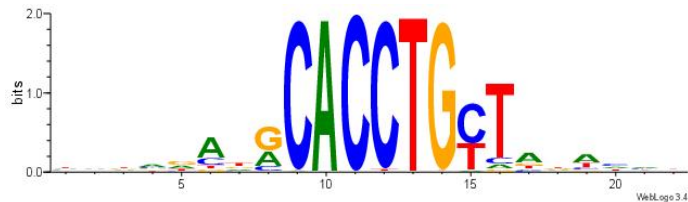
DHDHDTAKCAGGTGMDTHBDHH  
-----DCCACGTGCV-----

Original motif

Consensus sequence: HHDVDADRCACCTGYTADHHHD

Reverse complement motif

Consensus sequence: DHDHDTAKCAGGTGMDTHBDHH



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: Forward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.00250317

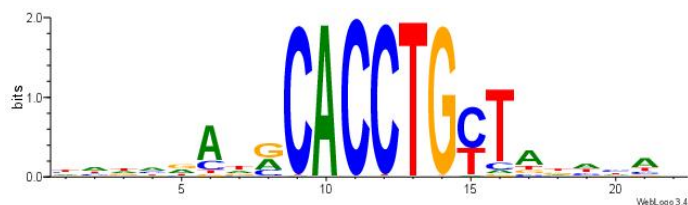
**Alignment:**

```

DTDHDTAKCAGGTGMDTHHDHH
-----DCCACGTGCV-----
  
```

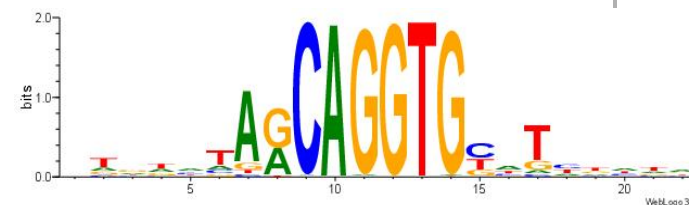
**Original motif**

Consensus sequence: HHDHDADRCACCTGYTADHHAD



**Reverse complement motif**

Consensus sequence: DTDHDTAKCAGGTGMDTHHDHH



Motif ID: [UP00605](#)



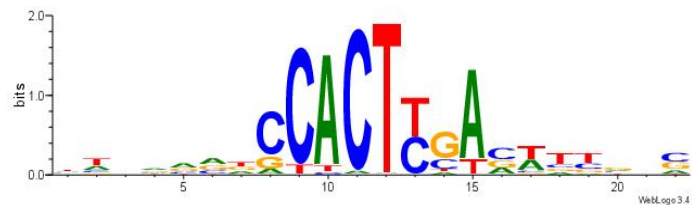
Motif name: NKX2-8  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.00749721

**Alignment:**

SBVMAWVTCMAGTGGDBBBDHH  
 -----DCCACGTGCV-----

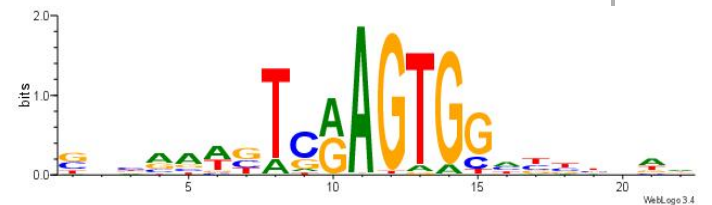
**Original motif**

Consensus sequence: HHDVVVDCCACTYGAVWTYVBS



**Reverse complement motif**

Consensus sequence: SBVMAWVTCMAGTGGDBBBDHH




---

Motif ID: [UP00522](#)  
 Motif name: FOXN4\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 10

Similarity score:

0.0117827

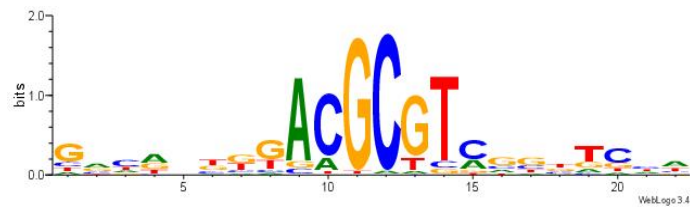
Alignment:

HDGAVBVGACGCGTCYVBDDBC

-----VGCACGTGGH-----

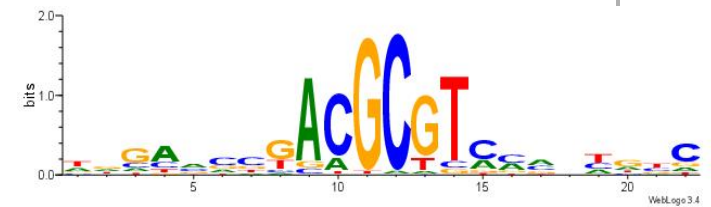
Original motif

Consensus sequence: GVHDBBKGACGCGTCVBBTCHH



Reverse complement motif

Consensus sequence: HDGAVBVGACGCGTCYVBDDBC



**Dataset #: 3**

**Motif ID: 35**

**Motif name: GABPA**

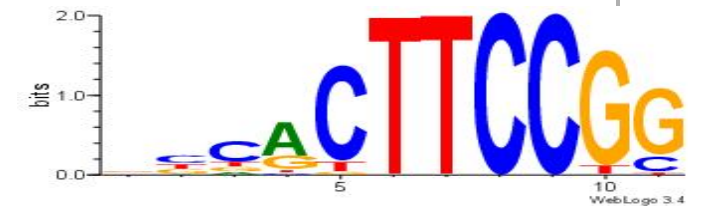
Original motif

Consensus sequence: CCGGAAGTG



Reverse complement motif

Consensus sequence: VVCACTTCCGG



### Best Matches for Motif ID 35 (Highest to Lowest)

Motif ID:

[UP00586](#)

Motif name:

CRX

Species:

Homo sapiens

Matching format of first motif:

Reverse Complement

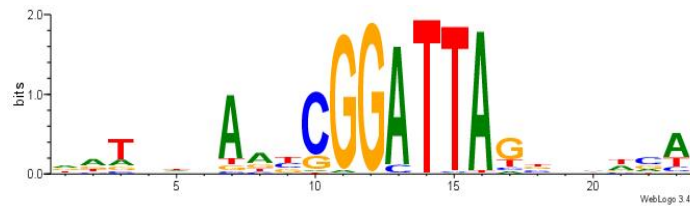
Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0482888

Alignment:

TVDHDVCTAATCCGVTTHDVADD  
 ----VVCACTTCCGG-----

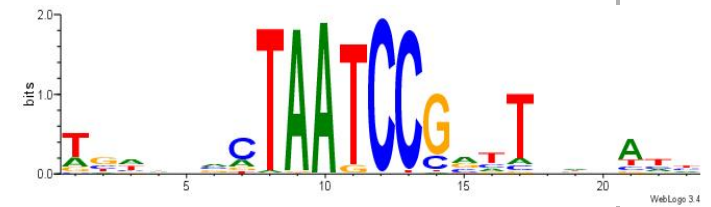
Original motif

Consensus sequence: DDTVDHAABCGGATTAGBDHDVA



Reverse complement motif

Consensus sequence: TVDHDVCTAATCCGVTTHDVADD




---

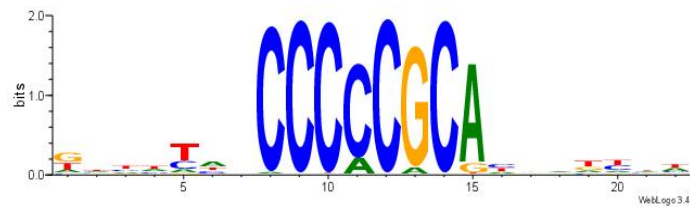
Motif ID: [UP00627](#)  
 Motif name: WT1\_R366C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 11  
 Similarity score: 0.0483091

Alignment:

HHHDHHD TGCGGGGGHHAHHY  
-VCACTTCGG-----

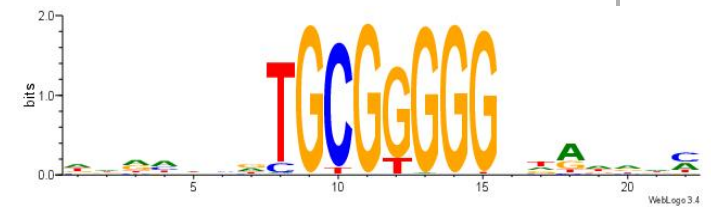
Original motif

Consensus sequence: KHHHTHHCCCCGCAHDHDDHH



Reverse complement motif

Consensus sequence: HHDHHD TGCGGGGGHHAHHY



Motif ID: [UP00608](#)  
Motif name: OVOL2  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 6  
Number of overlap: 11  
Similarity score: 0.0542546

Alignment:

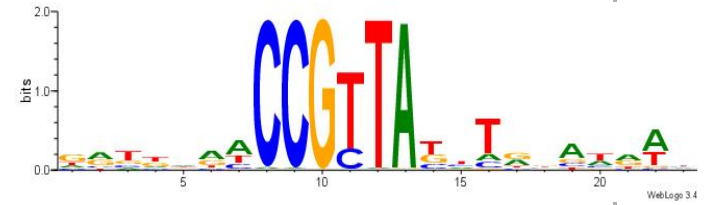
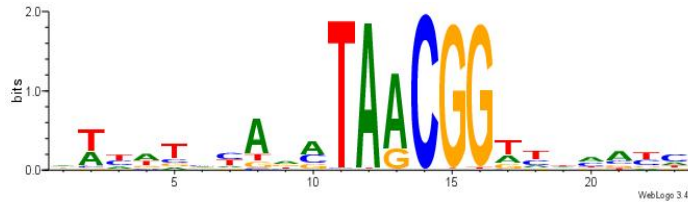
DWHDTVYADMTAACGGWYDHAYH  
-----VCACTTCGG-----

Original motif

Consensus sequence: DWHDTVYADMTAACGGWYDHAYH

Reverse complement motif

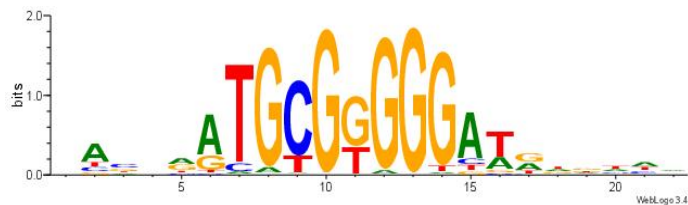
Consensus sequence: DMTHDMWCCGTTAYDTKVADHWD



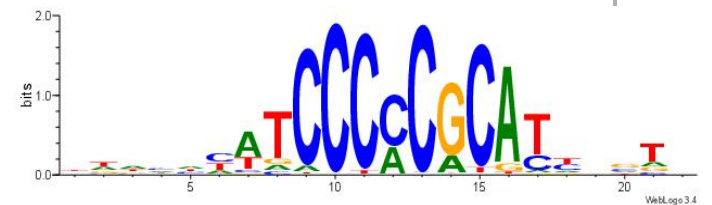
Motif ID: [UP00627](#)  
 Motif name: WT1\_R366L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 12  
 Number of overlap: 11  
 Similarity score: 0.0567917

Alignment:  
 HHHHDMATCCCYCGCATKVBTV  
 -----CCGGAAGTGVV

Original motif  
 Consensus sequence: VABVRATGCGKGGGATRDDHHH



Reverse complement motif  
 Consensus sequence: HHHHDMATCCCYCGCATKVBTV



Motif ID: [UP00612](#)

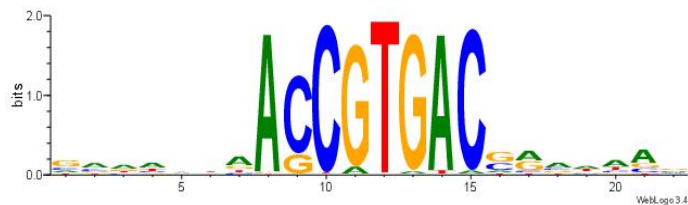
Motif name: PAX7  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 9  
 Number of overlap: 11  
 Similarity score: 0.0590324

Alignment:

VVDHDHAACCGTGACSRVDHAV  
 -----CCGGAAGTGVV----

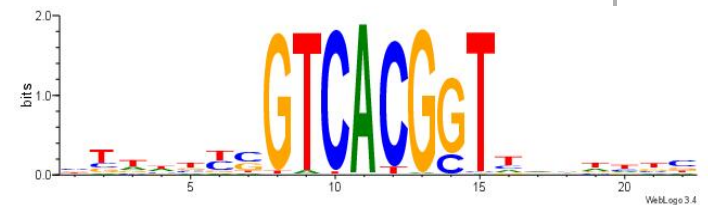
Original motif

Consensus sequence: VVDHDHAACCGTGACSRVDHAV



Reverse complement motif

Consensus sequence: VTHDBKSGTCACGGTTHDHDVBV



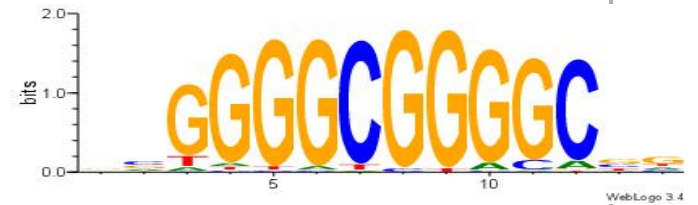
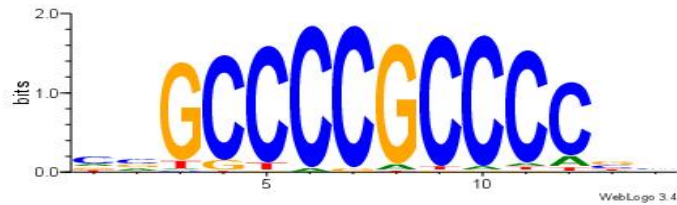
**Dataset #: 4      Motif ID: 36      Motif name: csGCCCCGCCCCsc**

Original motif

Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif

Consensus sequence: BBGGGGCGGGGCVD

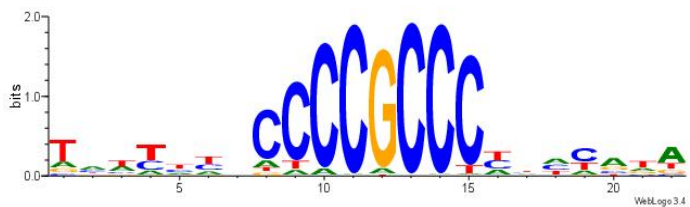


**Best Matches for Motif ID 36 (Highest to Lowest)**

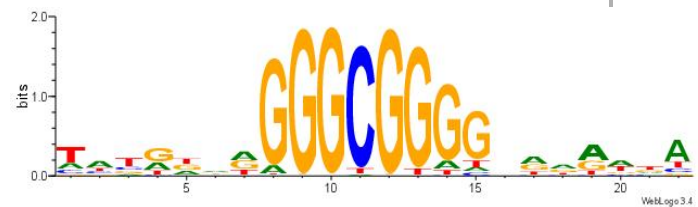
Motif ID: [UP00587](#)  
 Motif name: EGR2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0

Alignment:  
 THWYHHDCCCCGCCCHHHYADA  
 ----HVGCCCCGCCCCBB----

Original motif  
 Consensus sequence: THWYHHDCCCCGCCCHHHYADA



Reverse complement motif  
 Consensus sequence: TDTKHHHGGGCGGGGDHHMWHA



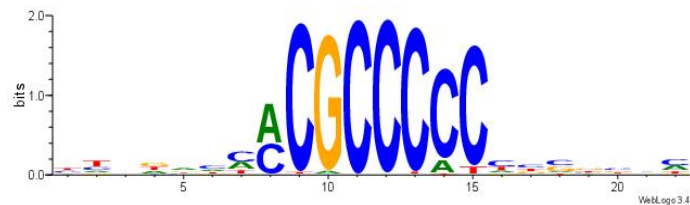
Motif ID: [UP00600](#)  
 Motif name: KLF11  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0197359

**Alignment:**

BHHDDHMMCGCCCCCHBSBBVH  
 --HVGCCCGCCCCBB-----

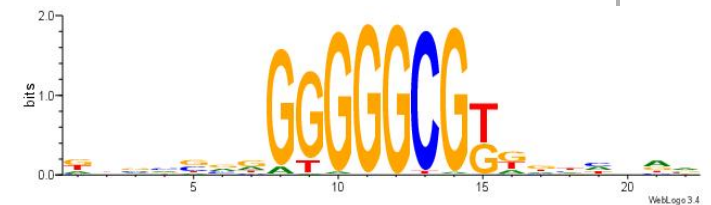
**Original motif**

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: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6



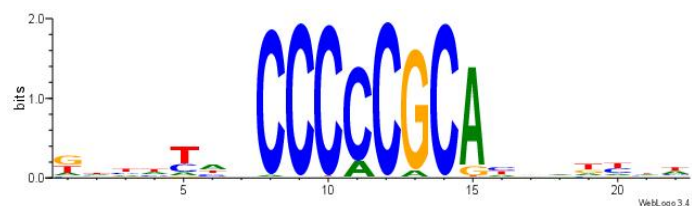
Number of overlap: 14  
Similarity score: 0.0359414

Alignment:

KHHHTHHCCCCCGCAHDHDH  
-----HVGCCCGCCCB

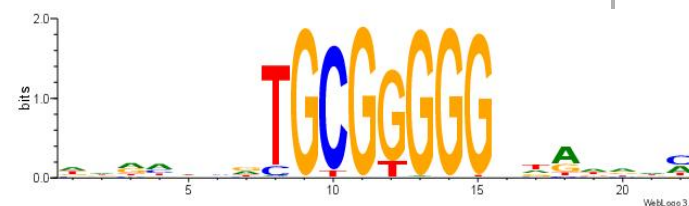
Original motif

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: Backward  
Position number: 7  
Number of overlap: 14  
Similarity score: 0.045601

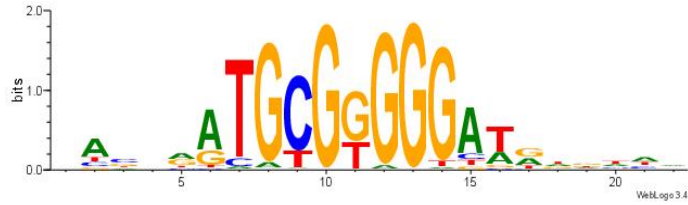
Alignment:

VABVRATGCGKGGGATRDDH  
--BBGGGCGGGCVD-----

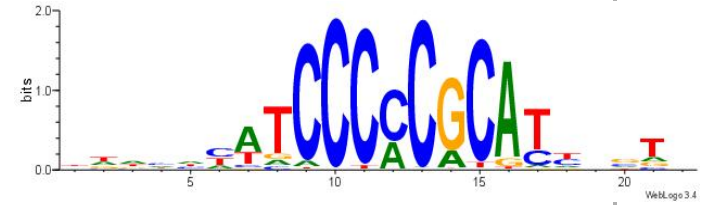
Original motif

Reverse complement motif

Consensus sequence: VABVRATGCGKGGGATRDDHHH



Consensus sequence: HHHHDMATCCCcCGCATKVBTV



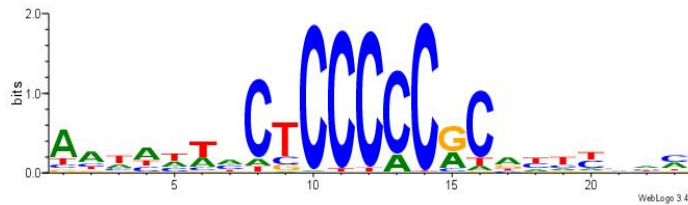
Motif ID: [UP00627](#)  
Motif name: WT1\_REF\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 14  
Similarity score: 0.0459004

Alignment:

```
AAHAHWHCTCCCCRCDDHHYVHM  
-----HVGCCCGCCCCBB---
```

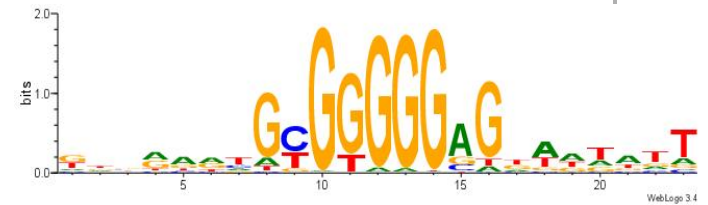
Original motif

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



Reverse complement motif

Consensus sequence: RHVMHHDGMGGGGGAGHWHTHT



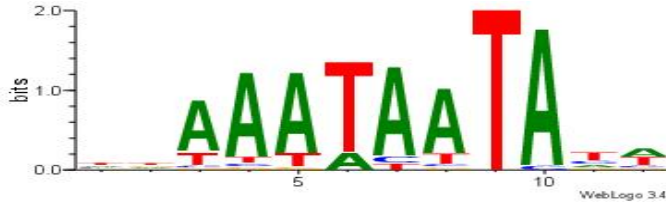
**Dataset #: 4**

**Motif ID: 37**

**Motif name: tkAAATAATatw**

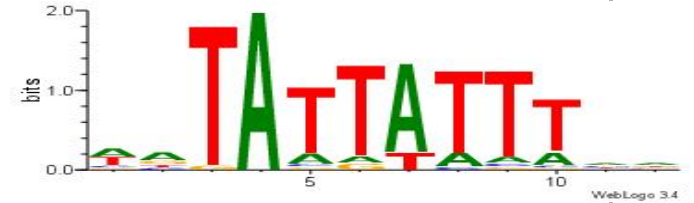
Original motif

Consensus sequence: HDAAATAATAHW



Reverse complement motif

Consensus sequence: WHTATTATTTDH



### Best Matches for Motif ID 37 (Highest to Lowest)

Motif ID: [UP00617](#)  
Motif name: POU4F3  
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: 12  
Similarity score: 0.0220779

Alignment:

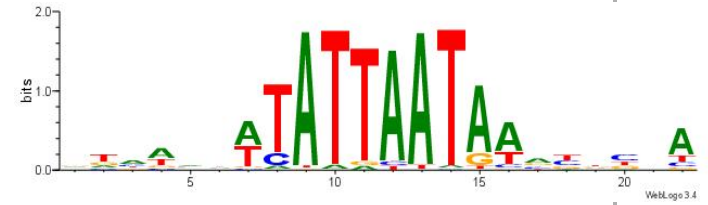
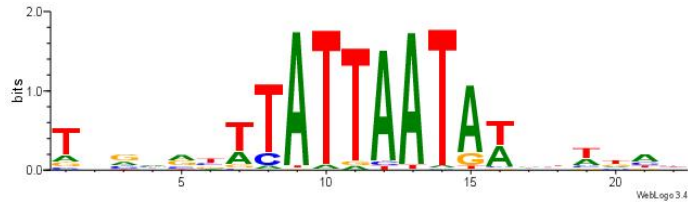
```
BHDWVHWTATTAATAAVBHVHA  
-----WHTATTATTTDH-----
```

Original motif

Consensus sequence: THVHVBTTATTAATAWHBWDHB

Reverse complement motif

Consensus sequence: BHDWVHWTATTAATAAVBHVHA

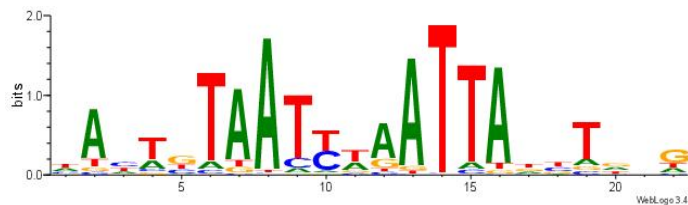


Motif ID: [UP00619](#)  
 Motif name: PROP1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 12  
 Similarity score: 0.0257795

Alignment:  
 HAHTBTAATYWAATTADBTDVG  
 -----WHTATTATTTDH-

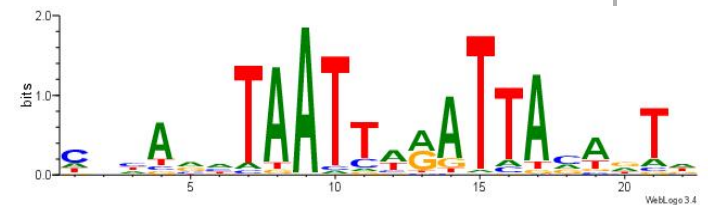
Original motif

Consensus sequence: HAHTBTAATYWAATTADBTDVG



Reverse complement motif

Consensus sequence: CBHAVDTAATTWMATTABADTH



Motif ID: [UP00627](#)

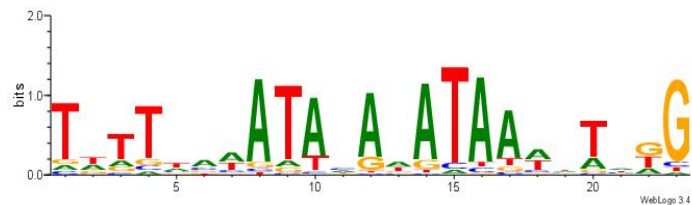
Motif name: WT1\_H373Y\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 12  
 Similarity score: 0.0258362

**Alignment:**

CYHAHWTTATD TDTATWBHAADA  
 --WHTATTATTTDH-----

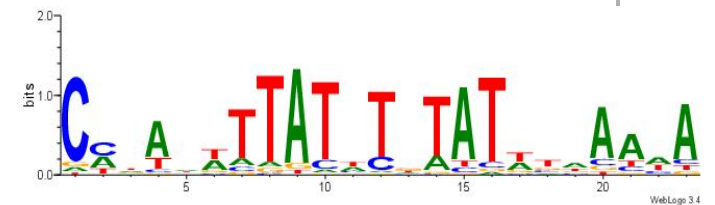
**Original motif**

Consensus sequence: TDTTHVWATAHADATAAWHHTHGK



**Reverse complement motif**

Consensus sequence: CYHAHWTTATD TDTATWBHAADA




---

Motif ID: [UP00606](#)  
 Motif name: NR1H4  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 12

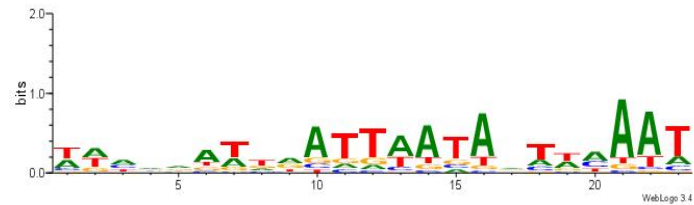
Similarity score: 0.0279126

Alignment:

```
ATTYWABTATWAATDDWTDBHWW  
-----WHTATTATTTDH-----
```

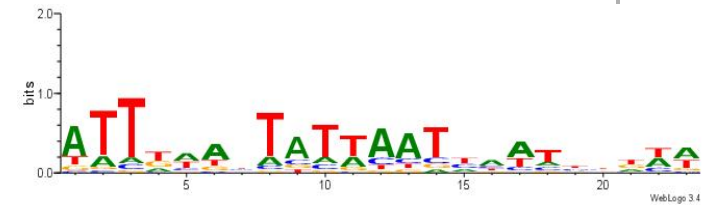
Original motif

Consensus sequence: WWHVDAWDDATTWATAVTWMAAT



Reverse complement motif

Consensus sequence: ATTYWABTATWAATDDWTDBHWW



Motif ID: [UP00599](#)  
Motif name: KLF1\_R328H\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 12  
Similarity score: 0.0289279

Alignment:

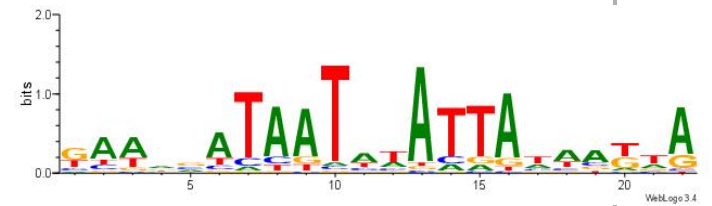
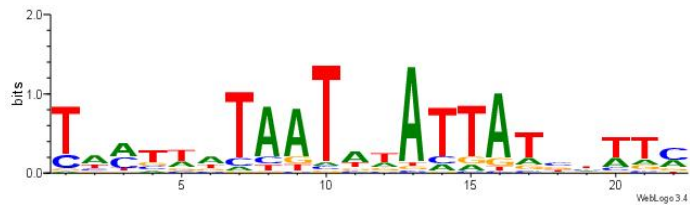
```
THMTWDTAATADATTATBHTTM  
-----WHTATTATTTDH-
```

Original motif

Consensus sequence: THMTWDTAATADATTATBHTTM

Reverse complement motif

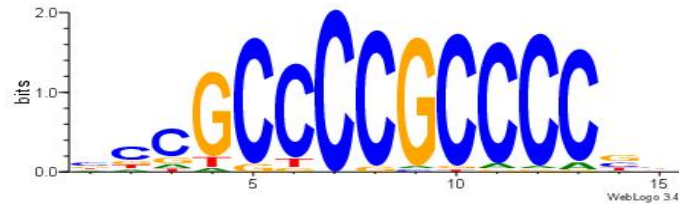
Consensus sequence: RAAHBATAATDTATTADWAYHA



**Dataset #: 4      Motif ID: 38      Motif name: cccGCCCCGCCCCsb**

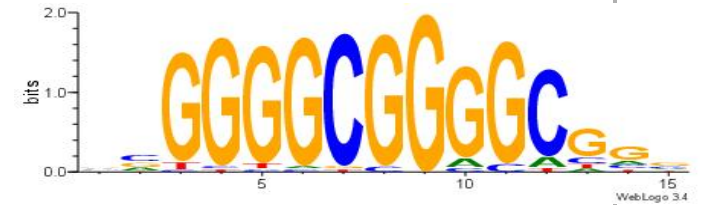
Original motif

Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif

Consensus sequence: BBGGGGCGGGGCGGB



**Best Matches for Motif ID 38 (Highest to Lowest)**

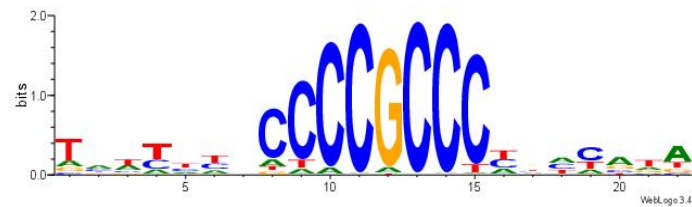
Motif ID:	<a href="#">UP00587</a>
Motif name:	EGR2
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	15
Similarity score:	0

Alignment:

THWYHHDCCCCGCCCHHHYADA  
---BCCGCCCCGCCCCBB----

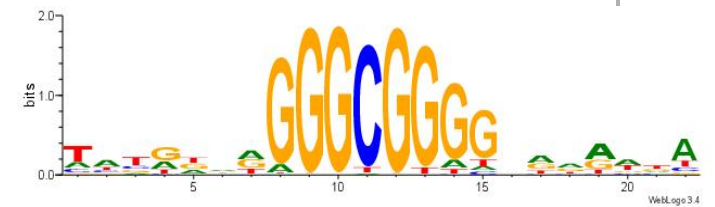
Original motif

Consensus sequence: THWYHHDCCCCGCCCHHHYADA



Reverse complement motif

Consensus sequence: TDTKHHHGGGCGGGGDHHMWHA



Motif ID: [UP00600](#)  
Motif name: KLF11  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 15  
Similarity score: 0.0183446

Alignment:

BHDDHMMCGCCCCCHBSBBVH  
-BCCGCCCCGCCCCBB-----

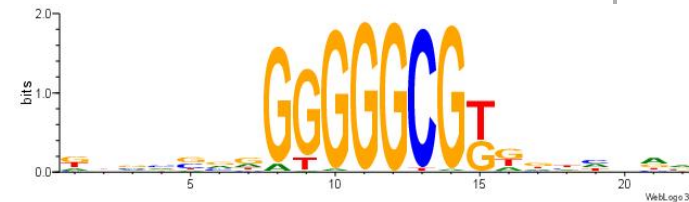
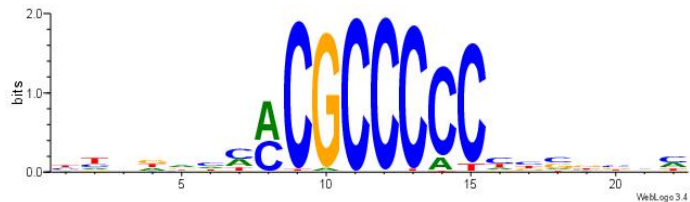
Original motif

Consensus sequence: BHDDHMMCGCCCCCHBSBBVH

Reverse complement motif

Consensus sequence: DBBBSBDGGGGGCGYRDDHHHV





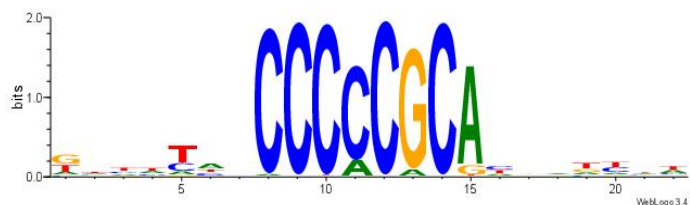
Motif ID: [UP00627](#)  
 Motif name: WT1\_R366C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 15  
 Similarity score: 0.0349416

**Alignment:**

KHHHTHHCCCCCGCAHDHDH  
 ---BCCGCCCGCCCCBB---

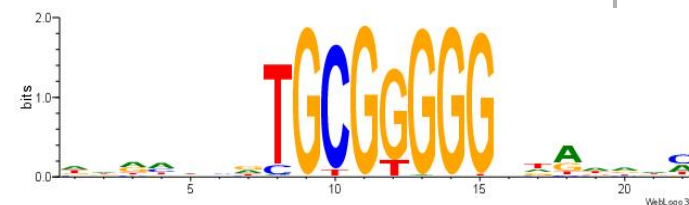
**Original motif**

Consensus sequence: KHHHTHHCCCCCGCAHDHDH



**Reverse complement motif**

Consensus sequence: HHHDHDTGCGGGGGHHAHHY



Motif ID: [UP00627](#)

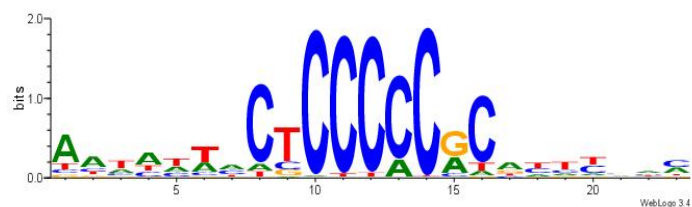
Motif name: WT1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 15  
 Similarity score: 0.0385263

**Alignment:**

AAHAHWHCTCCCCRCDDHHYVHM  
 -----BCCGCCCGCCCCBB--

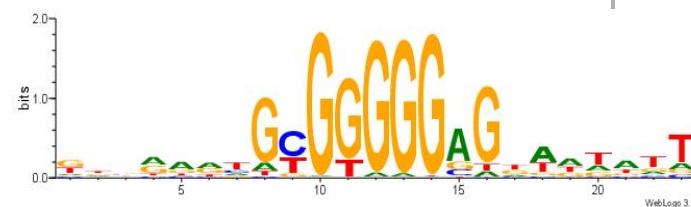
**Original motif**

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



**Reverse complement motif**

Consensus sequence: RHVMHHDGMGGGGGAGHWHHTHT




---

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: Backward  
 Position number: 6  
 Number of overlap: 15

Similarity score:

0.0405718

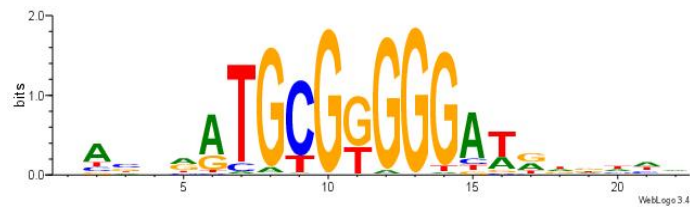
Alignment:

VABVRATGCGKGGGATRDDHHH

--BBGGGGCGGGGCGGB-----

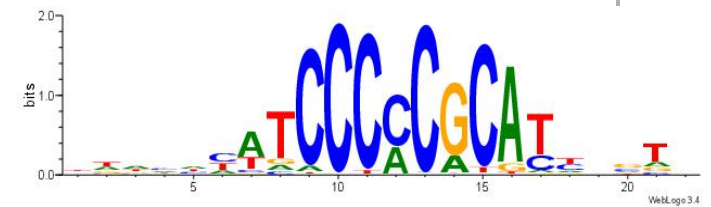
Original motif

Consensus sequence: VABVRATGCGKGGGATRDDHHH



Reverse complement motif

Consensus sequence: HHHHDMATCCCcCGCATKVBTV



**Dataset #: 4**

**Motif ID: 39**

**Motif name: kCAGCCAATmr**

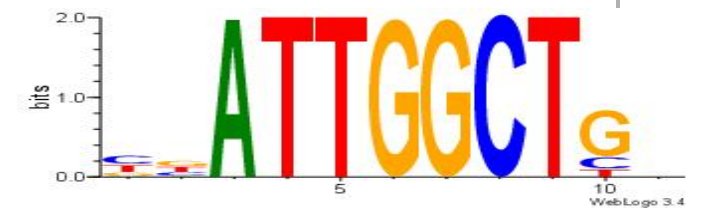
Original motif

Consensus sequence: DCAGCCAATVR



Reverse complement motif

Consensus sequence: MBATTGGCTGH



### Best Matches for Motif ID 39 (Highest to Lowest)

Motif ID:

[UP00584](#)

Motif name:

ARX\_T333N\_R2

Species:

Homo sapiens

Matching format of first motif:

Reverse Complement

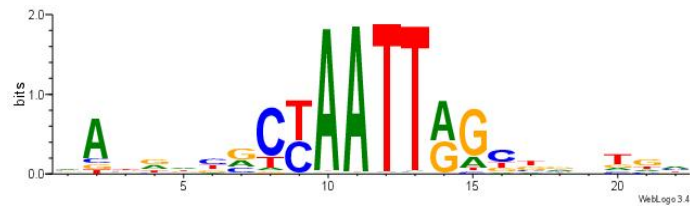
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 9  
 Number of overlap: 11  
 Similarity score: 0.00749807

Alignment:

VABDDBVCYAATTRGCBVDTDH  
 -----MBATTGGCTGH----

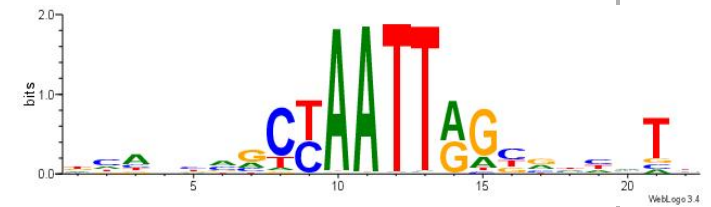
Original motif

Consensus sequence: VABDDBVCYAATTRGCBVDTDH



Reverse complement motif

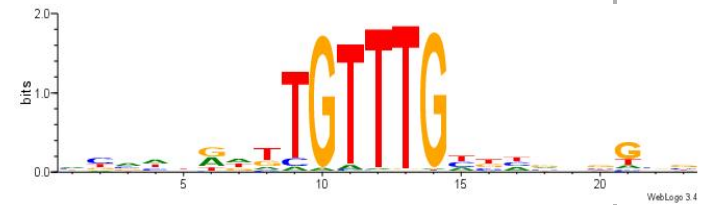
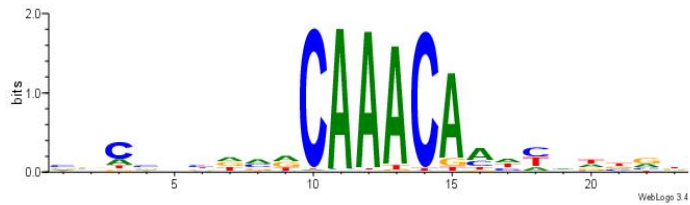
Consensus sequence: HHADVVGCKAATTMGVBDHVTB



Motif ID: [UP00605](#)  
 Motif name: NKX2-8  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0182048

Alignment:

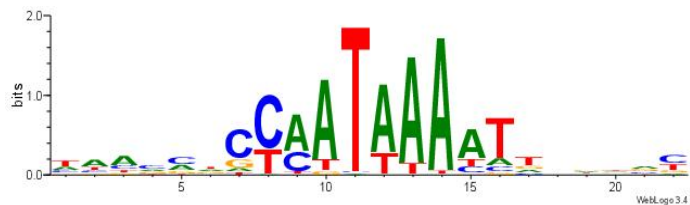




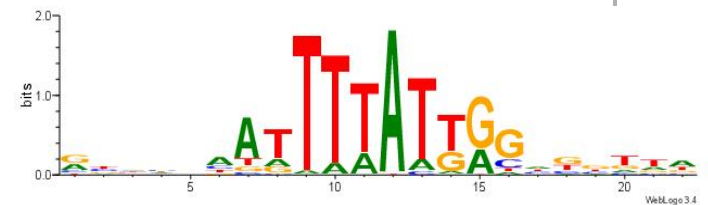
Motif ID: [UP00597](#)  
 Motif name: HOXD13\_S316C\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0203222

Alignment:  
 HHAVVDCCMATAAAAATDBDDVY  
 --DCAGCCAATVR-----

Original motif  
 Consensus sequence: HHAVVDCCMATAAAAATDBDDVY



Reverse complement motif  
 Consensus sequence: KBDHVDATTTTATYGGDVVTHH



Motif ID: [UP00625](#)

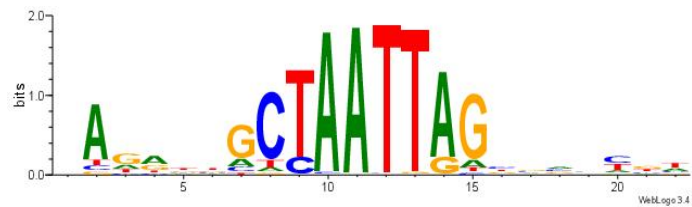
Motif name: VSX1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0208017

Alignment:

DAGRBBGCTAATTAGBVVBYBH  
 ---DCAGCCAATVR-----

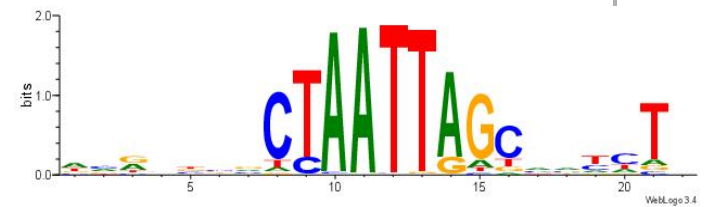
Original motif

Consensus sequence: DAGRBBGCTAATTAGBVVBYBH



Reverse complement motif

Consensus sequence: HBKBBVBCTAATTAGCVVKCTD



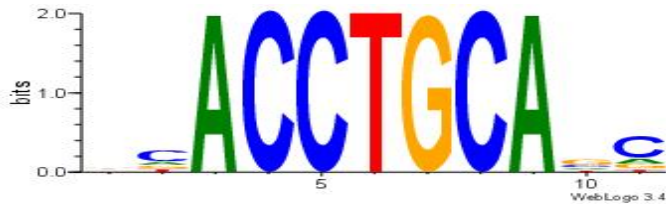
**Dataset #: 4      Motif ID: 40      Motif name: kcACCTGCAGc**

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

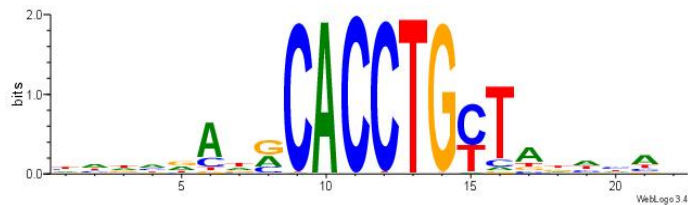
#### Alignment:

```

DTDHDTAKCAGGTGMDTHHDHH
----GBTGCAGGTGB-----
  
```

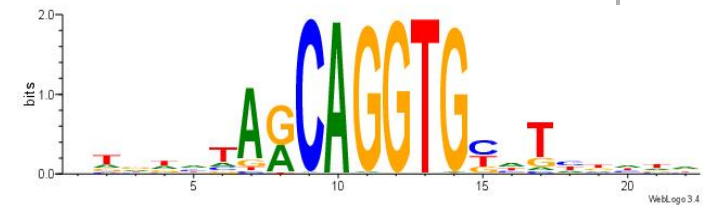
#### Original motif

Consensus sequence: HHDHDADRCACCTGYTADHHAD



#### Reverse complement motif

Consensus sequence: DTDHDTAKCAGGTGMDTHHDHH





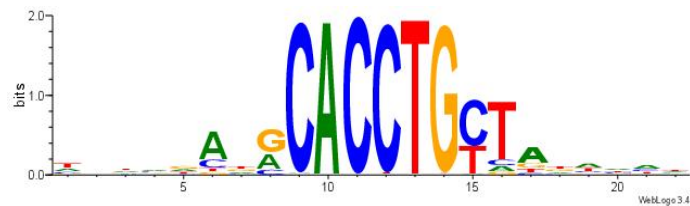
Motif ID: [UP00621](#)  
 Motif name: SNAI2\_D119E\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.000881825

**Alignment:**

HHHHDTAKCAGGTGMDTHBDDH  
 ----GBTGCAGGTGB-----

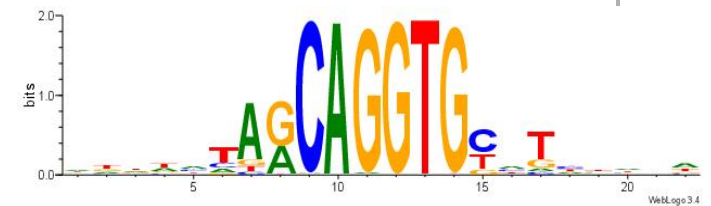
**Original motif**

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

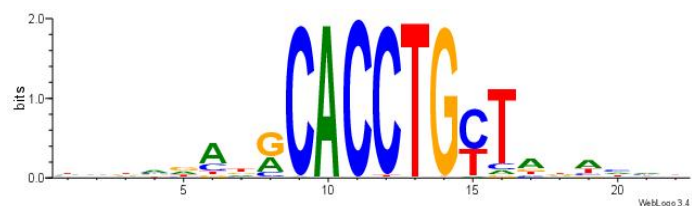
Number of overlap: 11  
Similarity score: 0.0013625

Alignment:

DHDHDTAKCAGGTGMDTHBDHH  
-----GBTGCAGGTGB-----

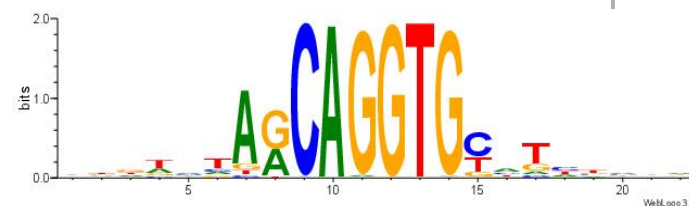
Original motif

Consensus sequence: HHDVDADRCACCTGYTADHHHD



Reverse complement motif

Consensus sequence: DHDHDTAKCAGGTGMDTHBDHH



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

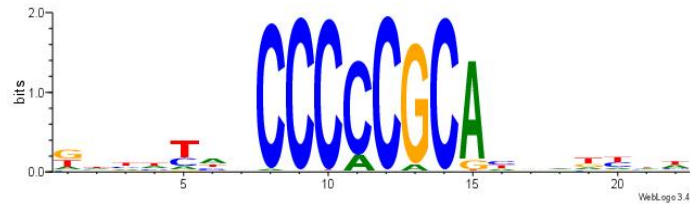
Alignment:

KHHHTHHCCCCGCAHDHDH  
-----BCACCTGCABC-----

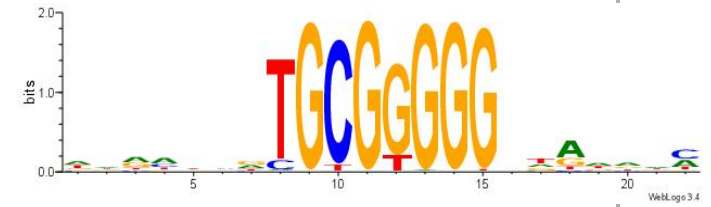
Original motif

Reverse complement motif

Consensus sequence: KHHHTHHCCCCGCAHDHDH HH



Consensus sequence: HHHDHDTGCGGGGGHHAHHHY



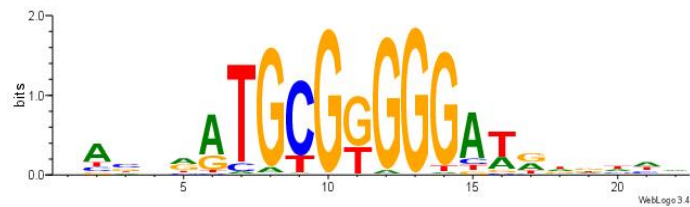
Motif ID: [UP00627](#)  
Motif name: WT1\_R366L\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 11  
Similarity score: 0.0381181

Alignment:

```
VABVRATGCGKGGGATRDDHHH  
----GBTGCAGGTGB-----
```

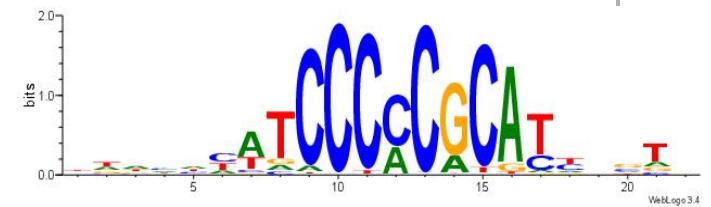
Original motif

Consensus sequence: VABVRATGCGKGGGATRDDHHH



Reverse complement motif

Consensus sequence: HHHHDMATCCCYCGCATKVBTV



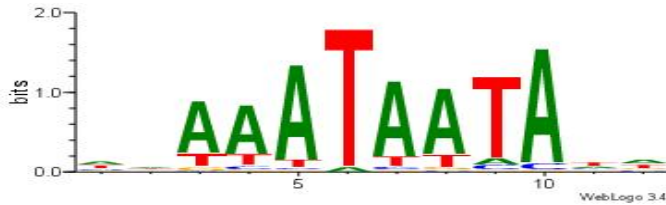
**Dataset #: 4**

**Motif ID: 41**

**Motif name: wwAAATAATAtw**

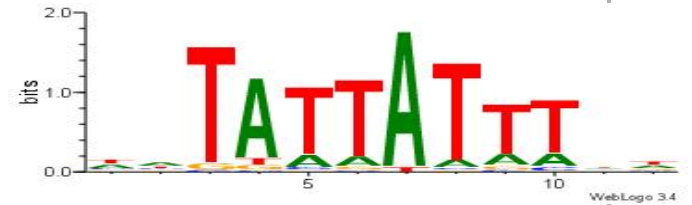
Original motif

Consensus sequence: HDAAATAATADD



Reverse complement motif

Consensus sequence: DDTATTATTTDH



### Best Matches for Motif ID 41 (Highest to Lowest)

Motif ID: [UP00627](#)  
Motif name: WT1\_H373Y\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 12  
Similarity score: 0.0155891

Alignment:

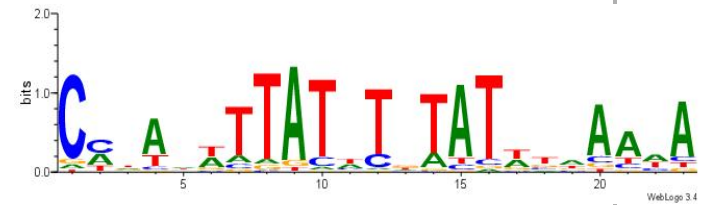
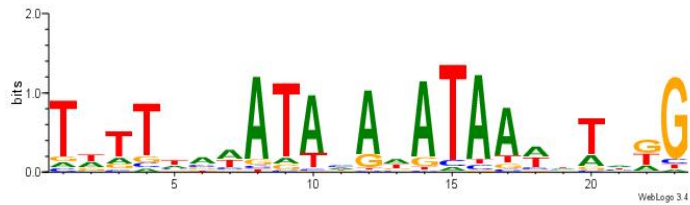
```
CYHAHWTTATD TDTATWBHAADA  
--DDTATTATTTDH-----
```

Original motif

Consensus sequence: TDTTHVWATAHADATAAWHTHKG

Reverse complement motif

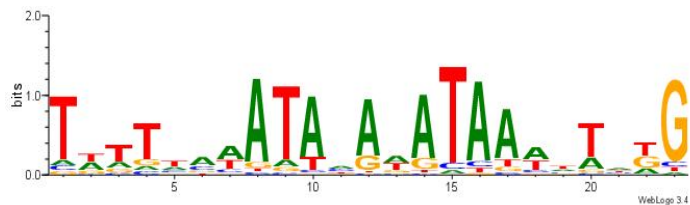
Consensus sequence: CYHAHWTTATD TDTATWBHAADA



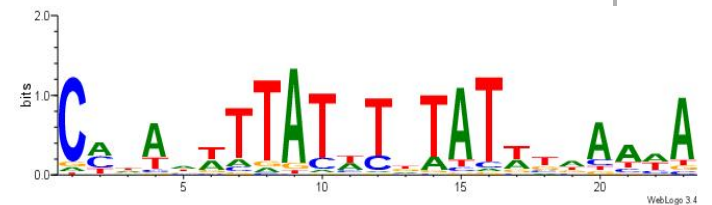
Motif ID: [UP00627](#)  
 Motif name: WT1\_R394L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 12  
 Similarity score: 0.0172798

Alignment:  
 TWTHVWATAHAWATAAWHTHKG  
 -----HDAAATAATADD--

Original motif  
 Consensus sequence: TWTHVWATAHAWATAAWHTHKG



Reverse complement motif  
 Consensus sequence: CRHAHWTTATWHTATWBHAAWA



Motif ID: [UP00627](#)

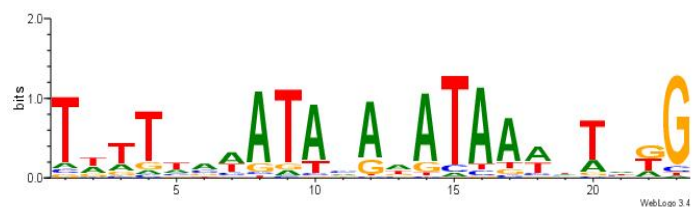
Motif name: WT1\_F392L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.0186508

**Alignment:**

CYHAHWTTATDTVTATWBHAAWA  
 --DDTATTATTTDH-----

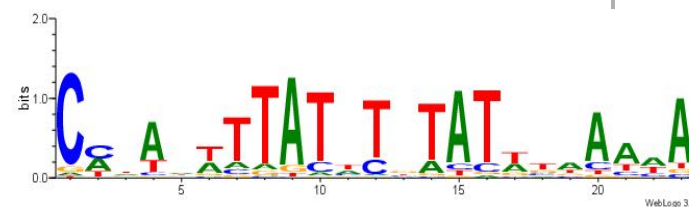
**Original motif**

Consensus sequence: TWTHVWATAVADATAAWHTHKG



**Reverse complement motif**

Consensus sequence: CYHAHWTTATDTVTATWBHAAWA




---

Motif ID: [UP00627](#)  
 Motif name: WT1\_R394W\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 12

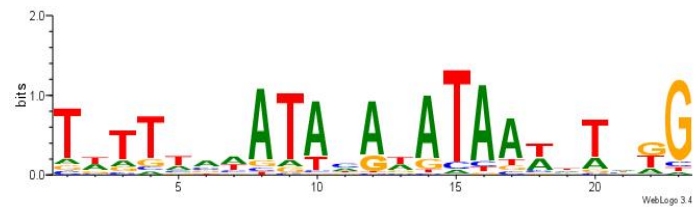
Similarity score: 0.0190508

Alignment:

CYHAHWTTATWTDATWBHAAWA  
--DDTATTATTTDH-----

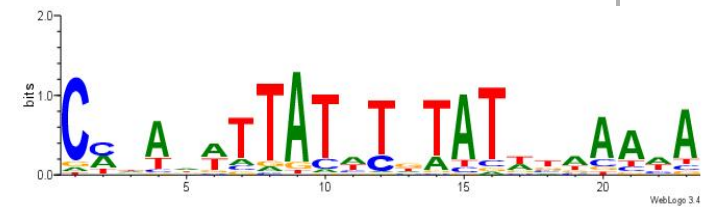
Original motif

Consensus sequence: TWTHVWATAHAWATAAWHCHKG



Reverse complement motif

Consensus sequence: CYHAHWTTATWTDATWBHAAWA



Motif ID: [UP00599](#)  
Motif name: KLF1\_R328H\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 12  
Similarity score: 0.0220346

Alignment:

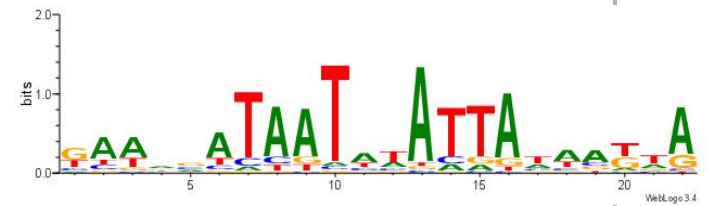
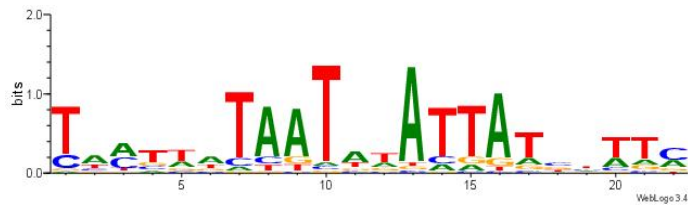
THMTWDTAATADATTATBHTTM  
-----DDTATTATTTDH-

Original motif

Consensus sequence: THMTWDTAATADATTATBHTTM

Reverse complement motif

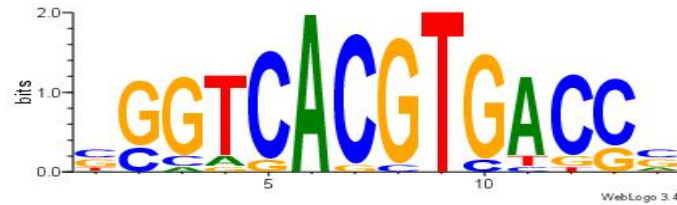
Consensus sequence: RAAHBATAATDTATTADWAYHA



**Dataset #: 4      Motif ID: 42      Motif name: sSGTCACGTGACCS**

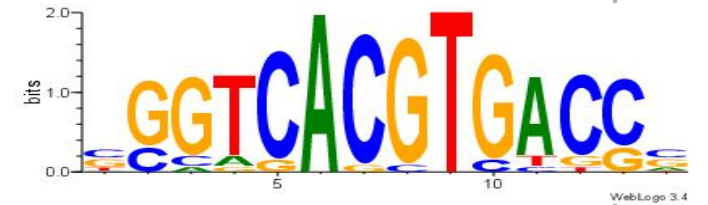
Original motif

Consensus sequence: SGGTCACGTGACCS



Reverse complement motif

Consensus sequence: SGGTCACGTGACCS



### Best Matches for Motif ID 42 (Highest to Lowest)

Motif ID:	<a href="#">UP00612</a>
Motif name:	PAX7
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.00859567

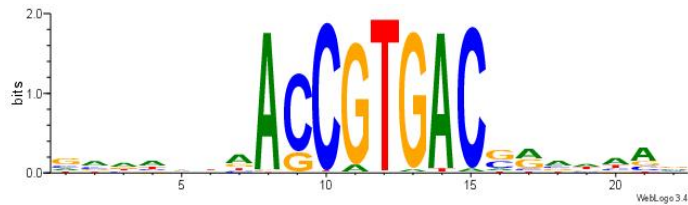
Alignment:



VTHDBKSGTCACGGTTHDHDBV  
-----SGGTCACGTGACCS----

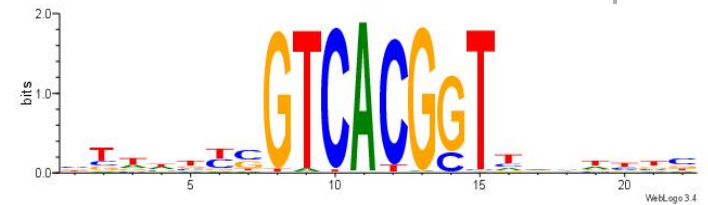
Original motif

Consensus sequence: VVDHDHAACCGTGACSRVDHAV



Reverse complement motif

Consensus sequence: VTHDBKSGTCACGGTTHDHDBV



Motif ID: [UP00605](#)  
Motif name: NKX2-8  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 5  
Number of overlap: 14  
Similarity score: 0.0145827

Alignment:

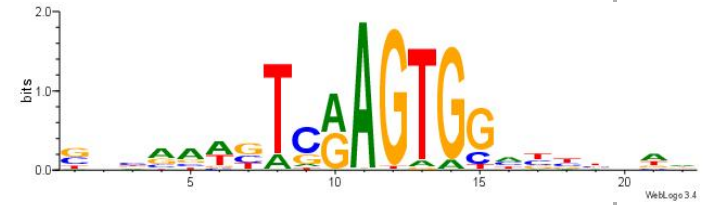
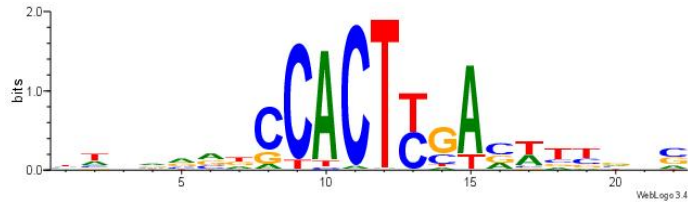
HHDVVVDCCACTYGAVWTVBS  
-----SGGTCACGTGACCS-----

Original motif

Consensus sequence: HHDVVVDCCACTYGAVWTVBS

Reverse complement motif

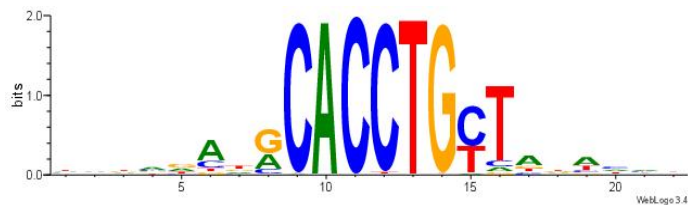
Consensus sequence: SBVMAWTCMAGTGGDBBDHH



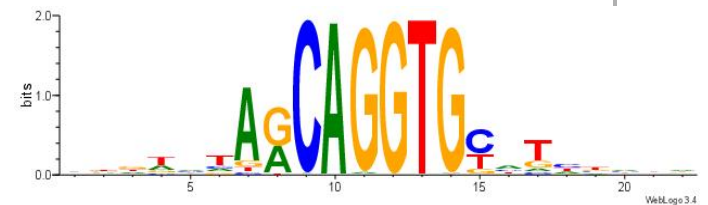
Motif ID: [UP00621](#)  
 Motif name: SNAI2\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0151743

Alignment:  
 DHDHDTAKCAGGTGMDTHBDHH  
 ----SGGTCACGTGACCS----

Original motif  
 Consensus sequence: HHDVDADRCACCTGYTADHHHD



Reverse complement motif  
 Consensus sequence: DHDHDTAKCAGGTGMDTHBDHH



Motif ID: [UP00599](#)

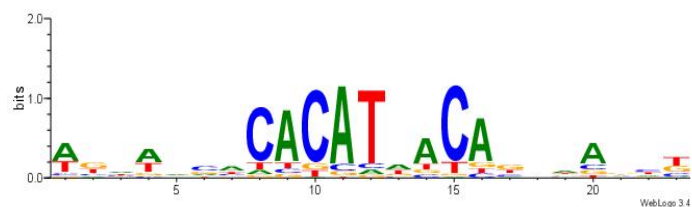
Motif name: KLF1\_R328H\_R2  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 7  
Number of overlap: 14  
Similarity score: 0.0168994

Alignment:

WBHWDVHCACATDACABDDADHK  
---SGGTCACGTGACCS-----

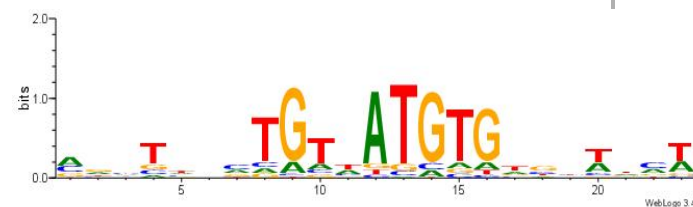
Original motif

Consensus sequence: WBHWDVHCACATDACABDDADHK



Reverse complement motif

Consensus sequence: RDHTDDBTGTDATGTGHVDWHBW



Motif ID: [UP00621](#)  
Motif name: SNAI2\_D119E\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 5  
Number of overlap: 14

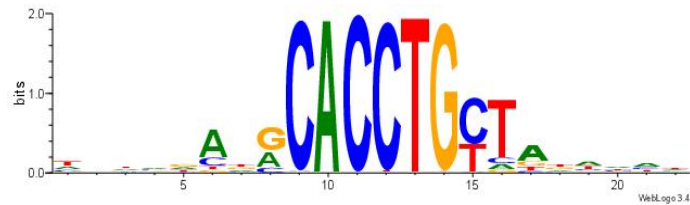
Similarity score: 0.0169037

Alignment:

```
HHHHDTAKCAGGTGMDTHBDDH  
----SGGTCACGTGACCS-----
```

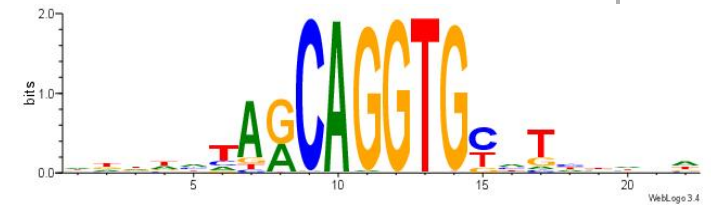
Original motif

Consensus sequence: HDDVDADRCACCTGYTADHHHH



Reverse complement motif

Consensus sequence: HHHHDTAKCAGGTGMDTHBDDH



**Dataset #: 4      Motif ID: 43      Motif name: wsTACwGTAsw**

Original motif

Consensus sequence: HVTACWGATABD



Reverse complement motif

Consensus sequence: DBTACWGTA VH



### Best Matches for Motif ID 43 (Highest to Lowest)

Motif ID: [UP00605](#)  
Motif name: NKX2-8  
Species: Homo sapiens  
Matching format of first motif: Original Motif

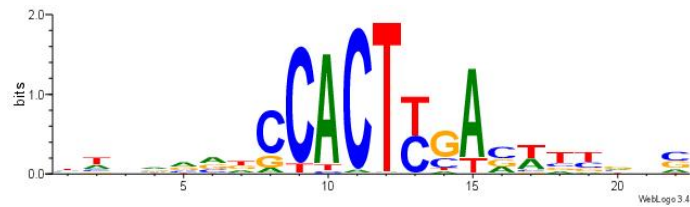
Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.0140465

Alignment:

SBVMAWVTCMAGTGGDBBBDHH  
 -----HVTACWGTABD-----

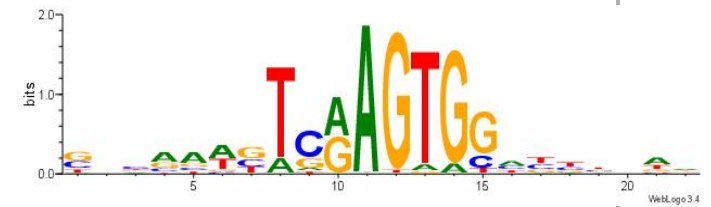
Original motif

Consensus sequence: HHDVVVDCCACTYGAVWTYVBS



Reverse complement motif

Consensus sequence: SBVMAWVTCMAGTGGDBBBDHH



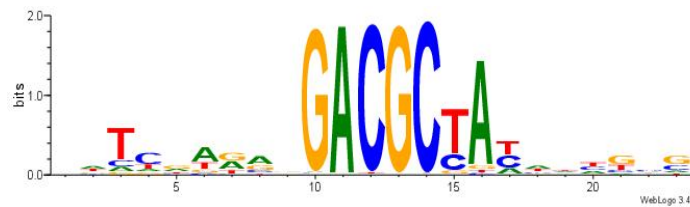
Motif ID: [UP00522](#)  
 Motif name: FOXN4\_primary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 11  
 Similarity score: 0.0186228

Alignment:

SDYHHHMTAGCGTCBBMTHGADH  
-----HVTACWGATABD-----

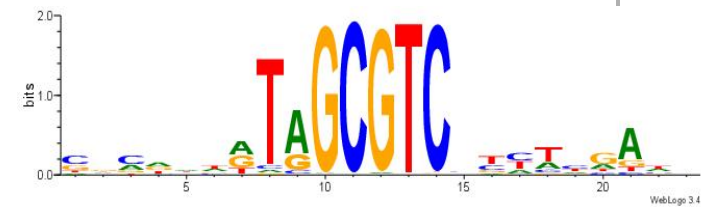
Original motif

Consensus sequence: HDTCDARVBGACGCTAYHHHKHS



Reverse complement motif

Consensus sequence: SDYHHHMTAGCGTCBBMTHGADH



Motif ID: [UP00608](#)  
Motif name: OVOL2  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 9  
Number of overlap: 11  
Similarity score: 0.0245566

Alignment:

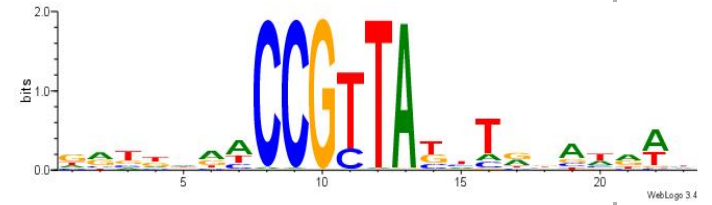
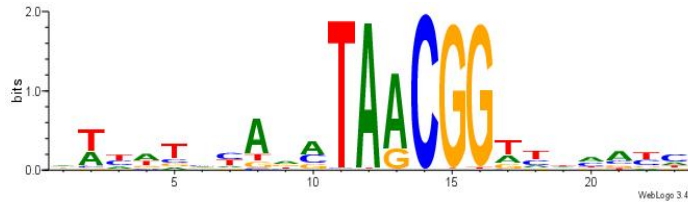
DMTHDMWCCGTTAYDTKVADHWD  
-----HVTACWGATABD-----

Original motif

Consensus sequence: DWHDTVYADMTAACGGWYDHAYH

Reverse complement motif

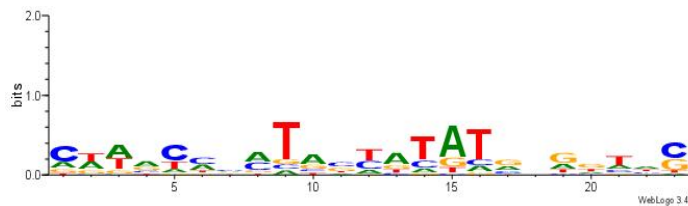
Consensus sequence: DMTHDMWCCGTTAYDTKVADHWD



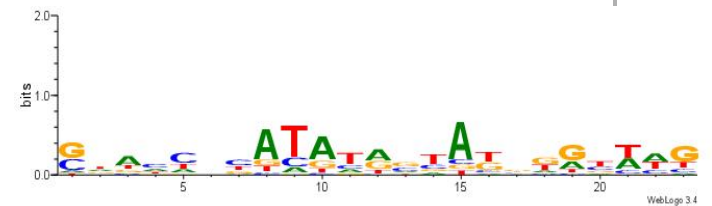
Motif ID: [UP00624](#)  
 Motif name: VENTX\_R143C\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.0247914

Alignment:  
 CWWVCMVMTABYATATVHDDTHS  
 -----HVTACWGTTABD-----

Original motif  
 Consensus sequence: CWWVCMVMTABYATATVHDDTHS



Reverse complement motif  
 Consensus sequence: SHAHHHVATATMBTAYVRGBWWG



Motif ID: [UP00627](#)

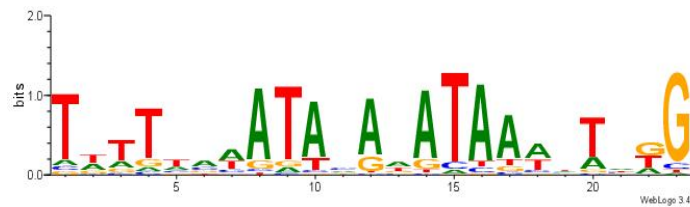
Motif name: WT1\_F392L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0266567

**Alignment:**

TWTTTHVWATAVADATAAAWHTHKG  
 -HVTACWGTABD-----

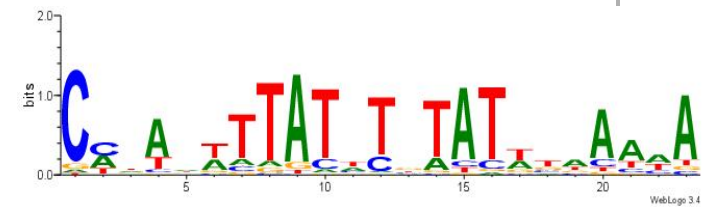
**Original motif**

Consensus sequence: TWTTTHVWATAVADATAAAWHTHKG



**Reverse complement motif**

Consensus sequence: CYHAHWTTATDTVTATWBHAAWA




---

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

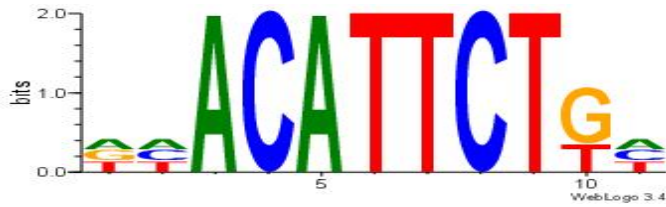
**Original motif**

Consensus sequence: DHACATTCTGH

**Reverse complement motif**

Consensus sequence: HCAGAATGTHD





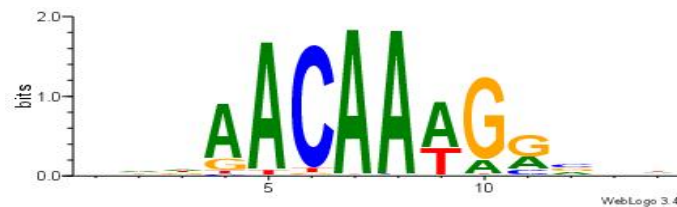
### Best Matches for Motif ID 44 (Highest to Lowest)

Motif ID: [UP00401](#)  
 Motif name: Sox4  
 Species: Homo sapiens  
 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

Alignment:  
 HBVMCWTGTGTTDDD  
 -DHACATTCTGH--

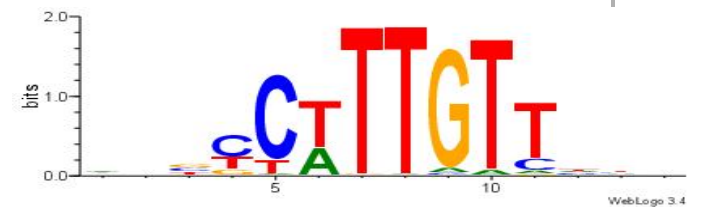
#### Original motif

Consensus sequence: DDDAACAAWGRVVH



#### Reverse complement motif

Consensus sequence: HBVMCWTGTGTTDDD



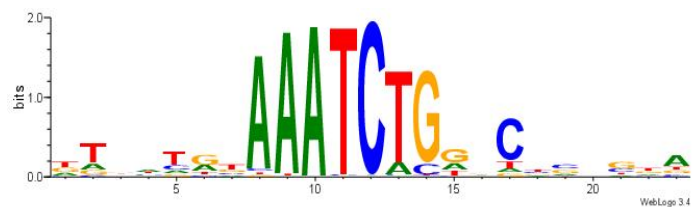
Motif ID: [UP00592](#)  
 Motif name: GFI1B\_A204T\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0061565

**Alignment:**

TDBHVVGVMCAGATTTVMAHHAD  
 -----HCAGAATGTHD-----

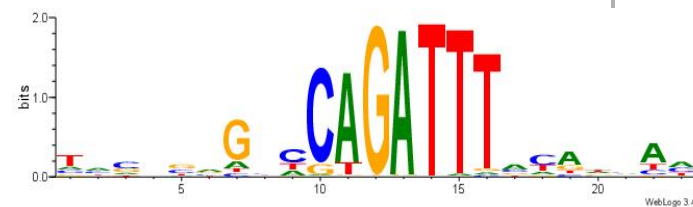
**Original motif**

Consensus sequence: DTDHTRBAAATCTGRVCBVHBD A



**Reverse complement motif**

Consensus sequence: TDBHVVGVMCAGATTTVMAHHAD



Motif ID: [UP00630](#)  
 Motif name: ZNF655\_E327G\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 9

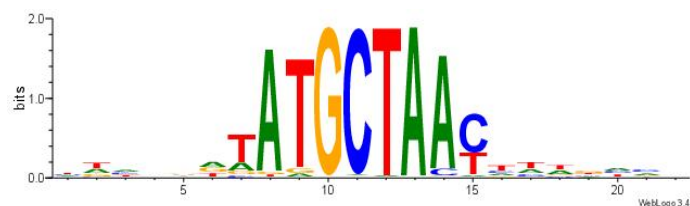
Number of overlap: 11  
Similarity score: 0.00867089

Alignment:

VVHBDHHKTTAGCATADHDHDH  
-----HCAGAATGTHD----

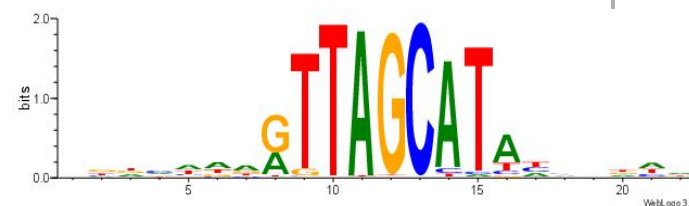
Original motif

Consensus sequence: HDHDDDTATGCTAAYHHDBHVV



Reverse complement motif

Consensus sequence: VVHBDHHKTTAGCATADHDHDH



---

Motif ID: [UP00630](#)  
Motif name: ZNF655\_S393L\_R1  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.00939906

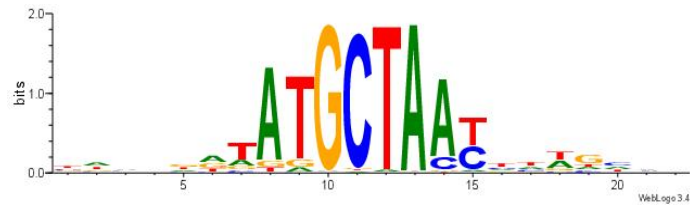
Alignment:

VBDCWHHMTTAGCATADHDHDV  
-----HCAGAATGTHD----

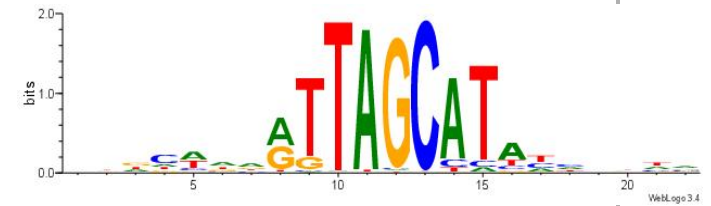
Original motif

Reverse complement motif

Consensus sequence: BDHDDDTATGCTAAYHHWGHVV



Consensus sequence: VBDCWHHMTTAGCATADHDHDV



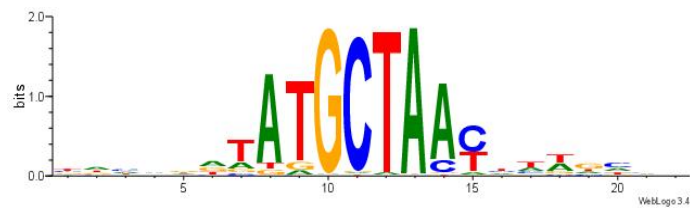
Motif ID: [UP00630](#)  
Motif name: ZNF655\_S393L\_R2  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.00973712

Alignment:

```
VVDHWHHKTTAGCATADHDDDV  
-----HCAGAATGTHD----
```

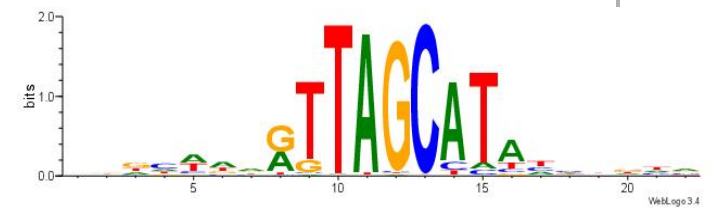
Original motif

Consensus sequence: BDHDDDTATGCTAAYHHWDHV



Reverse complement motif

Consensus sequence: VVDHWHHKTTAGCATADHDDDV



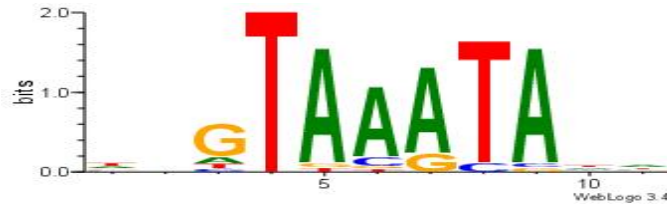
**Dataset #: 4**

**Motif ID: 45**

**Motif name: wbgTAAATAww**

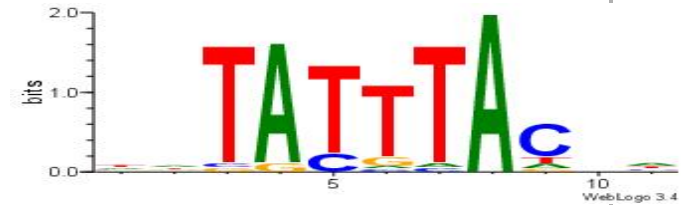
Original motif

Consensus sequence: DBGTAATAHD



Reverse complement motif

Consensus sequence: DHTATTTACBD



### Best Matches for Motif ID 45 (Highest to Lowest)

Motif ID:	<a href="#">UP00616</a>
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:

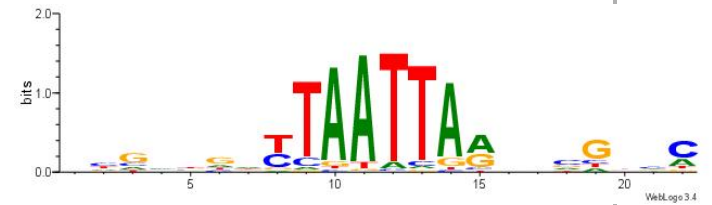
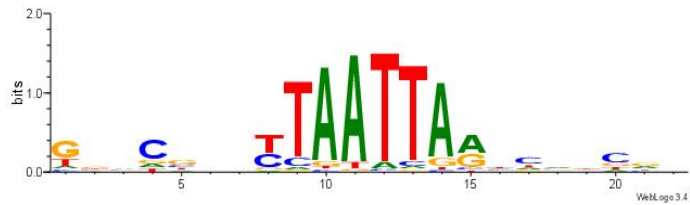
```
BHGDBDHKTAATTAMBBBGHBC
-----DHTATTTACBD-----
```

Original motif

Consensus sequence: GBHCBBBYAATTARHHVDCDB

Reverse complement motif

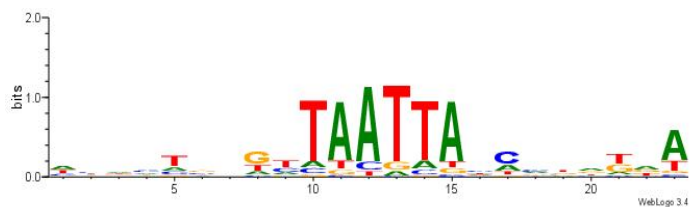
Consensus sequence: BHGDBDHKTAATTAMBBBGHBC



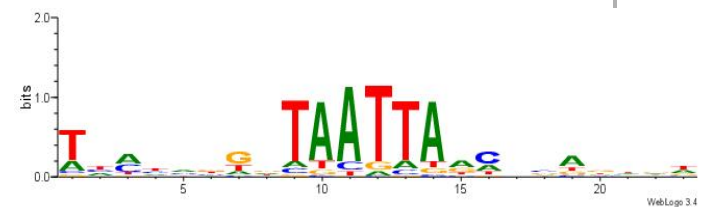
Motif ID: [UP00585](#)  
 Motif name: BCL6  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.00546358

Alignment:  
 TDRDVVGDTAATTAHCDBADDDH  
 -----DHTATTTACBD-----

Original motif  
 Consensus sequence: HHDHTBDGHTAATTAHCVBDKDA



Reverse complement motif  
 Consensus sequence: TDRDVVGDTAATTAHCDBADDDH



Motif ID: [UP00596](#)

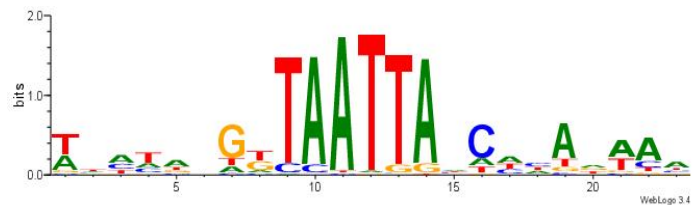
Motif name: HOXC4\_R158L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.00584685

**Alignment:**

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

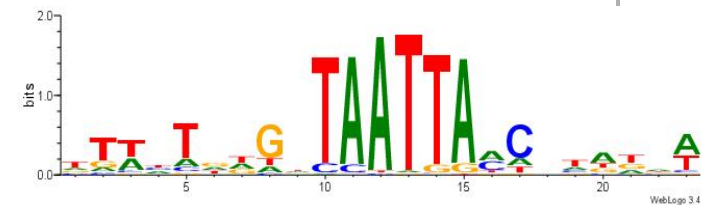
**Original motif**

Consensus sequence: WHHHDDGKTAATTAHCHHADWAH



**Reverse complement motif**

Consensus sequence: HTWDTDHGHTAATTARCDDHHHW




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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

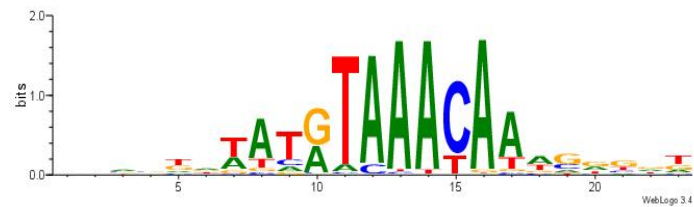
Similarity score: 0.00675467

Alignment:

BHVVDWATRTAAACAAWSDBDD  
-----DBGTAAATAHD-----

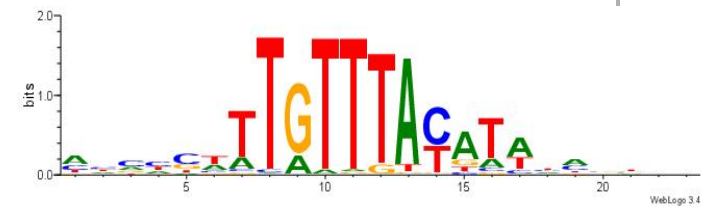
Original motif

Consensus sequence: BHVVDWATRTAAACAAWSDBDD



Reverse complement motif

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-----

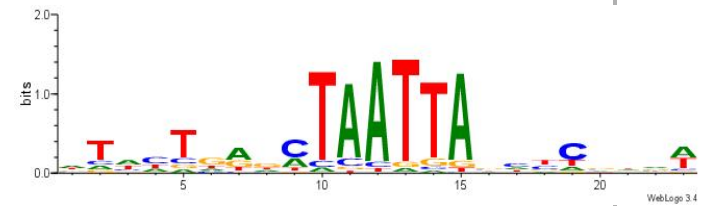
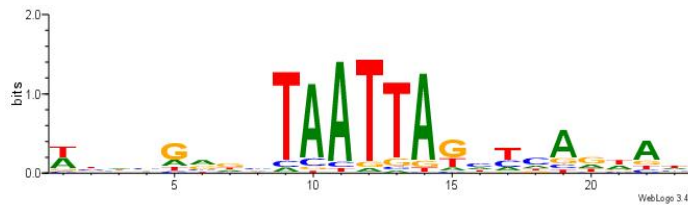
Original motif

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)**

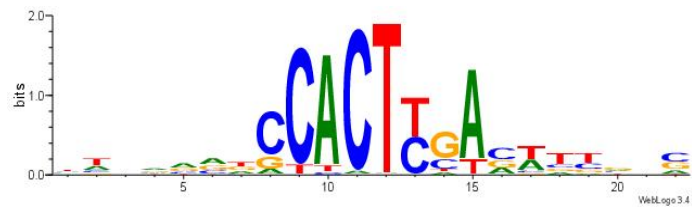
Motif ID:	<a href="#">UP00605</a>
Motif name:	NKX2-8
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	6
Similarity score:	0

Alignment:

SBVMAWVTCMAGTGGDBBBDHH  
-----CAGTGC-----

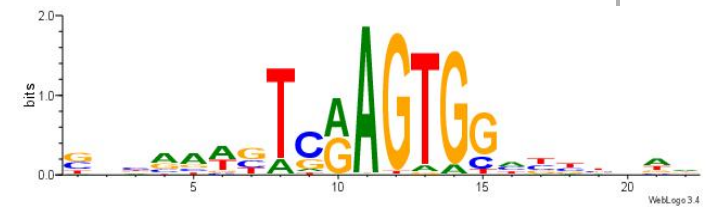
Original motif

Consensus sequence: HHDVVVDCCACTYGAVWTVVBS



Reverse complement motif

Consensus sequence: SBVMAWVTCMAGTGGDBBBDHH



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:

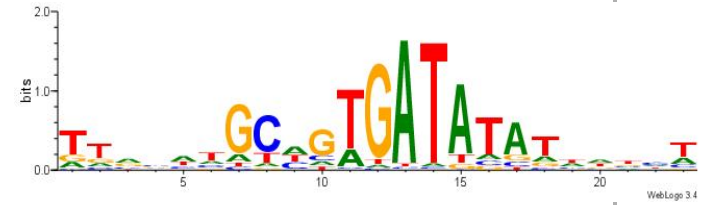
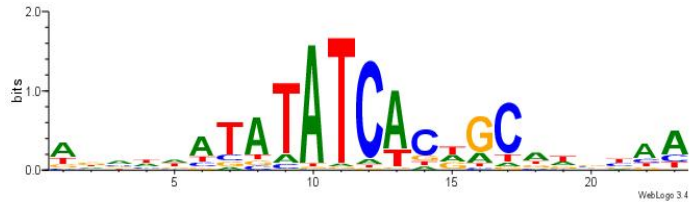
TTVBDDGCDGTGATATATDHBHT  
-----GCACTG-----

Original motif

Consensus sequence: ADVHDATATATCACDGCDDBBAA

Reverse complement motif

Consensus sequence: TTVBDDGCDGTGATATATDHBHT

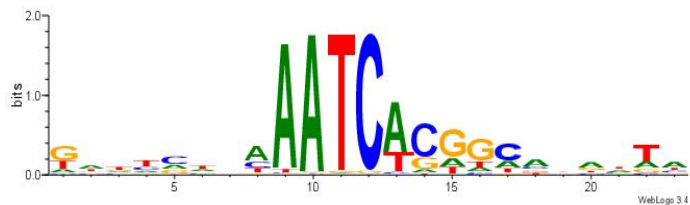


Motif ID: [UP00592](#)  
 Motif name: GFI1B\_A204T\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 6  
 Similarity score: 0.0198609

Alignment:  
 HAHDDBGCCGTGATTTTHDVHDDY  
 -----GCACTG-----

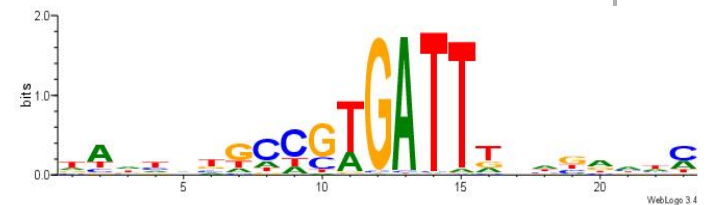
Original motif

Consensus sequence: KDDHVDDAAATCACGGCVDDHHTH



Reverse complement motif

Consensus sequence: HAHDDBGCCGTGATTTTHDVHDDY



Motif ID: [UP00592](#)

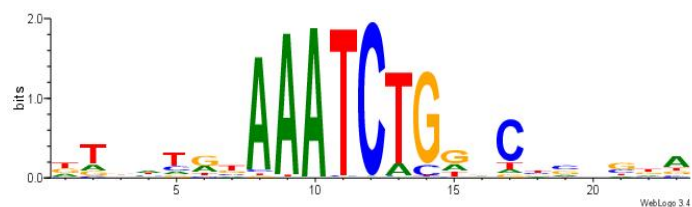
Motif name: GFI1B\_A204T\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 12  
 Number of overlap: 6  
 Similarity score: 0.0232927

**Alignment:**

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

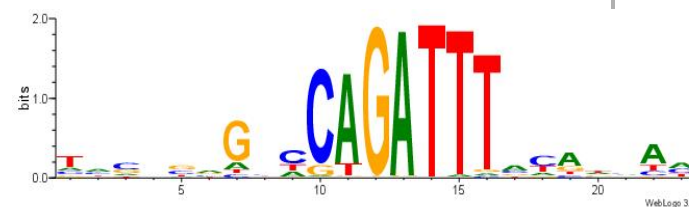
**Original motif**

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

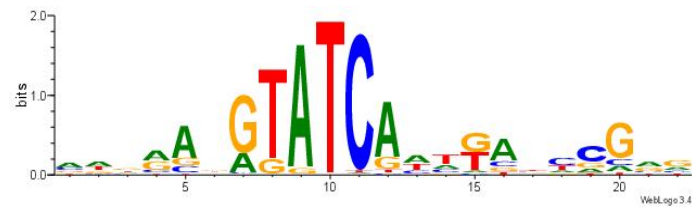
Alignment:

VBCGKVTYAWTGATACBTKHDB

-----GCACTG-----

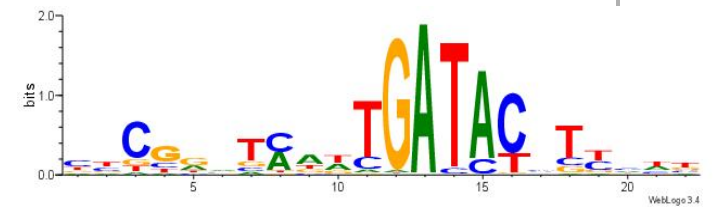
Original motif

Consensus sequence: VDDRABGTATCAWTKABYCGVV



Reverse complement motif

Consensus sequence: VBCGKVTYAWTGATACBTKHDB



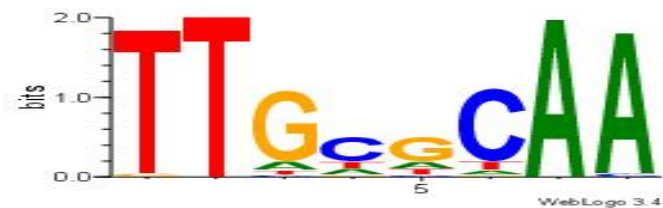
**Dataset #: 5**

**Motif ID: 47**

**Motif name: TFW1**

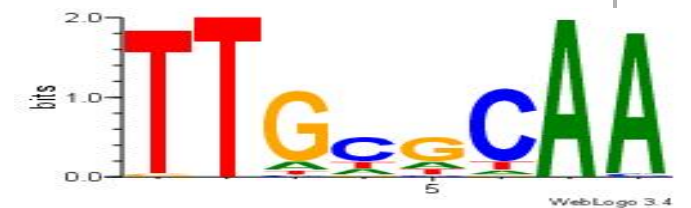
Original motif

Consensus sequence: TTGCGCAA



Reverse complement motif

Consensus sequence: TTGCGCAA



### Best Matches for Motif ID 47 (Highest to Lowest)

Motif ID:

[UP00523](#)

Motif name:

FOXR1\_primary

Species:

Homo sapiens

Matching format of first motif:

Reverse Complement

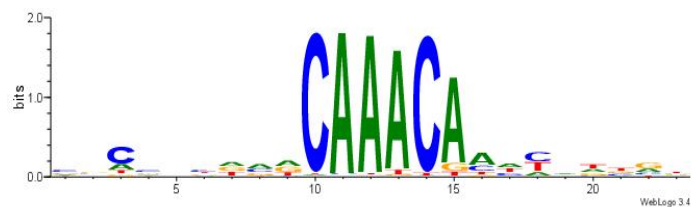
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 8  
Similarity score: 0.00299493

Alignment:

```
VVCVHBDVDCAAACAAHYVDBVD  
----TTGCGCAA-----
```

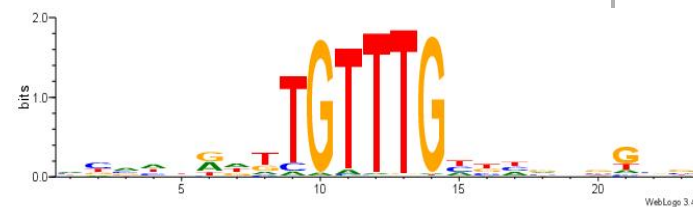
Original motif

Consensus sequence: VVCVHBDVDCAAACAAHYVDBVD



Reverse complement motif

Consensus sequence: DVVDBKHTTGTGGDBDBHVGVV



---

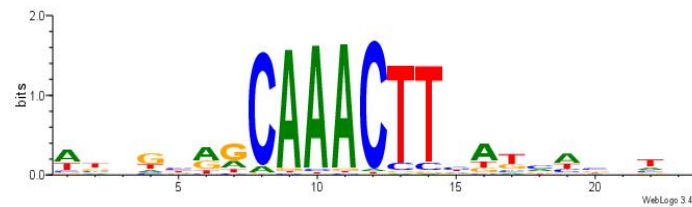
Motif ID: [UP00523](#)  
Motif name: FOXR1\_secondary  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 14  
Number of overlap: 8  
Similarity score: 0.00355095

Alignment:

DHHBHVRTDAAGTTTGCKBCHVW  
-----TTGCGCAA--

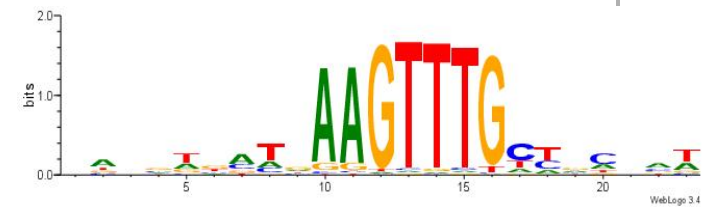
Original motif

Consensus sequence: WBHGBRGCAAACCTTHAKVHBHHD



Reverse complement motif

Consensus sequence: DHHBHVRTDAAGTTTGCKBCHVW



Motif ID: [UP00623](#)  
Motif name: VAX2\_L139M\_R2  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 12  
Number of overlap: 8  
Similarity score: 0.0110213

Alignment:

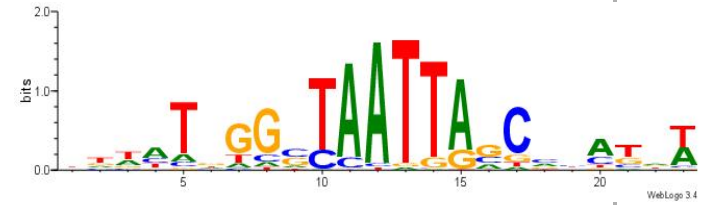
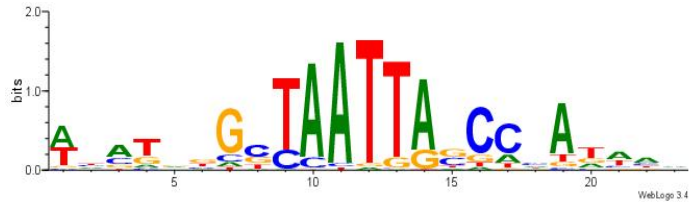
WHMTVBGSTAATTASCCHADWHD  
-----TTGCGCAA-----

Original motif

Consensus sequence: WHMTVBGSTAATTASCCHADWHD

Reverse complement motif

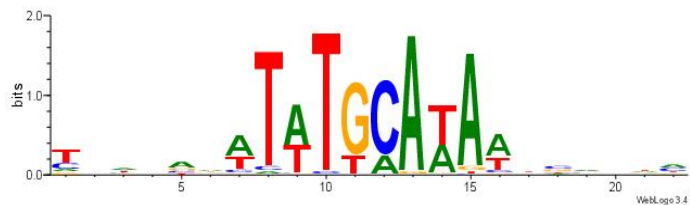
Consensus sequence: DHWDTDGGSTAATTASCBVAYHW



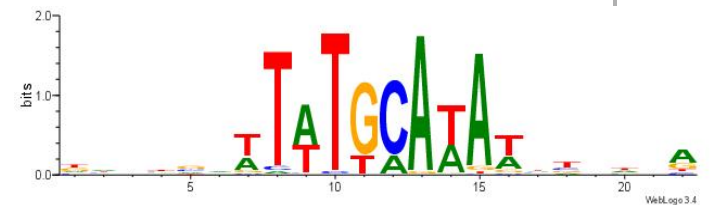
Motif ID: [UP00399](#)  
 Motif name: Oct-1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 8  
 Similarity score: 0.0113792

Alignment:  
 HDVBBVWTWTGCAWAWDBDHHA  
 -----TTGCGCAA-----

Original motif  
 Consensus sequence: THHDVDWTWTGCAWAWBBVVDH



Reverse complement motif  
 Consensus sequence: HDVBBVWTWTGCAWAWDBDHHA



Motif ID: [UP00623](#)



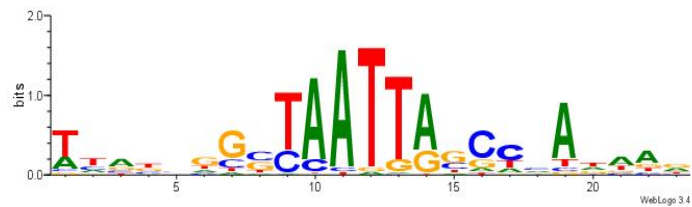
Motif name: VAX2\_REF\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.0115107

Alignment:

THVBVDGSTAATTASCCVADWAD  
 -----TTGCGCAA-----

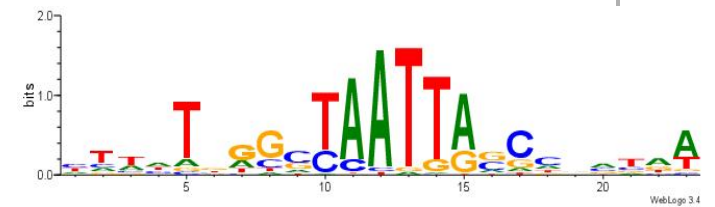
Original motif

Consensus sequence: THVBVDGSTAATTASCCVADWAD



Reverse complement motif

Consensus sequence: HTWDTVGGSTAATTASCHVVBHA



**Dataset #: 5      Motif ID: 48      Motif name: TFW2**

Original motif

Consensus sequence: YGGA CT TACG

Reverse complement motif

Consensus sequence: CGTAAGT CCK



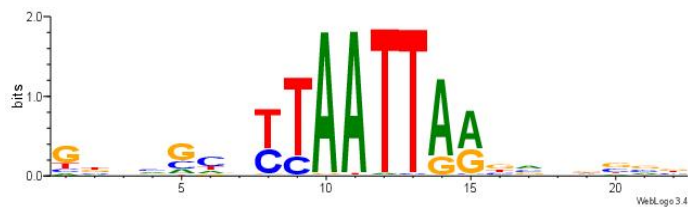
### Best Matches for Motif ID 48 (Highest to Lowest)

Motif ID: [UP00598](#)  
 Motif name: ISX\_R83Q\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0

Alignment:  
 BVBHDBBKTAATTAMVGCVDVC  
 -----YGGACTTACG-----

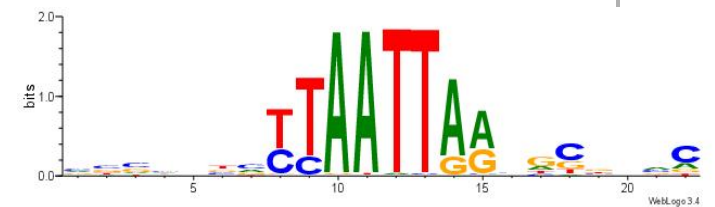
#### Original motif

Consensus sequence: GBHVCVYTAATTARBVHDBVB



#### Reverse complement motif

Consensus sequence: BVBHDBBKTAATTAMVGCVDVC



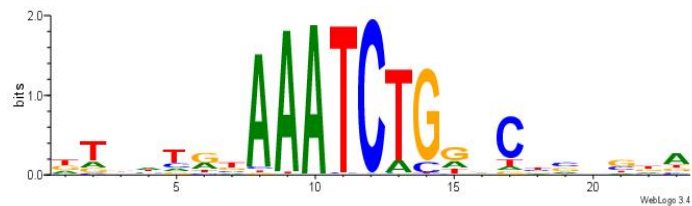
Motif ID: [UP00592](#)  
 Motif name: GFI1B\_A204T\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 10  
 Similarity score: 0.00513957

**Alignment:**

DTDHTRBAAATCTGRVCBVHBD  
 ----CGTAAGTCCK-----

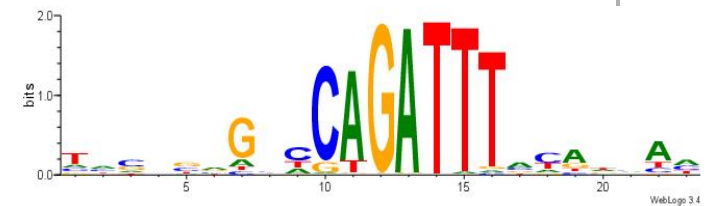
**Original motif**

Consensus sequence: DTDHTRBAAATCTGRVCBVHBD



**Reverse complement motif**

Consensus sequence: TDBHVVGVMCAGATTTVMAHHAD



Motif ID: [UP00616](#)  
 Motif name: POU3F4  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7

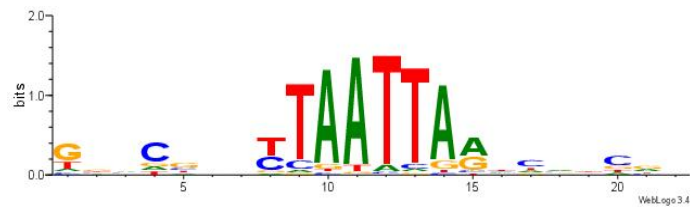
Number of overlap: 10  
Similarity score: 0.00646552

Alignment:

BHGDBDHKTAATTAMBBBGHBC  
-----YGGACTTACG-----

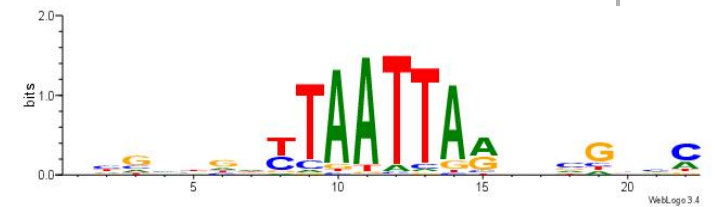
Original motif

Consensus sequence: GBHCBBBYTAATTARHHVDCDB



Reverse complement motif

Consensus sequence: BHGDBDHKTAATTAMBBBGHBC



---

Motif ID: [UP00610](#)  
Motif name: PAX4\_R192S\_R2  
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: 10  
Similarity score: 0.0102482

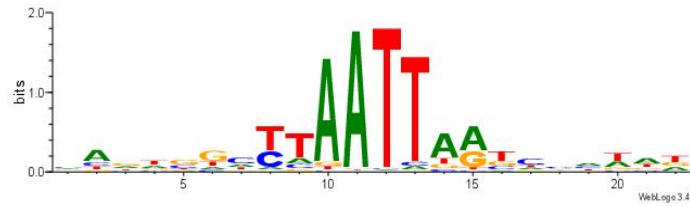
Alignment:

DDWHDDVKTAATTAMDCBDHTV  
-----CGTAAGTCCK-----

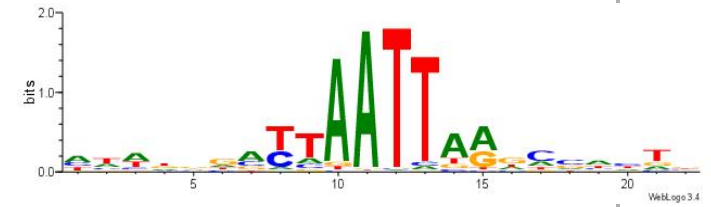
Original motif

Reverse complement motif

Consensus sequence: VADDBGHYTAATTARBHHHWDD



Consensus sequence: DDWHDDVKTAATTAMDCBDHTV



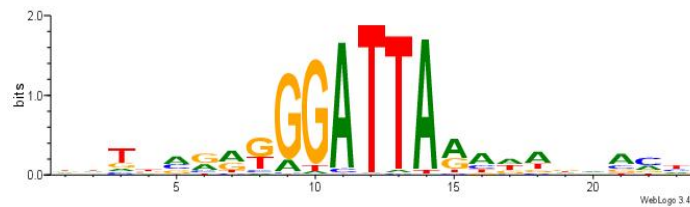
Motif ID: [UP00615](#)  
Motif name: PITX2  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 8  
Number of overlap: 10  
Similarity score: 0.0105906

Alignment:

```
HVTHHWDTKTAATCCYKMBVADD  
-----CGTAAGTCCK-----
```

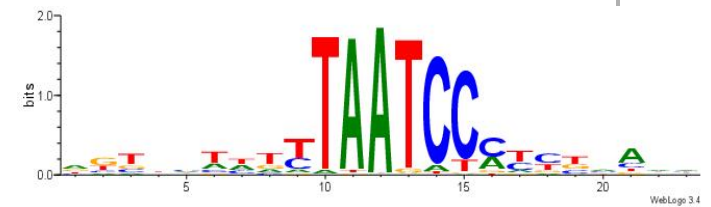
Original motif

Consensus sequence: DDTBVRRKGGATTARADWDHAVH



Reverse complement motif

Consensus sequence: HVTHHWDTKTAATCCYKMBVADD



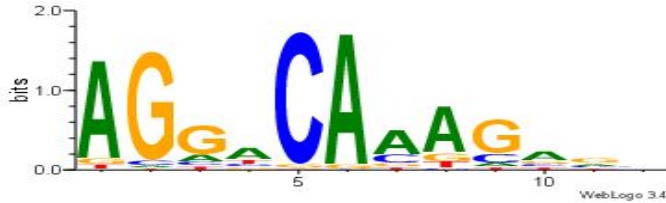
**Dataset #: 5**

**Motif ID: 49**

**Motif name: TFF1**

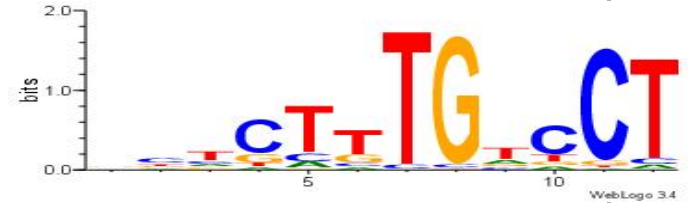
Original motif

Consensus sequence: AGGACAAAGAVV



Reverse complement motif

Consensus sequence: VVTCTTTGTCCT



### Best Matches for Motif ID 49 (Highest to Lowest)

Motif ID: [UP00599](#)  
Motif name: KLF1\_R328H\_R2  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 11  
Number of overlap: 12  
Similarity score: 0.0337556

Alignment:

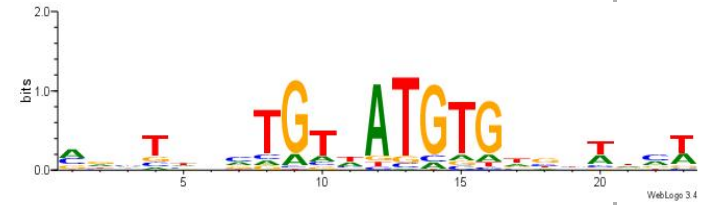
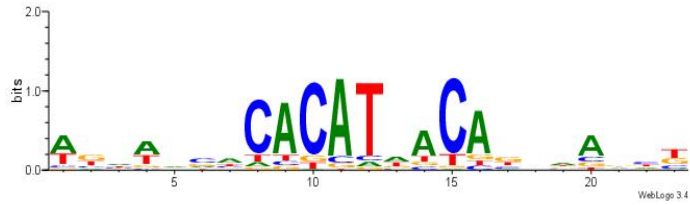
```
RDHTDDBTGTDATGTGHVDWHBW  
-VVTCTTTGTCCT-----
```

Original motif

Consensus sequence: WBHWDVHCACATDACABDDADHK

Reverse complement motif

Consensus sequence: RDHTDDBTGTDATGTGHVDWHBW

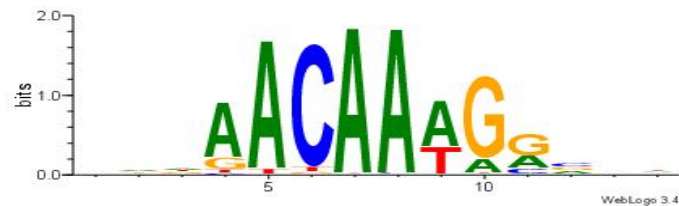


Motif ID: [UP00401](#)  
 Motif name: Sox4  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0367887

Alignment:  
 DDDAACAAWGRVVH  
 -AGGACAAAGAVV-

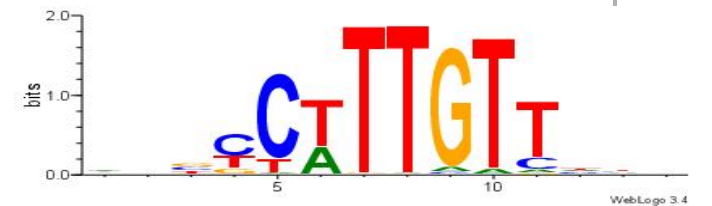
Original motif

Consensus sequence: DDDAACAAWGRVVH



Reverse complement motif

Consensus sequence: HBVMCWTGTGTTDDD



Motif ID: [UP00607](#)

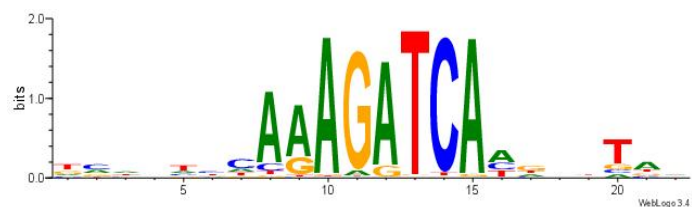
Motif name: NR2E3  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 12  
 Similarity score: 0.040146

**Alignment:**

DVDBHBCAAAGATCAHDHDTDD  
 -----AGGACAAAGAVV-

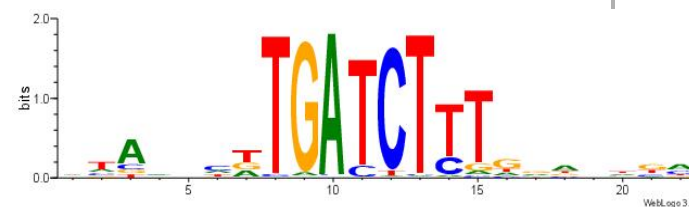
**Original motif**

Consensus sequence: DVDBHBCAAAGATCAHDHDTDD



**Reverse complement motif**

Consensus sequence: DDADHHHTGATCTTTGBHVDVD




---

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: 2  
 Number of overlap: 12



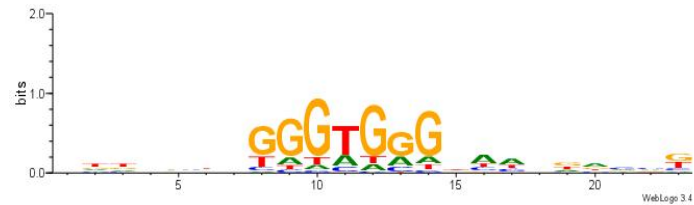
Similarity score: 0.0447887

Alignment:

DDDDHDGGGTGGGHHHDDDVVK  
-----AGGACAAAGAVV-

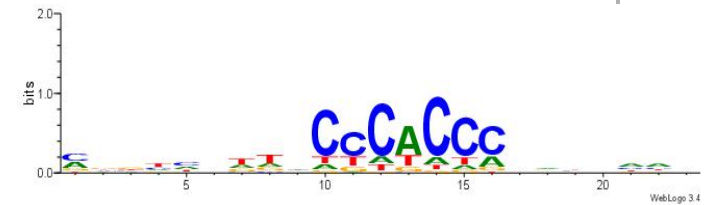
Original motif

Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



Reverse complement motif

Consensus sequence: YVVDHDHHHCCCACCCHHDDDDD



Motif ID: [UP00523](#)  
Motif name: FOXR1\_primary  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 7  
Number of overlap: 12  
Similarity score: 0.0496395

Alignment:

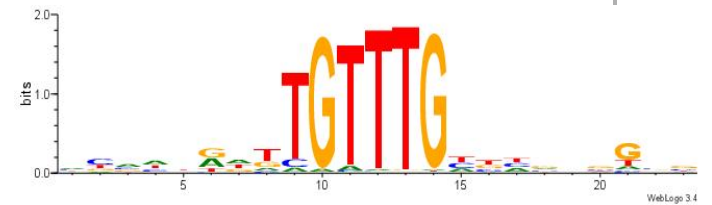
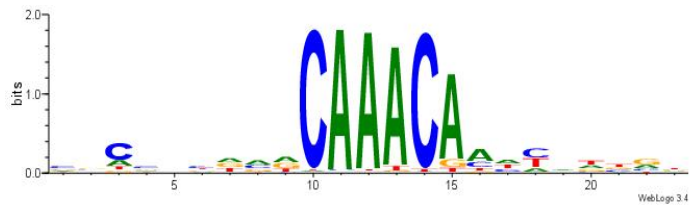
VVCVHBDVDCAAACAAHYVDBVD  
-----AGGACAAAGAVV-----

Original motif

Consensus sequence: VVCVHBDVDCAAACAAHYVDBVD

Reverse complement motif

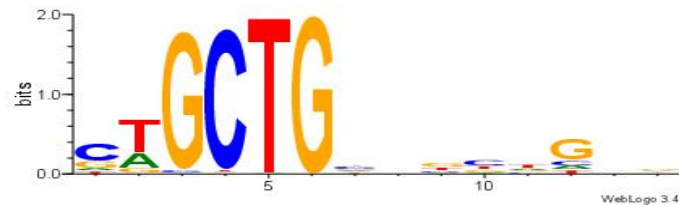
Consensus sequence: DVVDBKHTTGTTTGDBDBHVGVV



**Dataset #: 5      Motif ID: 50      Motif name: TFF11**

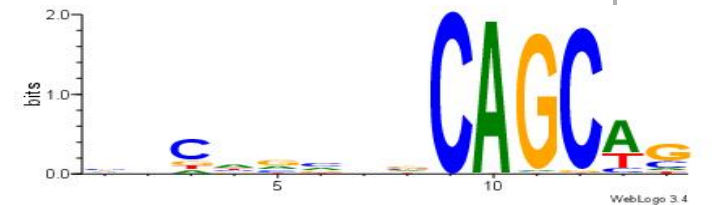
Original motif

Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif

Consensus sequence: HVCDBBDBCAGCAG



**Best Matches for Motif ID 50 (Highest to Lowest)**

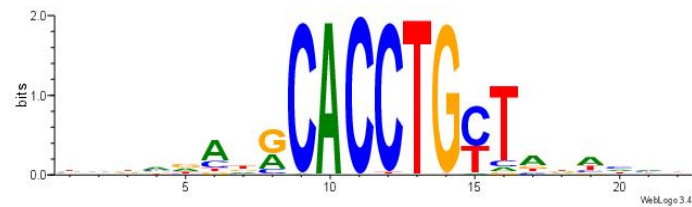
Motif ID:	<a href="#">UP00621</a>
Motif name:	SNAI2_REF_R1
Species:	Homo sapiens
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	14
Similarity score:	0.0352833

Alignment:

DHDHDTAKCAGGTGMDTHBDHH  
-----CTGCTGBDDBDGBD

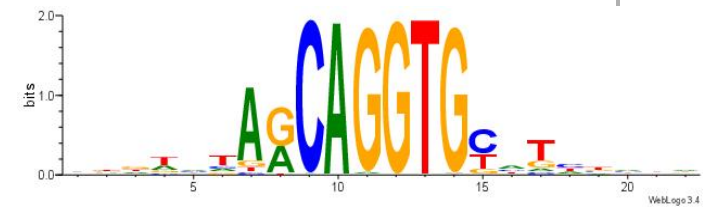
Original motif

Consensus sequence: HHDVDADRCACCTGYTADHHHD



Reverse complement motif

Consensus sequence: DHDHDTAKCAGGTGMDTHBDHH



Motif ID: [UP00621](#)  
Motif name: SNAI2\_T234I\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 9  
Number of overlap: 14  
Similarity score: 0.0382076

Alignment:

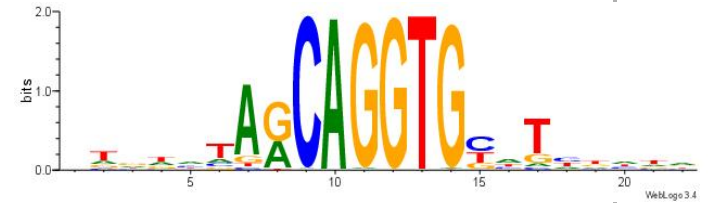
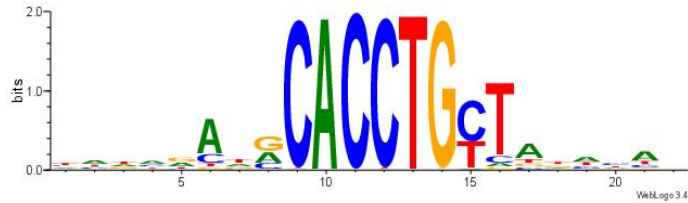
DTDHDTAKCAGGTGMDTHHDHH  
-----CTGCTGBDDBDGBD

Original motif

Consensus sequence: HHDHDADRCACCTGYTADHHAD

Reverse complement motif

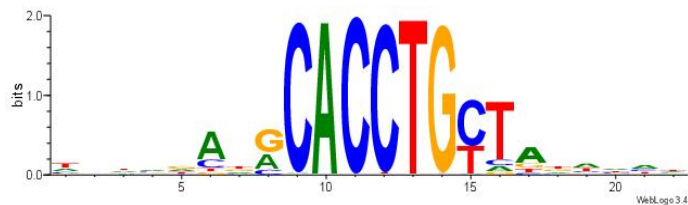
Consensus sequence: DTDHDTAKCAGGTGMDTHHDHH



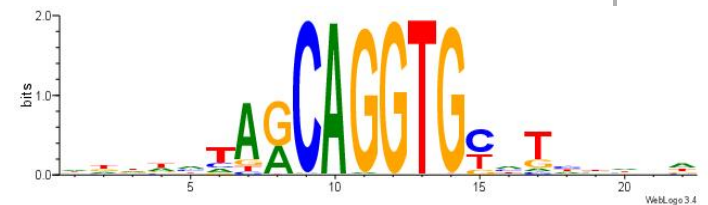
Motif ID: [UP00621](#)  
 Motif name: SNAI2\_D119E\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0390753

Alignment:  
 HHHHDTAKCAGGTGMDTHBDDH  
 -----CTGCTGBDBBDGBD

Original motif  
 Consensus sequence: HDDVDADRCACCTGYTADHHHH



Reverse complement motif  
 Consensus sequence: HHHHDTAKCAGGTGMDTHBDDH



Motif ID: [UP00630](#)

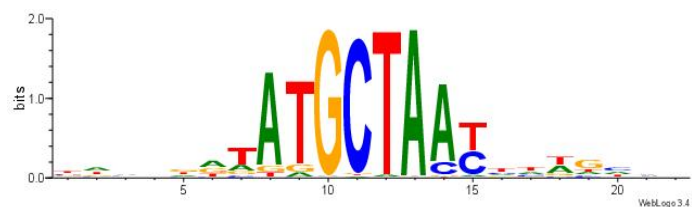
Motif name: ZNF655\_S393L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 14  
 Similarity score: 0.0448605

**Alignment:**

BDHDDDTATGCTAAYHHWGHVV  
 -----CTGCTGBDBBDGBD-

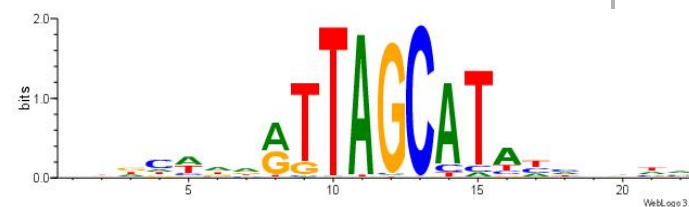
**Original motif**

Consensus sequence: BDHDDDTATGCTAAYHHWGHVV



**Reverse complement motif**

Consensus sequence: VBDCWHHMTTAGCATADHDHDV




---

Motif ID: [UP00630](#)  
 Motif name: ZNF655\_REF\_R2  
 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: 14



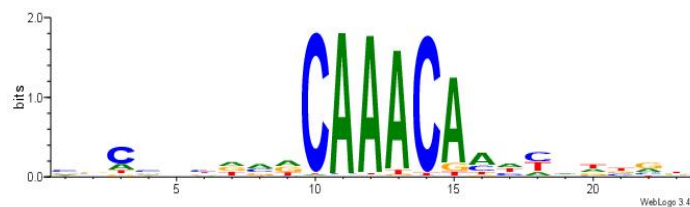
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 18  
 Similarity score: 0.0248291

Alignment:

VVCVHBDVDCAAACAAHYVDBVD  
 -----CACACACACACWCACACA

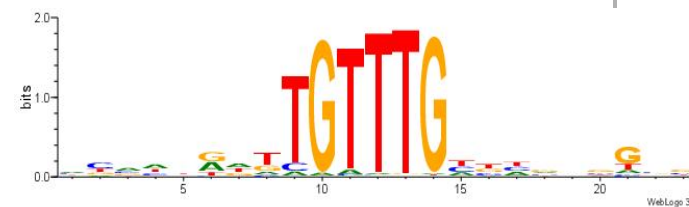
Original motif

Consensus sequence: VVCVHBDVDCAAACAAHYVDBVD



Reverse complement motif

Consensus sequence: DVVDBKHTTGTTTGDBDBHVGVV




---

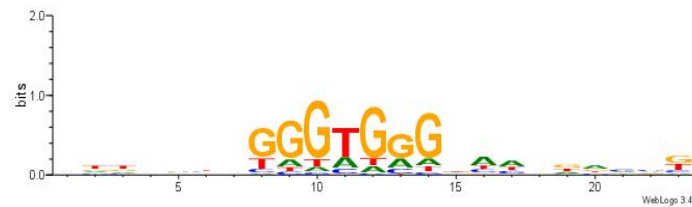
Motif ID: [UP00629](#)  
 Motif name: ZNF200\_H322Y\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0295798

Alignment:

YVVDHDHHHCCCACCCCHHDDDDD  
-----CACACACACACWCACACA

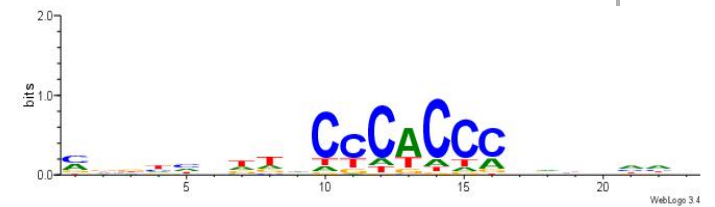
Original motif

Consensus sequence: DDDDDHDGGGTGGGHHHDDDDVVK



Reverse complement motif

Consensus sequence: YVVDHDHHHCCCACCCCHHDDDDD



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: Forward  
Position number: 6  
Number of overlap: 18  
Similarity score: 0.0343432

Alignment:

AAHAHWHCTCCCCRCDDHHYVHM  
-----CACACACACACWCACACA

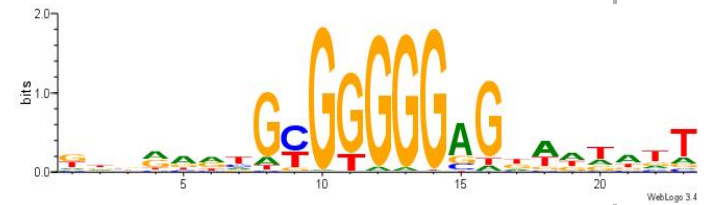
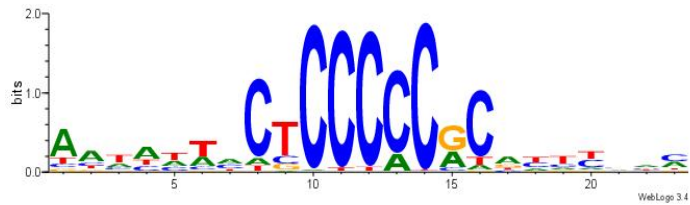
Original motif

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM

Reverse complement motif

Consensus sequence: RHVMHHDGMGGGGGAGHWHTHT



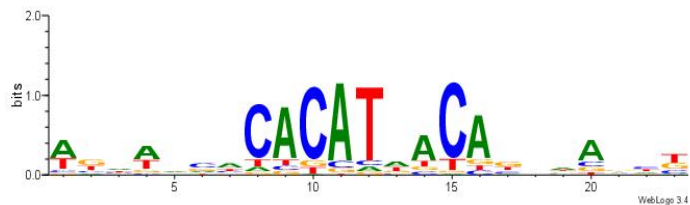


Motif ID: [UP00599](#)  
 Motif name: KLF1\_R328H\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 18  
 Similarity score: 0.0353298

Alignment:  
 RDHTDDBTGTDATGTGHVDWHBW  
 ----TGTGTGWGTGTGTGTGTG-

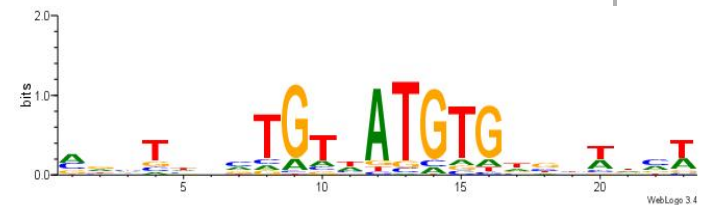
Original motif

Consensus sequence: WBHWDVHCACATDACABDDADHK



Reverse complement motif

Consensus sequence: RDHTDDBTGTDATGTGHVDWHBW



Motif ID: [UP00523](#)

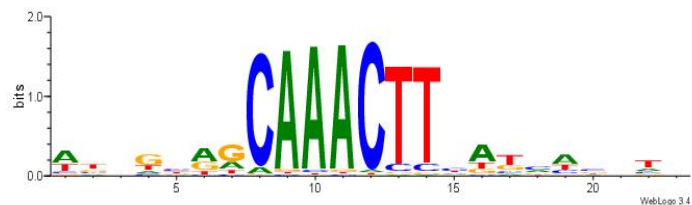
Motif name: FOXR1\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 18  
 Similarity score: 0.0372777

**Alignment:**

DHHBHVRTDAAGTTTGCKBCHVW  
 TGTGTGWTGTGTGTGTG-----

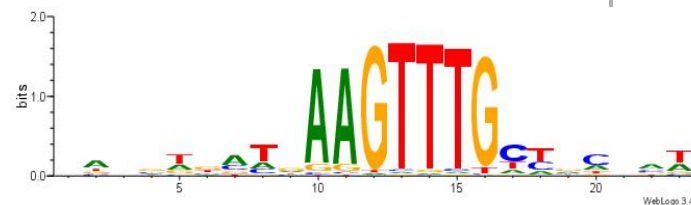
**Original motif**

Consensus sequence: WBHGBRGCAAACCTTHAKVHBHHD



**Reverse complement motif**

Consensus sequence: DHHBHVRTDAAGTTTGCKBCHVW




---

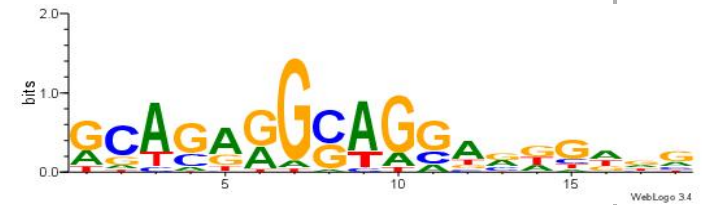
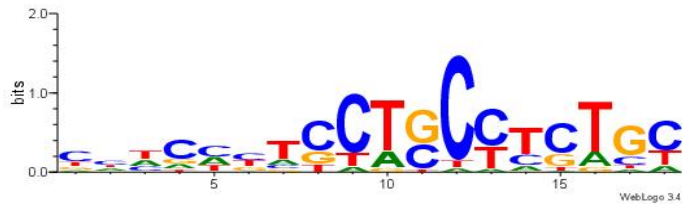
**Dataset #: 5      Motif ID: 52      Motif name: TFM2**

**Original motif**

Consensus sequence: CHHCHBTCCTSCYTCTGC

**Reverse complement motif**

Consensus sequence: GCAGAKGSAGGABDGHGDG



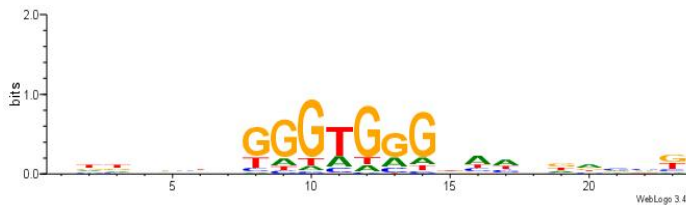
**Best Matches for Motif ID 52 (Highest to Lowest)**

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: 3  
 Number of overlap: 18  
 Similarity score: 0.0422436

Alignment:  
 YVVDHDDHHCCCACCCCHDDDDD  
 ---CHHCHBTCCTSCYTCTGC---

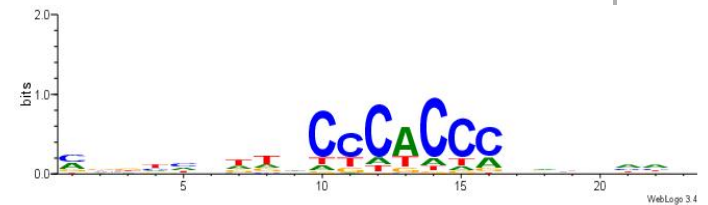
**Original motif**

Consensus sequence: DDDDDHDGGGTGGGHHHDDDDVVK



**Reverse complement motif**

Consensus sequence: YVVDHDDHHCCCACCCCHDDDDD





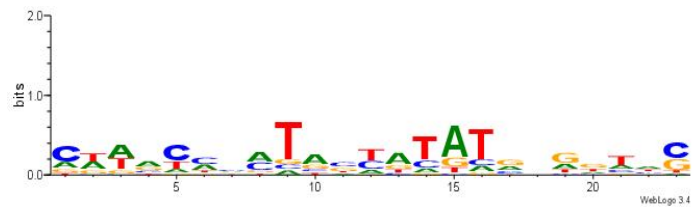
Number of overlap: 18  
Similarity score: 0.0508662

Alignment:

SHAHHHVATATMBTAYVRGBWWG  
-----GCAGAKGSAGGABDGHDG

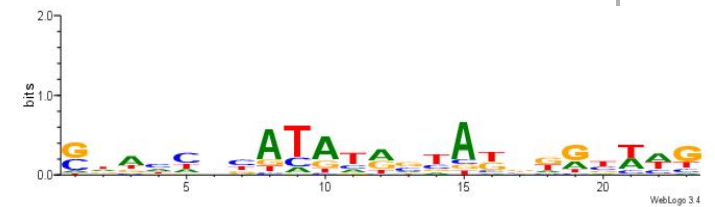
Original motif

Consensus sequence: CWWVCMVMTABYATATVHDDTHS



Reverse complement motif

Consensus sequence: SHAHHHVATATMBTAYVRGBWWG



Motif ID: [UP00594](#)  
Motif name: HESX1  
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: 18  
Similarity score: 0.0519761

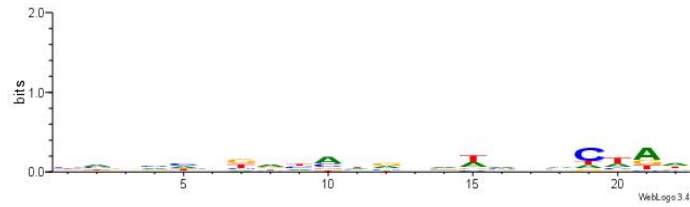
Alignment:

BHBVHVBDHVHVDHWVBVCHAD  
-CHHCHBTCCTSCYTCTGC---

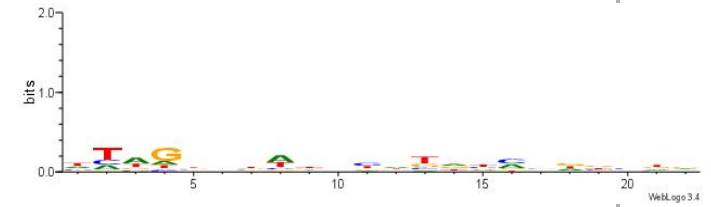
Original motif

Reverse complement motif

Consensus sequence: BHBVHVBDHVHVDHWVBVCHAD



Consensus sequence: DTHGBBBWHDVHBHDBVDVBHB



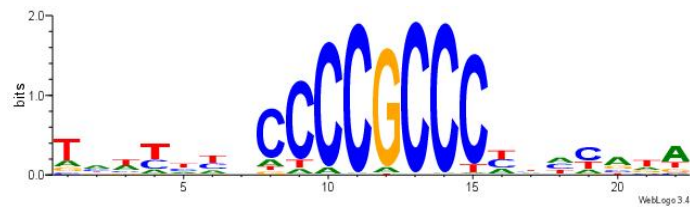
Motif ID: [UP00587](#)  
Motif name: EGR2  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 18  
Similarity score: 0.0521665

Alignment:

THWYHHDCCCCGCCCHHHYADA  
-CHHCHBTCCTSCYTCTGC---

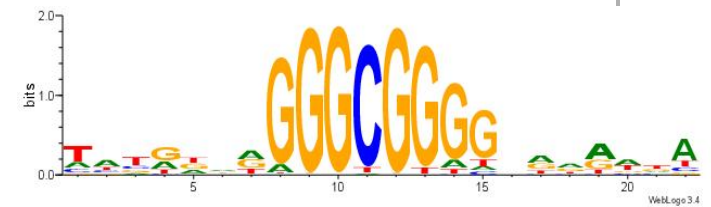
Original motif

Consensus sequence: THWYHHDCCCCGCCCHHHYADA



Reverse complement motif

Consensus sequence: TDTKHHHGGGCGGGGDHHMWHA



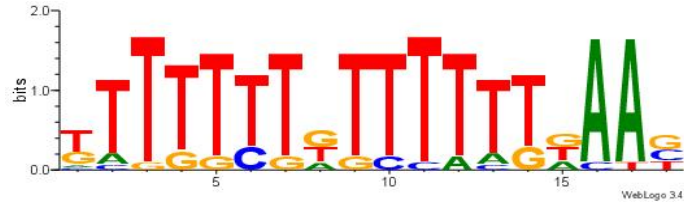
**Dataset #: 5**

**Motif ID: 53**

**Motif name: TFM3**

Original motif

Consensus sequence: KTTTTTTKTTTTTTDAAB



Reverse complement motif

Consensus sequence: BTTHAAAAAYAAAAAR



### Best Matches for Motif ID 53 (Highest to Lowest)

Motif ID:	<a href="#">UP00627</a>
Motif name:	WT1_H373Y_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:	18
Similarity score:	0.014126

Alignment:

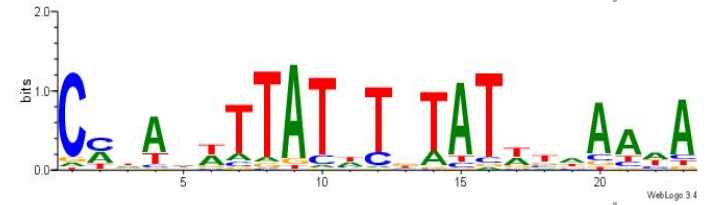
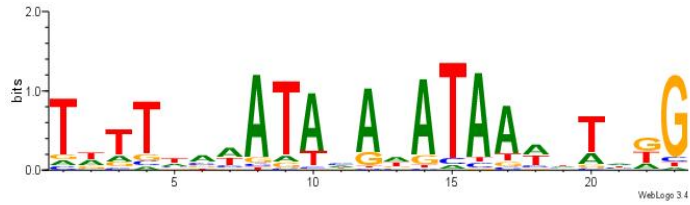
```
TDTTHVWATAHADATAAWHTHKG  
BTTHAAAAAYAAAAAR-----
```

Original motif

Consensus sequence: TDTTHVWATAHADATAAWHTHKG

Reverse complement motif

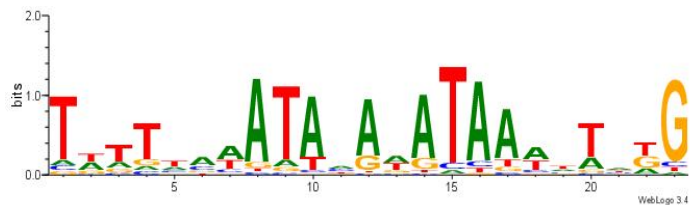
Consensus sequence: CYHAHWTTATD TDTATWBHAADA



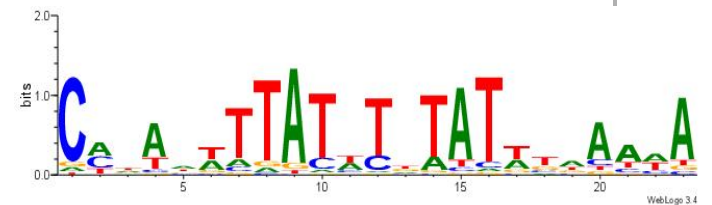
Motif ID: [UP00627](#)  
 Motif name: WT1\_R394L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 18  
 Similarity score: 0.0146039

Alignment:  
 CRHAHWTTATWHTATWBHAAWA  
 ---KTTTTTTKTTTTTTDAAB--

Original motif  
 Consensus sequence: TWTHVWATAHAWATAAWHTHKG



Reverse complement motif  
 Consensus sequence: CRHAHWTTATWHTATWBHAAWA



Motif ID: [UP00627](#)



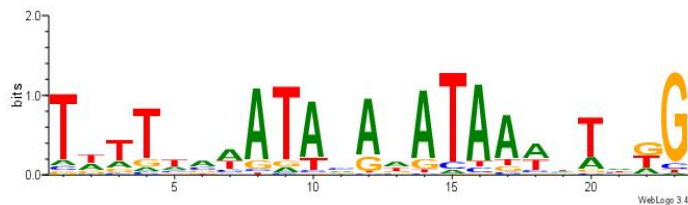
Motif name: WT1\_F392L\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 18  
 Similarity score: 0.0151319

**Alignment:**

TWTHVWATAVADATAAWHTHKG  
 BTTAAAAAYAAAAAR-----

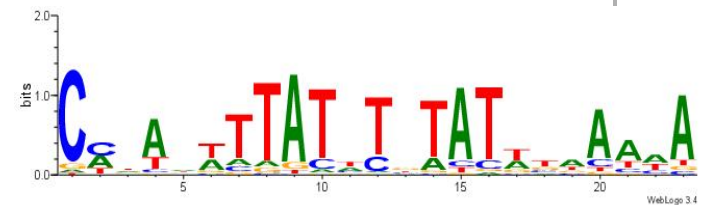
**Original motif**

Consensus sequence: TWTHVWATAVADATAAWHTHKG



**Reverse complement motif**

Consensus sequence: CYHAHWTTATDTVTATWBHAAWA




---

Motif ID: [UP00523](#)  
 Motif name: FOXR1\_primary  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 18

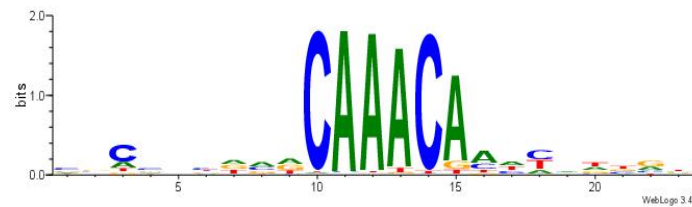
Similarity score: 0.0167729

Alignment:

```
DVVD BKHTTGT TTTGDBDBHVG VV  
--KTTTTTTKTTTTTTDAAB---
```

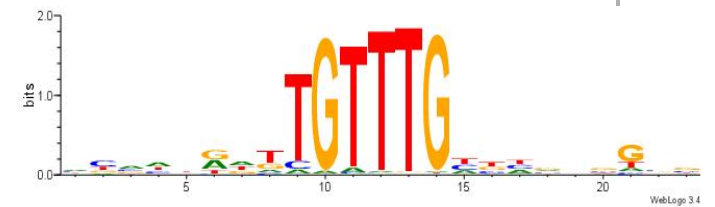
Original motif

Consensus sequence: VVCVHBDVDCAAACAAHYVDBVD



Reverse complement motif

Consensus sequence: DVVD BKHTTGT TTTGDBDBHVG VV



Motif ID: [UP00627](#)  
Motif name: WT1\_R394W\_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: 18  
Similarity score: 0.017136

Alignment:

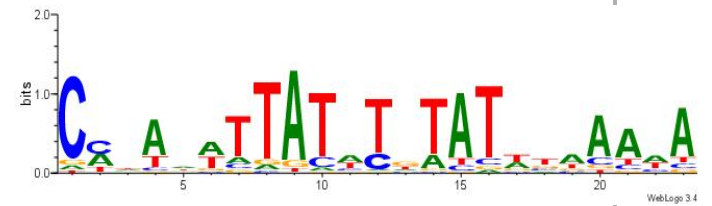
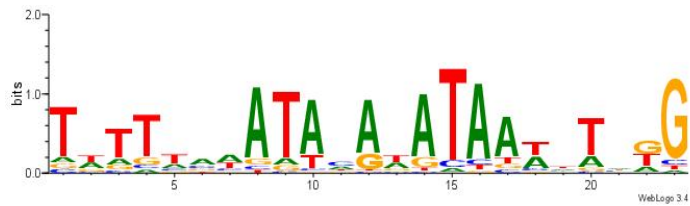
```
TWTHVWATAHAWATAAWH THKG  
BTTHAAAAAYAAAAAAR-----
```

Original motif

Consensus sequence: TWTHVWATAHAWATAAWH THKG

Reverse complement motif

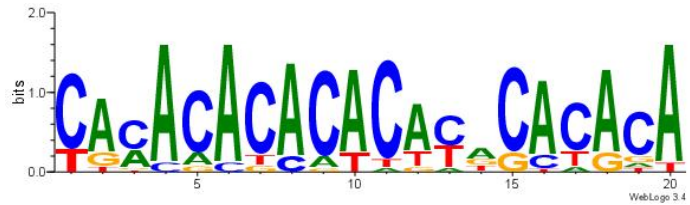
Consensus sequence: CYHAHWTTATWTDATWBHAAWA



**Dataset #: 5      Motif ID: 54      Motif name: TFM11**

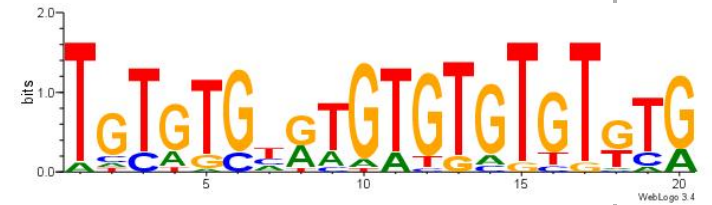
Original motif

Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif

Consensus sequence: TGTGTGDKTGTGTGTGTRTG



**Best Matches for Motif ID 54 (Highest to Lowest)**

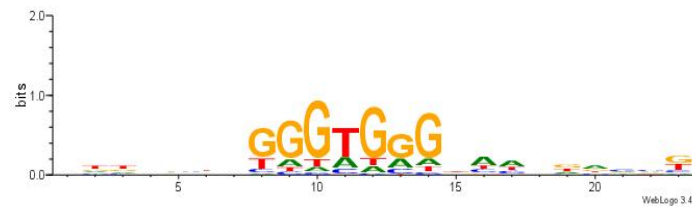
Motif ID:	<a href="#">UP00629</a>
Motif name:	ZNF200_H322Y_R1
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	20
Similarity score:	0.0391901

Alignment:

DDDDHDGGGTGGGHHHDDDVVK  
TGTGTGDKTGTGTGTGTRTG---

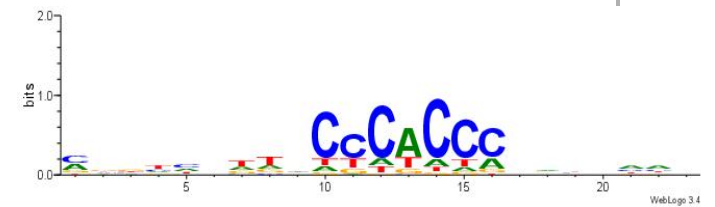
Original motif

Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



Reverse complement motif

Consensus sequence: YVVDHDHHHCCCACCCHHDDDDD



Motif ID: [UP00523](#)  
Motif name: FOXR1\_primary  
Species: Homo sapiens  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 20  
Similarity score: 0.0391934

Alignment:

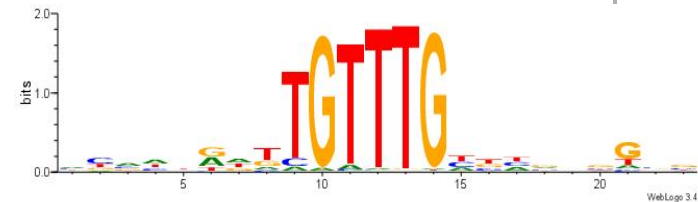
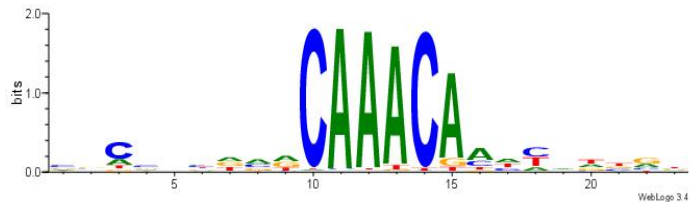
DVVD BKHTTGT TTTGDBDBHVG VV  
TGTGTGDKTGTGTGTGTRTG---

Original motif

Consensus sequence: VVCVHBDVDCAAACAAHYVDBVD

Reverse complement motif

Consensus sequence: DVVD BKHTTGT TTTGDBDBHVG VV

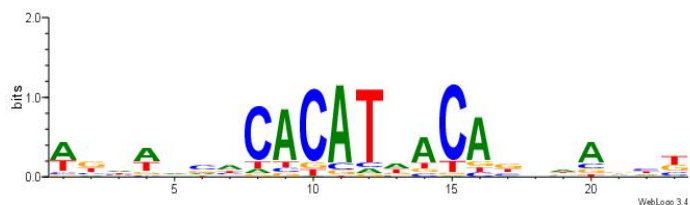


Motif ID: [UP00599](#)  
 Motif name: KLF1\_R328H\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 20  
 Similarity score: 0.0405918

Alignment:  
 RDHTDDBTGTDATGTGHVDWHBW  
 --TGTGTGDKTGTGTGTGTRTG--

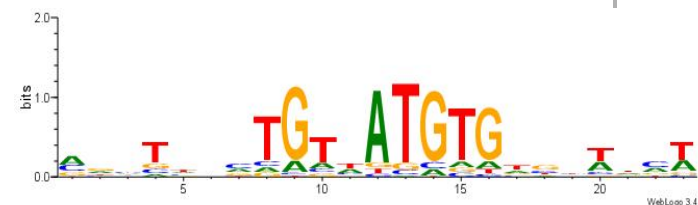
Original motif

Consensus sequence: WBHWDVHCACATDACABDDADHK



Reverse complement motif

Consensus sequence: RDHTDDBTGTDATGTGHVDWHBW



Motif ID: [UP00627](#)

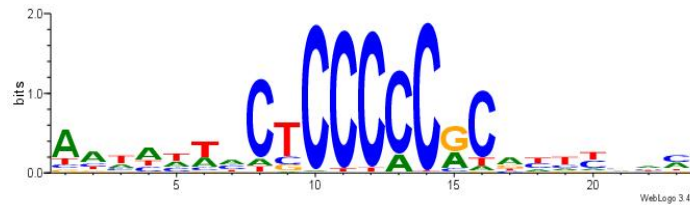
Motif name: WT1\_REF\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0438934

**Alignment:**

AAHAHWHCTCCCCRCDDHHYVHM  
 ---CAMACACACACAYDCACACA

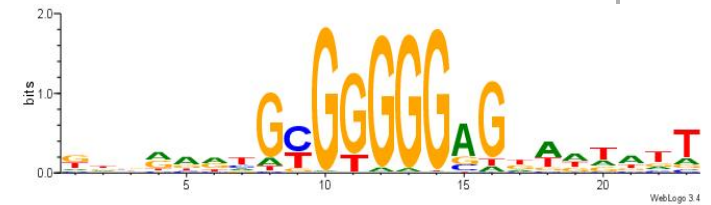
**Original motif**

Consensus sequence: AAHAHWHCTCCCCRCDDHHYVHM



**Reverse complement motif**

Consensus sequence: RHVMHHDGMGGGGGAGHWHHTHT




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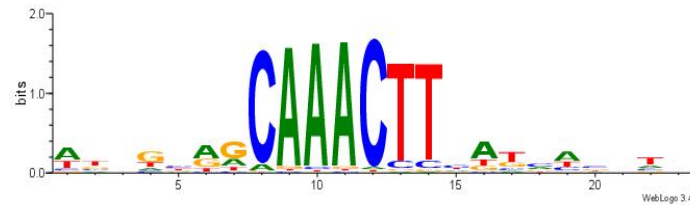
Motif ID: [UP00523](#)  
 Motif name: FOXR1\_secondary  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0442588

Alignment:

DHHBHVRTDAAGTTTGCKBCHVW  
TGTGTGDKTGTGTGTGTRTG---

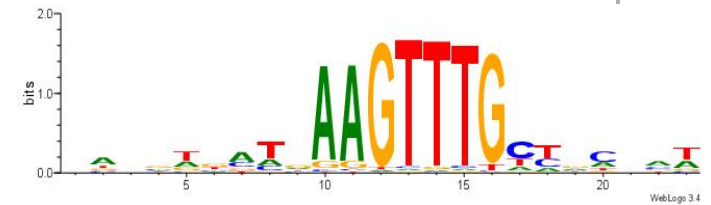
Original motif

Consensus sequence: WBHGBRGCAAACCTTHAKVHBHHD



Reverse complement motif

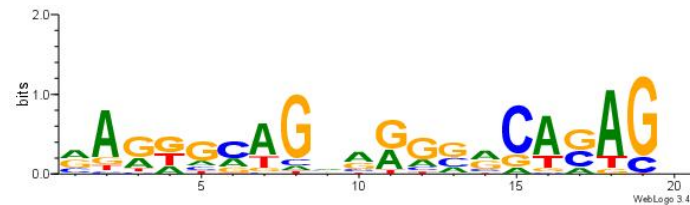
Consensus sequence: DHHBHVRTDAAGTTTGCKBCHVW



**Dataset #: 5      Motif ID: 55      Motif name: TFM12**

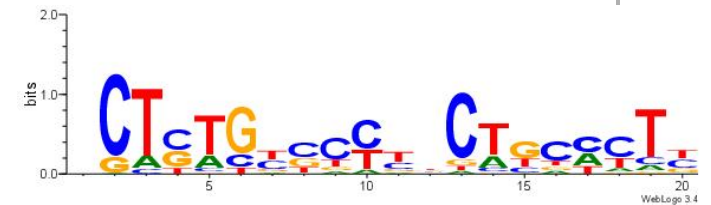
Original motif

Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif

Consensus sequence: VCTSTGKSCMKBCTRCYCTK



**Best Matches for Motif ID 55 (Highest to Lowest)**

Motif ID:	<a href="#">UP00594</a>
Motif name:	HESX1
Species:	Homo sapiens
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

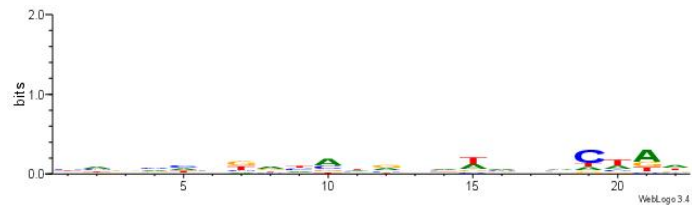
Direction: Forward  
Position number: 3  
Number of overlap: 20  
Similarity score: 0.0372823

Alignment:

DTHGBBBWHDVHBHDBVDVBHB  
--VCTSTGKSCMKBCTRCYCTK

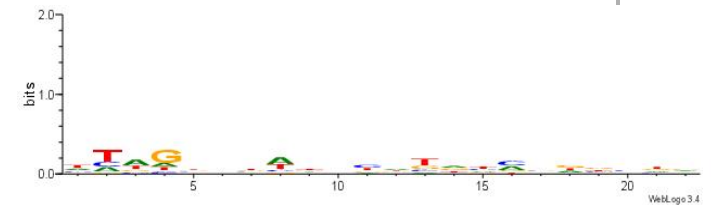
Original motif

Consensus sequence: BHBVHVBDHVHVDHWVBVCHAD



Reverse complement motif

Consensus sequence: DTHGBBBWHDVHBHDBVDVBHB



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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: 2  
Number of overlap: 20  
Similarity score: 0.0400251

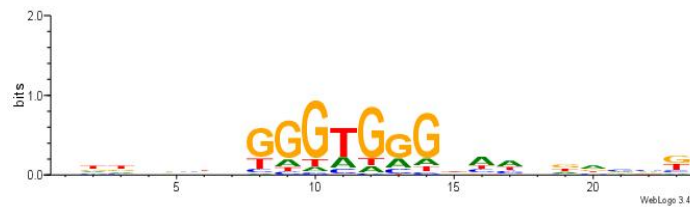
Alignment:



DDDDHDGGGTGGGHHHDDDVVK  
--RAGKGMAGVRRGSRCASAGV--

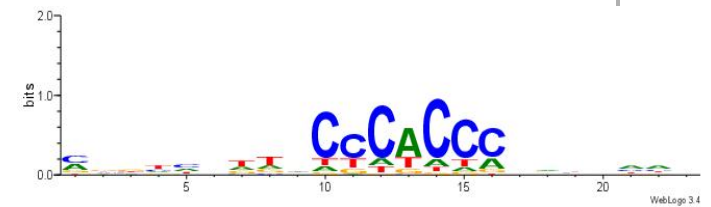
Original motif

Consensus sequence: DDDDDHDGGGTGGGHHHDDDVVK



Reverse complement motif

Consensus sequence: YVVDHDHHHCCCACCCHHDDDDD



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: 1  
Number of overlap: 20  
Similarity score: 0.044798

Alignment:

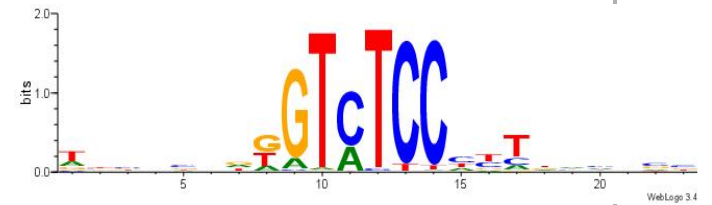
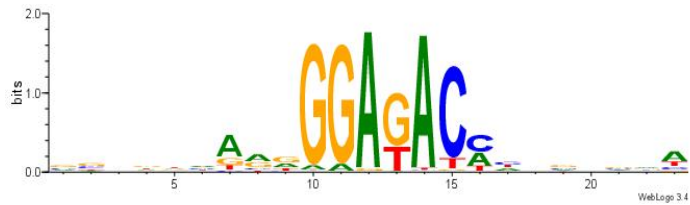
VBHDDHARDGGAGACMHDVDVVA  
RAGKGMAGVRRGSRCASAGV---

Original motif

Consensus sequence: VBHDDHARDGGAGACMHDVDVVA

Reverse complement motif

Consensus sequence: TBVDVDDRGTCCTCHKTHDHHBV

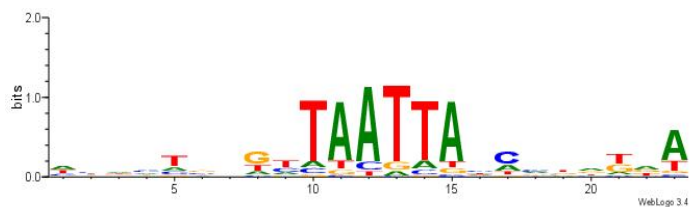


**Motif ID:** [UP00585](#)  
**Motif name:** BCL6  
**Species:** Homo sapiens  
**Matching format of first motif:** Reverse Complement  
**Matching format of second motif:** Original Motif  
**Direction:** Forward  
**Position number:** 3  
**Number of overlap:** 20  
**Similarity score:** 0.0451484

**Alignment:**  
 HDDHTBDGHTAATTAHCVBDKDA  
 --VCTSTGKSCMKBCTRCYCTK-

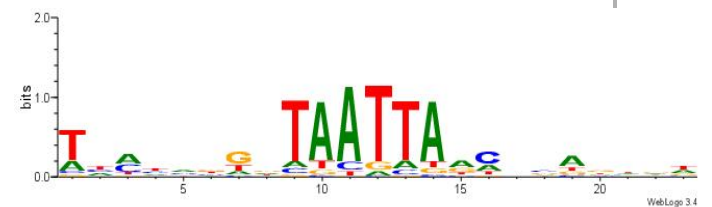
**Original motif**

Consensus sequence: HDDHTBDGHTAATTAHCVBDKDA



**Reverse complement motif**

Consensus sequence: TDRDVVGDTAATTAHCDBADDDH



**Motif ID:** [UP00611](#)

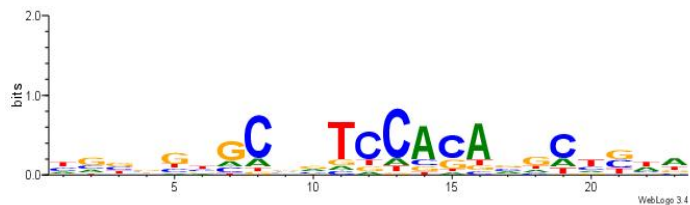
Motif name: PAX6  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0462503

**Alignment:**

DHBHGCVTGTGGAVVGCVCBBVH  
 RAGKGMAGVRRGSRCASAGV---

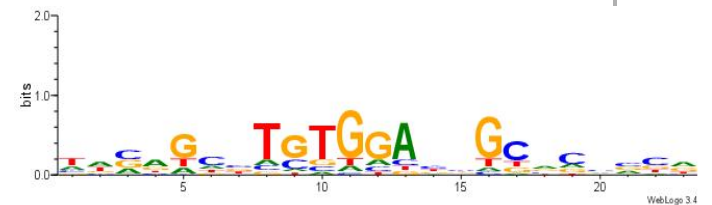
**Original motif**

Consensus sequence: HVBBGBGCVVTCCACAVGCHBHD



**Reverse complement motif**

Consensus sequence: DHBHGCVTGTGGAVVGCVCBBVH




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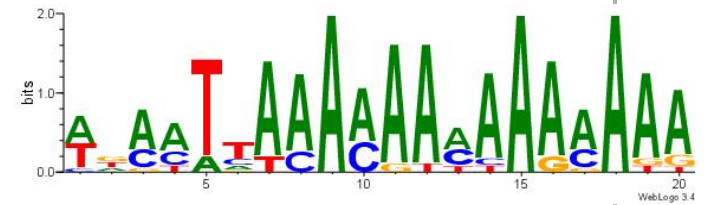
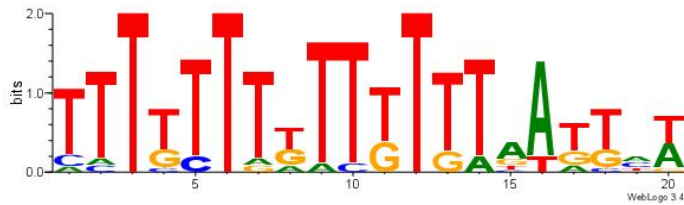
**Dataset #: 5      Motif ID: 56      Motif name: TFM13**

**Original motif**

Consensus sequence: TTTTTTKTKTTTAATTHW

**Reverse complement motif**

Consensus sequence: WHAATTAARAARAAAAAAA



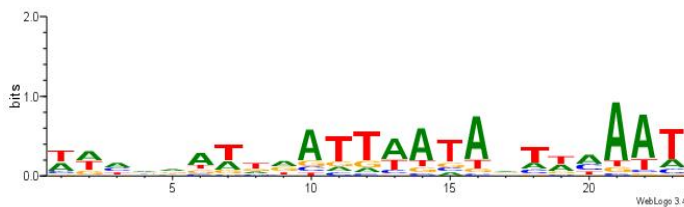
### Best Matches for Motif ID 56 (Highest to Lowest)

Motif ID: [UP00606](#)  
 Motif name: NR1H4  
 Species: Homo sapiens  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 20  
 Similarity score: 0.0492341

Alignment:  
 WWHVDAWDDATTWATAVTWMAAT  
 --WHAATTAAARAARAAAAAAA--

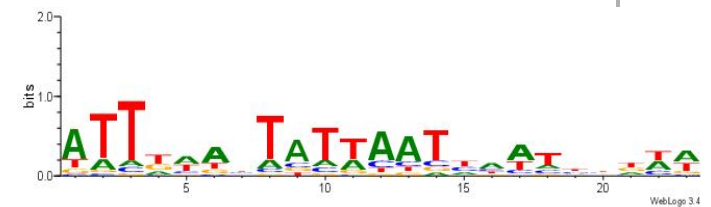
#### Original motif

Consensus sequence: WWHVDAWDDATTWATAVTWMAAT



#### Reverse complement motif

Consensus sequence: ATTYWABTATWAATDDWTDBHWW



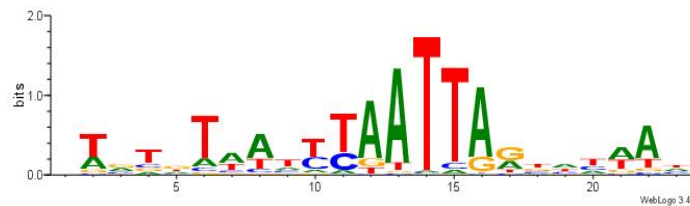
Motif ID: [UP00619](#)  
 Motif name: PROP1\_R112Q\_R1  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 20  
 Similarity score: 0.0577478

**Alignment:**

VWVTDTWAHYTAATTARBHHWAH  
 -TTTTTTTKTTKTTTAATTHW--

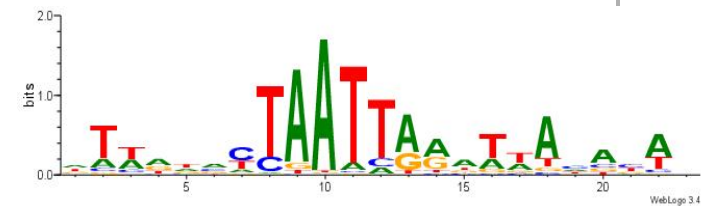
**Original motif**

Consensus sequence: VWVTDTWAHYTAATTARBHHWAH



**Reverse complement motif**

Consensus sequence: HTWHHVMTAATTAMHTWAHAVVW



Motif ID: [UP00599](#)  
 Motif name: KLF1\_R328H\_R2  
 Species: Homo sapiens  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20

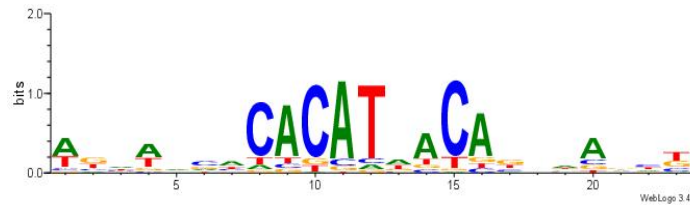
Similarity score: 0.0580026

Alignment:

WBHWDVHCACATDACABDDADHK  
---TTTTTTTCTTKTTTAATTHW

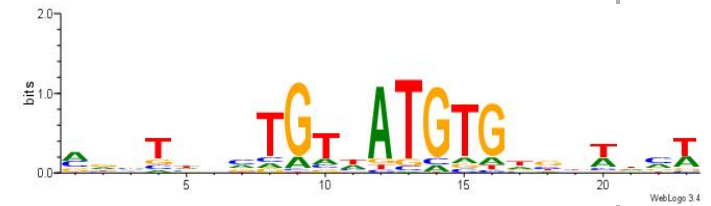
Original motif

Consensus sequence: WBHWDVHCACATDACABDDADHK



Reverse complement motif

Consensus sequence: RDHTDDBTGTDATGTGHVDWHBW



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Motif ID: [UP00626](#)  
Motif name: VSX2\_R200P\_R1  
Species: Homo sapiens  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.0613436

Alignment:

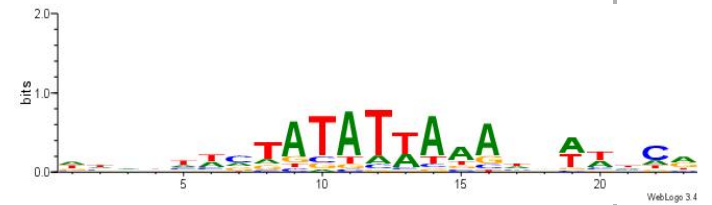
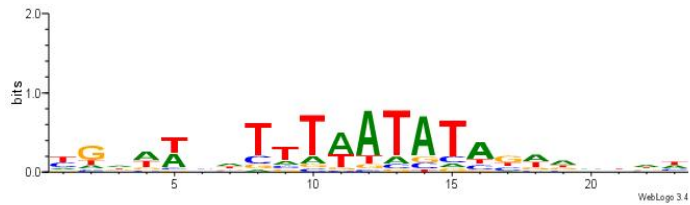
HGDWWHDTTTWTATATABWDDHDH  
TTTTTTTCTTKTTTAATTHW---

Original motif

Consensus sequence: HGDWWHDTTTWTATATABWDDHDH

Reverse complement motif

Consensus sequence: HDHDDWBTATATWAAADDWDC



Motif ID: [UP00599](#)  
 Motif name: KLF1\_R328H\_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: 20  
 Similarity score: 0.0614554

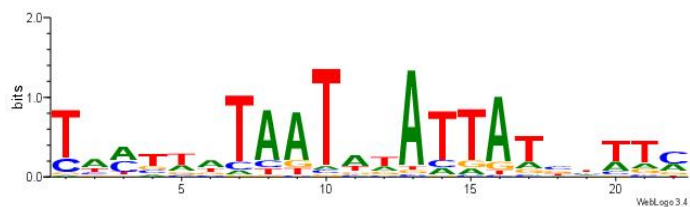
**Alignment:**

```

THMTWDTAATADATTATBHTTM
TTTTTTTKTTKTTTAATTHW--
  
```

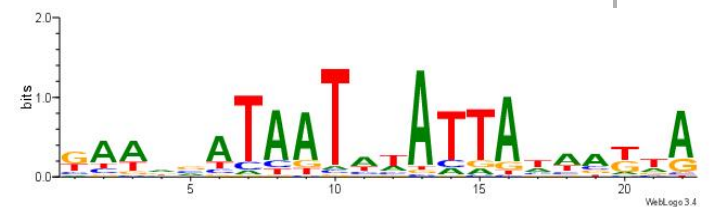
**Original motif**

Consensus sequence: THMTWDTAATADATTATBHTTM



**Reverse complement motif**

Consensus sequence: RAAHBATAATDTATTADWAYHA



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 [weblgo](#)