



For further information on how to interpret these results please access <https://meme-suite.org/meme/doc/spamo-output-format.html>.
To get a copy of the MEME software please access <https://meme-suite.org>.

If you use SpaMo in your research, please cite the following paper:

Tom Whittington, Martin C. Frith, James Johnson and Timothy L. Bailey "Inferring transcription factor complexes from ChIP-seq data", *Nucleic Acids Res.* **39**(15):e98, 2011. [\[full text\]](#)

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PRIMARY MOTIFS

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Database	Name	Preview	Significant Secondaries	List
meme.xml	TTTTTKTTTTTT (MEME-1)		8	TTTTTKTTTTTT (MEME-1), GCTGGGATTACAGGC (MEME-3), 3-
Alphabet				
Background source: the file './background'				
Name	Bg.		Bg.	Name
Adenine	0.2666	A ~ T	0.2666	Thymine
Cytosine	0.2334	C ~ G	0.2334	Guanine

SEQUENCE DATABASE

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Name	Last Modified	Contained	Too Short	Too Masked	No Primary	Too Similar	Used
Galaxy8-hyperacetylation_fasta	Thu Mar 2 08:04:26 2023	958	0	0	25	121	812

SECONDARY MOTIF DATABASES

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Name	Last Modified	Number of Motifs	Motifs Significant	Motifs Redundant
meme.xml	Thu Mar 2 13:34:08 2023	3	3	0
streme.xml	Thu Mar 2 13:34:29 2023	5	5	0

SETTINGS

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Match Score Threshold 7 (bits)

Margin size 150

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SPACING ANALYSIS FOR TTTTGTKTTTTTTT (MEME-1)

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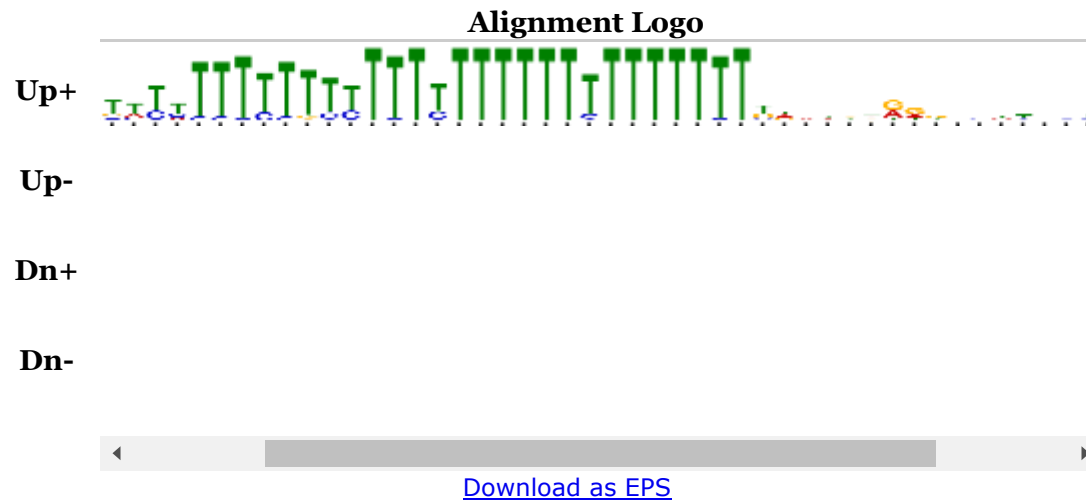
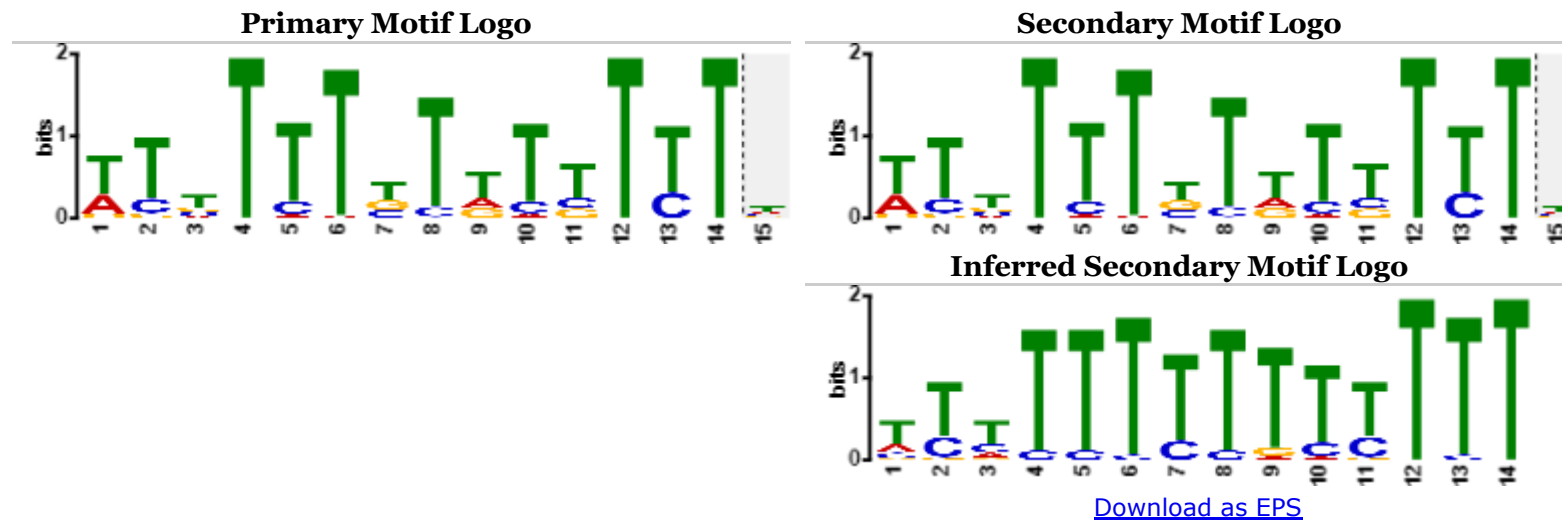
Secondary Motif: TTTTGTKTTTTTTT
(MEME-1)

Cluster: TTTTGTKTTTTTTT
(MEME-1)

E-value: 4.42e-24

Best Gap: 1

Best Orientation: upstream / same strand



Spacings

Gap	Orientation	p-value
1	up+	5.53e-25
0	up+	1.04e-23
1	up+/up-	1.88e-19
1	up+/dn-	1.87e-17
0	up+/up-	1.77e-16
0	up+/dn-	1.77e-16
2	up+	1.99e-16
0	all	6.84e-15
1	all	3.97e-14
3	up+	4.56e-13
7	up+	5.38e-12
2	all	6.43e-12
2	up+/up-	7.27e-12
2	up+/dn-	5.32e-11
4	up+	5.96e-11
3	up+/dn-	2.45e-9
7	up+/dn-	2.45e-9

Highlight: ☒ Selected ☒ All

Contributing Sequence IDs (27)

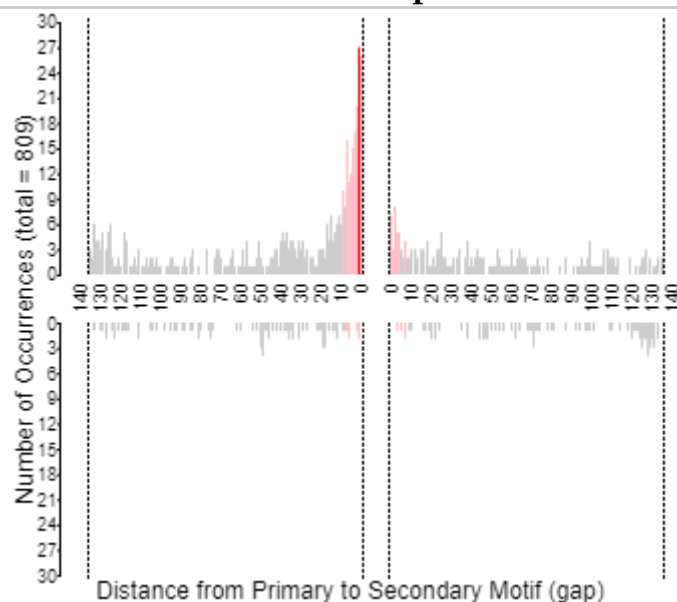
10103::chr4:169771180-169773199
 1028::chr1:39656450-39663179
 11997::chr5:172442450-172446299
 13075::chr6:43087580-43090349
 1417::chr1:60154730-60157629
 1549::chr1:67140630-67144229
 15642::chr7:134450630-134452829
 16351::chr8:29386780-29388829
 18313::chr9:115109780-115112349
 19054::chr10:4169350-4175299
 20418::chr10:104548200-104563899
 23938::chr12:93964430-93969879
 24401::chr12:122026880-122029699
 25597::chr14:27065800-27068999
 25635::chr14:33170880-33173099
 25675::chr14:35881380-35883499
 26038::chr14:69401530-69426999
 27090::chr15:60654580-60656599
 27984::chr15:101560730-101564299

Plain Format ▾

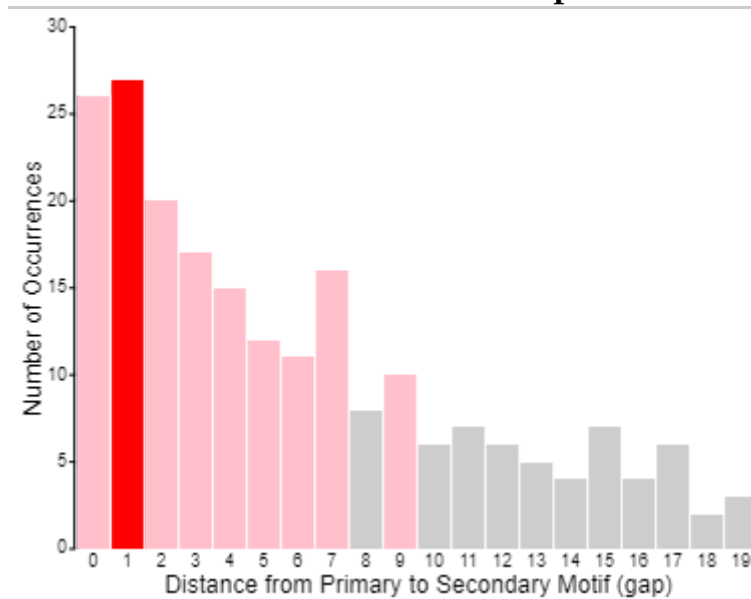
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Secondaries

Overview Graph

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Selected Orientation Graph

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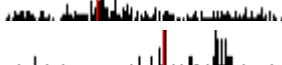

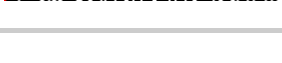
Filter

- ☐ Top 10
- ☐ ID matches .*
- ☐ Name matches .*
- ☐ Cluster matches .*
- ☐ E-value \leq 1
- ☐ Gaps (ranges allowed) 0-10

Sort

Sort by E-value ▼

Update

Lock	ID	Name	Cluster	E-value	Best Gap	Best Orientation	Spacings
<input type="checkbox"/>	TTTTTKTTTTTT	MEME-1	TTTTTKTTTTTT	4.42e-24	1	upstream / same strand	
<input type="checkbox"/>	GCTGGGATTACAGGC	MEME-3	GCTGGGATTACAGGC	2.05e-20	112	downstream / same strand	
<input type="checkbox"/>	3-TAATCCCAGCA	STREME-3	3-TAATCCCAGCA	1.77e-16	113	downstream / opposite strand	
<input type="checkbox"/>	1-CCACCCCCACCTCC	STREME-1	1-CCACCCCCACCTCC	4.63e-15	63	downstream / same strand	
<input type="checkbox"/>	GGGHGGCSGMGGSGG	MEME-2	GGGHGGCSGMGGSGG	9.77e-12	63	downstream / opposite strand	
<input type="checkbox"/>	5-GATGTCAG	STREME-5	5-GATGTCAG	1.86e-11	46	downstream / secondary palindromic	
<input type="checkbox"/>	2-ACTTTG	STREME-2	2-ACTTTG	1.80e+0	79	downstream / opposite strand	
<input type="checkbox"/>	4-AAATGCAAAA	STREME-4	4-AAATGCAAAA	7.48e+0	0	upstream / opposite strand	

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5.5.1 (Release date: Sun Jan 29 10:33:12 2023 -0800)

Reference

Tom Whittington, Martin C. Frith, James Johnson and Timothy L. Bailey "Inferring transcription factor complexes from ChIP-seq data", *Nucleic Acids Res.* **39**(15):e98, 2011. [\[full text\]](#)

Command line

```
spamo -verbosity 1 -oc spamo_out_1 -bgfile ./background -keepprimary -primary TTTTTKTTTTTTT ./Galaxy8-hyperacetylation_fasta.fasta
```

Result calculation took 2 seconds

