



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. [\[full text\]](#)

[PRIMARY MOTIFS](#) | [SEQUENCE DATABASE](#) | [SECONDARY MOTIF DATABASES](#) | [SPACING ANALYSIS](#) | [INPUTS AND SETTINGS](#) | [PROGRAM INFORMATION](#) | [RESULTS IN TSV FORMAT](#) | CONTRIBUTING SEQUENCE IDS [\[DOWNLOAD PLAIN\]](#) [\[DOWNLOAD BED\]](#)

PRIMARY MOTIFS

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Database	Name	Preview	Significant Secondaries	List																		
meme.xml	AAWAAAAAWAAAAAA (MEME-1)		7	4-CCAGGCTGGWST (STREME-4), CCTYRGCCTCCCRAR (MEME-3),																		
<div>Alphabet</div> <div>Background source: the file './background'</div> <table><thead><tr><th>Name</th><th>Bg.</th><th></th><th></th><th>Bg.</th><th>Name</th></tr></thead><tbody><tr><td>Adenine</td><td>0.2278</td><td>A</td><td>~</td><td>T</td><td>Thymine</td></tr><tr><td>Cytosine</td><td>0.2722</td><td>C</td><td>~</td><td>G</td><td>Guanine</td></tr></tbody></table>					Name	Bg.			Bg.	Name	Adenine	0.2278	A	~	T	Thymine	Cytosine	0.2722	C	~	G	Guanine
Name	Bg.			Bg.	Name																	
Adenine	0.2278	A	~	T	Thymine																	
Cytosine	0.2722	C	~	G	Guanine																	

SEQUENCE DATABASE

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Name	Last Modified	Contained	Too Short	Too Masked	No Primary	Too Similar	Used
Galaxy7-hypoacetylation_fasta	Thu Mar 2 08:11:33 2023	1148	0	0	210	254	684

SECONDARY MOTIF DATABASES

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Name	Last Modified	Number of Motifs	Motifs Significant	Motifs Redundant
meme.xml	Thu Mar 2 13:53:52 2023	3	3	0
streme.xml	Thu Mar 2 13:54:02 2023	4	2	2

SETTINGS

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Match Score Threshold 7 (bits)

Margin size 150

[Show Advanced Settings](#)

SPACING ANALYSIS FOR AAWAAAAAWAAAAA (MEME-1)

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Secondary 4-CCAGGCTGGWST
Motif: (STREME-4)

Cluster: 4-CCAGGCTGGWST
(STREME-4)

E- 5.06e-66
value:

Best 24
Gap:

Best upstream / opposite
Orientation: strand

Primary Motif Logo



Secondary Motif Logo



Inferred Secondary Motif Logo

[Download as EPS](#)

Alignment Logo

Up+

Up-

Dn+

Dn-

[Download as EPS](#)

Spacings

Gap	Orientation	p-value
24	up-	7.23e-67
24	up+/up-	2.35e-53
24	up-/dn+	2.35e-53
23	up-	2.49e-45
25	up-	9.45e-44
24	all	1.15e-39
23	up+/up-	1.32e-35
23	up-/dn+	1.32e-35
26	up-	1.51e-34
27	up-	1.51e-34
25	up-/dn+	2.58e-34
25	up+/up-	4.90e-33
27	up-/dn+	4.73e-28
26	up-/dn+	7.72e-27
23	all	1.04e-25
26	up+/up-	1.22e-25
27	up+/up-	1.22e-25

Highlight: ☒ Selected ☒ All

Contributing Sequence IDs (51)

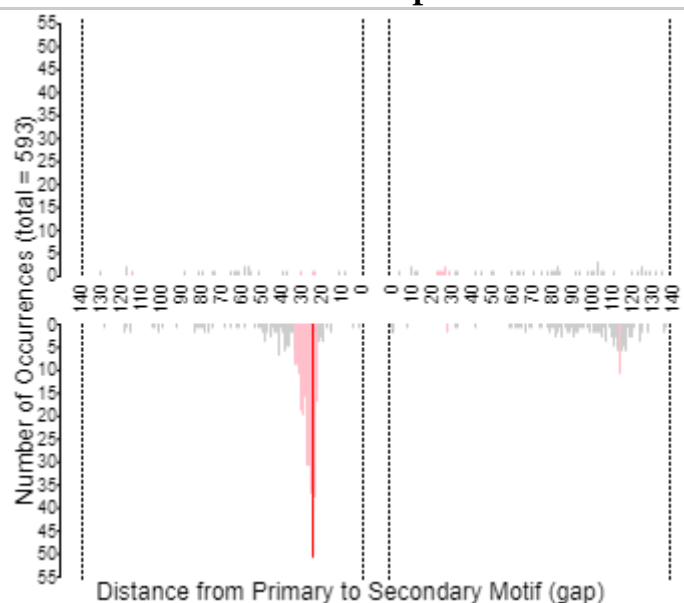
10298::chr5:1116580-1129679
 11372::chr5:138706750-138710079
 11401::chr5:139386650-139392579
 1160::chr1:44410650-44415499
 11978::chr5:172170330-172181049
 12006::chr5:172691050-172698049
 12941::chr6:36833600-36839979
 14134::chr6:163752550-163762479
 14795::chr7:44687380-44696229
 15840::chr7:151155400-151159279
 15981::chr8:8922650-8924899
 15989::chr8:9011450-9014329
 16974::chr8:107780580-107784049
 17090::chr8:125405600-125409029
 17387::chr8:145546230-145550849
 17650::chr9:33389350-33394899
 19272::chr10:18599300-18603599
 21763::chr11:64755730-64758599
 21781::chr11:65077050-65079229

Plain Format ▾

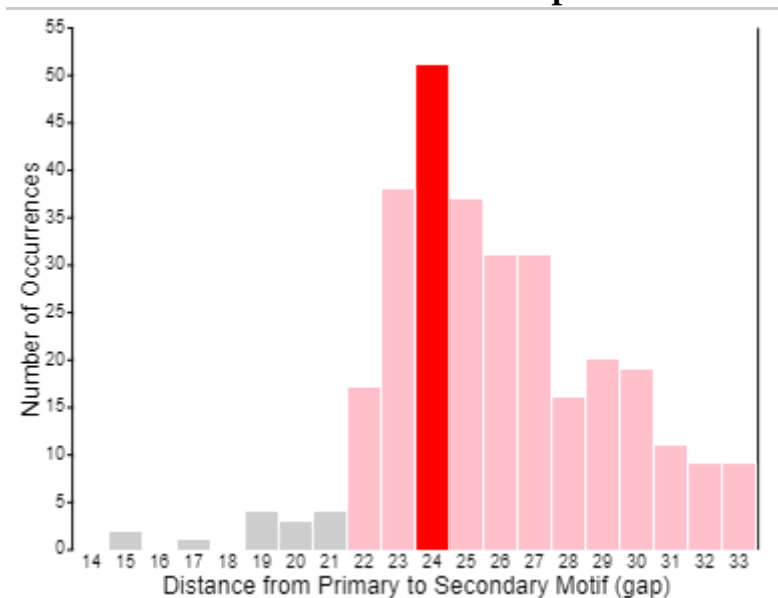
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Secondaries

Overview Graph

[Download as EPS](#)

Selected Orientation Graph

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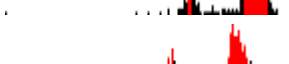

Filter

- ☐ Top 10
- ☐ ID matches .*
- ☐ Name matches .*
- ☐ Cluster matches .*
- ☐ E-value ≤ 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"/>	4-CCAGGCTGGWST	STREME-4	4-CCAGGCTGGWST	5.06e-66	24	upstream / opposite strand	
<input type="checkbox"/>	CCTYRGCCTCCCRAR	MEME-3	CCTYRGCCTCCCRAR	9.86e-37	65	upstream / opposite strand	
<input type="checkbox"/>	AAWAAAAAWAAAAAA	MEME-1	AAWAAAAAWAAAAAA	6.49e-24	1	all / both palindromic	
<input type="checkbox"/>	2-GCCTCRGCCTCCCAA	STREME-2	CCTYRGCCTCCCRAR	6.91e-24	64	upstream / opposite strand	
<input type="checkbox"/>	GCTGGGATTACAGGC	MEME-2	GCTGGGATTACAGGC	3.93e-23	112	upstream / opposite strand	
<input type="checkbox"/>	3-ACAGGCRTGAGCCAC	STREME-3	3-ACAGGCRTGAGCCAC	1.27e-19	123	upstream / opposite strand	
<input type="checkbox"/>	1-CTGGGAY	STREME-1	GCTGGGATTACAGGC	1.77e-16	113	upstream / opposite strand	

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

ReferenceTom 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 AAAAAAAAAAAAAA ./Galaxy7-hypoacetylation_fasta.fasta
```

Result calculation took 1 seconds

