



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	GCTGGGATTACAGGC (MEME-2)		7	CCTYRGCCCTCCCRAR (MEME-3), 2- GCCTCRGCCTCCCAA (STREME-2), 4-																		
Alphabet																						
Background source: the file './background'																						
<table><tr><th>Name</th><th>Bg.</th><th></th><th></th><th>Bg.</th><th>Name</th></tr><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></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	331	471	346

SECONDARY MOTIF DATABASES

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SETTINGS

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Best upstream / same
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
2	up+	0.00e+0
2	up+/up-	0.00e+0
2	up+/dn-	0.00e+0
2	all	0.00e+0
34	up+	1.93e-38
34	up+/up-	9.40e-31
34	up+/dn-	9.40e-31
34	all	8.61e-23
135	up+	1.02e-14
32	up+	1.97e-13
135	up+/up-	1.62e-10
135	up+/dn-	1.62e-10
32	up+/up-	1.57e-9
32	up+/dn-	1.57e-9
135	all	1.25e-6
134	up+	1.94e-6
32	all	6.13e-6

Highlight: ☒ Selected ☒ All

Contributing Sequence IDs (221)

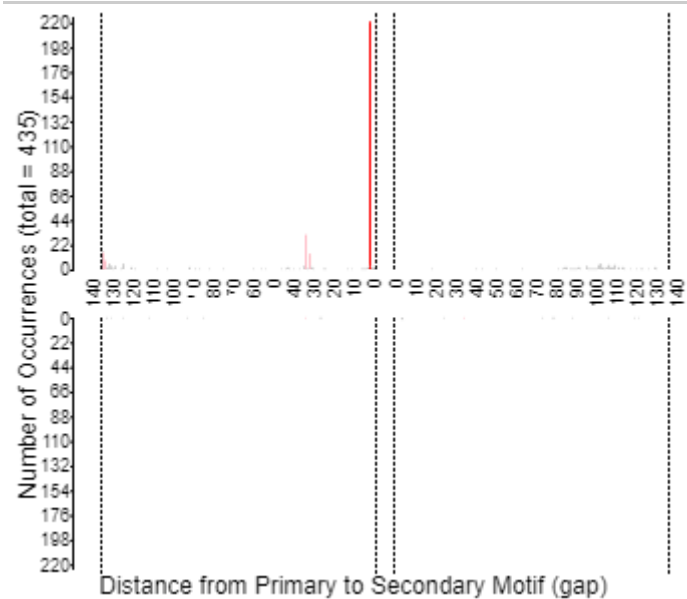
10174::chr4:184794050-184799749
 10176::chr4:184905150-184911799
 10183::chr4:185263550-185271629
 10185::chr4:185302650-185313499
 10244::chr4:186699930-186709749
 10254::chr4:186756200-186765249
 10256::chr4:186781430-186791099
 10283::chr5:269850-272399
 10298::chr5:1116580-1129679
 10667::chr5:56501430-56506299
 1107::chr1:42277230-42280499
 11264::chr5:133770180-133776179
 11268::chr5:133844100-133848449
 11272::chr5:133882480-133892179
 11401::chr5:139386650-139392579
 1140::chr1:43670600-43674649
 11652::chr5:149066280-149074249
 11664::chr5:149198800-149208899
 11914::chr5:170213550-170217499

Plain Format ▾

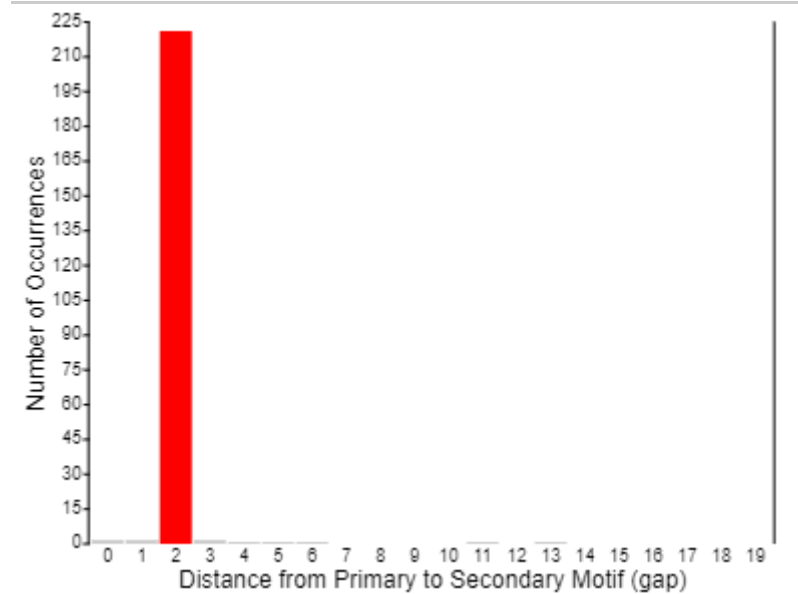
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Secondaries

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"/>	CCTYRGCCTCCCRAR	MEME-3	CCTYRGCCTCCCRAR	0.00e+0	2	upstream / same strand	
<input type="checkbox"/>	2-GCCTCRGCCTCCCAA	STREME-2	CCTYRGCCTCCCRAR	0.00e+0	3	upstream / same strand	
<input type="checkbox"/>	4-CCAGGCTGGWST	STREME-4	4-CCAGGCTGGWST	2.75e-160	46	upstream / same strand	
<input type="checkbox"/>	AAWAAAAAWAAAAAA	MEME-1	AAWAAAAAWAAAAAA	6.17e-56	82	upstream / opposite strand	
<input type="checkbox"/>	GCTGGGATTACAGGC	MEME-2	GCTGGGATTACAGGC	7.65e-28	121	upstream / same strand	
<input type="checkbox"/>	3-ACAGGCRTGAGCCAC	STREME-3	GCTGGGATTACAGGC	2.45e-27	112	upstream / same strand	
<input type="checkbox"/>	1-CTGGGAY	STREME-1	GCTGGGATTACAGGC	1.41e-21	128	upstream / same 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_3 -bgfile ./background -keepprimary -primary GCTGGGATTACAGGC ./Galaxy7-hypoacetylation_fasta.fasta
```

Result calculation took 1 seconds

