SpaMo
Spaced Motif Analysis Tool

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 Whitington, 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-3)		8	GGGHGGCSGMGGSGG (MEME-2), 1- CCACCCCCACCTCC (STREME-1), 2-

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	388	321	249

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	2	1
streme.xml	Thu Mar 2 13:34:29 2023	5	4	1

SETTINGS

Match Score Threshold	7 (bits)
Margin size	150

Show Advanced Settings

SPACING ANALYSIS FOR GCTGGGATTACAGGC (MEME-3)

Secondary Motif: GGGHGGCSGMGGSGG (MEME-2)   **Cluster:** GGGHGGCSGMGGSGG (MEME-2)   **E-value:** 4.68e-273   **Best Gap:** 5   **Best Orientation:** all / both palindromic

Primary Motif Logo

Secondary Motif Logo

Inferred Secondary Motif Logo
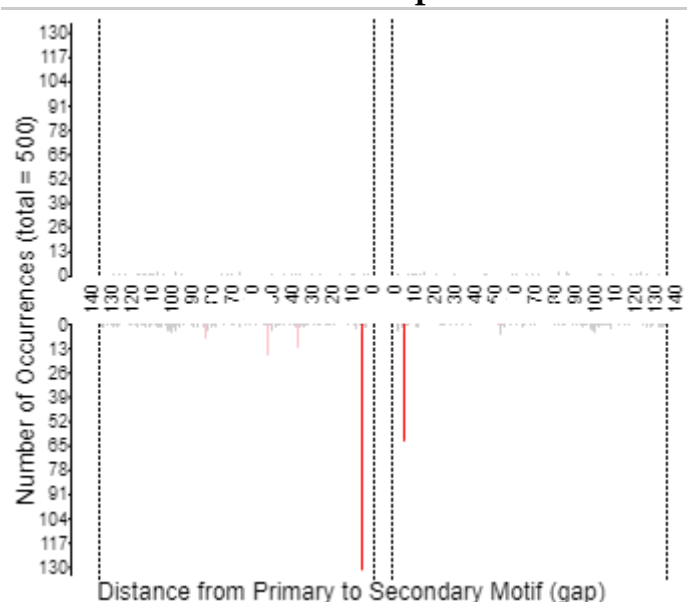

[Download as EPS](#)

Alignment Logo

Up+

Up-
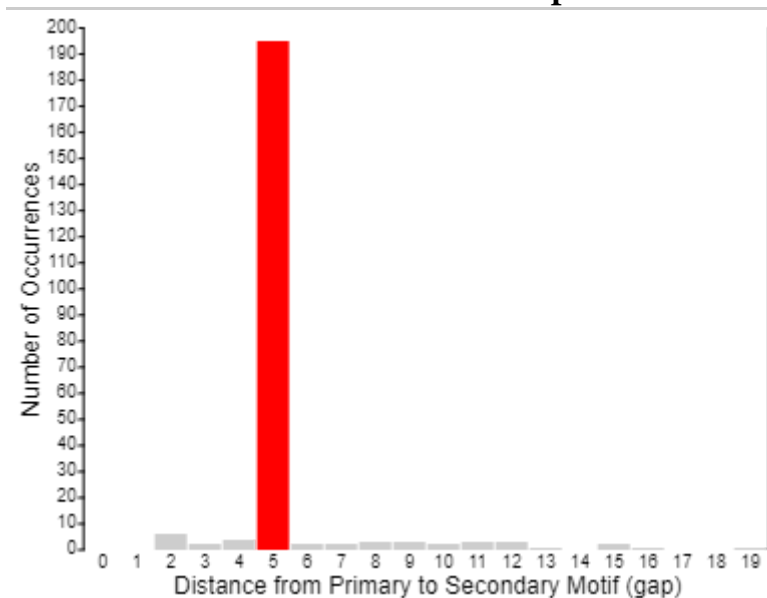

Dn+

Dn-

[Download as EPS](#)

Spacings

Gap	Orientation	*p*-value
5	all	5.85e-274
5	up-	3.57e-238
5	up+/up-	9.93e-199
5	up-/dn+	9.93e-199
5	dn-	1.90e-92
5	up+/dn-	7.95e-74
5	dn+/dn-	7.95e-74
52	up-	2.20e-16
52	up+/up-	1.25e-11
52	up-/dn+	1.25e-11
37	up-	2.00e-11
52	all	6.04e-8
37	up+/up-	7.16e-8
37	up-/dn+	7.16e-8
83	up-	5.36e-6

Overview Graph

Distance from Primary to Secondary Motif (gap)

[Download as EPS](#)

Selected Orientation Graph

Distance from Primary to Secondary Motif (gap)

[Download as EPS](#)

Highlight: ☑ Selected ☑ All

Contributing Sequence IDs (195)

```
10020::chr4:156415650-15641839
10097::chr4:169685400-16969259
10103::chr4:169771180-16977319
1019::chr1:39551200-39554149
10222::chr4:186452830-18645964
10511::chr5:36689100-36693599
10543::chr5:39420680-39425729
10554::chr5:40913950-40916279
10641::chr5:54827750-54832679
10645::chr5:54886300-54890379
10860::chr5:76085030-76088849
10943::chr5:81629380-81632299
10978::chr5:90414500-90422099
11411::chr5:139559130-13956194
11483::chr5:141695980-14170844
11853::chr5:159590900-15959472
11997::chr5:172442450-17244629
1201::chr1:46267830-46271029
12239::chr6:4646700-4649179
```

Plain Format ▾   [Download](#)

Secondaries

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
☐	GGGHGGCSGMGGSGG	MEME-2	GGGHGGCSGMGGSGG	4.68e-273	5	all / both palindromic	
☐	1-CCACCCCCACCTCC	STREME-1	GGGHGGCSGMGGSGG	1.24e-178	6	upstream / same strand	
☐	2-ACTTTG	STREME-2	2-ACTTTG	3.29e-169	0	upstream / opposite strand	
☐	5-GATGTCAG	STREME-5	5-GATGTCAG	2.88e-65	31	upstream / opposite strand	
☐	4-AAATGCAAAA	STREME-4	4-AAATGCAAAA	5.37e-29	23	downstream / opposite strand	
☐	TTTTTTKTTTTTTTT	MEME-1	TTTTTTKTTTTTTTT	4.89e-26	85	upstream / same strand	
☐	3-TAATCCCAGCA	STREME-3	3-TAATCCCAGCA	6.60e-17	126	upstream / opposite strand	
☐	GCTGGGATTACAGGC	MEME-3	3-TAATCCCAGCA	1.05e-16	121	upstream / same strand	

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

Reference

Tom Whitington, 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_2 -bgfile ./background -keepprimary -primary GCTGGGATTACAGGC ./Galaxy8-hyperacetylation_fasta.fasta
```

Result calculation took 1 seconds