STREME
Sensitive, Thorough, Rapid, Enriched Motif Elicitation

For further information on how to interpret these results please access https://meme-suite.org/meme/doc/streme.html.

To get a copy of the MEME software please access https://meme-suite.org.

If you use STREME in your research, please cite the following paper:
Timothy L. Bailey, "STREME: accurate and versatile sequence motif discovery", *Bioinformatics*, Mar. 24, 2021. [full text]

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DISCOVERED MOTIFS

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Motif	Logo	RC Logo	P-value	E-value	Sites	More	Submit/Download
1−CTGGGAY			3.0e-002	1.2e-001	316 (27.5%)	↧	⋯→
2−GCCTCRGCCTCCCAA			1.4e-001	5.6e-001	65 (5.7%)	↧	⋯→

Stopped because 3 consecutive motifs exceeded the p-value threshold (0.05).
STREME ran for 9.91 seconds.

Motif	Logo	RC Logo	P-value	E-value	Sites	More	Submit/Download
3–ACAGGCRTGAGCCAC			1.8e-001	7.4e-001	41 (3.6%)	↓	⋯→
4–CCAGGCTGGWST			2.5e-001	1.0e+000	50 (4.4%)	↓	⋯→

Stopped because 3 consecutive motifs exceeded the p-value threshold (0.05).
STREME ran for 9.91 seconds.

INPUTS & SETTINGS

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Positive (primary) Sequences	./seqs-centered	DNA	1148	114800
Negative (control) Sequences	2-Order Shuffled Positive Sequences	DNA	1148	114800

Background Model

Source: built from the negative (control) sequences

Order: 2 (only order-0 shown)

Name	Freq.	Bg.			Bg.	Freq.	Name
Adenine	0.219	0.219	A	~ T	0.219	0.219	Thymine
Cytosine	0.281	0.281	C	~ G	0.281	0.281	Guanine

Other Settings

Strand Handling   Both the given and reverse complement strands are processed.

Objective Function	Differential Enrichment
Statistical Test	Fisher Exact Test
Minimum Motif Width	6
Maximum Motif Width	15
Sequence Shuffling	Negative sequences are positives shuffled preserving 3-mer frequencies.
Test Set	10% of the input sequences were randomly assigned to the test set.
Word Evaluation	Up to 25 words of each width from 6 to 15 were evaluated to find seeds.
Seed Refinement	Up to 4 seeds of each width from 6 to 15 were further refined.
Refinement Iterations	Up to 20 iterations were allowed when refining a seed.
Random Number Seed	0
Total Length	The total length of each sequence set was limited to 4.00e+6.
Maximum Motif p-value	Stop when the p-value is greater than 0.05 for 3 consecutive motifs.
Maximum Motifs to Find	No maximum number of motifs.
Maximum Run Time	5707 seconds.

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

Reference
Timothy L. Bailey, "STREME: accurate and versatile sequence motif discovery", *Bioinformatics*, Mar. 24, 2021. [full text]

Command line

```
streme --verbosity 1 --oc streme_out -dna --p ./seqs-centered --minw 6 --maxw 15 --time 5707 --order 2 --thresh 0.05 --totallength 4000000
```