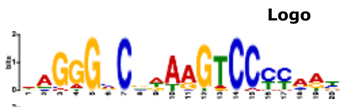
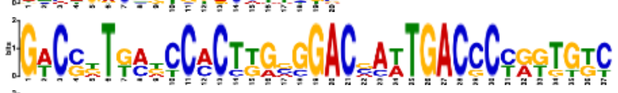
MEME
Multiple Em for Motif Elicitation

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

If you use MEME in your research, please cite the following paper:
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [pdf]

DISCOVERED MOTIFS | MOTIF LOCATIONS | INPUTS & SETTINGS | PROGRAM INFORMATION | RESULTS IN TEXT FORMAT NEW | RESULTS IN XML FORMAT NEW

DISCOVERED MOTIFS

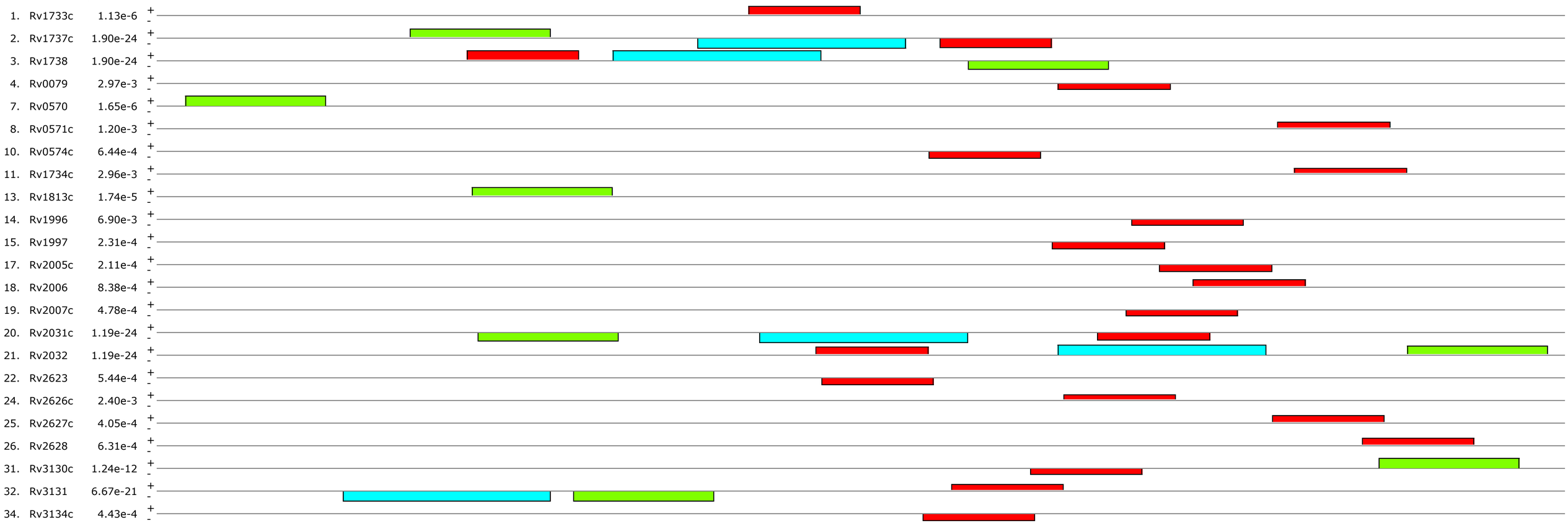
	Logo	E-value	Sites	Width	More	Submit/Download
1.		2.8e-022	21	20		
2.		7.2e-005	5	37		
3.		5.0e-003	8	25		

Stopped because requested number of motifs (3) found.

MOTIF LOCATIONS

Only Motif Sites | Motif Sites+Scanned Sites | All Sequences | Download PDF NEW | Download SVG NEW

Name **p-value** **Motif Locations**



INPUTS & SETTINGS

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	upstream250.txt	DNA	36	9000

Background Model

Source: built from the (primary) sequences

Order: 0

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.188	0.188	A	~	T	0.188	0.188	Thymine
Cytosine	0.312	0.312	C	~	G	0.312	0.312	Guanine

Other Settings

Motif Site Distribution	ZOOPS: Zero or one site per sequence
Objective Function	E-value of product of p-values
Starting Point Function	E-value of product of p-values
Site Strand Handling	Sites may be on either strand
Maximum Number of Motifs	3
Motif E-value Threshold	no limit
Minimum Motif Width	6
Maximum Motif Width	50
Minimum Sites per Motif	2
Maximum Sites per Motif	36

Show Advanced Settings

MEME version
5.3.3 (Release date: Sun Feb 7 15:39:52 2021 -0800)

Reference
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994.

Command line

```
meme upstream250.txt -dna -oc . -nostatus -time 14400 -mod zoops -nmotifs 3 -minw 6 -maxw 50 -objfun classic -revcomp -markov_order 0
```