



MAST

Motif Alignment & Search Tool

For further information on how to interpret these results <https://meme-suite.org/meme/doc/mast.html>.

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

If you use MAST in your research, please cite the following paper:

Timothy L. Bailey and Michael Gribskov, "Combining evidence using p-values: application to sequence homology searches", *Bioinformatics*, **14**(1):48-54, 1998. [\[full text\]](#)

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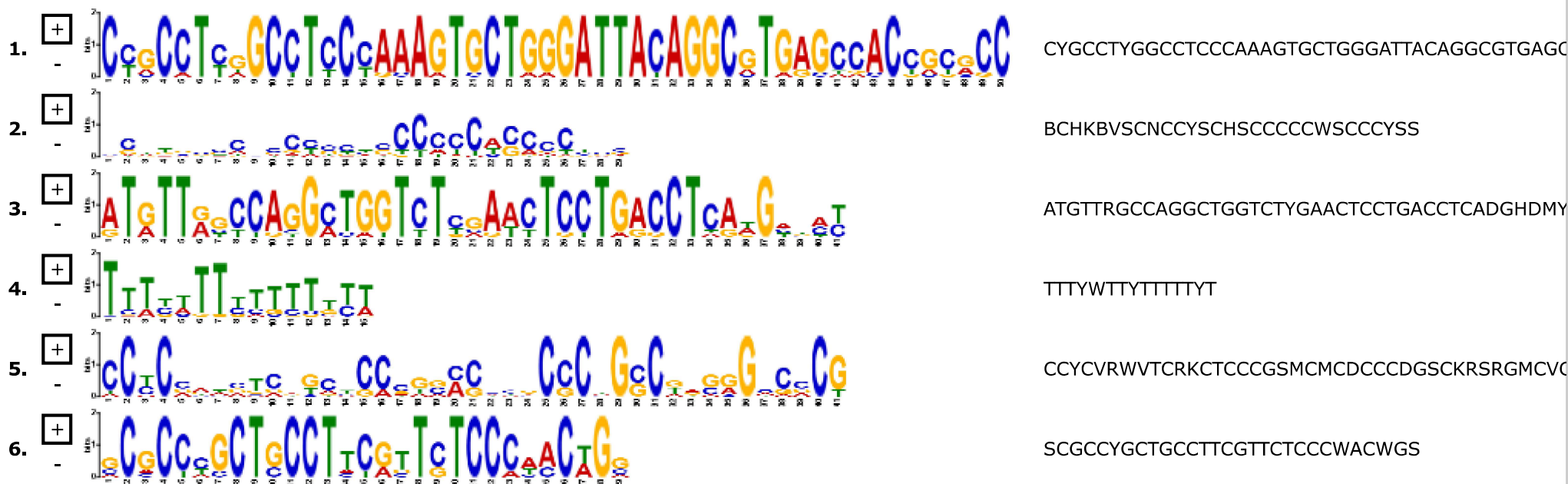
MOTIFS

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Motifs with a pale red background are very similar to other earlier specified motifs and may be biasing the results. It is recommended that you re-run MAST and request it to remove redundant motifs.

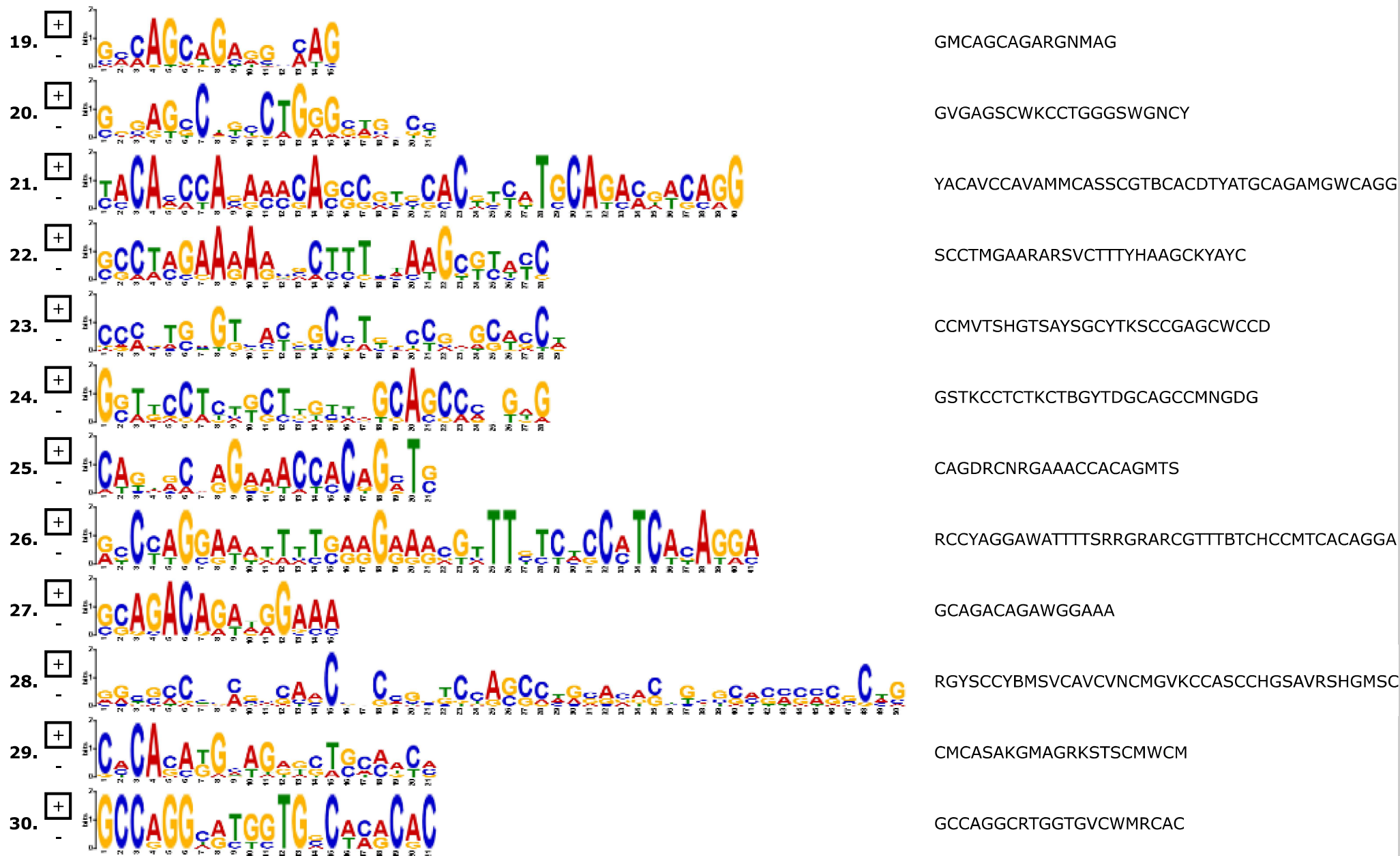
Logo

Name



Logo

Name



Top Scoring Sequences

Each of the following 205 sequences has an *E*-value less than 10.
The motif matches shown have a position *p*-value less than 0.0001.
Hover the cursor over the sequence name to view more information about a sequence.
Hover the cursor over a motif for more information about the match.
Click on the arrow (↕) next to the *E*-value to see the sequence surrounding each match.

CYGCCTYGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCRCC

BCHKBVSCNCCYSCHSCCCCCWSCCCYSS

ATGTTRGCCAGGCTGGTCTYGAACCTCTGACCTCADGHDMY

TTYWTTYTTTTYT

CCYCVRWVTRKCTCCCGSMCMDCCCDGSCKRSRGMVCVG

SCGCCYGCTGCCTTCGTTCTCCCWACWGS

TCGCACTAGTGGGCATTGCTAAACTACG

ATGCTGCTCTTATCGACTTACGAAAAGCTCCAGCAGCAACGTGGAAACCC

KCMGGSCVYGGGCMYKDGGCM

AGCRCCBTBYVGTGACTCWGCACTCTGCTCYAGTCTGVHCMCCBAACTG

GKRHCVRKATGAASAAGGAGGGTAWHHCGAAGRCA

CACTDTRCACGCAGGMMTTVNHTGTGGCAGCGABVWGGRCT

YTTCDMHTKTTSCWAHCACWBRHWCACDCAVACACACACACWBBAC

KDAAAAMWKCTTTTHTTTSA

TRRWNRWAWYTSCMRRYGTSRTKKCDAMGMTGRKATGAGRTYWRYWT

TRTTCCSWSTYNATKGAARCDGTCMNCYCCYYTGTGWGKATWKWRMWGT

CCYBWGGDYKKCCACDTCTCRTYKGCVAM

AGARADKAATTCWCTGAAGMRCRAMGGKC

GMCAGCAGARGNMAG

GVGAGSCWKCTGGGSWGNCY

YACAVCCAVAMMCASSCGTBCACDTYATGCAGAMGWCAGG

SCCTMGAARARSVCTTTYHAAGCKYAYC

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GSTKCCTCTKCTBGYTDGCAGCCMNGDG

CAGDRCNRGAAACCACAGMTS

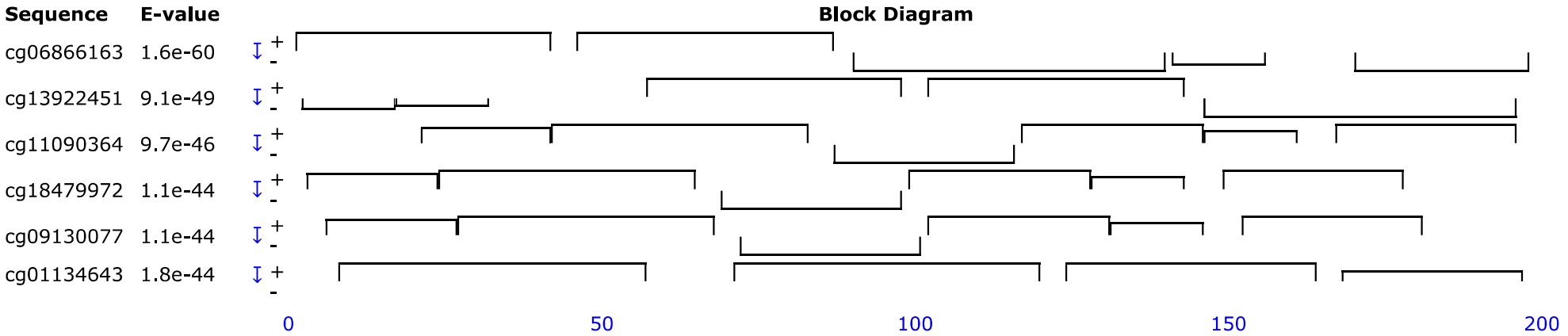
RCCYAGGAWATTTTSRRGRARCGTTTBTCHCCMTCACAGGA

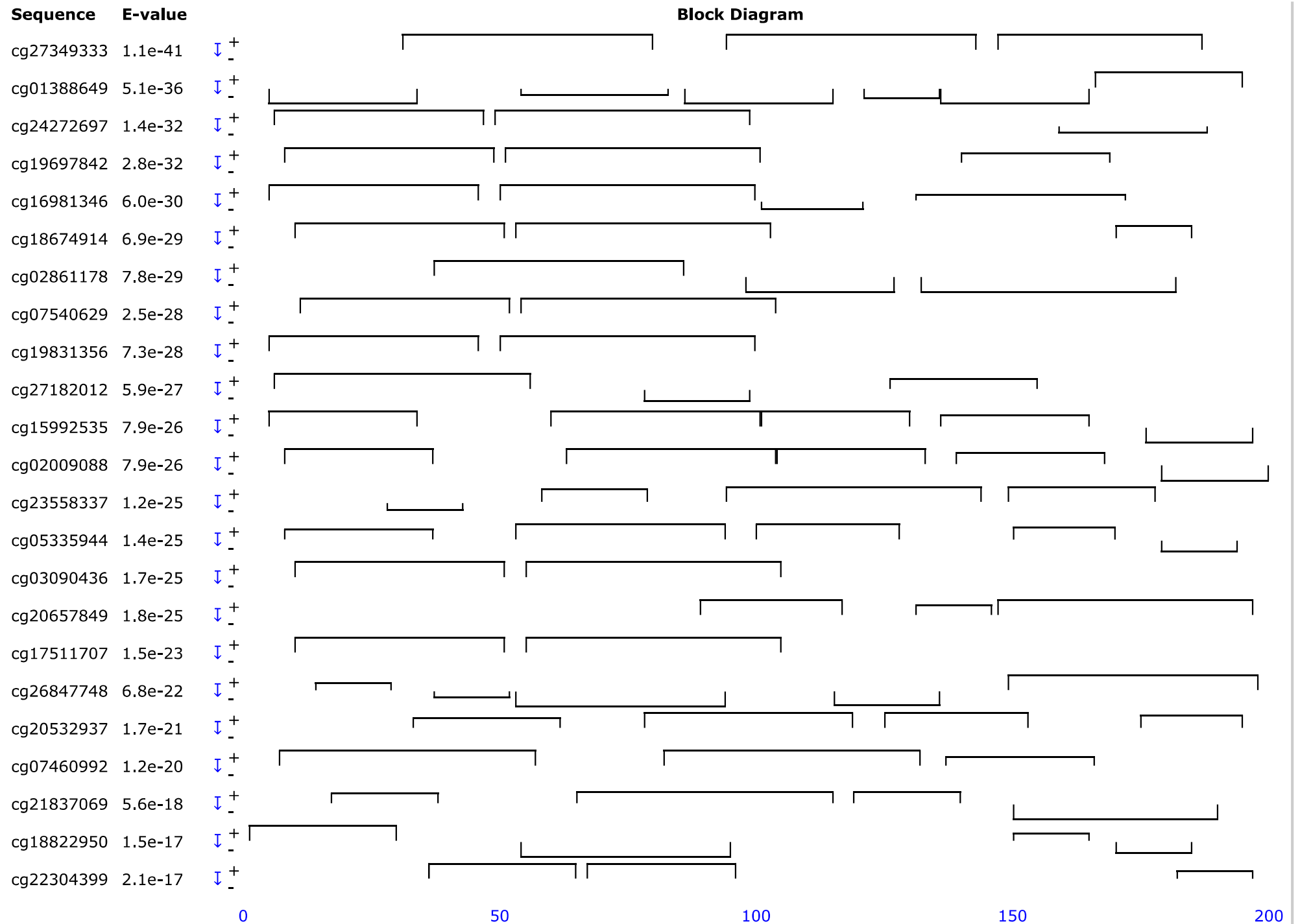
GCAGACAGAWGGAAA

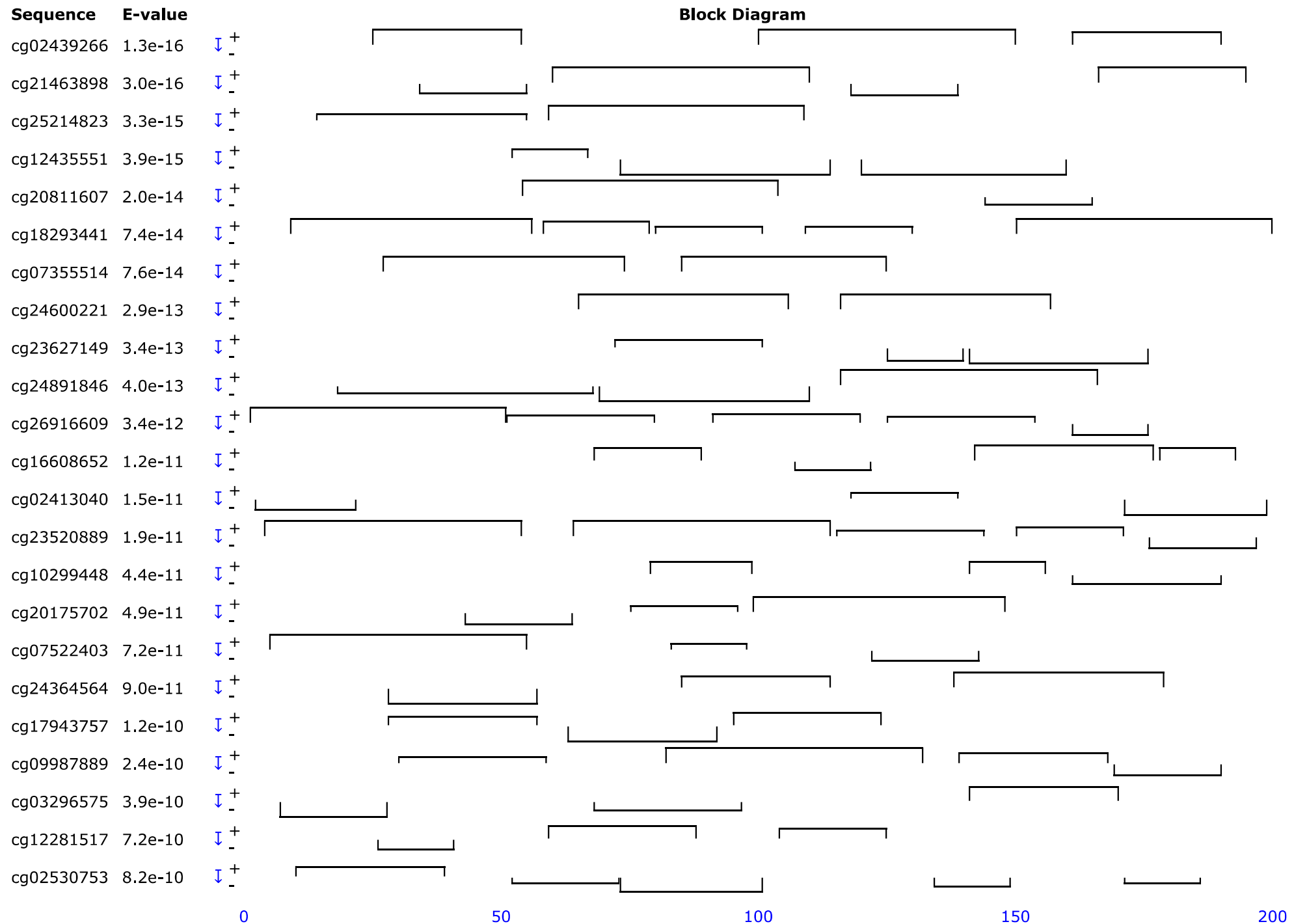
RGYSCCYBMSVCAVCVNCMGVKCCASCCHGSAVRSHGMSMSMSMCSCHG

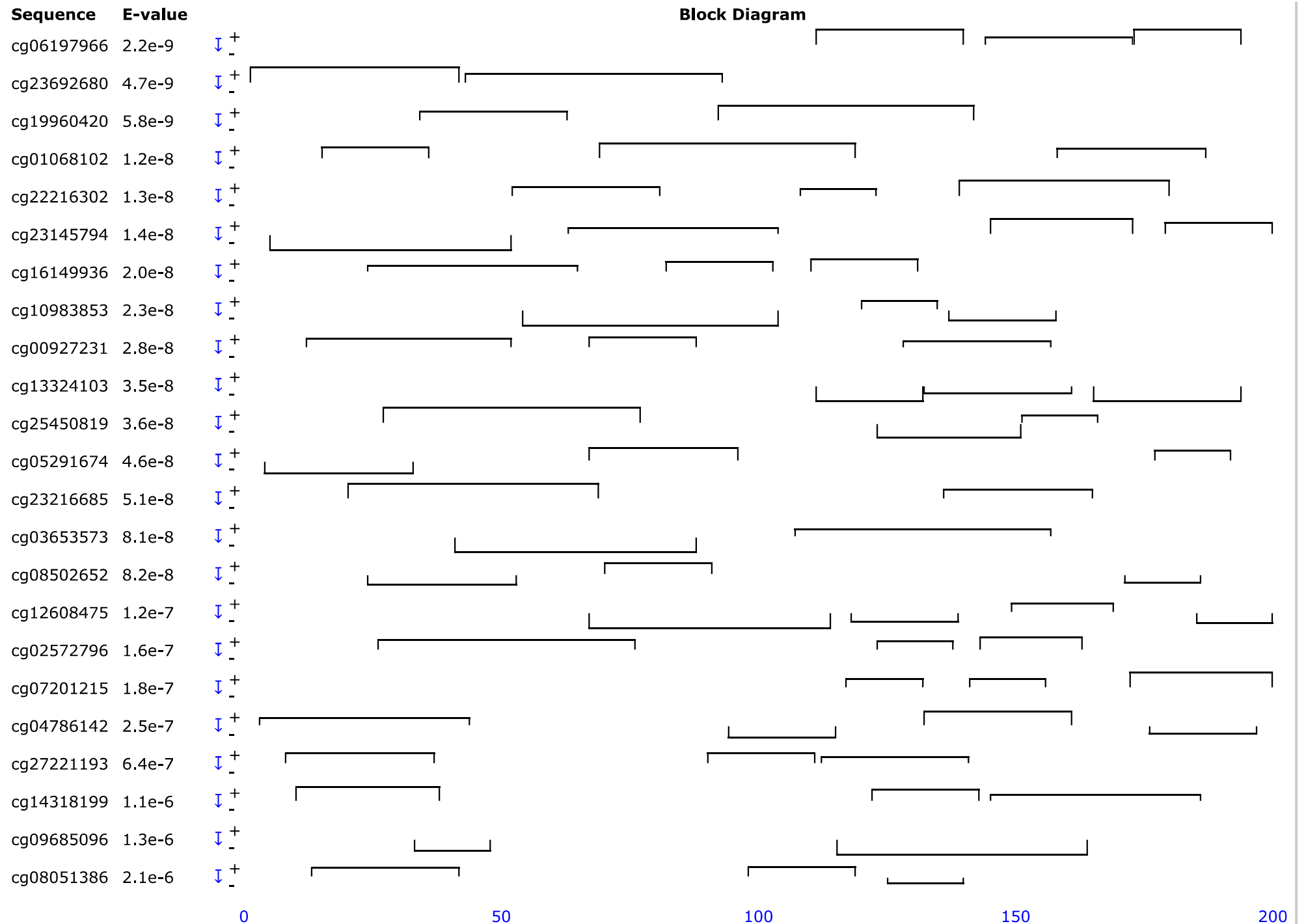
CMCASAKGMAGRKSTSCMWCM

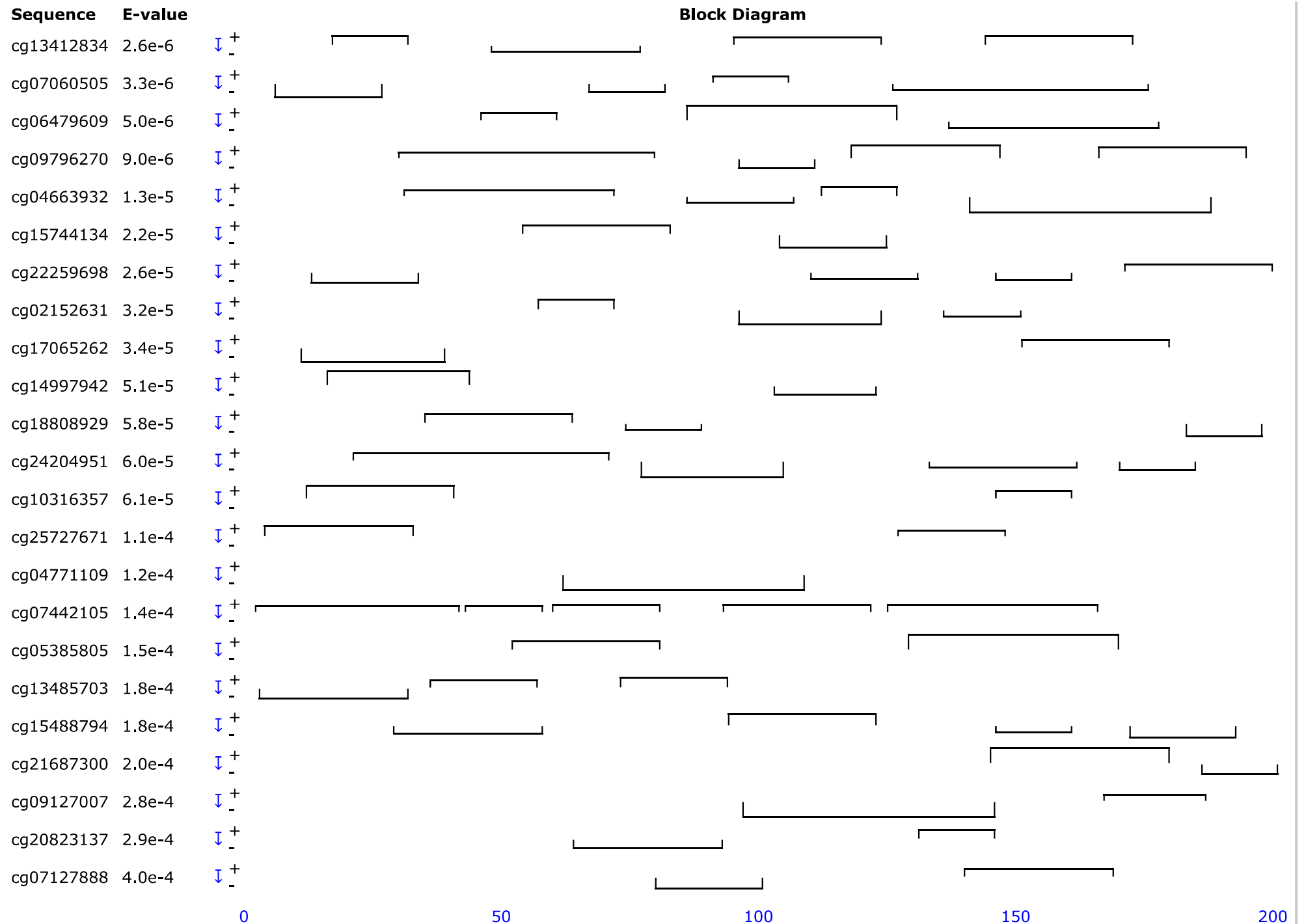
GCCAGGCRTGGTGVCWMRCAC

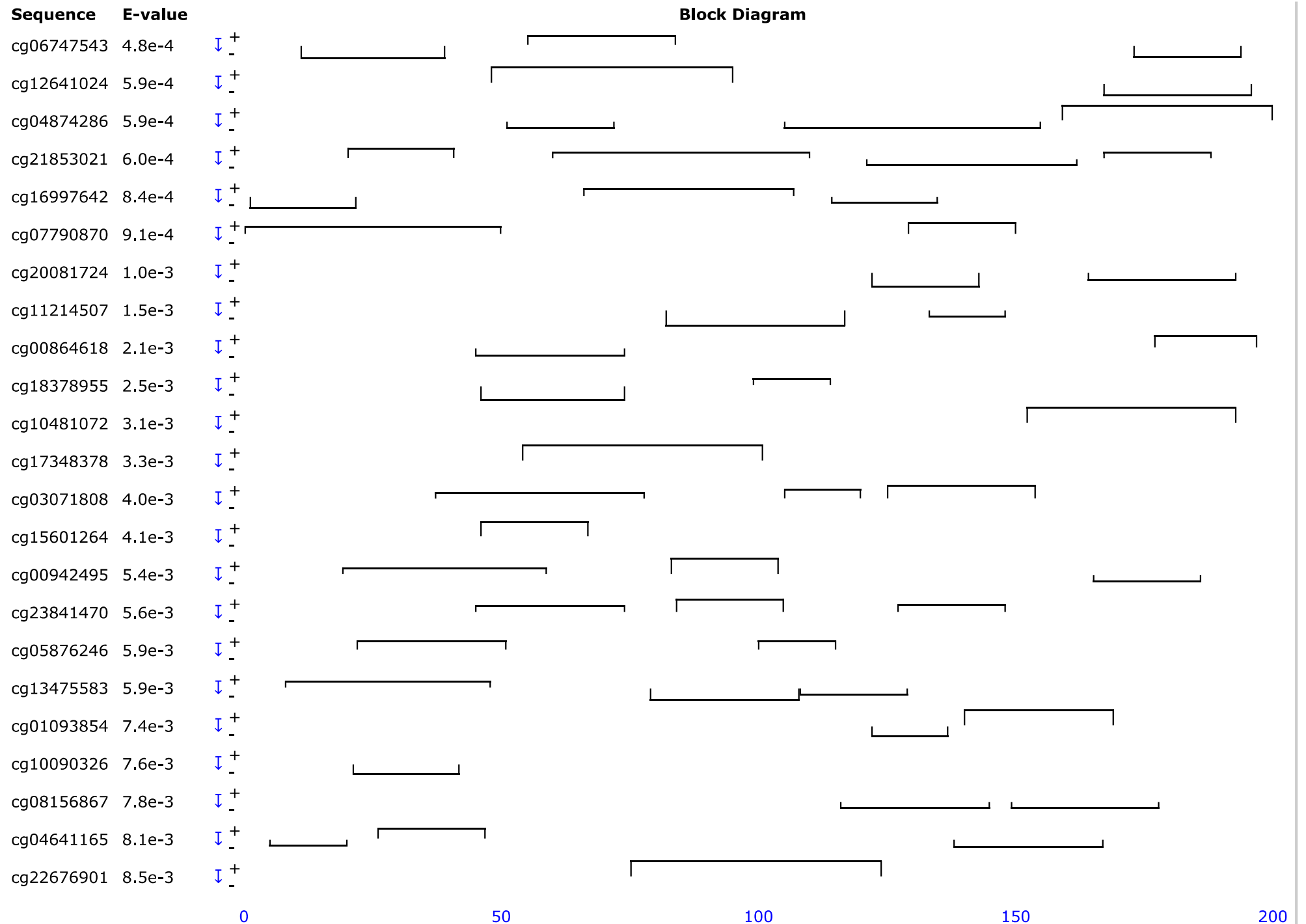












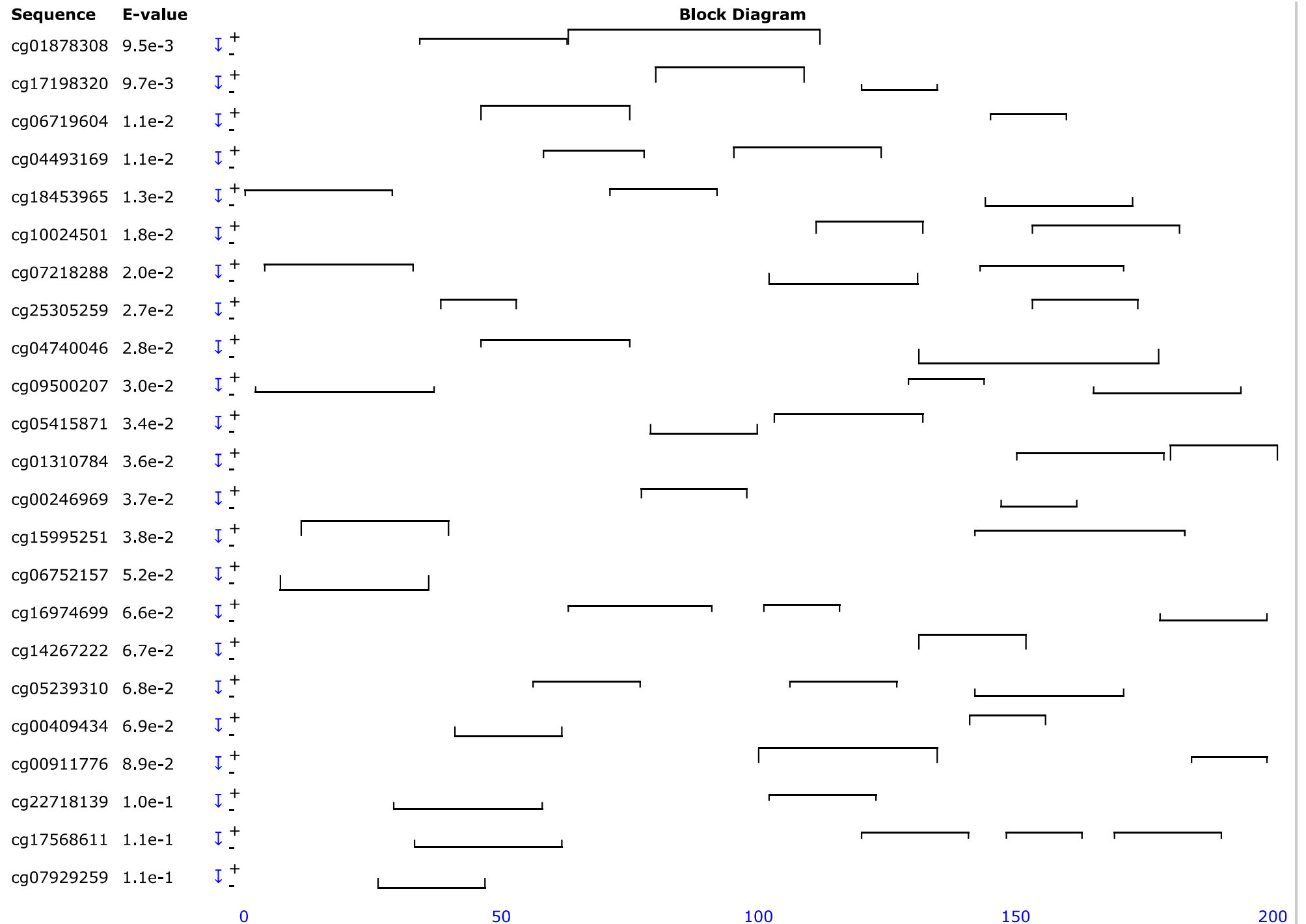
0

50

100

150

200



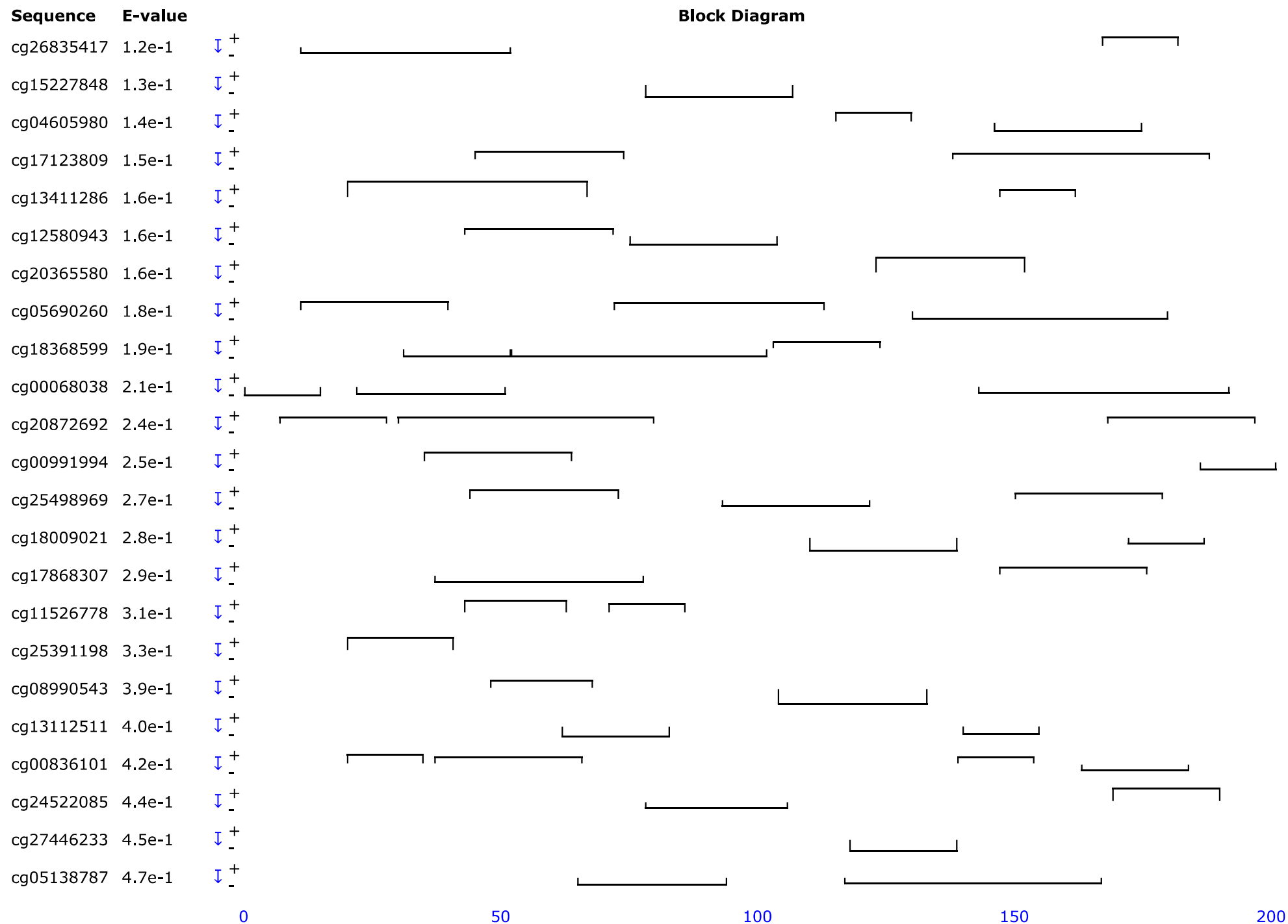
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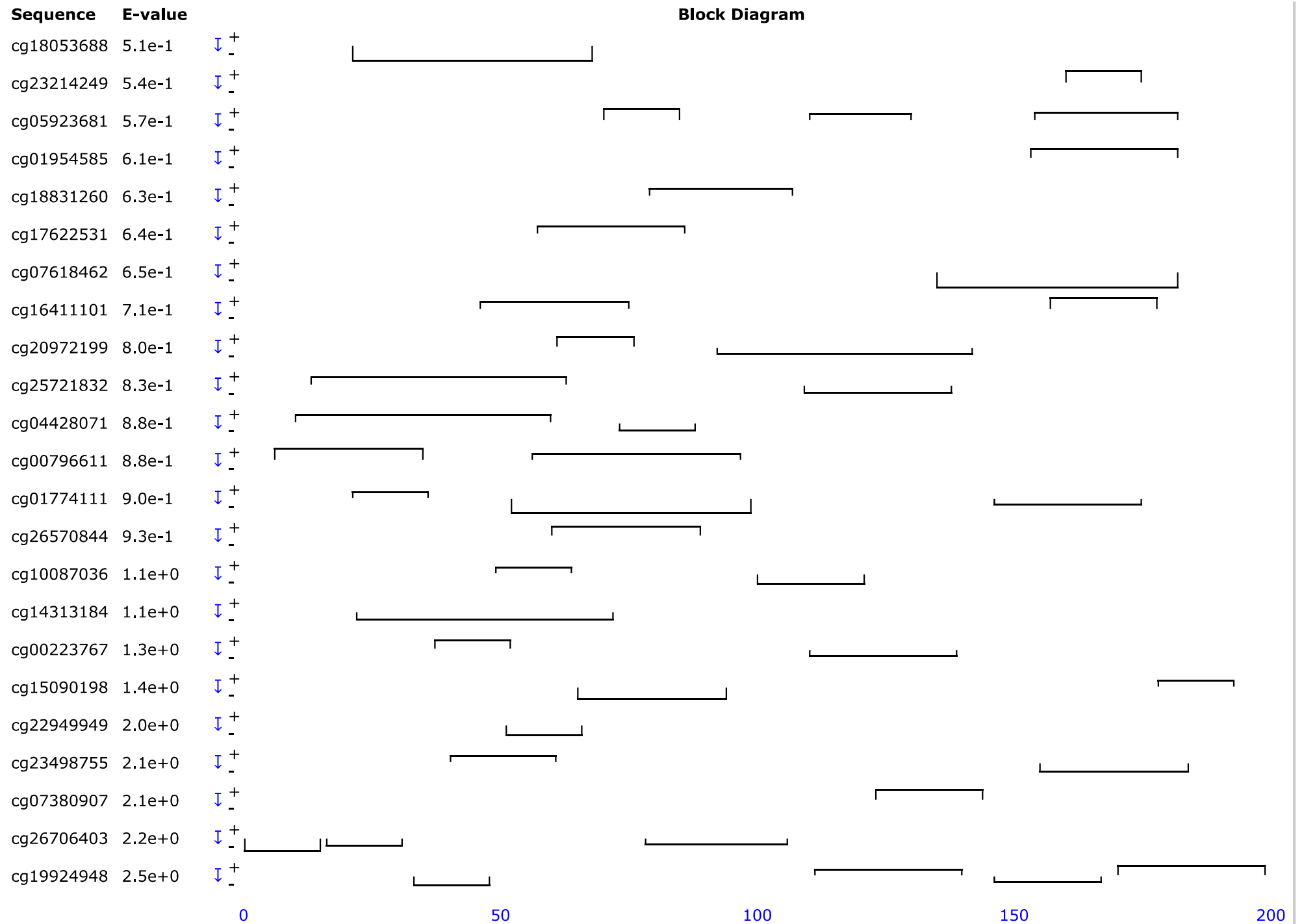
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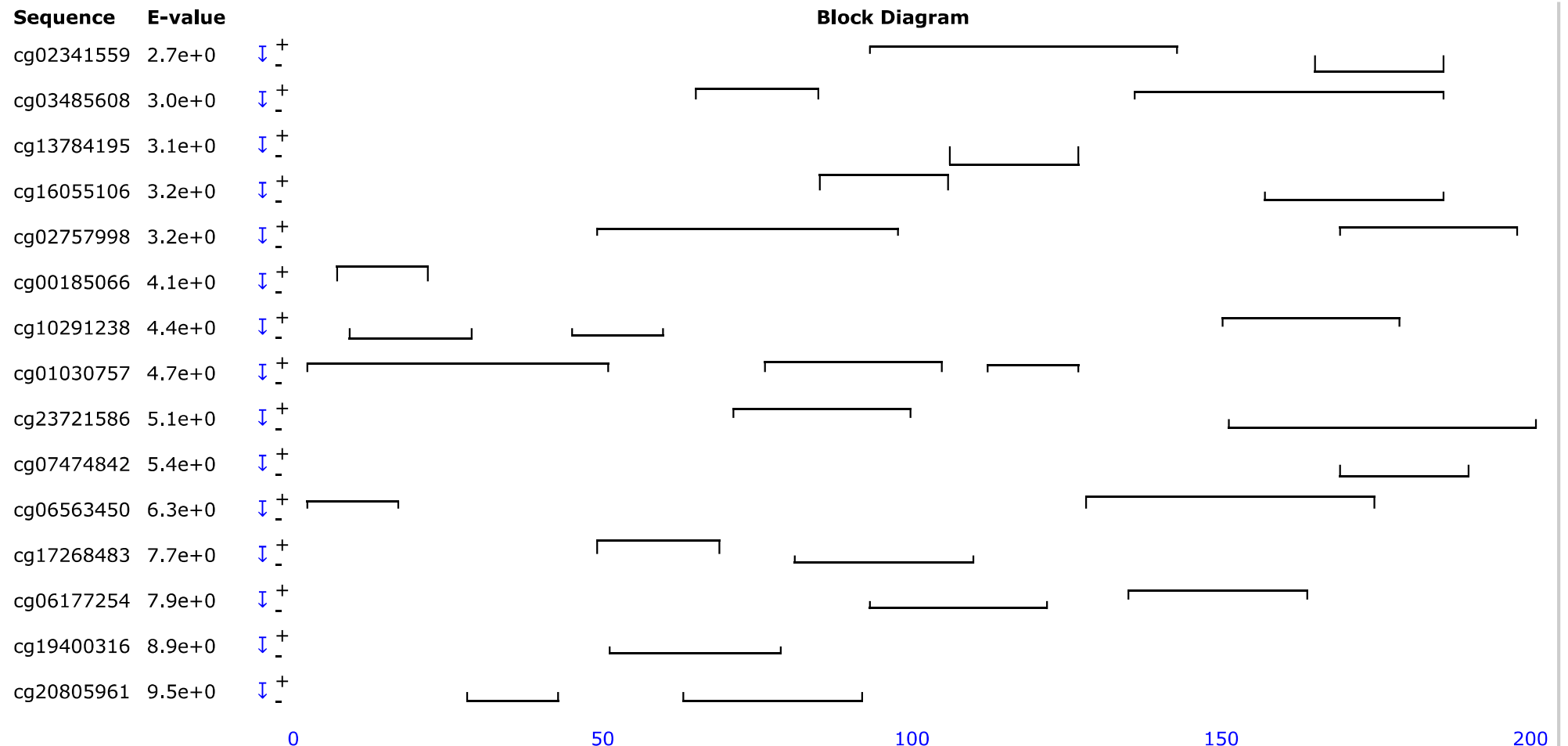
100

150

200







□ CYGCCTYGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCRCC □ BCHKBVSCNCCYSCHSCCCCCWSCCCYSS
□ ATGTTTRGCCAGGCTGGTCTYGAACCTCTGACCTCADGHDMY □ TTTYWTTYTTTTTYT □ CCYCVRWVTCRKCTCCCGSMCMCDCCCDGSCKRSRGMCVCG
□ SCGCCYGCTGCCTTCGTTCTCCCWACWGS □ TCGCACTAGTGGGCATTGCTAAACTACG
□ ATGCTGCTCTTATCGACTTACGAAAAGCTCCAGCAGCAACGTGGAAACCC □ KCMGGSCVYGGGCMYKDGGCM
□ AGCRCCBTBYVGTGACTCWGCACTCTGCTCYCAGTCTGVHCMCCBAACTG □ GKRHCVRKATGAASAAGGAGGGTAWHHCGAAGRCA
□ CACTDTRCACGCAGGMMTTVNHTGTGGCAGCGABVWGGRCT □ YTTCDMHTKTTSCWAHCACWBRHWCACDCAVACACACACACWBBAC
□ KDAAAAMWKCTTTTHTTTSA □ TRRWNHRWAWYTSCMRRYGTSRTKKCDAMGMTGRKATGAGRTYWYRYWT
□ TRTTCCSWSTYNATKGAARCDGTCMNCCYYTGTGWGKATWKWRMWGT □ CCYBWGGDYKKCCACDTCTCRTYKGCVAM
□ AGARADKAATTCWCTGAAGMRCRAMGGKC □ GMCAGCAGARGNMAG □ GVGAGSCWKCTGGGSGWNCY

☐ YACAVCCA VAMMCASSCGTBCACD TYATGCAGAMGWCAGG ☐ SCCTMGAARARSVCTTTYHAAGCKYAYC ☐ CCMVTSHGTSAYSGCYTKSCCGAGCWCCD
☐ GSTKCCTCTKCTBGYTDGCAGCCMNGDG ☐ CAGDRCNRGAAACCACAGMTS ☐ RCCYAGGAWATTTTSRRGRARCGTTTBTCHCCMTACAGGA
☐ GCAGACAGAWGGAAA ☐ RGYSCCYBMSVCAVCVNCMGVKCCASCCHGSAVRSHGMSMSMSMC SCHG ☐ CMCASAKGMAGRKSTSCMWCM
☐ GCCAGGCRTGGTGVCWMRCAC

INPUTS & SETTINGS

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Alphabet

Background Source: an old version of the NCBI non-redundant database

Name	Bg.				Bg.	Name
Adenine	0.274262	A	~	T	0.274262	Thymine
Cytosine	0.22521	C	~	G	0.22521	Guanine

Sequences

The following sequence database was supplied to MAST.

Database	Sequence Count	Residue Count	Last Modified
UC_dmp_cpg_sequences.fasta	334	67134	Sat Jun 21 02:18:32 2025
Total	334	67134	

Motifs

The following motif database was supplied to MAST.

Database	Last Modified
meme.xml	Sat Jun 21 04:46:21 2025

Other Settings

Strand Handling
Max Correlation
Remove Correlated

The result of scanning both strands is **combined**. When matches overlap the non-overlapping combination with the best p-value is shown.
Motifs with a correlation greater than **0.6** are marked for potential removal dependant on the --remcorr option.
Correlated motifs exceeding the threshold are **highlighted** and their removal is recommended.

Max Sequence E -value

Sequences with an E -value less than **10** are included in the output.

Adjust Hit p -value

The hit p -value is **not adjusted** for the length of the sequence.

Displayed Hits

The p -value of a hit must be less than **0.0001** to be shown in the output.

Displayed Weak Hits

Weak hits are **not displayed**.

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MAST version 5.5.8

(Release date: Thu May 15 15:01:46 2025 -0700)

Reference

Timothy L. Bailey and Michael Gribskov, "Combining evidence using p -values: application to sequence homology searches", *Bioinformatics*, **14**(1):48-54, 1998. [\[full text\]](#)

Command line summary

```
mast -oc . -nostatus meme.xml UC_dmp_cpg_sequences.fasta
```

Ran in 0.472 seconds on Sat Jun 21 04:46:22 2025 on noble-meme.grid.gs.washington.edu