



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. [\[full text\]](#)

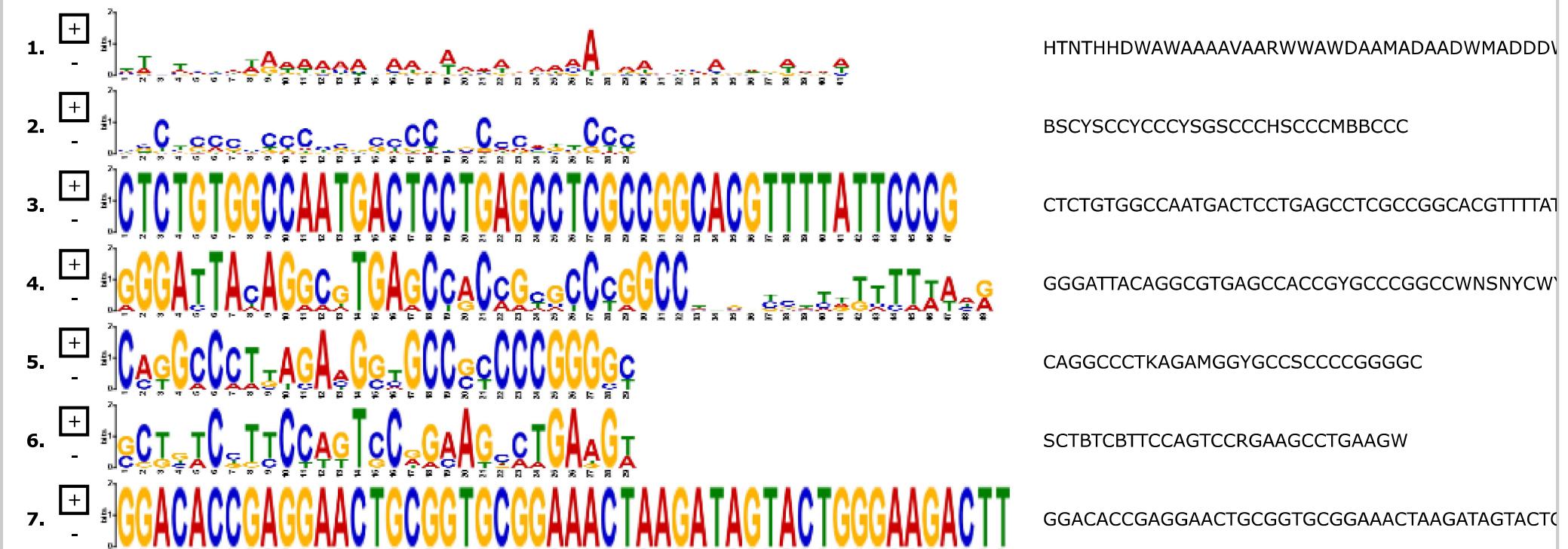
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MOTIFS

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Logo

Name



Logo

Name



TTTCCCCATCGCACTGAGCACTGAGATCCTGCTGGAAAGCTCTGCGGCCAGCA
TGCAGTGAGCHGWATCGTGCCACTGCACTCCAGCCTGGG
GGGCTGTCTGTGGCCTCAGCGCTCGGCAGGCGCGCACTCA
CCTGSCSKMTCTSSGMKSCCCYSCCYGMCCYCATTCCYKG
TCWGTYYCHAYATYTGCAAAAWRRR
CGATSKGCCACMTSSTSPTYCTYCMAMARRWGSCAAWKC
TKTSMCCWKGTGBSCASRSTGRTCWYGAWCWCYTGRVCT
CARMYSYYCKGNMGGCCTYGAGYCKCYCCDMCWSGATCT
SKGGGGGGGGC
RCACAGCTGCMWGGAGHVSGBGCCASCT
CCDCMCTGYCGCWGMAGMRMTCCMCABKCKSWBGWGGC
GTGYKTGDGSGTGTGTSTDYSTGBTGTGKGTHKTGKAYR

Logo

Name

20.		CCCGRGACCASCCCAGACCAAG
21.		GWNGKBYTHTYTYCTKTCTGM
22.		CAAARCCGGCASWGTMCVCWCACKGAARCTCATGGACWTI
23.		GTDDAGSDGSTGAGTKAADCMMAGAGGBGGKSWTTGDTG
24.		GCAGGAAGGTAGGTAGATCTGTCCGGCTTTCGATCCTAATG
25.		THTRMAKGWGTGASTTDTTYNWAARMMAMWCYYATGYDR
26.		CTAAAAANGATWAAHCDTTAYTTAAAT
27.		TKGGKGTTGGTGTGG
28.		TTTMABGTGTVBTTAKBVHNKRGCAGTGKKTWHTAADYTWT
29.		AWGKAABAGHTAAKTATGAADAATT
30.		ARAAAABARMWBAGAAGWARC

SEARCH RESULTS

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Top Scoring Sequences

Each of the following 303 sequences has an *E*-value less than 10.

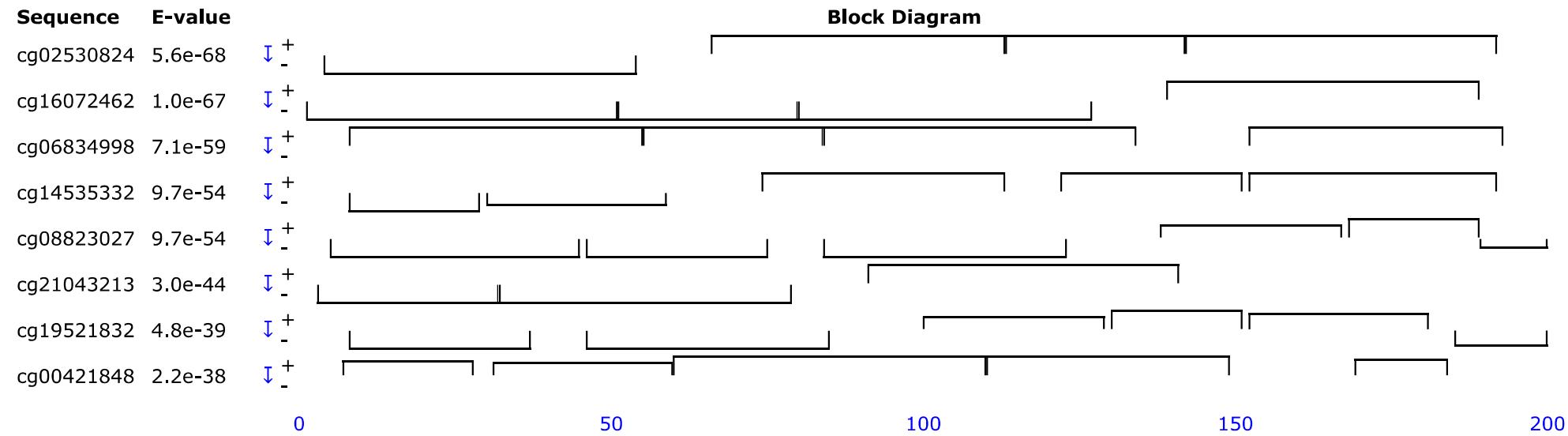
The motif matches shown have a position *p*-value less than 0.0001.

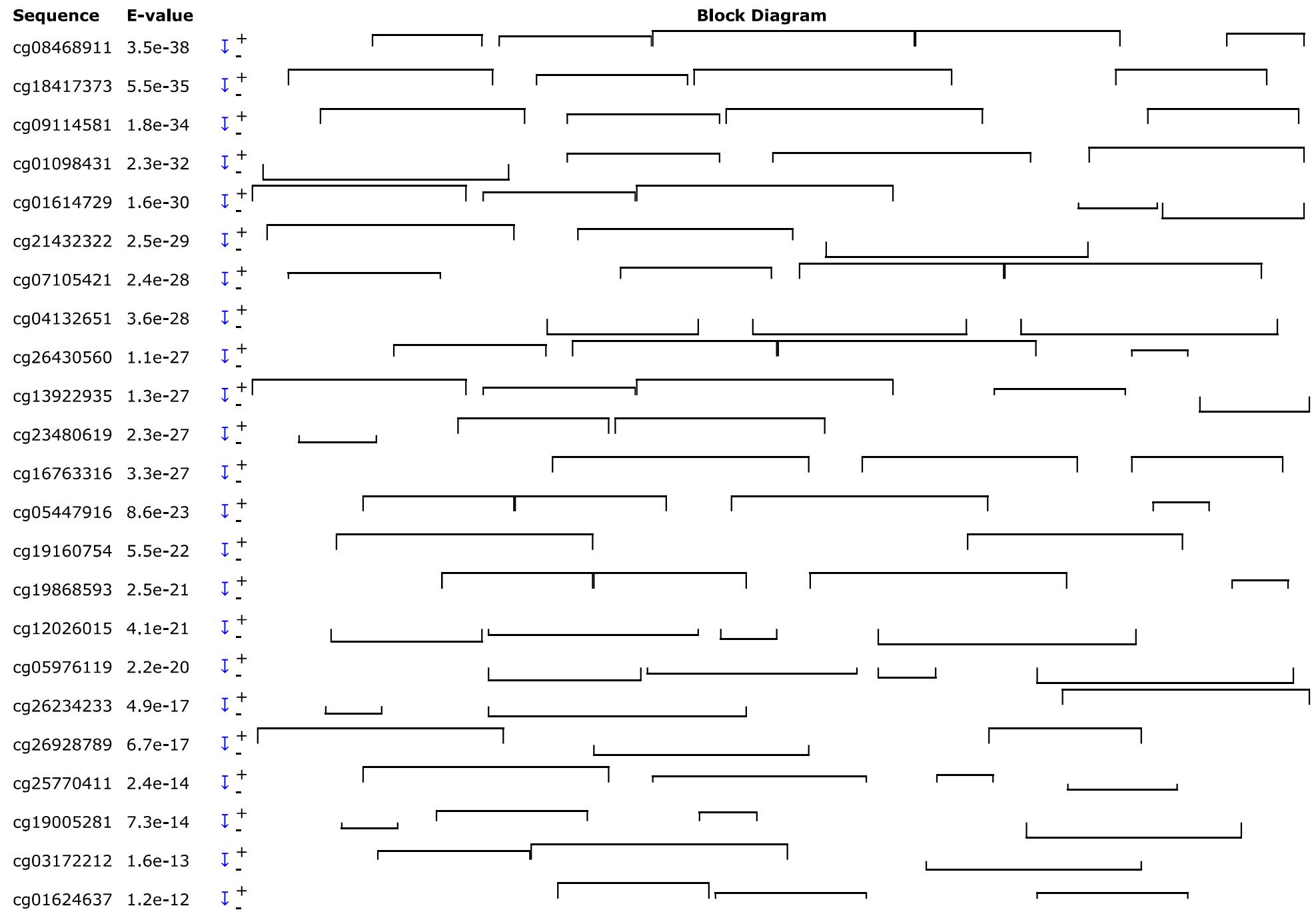
Hover the cursor over the sequence name to view more information about a sequence.

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.

□ HTNTHHDWA AAAA AVARWW AWDAAMADA ADWM ADDD WWWW □ BSCYSCCYCCCYS GSCCC HSCCC MBBCCC
□ CTCTGTGGCCAATGACTCCTGAGCCTGCCGGCACGTTTATTCCCG □ GGGATTACAGGC GTGAGCC ACCGYGCCC GCCWNSNYC WYDTTT WAHR
□ CAGGCCCTKAGAMGGYGCSCCCGGGGC □ SCTB TCBTTCCAGTCCRGAAGCCTGAAGW
□ GGACACCGAGGAACTGCGGTGCGGAAACTAAGATAGTACTGGGAAGACTT □ TTTCCCATCGCACTGAGGACTTGAGATCCTGCTGGAGCTCTGCCAGCA
□ TGCAGTGAGCHGWGATCGCCACTGC ACTCCAGCCTGGCGACAGA □ GGGCTGTCTGTGGCCTCAGCGCTCGGCAGGCGCGCACTCA
□ CCTGSCSKMTCTSSGMKSCCCYSCCYGMCCYC ATCCYKG □ TCWGTTTYCHYATYTGCAAAAWRRR
□ CGATSKGCCACMTSSTS KTYCTYCMMA MARRWGSCAAWKCRSCKGSAGA □ TKTS MCCWK GTTGBSCASRSTGR TCWYGAWCWCYTGRVCTC
□ CARMYSYYCKGNMGGCCTY GAGYCKCYCCDMCWSGATCT □ SKGGCGGGGC □ RCACAGCTGCMWGGAGHVSGBGCCASCT
□ CCDCMCTGYCGCWGMAGMRMTCCMCABCKSWBGWGGCTYARSYCCST □ GTGYKTGDGSGTGTGTSTDY STGBRTGTGKGTHKTGKAYR
□ CCCRGACCA SC CAGACCA G □ GWNGKB YHT TYCTKTCTGM □ CAAARCCGGCASWGTMCVCWCACKGAARCTCATGGACWTMA
□ GTDDAGSDGSTGAGTKAAC DMMAGAGGBGGKS TTGDTGWC VAGCTYCC □ GCAGGAAGGTAGGTAGATCTGTCGTTGGCTTCTCGAT CCTAATG
□ THTRMAKGWGTGASTTD TTYNWAARMMAMWCYYATKGYDRGMM DWAAAAA □ CTAAA AANGATWAAHCDTTAYTTAAAT □ TKGGKGTTGGTGTGG
□ TTTMABGTGTVBTTAKBVHNKRGCASTGKKTWHTAADYTWWGTTCA □ AWGKAABAGHTAAKTATGAADAATT □ ARAAAABARMWBAGAAGWARC





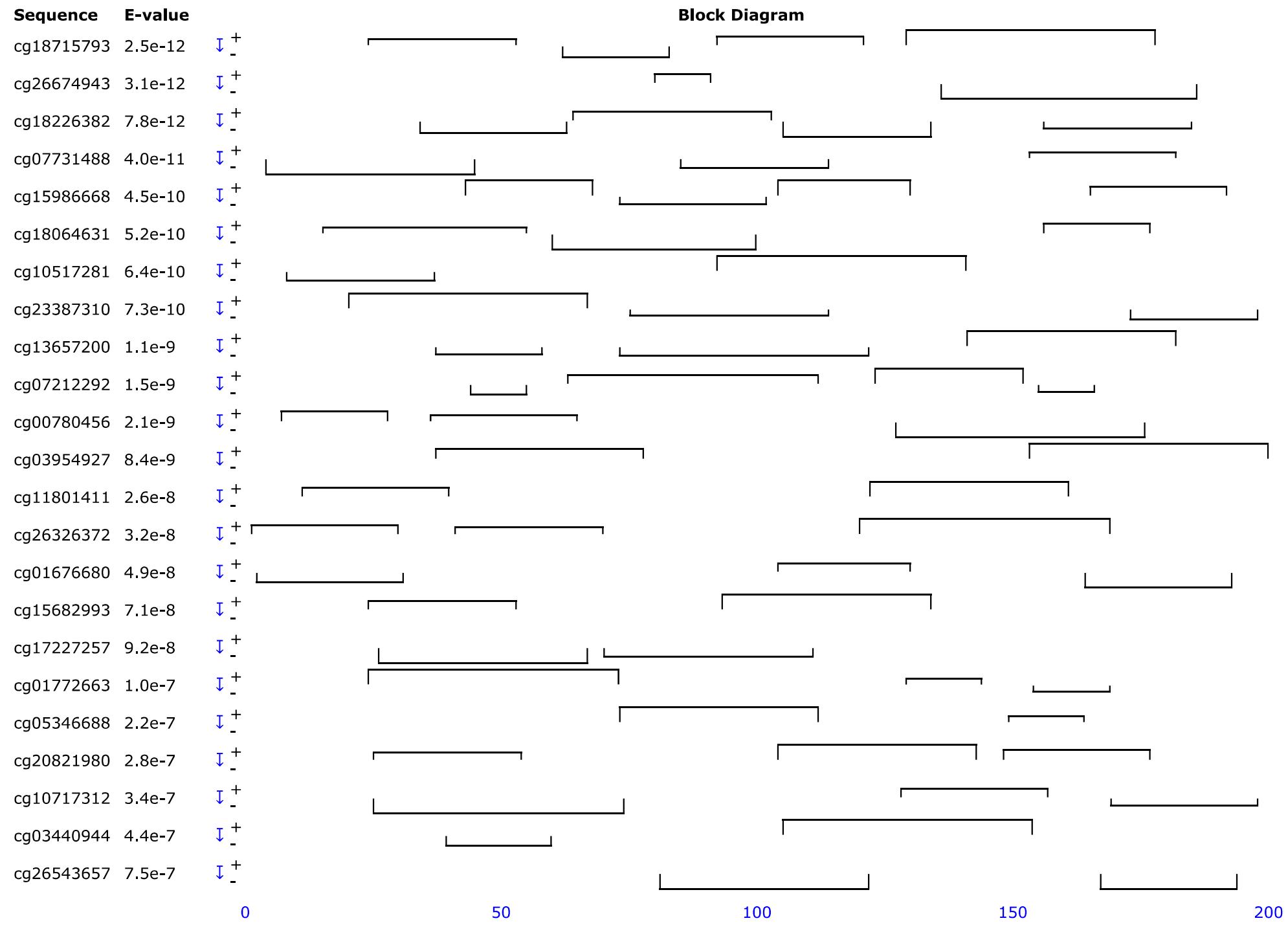
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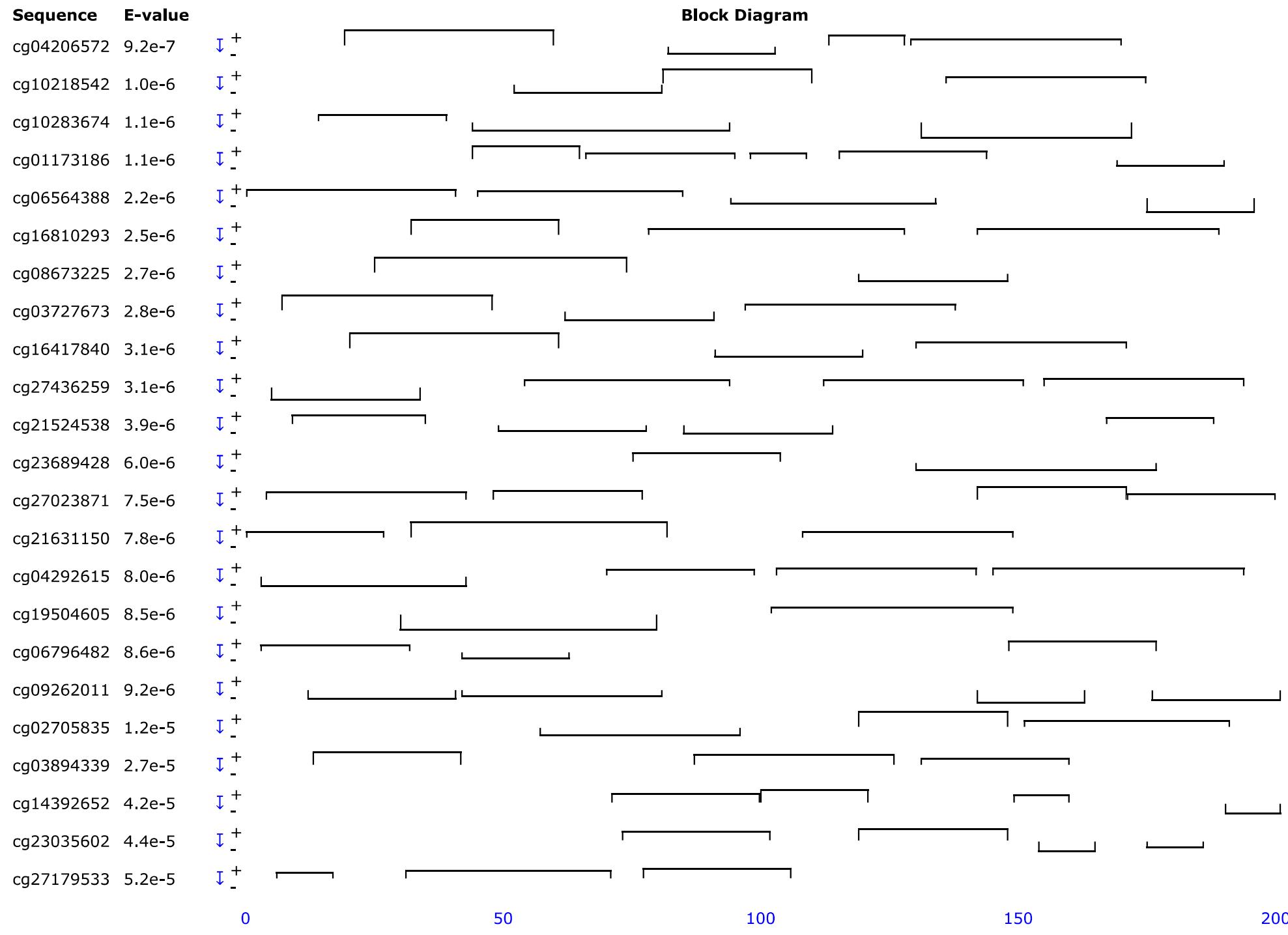
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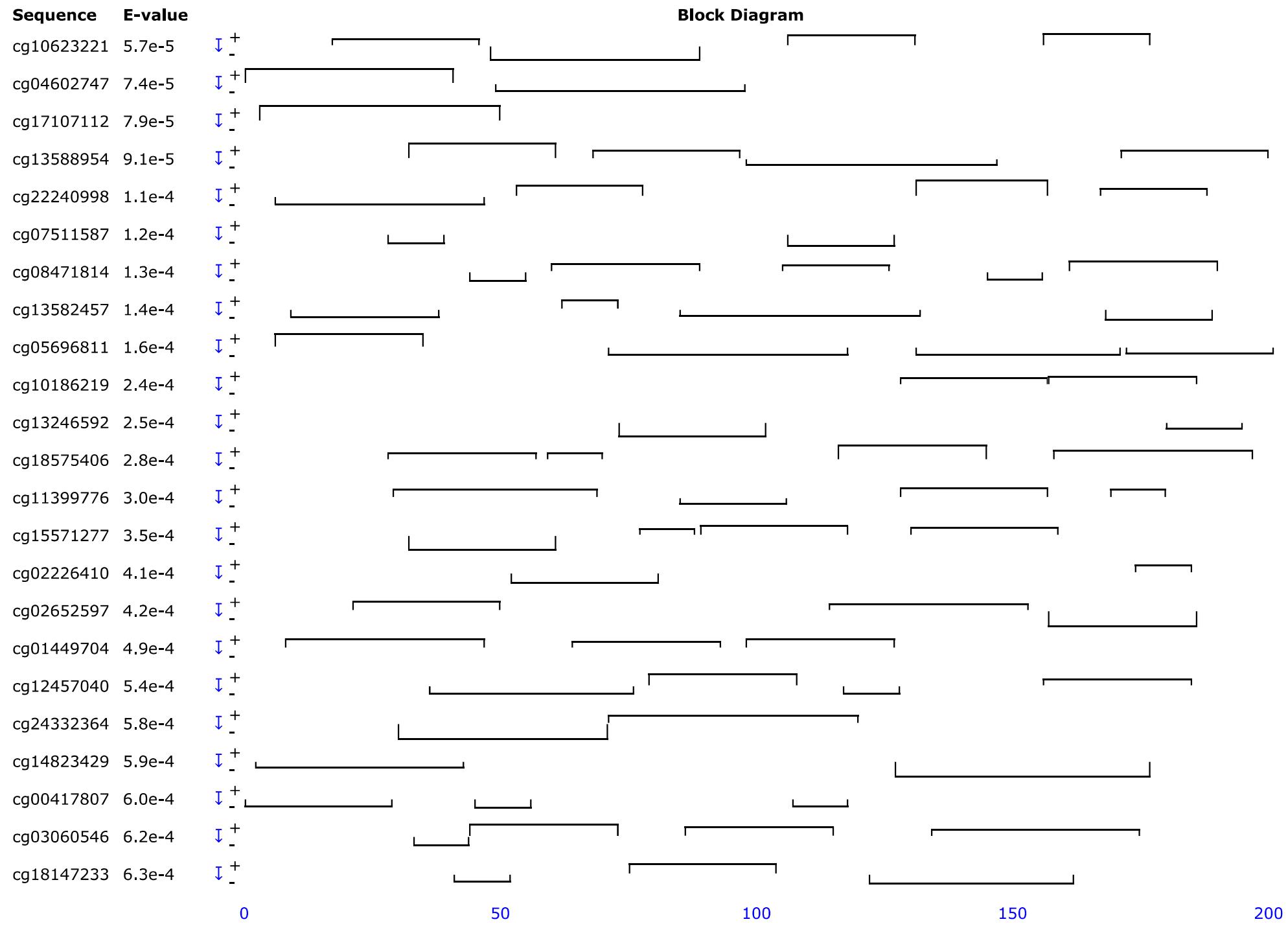
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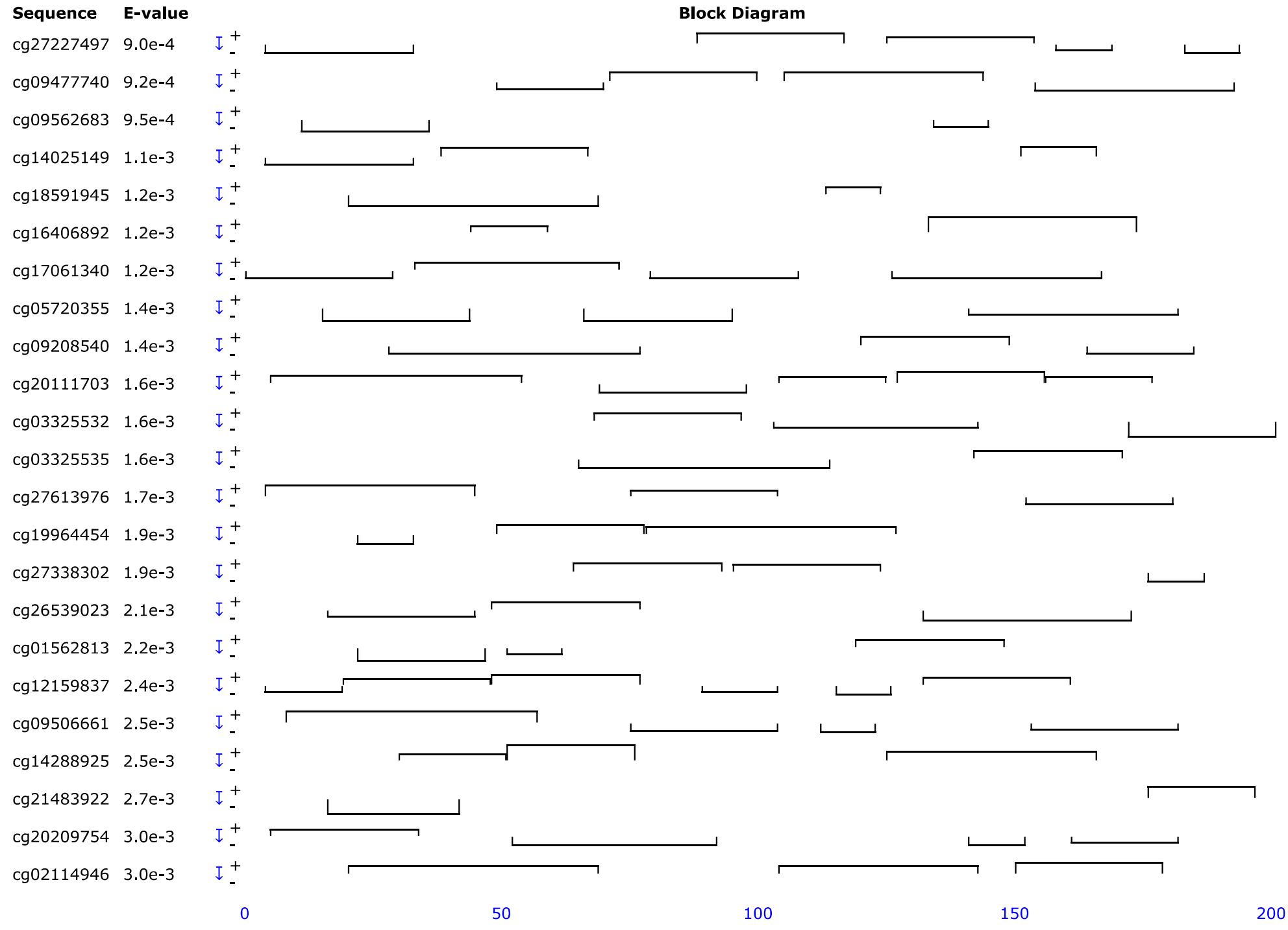
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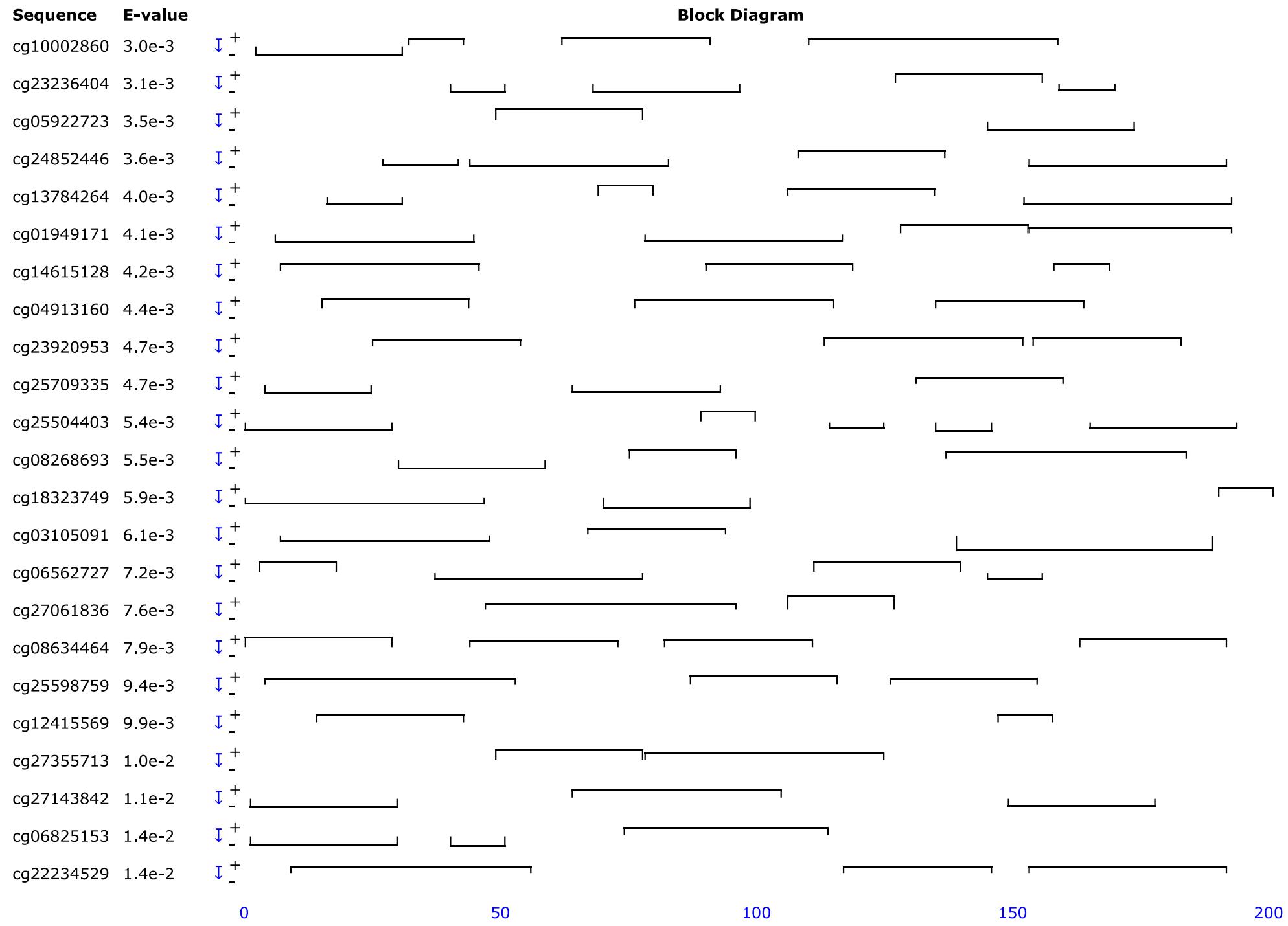
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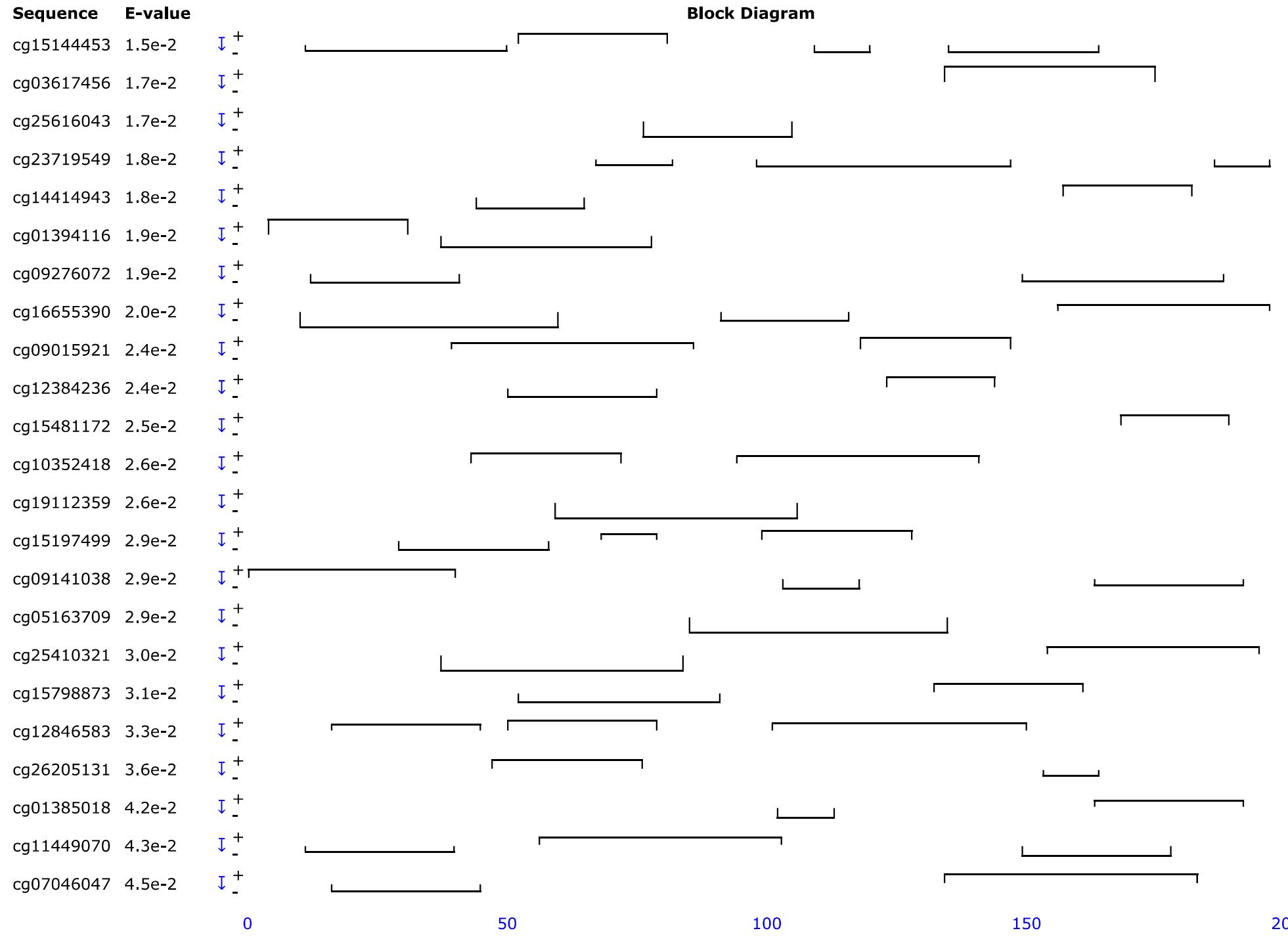


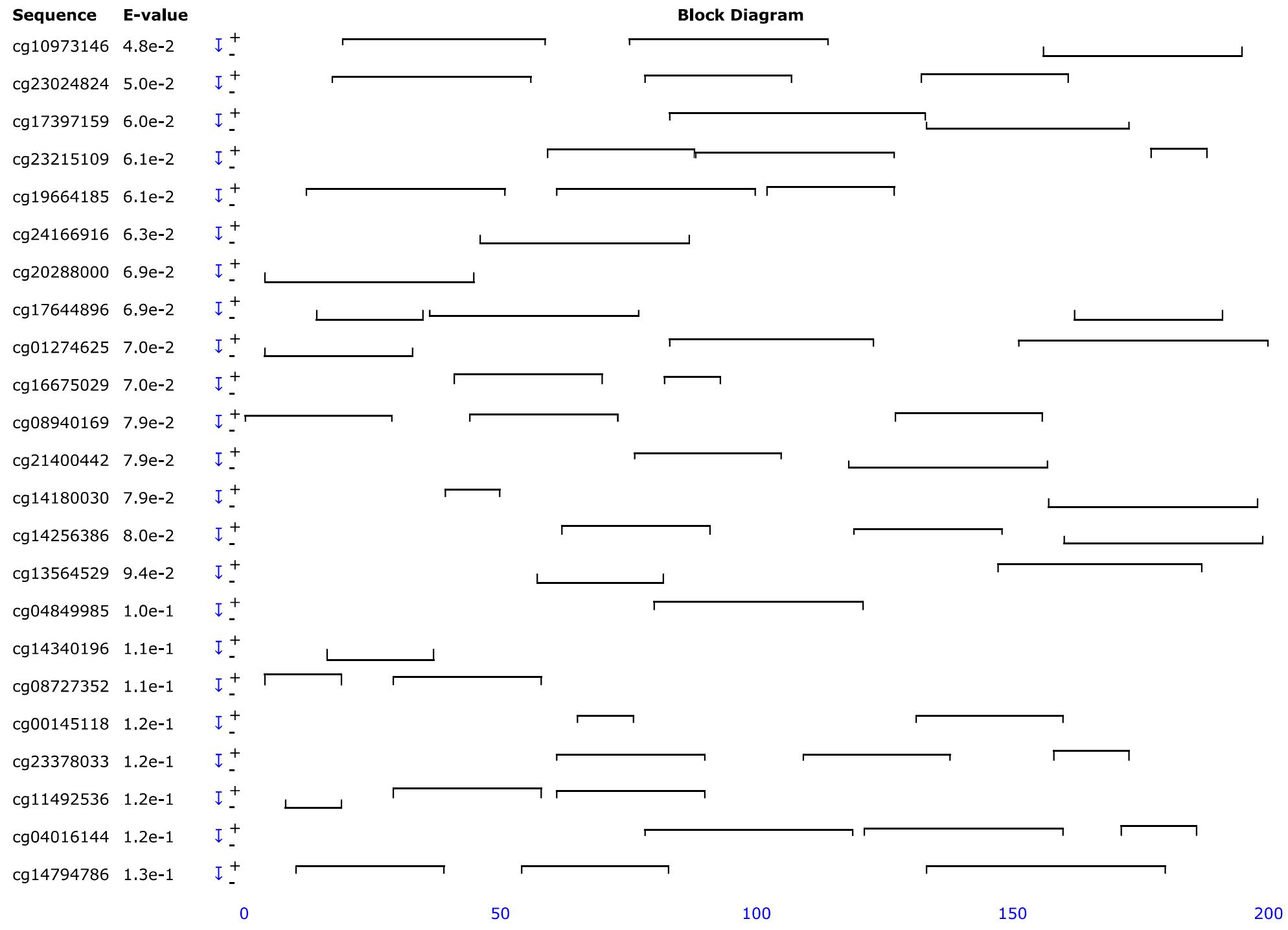


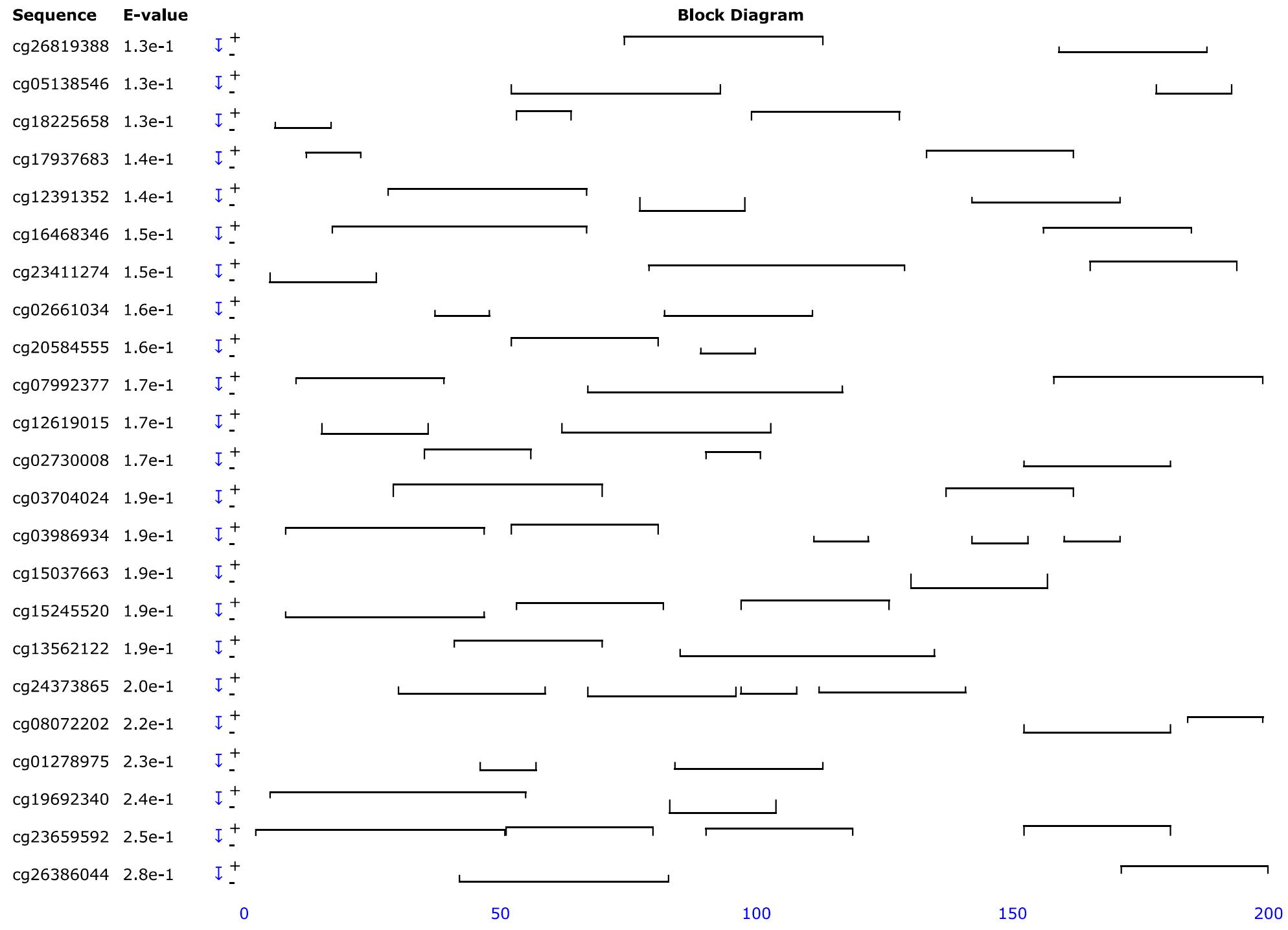


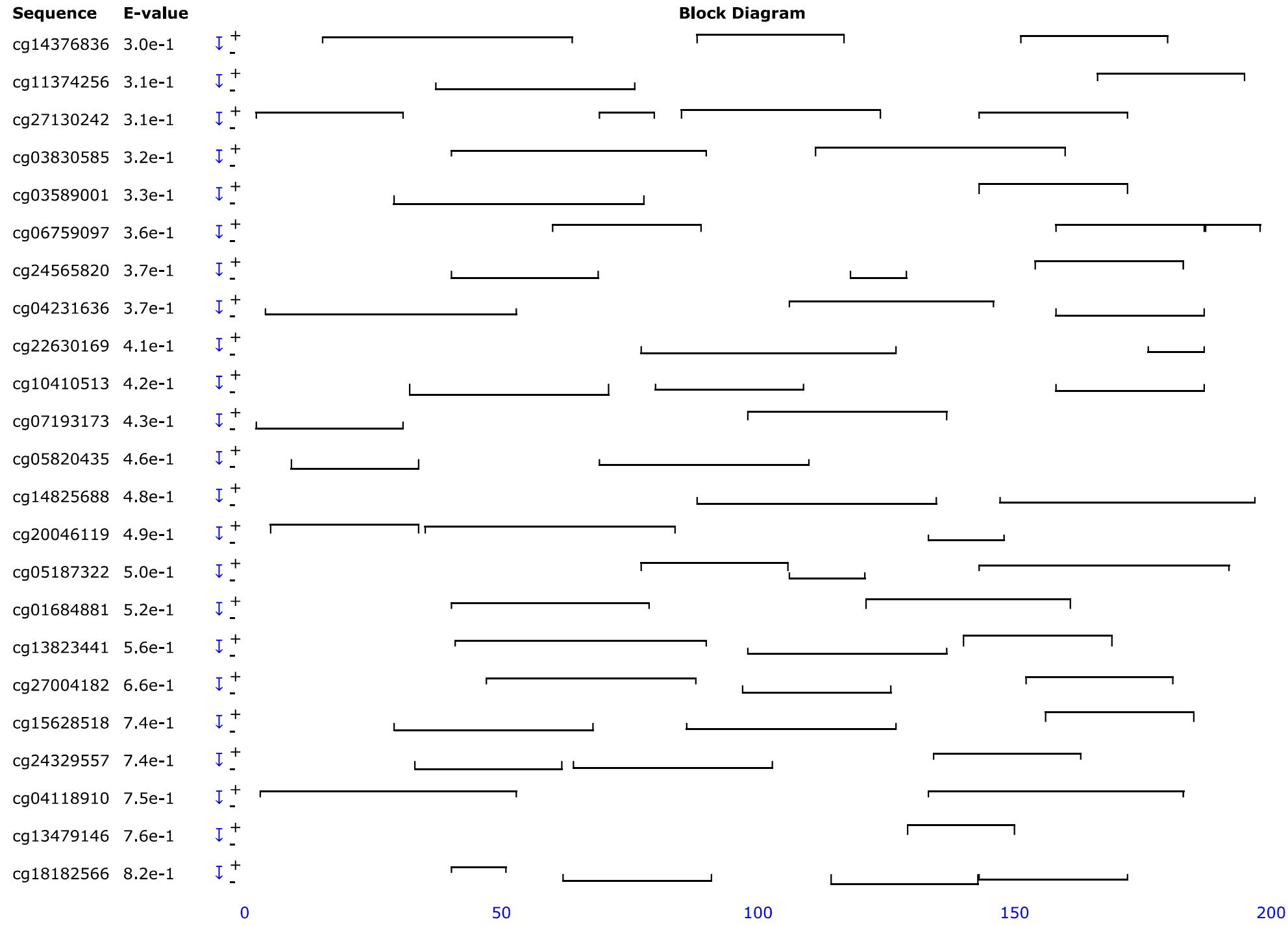


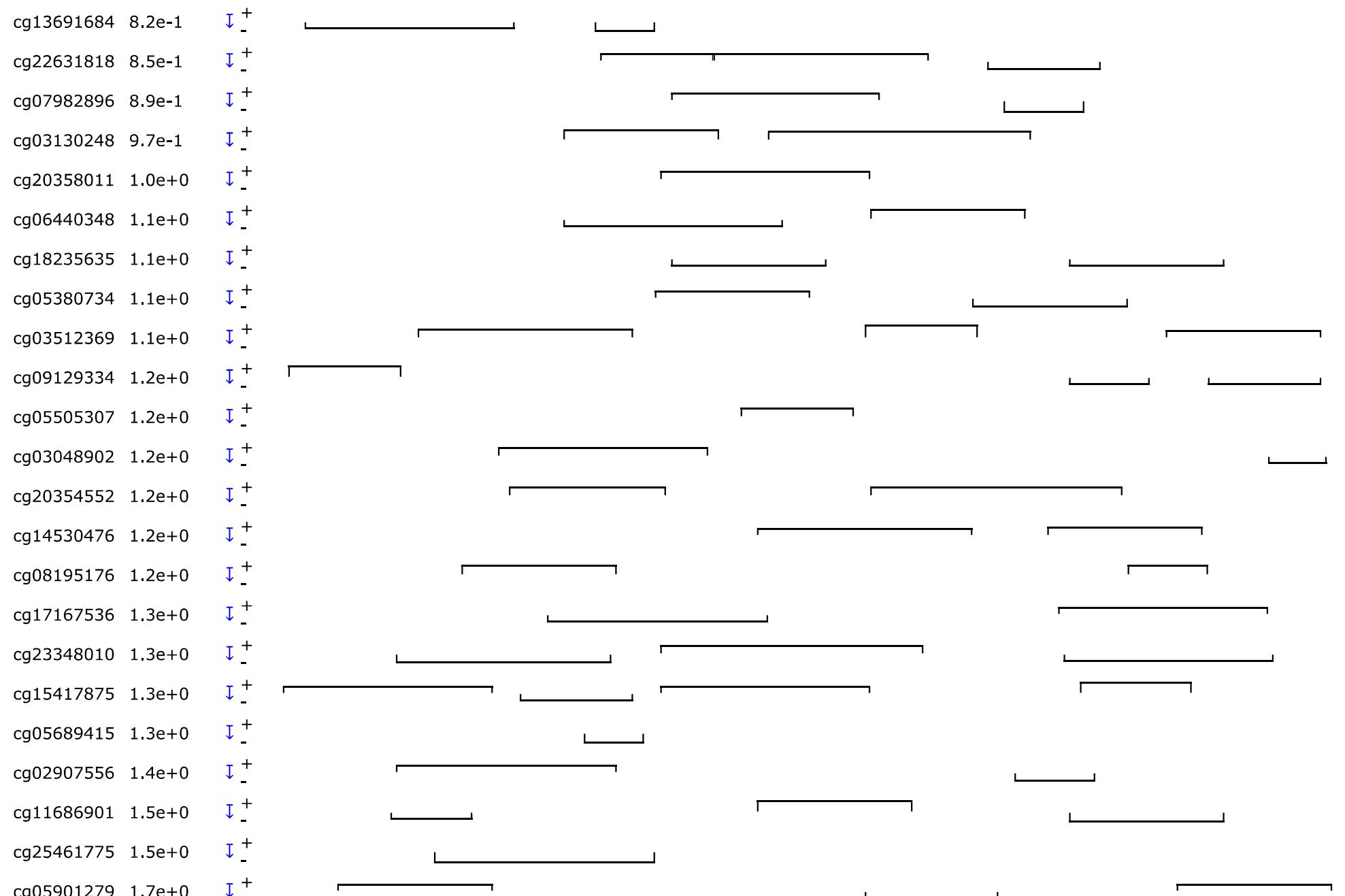










Sequence E-value**Block Diagram**

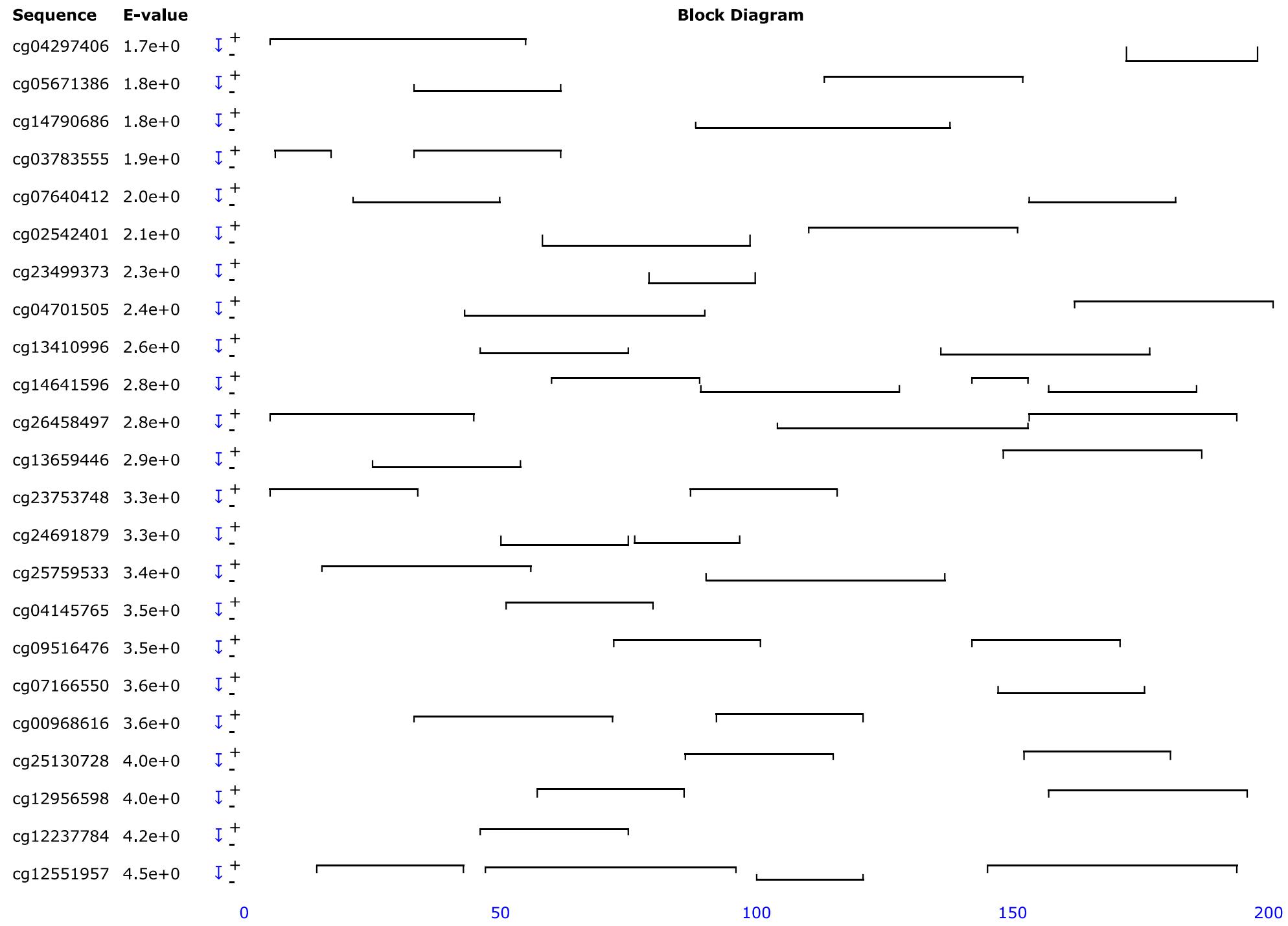
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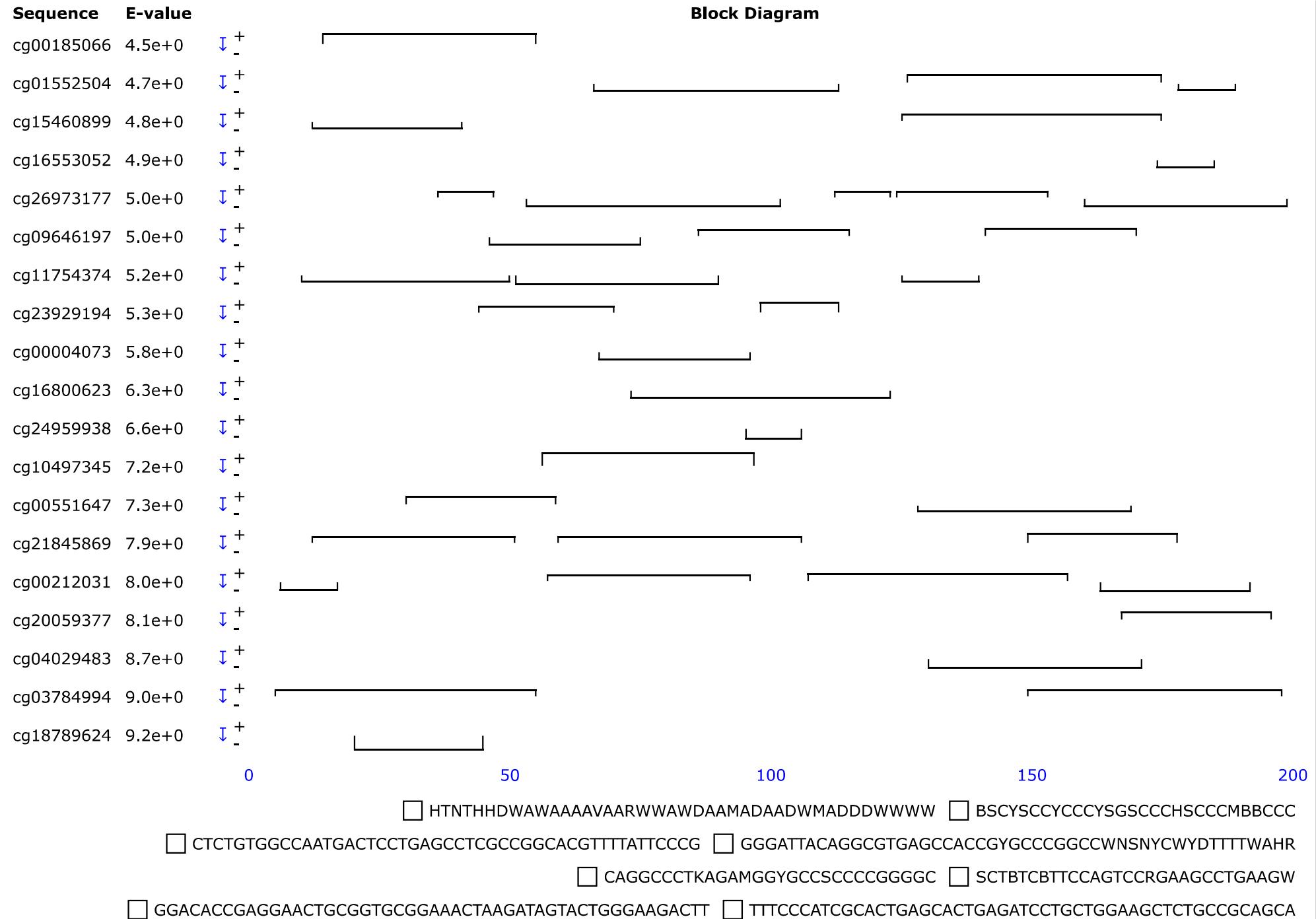
50

100

150

200





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 CGATSKGCCACMTSSTSCKTYCTYCMMAMARRWGSCAAWKRCSCKGSAGA TKTSMCCWKTTGBSCASRSTGRTCWYGAWCWCYTGRVCTC
 CARMYSYYCKGNMGGCCTYGAGYCKCYCCDMCWSGATCT SKGGGGGGGC RCACAGCTGCMWGGAGHVSGBGCCASCT
 CCDCMCTGYCGCWGMAGMRMTCCMCABKCKSWBGWGGCTYARSYCCST GTGYKTGDGSGTGTSTDYSTGBRTGTGKTTHKTGAYR
 CCCGRGACCASCCCAGACCAAG GWNGKBYTHTYTYCTKTCTGM CAAARCCGGCASWGTMCVCWACKGAARCTCATGGACWTMA
 GTDDAGSDGSTGAGTKAACDCMMAGAGGBGGKSWTTGDTGWCVAGCTYCC GCAGGAAGGTAGGTAGATCTGTCCGTTGGCTGGCTTCGATCCTAATG
 THTRMAKGWGTGASTTDTTYNWAARMMAMWCYYATKGYDRGMDWAAAAA CTAAAAAANGATWAAHCDTTAYTTAAAT TKGGKGTTGGTGTGG
 TTTMABGTGTVBTTAKBVHNKRGCAGTGKKTWHTAADYTWWGTTCA AWGKAABAGHTAAKTATGAADAATT ARAAAABARMWBAGAAGWARC

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	~	Thymine
Cytosine	0.22521	C	~	Guanine

Sequences

The following sequence database was supplied to MAST.

Database	Sequence Count	Residue Count	Last Modified
dmp_cpg_sequences.fasta	384	77184	Fri Jun 20 14:45:49 2025
Total	384	77184	

Motifs

The following motif database was supplied to MAST.

Database	Last Modified
meme.xml	Fri Jun 20 17:28:01 2025

Other Settings

Strand Handling	The result of scanning both strands is combined . When matches overlap the non-overlapping combination with the best p-value is shown.
Max Correlation	Motifs with a correlation greater than 0.6 are marked for potential removal dependant on the --remcorr option.
Remove Correlated	Correlated motifs exceeding the threshold are highlighted and their removal is recommended.
Max Sequence <i>E</i>-value	Sequences with an <i>E</i> -value less than 10 are included in the output.
Adjust Hit <i>p</i>-value	The hit <i>p</i> -value is not adjusted for the length of the sequence.
Displayed Hits	The <i>p</i> -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 dmp_cpg_sequences.fasta
```

Ran in 0.648 seconds on Fri Jun 20 17:28:02 2025 on noble-meme.grid.gs.washington.edu