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## MAST - Motif Alignment and Search Tool

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MAST version 5.5.8 (Release date: Thu May 15 15:01:46 2025 -0700)

For further information on how to interpret these results please access <https://meme-suite.org/meme>.

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

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## REFERENCE

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If you use this program in your research, please cite:

Timothy L. Bailey and Michael Gribskov,  
"Combining evidence using p-values: application to sequence homology  
searches", Bioinformatics, 14(48-54), 1998.

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## DATABASE AND MOTIFS

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DATABASE dmp\_cpg\_sequences.fasta (nucleotide)  
Last updated on Fri Jun 20 07:54:51 2025  
Database contains 75 sequences, 15075 residues

Scores for positive and reverse complement strands are combined.

MOTIFS meme.xml (nucleotide)

MOTIF ID	ALT ID	WIDTH	BEST POSSIBLE MATCH
-----	-----	-----	-----
1 HAWTNWBATRVAKWDAVAYWRWRADAAMMAWKHARADMA	MEME-1	41	TAATATCATAAATTTAGAAATAAAAAAAAAAATTA
2 SCCCCMSCCCCCGCMCYSCCACKCMCCV	MEME-2	28	CCCCAGCCCCCGCCCGCCACTCCCCA
3 WKTVTRTBDTCAYATTATARBTRAKGMA	MEME-3	28	ATTATATGATCATATTATAACTAAGGAA
4 AMAYWAAATAWATRWAMTC	MEME-4	19	AAATTAAATAAATATAATC
5 TTTCWHRTYTT	MEME-5	11	TTTCATATTTT
6 CBSCCCBCCNCHCCCNCTCC	MEME-6	21	CTGCCCTCCTACCCCACTCC
7 AAARWRTTYKTGWTWG	MEME-7	15	AAATATTTTTGTTTG
8 TTAAGTWSAGAA	MEME-8	12	TTAAGTACAGAA
9 ATAMAAAGSTCAVTTCCMAWGATBNT	MEME-9	26	ATAAAAAGGTCAATTCCTCAAGATTAT
10 TWWTWTAGMAGWAGCAARA	MEME-10	19	TATTTTAGAAGTAGCAAAA
11 CCCGCSCCCGCCCCG	MEME-11	15	CCCGCCCCGCCCCG
12 ARWCCYACASAVGC	MEME-12	15	AAACCTCACAGAAGC
13 CBMCTCTCAGGAA	MEME-13	13	CTACTCTCAGGAA
14 TCWTCTAAGAA	MEME-14	11	TCATCTAAGAA

MEME-15	8	TGTGAAAT
MEME-16	10	ATCTAGAAAA
MEME-17	7	ATAAAAT
MEME-18	15	CTGCACCACGATCAC
MEME-19	11	AGACACATTCA
MEME-20	14	TTATTCTCTTAA
MEME-21	6	AAATGA
MEME-22	10	AACTCATGAA
MEME-23	11	TTTGCACTGCT
MEME-24	10	AGCTATTTTT
MEME-25	8	TTTAGAAT
MEME-26	11	AAACTTGAGCA
MEME-27	9	AATAACCTT
MEME-28	10	ATAAAGTAAT
MEME-29	8	TATTAATT
MEME-30	8	TGAAATGT

	MOTIF	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	
22	23	24	25	26	27	28	29																
		2	0.16																				
		3	0.39	0.09																			
		4	0.49	0.15	0.45																		
		5	0.52	0.20	0.47	0.43																	
		6	0.17	0.28	0.15	0.07	0.20																
		7	0.40	0.10	0.33	0.29	0.26	0.09															
		8	0.48	0.25	0.33	0.51	0.17	0.13	0.37														
		9	0.28	0.18	0.23	0.25	0.45	0.21	0.26	0.30													
		10	0.50	0.21	0.37	0.30	0.29	0.17	0.23	0.42	0.30												
		11	0.10	0.45	0.10	0.03	0.08	0.37	0.07	0.17	0.19	0.24											
		12	0.24	0.34	0.24	0.20	0.29	0.25	0.21	0.20	0.27	0.21	0.24										
		13	0.25	0.35	0.23	0.15	0.20	0.43	0.18	0.10	0.30	0.21	0.34	0.38									
		14	0.44	0.19	0.52	0.52	0.40	0.25	0.33	0.31	0.33	0.41	0.20	0.42	0.47								
		15	0.45	0.29	0.49	0.49	0.36	0.23	0.42	0.44	0.41	0.40	0.08	0.33	0.28	0.42							
		16	0.51	0.25	0.40	0.46	0.18	0.17	0.32	0.50	0.35	0.45	0.23	0.30	0.28	0.55	0.36						
		17	0.58	0.34	0.54	0.68	0.50	0.20	0.51	0.44	0.60	0.57	-0.03	0.38	0.27	0.39	0.56	0.55					
		18	0.29	0.41	0.24	0.13	0.25	0.29	0.08	0.13	0.27	0.30	0.27	0.29	0.28	0.22	0.12	0.27	0.20				
		19	0.41	0.38	0.31	0.39	0.33	0.28	0.25	0.19	0.38	0.29	0.35	0.25	0.33	0.23	0.45	0.36	0.33	0.38			
		20	0.32	0.28	0.34	0.21	0.38	0.35	0.24	0.28	0.33	0.22	0.22	0.48	0.36	0.48	0.46	0.30	0.36	0.24	0.24		
		21	0.54	0.31	0.57	0.60	0.33	0.17	0.51	0.47	0.57	0.46	0.18	0.40	0.26	0.33	0.67	0.44	0.60	0.36	0.33	0.44	
		22	0.45	0.31	0.54	0.43	0.21	0.20	0.28	0.26	0.52	0.32	0.10	0.32	0.42	0.35	0.39	0.40	0.46	0.20	0.38	0.35	0.71
		23	0.30	0.20	0.30	0.27	0.34	0.50	0.30	0.20	0.33	0.20	0.32	0.23	0.22	0.26	0.50	0.13	0.18	0.34	0.18	0.28	0.33
0.39																							
		24	0.30	0.14	0.38	0.32	0.30	0.21	0.51	0.26	0.31	0.28	0.24	0.22	0.35	0.23	0.27	0.23	0.33	0.18	0.30</		

0.46	0.49	0.40	0.42	0.30	0.27	0.49	0.22	0.22	0.33	0.38	0.44	0.42	0.25	0.30	0.26	0.26	0.45	0.28	0.39	0.57	0.55	0.29	0.38	0.37	0.50	0.50	0.29	0.41	0.41	0.41	0.39	0.36
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Correlations above 0.60 may cause some combined p-values and E-values to be underestimates.  
 Removing motifs 17, 21, 25, 26, 29 and 30 from the query may be advisable.

Random model letter frequencies (from non-redundant database):  
 A 0.274 C 0.225 G 0.225 T 0.274

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## SECTION I: HIGH-SCORING SEQUENCES

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- Each of the following 37 sequences has E-value less than 10.
- The E-value of a sequence is the expected number of sequences in a random database of the same size that would match the motifs as well as the sequence does and is equal to the combined p-value of the sequence times the number of sequences in the database.
- The combined p-value of a sequence measures the strength of the match of the sequence to all the motifs and is calculated by
  - o finding the score of the single best match of each motif to the sequence (best matches may overlap),
  - o calculating the sequence p-value of each score,
  - o forming the product of the p-values,
  - o taking the p-value of the product.
- The sequence p-value of a score is defined as the probability of a random sequence of the same length containing some match with as good or better a score.
- The score for the match of a position in a sequence to a motif is computed by by summing the appropriate entry from each column of the position-dependent scoring matrix that represents the motif.
- Sequences shorter than one or more of the motifs are skipped.
- The table is sorted by increasing E-value.

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SEQUENCE NAME	DESCRIPTION	E-VALUE	LENGTH
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cg00957886	8.6e-17	201
cg02632822	1.6e-13	201
cg04156077	1.3e-10	201
cg17040924	2.1e-10	201
cg02573152	3.1e-10	201
cg07747690	1.3e-06	201
cg00896220	2.4e-06	201
cg24872610	2.9e-06	201
cg19931348	4.8e-05	201
cg12500857	0.00023	201
cg10637260	0.0039	201
cg20667822	0.0066	201
cg03532422	0.015	201
cg25917893	0.039	201
cg13936911	0.078	201
cg10857807	0.12	201
cg16139664	0.16	201
cg12509424	0.19	201
cg05725080	0.37	201
cg03983713	0.48	201
cg07724977	0.51	201
cg05541867	0.59	201
cg02163400	0.84	201
cg13752114	0.88	201
cg21813265	1.4	201
cg07265976	1.4	201
cg08590601	1.5	201
cg25613667	1.7	201
cg19729672	2	201
cg17775727	2.4	201
cg17862404	2.5	201
cg22824635	3.7	201
cg02467054	3.9	201
cg09588770	5.5	201
cg22040815	6.6	201
cg14491776	6.8	201
cg09368670	7.4	201

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## SECTION II: MOTIF DIAGRAMS

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- The ordering and spacing of all non-overlapping motif occurrences

are shown for each high-scoring sequence listed in Section I.

- A motif occurrence is defined as a position in the sequence whose match to the motif has POSITION p-value less than 0.0001.
  - The POSITION p-value of a match is the probability of a single random subsequence of the length of the motif scoring at least as well as the observed match.
  - For each sequence, all motif occurrences are shown unless there are overlaps. In that case, a motif occurrence is shown only if its p-value is less than the product of the p-values of the other (lower-numbered) motif occurrences that it overlaps.
  - The table also shows the E-value of each sequence.
  - Spacers and motif occurrences are indicated by
    - o -d-    `d' residues separate the end of the preceding motif occurrence and the start of the following motif occurrence
    - o [sn] occurrence of motif `n' with p-value less than 0.0001.
- A minus sign indicates that the occurrence is on the reverse complement strand.

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SEQUENCE NAME	E-VALUE	MOTIF DIAGRAM
-----	-----	-----
cg00957886	8.6e-17	4-[-7]-11-[+25]-10-[+4]-5-[+3]-2-[+10]-9-[-5]-15-[-1]-4
cg02632822	1.6e-13	16-[+15]-49-[-6]-8-[+1]-4-[+8]-11-[+3]-3
cg04156077	1.3e-10	9-[-5]-6-[+28]-1-[-13]-1-[-1]-27-[+7]-22-[-3]-17
cg02573152	3.1e-10	21-[+10]-2-[+8]-8-[+9]-50-[+1]-22
cg07747690	1.3e-06	10-[+13]-6-[+30]-6-[+5]-70-[+1]-10-[-10]-7
cg00896220	2.4e-06	[+4]-7-[+26]-4-[+3]-45-[+22]-10-[-5]-56
cg24872610	2.9e-06	6-[-10]-13-[-9]-51-[-4]-1-[+1]-14-[-24]-1
cg19931348	4.8e-05	18-[-3]-3-[+1]-11-[-27]-25-[+8]-29-[+6]-4
cg12500857	0.00023	24-[-3]-68-[-7]-9-[+12]-17-[-4]-6
cg10637260	0.0039	8-[+2]-26-[+20]-38-[+5]-21-[-6]-11-[+14]-12
cg20667822	0.0066	2-[+7]-117-[-4]-19-[+3]-1
cg03532422	0.015	11-[-11]-15-[-11]-10-[-2]-36-[+5]-1-[-9]-33
cg25917893	0.039	11-[+6]-9-[+2]-25-[+5]-45-[+13]-38
cg13936911	0.078	4-[+3]-19-[-5]-16-[+7]-11-[+12]-82
cg10857807	0.12	4-[-2]-4-[-2]-60-[+11]-31-[+6]-10
cg16139664	0.16	4-[-9]-36-[+27]-21-[+28]-95
cg12509424	0.19	75-[+5]-41-[-1]-16-[-8]-5
cg05725080	0.37	58-[+11]-19-[+11]-[+6]-73
cg03983713	0.48	29-[+8]-48-[+11]-24-[+12]-30-[+7]-13
cg05541867	0.59	72-[-6]-13-[+18]-31-[+13]-36
cg13752114	0.88	9-[+2]-48-[-11]-41-[+30]-52
cg21813265	1.4	42-[+26]-23-[+13]-85-[-10]-8
cg07265976	1.4	14-[-2]-14-[+6]-71-[+12]-38
cg08590601	1.5	1-[+4]-10-[+19]-67-[+2]-12-[+2]-25
cg25613667	1.7	8-[-8]-118-[+2]-[-20]-21
cg19729672	2	10-[+11]-12-[+11]-32-[+2]-22-[+2]-2-[+2]-9

cg17775727	2.4	62-[+18]-38-[+2]-3-[+6]-34
cg17862404	2.5	42-[-13]-63-[+2]-1-[+11]-39
cg22824635	3.7	8-[-2]-13-[+9]-85-[+2]-13
cg02467054	3.9	47-[+6]-6-[+2]-28-[-4]-12-[+6]-19
cg09588770	5.5	18-[+16]-2-[+6]-36-[+12]-37-[+6]-11-[-2]-2
cg22040815	6.6	84-[+12]-3-[+2]-71
cg14491776	6.8	[+6]-44-[+12]-6-[+2]-18-[+2]-11-[+2]-2
cg09368670	7.4	15-[+6]-107-[-12]-4-[-2]-11

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### SECTION III: ANNOTATED SEQUENCES

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- The positions and p-values of the non-overlapping motif occurrences are shown above the actual sequence for each of the high-scoring sequences from Section I.
- A motif occurrence is defined as a position in the sequence whose match to the motif has POSITION p-value less than 0.0001 as defined in Section II.
- For each sequence, the first line specifies the name of the sequence.
- The second (and possibly more) lines give a description of the sequence.
- Following the description line(s) is a line giving the length, combined p-value, and E-value of the sequence as defined in Section I.
- The next line reproduces the motif diagram from Section II.
- The entire sequence is printed on the following lines.
- Motif occurrences are indicated directly above their positions in the sequence on lines showing
  - o the motif number of the occurrence (a minus sign indicates that the occurrence is on the reverse complement strand),
  - o the position p-value of the occurrence,
  - o the best possible match to the motif (or its reverse complement), and
  - o columns whose match to the motif has a positive score (indicated by a plus sign).

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cg00957886

LENGTH = 201 COMBINED P-VALUE = 1.15e-18 E-VALUE = 8.6e-17

DIAGRAM: 4-[-7]-11-[+25]-10-[+4]-5-[+3]-2-[+10]-9-[-5]-15-[-1]-4

[-7]	[+25]	[+4]	[+3]
1.8e-06	5.3e-05	3.0e-08	3.1
CAAACAAAAATATTT	TTTAGAAT	AAATTAAATAAATATAATC	ATT

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      ++++++ + ++++++ ++++++ ++++++ ++++++
1  CATTCTATCAAGAATTTCTCAAGCCTGACATTTAGAATTCAACTTCAAAAACAACATATATGTAATCCTACATTT

      ]      [+10]      [-5]
      e-12      4.1e-10      4.2e-05
      ATATGATCATATTATAACTAAGGAA  TATTTTAGAAGTAGCAAAA  AAAATATGAAA
      ++++ ++++++ ++++++ ++++++ ++++++ +
76  ATGTCATTATATTATAGCTAAGGCACGTATTTTAGCAGTAGCAAGACCTTAGGAGAAAACATGATAGACGGTGGT

      [-1]
      4.6e-10
      TTTTTTAATTTTTTTTTTTTATTTCTAAATTTATGATATTA
      ++++++ ++++++ ++++++ ++++++ ++ +++++
151  TTTTCGTTTTTAAAAAGTTTATAATTGTTTAGAAATCCTCAACATTATACT

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cg02632822

LENGTH = 201 COMBINED P-VALUE = 2.15e-15 E-VALUE = 1.6e-13

DIAGRAM: 16-[+15]-49-[-6]-8-[+1]-4-[+8]-11-[+3]-3

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      [+15]      [-]
      2.2e-05      1.
      TGTGAAAT      GG
      ++++++      +
1  AGGCAGAATGGTGTCTGTGAAATTCAGTATGGGGGGAGTGAGGGGTCCCAAAGATGGGGTGATGGAGATTTAG

      6]      [+1]      [+8]
      4e-07      7.1e-16      5.4
      AGTGGGGTGAGGAGGGCAG  TAATATCATAAATTTAGAAATAAAAAAAAAAATTAATAAAAA  TTA
      + ++++++ ++++++ ++++++ ++++++ ++++++ +
76  AAGGGGGAAAGGGTGGGAGAAATACCGAAATTACATGCAGTGAAATATAAAGAAAAAAATCAGAAAAGGTGTTA

      ]      [+3]
      e-06      1.9e-07
      AGTACAGAA  ATTATATGATCATATTATAACTAAGGAA
      ++++ +++  ++ + +++ +++ ++++++ +++++
151  AGTATAGATCCATATTAATTTTGGGGTGGTCAAATTATAATTACTAAAAGG

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cg04156077

LENGTH = 201 COMBINED P-VALUE = 1.78e-12 E-VALUE = 1.3e-10

DIAGRAM: 9-[-5]-6-[+28]-1-[-13]-1-[-1]-27-[+7]-22-[-3]-17

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      [-5]      [+28]      [-13]      [-1]
      6.5e-05      2.0e-06      3.8e-07      1.1e-09
      AAAATATGAAA  ATAAAGTAAT TTCCTGAGAGTAG TTTTTTAATTTTTTTTTTTATTT
      ++ ++++++  ++++++ + ++++++ +++ +++ +++++ ++++++ ++++++

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1 AGAATCCCAAATCTAAGAAATCTAAGATAAAGTAATGTGCCTGAGAATAGCTTTGTAAATGTGTTTCATTTAATTT

[+7]  
5.0e-08  
AAATATTTTGTGTTG  
+++++++ ++++++

CTAAATTTATGATATTA  
76 CTAAC TGGGTTTAAATATTTTGGCCGTCATAACTGTTGTGTGGTAAATATTTCTGTTTGTGGCAAACCTTTT

[-3]  
4.4e-08  
TTCCTTAGTTATAATATGATCATATAAT  
+++++++ ++++++++ ++ +++++

151 GGGTTGTTTCATCACCTTTTATGTCATTATAGATGTAACAACATGTGTGCT

cg17040924

LENGTH = 201 COMBINED P-VALUE = 2.79e-12 E-VALUE = 2.1e-10

[-5] [-1] [+3]  
1.3e-05 7.3e-11 1.0e-0  
AAAAATAGAAA TTTTTTAATTTTTTTTTTTTATTCTAAATTTATGATATTA ATTATA  
++ ++++++++ ++ ++++++++ +++++ +++++ +++++ ++ + ++ ++ +

1 AAGCAAATACATGAAAACAATGTGTTGTCTGATTTTTTTTTTTTTTAAATCTTTGTCTAAAAGACTATACCAGAATG

[-12]  
2.0e-06  
GCTTCTGTGAGGTTT  
++++ + ++++++

7 TGATCATATTATACTAAGGAA  
76 TGTTCTTATATATCAGAGGAATACGAAAGGTGAGGAGCGTGTAAGAAGTTTAAATGCAGTACATCTTAAGCCTAG

[+8] [-16]  
1.9e-06 1.6e-06  
TTAAGTACAGAA TTTTCTAGAT  
++ ++++++++ ++++++

151 TTAGGTTGATTACAGAATAGTCAGCAATCTGGGCTTAGGACTTTTCTAGAT

cg02573152

LENGTH = 201 COMBINED P-VALUE = 4.08e-12 E-VALUE = 3.1e-10

DIAGRAM: 21-[+10]-2-[+8]-8-[+9]-50-[+1]-22

[+10] [+8] [+9]  
6.4e-07 1.2e-06 4.1e-11  
TATTTTAGAAGTAGCAAAA TTAAGTACAGAA ATAAAAAGGTCAA  
+++ ++++++ +++++ + ++++++ +++++ ++++++ +

1 GCCTGGAATAATATAGGAGGCTTTATTAGCAGCAGCAGCAGTTTAAGTTGAGAATCTGATAGATACAAAGGTGAA



TTCCAAAGATTAT  
+++++ ++++++  
76 TACCAGAGATTATAAACTAAGTCACCGAGTCAGGTGTCTGAGAGCACACACAGCTATTACTTAAAATAACATAAA

[+1]  
1.3e-11  
TAATATCATAAA  
+++++

TTTAGAAATAAAAAAAAAATTAAAAAA  
++ ++++++ ++++++  
151 ATTGGAATTTGAGATAAGCATGAAAATCATTTAATCAGAGCAGAGGGTTAA

cg07747690  
LENGTH = 201 COMBINED P-VALUE = 1.77e-08 E-VALUE = 1.3e-06  
DIAGRAM: 10-[+13]-6-[+30]-6-[+5]-70-[+1]-10-[-10]-7

[+13] [+30] [+5]  
2.4e-07 2.2e-05 5.6e-05  
CTACTCTCAGGAA TGAAATGT TTTCATATTT  
+++++ ++++++ ++++++  
1 GGTTTCTGGGCCACTCTCAGGATCAGTCATGAAATGTCCTTAGCTTCTCATTTTTGTTGGAGGATATGTGGAGGC

[+1]  
7.7e-09  
TAATATCATAAATTTAGAAATAAAAA  
+ ++ + ++++++ +++++ ++  
76 ATAGAGCTTGGTCACATTGAGCTGACGCAAGTCACTGATTCTGCAACCTCTAGTGATGCATTTCCAAACCTCAGG

[-10]  
1.7e-08  
AAAAAATTAATAAA  
+++++ + + ++++++  
151 TTAAAATGAAGGTCAAGAACTCCTGTTTTGCCATTTCTAAATTATTGGGAT

cg00896220  
LENGTH = 201 COMBINED P-VALUE = 3.19e-08 E-VALUE = 2.4e-06  
DIAGRAM: [+4]-7-[+26]-4-[+3]-45-[+22]-10-[-5]-56

[+4] [+26] [+3]  
9.6e-08 6.0e-07 2.3e-08  
AAATTAATAAATATAATC AAACCTTGAGCA ATTATATGATCATATTATACTAAGGAA  
+++++ + ++++++ ++++++ ++++++ ++ ++++++  
1 ACACATATTATATATAATCCTACCATAATCTTGAGCAGGGGTGTCTAATCTCATTTTACAGATAAGGCAATTGGG

[+22] [-5]

2.7e-06	2.6e-05
AACTCATGAA	AAAATATGAAA
+++++	+++++

76 GATCAGAGAGTGGTCCACTGATGGCGCTCAATGCCACAGAACTGATGAATGGCACTGCCAAGATTTGAATCAAGA

cg24872610

LENGTH = 201    COMBINED P-VALUE = 3.82e-08    E-VALUE = 2.9e-06

DIAGRAM: 6-[-10]-13-[-9]-51-[-4]-1-[+1]-14-[-24]-1

[-10]	[-9]
1.6e-07	4.4e-09
TTTTGCTACTTCTAAAATA	ATAATCTTTGGAATTGACCTTTTTAT
++++ ++++++ +++++	++ + ++++++ +++++ +

1 CACGGCTCTTCCTTCTTCCTTAAAAGCAGGTCATAGAGTTGAGATTTGGAAGTTACCGTTTTGTCCCAAGAATGG

<b>[-4]</b>	<b>[+1]</b>
5.0e-07	2.2e-08
GATTATATTTATTTAATTT	TAATATCATAAATTT
++++++ ++ ++ ++++++	+++ +++ ++ +++

76 AGCCTCCTTGCCGGTCCAGCCCCGACATCTGTCCAGCCGATTTCTTTGATCTAATGTGCAAACACAGAACGAA

	[ -24]
	1.6e-06
AGAAATAAAAAAAAAAATTA	AAAAATAGCT
+ + ++++++++ +	+++++++

151 ACAGCTAAAGTGAACAATGAAAGGCAAGTTGCAAAGTGCTAAAAATAGCTT

cg19931348

LENGTH = 201 COMBINED P-VALUE = 6.37e-07 E-VALUE = 4.8e-05

DIAGRAM: 18-[-3]-3-[+1]-11-[-27]-25-[+8]-29-[+6]-4

[-3]	[+1]
2.2e-07	4.0e-09
TTCCTTAGTTATAATATGATCATATAAT	TAATATCATAAATTTAGAAATAAAAA
++ ++++ ++++++ ++++++ ++++++	+ + ++++++ ++++++

1 CTCACAGAGTAGAAGTGCTGGCTCACTTATTAGGTAACATTACAATGAAATTCTTCATGTTTTGAAATACAGTGA

	[-27]	[+8]
	1.2e-05	7.8e-06
AAAAAATTAAAAAA	AAGGTTATT	TTAAGTACAGAA
++ ++++++	+++++	++ ++++++

76 GACCCAAGAAGAGAAAGGAATCACCGAAGGTTATTCAGCAAGTCACTGGTAGATCCAGTCTTGATTACAAAACCA

[+6]  
1.3e-05

CTGCCCTCCTCACCCCACTCC  
++ ++ ++ +++++ ++  
151 AGGTGTTTCTCCATTATGCTCTGGTGCTACAAACCCACCCAGATCTACTT

cg12500857  
LENGTH = 201 COMBINED P-VALUE = 3.01e-06 E-VALUE = 0.00023  
DIAGRAM: 24-[-3]-68-[-7]-9-[+12]-17-[-4]-6

[-3]  
7.2e-09  
TTCCTTAGTTATAATATGATCATATAAT  
+++++ +++++ ++ +++++  
1 TATTGCCAACAAACACTGCAAGGCTTTATTAGCTAAAATGTCAACCCACACACAGATCAGAGACCGCCCTCAGCT

[-7] [+12]  
2.3e-06 4.8e-0  
CAAACAAAAATATT AACCT  
+++++ +++++ ++ +++++ +  
76 TCTCTGCGCCTTTCGCCCCGTCAACGCATCAATGGGGTGGAGGCCAAACTCAAACACTTGCGGGGCACAGACGT

[-4]  
6 7.0e-10  
CACAGAAGC GATTATATTTATTTAATTT  
+ +++++ ++ +++++  
151 CCCAGAAGCAAACATGCAAGTCACGGGAGTTTATTTATTTAATTTTTTTTCC

cg10637260  
LENGTH = 201 COMBINED P-VALUE = 5.18e-05 E-VALUE = 0.0039  
DIAGRAM: 8-[+2]-26-[+20]-38-[+5]-21-[-6]-11-[+14]-12

[+2] [+20]  
5.8e-08 2.6e-08  
CCCCCAGCCCCGCCCGCCACTCCCCA TTATTCCTCTTAA  
+ + +++++ +++++ +++++ +++++  
1 CCTGGTGGGTCGCCCCCTCTTCCCTCCCAAGTCCAAACCAGGCATAGCATTTCTCACCCAGTTATTCCTCTCAA

[+5] [-6]  
2.3e-05 7.3e  
A TTTCATATTT GGAG  
+ +++++ ++ +  
76 ATCCCTTCTGCAGCCCTAGGGTCCCGACGTTGACCCCTCATTACGTTTTATTGATACCTGCCCCAGCTGGGTG

[-07] [+14]  
7.3e-07  
TGGGGTGAGGAGGGCAG TCATCTAAGAA

++ + ++++++++ ++++++++  
151 CTGGAGATGGAGGGGAGGAAGATCCCTGTCATCTAAGAACTGGCTTTCTGG

cg20667822

LENGTH = 201 COMBINED P-VALUE = 8.85e-05 E-VALUE = 0.0066

DIAGRAM: 2-[+7]-117-[-4]-19-[+3]-1

[+7]  
3.5e-08  
AAATATTTTTGTTG  
+++++++ ++  
1 AAAAAAATTTTTTTTGAGACAGGGTCTCCAGGCTGGTGCTAGTCTGCAACTGTTGGGCCAAGCAATCCTCCTG

[-4]  
5.3e-07  
GATTATATTTATTAA  
+++++++ +++ +  
76 CCGCAGCCTCTCAAGTAGCTGGGACGATGGGTGCAGGCCACCGTAGCTGACTATAAAATGATTTTATCAATTCA

[+3]  
1.7e-07  
TTT ATTATATGATCATATTATAACTAAGGAA  
++ +++++ + +++++ + + +++ +++++  
151 ATTAGCCTTCTAGAACTAACAAAGTATCTCATCACAGTGTTGTTTAGGAAA

cg03532422

LENGTH = 201 COMBINED P-VALUE = 1.97e-04 E-VALUE = 0.015

DIAGRAM: 11-[-11]-15-[-11]-10-[-2]-36-[+5]-1-[-9]-33

[-11] [-11] [-2]  
1.0e-07 7.7e-05 2.2e-06  
CGGGGCGGGGCGGG CGGGGCGGGGCGGG TGGGGAGTG  
++++ +++ +++++ + ++ +++++ + +++++  
1 GTGGGGAACGCCGGGCGGTGGCGGGACTTCCGCCACGGGACTCGGAAGGGGCCGCGCCGCGCTGCTGGGAGTT

[+5] [-9]  
3.7e-05 1.2e-09  
GCGGGGCGGGGCTGGGGG TTTCATATTT ATAATCTT  
+ +++ +++ + ++ ++ ++++++ ++++++  
76 GTAGTCCGGCCGTGGTTGGGGGAGCCGCGGCTCATGCGCGGTGCACAGAGGCTTGTTTCACATCTGTAACAACAG

TGGAATTGACCTTTTTAT  
+++++++ ++++++++

151 GTGAATTGGGCTTTTTATTCTCCCCTTTCGTGCCCTCTTGAGGAGCCTGCC

cg25917893

LENGTH = 201 COMBINED P-VALUE = 5.25e-04 E-VALUE = 0.039

DIAGRAM: 11-[+6]-9-[+2]-25-[+5]-45-[+13]-38

	[+6] 3.3e-07 CTGCCCTCCTCACCCCACTCC + +++ + +++ + + + +	[+2] 5.2e-09 CCCCCAGCCCCCGCCCCGCCACTCCCCA +++++ ++ + + + + + + + + + + + + +
1	CGCCTCCTGCGCGCCGCCATCTTCCCGCTCCGGTCCCCGCCCGCCGCCAGCCCCGCCCGTCCCCGACTTC	

	[+5] 6.5e-05 TTTCATATTTT +++++++ + + +
76	GCAGCGCAATCGCGCGAGATTTACGCTTTCCTAGCCCCGCCGGGCCACCCTATCCGGCAAGAGTGCCGCGAGCCA

	[+13] 1.5e-07 CTACTCTCAGGAA +++++++ + + + + + + + + + + +
151	CGCCTCTCAGGAAGGCCACTTCCGGCTATGGAAGGACCAACCTGGCCACCG

cg13936911

LENGTH = 201 COMBINED P-VALUE = 1.03e-03 E-VALUE = 0.078

DIAGRAM: 4-[+3]-19-[-5]-16-[+7]-11-[+12]-82

	[+3] 6.6e-08 ATTATATGATCATATTATAACTAAGGAA ++ ++ + + + + + + + + + + + + + + +	[-5] 9.1e-06 AAAATATGAAA +++++++ + + +
1	GAGAAGCCTTTGATCTATCAAAACAAAGGAAAACCACTCTGGCCTTGCTGAAGATGAGAAAAAGACTGGGGGGG	

	[+7] 1.0e-06 AAATATTTTGTGTTG +++ + + + + + + + + + + + + + + +	[+12] 8.2e-06 AAACCTCACAGAAGC +++++++ + + +
76	ACCAAAGATTCTGTGTAGGAAAGCCGCTAGACCCACACCTCCCGCCCCGGCATGTTCTGGCAACCCCTGGGG	

cg10857807

LENGTH = 201 COMBINED P-VALUE = 1.65e-03 E-VALUE = 0.12

DIAGRAM: 4-[-2]-4-[-2]-60-[+11]-31-[+6]-10

	[ -2]		[ -2]
	6.4e-05		5.9e-07
	TGGGGAGTGGCGGGGCGGGGGCTGGGGG		TGGGGAGTGGCGGGGCGGGGGCTGGGGG
	+ +++++ + +++ +++++ +++		++++ +++++ ++ +++++ +++++

1 TC GCGCGGGGCGGCGGGGTCCCGGGGTCCCGGGGTCCCGGGAATGGCAAGGGAGGGGCCGAGGGCCCGGACCGGG

		[+11]
		8.2e-10
		CCCCCCCCGCCCCG
		+++++

76 TGTGCTCGCCAGGGTGGGGCACAACGACCCAGACCCGTGCCTCAGGACCCCGCGCCGCCCCGTCTCCCATGGG

	[+6]
	9.3e-13
	CTGCCCTCCTCACCCACTCC
	+++++

151 CGCGCTCTCCTCTCTGTGCTCTCCCTCCTCTCCCCACTCCCTGTCCCA

cg16139664  
 LENGTH = 201 COMBINED P-VALUE = 2.19e-03 E-VALUE = 0.16  
 DIAGRAM: 4-[-9]-36-[+27]-21-[+28]-95

	[-9]		[+27]
	2.4e-09		1.2e-05
	ATAATCTTTGGAATTGACCTTTTAT		AATAACCTT
	+ ++++++		+++++

1 AGAGAGAATCATGGGAAGAGACCTTATAAGGTCGCTGCGGGGATGGGGGCCGGAATCTCCTCCCAATATCCTT

	[+28]
	6.6e-06
	ATAAAGTAAT
	+++++

76 CGATGCTCCTGGCCCTCCTTGATGACGTAATCATCGCGAGGCGAAAGATCTCGTTTTCCCTGACAGCTGACTTCC

cg12509424  
 LENGTH = 201 COMBINED P-VALUE = 2.54e-03 E-VALUE = 0.19  
 DIAGRAM: 75-[+5]-41-[-1]-16-[-8]-5

	[+5]		[-1]
	8.3e-05		3.4e-09
	TTTCATATTTT		TTTTTTTAATTTTTTTTTTATT
	+++++ +		+++++ +++++

76 TTTCAAATCCTCCCGTGTTACTAAGCGACAGTCCCTGCTTTAGGCACACTTCTGCTCTGAATTGAATTTACTATT

[-8]

TCTAAATTTATGATATTA  
 + ++++++ ++ ++  
 151 ACCCTATCCACCATGTTGAGCTGTGCTGTTTTTTCCTGTACTTAAAATTA

3.3e-06  
 TTCTGTACTTAA  
 + ++++++

cg05725080

LENGTH = 201 COMBINED P-VALUE = 4.96e-03 E-VALUE = 0.37  
 DIAGRAM: 58-[+11]-19-[+11]-[+6]-73

1 ACTGAACTGCTCTGCGGCCGCCAGCCACATGCAGAGGAAGAAGGAGCCAGAGGCCGCCCCGCCCCGCCCCGCC  
 [+11] 1.0e-08 [+6] 8.2e-07  
 CCGCCCCCGCCCCGCTGCCCTCCTCACCCTACTCC  
 ++++ ++++++ ++ ++ ++ ++ ++  
 76 GGGCCGCCACCCTCCAGCCAGTCCCCGCCCGCTCTCCGCCACAGCCCGCTCAAGGGGGTACCATGACTGCCCG

[+11]  
 1.9e-10  
 CCGCCCCCGCCCCG  
 ++++++

cg03983713

LENGTH = 201 COMBINED P-VALUE = 6.41e-03 E-VALUE = 0.48  
 DIAGRAM: 29-[+8]-48-[+11]-24-[+12]-30-[+7]-13

1 ATAACGCGGGCGCGCTCCCTTGAGTACGTGTAAGTGCAGAATTCACCAGGCACCCCTGAGACCCACGGCCCCAG  
 [+8] 1.6e-05  
 TTAAGTACAGAA  
 +++++ +++++  
 [+11] 6.8e-05 [+12] 2.6e-07  
 CCGCCCCCGCCCCG AACCTCACAGAAGC  
 ++ + ++ ++ ++ ++++++  
 76 GGGTCTCCATCTCACCTGTCCGTTCCGCGAACACACCTCGATGAAGTCCACAGTCCCCACAGAATCCTGCGTG

[+7]  
 2.1e-06  
 AAATATTTTGTG  
 ++++++ ++ ++

151 TGACATCCCCCTCTCTAATGGTAAATGTTTTGGAATGTCCATAGATAAGA

cg07724977

LENGTH = 201 COMBINED P-VALUE = 6.86e-03 E-VALUE = 0.51

[+6]  
4.7e-08  
CTGCCCTCCTCACCCCACTCC  
+ ++++ ++ + +++ +++++

1 CATCACCCGCGCCGCCGCTCGGGCAACTCCTTTAACCGCGCCCCCGCCCCATCTCCAGTCGCGGTCCCTCC

[+6] [-5]  
4.2e-07 2.6e-05  
CTGCCCTCCTCACCCCACTCC AAAATATGAAA  
+++++ +++ + +++++ ++ ++++++

76 TCTGCCATCCCTCCCCCAGCCTCTCGCCATAAATTAGCCAAATAAGAAAAGAGGCCCGCGCTCGTCCGGGAA

[-6] [+24]  
2.3e-06 3.0e-06  
GGAGTGGGGTGAGGAGGGCAG AGCTATTTT  
++ +++++ ++ + +++++ ++++++

151 GGCTTGGGCAGCCGGTGGCAGGAGCCAGGATCTAAGGAGTAGCTATTGTT

cg05541867

LENGTH = 201 COMBINED P-VALUE = 7.83e-03 E-VALUE = 0.59

DIAGRAM: 72-[-6]-13-[-18]-31-[-13]-36

[-6  
4.7  
GGA  
+++

1 CCAGAGGAGGCATCTGGCCACGGCACCAAGGTGAGATGGGGGACAAAACCACCCACATGGTGCAGGAGGATGGA

] [+18]  
e-08 8.1e-09  
GTGGGGTGAGGAGGGCAG CTGCACCACGATCAC  
++ + +++ ++++++ ++++++

76 GGCCTGAGCGGAGGGCAGGGGACCGCATACCATCACGATCACACAGAGCCGGCCAGCATGCGGCGCGCGC

[+13]  
4.7e-07  
CTACTCTCAGGAA  
+++++ +

151 GGCTCCTCTCAGGGAAGTAGGGCTCGTCCTCACCCGTGATGGGGTTCGGGG

cg02163400

LENGTH = 201 COMBINED P-VALUE = 1.12e-02 E-VALUE = 0.84



	[-6]		[+2]
	4.2e-07		6.0e-06
	GGAGTGGGGT		CCCCAGCCCCGCCCCGCCA
	++ ++ + ++ +++++ +++++		++++ +++++ + ++++++

1 GCGGCGGCGTCGGCGGCAGGCGCTGGGGAGAGCAGAGCCCGGCCAGTAGGGCCGCCACGCCACGCCCCCTCCG

	[+2]		[+11]
	2.4e-11		1.3e-05
	CTCCCCA		CCCCAGCCCCGCCCCGCCACTCCCCA
	+ + + + +		+++++ +++++ +++++ +++++ +

76 CCTGCCCCGCCACGCCCTTCCCCGCCCTGCCACGCCCCCTCCGCGGCCCGGCCACGCCCTTCGGCTGCCC

	[+6]		[+11]
	1.2e-07		4.9e-06
	CTGCCCTCCTC		CCCCCCCCGCCCCG
	+ +++++ ++ +++++ + + +		+++++ +++++ + +

151 TCGCCACGCCCCCTCCGCCGCCCTCGCCACGCCCCCTCCGCCCTCGCCACG

cg13752114  
 LENGTH = 201 COMBINED P-VALUE = 1.17e-02 E-VALUE = 0.88  
 DIAGRAM: 9-[+2]-48-[-11]-41-[+30]-52

	[+2]
	1.9e-08
	CCCCAGCCCCGCCCCGCCACTCCCCA
	++ +++++ +++++ +++++ + +

1 CACCACAACGCACCCGGCCCTGCACCGCCACGCGCCCGGCCCTGCACCGCAACGCGGCTTCCCGCCACCTCGCT

	[-11]		[+30]
	2.6e-08		2.2e-05
	CGGGGCGGGGCGGG		TGAAATGT
	+++++ ++++++		+++++ ++++++

76 GCTCCCGGTGCGGGGAGGGGGCGGCCGCTCCCCAACCTACCTCCGCCGTCTTCATGGTCAGGCTGAAATGTC

cg21813265  
 LENGTH = 201 COMBINED P-VALUE = 1.82e-02 E-VALUE = 1.4  
 DIAGRAM: 42-[+26]-23-[+13]-85-[-10]-8

	[+26]
	6.0e-07
	AAACTTGAGCA
	+++++ ++++++

1 TGTCTACCTGGGATCAGTTCCTAGCCAAAGCCAAGCGTCAGGAACTTGAGCATAAACACCCCTTCCATCCTGGT

[+13]

4.0e-08  
CTACTCTCAGGAA  
+++++  
76 GCGACTCTCAGGAAGTGAGAAAAGCCGAGCCTACCGTGTGGTTAGCGCCACAGGCCACGTCTCGTACAACCACG

[-10]  
3.7e-07  
TTTTGCTACTTCTAAAATA  
++++ + +++++ + + +  
151 TTTGGTACAGGCAGAATCTGTCCATCTTTCGTCTTCTCAATGAAGATGGCC

cg07265976  
LENGTH = 201 COMBINED P-VALUE = 1.92e-02 E-VALUE = 1.4  
DIAGRAM: 14-[-2]-14-[+6]-71-[+12]-38

[-2] [+6]  
1.1e-07 7.3e-07  
TGGGGAGTGGCGGGGCGGGGGCTGGGGG CTGCCCTCCTCACCCACT  
++++ ++++++ ++++++ ++++++  
1 ACTTGCCCTCCTTCTGGTTGGTGGAGGTCGAGGTGCTGGAGCTGTGCTCAGAGCAGCTGTCCTCATCTGCACTCT

[+]  
2.  
CC AA  
+ ++  
76 CGTCCCCATCATCCTGCTGTGGGTCGTAGACACCATTTCTCGCAGCGGTGCCCTTCGCAGTCAGGGTCACTGCAAA

12]  
5e-06  
ACCTCACAGAAGC  
+++ ++ + +++++  
151 ACCGCATACAAGCTCATCAGCAAGTGGCCGGCCCGGGAGGCAATGACTCAC

cg08590601  
LENGTH = 201 COMBINED P-VALUE = 1.96e-02 E-VALUE = 1.5  
DIAGRAM: 1-[+4]-10-[+19]-67-[+2]-12-[+2]-25

[+4] [+19]  
1.6e-07 6.0e-07  
AAATTAAATAAATATAATC AGACACATTCA  
+++++ ++++++ + ++++++  
1 CACACTATATAAATATACGCGGAGATGCCAGACACATTCATGCGCTGCGCACACAGGATACTTGCTCCTGGGAG

[+2] [+]  
7.6e-05 1.

```

                CCCCCAGCCCCCGCCCCGCCACTCCCCA      CC
                + ++++++ +++++ ++   + +++++ +      ++
76  ATAAGAGCTAGCCGGGAACAATGACGGGGTCCACGCCCAGCGTCCGCGCCCTGATTCCCGAAGTCTGAACCTCCC

    2]
    8e-09
    CCCAGCCCCCGCCCCGCCACTCCCCA
    +++++ ++++++++ ++++++++
151 CCCATCACCTTCCCCAAAATCCAAAGCCAAAGACCTTTGGCTTCTTTGCT

```

cg25613667  
 LENGTH = 201 COMBINED P-VALUE = 2.32e-02 E-VALUE = 1.7  
 DIAGRAM: 8-[-8]-118-[+2]-[-20]-21

```

    [-8]
    7.8e-06
    TTCTGTAATAA
    +++++ +++++ +
1  ACACGCAGTTCTCAACTTTACGTGACGTGACTAGGGAGGGAATTGACGGTCGCACCGTCTACCTAGCCCAAACGG

```

```

                                                    [+2]
                                                    1.7e-06
                                                    CCCCCAGCCCC
                                                    ++ +++++ +
76  GGTCACAGCAGGACAAGGAAGTAGCCGATCTCCAGATGCGGTCTCTTCGCTCCGCTCCACCCGCACCAGCAGCG

```

```

                [-20]
                4.1e-08
                GCCCCGCCACTCCCCATTTAAGAGGAATAA
                +++++ +++++ ++ ++++++++
151 GCCCACCCACCTCTCCTGTAAGAGGAAGAACGTCCCGGAGACACTTCCGGC

```

cg19729672  
 LENGTH = 201 COMBINED P-VALUE = 2.60e-02 E-VALUE = 2  
 DIAGRAM: 10-[+11]-12-[+11]-32-[+2]-22-[+2]-2-[+2]-9

```

                [+11]                [+11]
                3.8e-06                4.3e-10
                CCCGCCCCGCCCCG        CCCGCCCCGCCCCG
                ++ ++++ ++++++        ++++++++
1  CCCGCCGCTCCCGGCCGCGCCCCGCCCTCGCTGTGCCGCCCTCGCCCCGCCCGGCCACCCGGAGCCCCGC

```

```

                [+2]                [+2]
                9.4e-08                1.1e-06
                CCCCCAGCCCCCGCCCCGCCACTCCCCA        CCCCCAGCCCCCGCCC

```



76 CCCCAGCTGAGACCAGCAGCGGGGACGTCCAAGCCACAGCGCGCCACCGCGTCCCCGCCCCAGGCCCCGCCCC

1]  
e-09  
GCCCCCGCCCCG  
+++++

151 GCGCTCGCCCGAGCCGCCTCCTTCAGCACCGGCTGCAGCCAGTTCCTACC

cg22824635

LENGTH = 201 COMBINED P-VALUE = 4.94e-02 E-VALUE = 3.7

DIAGRAM: 8-[-2]-13-[+9]-85-[+2]-13

	[-2]		[+9]
	6.1e-05		1.1e-09
	TGGGGAGTGGCGGGGCGGGGGCTGGGGG		ATAAAAAGGTCAATTCCAAAGATTAT
	++++ + + + + + + + + +		++++ + + + + + + + + +

1 AAACACTGCTGTAGATGTGACGCATGTCGCTGGGACACTGTCACCCCAGATACAAAGCGCAGATACAAAGATGGT

	[+2]
	1.7e-07
	CCCCAGCCCCCGCCCCGCACTCCCCA
	++++ + + + + + + + + +

151 ATGGTGGCACGCTCCCCGACCCCCACTACCAAATACACAAGAGACAGGGCG

cg02467054

LENGTH = 201 COMBINED P-VALUE = 5.15e-02 E-VALUE = 3.9

DIAGRAM: 47-[+6]-6-[+2]-28-[-4]-12-[+6]-19

	[+6]		[-4]
	1.2e-05		5.3e-07
	CTGCCCTCCTACCCCACTCC		GATTATATTTATTTAATTT
	+ + + + + + + + +		+ + + + + + + + +

1 GTTGATCATGACCTGGTGCTTGAGCTCGTCCATGTTACGGACATGGCGCCGCCGCGCTGCCCGCTCCGGCCTCC

	+2]		[-4]
	.1e-07		5.3e-07
	CCCCAGCCCCCGCCCCGCACTCCCCA		GATTATATTTATTTAATTT
	++++ + + + + + + + + +		+ + + + + + + + +

76 CTCCTCCGCCCGCGCTCCGCCTCACGCGTCCACCATTAGCGAGCCGGCTCCGGCTAATACAAATATTTACTGTG

	[+6]
	1.4e-06
	CTGCCCTCCTACCCCACTCC
	+ + + + + + + + +

151 CGGCTCTGACTCACCGCGCCTCGCTCCGCCGGCGCCGCGGCATGCT

cg09588770

LENGTH = 201 COMBINED P-VALUE = 7.39e-02 E-VALUE = 5.5

DIAGRAM: 18-[+16]-2-[+6]-36-[+12]-37-[+6]-11-[-2]-2

		[+16]		[+6]	
		3.0e-06		7.9e-05	
		ATCTAGAAAA		CTGCCCTCCTCACCCCACTCC	
		+++++++	+	+	++ ++ + +++
1	TCCCATTGGGTATTGGATATCTAGAGAAGCCAATCAGCGTCGCCGCGGTCCCAGTTCTAAAGTCCCCACGCACCC				
		[+12]		[+6]	
		2.0e-06		1.0e-05	
		AAACCTCACAGAAGC		CTGCCCTCCTC	
		+++++++		++++ ++ +	
76	ACCCGGACTCAGAGTCTCCTCAGACGCCGAGATGCTGGTCATGGCGCCCCGAACCGTCCTCCTGCTGCTCTCGGC				
		[-2]			
		2.9e-07			
	ACCCCACTCC		TGGGGAGTGGCGGGGCGGGGGCTGGGGG		
	++++ ++	++++ ++	+++++++	+++++++	
151	GGCCCTGGCCCTGACCGAGACCTGGGCCGGTGAGTGCGGGTCGGGAGGGAA				

cg22040815

LENGTH = 201 COMBINED P-VALUE = 8.76e-02 E-VALUE = 6.6

DIAGRAM: 84-[+12]-3-[+2]-71

		[+12]		[+2]	
		4.4e-07		3.5e-08	
		AAACCTCACAGAAGC		CCCCCAGCCCCGCCCCGCCACTCCCCA	
		+++++++	++++ +	+++++ ++ ++	+++ ++++++++
76	CGGCTGTCTAATCCTCAGAGAACCCCGCCCCATCCACAAACCACCACTCACAGGCGGTCCCGCCTGGTTCCAG				

cg14491776

LENGTH = 201 COMBINED P-VALUE = 9.12e-02 E-VALUE = 6.8

DIAGRAM: [+6]-44-[+12]-6-[+2]-18-[+2]-11-[+2]-2

		[+6]		[+12]	
		8.2e-08		3.4e-08	
		CTGCCCTCCTCACCCCACTCC		AAACCTCACA	
		+ +++ +	+++++++	+++++	
1	CAACCCCAACACCCCAATCCCTGCCCCACAGACGCCCGAATCCCCACCCACAGTCGACACCCGAATCCCCACA				
		[+2]		[+2]	

		4.0e-07		1.7e-07
	GAAGC	CCCCCAGCCCCCGCCCCGCGCCACTCCCCA		CCCCCAGCCCCCGCCCCG
	+++++	++++ +++++ + + + + + + + + + + +		++++ +++++ + + + + +
76	GACGCCCCGAATCCCCACCCCGCAGACGCCCCGAATCTCCACCCCGCAGACGCCGAATCCCCACCCACAGACGCC			

		[+2]	
		3.4e-06	
	CCACTCCCCA	CCCCCAGCCCCCGCCCCGCGCCACTCCCCA	
	+ ++++++	+++ + +++++ + + + + +++++ +	
151	CGAATCCCCACCCACAGACGCCCGAATCCCCACCCACAGACGCCCGAAT		

cg09368670  
 LENGTH = 201 COMBINED P-VALUE = 9.93e-02 E-VALUE = 7.4  
 DIAGRAM: 15-[+6]-107-[-12]-4-[-2]-11

		[+6]	
		7.4e-06	
		CTGCCCTCCTCACCCCACTCC	
		+ +++++ + + + + + + +	
1	GCCCGGCGGATATGACGCCACGCACCCAGCGTTCCAAGCTGAGCTGGCGGCAATCAGAGACGCTCAGTTGGGC		

				[-12]
				4.4e-06
				GCTTCTG
				++ +++
76	TGGAGCGTCCTCTTCCTAGGTCCCCGCGTTCTCTGCACGCTGAAGTCGCTGCAGTGACCTCCGTACCTGACTCTT			

		[-2]	
		3.5e-08	
	TGAGGTTT	TGGGGAGTGGCGGGCGGGGGCTGGGGG	
	+++++	++ ++ +++ +++++ +++++ +++++	
151	AGGGGATTTCTCTGAGAATTTGGGGGCCGGGGGAGAGGGTTGTAGGCCTA		

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CPU: noble-meme.grid.gs.washington.edu  
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