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MEME - Motif discovery tool

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MEME 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 MEME Suite 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 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.

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## TRAINING SET

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PRIMARY SEQUENCES= dmp\_cpg\_sequences.fasta

CONTROL SEQUENCES= --none--

ALPHABET= ACGT

Sequence name	Weight	Length	Sequence name	Weight	Length
cg00896220	1.0000	201	cg00957886	1.0000	201
cg01277910	1.0000	201	cg01724041	1.0000	201
cg02163400	1.0000	201	cg02467054	1.0000	201
cg02573152	1.0000	201	cg02632822	1.0000	201
cg02907176	1.0000	201	cg03147312	1.0000	201
cg03532422	1.0000	201	cg03796003	1.0000	201
cg03983713	1.0000	201	cg04039667	1.0000	201
cg04156077	1.0000	201	cg04784471	1.0000	201
cg05004480	1.0000	201	cg05541867	1.0000	201
cg05725080	1.0000	201	cg05834845	1.0000	201
cg06805280	1.0000	201	cg06840699	1.0000	201
cg07265976	1.0000	201	cg07724977	1.0000	201
cg07747690	1.0000	201	cg08034643	1.0000	201
cg08590601	1.0000	201	cg09368670	1.0000	201
cg09588770	1.0000	201	cg09808690	1.0000	201

cg10112022	1.0000	201	cg10280383	1.0000	201
cg10637260	1.0000	201	cg10857807	1.0000	201
cg10889506	1.0000	201	cg10990040	1.0000	201
cg11275803	1.0000	201	cg11847597	1.0000	201
cg12500857	1.0000	201	cg12509424	1.0000	201
cg13233166	1.0000	201	cg13738327	1.0000	201
cg13752114	1.0000	201	cg13936911	1.0000	201
cg14491776	1.0000	201	cg14685095	1.0000	201
cg16139664	1.0000	201	cg16347828	1.0000	201
cg16456906	1.0000	201	cg17040924	1.0000	201
cg17775727	1.0000	201	cg17862404	1.0000	201
cg17891735	1.0000	201	cg18255614	1.0000	201
cg18768400	1.0000	201	cg19729672	1.0000	201
cg19801460	1.0000	201	cg19931348	1.0000	201
cg20128772	1.0000	201	cg20667822	1.0000	201
cg21380181	1.0000	201	cg21813265	1.0000	201
cg22040815	1.0000	201	cg22664157	1.0000	201
cg22780612	1.0000	201	cg22824635	1.0000	201
cg22889584	1.0000	201	cg22973789	1.0000	201
cg24872610	1.0000	201	cg25208863	1.0000	201
cg25613667	1.0000	201	cg25917893	1.0000	201
cg26305881	1.0000	201	cg26673609	1.0000	201
cg27099625	1.0000	201			

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#### COMMAND LINE SUMMARY

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This information can also be useful in the event you wish to report a problem with the MEME software.

command: meme dmp\_cpg\_sequences.fasta -dna -oc . -nostatus -time 14400 -mod zoops -nmotifs 30 -minw 6 -maxw 50 -objfun classic -revcomp -markov\_order 0

model:	mod=	zoops	nmotifs=	30	evt=	inf
objective function:			em=	E-value of product of p-values		
			starts=	E-value of product of p-values		
strands:	+ -					
width:	minw=	6	maxw=	50		
nsites:	minsites=	2	maxsites=	75	wnsites=	0.8
theta:	spmap=	uni	spfuzz=	0.5		
em:	prior=	dirichlet	b=	0.01	maxiter=	50
	distance=	1e-05				
trim:	wg=	11	ws=	1	endgaps=	yes
data:	n=	15075	N=	75		
sample:	seed=	0	hsfrac=	0		
	searchsize=	15075	norand=	no	csites=	1000

Letter frequencies in dataset:

A 0.187 C 0.313 G 0.313 T 0.187

Background letter frequencies (from file dataset with add-one prior applied):

A 0.187 C 0.313 G 0.313 T 0.187

Background model order: 0

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MOTIF HAWTNWBATRVAKWDAVAWAYWRWRADAAMMAWKHARADMA MEME-1 width = 41 sites = 9 llr = 254 E-value = 7.0e-014

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Motif HAWTNWBATRVAKWDAVAWAYWRWRADAAMMAWKHARADMA MEME-1 Description

Simplified A 38623417132813262967:767373884784:484736a  
pos.-specific C 21:22:4:11311::22::13:1::::1431::3::114:  
probability G ::1:2:22163:3:324:1::::3:613::1::4:623:::  
matrix T 413626217:11474:113273:312321::16622::2::

bits 2.4 \*  
2.2 \*  
1.9 \* \*  
1.7 \* \* \* \* \*  
Relative 1.5 \* \* \* \* \* \* \* \* \* \* \*  
Entropy 1.2 \* \* \* \* \* \* \* \* \* \* \*  
(40.7 bits) 1.0 \*\* \* \* \* \* \* \* \* \* \* \* \*  
0.7 \*\*\*\* \* \*\* \* \*\*\* \* \* \* \* \* \* \* \*  
0.5 \*\*\*\* \* \*\*\* \* \*\*\* \* \* \* \* \* \* \*  
0.2 \*\*\*\* \* \*\*\* \* \*\*\* \* \* \* \* \* \* \*  
0.0 -----

Multilevel TAATATCATGCATTTAGAAATAAAGAAAAAAATTAAGAAAA  
consensus A TACAGG AG GAGCA TTCTGTATGT CC AGCTAGGC  
sequence C CG T A AGC T T T  
T

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Motif HAWTNWBATRVAKWDAVAWAYWRWRADAAMMAWKHARADMA MEME-1 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg02632822	+	103	5.11e-21	AGAAATACCG AAATTACATGCAGTGAAATATAAGAAAAAAATCAGAAAA GGTGTTAAGT
cg02573152	+	139	6.28e-16	CTATTACTTA AAATAACATAAAATTGGAATTGAGATAAGCATGAAAATCA TTTAACATCAGA
cg17040924	-	25	5.42e-15	CATTCTGGTA TAGTCTTTAGACAAAGATTAAAAAAAATCAGACAA CACATTGTTT
cg00957886	-	157	5.82e-14	AGTA TAATGTTGAGGATTCTAACATTATAAACTTTAAAAA CGAAAAACCA
cg04156077	-	52	1.92e-13	ACGGCCAAAA TATTAACCCAGTTAGAAATTAAATGAACACATTACAAA GCTATTCTCA

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cg12509424      -    128  8.39e-13 CAGCACAGCT CAACATGGTGGATAGGGTAATAGTAAATTCAATTCAAGAGCA GAAGTGTGCC
cg19931348      +    50   1.05e-12 TTACAATGAA ATTCTTCATGTTTGAAATACAGTGAGACCCAAGAAGAGAA AGGAATCACC
cg07747690      +    125  2.59e-12 TCCTGCAACC TCTAGTGATGCATTCCAAACTCAGGTTAAAATGAAGGTCA AGAACTCCTG
cg24872610      +    136  1.11e-11 ATCTAATGTG CAAACACAGAACGAAACAGCTAAAGTGAACAATGAAAGGCA AGTTGCAAAG

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Motif HAWTNWBATRVAKWDAVAWAYWRWRADAAMMAWKHARADMA MEME-1 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg02632822		5.1e-21	102_[+1]_58
cg02573152		6.3e-16	138_[+1]_22
cg17040924		5.4e-15	24_-[-1]_136
cg00957886		5.8e-14	156_-[-1]_4
cg04156077		1.9e-13	51_-[-1]_109
cg12509424		8.4e-13	127_-[-1]_33
cg19931348		1e-12	49_[+1]_111
cg07747690		2.6e-12	124_[+1]_36
cg24872610		1.1e-11	135_[+1]_25

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Motif HAWTNWBATRVAKWDAVAWAYWRWRADAAMMAWKHARADMA MEME-1 in BLOCKS format

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BL MOTIF HAWTNWBATRVAKWDAVAWAYWRWRADAAMMAWKHARADMA width=41 seqs=9
cg02632822      ( 103) AAATTACATGCGAGTAAAGATAAGAAAAAAATCAGAAAA 1
cg02573152      ( 139) AAATAACATAAAATTGGAATTGAGATAAGCATGAAAATCA 1
cg17040924      ( 25) TAGTCTTTAGACAAAGATTAAAAAATCAGACAA 1
cg00957886      ( 157) TAATGTTGAGGATTCTAACAAATTATAAACTTTTTAAAAA 1
cg04156077      ( 52) TATTAACCCAGTTAGAAATTAAATGAACACATTTACAAA 1
cg12509424      ( 128) CAACATGGTGGATAGGGTAATAGTAAATTCAATTCAAGAGCA 1
cg19931348      ( 50) ATTCTTCATGTTTGAAATACAGTGAGACCCAAGAAGAGAA 1
cg07747690      ( 125) TCTAGTGATGCATTCCAAACTCAGGTTAAAATGAAGGTCA 1
cg24872610      ( 136) CAAACACAGAACGAAACAGCTAAAGTGAACAATGAAAGGCA 1
//
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Motif HAWTNWBATRVAKWDAVAWAYWRWRADAAMMAWKHARADMA MEME-1 position-specific scoring matrix

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log-odds matrix: alength= 4 w= 41 n= 12075 bayes= 11.7938 E= 7.0e-014
  84   -50   -982    125
 206   -149   -982    -75
 157   -982   -149     84
   25    -50   -982    157

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84	-50	-50	25
125	-982	-982	157
-75	50	-50	25
184	-982	-50	-75
-75	-149	-149	184
84	-149	83	-982
25	9	9	-75
206	-149	-982	-75
-75	-149	9	125
84	-982	-982	184
25	-982	9	125
157	-50	-50	-982
25	-50	50	-75
225	-982	-982	-75
157	-982	-149	84
184	-149	-982	25
-982	9	-982	184
184	-982	-982	84
157	-149	9	-982
184	-982	-982	84
84	-982	83	-75
184	-982	-149	25
84	-982	9	84
206	-982	-982	25
206	-149	-982	-75
125	50	-149	-982
184	9	-982	-982
206	-149	-982	-75
125	-982	-982	157
-982	-982	50	157
125	9	-982	25
206	-982	-982	25
125	-982	83	-982
184	-149	-50	-982
84	-149	9	25
157	50	-982	-982
242	-982	-982	-982

Motif HAWTNWBATRVAKWDAAWAYWRWRADAAMMAWKHARADMA MEME-1 position-specific probability matrix

letter-probability matrix: alength= 4 w= 41 nsites= 9 E= 7.0e-014

0.333333	0.222222	0.000000	0.444444
0.777778	0.111111	0.000000	0.111111
0.555556	0.000000	0.111111	0.333333
0.222222	0.222222	0.000000	0.555556

0.333333	0.222222	0.222222	0.222222
0.444444	0.000000	0.000000	0.555556
0.111111	0.444444	0.222222	0.222222
0.666667	0.000000	0.222222	0.111111
0.111111	0.111111	0.111111	0.666667
0.333333	0.111111	0.555556	0.000000
0.222222	0.333333	0.333333	0.111111
0.777778	0.111111	0.000000	0.111111
0.111111	0.111111	0.333333	0.444444
0.333333	0.000000	0.000000	0.666667
0.222222	0.000000	0.333333	0.444444
0.555556	0.222222	0.222222	0.000000
0.222222	0.222222	0.444444	0.111111
0.888889	0.000000	0.000000	0.111111
0.555556	0.000000	0.111111	0.333333
0.666667	0.111111	0.000000	0.222222
0.000000	0.333333	0.000000	0.666667
0.666667	0.000000	0.000000	0.333333
0.555556	0.111111	0.333333	0.000000
0.666667	0.000000	0.000000	0.333333
0.333333	0.000000	0.555556	0.111111
0.666667	0.000000	0.111111	0.222222
0.333333	0.000000	0.333333	0.333333
0.777778	0.000000	0.000000	0.222222
0.777778	0.111111	0.000000	0.111111
0.444444	0.444444	0.111111	0.000000
0.666667	0.333333	0.000000	0.000000
0.777778	0.111111	0.000000	0.111111
0.444444	0.000000	0.000000	0.555556
0.000000	0.000000	0.444444	0.555556
0.444444	0.333333	0.000000	0.222222
0.777778	0.000000	0.000000	0.222222
0.444444	0.000000	0.555556	0.000000
0.666667	0.111111	0.222222	0.000000
0.333333	0.111111	0.333333	0.222222
0.555556	0.444444	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000

Motif HAWTNWBATRVAKWDAVA WAYWRWRADAAMMAWKHARADMA MEME-1 regular expression

[TAC]A[AT][TAC][ACGT][TA][CGT][AG]T[GА][CGA]A[TG][TA][TGA][ACG][GAC]A[AT][AT][TC][AT][AG][AT][GA][AT][AGT][AT]A[AC][AC]A[TA][TG][ACT][AT][GA][AG][AGT][AC]A

Time 22.68 secs.

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MOTIF SCCCCMSCCCCGCMCYSCCACKCMCCV MEME-2 width = 28 sites = 43 llr = 472 E-value = 1.4e-011

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Motif SCCCCMSCCCCGCMCYSCCACKCMCCV MEME-2 Description

-----  
Simplified A ::2113::21:2113:112262::3234  
pos.-specific C 6966744856a51869638716275873  
probability G 4:::2225212:16121:4:1214:::13  
matrix T :122:21:11:22:::32:::1332:::

bits 2.4  
2.2  
1.9  
1.7 \*  
Relative 1.5 \*  
Entropy 1.2 \*  
(15.8 bits) 1.0 \* \* \* \* \*  
0.7 \*\* \* \* \* \* \* \* \*  
0.5 \*\*\* \* \* \* \*\*\* \* \*\*\*  
0.2 \*\*\*\* \* \* \* \* \* \* \*  
0.0 -----

Multilevel  
consensus sequence  
CCCCCCGCCCGCCCCGCCACGCCA  
G T ACGA AT A TC AGATTAAC  
T C G

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Motif SCCCCMSCCCCGCMCYSCCACKCMCCV MEME-2 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg10889506	+	90	7.19e-10	CGCAGCGCCC CCTCCCGCCGCCGGCCGCAACTCACCC CGGCGGCCCC
cg02163400	+	90	1.30e-09	CCCGCGCCAC GCCCCCTCCCCCGCCCTGCCACGCCCGCC TCCGCGGCC
cg10112022	-	146	1.69e-08	CGGCGCTCCT CCCTCTCCTGCCCTCCCCGCCAAGCAACA ACAATTGAG
cg05834845	+	126	3.09e-08	GCACCGCCAC GCACCGGGCCCTGCACCGCCACGCACCG GGCCCGGGCAC
cg08590601	+	149	5.48e-08	TCTGAACCTC CCCCCATCACCTCCCCCAAATCCAAA GCCAAAGACC
cg25917893	+	42	1.40e-07	CGGGTCCCCG CCCCCGCCAGCCCCGCCGTCCCC GACTTCGCAG

cg16347828	+	26	4.21e-07	GACGGCCGCC	CCTCCCCGCCCCGCCCTCAGCGCCCGC	CCCCGCCTCC
cg13752114	+	10	4.21e-07	CACCACAAC	GCACCCGGCCCTGCACCGCCACCGCCC	GGCCCTGCAC
cg05725080	+	64	5.94e-07	CCGGCCCCGC	CCCCGCCCGCCGGCCGCCACCCCTCA	GCCAGTCCCC
cg22040815	+	103	7.43e-07	GAGAACCCCG	CCCCCATCCACAAACCCACCACTCACAG	GCGGTCCCCG
cg09368670	-	163	7.43e-07	AGGCCTACAA	CCCTCTCCCCGGGCCCCAAATTCTAG	GAGAAATCCC
cg11847597	+	163	8.29e-07	ATCCACTTGG	CCCTGGCCACCTTCCCCAAAATTCCACC	AGCCACAGAG
cg10637260	+	9	1.14e-06	CCTGGTGG	GTCGCCCCCTCTTCCCTCCAAAGTCAA	ACCAGGCATA
cg14685095	+	68	1.27e-06	CTAGGGGTCT	CTCGGAGCCCCCTGCACTCACACCCCTCA	TCTCCGAGTT
cg19729672	+	85	1.73e-06	CCCCCTCCGG	GAACCCC GCCCTGCACCGCCCGTACCC	GGGTCTCCAA
cg07265976	-	15	1.92e-06	TCTGAGCACA	GCTCCAGCACCTCGACCTCCACCAACCA	GAAGGAGGGC
cg02467054	+	75	1.92e-06	CTCGGGCTC	CCTCCTCCGCCGCCCTCCGCCCTCACG	CGTCCACCAT
cg01724041	+	156	2.12e-06	TGGAAATATG	CCCCATCCTACCTCCCCGCCCTTCTCA	GACAACATCC
cg09808690	+	90	2.34e-06	CCCTTACCCCT	CCCGAAGCTCCGCACCTGCCACGCCCG	GCGCTCAGCT
cg22824635	+	161	2.84e-06	ATGGTGGCAC	GCTCCCCGACCCCCACTACCAATACAC	AAGAGACAGG
cg14491776	+	156	2.84e-06	ACGCCGAAT	CCCCACCCCACAGACGCCGAATCCCA	CCCCACAGAC
cg26305881	+	131	3.44e-06	CTCCC GGCG	GCCCCACGACCCGCCCTCGGGCCCCA	GCGGGGGGCA
cg26673609	+	128	3.78e-06	GTCCC GAGAC	GCCCCCGGCCCGCCCATACTCCCTCCC	GGCTCC CAGG
cg18768400	+	80	3.78e-06	CTCAGGGCGT	AAAGCAGCCCCAGCCCCGCCACGAACCA	CAACGAGGCC
cg08034643	+	125	4.15e-06	CCCGAGACGC	CCCTGAGCCTCCGACCTCCAGACCCCAA	TTCGGTTCGA
cg16456906	+	102	4.55e-06	GGCTCGGCC	GCAGCGCTCCAGCCCCGAGCCGCTCAA	CTCCCGGAGG
cg09588770	-	172	4.55e-06	TT	CCCTCCCAGACCCGCACTCACCGGCCAG	GTCTCGGTCA
cg06805280	+	68	5.97e-06	CGCCGCCAG	CCCTCGCCTCCCTGCCACCGGGCCAC	CGCGCCGCCA
cg17891735	+	14	6.53e-06	CCTGGAGAGC	ACCAACACACCCGCCACCGCAAAACACCA	ATCCGGAACC
cg17775727	+	116	7.77e-06	AGACGTGGCA	CCTCGCCCCACAACTTCCCAAGTACCC	GTGCAGCTAT
cg10857807	-	37	8.47e-06	CCGGTCCGGG	CCCTCGGCCCTCCCTTGCCATTCCC GG	GACCCCCGGG
cg10280383	+	24	9.22e-06	AGGTGCTGCT	GCTCCCGACCCAGGGCTCAGCTTCACC	CACCTCCCAG
cg02907176	+	123	9.22e-06	GACTCCACCG	CCCACGGCCGCATCCATGCCGCACAA	GATGCCCGGA
cg19801460	+	35	1.00e-05	CTGCGGGGAG	GCCTGAGTCCC GCCACAGCCAC TCCC	CCGGTTACAA
cg13233166	-	3	1.00e-05	CGGCCGCCG	CCCCCGCCCGCCGCCGCCGCCAGG	AG
cg04784471	+	135	1.00e-05	CTCCCTGGGG	GCTCCTGGTCCAGCCCCCTCCACCCAGA	TGCTTCCCTT
cg17862404	+	119	1.29e-05	CCACAGCGCG	CCCACCGCGTCCCCGCCCGCCAGG	CCCCCGCGCTC
cg18255614	+	83	1.64e-05	ACACTTCCGC	CTTGGTGCCGCCCTGCCCGACTTCCA	GTATGCCCG
cg05004480	+	99	1.91e-05	GGCCCGAGACT	GCCGCCGCCACCTCGGCTCGGCTCACCC	AAACCCCCAGC
cg25613667	+	139	2.07e-05	CGCTCCACCC	GCACCAGCAGCGGGCCACCCACCTCTCC	TGTAAGAGGA
cg01277910	-	50	2.23e-05	CCTACAAACT	CGCCAGCCGCCATACCAACCAACTCACA	CCGACAGAGC
cg03532422	-	67	2.59e-05	CGCGGCTCCC	CCAACCACGGCCGGACTACAAC TCCCAG	CAGCGGCCGG
cg27099625	+	74	3.23e-05	CAAGCAGCGC	GCCCCAGCACCGGAAGTGACGCCGTACG	TGCCC CGCGTA

Motif SCCCCMSCCCCGCMYCSCACKMCCV MEME-2 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg10889506		7.2e-10	89_[+2]_84
cg02163400		1.3e-09	89_[+2]_84
cg10112022		1.7e-08	145_-[-2]_28

cg05834845	3.1e-08	125_[+2]_48
cg08590601	5.5e-08	148_[+2]_25
cg25917893	1.4e-07	41_[+2]_132
cg16347828	4.2e-07	25_[+2]_148
cg13752114	4.2e-07	9_[+2]_164
cg05725080	5.9e-07	63_[+2]_110
cg22040815	7.4e-07	102_[+2]_71
cg09368670	7.4e-07	162_[-2]_11
cg11847597	8.3e-07	162_[+2]_11
cg10637260	1.1e-06	8_[+2]_165
cg14685095	1.3e-06	67_[+2]_106
cg19729672	1.7e-06	84_[+2]_89
cg07265976	1.9e-06	14_[-2]_159
cg02467054	1.9e-06	74_[+2]_99
cg01724041	2.1e-06	155_[+2]_18
cg09808690	2.3e-06	89_[+2]_84
cg22824635	2.8e-06	160_[+2]_13
cg14491776	2.8e-06	155_[+2]_18
cg26305881	3.4e-06	130_[+2]_43
cg26673609	3.8e-06	127_[+2]_46
cg18768400	3.8e-06	79_[+2]_94
cg08034643	4.2e-06	124_[+2]_49
cg16456906	4.6e-06	101_[+2]_72
cg09588770	4.6e-06	171_[-2]_2
cg06805280	6e-06	67_[+2]_106
cg17891735	6.5e-06	13_[+2]_160
cg17775727	7.8e-06	115_[+2]_58
cg10857807	8.5e-06	36_[-2]_137
cg10280383	9.2e-06	23_[+2]_150
cg02907176	9.2e-06	122_[+2]_51
cg19801460	1e-05	34_[+2]_139
cg13233166	1e-05	2_[-2]_171
cg04784471	1e-05	134_[+2]_39
cg17862404	1.3e-05	118_[+2]_55
cg18255614	1.6e-05	82_[+2]_91
cg05004480	1.9e-05	98_[+2]_75
cg25613667	2.1e-05	138_[+2]_35
cg01277910	2.2e-05	49_[-2]_124
cg03532422	2.6e-05	66_[-2]_107
cg27099625	3.2e-05	73_[+2]_100

Motif SCCCCMSCCCCGCMCYSCCACKCMCCV MEME-2 in BLOCKS format

BL MOTIF SCCCCMSCCCCGCMCYSCCACKCMCCV width=28 seqs=43  
cg10889506 ( 90) CCTCCCGCCGCCGGCAACTCACCC 1

cg02163400 ( 90) GCCCCCTTCCCCCGCCCTGCCACGGCCCC 1  
cg10112022 ( 146) CCCTCTCTGCCTCCCCGCCAAGCAACA 1  
cg05834845 ( 126) GCACCGGGCCCTGCACCGCCACGCACCG 1  
cg08590601 ( 149) CCCCCATCACCTCCCCAAAATCCAAA 1  
cg25917893 ( 42) CCCCCGCCGCCAGCCCCGCCCGTCCCC 1  
cg16347828 ( 26) CCTCCCCGCCCGCCCTCAGCGCCCGC 1  
cg13752114 ( 10) GCACCCGGCCCTGCACCGCCACGCGCCC 1  
cg05725080 ( 64) CCCCAGCCCCGCCGGGGCGCCACCTCCA 1  
cg22040815 ( 103) CCCCCATCCACAAACCCACCACTCACAG 1  
cg09368670 ( 163) CCCTCTCCCCGGCCCCAAATTTCAG 1  
cg11847597 ( 163) CCCTGCCAACCTTCCCCAAAATTCCACC 1  
cg10637260 ( 9) GTCGCCCTCTTCCCTCCCAAGTCAA 1  
cg14685095 ( 68) CTCGGAGCCCCCTGCACTCACACCCCTCCA 1  
cg19729672 ( 85) GAACCCCGCCCTGCACCGCCGCGTACCC 1  
cg07265976 ( 15) GCTCCAGCACCTGACCTCCACCAACCA 1  
cg02467054 ( 75) CCTCCTCCGCCGCCGCGCTCCGCCTCACG 1  
cg01724041 ( 156) CCCCATCTACCTCCCCGCCCTTCTCCA 1  
cg09808690 ( 90) CCCGAAGCTCCGCACCTGCCACGGCCCG 1  
cg22824635 ( 161) GCTCCCCGACCCCCACTACCAAATACAC 1  
cg14491776 ( 156) CCCCACCCCCACAGACGCCGAATCCCCA 1  
cg26305881 ( 131) GCCCCACGACCCGCCCTCTGGGGCCCA 1  
cg26673609 ( 128) GCCCCCGGGCCCCGCCCATACTCCCTCCC 1  
cg18768400 ( 80) AAAGCAGCCCCAGCCCCGCCACGAACCA 1  
cg08034643 ( 125) CCCTGAGCTCCGACCTCCAGACCCCCAA 1  
cg16456906 ( 102) GCAGCCGCTCCAGCCCCGAGCCGCTCAA 1  
cg09588770 ( 172) CCCTCCCGACCCGCACTCACCGGGCCAG 1  
cg06805280 ( 68) CCCTCGCCCTCCGTGCCACCGGGGGCCAC 1  
cg17891735 ( 14) ACCAACACACCGCACCGCAAAACACCA 1  
cg17775727 ( 116) CCTCGCCCCACAACCTCCCAAGTACCC 1  
cg10857807 ( 37) CCCTCGGGCCCTCCCTTGCCATTCCGG 1  
cg10280383 ( 24) GCTCCCGCACCCAGGCCCTCAGCTTCACC 1  
cg02907176 ( 123) CCCACGGCCGCATCCCATGCCGCACAA 1  
cg19801460 ( 35) GCCTGAGTCCCGCCACAGCCACTTCCA 1  
cg13233166 ( 3) CCCCCGCCGCCGCCGCCGCCAGGGCAGG 1  
cg04784471 ( 135) GCTCCTGGTCCAGCCCCCTCCCACCCAGA 1  
cg17862404 ( 119) CCCACCGCGTCCCCGCCACGGCCCCG 1  
cg18255614 ( 83) CTTGGTGCCGCCCTGCCCTCGGCTCACCC 1  
cg05004480 ( 99) GCCGCCGCCACCTCGGCTCGGCTCACCC 1  
cg25613667 ( 139) GCACCAGCAGCGGCCACCCACCTCTCC 1  
cg01277910 ( 50) CGCCAGCCGCATCACCACCAACTCACA 1  
cg03532422 ( 67) CCAACCACGGCCGGACTACAACCTCCAG 1  
cg27099625 ( 74) GCCCCAGCACCGGAAGTGACGCAGTACG 1  
//

---

---

Motif SCCCCMSCCCCGCMCYSCCACKCMCCV MEME-2 position-specific scoring matrix

-----  
log-odds matrix: alength= 4 w= 28 n= 13050 bayes= 9.24986 E= 1.4e-011  
-200 89 25 -1207  
-200 146 -375 -142  
-20 100 -1207 17  
-100 83 -94 0  
-68 120 -94 -1207  
46 42 -94 -20  
-200 42 57 -142  
-1207 129 -58 -300  
32 71 -143 -42  
-68 100 -75 -142  
-1207 167 -1207 -1207  
17 57 -143 17  
-142 -117 83 32  
-68 129 -143 -1207  
58 83 -94 -1207  
-1207 150 -217 -200  
-100 95 -1207 70  
-42 -17 34 0  
0 133 -1207 -300  
17 105 -117 -1207  
170 -143 -43 -200  
32 89 -175 -100  
-200 -58 50 70  
-200 111 -1207 58  
58 77 -375 -20  
17 129 -1207 -300  
46 105 -175 -1207  
117 6 -29 -1207

-----

Motif SCCCCMSCCCCGCMCYSCCACKCMCCV MEME-2 position-specific probability matrix

-----  
letter-probability matrix: alength= 4 w= 28 nsites= 43 E= 1.4e-011  
0.046512 0.581395 0.372093 0.000000  
0.046512 0.860465 0.023256 0.069767  
0.162791 0.627907 0.000000 0.209302  
0.093023 0.558140 0.162791 0.186047  
0.116279 0.720930 0.162791 0.000000  
0.255814 0.418605 0.162791 0.162791  
0.046512 0.418605 0.465116 0.069767  
0.000000 0.767442 0.209302 0.023256  
0.232558 0.511628 0.116279 0.139535  
0.116279 0.627907 0.186047 0.069767

```
0.000000 1.000000 0.000000 0.000000
0.209302 0.465116 0.116279 0.209302
0.069767 0.139535 0.558140 0.232558
0.116279 0.767442 0.116279 0.000000
0.279070 0.558140 0.162791 0.000000
0.000000 0.883721 0.069767 0.046512
0.093023 0.604651 0.000000 0.302326
0.139535 0.279070 0.395349 0.186047
0.186047 0.790698 0.000000 0.023256
0.209302 0.651163 0.139535 0.000000
0.604651 0.116279 0.232558 0.046512
0.232558 0.581395 0.093023 0.093023
0.046512 0.209302 0.441860 0.302326
0.046512 0.674419 0.000000 0.279070
0.279070 0.534884 0.023256 0.162791
0.209302 0.767442 0.000000 0.023256
0.255814 0.651163 0.093023 0.000000
0.418605 0.325581 0.255814 0.000000
```

---

```
Motif SCCCCMSCCCCGCMCYSCCACKCMCCV MEME-2 regular expression
```

```
[CG]C[CT]CC[CA][GC][CG][CA]CC[CAT][GT]C[CA]C[CT][GC]C[CA][AG][CA][GTC][CT][CA][CA][ACG]
```

---

Time 44.92 secs.

```
*****
```

```
*****  
MOTIF WKTVRTBDTCAYATTATARBTRAKGMA MEME-3 width = 28 sites = 9 llr = 185 E-value = 8.7e-004  
*****
```

---

```
Motif WKTVRTBDTCAYATTATARBTRAKGMA MEME-3 Description
```

---

```
Simplified A 4113:3214::8171282931269:27a
pos.-specific C 1:13:1:21:6241:1:1::4::1:13:
probability G :61314142:2:::1:1::62:3:77::
matrix T 437:91722a2:42871711281:3:::
```

```
bits 2.4 *
      *
      *
```

	1.9	*	*	*	*	*
	1.7	*	*	*	*	*
Relative Entropy (29.7 bits)	1.5	*	*	*	*	*
	1.2	*	*	*****	*	**
	1.0	*	*	*****	*	**
	0.7	***	*	*****	*****	
	0.5	***	*	*****	*****	
	0.2	*****	*****	*****	*****	
	0.0	-----				

Multilevel consensus sequence      AGTATGTGATCACATTATAGCTAAGGAA  
     TT C AACG GCTT A A AGAG TAC  
     G T T T                            T

---

#### Motif WKTVRTBDCAYATTATARBTRAKGMA MEME-3 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg00957886	+	73	4.50e-15	TAATCCTACA TTTATGTCATTATATTATAGCTAAGGCA CGTATTTAG
cg12500857	-	25	2.23e-11	CTCTGATCTG TGTGTGGTTGACATTTAGCTAATAAA GCCTTGCAGT
cg00896220	+	42	8.56e-11	TGAGCAGGGG TGTCTAATCTCATTTACAGATAAGGCA ATTGGGGATC
cg04156077	-	157	1.90e-10	ATGTTGTTA CATCTATAATGACATAAAAGGTGATGAA CAACCCAAAA
cg13936911	+	5	3.13e-10	GAGA AGCCTTGATCCTATCAAACAAAGGAA AACCACTCTG
cg17040924	+	70	5.49e-10	AGACTATACC AGAATGTGTTCTTATATATCAGAGGAA TACGAAAGGT
cg20667822	+	173	1.01e-09	GAACTAACAA AGTATCTCATCACAGTGTGTTAGGAA A
cg02632822	+	171	1.17e-09	CATATTAATT TTGGGGTGGTCAAATTATAATTACTAAA AGG
cg19931348	-	19	1.35e-09	GAAGAATTTC ATTGTAATGTTACCTAATAAGTGAGCCA GCACTTCTAC

#### Motif WKTVRTBDCAYATTATARBTRAKGMA MEME-3 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg00957886		4.5e-15	72_[+3]_101
cg12500857		2.2e-11	24_-[-3]_149
cg00896220		8.6e-11	41_[+3]_132
cg04156077		1.9e-10	156_-[-3]_17
cg13936911		3.1e-10	4_[+3]_169
cg17040924		5.5e-10	69_[+3]_104
cg20667822		1e-09	172_[+3]_1
cg02632822		1.2e-09	170_[+3]_3
cg19931348		1.3e-09	18_-[-3]_155

Motif WKTVRTBDBTCAYATTATARBTRAKGMA MEME-3 in BLOCKS format

```
BL MOTIF WKTVRTBDBTCAYATTATARBTRAKGMA width=28 seqs=9
cg00957886      ( 73) TTTATGTCATTATATTATAGCTAAGGCA  1
cg12500857      ( 25) TGTGTGGGTTGACATTTAGCTAATAAA  1
cg00896220      ( 42) TGTCTAACATCATTACAGATAAGGCA  1
cg04156077      ( 157) CATCTATAATGACATAAAAGGTGATGAA 1
cg13936911       ( 5) AGCCTTGATCCTATCAAACAAAGGAA 1
cg17040924       ( 70) AGAATGTGTTCTTATATATCAGAGGAA 1
cg20667822       ( 173) AGTATCTCATCACAGTGTGTTAGGAA 1
cg02632822       ( 171) TTGGGGTGGTCAAATTATAATTACTAAA 1
cg19931348       ( 19) ATTGTAATGTTACCTAATAAGTGAGCCA 1
//
```

Motif WKTVRTBDBTCAYATTATARBTRAKGMA MEME-3 position-specific scoring matrix

log-odds matrix: alength= 4 w= 28 n= 13050 bayes= 10.6352 E= 8.7e-004

125	-149	-982	125
-75	-982	83	84
-75	-149	-149	184
84	9	9	-982
-982	-982	-149	225
84	-149	50	-75
25	-982	-149	184
-75	-50	50	25
125	-149	-50	25
-982	-982	-982	242
-982	83	-50	25
206	-50	-982	-982
-75	50	-982	125
184	-149	-982	25
-75	-982	-149	206
25	-149	-982	184
206	-982	-149	-75
25	-149	-982	184
225	-982	-982	-75
84	-982	83	-75
-75	50	-50	25
25	-982	-982	206
157	-982	9	-75
225	-149	-982	-982
-982	-982	109	84

```
25   -149    109   -982
184      9   -982   -982
242   -982   -982   -982
```

---

```
Motif WKTVRTBDCAYATTATARBTRAKGMA MEME-3 position-specific probability matrix
```

---

```
letter-probability matrix: alength= 4 w= 28 nsites= 9 E= 8.7e-004
```

```
0.444444  0.111111  0.000000  0.444444
0.111111  0.000000  0.555556  0.333333
0.111111  0.111111  0.111111  0.666667
0.333333  0.333333  0.333333  0.000000
0.000000  0.000000  0.111111  0.888889
0.333333  0.111111  0.444444  0.111111
0.222222  0.000000  0.111111  0.666667
0.111111  0.222222  0.444444  0.222222
0.444444  0.111111  0.222222  0.222222
0.000000  0.000000  0.000000  1.000000
0.000000  0.555556  0.222222  0.222222
0.777778  0.222222  0.000000  0.000000
0.111111  0.444444  0.000000  0.444444
0.666667  0.111111  0.000000  0.222222
0.111111  0.000000  0.111111  0.777778
0.222222  0.111111  0.000000  0.666667
0.777778  0.000000  0.111111  0.111111
0.222222  0.111111  0.000000  0.666667
0.888889  0.000000  0.000000  0.111111
0.333333  0.000000  0.555556  0.111111
0.111111  0.444444  0.222222  0.222222
0.222222  0.000000  0.000000  0.777778
0.555556  0.000000  0.333333  0.111111
0.888889  0.111111  0.000000  0.000000
0.000000  0.000000  0.666667  0.333333
0.222222  0.111111  0.666667  0.000000
0.666667  0.333333  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000
```

---

```
Motif WKTVRTBDCAYATTATARBTRAKGMA MEME-3 regular expression
```

---

```
[AT][GT]T[ACG]T[GA][TA][GCT][AGT]T[CGT][AC][CT][AT]T[TA]A[TA]A[GA][CGT][TA][AG]A[GT][GA][AC]A
```

---

Time 64.65 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF AMAYWAAATAWATRWAMTC MEME-4 width = 19 sites = 7 llr = 135 E-value = 8.9e-004

\*\*\*\*\*

Motif AMAYWAAATAWATRWAMTC MEME-4 Description

Simplified A a49:3969:749164a6:1  
pos.-specific C :6:4::1::1:::::3:9  
probability G :::11:1::::1::4:::1:  
matrix T ::146111a1419:6:19:

bits 2.4 \* \* \*  
2.2 \* \* \*  
1.9 \* \* \* \*\* \*\* \*  
1.7 \* \* \* \*\* \*\* \* \*  
Relative 1.5 \* \* \* \*\* \*\* \* \*  
Entropy 1.2 \* \* \* \*\*\* \*\*\*\* \* \*  
(27.8 bits) 1.0 \*\*\* \*\* \*\*\*\*\* \* \*  
0.7 \*\*\* \*\* \*\*\*\*\* \* \*  
0.5 \*\*\*\*\* \* \* \* \* \* \*  
0.2 \*\*\*\*\* \* \* \* \* \* \*  
0.0 -----

Multilevel ACAC TAAATAA ATATAATC  
consensus A TA T GA C  
sequence

\*\*\*\*\*

Motif AMAYWAAATAWATRWAMTC MEME-4 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg12500857	-	177	2.05e-12	GGAAAA AAATTAATAAATAAACTC CGTGACTTG
cg00957886	+	49	1.29e-10	TCAACTTCAA AAACAACATATATGTAATC CTACATTAT
cg00896220	+	1	5.10e-10	. ACACATATTATATAATC CTACCATAAT
cg08590601	+	2	9.35e-10	C ACACTATATAAAATACGC GGAGATGCC
cg24872610	-	116	3.60e-09	CTGTGTTTGC ACATTAGATCAAAGAAATC GGCTGGACAG
cg20667822	-	135	3.87e-09	CTAGAAGGCT AATTGAAATTGATAAAATC ATTTTATAGT
cg02467054	-	131	3.87e-09	TCAGAGCCGC ACAGTAAATATTGTATTA GCCGGAGCCG

Motif AMAYWAAATAWATRWAMTC MEME-4 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg12500857		2e-12	176_-[-4]_6
cg00957886		1.3e-10	48_+[+4]_134
cg00896220		5.1e-10	[+4]_182
cg08590601		9.3e-10	1_[+4]_181
cg24872610		3.6e-09	115_-[-4]_67
cg20667822		3.9e-09	134_-[-4]_48
cg02467054		3.9e-09	130_-[-4]_52

Motif AMAYWAAATAWATRWAMTC MEME-4 in BLOCKS format

```
BL MOTIF AMAYWAAATAWATRWAMTC width=19 seqs=7
cg12500857      ( 177) AAATTAAATAAAATAACTC  1
cg00957886      (  49) AAACAAACATATATGTAATC  1
cg00896220      (   1) ACACATATTATATATAATC  1
cg08590601      (   2) ACACTATATAAATATACGC  1
cg24872610      ( 116) ACATTAGATCAAAGAAATC  1
cg20667822      ( 135) AATTGAAATTGATAAAAATC  1
cg02467054      ( 131) ACAGTAAATATTTGTATTA  1
//
```

Motif AMAYWAAATAWATRWAMTC MEME-4 position-specific scoring matrix

```
log-odds matrix: alength= 4 w= 19 n= 13725 bayes= 10.7802 E= 8.9e-004
 242  -945  -945  -945
 120    87  -945  -945
 220  -945  -945   -38
 -945    45  -113   120
   61  -945  -113   161
 220  -945  -945   -38
 161  -113  -113   -38
 220  -945  -945   -38
 -945  -945  -945   242
 194  -113  -945   -38
 120  -945  -113   120
 220  -945  -945   -38
```

```
-38   -945   -945    220
161   -945     45   -945
120   -945   -945    161
242   -945   -945   -945
161     -13   -945    -38
-945   -945   -113    220
-38     145   -945   -945
```

---

---

Motif AMAYWAAATAWATRWAMTC MEME-4 position-specific probability matrix

---

letter-probability matrix: alength= 4 w= 19 nsites= 7 E= 8.9e-004

```
1.000000  0.000000  0.000000  0.000000
0.428571  0.571429  0.000000  0.000000
0.857143  0.000000  0.000000  0.142857
0.000000  0.428571  0.142857  0.428571
0.285714  0.000000  0.142857  0.571429
0.857143  0.000000  0.000000  0.142857
0.571429  0.142857  0.142857  0.142857
0.857143  0.000000  0.000000  0.142857
0.000000  0.000000  0.000000  1.000000
0.714286  0.142857  0.000000  0.142857
0.428571  0.000000  0.142857  0.428571
0.857143  0.000000  0.000000  0.142857
0.142857  0.000000  0.000000  0.857143
0.571429  0.000000  0.428571  0.000000
0.428571  0.000000  0.000000  0.571429
1.000000  0.000000  0.000000  0.000000
0.571429  0.285714  0.000000  0.142857
0.000000  0.000000  0.142857  0.857143
0.142857  0.857143  0.000000  0.000000
```

---

---

Motif AMAYWAAATAWATRWAMTC MEME-4 regular expression

---

A[CA]A[CT][TA]AAATA[AT]AT[AG][TA]A[AC]TC

---

Time 83.91 secs.

\*\*\*\*\*

\*\*\*\*\*  
MOTIF TTTCWHRTYTT MEME-5 width = 11 sites = 13 llr = 146 E-value = 2.2e+003  
\*\*\*\*\*

-----  
Motif TTTCWHRTYTT MEME-5 Description

Simplified A 21::625:2::  
pos.-specific C 1::a:5:141:  
probability G ::::::52::2  
matrix T 89a:43:8598

bits 2.4 \*  
2.2 \*  
1.9 \*\* \*  
1.7 \*\*\* \*\*  
Relative 1.5 \*\*\*\*\* \*\*  
Entropy 1.2 \*\*\*\*\* \* \*\*  
(16.2 bits) 1.0 \*\*\*\*\* \*\* \*\*  
0.7 \*\*\*\*\* \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel TTTCACATTTT  
consensus TTG C  
sequence A

-----  
Motif TTTCWHRTYTT MEME-5 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg13738327	+	129	2.67e-07	AGCGACAGAA TTTCACGTTT CTTCACGTTG
cg13936911	-	52	5.74e-07	CCCCAGTCTT TTTCTCATCTT CAGCAAGGCC
cg17040924	-	6	8.66e-07	AACACATTGT TTTCATGTATT TGCTT
cg10637260	+	115	1.61e-06	TTGACCCCTC ATTACAGTTT ATTGATAACCT
cg00896220	-	135	1.79e-06	TGGAATCTTG ATTCAAATCTT GGCAGTGCCA
cg07724977	-	115	1.82e-06	CGGGGCCTCT TTTCTTATTTG GCTAATTAT
cg03532422	+	131	2.90e-06	CAGAGGCTTG TTTCACATCTG TAACAACAGG
cg00957886	-	131	3.35e-06	AACCACCGTC TATCATGTTT CTCTTAAGGT
cg07747690	+	44	4.77e-06	ATGTCCTTAG CTTCTCATTT TGTTGGAGGA
cg25917893	+	95	5.99e-06	TCGCGCGAGA TTTCACGCTT CCTAGCCCCG
cg04156077	-	10	5.99e-06	TTATCTTAGA TTTCTTAGATT TGGGATTCT
cg12509424	+	76	8.15e-06	GCCTCCCTTC TTTCAAATCCT CCCGTGTTAC

cg19801460 + 119 1.08e-05 ACTCTCACCA TTTCTAGGCTT TCAGGGGGTC

Motif TTTCWHRTYTT MEME-5 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg13738327		2.7e-07	128_[+5]_62
cg13936911		5.7e-07	51_-[-5]_139
cg17040924		8.7e-07	5_-[-5]_185
cg10637260		1.6e-06	114_[+5]_76
cg00896220		1.8e-06	134_-[-5]_56
cg07724977		1.8e-06	114_-[-5]_76
cg03532422		2.9e-06	130_[+5]_60
cg00957886		3.3e-06	130_-[-5]_60
cg07747690		4.8e-06	43_[+5]_147
cg25917893		6e-06	94_[+5]_96
cg04156077		6e-06	9_-[-5]_181
cg12509424		8.2e-06	75_[+5]_115
cg19801460		1.1e-05	118_[+5]_72

Motif TTTCWHRTYTT MEME-5 in BLOCKS format

BL MOTIF TTTCWHRTYTT width=11 seqs=13  
cg13738327 ( 129) TTTCACGTTTT 1  
cg13936911 ( 52) TTTCTCATCTT 1  
cg17040924 ( 6) TTTCATGTATT 1  
cg10637260 ( 115) ATTCACTGGTTTT 1  
cg00896220 ( 135) ATTCAAATCTT 1  
cg07724977 ( 115) TTTCTTATTG 1  
cg03532422 ( 131) TTTCACATCTG 1  
cg00957886 ( 131) TATCATGTTTT 1  
cg07747690 ( 44) CTTCTCATT 1  
cg25917893 ( 95) TTTCACGCTTT 1  
cg04156077 ( 10) TTTCTTAGATT 1  
cg12509424 ( 76) TTTCAAATCCT 1  
cg19801460 ( 119) TTTCCTAGGCTT 1  
//

Motif TTTCWHRTYTT MEME-5 position-specific scoring matrix

```
log-odds matrix: alength= 4 w= 11 n= 14325 bayes= 11.2696 E= 2.2e+003
 -28   -202   -1035   204
 -128   -1035   -1035   231
 -1035   -1035   -1035   242
 -1035    167   -1035  -1035
  172   -1035   -1035   104
   31     56   -1035    72
  153   -1035      56  -1035
 -1035   -202   -103    204
  -28     30   -1035   131
 -1035   -202   -1035   231
 -1035   -1035   -103   218
```

---

```
Motif TTTCWHRTYTT MEME-5 position-specific probability matrix
```

```
letter-probability matrix: alength= 4 w= 11 nsites= 13 E= 2.2e+003
 0.153846  0.076923  0.000000  0.769231
 0.076923  0.000000  0.000000  0.923077
 0.000000  0.000000  0.000000  1.000000
 0.000000  1.000000  0.000000  0.000000
 0.615385  0.000000  0.000000  0.384615
 0.230769  0.461538  0.000000  0.307692
 0.538462  0.000000  0.461538  0.000000
 0.000000  0.076923  0.153846  0.769231
 0.153846  0.384615  0.000000  0.461538
 0.000000  0.076923  0.000000  0.923077
 0.000000  0.000000  0.153846  0.846154
```

---

```
Motif TTTCWHRTYTT MEME-5 regular expression
```

```
TTTC[AT][CTA][AG]T[TC]TT
```

---

```
Time 103.06 secs.
```

```
*****
```

```
*****
```

```
MOTIF CBSCCCBCCNCCHCCCCNCTCC MEME-6      width =  21  sites =  39  llr = 377  E-value = 9.6e+003
```

\*\*\*\*\*

Motif CBSCCCBCCNCHCCCCNCTCC MEME-6 Description

Simplified A :11:31::22:3:111212::  
pos.-specific C 9248683a7382686837:a8  
probability G :35:113:13:13121312:1  
matrix T 14:11:4::3231:1:216:1

bits 2.4  
2.2  
1.9  
1.7 \*  
Relative 1.5 \* \*  
Entropy 1.2 \* \* \* \*  
(13.9 bits) 1.0 \* \* \* \* \* \*\*  
0.7 \* \* \* \* \* \* \*\*\*  
0.5 \* \* \* \* \* \* \* \*\*\*\*  
0.2 \* \* \* \* \* \* \* \*\*\*  
0.0 -----

Multilevel CTGCCCTCCCCACCCCCCTCC  
consensus GC A C TTTG G G  
sequence C G G C A  
T

Motif CBSCCCBCCNCHCCCCNCTCC MEME-6 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg10857807	+	171	1.70e-11	TCTCTGTGCT CTCCCCCTCCTCTCCCCACTCC CCTGTCCCCA
cg02163400	+	145	4.90e-07	GCCCCTTCGG CTGCCCTCGCCACGCCCTCC GCCCCGCCCTC
cg19729672	+	153	6.40e-07	CCCGGGACCC CGGCCCTCCGTGGCCCCCTCC CGGGGAGCTC
cg07724977	+	40	6.40e-07	CCTTAACCG CGCCCCCCCAGCCCCATCTCC AGTCGCGGTC
cg05541867	-	73	6.40e-07	TGCGGTCCCC CTGCCCTCCGCTCACGCCCTCC ATCCTCTGC
cg04784471	+	26	6.40e-07	GCAAGTGAGT CGGCCCGCCCCCTGCCCGGCC CATAGCGCTG
cg14491776	+	1	1.07e-06	. CAACCCCCAACACCCCAATCC CTGCCCAACA
cg09808690	+	153	1.74e-06	CCAGGAGCTC CGCCCCGCCCGCCCCCTTC AGAAGCCCCG
cg02632822	-	74	1.74e-06	TTCGGTATTCTT CTCCCACCCCTTCCCCCTTCT AAATCTCCAT
cg26305881	+	46	2.75e-06	CCCTTTCCGT CCCCACCCCATACCCCTCT TCCGAACAGA
cg13752114	-	82	2.75e-06	TGGGGAGCGC CGGCCGCCCTCCCCGACC GGGAGCAGCG
cg25917893	+	12	3.83e-06	GCCTCCTGCG CGGCCGCATCTTCCCGCTCC GGGTCCCCGC
cg04039667	+	18	4.26e-06	CTCGATATCA CTGCTCCCCCACCGCAAGCC CCCGGAACCC
cg22664157	-	1	7.13e-06	CCCCCGGGGT CCCCACCGACACCCGCCCTCC
cg19801460	+	70	7.87e-06	CCACCGGTTA CAACCAGCCCTTCCCCCTCT CGGGATGTCC

cg10637260	-	147	7.87e-06	AGGGATCTTC	CTCCCCCTCCATCTCCAGCACC	CAGCTGGGGG
cg07265976	+	57	7.87e-06	CTCAGAGCAG	CTGTCCCTCATCTGCACTCTCG	TCCCCATCAT
cg26673609	+	101	8.68e-06	ACCCACTGGG	CGCCACCCCACCTCCCGTGTCC	CGAGACGCC
cg05725080	+	108	8.68e-06	CCCCGCCCG	CTCTCCGCCACAGCCCGCTCA	AGGGGGTACC
cg25208863	+	83	9.57e-06	TCACCAAGAG	CGGCCGCCCGCAGCCCCGCGCC	GGCTCAGCGC
cg18768400	+	134	9.57e-06	CCCGCCAGCC	CGGCCCGCAGTCGCTCCCTCC	AGCCTAGCGT
cg18255614	+	34	1.05e-05	CTTGGCCCGC	CGGTCCCTCCTCTGCTTCTCC	GCCTACTTGG
cg02467054	+	162	1.40e-05	GGCTCTGACT	CACCGCGCCTCGCCTCGCTCC	GCCGGCGCC
cg13233166	-	36	2.00e-05	CGCGCTGGCC	CGGCCCGCAGCTCCTCCGGCC	GCCGGCCCCC
cg05004480	-	47	2.18e-05	TCTGTGGGGG	CTACCCCCGTCCTCGCTTCC	ACTCGACCCC
cg16347828	+	162	2.38e-05	GCAACCTTCT	TTCTTCTCCGCCCGCCCTCC	AGCGGGTAAC
cg08034643	+	68	2.38e-05	GCTGGACGGC	CTCCACCCCTCCGGACACGCC	TGCAGGGGCT
cg14685095	+	116	2.82e-05	CCTCCGGGAA	TCGCACCGGCCACCCACACC	GACACGCACA
cg06840699	+	69	3.62e-05	ACGCAAGGTA	CTCCAGTCCGCGCCCCAAACT	CTTGGAGGAC
cg01277910	-	14	3.62e-05	AGAGCACCCC	CAGCACTCCCCACGGAGCACC	TATCATGTTA
cg10112022	+	116	4.25e-05	TGACGTTTCA	CGAGCCTCCCCGCGCTCGCTCC	TCGAATTGTT
cg01724041	+	117	4.25e-05	CCTCGGAGGC	CTCCAAGCCACACAACCTGCC	CGGACCCCTG
cg02907176	-	61	4.97e-05	ACCGCAGGGC	GCCTCCTCCTCACCGCTCGCC	GGCTTCAAAG
cg17775727	+	147	5.37e-05	AGTACCCGTG	CAGCTATCATTACCAACAAACC	AAGCCCCACC
cg09368670	+	16	6.25e-05	GCGGATATGA	CGCCACCGACCCCCAGCGTTCC	AAGCTGAGCT
cg27099625	+	129	7.81e-05	CGCGTATTTC	CCGCCCTGCTTTCGCCCGCC	GTTCCGTGGC
cg09588770	+	140	8.39e-05	CGTCCTCCTG	CTGCTCTCGCGGGCCCTGGCC	CTGACCGAGA
cg19931348	+	177	1.04e-04	TGCTCTGGTG	CTACAAACCCCACCCAGATCT	ACTT
cg10280383	+	101	1.19e-04	CAGCCGGGCC	CGCCCGCCGCTGCCAACTCG	CACAGTGCCT

Motif CBSCCBCCNCHCCCCNCTCC MEME-6 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg10857807		1.7e-11	170_[+6]_10
cg02163400		4.9e-07	144_[+6]_36
cg19729672		6.4e-07	152_[+6]_28
cg07724977		6.4e-07	39_[+6]_141
cg05541867		6.4e-07	72_-[-6]_108
cg04784471		6.4e-07	25_[+6]_155
cg14491776		1.1e-06	[+6]_180
cg09808690		1.7e-06	152_[+6]_28
cg02632822		1.7e-06	73_-[-6]_107
cg26305881		2.7e-06	45_[+6]_135
cg13752114		2.7e-06	81_-[-6]_99
cg25917893		3.8e-06	11_[+6]_169
cg04039667		4.3e-06	17_[+6]_163
cg22664157		7.1e-06	[-6]_180
cg19801460		7.9e-06	69_[+6]_111
cg10637260		7.9e-06	146_-[-6]_34

cg07265976	7.9e-06	56_[+6]_124
cg26673609	8.7e-06	100_[+6]_80
cg05725080	8.7e-06	107_[+6]_73
cg25208863	9.6e-06	82_[+6]_98
cg18768400	9.6e-06	133_[+6]_47
cg18255614	1.1e-05	33_[+6]_147
cg02467054	1.4e-05	161_[+6]_19
cg13233166	2e-05	35_[-6]_145
cg05004480	2.2e-05	46_[-6]_134
cg16347828	2.4e-05	161_[+6]_19
cg08034643	2.4e-05	67_[+6]_113
cg14685095	2.8e-05	115_[+6]_65
cg06840699	3.6e-05	68_[+6]_112
cg01277910	3.6e-05	13_[-6]_167
cg10112022	4.3e-05	115_[+6]_65
cg01724041	4.3e-05	116_[+6]_64
cg02907176	5e-05	60_[-6]_120
cg17775727	5.4e-05	146_[+6]_34
cg09368670	6.3e-05	15_[+6]_165
cg27099625	7.8e-05	128_[+6]_52
cg09588770	8.4e-05	139_[+6]_41
cg19931348	0.0001	176_[+6]_4
cg10280383	0.00012	100_[+6]_80

---

Motif CBSCCCBCCNCCHCCCCNCTCC MEME-6 in BLOCKS format

---

BL	MOTIF	CBSCCCBCCNCCHCCCCNCTCC	width=21	seqs=39
cg10857807	( 171)	CTCCCCCTCCTCTCCCCACTCC	1	
cg02163400	( 145)	CTGCCCTCGCCACGCCCCCTCC	1	
cg19729672	( 153)	CGGGCCCTCCGTGGCCCCCTCC	1	
cg07724977	( 40)	CCGGCCCCCGCCCCCATCTCC	1	
cg05541867	( 73)	CTGCCCTCCGCTCACGCCTCC	1	
cg04784471	( 26)	CCGGCCCAGCCCTGCCCCCGCC	1	
cg14491776	( 1)	CAACCCCCAACACCCCCAATCC	1	
cg09808690	( 153)	CGCCCCGCCCCCGCCCCCTTCC	1	
cg02632822	( 74)	CTCCCACCCCTTCCCCCTTCT	1	
cg26305881	( 46)	CCCCACCCCATACCACCCCTCT	1	
cg13752114	( 82)	CGGCCGCCCCCTCCCCGACC	1	
cg25917893	( 12)	CCGCCGCCATCTTCCCCGTCTCC	1	
cg04039667	( 18)	CTGCTCCCCCACCGCAAGCC	1	
cg22664157	( 1)	CCCCACGCGACACCCGCCCTCC	1	
cg19801460	( 70)	CAACCAGCCCTTCCCCCTCTCT	1	
cg10637260	( 147)	CTCCCCCTCCATCTCCAGCACC	1	
cg07265976	( 57)	CTGTCTCATCTGCACTCTCG	1	
cg26673609	( 101)	CGCCACCCACTCCCGTGTCC	1	

cg05725080 ( 108) CTCTCCGCCACAGCCGCTCA 1  
cg25208863 ( 83) CCGCCGCCCGCAGCCCGGCC 1  
cg18768400 ( 134) CGGCCCGCAGTCGCTCCCTCC 1  
cg18255614 ( 34) CGGTCTCCTCTGCTTCTCC 1  
cg02467054 ( 162) CACCGCGCTCGCCTCGCTCC 1  
cg13233166 ( 36) CGGGCCCCAGCTCCTCCGGCC 1  
cg05004480 ( 47) CTACCCCCGTCCTCGCTTCC 1  
cg16347828 ( 162) TTCTTCTCGCCCCGCCCTCC 1  
cg08034643 ( 68) CTCCACCCCTCCGGACACGCC 1  
cg14685095 ( 116) TCGCACGCCACCCCCACACC 1  
cg06840699 ( 69) CTCCAGTCCGCGCCCCAAACT 1  
cg01277910 ( 14) CAGCACTCCCCACGGAGCACC 1  
cg10112022 ( 116) CGAGCCTCCCCGCCCTCGCTCC 1  
cg01724041 ( 117) CTCCAAGGCCACACAACCTGCC 1  
cg02907176 ( 61) GCCTCCTCCTCACCGCTCGCC 1  
cg17775727 ( 147) CAGCTATCATTACCACAAACC 1  
cg09368670 ( 16) CGCCACGCACCCCAGCGTTCC 1  
cg27099625 ( 129) CGGCCCTGCTTTCGCCCGGCC 1  
cg09588770 ( 140) CTGCTCTCGGCGGCCCTGGCC 1  
cg19931348 ( 177) CTACAAACCCCACCCAGATCT 1  
cg10280383 ( 101) CGCCGCGCCGCTGCCAACTCG 1  
//

---

---

Motif CBSCCCBCNCNCHCCCCNCTCC MEME-6 position-specific scoring matrix

---

log-odds matrix: alength= 4 w= 21 n= 13575 bayes= 8.66333 E= 9.6e+003

-1193	156	-361	-186
-54	-44	-29	104
-54	39	56	-1193
-1193	143	-361	-54
46	91	-261	-86
-54	130	-161	-1193
-286	-3	-15	104
-1193	164	-361	-1193
-6	114	-129	-1193
-6	-15	-29	60
-1193	134	-1193	14
84	-61	-129	84
-1193	97	-15	-86
-128	143	-203	-1193
-54	85	-80	-54
-54	130	-203	-286
14	9	-29	14
-54	109	-203	-54

```
-28 -1193 -44 172
-1193 167 -1193 -1193
-286 134 -261 -54
```

```
-----  
Motif CBSCCCCBCCNCNCHCCCCNCTCC MEME-6 position-specific probability matrix  
-----
```

```
letter-probability matrix: alength= 4 w= 21 nsites= 39 E= 9.6e+003
```

```
0.000000 0.923077 0.025641 0.051282
0.128205 0.230769 0.256410 0.384615
0.128205 0.410256 0.461538 0.000000
0.000000 0.846154 0.025641 0.128205
0.256410 0.589744 0.051282 0.102564
0.128205 0.769231 0.102564 0.000000
0.025641 0.307692 0.282051 0.384615
0.000000 0.974359 0.025641 0.000000
0.179487 0.692308 0.128205 0.000000
0.179487 0.282051 0.256410 0.282051
0.000000 0.794872 0.000000 0.205128
0.333333 0.205128 0.128205 0.333333
0.000000 0.615385 0.282051 0.102564
0.076923 0.846154 0.076923 0.000000
0.128205 0.564103 0.179487 0.128205
0.128205 0.769231 0.076923 0.025641
0.205128 0.333333 0.256410 0.205128
0.128205 0.666667 0.076923 0.128205
0.153846 0.000000 0.230769 0.615385
0.000000 1.000000 0.000000 0.000000
0.025641 0.794872 0.051282 0.128205
```

```
-----  
Motif CBSCCCCBCCNCNCHCCCCNCTCC MEME-6 regular expression  
-----
```

```
C[TGC][GC]C[CA]C[TCG]CC[CTG][CT][ATC][CG]CCC[CGAT]C[TG]CC
```

```
Time 121.95 secs.
```

```
*****  
*****
```

```
*****  
*****
```

MOTIF AAAWRTTYKTGWTWG MEME-7 width = 15 sites = 6 llr = 96 E-value = 1.5e+004  
\*\*\*\*\*

-----  
Motif AAAWRTTYKTGWTWG MEME-7 Description

Simplified A a8837:::::2:323:  
pos.-specific C :::::::32:::::  
probability G :2223::::328::::a  
matrix T ::::5:aa7572787:

bits 2.4 \* \*\*  
2.2 \* \*\*  
1.9 \* \*\*  
1.7 \*\*\* \*\* \* \*  
Relative 1.5 \*\*\* \*\* \*\*\*\*  
Entropy 1.2 \*\*\* \*\*\*\* \*\*\*\*  
(23.1 bits) 1.0 \*\*\* \*\*\*\* \*\*\*\*\*  
0.7 \*\*\*\*\* \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel AAATATTTTGTGG  
consensus AG CG A A  
sequence

-----  
Motif AAAWRTTYKTGWTWG MEME-7 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg20667822	+	3	5.32e-10	AA AAAAATTTTTTTTG AGACAGGGTC
cg04156077	+	120	9.02e-10	GTTGTGTGGT AAATATTTCTGTTTG TTGGCAAAAC
cg13936911	+	79	3.28e-08	GGGGGGGACC AAAGATTCTGTGTTAG GAAAGCCGCG
cg00957886	-	5	6.73e-08	GTCAGGCTTG AGAAATTCTTGATAG AATG
cg03983713	+	174	8.37e-08	CTCTAATGGT AAATGTTTGGAAATG TCCATAGATA
cg12500857	-	121	9.25e-08	TGTGCCCGC AAGTGTGGAGTTG GCCTCCACCC

-----  
Motif AAAWRTTYKTGWTWG MEME-7 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg20667822		5.3e-10	2_[+7]_184

```
cg04156077          9e-10  119_[+7]_67
cg13936911          3.3e-08 78_[+7]_108
cg00957886          6.7e-08 4_-[-7]_182
cg03983713          8.4e-08 173_[+7]_13
cg12500857          9.3e-08 120_-[-7]_66
```

---

```
Motif AAAWRTTYKTGWTWG MEME-7 in BLOCKS format
```

---

```
BL MOTIF AAAWRTTYKTGWTWG width=15 seqs=6
cg20667822          (   3) AAAAATTTTTTTTG  1
cg04156077          ( 120) AAATATTTCTGTTTG  1
cg13936911          (   79) AAAGATTCTGTGTTAG  1
cg00957886          (    5) AGAAATTCTTGATAG  1
cg03983713          ( 174) AAATGTTTGGAAATG  1
cg12500857          ( 121) AAGTGTGGAGTTTG  1
//
```

---

```
Motif AAAWRTTYKTGWTWG MEME-7 position-specific scoring matrix
```

---

```
log-odds matrix: alength= 4 w= 15 n= 14025 bayes= 12.29 E= 1.5e+004
```

242	-923	-923	-923
216	-923	-91	-923
216	-923	-91	-923
84	-923	-91	142
184	-923	9	-923
-923	-923	-923	242
-923	-923	-923	242
-923	9	-923	184
-923	-91	9	142
-16	-923	-91	184
-923	-923	141	-16
84	-923	-923	184
-16	-923	-923	216
84	-923	-923	184
-923	-923	167	-923

---

```
Motif AAAWRTTYKTGWTWG MEME-7 position-specific probability matrix
```

---

```
letter-probability matrix: alength= 4 w= 15 nsites= 6 E= 1.5e+004
1.000000 0.000000 0.000000 0.000000
```

```
0.833333 0.000000 0.166667 0.000000
0.833333 0.000000 0.166667 0.000000
0.333333 0.000000 0.166667 0.500000
0.666667 0.000000 0.333333 0.000000
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 0.000000 1.000000
0.000000 0.333333 0.000000 0.666667
0.000000 0.166667 0.333333 0.500000
0.166667 0.000000 0.166667 0.666667
0.000000 0.000000 0.833333 0.166667
0.333333 0.000000 0.000000 0.666667
0.166667 0.000000 0.000000 0.833333
0.333333 0.000000 0.000000 0.666667
0.000000 0.000000 1.000000 0.000000
```

---

```
Motif AAAWRTTYKTGWTWG MEME-7 regular expression
```

```
AAA[TA][AG]TT[TC][TG]TG[TA]T[TA]G
```

---

Time 138.94 secs.

```
*****
```

```
*****  
MOTIF TTAAGTWSAGAA MEME-8      width = 12 sites = 7 llr = 94 E-value = 3.1e+004  
*****
```

---

```
Motif TTAAGTWSAGAA MEME-8 Description
```

---

```
Simplified      A :17a::6:a199
pos.-specific   C :::::::6::::
probability     G 1:3:7:13:91:
matrix          T 99::3a31:::1
```

```
bits    2.4    * * *
       2.2    * * *
       1.9    * * * * *
       1.7 ** * * * **
Relative      1.5 **** * * **
Entropy       1.2 **** * ****
```

(19.3 bits) 1.0 \*\*\*\*\* \*\*\*  
0.7 \*\*\*\*\* \*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel  
consensus  
sequence

TTAAGTACAGAA  
G T TG

---

Motif TTAAGTWSAGAA MEME-8 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg02573152	+	43	6.30e-08	CAGCAGCAGT TTAAGTTGAGAA TCTGATAGAT
cg17040924	+	156	1.16e-07	CCTAGTTAGG TTGATTACAGAA TAGTCAGCAA
cg12509424	-	185	2.32e-07	TAATT TTAAGTACAGGA AAAAAACAGC
cg02632822	+	148	3.66e-07	AGAAAAGGTG TTAAGTATAGAT CCATATTAAAT
cg25613667	-	9	5.23e-07	TCACGTCACG TAAAGTTGAGAA CTGCGTGT
cg19931348	+	136	5.23e-07	AGATCCAGTC TTGATTACAAAA CCAAGGTGTT
cg03983713	+	30	1.27e-06	TTGAGTACGT GTAAGTGCAGAA TTCACCAGGC

---

Motif TTAAGTWSAGAA MEME-8 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg02573152		6.3e-08	42_[+8]_147
cg17040924		1.2e-07	155_[+8]_34
cg12509424		2.3e-07	184_-[-8]_5
cg02632822		3.7e-07	147_[+8]_42
cg25613667		5.2e-07	8_-[-8]_181
cg19931348		5.2e-07	135_[+8]_54
cg03983713		1.3e-06	29_[+8]_160

---

Motif TTAAGTWSAGAA MEME-8 in BLOCKS format

BL MOTIF TTAAGTWSAGAA width=12 seqs=7

cg02573152	( 43)	TTAAGTTGAGAA	1
cg17040924	( 156)	TTGATTACAGAA	1
cg12509424	( 185)	TTAAGTACAGGA	1

```
cg02632822      ( 148) TTAAGTATAGAT  1
cg25613667      (   9) TAAAGTTGAGAA  1
cg19931348      ( 136) TTGATTACAAAA  1
cg03983713      (  30) GTAAGTGCAGAA  1
//
```

---

---

```
Motif TTAAGTWSAGAA MEME-8 position-specific scoring matrix
```

---

```
log-odds matrix: alength= 4 w= 12 n= 14250 bayes= 12.2134 E= 3.1e+004
```

```
-945 -945 -113  220
 -38 -945 -945  220
 194 -945 -13   -945
 242 -945 -945 -945
-945 -945  119  61
-945 -945 -945  242
 161 -945 -113  61
-945  87   -13  -38
 242 -945 -945 -945
 -38 -945  145 -945
 220 -945 -113 -945
 220 -945 -945  -38
```

---

---

```
Motif TTAAGTWSAGAA MEME-8 position-specific probability matrix
```

---

```
letter-probability matrix: alength= 4 w= 12 nsites= 7 E= 3.1e+004
```

```
0.000000 0.000000 0.142857 0.857143
0.142857 0.000000 0.000000 0.857143
0.714286 0.000000 0.285714 0.000000
1.000000 0.000000 0.000000 0.000000
0.000000 0.000000 0.714286 0.285714
0.000000 0.000000 0.000000 1.000000
0.571429 0.000000 0.142857 0.285714
0.000000 0.571429 0.285714 0.142857
1.000000 0.000000 0.000000 0.000000
0.142857 0.000000 0.857143 0.000000
0.857143 0.000000 0.142857 0.000000
0.857143 0.000000 0.000000 0.142857
```

---

---

```
Motif TTAAGTWSAGAA MEME-8 regular expression
```

---

TT[AG]A[GT]T[AT][CG]AGAA

Time 155.73 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF ATAMAAAGSTCAVTTCCMAWGATBNT MEME-9 width = 26 sites = 5 llr = 115 E-value = 2.8e+004

\*\*\*\*\*

-----  
Motif ATAMAAAGSTCAVTTCCMAWGATBNT MEME-9 Description

Simplified A 8:868a8:::2842222666:6::42  
pos.-specific C 22:4::2:426:4::8842::2:22:  
probability G :::::::a622:2:::::2:8::42:  
matrix T :82:2::::6:2:88::::422a428

bits 2.4 \* \*  
2.2 \* \*  
1.9 \* \*  
1.7 \* \*\* \* \* \*\* \* \*  
Relative 1.5 \*\*\* \*\*\* \* \*\* \* \* \*  
Entropy 1.2 \*\*\*\*\* \* \*\*\*\*\* \* \* \*  
(33.1 bits) 1.0 \*\*\*\*\* \* \*\*\*\*\* \* \*  
0.7 \*\*\*\*\* \* \*\*\*\*\* \*  
0.5 \*\*\*\*\* \*  
0.2 \*\*\*\*\* \*  
0.0 -----

Multilevel ATAAAAAGGTCAATTCAAAGATGAT  
consensus CCTCT C CCATCAAAACCTTC TCA  
sequence GG G G T CG  
T

-----  
Motif ATAMAAAGSTCAVTTCCMAWGATBNT MEME-9 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg02573152	+	63	3.41e-13	AATCTGATAG ATACAAAGGTGAATACCAGAGATTAT AACTAAGTC
cg22824635	+	50	1.63e-11	GTCACCCAG ATACAAAGCGCAGATACAAAGATGGT GACCGGTACA

```
cg03532422      -    143  1.93e-11 AAAGGGGAGA ATAAAAAGCCAATTCACCTGTTGTT ACAGATGTGA
cg16139664      -     5  4.26e-11 CCGCAGCGAC CTTATAAGGTCTTCCCATGATTCT CTCT
cg24872610      -    39  9.35e-11 CATTCTTGGG ACAAAACGGTAACCTCAAATCTCAA CTCTATGACC
```

Motif ATAMAAAGSTCAVTTCCMAWGATBNT MEME-9 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg02573152		3.4e-13	62_[+9]_113
cg22824635		1.6e-11	49_[+9]_126
cg03532422		1.9e-11	142_[-9]_33
cg16139664		4.3e-11	4_[-9]_171
cg24872610		9.4e-11	38_[-9]_137

Motif ATAMAAAGSTCAVTTCCMAWGATBNT MEME-9 in BLOCKS format

```
BL MOTIF ATAMAAAGSTCAVTTCCMAWGATBNT width=26 seqs=5
cg02573152      (   63) ATACAAAGGTGAATACCAAGAGATTAT  1
cg22824635      (   50) ATACAAAGCGCAGATAAAAAGATGGT  1
cg03532422      (  143) ATAAAAAGCCAATTCACCTGTTGTT  1
cg16139664      (     5) CTTATAAGGTCTTCCCATGATTCT  1
cg24872610      (    39) ACAAAACGGTAACCTCAAATCTCAA  1
//
```

Motif ATAMAAAGSTCAVTTCCMAWGATBNT MEME-9 position-specific scoring matrix

```
log-odds matrix: alength= 4 w= 26 n= 13200 bayes= 12.3095 E= 2.8e+004
 210    -65    -897    -897
 -897    -65    -897    210
 210    -897    -897     10
 168     35    -897    -897
 210    -897    -897     10
 242    -897    -897    -897
 210    -65    -897    -897
 -897    -897    167    -897
 -897     35     94    -897
 -897    -65     -65    168
   10     94    -65    -897
 210    -897    -897     10
 110     35    -65    -897
```

```
10  -897  -897   210
10  -897  -897   210
10   135  -897  -897
10   135  -897  -897
168    35  -897  -897
168    -65   -65  -897
168   -897  -897   110
-897  -897   135    10
168    -65  -897    10
-897  -897  -897   242
-897    -65    35   110
110    -65   -65    10
10  -897  -897   210
```

---

---

Motif ATAMAAAGSTCAVTTCCMAWGATBNT MEME-9 position-specific probability matrix

---

letter-probability matrix: alength= 4 w= 26 nsites= 5 E= 2.8e+004

```
0.800000  0.200000  0.000000  0.000000
0.000000  0.200000  0.000000  0.800000
0.800000  0.000000  0.000000  0.200000
0.600000  0.400000  0.000000  0.000000
0.800000  0.000000  0.000000  0.200000
1.000000  0.000000  0.000000  0.000000
0.800000  0.200000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000
0.000000  0.400000  0.600000  0.000000
0.000000  0.200000  0.200000  0.600000
0.200000  0.600000  0.200000  0.000000
0.800000  0.000000  0.000000  0.200000
0.400000  0.400000  0.200000  0.000000
0.200000  0.000000  0.000000  0.800000
0.200000  0.000000  0.000000  0.800000
0.200000  0.800000  0.000000  0.000000
0.200000  0.800000  0.000000  0.000000
0.600000  0.400000  0.000000  0.000000
0.600000  0.200000  0.200000  0.000000
0.600000  0.000000  0.000000  0.400000
0.000000  0.000000  0.800000  0.200000
0.600000  0.200000  0.000000  0.200000
0.000000  0.000000  0.000000  1.000000
0.000000  0.200000  0.400000  0.400000
0.400000  0.200000  0.200000  0.200000
0.200000  0.000000  0.000000  0.800000
```

---

Motif ATAMAAAGSTCAVTTCCMAWGATBNT MEME-9 regular expression

[AC][TC][AT][AC][AT]A[AC]G[GC][TCG][CAG][AT][ACG][TA][CA][CA][AC][ACG][AT][GT][ACT]T[GTC][ACGT][TA]

Time 172.54 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF TWWTWTAGMAGWAGCAARA MEME-10 width = 19 sites = 6 llr = 106 E-value = 5.4e+004

\*\*\*\*\*

Motif TWWTWTAGMAGWAGCAARA MEME-10 Description

Simplified A :532327:78237:2883a  
pos.-specific C ::::::2:32:22:5::2:  
probability G ::::::22a:::8:2a2:25:  
matrix T a37877:::::5::22:::

bits 2.4 \* \*  
2.2 \* \*  
1.9 \* \*  
1.7 \* \* \* \* \* \*\* \*  
Relative 1.5 \* \*\*\* \* \* \* \*\*\* \*  
Entropy 1.2 \* \*\*\* \*\*\*\* \* \*\* \*  
(25.6 bits) 1.0 \* \*\*\*\*\* \* \* \*\* \*  
0.7 \*\*\*\*\* \* \* \*  
0.5 \*\*\*\*\* \* \*\*\*  
0.2 \*\*\*\*\* \* \* \* \*  
0.0 -----

Multilevel TATTTAGAAGTAGCAAGA  
consensus TA A C A A  
sequence

Motif TWWTWTAGMAGWAGCAARA MEME-10 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
---------------	--------	-------	---------	------

```

-----+
cg00957886      +  103  5.64e-12 CTAAGGCACG TATTTTAGCAGTAGCAAGA CCTTAGGAGA
cg07747690      -  176  3.23e-10 ATCCCAA TAATTTAGAAATGGCAAAA CAGGAGTTCT
cg24872610      -   7  4.95e-09 TATGACCTGC TTTTAAGGAAGAAGGAAGA GCCGTG
cg02907176      +  165  1.21e-08 GCCGGAGTC A TATTATCGACGTAGTTAAA GCCCACTAGC
cg21813265      -  175  1.49e-08 GGCCATCT TCATTGAGAAGACGAAAGA TGGACAGATT
cg02573152      +   22  3.18e-08 TATAGGAGGC TTTATTAGCAGCAGCAGCA GTTTAAGTTG
-----+

```

Motif TWWTWTAGMAGWAGCAARA MEME-10 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg00957886		5.6e-12	102_[+10]_80
cg07747690		3.2e-10	175_-[-10]_7
cg24872610		4.9e-09	6_-[-10]_176
cg02907176		1.2e-08	164_[+10]_18
cg21813265		1.5e-08	174_-[-10]_8
cg02573152		3.2e-08	21_[+10]_161

Motif TWWTWTAGMAGWAGCAARA MEME-10 in BLOCKS format

```

BL MOTIF TWWTWTAGMAGWAGCAARA width=19 seqs=6
cg00957886      ( 103) TATTTTAGCAGTAGCAAGA 1
cg07747690      ( 176) TAATTTAGAAATGGCAAAA 1
cg24872610      (   7) TTTTAAGGAAGAAGGAAGA 1
cg02907176      ( 165) TATTATCGACGTAGTTAAA 1
cg21813265      ( 175) TCATTGAGAAGACGAAAGA 1
cg02573152      (   22) TTTATTAGCAGCAGCAGCA 1
//
```

Motif TWWTWTAGMAGWAGCAARA MEME-10 position-specific scoring matrix

```

log-odds matrix: alength= 4 w= 19 n= 13725 bayes= 12.2588 E= 5.4e+004
-923  -923  -923  242
 142   -91  -923   84
   84  -923  -923  184
  -16  -923  -923  216
   84  -923  -923  184
  -16  -923   -91  184
  184   -91   -91  -923

```

```
-923 -923 167 -923
184 9 -923 -923
216 -91 -923 -923
-16 -923 141 -923
84 -91 -923 142
184 -91 -91 -923
-923 -923 167 -923
-16 67 -91 -16
216 -923 -923 -16
216 -923 -91 -923
84 -91 67 -923
242 -923 -923 -923
```

---

---

Motif TWWTWTAGMAGWAGCAARA MEME-10 position-specific probability matrix

---

letter-probability matrix: alength= 4 w= 19 nsites= 6 E= 5.4e+004

```
0.000000 0.000000 0.000000 1.000000
0.500000 0.166667 0.000000 0.333333
0.333333 0.000000 0.000000 0.666667
0.166667 0.000000 0.000000 0.833333
0.333333 0.000000 0.000000 0.666667
0.166667 0.000000 0.166667 0.666667
0.666667 0.166667 0.166667 0.000000
0.000000 0.000000 1.000000 0.000000
0.666667 0.333333 0.000000 0.000000
0.833333 0.166667 0.000000 0.000000
0.166667 0.000000 0.833333 0.000000
0.333333 0.166667 0.000000 0.500000
0.666667 0.166667 0.166667 0.000000
0.000000 0.000000 1.000000 0.000000
0.166667 0.500000 0.166667 0.166667
0.833333 0.000000 0.000000 0.166667
0.833333 0.000000 0.166667 0.000000
0.333333 0.166667 0.500000 0.000000
1.000000 0.000000 0.000000 0.000000
```

---

---

Motif TWWTWTAGMAGWAGCAARA MEME-10 regular expression

---

T[AT][TA]T[TA]TAG[AC]AG[TA]AGCAA[GA]A

---

Time 188.89 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF CCCGCSCCGCCSG MEME-11 width = 15 sites = 15 llr = 178 E-value = 3.8e+005

\*\*\*\*\*

-----  
Motif CCCGCSCCGCCSG MEME-11 Description  
-----

Simplified A ::2:1:1:::1:11:  
pos.-specific C 8a8:77969:9a96:  
probability G 2::a:3:1:91:13a  
matrix T ::::1:::311:::::

bits 2.4  
2.2  
1.9  
1.7 \* \* \* \*  
Relative 1.5 \* \* \* \*  
Entropy 1.2 \*\*\* \* \*\* \* \*  
(17.1 bits) 1.0 \*\*\*\* \* \*\*\*\*\* \*  
0.7 \*\*\*\*\* \* \*\*\*\* \*  
0.5 \*\*\*\*\* \* \* \* \*  
0.2 \*\*\*\*\* \* \* \* \*  
0.0 -----

Multilevel CCCGGCCCCGCCCCG  
consensus G A G T G  
sequence

-----  
Motif CCCGCSCCGCCSG MEME-11 sites sorted by position p-value  
-----

Sequence name	Strand	Start	P-value	Site
cg19729672	+	38	4.33e-08	CCTCGCTGTG CCCGCCCTCGCCCCG CCCCAGCGCCA
cg10857807	+	125	9.75e-08	GCCTCAGGAC CCCGCGCCCGCCCCG TCTCCCATGG
cg25208863	-	1	1.88e-07	CGAGGGCACG CCCGACCCCGCCCCG
cg17862404	+	148	3.70e-07	CAGGCCCCGC CCCGCGCTCGCCCCG AGCCGGCTCC
cg05725080	+	93	7.06e-07	CACCTCCAG CCAGTCCCCGCCCCG CTCTCCGCCA
cg09808690	+	180	7.84e-07	TTCCAGAACG CCCGCCCCCTGCCCG CCCCCAG
cg06805280	+	164	9.49e-07	CGTTCGTC GCCGCCTCGCCCCG GGCTACTCCT

cg02163400	+	167	9.49e-07	CGCCCCCTCCG	CCC GCCCTGCCACG	CCCCCTCCGC
cg22889584	+	141	1.31e-06	GCGGTGGGCC	CCAGTCCCCGCCGG	TCC GCGGCCGC
cg04039667	+	46	2.37e-06	GCCCCCGGAA	CCCGCCCGCGCCAG	CAGC GGGCGGA
cg26305881	+	113	2.54e-06	GAACCTCAGT	GCCGCCCTCCCGG	GC GGCCCCAC
cg03532422	-	12	4.23e-06	TGGCGGAAGT	CCCGCCACC GGCCCC	GCGTTCCCCA
cg10889506	-	61	7.08e-06	GCTGCGAAGC	CCCGCGACCGGCCGG	CGGAGGAAGT
cg04784471	+	64	8.58e-06	CTGACAGCGC	CCCGCGCGGACCGG	TTCAGCACCG
cg05834845	-	30	1.16e-05	CGCCTCAGT	GCAGACCCCTCCCG	CTTCAGCCCC

Motif CCCGCSCCGCCSG MEME-11 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg19729672		4.3e-08	37_[+11]_149
cg10857807		9.8e-08	124_[+11]_62
cg25208863		1.9e-07	[-11]_186
cg17862404		3.7e-07	147_[+11]_39
cg05725080		7.1e-07	92_[+11]_94
cg09808690		7.8e-07	179_[+11]_7
cg06805280		9.5e-07	163_[+11]_23
cg02163400		9.5e-07	166_[+11]_20
cg22889584		1.3e-06	140_[+11]_46
cg04039667		2.4e-06	45_[+11]_141
cg26305881		2.5e-06	112_[+11]_74
cg03532422		4.2e-06	11_-[-11]_175
cg10889506		7.1e-06	60_-[-11]_126
cg04784471		8.6e-06	63_[+11]_123
cg05834845		1.2e-05	29_-[-11]_157

Motif CCCGCSCCGCCSG MEME-11 in BLOCKS format

```
BL MOTIF CCCGCSCCGCCSG width=15 seqs=15
cg19729672      ( 38) CCCGCCCTGCCCG 1
cg10857807      ( 125) CCCGCGCCGCCCG 1
cg25208863      (  1) CCCGACCCGCCCG 1
cg17862404      ( 148) CCCGCGCTGCCGG 1
cg05725080      (  93) CCAGTCCCCGCCCG 1
cg09808690      ( 180) CCCGCCCTGCCCG 1
cg06805280      ( 164) GCCGCGCTGCCCG 1
cg02163400      ( 167) CCCGCCCTGCCACG 1
cg22889584      ( 141) CCAGTCCCCGCCGG 1
cg04039667      (  46) CCCGCCCGGCCAG 1
cg26305881      ( 113) GCCGCCCTGCCGG 1
```

```
cg03532422      ( 12) CCCGCCACCGGGCCCG  1  
cg10889506      ( 61) CCCGCGACCGCCGCG  1  
cg04784471      ( 64) CCCGCGCGCGACCGG  1  
cg05834845      ( 30) GCAGACCCCTCCCGG  1  
//
```

---

```
Motif CCCGCSCCGCCSG MEME-11 position-specific scoring matrix
```

---

```
log-odds matrix: alength= 4 w= 15 n= 14025 bayes= 10.5421 E= 3.8e+005
```

-1055	135	-65	-1055
-1055	167	-1055	-1055
10	135	-1055	-1055
-1055	-1055	167	-1055
-48	123	-1055	-48
-1055	109	9	-1055
-48	147	-1055	-1055
-1055	94	-123	51
-1055	157	-1055	-148
-1055	-1055	147	-48
-148	147	-223	-1055
-1055	167	-1055	-1055
-148	147	-223	-1055
-148	94	9	-1055
-1055	-1055	167	-1055

---

```
Motif CCCGCSCCGCCSG MEME-11 position-specific probability matrix
```

---

```
letter-probability matrix: alength= 4 w= 15 nsites= 15 E= 3.8e+005
```

0.000000	0.800000	0.200000	0.000000
0.000000	1.000000	0.000000	0.000000
0.200000	0.800000	0.000000	0.000000
0.000000	0.000000	1.000000	0.000000
0.133333	0.733333	0.000000	0.133333
0.000000	0.666667	0.333333	0.000000
0.133333	0.866667	0.000000	0.000000
0.000000	0.600000	0.133333	0.266667
0.000000	0.933333	0.000000	0.066667
0.000000	0.000000	0.866667	0.133333
0.066667	0.866667	0.066667	0.000000
0.000000	1.000000	0.000000	0.000000
0.066667	0.866667	0.066667	0.000000
0.066667	0.600000	0.333333	0.000000

0.000000 0.000000 1.000000 0.000000

---

---

Motif CCCGCSCCGCCSG MEME-11 regular expression

---

[CG]C[CA]GC[CG]C[CT]GCCCG[CG]G

---

Time 205.12 secs.

\*\*\*\*\*

\*\*\*\*\*  
MOTIF ARWCCYCACASAVGC MEME-12 width = 15 sites = 14 llr = 168 E-value = 1.0e+005  
\*\*\*\*\*

---

Motif ARWCCYCACASAVGC MEME-12 Description

---

Simplified A a65::1:61a184::  
pos.-specific C ::964a16:3241a  
probability G :4::11::2:6:36:  
matrix T ::5124:21::::2:

bits 2.4 \* \*  
2.2 \* \*  
1.9 \* \*  
1.7 \* \* \* \*  
Relative 1.5 \* \*\* \* \* \*  
Entropy 1.2 \*\*\*\* \* \* \*  
(17.3 bits) 1.0 \*\*\*\* \*\* \* \*  
0.7 \*\*\*\* \*\* \* \*  
0.5 \*\*\*\*\* \*\*\*\*\*  
0.2 \*\*\*\*\* \*\*\*\*\*  
0.0 -----

Multilevel AAACCCCACAGAAGC  
consensus GT TT TG CCCT  
sequence G

---

Motif ARWCCYCACASAVGC MEME-12 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg14491776	+	66	1.78e-08	TCGACACCCG AATCCCCACAGACGC CCGAATCCCC
cg03983713	+	129	1.33e-07	TGAAGTCCAC AGTCCCCACAGAACCT CTGCGTGTGA
cg22040815	+	85	2.20e-07	TCGGCTGTCT AATCCTCAGAGAACCC CGGCCCAT
cg17040924	-	113	1.15e-06	GTACTGCATT AAACTTCTTACACGC TCCTCACCTT
cg10990040	+	35	1.15e-06	ACACGTACTC AGACCACACAGAGGC TCAGATGCAC
cg09588770	+	88	1.15e-06	CCGGACTCAAG AGTCTCCTCAGACGC CGAGATGCTG
cg20128772	-	161	1.29e-06	TTTGGGTGTG AAACTTCACACCGGC CGGGTCCAGC
cg26673609	+	45	1.44e-06	GGGGTGAGG AATCCTCCGAAAAGC GATGGAAGT
cg07265976	+	149	1.44e-06	GGTCACTGCA AAACCGCATACAAGC TCATCAGCAA
cg09368670	-	144	2.64e-06	TCTCAGGAGA AATCCCCTAACAGAGTC AGGTACGGAG
cg12500857	+	145	2.92e-06	TGCGGGGCAC AGACGTCCCAGAACAGC AAACATGCAA
cg18768400	+	44	4.25e-06	CCCGCTGCCA ATTCTCACACAGCC TCAAAGGGAT
cg13936911	+	105	5.25e-06	AAAGCCGCGT AGACCCCACAAACCTC CCGCCCCGGC
cg10280383	+	65	5.25e-06	CTCCCAGAGGG AACGCCAGAGCCGC CGTGATTCCCT

Motif ARWCCYCACASAVGC MEME-12 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg14491776		1.8e-08	65_[+12]_121
cg03983713		1.3e-07	128_[+12]_58
cg22040815		2.2e-07	84_[+12]_102
cg17040924		1.2e-06	112_-[-12]_74
cg10990040		1.2e-06	34_[+12]_152
cg09588770		1.2e-06	87_[+12]_99
cg20128772		1.3e-06	160_-[-12]_26
cg26673609		1.4e-06	44_[+12]_142
cg07265976		1.4e-06	148_[+12]_38
cg09368670		2.6e-06	143_-[-12]_43
cg12500857		2.9e-06	144_[+12]_42
cg18768400		4.3e-06	43_[+12]_143
cg13936911		5.2e-06	104_[+12]_82
cg10280383		5.2e-06	64_[+12]_122

Motif ARWCCYCACASAVGC MEME-12 in BLOCKS format

```
BL MOTIF ARWCCYCACASAVGC width=15 seqs=14
cg14491776      ( 66) AATCCCCACAGACGC 1
cg03983713      ( 129) AGTCCCCACAGAACTC 1
```

```
cg22040815      (  85) AATCCTCAGAGAACCC 1
cg17040924      ( 113) AAAACTTCTTACACGC 1
cg10990040      (  35) AGACCACACAGAGGGC 1
cg09588770      (  88) AGTCTCCTCAGACGC 1
cg20128772      ( 161) AAACTTCACACCCGGC 1
cg26673609      (  45) AATCCTCCGAAAAGC 1
cg07265976      ( 149) AAACCGCATACAAGC 1
cg09368670      ( 144) AATCCCCTAAGAGTC 1
cg12500857      ( 145) AGACGTCCCAGAAAGC 1
cg18768400      (  44) AATTCTCACACAGGCC 1
cg13936911      ( 105) AGACCCCCACAACCTC 1
cg10280383      (   65) AACGCCAGAGGCCGC 1
//
```

---

```
Motif ARWCCYCACASAVGC MEME-12 position-specific scoring matrix
```

---

```
log-odds matrix: alength= 4 w= 15 n= 14025 bayes= 10.5731 E= 1.0e+005
```

```
 242 -1045 -1045 -1045
 178 -1045    19 -1045
 142 -1045 -1045    142
-1045    157 -1045 -138
-1045    104 -113    20
 -138     45 -213    120
-1045    167 -1045 -1045
 178 -113 -1045    20
 -138     87    -55   -39
 242 -1045 -1045 -1045
 -39    -13     87 -1045
 207    -55 -1045 -1045
   94     19    -13 -1045
-1045   -113    104    20
-1045    167 -1045 -1045
```

---

```
Motif ARWCCYCACASAVGC MEME-12 position-specific probability matrix
```

---

```
letter-probability matrix: alength= 4 w= 15 nsites= 14 E= 1.0e+005
```

```
1.000000  0.000000  0.000000  0.000000
0.642857  0.000000  0.357143  0.000000
0.500000  0.000000  0.000000  0.500000
0.000000  0.928571  0.000000  0.071429
0.000000  0.642857  0.142857  0.214286
0.071429  0.428571  0.071429  0.428571
```

```
0.000000 1.000000 0.000000 0.000000
0.642857 0.142857 0.000000 0.214286
0.071429 0.571429 0.214286 0.142857
1.000000 0.000000 0.000000 0.000000
0.142857 0.285714 0.571429 0.000000
0.785714 0.214286 0.000000 0.000000
0.357143 0.357143 0.285714 0.000000
0.000000 0.142857 0.642857 0.214286
0.000000 1.000000 0.000000 0.000000
```

---

```
Motif ARWCCYCACASAVGC MEME-12 regular expression
```

```
A[AG][AT]C[CT][CT]C[AT][CG]A[GC][AC][ACG][GT]C
```

---

Time 220.81 secs.

```
*****
```

```
*****  
MOTIF CBMCTCTCAGGAA MEME-13      width = 13  sites = 6  llr = 85  E-value = 3.3e+005  
*****
```

---

```
Motif CBMCTCTCAGGAA MEME-13 Description
```

---

```
Simplified      A ::7:::::a:::78
pos.-specific   C a337:a:a:::2:
probability     G :3:2:::::aa2:
matrix          T :3:2a:a:::::2
```

```
bits    2.4      * * *
        2.2      * * *
        1.9      * * *
        1.7 *    ***** *
Relative      1.5 *    ***** *
Entropy       1.2 * *    ***** *
(20.5 bits)  1.0 * *    *****
                           0.7 * *    *****
                           0.5 *    *****
                           0.2 *****
                           0.0 -----
```

Multilevel  
consensus  
sequence

CCACTCTCAGGAA  
GC  
T

Motif CBMCTCTCAGGAA MEME-13 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg21813265	+	77	3.27e-08	CATCCTGGTG CGACTCTCAGGAA GTGAGAAAAG
cg25917893	+	151	1.22e-07	GCCGCAGCCA CGCCTCTCAGGAA GGCCACTTCC
cg17862404	-	43	1.72e-07	CGGCTCTGGC CCAGTCTCAGGAA GCCTTACTTG
cg07747690	+	11	2.05e-07	GGTTTCTGGG CCACTCTCAGGAT CAGTCATGAA
cg04156077	-	38	3.59e-07	ATTTACAAAG CTATTCTCAGGCA CATTACTTTA
cg05541867	+	153	4.66e-07	GCGCGCGCGG CTCCCTCTCAGGGA AGTAGGGCTC

Motif CBMCTCTCAGGAA MEME-13 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg21813265		3.3e-08	76_[+13]_112
cg25917893		1.2e-07	150_[+13]_38
cg17862404		1.7e-07	42_-[-13]_146
cg07747690		2.1e-07	10_[+13]_178
cg04156077		3.6e-07	37_-[-13]_151
cg05541867		4.7e-07	152_[+13]_36

Motif CBMCTCTCAGGAA MEME-13 in BLOCKS format

BL MOTIF CBMCTCTCAGGAA width=13 seqs=6

cg21813265 ( 77) CGACTCTCAGGAA 1  
cg25917893 ( 151) CGCCTCTCAGGAA 1  
cg17862404 ( 43) CCAGTCTCAGGAA 1  
cg07747690 ( 11) CCACTCTCAGGAT 1  
cg04156077 ( 38) CTATTCTCAGGCA 1  
cg05541867 ( 153) CTCCCTCTCAGGGA 1

//

Motif CBMCTCTCAGGAA MEME-13 position-specific scoring matrix

log-odds matrix: alength= 4 w= 13 n= 14175 bayes= 10.8643 E= 3.3e+005

-923	167	-923	-923
-923	9	9	84
184	9	-923	-923
-923	109	-91	-16
-923	-923	-923	242
-923	167	-923	-923
-923	-923	-923	242
-923	167	-923	-923
242	-923	-923	-923
-923	-923	167	-923
-923	-923	167	-923
184	-91	-91	-923
216	-923	-923	-16

Motif CBMCTCTCAGGAA MEME-13 position-specific probability matrix

letter-probability matrix: alength= 4 w= 13 nsites= 6 E= 3.3e+005

0.000000	1.000000	0.000000	0.000000
0.000000	0.333333	0.333333	0.333333
0.666667	0.333333	0.000000	0.000000
0.000000	0.666667	0.166667	0.166667
0.000000	0.000000	0.000000	1.000000
0.000000	1.000000	0.000000	0.000000
0.000000	0.000000	0.000000	1.000000
0.000000	1.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.000000	0.000000	1.000000	0.000000
0.000000	0.000000	1.000000	0.000000
0.666667	0.166667	0.166667	0.000000
0.833333	0.000000	0.000000	0.166667

Motif CBMCTCTCAGGAA MEME-13 regular expression

C[CGT][AC]CTCTCAGGAA

Time 236.17 secs.

\*\*\*\*\*

\*\*\*\*\*  
MOTIF TCWTCTAAGAA MEME-14 width = 11 sites = 2 llr = 32 E-value = 5.4e+005  
\*\*\*\*\*

-----  
Motif TCWTCTAAGAA MEME-14 Description

Simplified A ::5:::aa:aa  
pos.-specific C :a:::a:::::  
probability G :::::::a:::  
matrix T a:5a:a:::::

bits 2.4 \* \* \*\*\* \*\*  
2.2 \* \* \*\*\* \*\*  
1.9 \* \* \*\*\* \*\*  
1.7 \*\* \*\*\*\*\*  
  
Relative 1.5 \*\*\*\*\*  
Entropy 1.2 \*\*\*\*\*  
(23.4 bits) 1.0 \*\*\*\*\*  
0.7 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel TCATCTAAGAA  
consensus T  
sequence

-----

Motif TCWTCTAAGAA MEME-14 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg10637260	+	179	9.17e-08	AAGATCCCTG TCATCTAAGAA CTGGCTTCT
cg06840699	+	9	9.17e-08	TCAAGTAC TCTTCTAAGAA CCGCGAAATG

-----

Motif TCWTCTAAGAA MEME-14 block diagrams

-----  
SEQUENCE NAME POSITION P-VALUE MOTIF DIAGRAM

```
-----  
cg10637260          9.2e-08 178_[+14]_12  
cg06840699          9.2e-08 8_[+14]_182  
-----
```

```
Motif TCWTCTAAGAA MEME-14 in BLOCKS format
```

```
BL MOTIF TCWTCTAAGAA width=11 seqs=2  
cg10637260          ( 179) TCATCTAAGAA 1  
cg06840699          (    9) TCTTCTAAGAA 1  
//
```

```
Motif TCWTCTAAGAA MEME-14 position-specific scoring matrix
```

```
log-odds matrix: alength= 4 w= 11 n= 14325 bayes= 12.806 E= 5.4e+005  
-765 -765 -765 242  
-765 167 -765 -765  
142 -765 -765 142  
-765 -765 -765 242  
-765 167 -765 -765  
-765 -765 -765 242  
242 -765 -765 -765  
242 -765 -765 -765  
-765 -765 167 -765  
242 -765 -765 -765  
242 -765 -765 -765
```

```
Motif TCWTCTAAGAA MEME-14 position-specific probability matrix
```

```
letter-probability matrix: alength= 4 w= 11 nsites= 2 E= 5.4e+005  
0.000000 0.000000 0.000000 1.000000  
0.000000 1.000000 0.000000 0.000000  
0.500000 0.000000 0.000000 0.500000  
0.000000 0.000000 0.000000 1.000000  
0.000000 1.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 1.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000
```

Motif TCWTCTAAGAA MEME-14 regular expression

TC[AT]TCTAAGAA

Time 251.39 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF TGTGAAAT MEME-15 width = 8 sites = 2 llr = 25 E-value = 8.2e+005

\*\*\*\*\*

Motif TGTGAAAT MEME-15 Description

Simplified      A    ::::aaa:  
pos.-specific    C    :::::::  
probability     G    :a:a:::  
matrix           T    a:a:::a

bits    2.4 \* \* \*\*\*\*  
      2.2 \* \* \*\*\*\*  
      1.9 \* \* \*\*\*\*  
      1.7 \*\*\*\*\*  
Relative      1.5 \*\*\*\*\*  
Entropy       1.2 \*\*\*\*\*  
(17.9 bits) 1.0 \*\*\*\*\*  
             0.7 \*\*\*\*\*  
             0.5 \*\*\*\*\*  
             0.2 \*\*\*\*\*  
             0.0 -----

Multilevel            TGTGAAAT  
consensus  
sequence

Motif TGTGAAAT MEME-15 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg02632822	+	17	4.19e-06	AATGGTGTTC TGTGAAAT TCAGTATGGG
cg01277910	-	110	4.19e-06	GGATGATGCG TGTGAAAT ACTCCATGCG

Motif TGTGAAAT MEME-15 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg02632822		4.2e-06	16_[+15]_177
cg01277910		4.2e-06	109_[-15]_84

Motif TGTGAAAT MEME-15 in BLOCKS format

```
BL MOTIF TGTGAAAT width=8 seqs=2
cg02632822      ( 17) TGTGAAAT 1
cg01277910      ( 110) TGTGAAAT 1
//
```

Motif TGTGAAAT MEME-15 position-specific scoring matrix

```
log-odds matrix: alength= 4 w= 8 n= 14550 bayes= 12.8285 E= 8.2e+005
 -765 -765 -765 242
 -765 -765 167 -765
 -765 -765 242 -765
 -765 -765 167 -765
 242 -765 -765 -765
 242 -765 -765 -765
 242 -765 -765 -765
 -765 -765 -765 242
```

Motif TGTGAAAT MEME-15 position-specific probability matrix

```
letter-probability matrix: alength= 4 w= 8 nsites= 2 E= 8.2e+005
 0.000000 0.000000 0.000000 1.000000
 0.000000 0.000000 1.000000 0.000000
 0.000000 0.000000 0.000000 1.000000
```

```
0.000000 0.000000 1.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000
```

---

```
Motif TGTGAAAT MEME-15 regular expression
```

```
TGTGAAAT
```

---

Time 266.61 secs.

```
*****
```

```
*****  
MOTIF ATCTAGARAA MEME-16 width = 10 sites = 2 llr = 30 E-value = 8.4e+005  
*****
```

```
Motif ATCTAGARAA MEME-16 Description
```

---

```
Simplified      A a::::a:a5aa  
pos.-specific   C ::a:::::::  
probability     G :::::a:5:::  
matrix          T :a:a:::::::
```

```
bits    2.4 ** ** * **  
       2.2 ** ** * **  
       1.9 ** ** * **  
       1.7 ***** **  
Relative      1.5 ***** **  
Entropy       1.2 ***** **  
(21.3 bits)  1.0 *****  
               0.7 *****  
               0.5 *****  
               0.2 *****  
               0.0 -----
```

```
Multilevel      ATCTAGAAAA  
consensus           G  
sequence
```

Motif ATCTAGARAA MEME-16 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg17040924	-	192	1.46e-07	. ATCTAGAAAAA GTCCTAAGCC
cg09588770	+	19	3.92e-07	GGTATTGGAT ATCTAGAGAA GCCAATCAGC

Motif ATCTAGARAA MEME-16 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg17040924		1.5e-07	191_-[-16]
cg09588770		3.9e-07	18_+[+16]_173

Motif ATCTAGARAA MEME-16 in BLOCKS format

```
BL MOTIF ATCTAGARAA width=10 seqs=2
cg17040924      ( 192) ATCTAGAAAA  1
cg09588770      (   19) ATCTAGAGAA 1
//
```

Motif ATCTAGARAA MEME-16 position-specific scoring matrix

log-odds matrix: alength= 4 w= 10 n= 14400 bayes= 12.8136 E= 8.4e+005

242	-765	-765	-765
-765	-765	-765	242
-765	167	-765	-765
-765	-765	-765	242
242	-765	-765	-765
-765	-765	167	-765
242	-765	-765	-765
142	-765	67	-765
242	-765	-765	-765
242	-765	-765	-765

Motif ATCTAGARAA MEME-16 position-specific probability matrix

letter-probability matrix: alength= 4 w= 10 nsites= 2 E= 8.4e+005  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 1.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 1.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.500000 0.000000 0.500000 0.000000  
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000

Motif ATCTAGARAA MEME-16 regular expression

ATCTAGA[AG]AA

Time 281.81 secs.

\*\*\*\*\*  
\*\*\*\*\*

\*\*\*\*\*  
\*\*\*\*\*  
MOTIF ATAAWAT MEME-17 width = 7 sites = 2 llr = 22 E-value = 8.4e+005  
\*\*\*\*\*  
\*\*\*\*\*

Motif ATAAWAT MEME-17 Description

Simplified A a:aa5a:  
pos.-specific C :::::::  
probability G :::::::  
matrix T :a::5:a

bits 2.4 \*\*\*\* \*\*  
2.2 \*\*\*\* \*\*  
1.9 \*\*\*\* \*\*  
1.7 \*\*\*\* \*\*

Relative Entropy 1.5 \*\*\*\*\*  
Entropy 1.2 \*\*\*\*\*

(16.0 bits) 1.0 \*\*\*\*\*  
0.7 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel ATAAAAT  
consensus T  
sequence

Motif ATAAWAT MEME-17 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg20667822	+	128	1.60e-05	GTAGCTGACT ATAAAAT GATTTTATCA
cg02573152	+	8	1.60e-05	GCCTGGA ATAATAT AGGAGGCTT

Motif ATAAWAT MEME-17 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg20667822		1.6e-05	127_[+17]_67
cg02573152		1.6e-05	7_[+17]_187

Motif ATAAWAT MEME-17 in BLOCKS format

BL MOTIF ATAAWAT width=7 seqs=2  
cg20667822 ( 128) ATAAAAT 1  
cg02573152 ( 8) ATAATAT 1  
//

Motif ATAAWAT MEME-17 position-specific scoring matrix

log-odds matrix: alength= 4 w= 7 n= 14625 bayes= 12.836 E= 8.4e+005  
242 -765 -765 -765  
-765 -765 -765 242  
242 -765 -765 -765

```
242 -765 -765 -765  
142 -765 -765 142  
242 -765 -765 -765  
-765 -765 -765 242
```

---

---

Motif ATAAWAT MEME-17 position-specific probability matrix

---

letter-probability matrix: alength= 4 w= 7 nsites= 2 E= 8.4e+005

```
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.500000 0.000000 0.000000 0.500000  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000
```

---

---

Motif ATAAWAT MEME-17 regular expression

---

ATAA[AT]AT

---

Time 297.07 secs.

```
*****
```

```
*****  
MOTIF CTGACCACTGAYCAC MEME-18 width = 15 sites = 4 llr = 70 E-value = 9.9e+005  
*****
```

---

Motif CTGACCACTGAYCAC MEME-18 Description

---

Simplified A :3::a::a:38::a:  
pos.-specific C a::a:aa:a::5a:a  
probability G ::8:::::83::::  
matrix T :83:::::5:::

bits	2.4	*	*	*
	2.2	*	*	*
	1.9	*	*	*

Relative Entropy (25.2 bits)

1.7	*****	***
1.5	** *****	* ***
1.2	** *****	* ***
1.0	*****	*****
0.7	*****	*****
0.5	*****	*****
0.2	*****	*****
0.0	- - - - -	

Multilevel consensus sequence

CTGCACCACGACCAC	
AT	AGT

---

Motif CTGCACCACGAYCAC MEME-18 sites sorted by position p-value

---

Sequence name	Strand	Start	P-value	Site
cg03796003	+	108	1.23e-09	GGCGCCGTCC CTGCACCACGATCAC TCAGAATGGA
cg17775727	+	63	3.30e-09	GGTCTTCCA CTGCACCACGACCAC CTACGGCATT
cg05541867	+	107	1.45e-08	GACCGCATAAC CATCACCACGATCAC CACAGAGCCG
cg22973789	+	2	3.03e-08	G CTGCACCACAGCCAC ACAAACTTCC

---

Motif CTGCACCACGAYCAC MEME-18 block diagrams

---

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg03796003		1.2e-09	107_[+18]_79
cg17775727		3.3e-09	62_[+18]_124
cg05541867		1.5e-08	106_[+18]_80
cg22973789		3e-08	1_[+18]_185

---

Motif CTGCACCACGAYCAC MEME-18 in BLOCKS format

---

BL	MOTIF	CTGCACCACGAYCAC	width=15	seqs=4
cg03796003	( 108)	CTGCACCACGATCAC	1	
cg17775727	( 63)	CTGCACCACGACCAC	1	
cg05541867	( 107)	CATCACCACGATCAC	1	
cg22973789	( 2)	CTGCACCACAGCCAC	1	
//				

Motif CTGCACCACGAYCAC MEME-18 position-specific scoring matrix

log-odds matrix: alength= 4 w= 15 n= 14025 bayes= 11.7753 E= 9.9e+005

-865	167	-865	-865
42	-865	-865	200
-865	-865	126	42
-865	167	-865	-865
242	-865	-865	-865
-865	167	-865	-865
-865	167	-865	-865
242	-865	-865	-865
-865	167	-865	-865
42	-865	126	-865
200	-865	-33	-865
-865	67	-865	142
-865	167	-865	-865
242	-865	-865	-865
-865	167	-865	-865

Motif CTGCACCACGAYCAC MEME-18 position-specific probability matrix

letter-probability matrix: alength= 4 w= 15 nsites= 4 E= 9.9e+005

0.000000	1.000000	0.000000	0.000000
0.250000	0.000000	0.000000	0.750000
0.000000	0.000000	0.750000	0.250000
0.000000	1.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000
0.250000	0.000000	0.750000	0.000000
0.750000	0.000000	0.250000	0.000000
0.000000	0.500000	0.000000	0.500000
0.000000	1.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000

Motif CTGCACCACGAYCAC MEME-18 regular expression

C[TA][GT]CACCAC[GA][AG][CT]CAC

---

Time 312.35 secs.

\*\*\*\*\*

\*\*\*\*\*  
MOTIF AGASACATTCA MEME-19 width = 11 sites = 2 llr = 31 E-value = 1.0e+006  
\*\*\*\*\*

---

Motif AGASACATTCA MEME-19 Description

---

Simplified A a:a:a:a::::a  
pos.-specific C ::::5:a::::a:  
probability G :a:5:::::::  
matrix T ::::::aa:::

bits 2.4 \* \* \* \*\*\* \*  
2.2 \* \* \* \*\*\* \*  
1.9 \* \* \* \*\*\* \*  
1.7 \*\*\* \*\*\*\*\*  
Relative 1.5 \*\*\* \*\*\*\*\*  
Entropy 1.2 \*\*\* \*\*\*\*\*  
(22.6 bits) 1.0 \*\*\* \*\*\*\*\*  
0.7 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel AGACACATTCA  
consensus G  
sequence

---

---

Motif AGASACATTCA MEME-19 sites sorted by position p-value

---

Sequence name	Strand	Start	P-value	Site
cg08590601	+	31	1.53e-07	GGAGATGCC AGACACATTCA TGCGCTGCGC
cg03796003	+	176	1.53e-07	GTGATGGCAC AGAGACATTCA CCACCCTTGG

Motif AGASACATTCA MEME-19 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
---------------	----------	---------	---------------

cg08590601		1.5e-07	30_[+19]_160
cg03796003		1.5e-07	175_[+19]_15

Motif AGASACATTCA MEME-19 in BLOCKS format

```
BL MOTIF AGASACATTCA width=11 seqs=2
cg08590601      ( 31) AGACACATTCA 1
cg03796003      ( 176) AGAGACATTCA 1
//
```

Motif AGASACATTCA MEME-19 position-specific scoring matrix

```
log-odds matrix: alength= 4 w= 11 n= 14325 bayes= 12.806 E= 1.0e+006
 242   -765   -765   -765
 -765   -765    167   -765
 242   -765   -765   -765
 -765     67     67   -765
 242   -765   -765   -765
 -765    167   -765   -765
 242   -765   -765   -765
 -765   -765   -765    242
 -765   -765   -765    242
 -765    167   -765   -765
 242   -765   -765   -765
```

Motif AGASACATTCA MEME-19 position-specific probability matrix

```
letter-probability matrix: alength= 4 w= 11 nsites= 2 E= 1.0e+006
 1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000
 1.000000  0.000000  0.000000  0.000000
 0.000000  0.500000  0.500000  0.000000
 1.000000  0.000000  0.000000  0.000000
```

```
0.000000 1.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 1.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000
```

---

```
Motif AGASACATTCA MEME-19 regular expression
```

```
AGA[CG]ACATTCA
```

---

Time 327.39 secs.

```
*****
```

```
*****  
MOTIF TTMTTCCTCTYAMA MEME-20      width = 14  sites = 2  llr = 38  E-value = 1.6e+006  
*****
```

---

```
Motif TTMTTCCTCTYAMA MEME-20 Description
```

```
Simplified      A  ::5::::::::::a5a  
pos.-specific   C  ::5::aa:a:5:5:  
probability     G  :::::::::::::::  
matrix          T  aa:aa:::a:a5:::
```

```
bits      2.4 ** ** * * *  
          2.2 ** ** * * *  
          1.9 ** ** * * *  
          1.7 ** ***** * *  
Relative      1.5 ** ***** * *  
Entropy       1.2 ** ***** * *  
(27.5 bits)  1.0 *****  
          0.7 *****  
          0.5 *****  
          0.2 *****  
          0.0 -----
```

```
Multilevel      TTATTCCTCTCAAA  
consensus        C          T C
```

sequence

Motif TTMTTCCTCTYAMA MEME-20 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg10637260	+	63	1.81e-09	CCTCACCCAG TTATTCTCTCAA TCCCTCTGC
cg25613667	-	167	4.33e-09	CTCCGGGACG TTCTCCTCTTACA GGAGAGGTGG

Motif TTMTTCCTCTYAMA MEME-20 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg10637260		1.8e-09	62_[+20]_125
cg25613667		4.3e-09	166_[-20]_21

Motif TTMTTCCTCTYAMA MEME-20 in BLOCKS format

BL MOTIF TTMTTCCTCTYAMA width=14 seqs=2  
cg10637260 ( 63) TTATTCTCTCAA 1  
cg25613667 ( 167) TTCTCCTCTTACA 1  
//

Motif TTMTTCCTCTYAMA MEME-20 position-specific scoring matrix

log-odds matrix: alength= 4 w= 14 n= 14100 bayes= 12.7832 E= 1.6e+006

-765	-765	-765	242
-765	-765	-765	242
142	67	-765	-765
-765	-765	-765	242
-765	-765	-765	242
-765	167	-765	-765
-765	167	-765	-765
-765	-765	-765	242
-765	167	-765	-765
-765	-765	-765	242
-765	67	-765	142

```
242 -765 -765 -765  
142 67 -765 -765  
242 -765 -765 -765
```

```
-----  
Motif TTMTTCCTCTYAMA MEME-20 position-specific probability matrix
```

```
-----  
letter-probability matrix: alength= 4 w= 14 nsites= 2 E= 1.6e+006
```

```
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.000000 1.000000  
0.500000 0.500000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 1.000000 0.000000 0.000000  
0.000000 1.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 1.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.500000 0.000000 0.500000  
1.000000 0.000000 0.000000 0.000000  
0.500000 0.500000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000
```

```
-----  
Motif TTMTTCCTCTYAMA MEME-20 regular expression
```

```
-----  
TT[AC]TTCCTCT[CT]A[AC]A
```

Time 342.30 secs.

```
*****
```

```
*****
```

```
MOTIF AAATGA MEME-21 width = 6 sites = 2 llr = 19 E-value = 1.5e+006
```

```
*****
```

```
-----  
Motif AAATGA MEME-21 Description
```

```
-----  
Simplified A aaa::a  
pos.-specific C ::::::
```

probability      G    ::::a:  
matrix            T    ::::a:::  
  
bits    2.4 \*\*\*\* \*  
       2.2 \*\*\*\* \*  
       1.9 \*\*\*\* \*  
       1.7 \*\*\*\*\*  
  
Relative        1.5 \*\*\*\*\*  
Entropy        1.2 \*\*\*\*\*  
(13.8 bits) 1.0 \*\*\*\*\*  
          0.7 \*\*\*\*\*  
          0.5 \*\*\*\*\*  
          0.2 \*\*\*\*\*  
          0.0 -----  
  
Multilevel      AAATGA  
consensus  
sequence

---

---

Motif AAATGA MEME-21 sites sorted by position p-value

---

Sequence name	Strand	Start	P-value	Site
cg22040815	+	179	7.16e-05	GTA <u>G</u> T <u>C</u> GAG AAATGA GCAAGCGGCC
cg14685095	+	16	7.16e-05	ACCCGAGAGG AAATGA GGTCCC <u>T</u> GG

---

---

Motif AAATGA MEME-21 block diagrams

---

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg22040815		7.2e-05	178_[+21]_17
cg14685095		7.2e-05	15_[+21]_180

---

---

Motif AAATGA MEME-21 in BLOCKS format

---

BL MOTIF AAATGA width=6 seqs=2  
cg22040815        ( 179) AAATGA 1  
cg14685095        ( 16) AAATGA 1  
//

Motif AAATGA MEME-21 position-specific scoring matrix

log-odds matrix: alength= 4 w= 6 n= 14700 bayes= 12.8433 E= 1.5e+006

242	-765	-765	-765
242	-765	-765	-765
242	-765	-765	-765
-765	-765	-765	242
-765	-765	167	-765
242	-765	-765	-765

Motif AAATGA MEME-21 position-specific probability matrix

letter-probability matrix: alength= 4 w= 6 nsites= 2 E= 1.5e+006

1.000000	0.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	1.000000
0.000000	0.000000	1.000000	0.000000
1.000000	0.000000	0.000000	0.000000

Motif AAATGA MEME-21 regular expression

AAATGA

Time 357.15 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF AACTSATGAA MEME-22 width = 10 sites = 2 llr = 29 E-value = 9.6e+005

\*\*\*\*\*

Motif AACTSATGAA MEME-22 Description

Simplified      A aa:::a::aa

pos.-specific C ::a:5:::::  
probability G ::::5::a:::  
matrix T ::::a::a:::  
  
bits 2.4 \*\* \* \*\* \*\*  
2.2 \*\* \* \*\* \*\*  
1.9 \*\* \* \*\* \*\*  
1.7 \*\*\*\*\* \*\*\*\*\*  
Relative 1.5 \*\*\*\*\* \*\*\*\*\*  
Entropy 1.2 \*\*\*\*\* \*\*\*\*\*  
(21.0 bits) 1.0 \*\*\*\*\* \*\*\*\*\*  
0.7 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel AACTCATGAA  
consensus G  
sequence

---

Motif AACTSATGAA MEME-22 sites sorted by position p-value

---

Sequence name	Strand	Start	P-value	Site
cg22780612	+	18	4.90e-07	GAGCGGCTGG AACTCATGAA CGCAGAGCTG
cg00896220	+	115	4.90e-07	AATGCCACAG AACTGATGAA TGGCACTGCC

---

---

Motif AACTSATGAA MEME-22 block diagrams

---

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg22780612		4.9e-07	17_[+22]_174
cg00896220		4.9e-07	114_[+22]_77

---

---

Motif AACTSATGAA MEME-22 in BLOCKS format

---

BL MOTIF AACTSATGAA width=10 seqs=2  
cg22780612 ( 18) AACTCATGAA 1  
cg00896220 ( 115) AACTGATGAA 1  
//

Motif AACTSATGAA MEME-22 position-specific scoring matrix

log-odds matrix: alength= 4 w= 10 n= 14400 bayes= 12.8136 E= 9.6e+005

242	-765	-765	-765
242	-765	-765	-765
-765	167	-765	-765
-765	-765	-765	242
-765	67	67	-765
242	-765	-765	-765
-765	-765	-765	242
-765	-765	167	-765
242	-765	-765	-765
242	-765	-765	-765

Motif AACTSATGAA MEME-22 position-specific probability matrix

letter-probability matrix: alength= 4 w= 10 nsites= 2 E= 9.6e+005

1.000000	0.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000
0.000000	0.000000	0.000000	1.000000
0.000000	0.500000	0.500000	0.000000
1.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	1.000000
0.000000	0.000000	1.000000	0.000000
1.000000	0.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000

Motif AACTSATGAA MEME-22 regular expression

AACT[CG]ATGAA

Time 371.95 secs.

\*\*\*\*\*

```
*****  
MOTIF TTTGCACTGCT MEME-23      width = 11 sites = 2 llr = 32 E-value = 1.0e+006  
*****
```

```
-----  
Motif TTTGCACTGCT MEME-23 Description
```

```
Simplified      A ::::::a:::::  
pos.-specific   C ::::::a:a:::a:  
probability     G ::::a:::::a:::  
matrix          T aaa:::::a:::a
```

```
bits    2.4 *** * * *  
       2.2 *** * * *  
       1.9 *** * * *  
       1.7 *****  
  
Relative Entropy  
(22.9 bits)  1.5 *****  
              1.2 *****  
              1.0 *****  
              0.7 *****  
              0.5 *****  
              0.2 *****  
              0.0 -----
```

```
Multilevel      TTTGCACTGCT  
consensus  
sequence
```

```
-----  
Motif TTTGCACTGCT MEME-23 sites sorted by position p-value
```

Sequence name	Strand	Start	P-value	Site
cg21380181	+	31	1.28e-07	GGAGGGTGGC TTTGCACTGCT GATCTGAACA
cg11847597	+	107	1.28e-07	TTCCGTCACA TTTGCACTGCT TCCCTCGTGA

```
-----  
Motif TTTGCACTGCT MEME-23 block diagrams
```

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg21380181		1.3e-07	30_[+23]_160
cg11847597		1.3e-07	106_[+23]_84

Motif TTTGCACTGCT MEME-23 in BLOCKS format

```
BL MOTIF TTTGCACTGCT width=11 seqs=2
cg21380181      ( 31) TTTGCACTGCT 1
cg11847597      ( 107) TTTGCACTGCT 1
//
```

Motif TTTGCACTGCT MEME-23 position-specific scoring matrix

```
log-odds matrix: alength= 4 w= 11 n= 14325 bayes= 12.806 E= 1.0e+006
-765 -765 -765 242
-765 -765 -765 242
-765 -765 -765 242
-765 -765 167 -765
-765 167 -765 -765
242 -765 -765 -765
-765 167 -765 -765
-765 -765 -765 242
-765 -765 167 -765
-765 167 -765 -765
-765 -765 -765 242
```

Motif TTTGCACTGCT MEME-23 position-specific probability matrix

```
letter-probability matrix: alength= 4 w= 11 nsites= 2 E= 1.0e+006
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 1.000000 0.000000
0.000000 1.000000 0.000000 0.000000
1.000000 0.000000 0.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 1.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 0.000000 0.000000 1.000000
```

Motif TTTGCACTGCT MEME-23 regular expression

-----  
TTTGCACTGCT  
-----

Time 386.71 secs.

\*\*\*\*\*  
\*\*\*\*\*

\*\*\*\*\*  
\*\*\*\*\*  
MOTIF AGCTATTKTT MEME-24 width = 10 sites = 2 llr = 30 E-value = 8.4e+005  
\*\*\*\*\*  
\*\*\*\*\*

-----  
Motif AGCTATTKTT MEME-24 Description

Simplified A a:::a:::::  
pos.-specific C ::a:::::::  
probability G :a:::::5:::  
matrix T ::::a:aa5aa

bits 2.4 \* \*\*\*\* \*\*  
2.2 \* \*\*\*\* \*\*  
1.9 \* \*\*\*\* \*\*  
1.7 \*\*\*\*\* \*\*  
Relative 1.5 \*\*\*\*\* \*\*  
Entropy 1.2 \*\*\*\*\* \*\*  
(21.3 bits) 1.0 \*\*\*\*\*  
0.7 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel AGCTATTGTT  
consensus T  
sequence

-----  
Motif AGCTATTKTT MEME-24 sites sorted by position p-value

Sequence name Strand Start P-value Site  
----- ----- ----- -----

```
cg24872610      -    191  1.46e-07          A AGCTATTTT AGCACTTG  
cg07724977      +    192  3.92e-07 TCTAAGGAGT AGCTATTGTT
```

---

Motif AGCTATTKTT MEME-24 block diagrams

---

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg24872610		1.5e-07	190_-[-24]_1
cg07724977		3.9e-07	191_[+24]

---

---

Motif AGCTATTKTT MEME-24 in BLOCKS format

---

```
BL MOTIF AGCTATTKTT width=10 seqs=2  
cg24872610      ( 191) AGCTATTTT  1  
cg07724977      ( 192) AGCTATTGTT 1  
//
```

---

---

Motif AGCTATTKTT MEME-24 position-specific scoring matrix

---

```
log-odds matrix: alength= 4 w= 10 n= 14400 bayes= 12.8136 E= 8.4e+005  
 242  -765  -765  -765  
-765  -765  167  -765  
-765  167  -765  -765  
-765  -765  -765  242  
 242  -765  -765  -765  
-765  -765  -765  242  
-765  -765  -765  242  
-765  -765   67  142  
-765  -765  -765  242  
-765  -765  -765  242
```

---

---

Motif AGCTATTKTT MEME-24 position-specific probability matrix

---

```
letter-probability matrix: alength= 4 w= 10 nsites= 2 E= 8.4e+005  
1.000000  0.000000  0.000000  0.000000  
0.000000  0.000000  1.000000  0.000000  
0.000000  1.000000  0.000000  0.000000  
0.000000  0.000000  0.000000  1.000000
```

```
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.500000 0.500000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.000000 1.000000
```

---

```
Motif AGCTATTKTT MEME-24 regular expression
```

```
AGCTATT[GT]TT
```

---

Time 401.37 secs.

```
*****
```

```
*****
```

```
MOTIF TTTWGAAT MEME-25 width = 8 sites = 2 llr = 24 E-value = 9.6e+005
```

```
*****
```

```
Motif TTTWGAAT MEME-25 Description
```

```
Simplified      A ::::5:aa:  
pos.-specific   C :::::::  
probability     G :::::a:::  
matrix          T aaa5:::a
```

```
bits      2.4 *** ***  
          2.2 *** ***  
          1.9 *** ***  
          1.7 *** ****  
Relative      1.5 *****  
Entropy       1.2 *****  
(17.6 bits) 1.0 *****  
          0.7 *****  
          0.5 *****  
          0.2 *****  
          0.0 -----
```

```
Multilevel      TTTAGAAT  
consensus        T
```

sequence

Motif TTTWGAAT MEME-25 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg21380181	-	65	5.01e-06	CAAAAGGACG TTTTGAAT CAGTGAGAGG
cg00957886	+	31	5.01e-06	AAGCCTGACA TTTAGAAT TCAACTTCAA

Motif TTTWGAAT MEME-25 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg21380181		5e-06	64_-[-25]_129
cg00957886		5e-06	30_+[+25]_163

Motif TTTWGAAT MEME-25 in BLOCKS format

```
BL MOTIF TTTWGAAT width=8 seqs=2
cg21380181      ( 65) TTTTGAAT 1
cg00957886      ( 31) TTTAGAAT 1
//
```

Motif TTTWGAAT MEME-25 position-specific scoring matrix

log-odds matrix: alength= 4 w= 8 n= 14550 bayes= 12.8285 E= 9.6e+005

-765	-765	-765	242
-765	-765	-765	242
-765	-765	-765	242
142	-765	-765	142
-765	-765	167	-765
242	-765	-765	-765
242	-765	-765	-765
-765	-765	-765	242

Motif TTTWGAAT MEME-25 position-specific probability matrix

```
-----  
letter-probability matrix: alength= 4 w= 8 nsites= 2 E= 9.6e+005  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.000000 1.000000  
0.500000 0.000000 0.000000 0.500000  
0.000000 0.000000 1.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
-----
```

Motif TTTWGAAT MEME-25 regular expression

```
-----  
TTT[AT]GAAT  
-----
```

Time 415.95 secs.

```
*****  
*****
```

```
*****  
*****  
MOTIF AAWCTTGAGCA MEME-26 width = 11 sites = 2 llr = 31 E-value = 1.2e+006  
*****  
*****
```

Motif AAWCTTGAGCA MEME-26 Description

```
-----  
Simplified pos.-specific probability matrix  
A aa5::::a:::a  
C ::::a::::::a:  
G :::::::a:a:::  
T :::5:aa:::::  
  
bits 2.4 ** ** * *  
      2.2 ** ** * *  
      1.9 ** ** * *  
      1.7 ** *****  
  
Relative Entropy (22.6 bits)  
1.5 *****  
1.2 *****  
1.0 *****  
0.7 *****  
0.5 *****  
-----
```

0.2 \*\*\*\*\*  
0.0 -----

Multilevel  
consensus  
sequence

AAACTTGAGCA  
T

Motif AAWCTTGAGCA MEME-26 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg21813265	+	43	1.53e-07	AAGCGTCAGG AAACATTGAGCA TAAACACCCC
cg00896220	+	27	1.53e-07	ATCCTTACCAT AATCTTGAGCA GGGGTGTCTA

Motif AAWCTTGAGCA MEME-26 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg21813265		1.5e-07	42_[+26]_148
cg00896220		1.5e-07	26_[+26]_164

Motif AAWCTTGAGCA MEME-26 in BLOCKS format

BL MOTIF AAWCTTGAGCA width=11 seqs=2  
cg21813265 ( 43) AAACATTGAGCA 1  
cg00896220 ( 27) AATCTTGAGCA 1  
//

Motif AAWCTTGAGCA MEME-26 position-specific scoring matrix

log-odds matrix: alength= 4 w= 11 n= 14325 bayes= 12.806 E= 1.2e+006  
242 -765 -765 -765  
242 -765 -765 -765  
142 -765 -765 142  
-765 167 -765 -765  
-765 -765 -765 242  
-765 -765 -765 242

```
-765 -765 167 -765  
242 -765 -765 -765  
-765 -765 167 -765  
-765 167 -765 -765  
242 -765 -765 -765
```

---

---

Motif AAWCTTGAGCA MEME-26 position-specific probability matrix

---

letter-probability matrix: alength= 4 w= 11 nsites= 2 E= 1.2e+006

```
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.500000 0.000000 0.000000 0.500000  
0.000000 1.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 0.000000 1.000000  
0.000000 0.000000 1.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 1.000000 0.000000  
0.000000 1.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000
```

---

---

Motif AAWCTTGAGCA MEME-26 regular expression

---

AA[AT]CTTGAGCA

---

Time 430.47 secs.

```
*****
```

```
*****
```

MOTIF AATAWCCTT MEME-27 width = 9 sites = 2 llr = 27 E-value = 1.0e+006

```
*****
```

---

Motif AATAWCCTT MEME-27 Description

---

Simplified        A aa:a5::::  
pos.-specific    C :::::aa:::  
probability      G ::::::::::::

matrix T ::a::5::aa

bits 2.4 \*\*\*\* \*\*  
2.2 \*\*\*\* \*\*  
1.9 \*\*\*\* \*\*  
1.7 \*\*\*\* \*\*\*  
Relative 1.5 \*\*\*\*\*  
Entropy 1.2 \*\*\*\*\*  
(19.3 bits) 1.0 \*\*\*\*\*  
0.7 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel AATAACCTT  
consensus T  
sequence

Motif AATAWCCTT MEME-27 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg19931348	-	102	1.57e-06	TGACTTGCTG AATAACCTT CGGTGATTCC
cg16139664	+	67	1.57e-06	TCTCCTCCCC AATATCCTT CGATGCTCCT

Motif AATAWCCTT MEME-27 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg19931348		1.6e-06	101_-[-27]_91
cg16139664		1.6e-06	66_+[+27]_126

Motif AATAWCCTT MEME-27 in BLOCKS format

BL MOTIF AATAWCCTT width=9 seqs=2  
cg19931348 ( 102) AATAACCTT 1  
cg16139664 ( 67) AATATCCTT 1  
//

Motif AATAWCCTT MEME-27 position-specific scoring matrix

log-odds matrix: alength= 4 w= 9 n= 14475 bayes= 12.8211 E= 1.0e+006

242	-765	-765	-765
242	-765	-765	-765
-765	-765	-765	242
242	-765	-765	-765
142	-765	-765	142
-765	167	-765	-765
-765	167	-765	-765
-765	-765	-765	242
-765	-765	-765	242

Motif AATAWCCTT MEME-27 position-specific probability matrix

letter-probability matrix: alength= 4 w= 9 nsites= 2 E= 1.0e+006

1.000000	0.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	1.000000
1.000000	0.000000	0.000000	0.000000
0.500000	0.000000	0.000000	0.500000
0.000000	1.000000	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000
0.000000	0.000000	0.000000	1.000000
0.000000	0.000000	0.000000	1.000000

Motif AATAWCCTT MEME-27 regular expression

AATA[AT]CCTT

Time 444.98 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF ATRAMGTAAT MEME-28 width = 10 sites = 2 llr = 29 E-value = 1.6e+006

\*\*\*\*\*

Motif ATRAMGTAAT MEME-28 Description

Simplified            A    a:5a5::aa:  
pos.-specific      C    ::::5:::::  
probability        G    ::5::a::::  
matrix              T    :a::::a::a

bits      2.4 \*\*\* \*    \*\*\*  
            2.2 \*\* \*    \*\*\*  
            1.9 \*\* \*    \*\*\*  
            1.7 \*\* \*    \*\*\*\*  
Relative     1.5 \*\* \*    \*\*\*\*\*  
Entropy      1.2 \*\* \*    \*\*\*\*\*  
(20.7 bits) 1.0 \*\*\*\*\*  
            0.7 \*\*\*\*\*  
            0.5 \*\*\*\*\*  
            0.2 \*\*\*\*\*  
            0.0 -----

Multilevel            ATAAAGTAAT  
consensus            G C  
sequence

Motif ATRAMGTAAT MEME-28 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg04156077	+	27	8.75e-08	GAAATCTAAG ATAAAGTAAT GTGCCTGAGA
cg16139664	+	97	6.26e-07	GCCCTCCTTG ATGACGTAAT CATCGCGAGG

Motif ATRAMGTAAT MEME-28 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg04156077		8.8e-08	26_[+28]_165
cg16139664		6.3e-07	96_[+28]_95

Motif ATRAMGTAAT MEME-28 in BLOCKS format

```
-----  
BL MOTIF ATRAMGTAAT width=10 seqs=2  
cg04156077 ( 27) ATAAAGTAAT 1  
cg16139664 ( 97) ATGACGTAAT 1  
//
```

---

```
-----  
Motif ATRAMGTAAT MEME-28 position-specific scoring matrix
```

---

```
log-odds matrix: alength= 4 w= 10 n= 14400 bayes= 12.8136 E= 1.6e+006  
242 -765 -765 -765  
-765 -765 -765 242  
142 -765 67 -765  
242 -765 -765 -765  
142 67 -765 -765  
-765 -765 167 -765  
-765 -765 -765 242  
242 -765 -765 -765  
242 -765 -765 -765  
-765 -765 -765 242
```

---

```
-----  
Motif ATRAMGTAAT MEME-28 position-specific probability matrix
```

---

```
letter-probability matrix: alength= 4 w= 10 nsites= 2 E= 1.6e+006  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
0.500000 0.000000 0.500000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.500000 0.500000 0.000000 0.000000  
0.000000 0.000000 1.000000 0.000000  
0.000000 0.000000 0.000000 1.000000  
1.000000 0.000000 0.000000 0.000000  
1.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 1.000000
```

---

```
-----  
Motif ATRAMGTAAT MEME-28 regular expression
```

---

```
AT[AG]A[AC]GTAAT
```

---

Time 459.42 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF TWTTAWTT MEME-29 width = 8 sites = 2 llr = 24 E-value = 1.1e+006

\*\*\*\*\*

-----  
Motif TWTTAWTT MEME-29 Description

Simplified A :5::a5:::  
pos.-specific C :::::::  
probability G :::::::  
matrix T a5aa:5aa

bits 2.4 \* \*\*\* \*\*  
2.2 \* \*\*\* \*\*  
1.9 \* \*\*\* \*\*  
1.7 \* \*\*\* \*\*  
Relative 1.5 \*\*\*\*\*  
Entropy 1.2 \*\*\*\*\*  
(17.4 bits) 1.0 \*\*\*\*\*  
0.7 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel TATTAATT  
consensus T T  
sequence

-----  
Motif TWTTAWTT MEME-29 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
cg27099625	-	32	5.98e-06	CCGTATAACGG TTTTATT AGGCAGGTGA
cg02632822	+	163	5.98e-06	TATAGATCCA TATTAATT TTGGGGTGTT

-----  
Motif TWTTAWTT MEME-29 block diagrams

```
-----  
SEQUENCE NAME      POSITION P-VALUE MOTIF DIAGRAM  
-----  
cg27099625          6e-06  31_[-29]_162  
cg02632822          6e-06  162_[+29]_31  
-----
```

```
Motif TWTTAWTT MEME-29 in BLOCKS format
```

```
BL  MOTIF TWTTAWTT width=8 seqs=2  
cg27099625          (   32) TTTTATTT  1  
cg02632822          ( 163) TATTAATT  1  
//
```

```
Motif TWTTAWTT MEME-29 position-specific scoring matrix
```

```
log-odds matrix: alength= 4 w= 8 n= 14550 bayes= 12.8285 E= 1.1e+006  
 -765    -765    -765    242  
  142    -765    -765    142  
 -765    -765    -765    242  
 -765    -765    -765    242  
  242    -765    -765   -765  
  142    -765    -765    142  
 -765    -765    -765    242  
 -765    -765    -765    242
```

```
Motif TWTTAWTT MEME-29 position-specific probability matrix
```

```
letter-probability matrix: alength= 4 w= 8 nsites= 2 E= 1.1e+006  
 0.000000  0.000000  0.000000  1.000000  
 0.500000  0.000000  0.000000  0.500000  
 0.000000  0.000000  0.000000  1.000000  
 0.000000  0.000000  0.000000  1.000000  
 1.000000  0.000000  0.000000  0.000000  
 0.500000  0.000000  0.000000  0.500000  
 0.000000  0.000000  0.000000  1.000000  
 0.000000  0.000000  0.000000  1.000000
```

```
Motif TWTTAWTT MEME-29 regular expression
```

T[AT]TTA[AT]TT

Time 473.89 secs.

\*\*\*\*\*

\*\*\*\*\*

MOTIF TGAAATGT MEME-30 width = 8 sites = 2 llr = 25 E-value = 8.2e+005

\*\*\*\*\*

Motif TGAAATGT MEME-30 Description

Simplified A ::aaa:::  
pos.-specific C :::::::  
probability G :a::::a:  
matrix T a::::a:a

bits 2.4 \* \*\*\*\* \*  
2.2 \* \*\*\*\* \*  
1.9 \* \*\*\*\* \*  
1.7 \*\*\*\*\*  
Relative 1.5 \*\*\*\*\*  
Entropy 1.2 \*\*\*\*\*  
(17.9 bits) 1.0 \*\*\*\*\*  
0.7 \*\*\*\*\*  
0.5 \*\*\*\*\*  
0.2 \*\*\*\*\*  
0.0 -----

Multilevel TGAAATGT  
consensus  
sequence

Motif TGAAATGT MEME-30 sites sorted by position p-value

Sequence name Strand Start P-value Site

cg13752114 + 142 4.19e-06 ATGGTCAGGC TGAAATGT CACAGTCTGG

```
cg07747690          +    30  4.19e-06 GGATCAGTCA TGAAATGT CCTTAGCTTC
```

---

Motif TGAAATGT MEME-30 block diagrams

---

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
cg13752114		4.2e-06	141_[+30]_52
cg07747690		4.2e-06	29_[+30]_164

---

---

Motif TGAAATGT MEME-30 in BLOCKS format

---

```
BL MOTIF TGAAATGT width=8 seqs=2
cg13752114      ( 142) TGAAATGT 1
cg07747690      ( 30) TGAAATGT 1
//
```

---

---

Motif TGAAATGT MEME-30 position-specific scoring matrix

---

```
log-odds matrix: alength= 4 w= 8 n= 14550 bayes= 12.8285 E= 8.2e+005
 -765  -765  -765   242
 -765  -765   167  -765
  242  -765  -765  -765
  242  -765  -765  -765
  242  -765  -765  -765
 -765  -765  -765  242
 -765  -765   167  -765
 -765  -765  -765   242
```

---

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Motif TGAAATGT MEME-30 position-specific probability matrix

---

```
letter-probability matrix: alength= 4 w= 8 nsites= 2 E= 8.2e+005
 0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  1.000000  0.000000
 1.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  1.000000  0.000000
```

0.000000 0.000000 0.000000 1.000000

---

Motif TGAAATGT MEME-30 regular expression

TGAAATGT

Time 488.26 secs.

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SUMMARY OF MOTIFS

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Combined block diagrams: non-overlapping sites with p-value < 0.0001

SEQUENCE NAME	COMBINED P-VALUE	MOTIF DIAGRAM
cg00896220	2.38e-21	[+4(5.10e-10)]_7_[+26(1.53e-07)]_4_\n[+3(8.56e-11)]_45_[+22(4.90e-07)]_10_[-5(1.79e-06)]_56
cg00957886	2.48e-38	4_-[-7(6.73e-08)]_11_[+25(5.01e-06)]_\n10_[+4(1.29e-10)]_5_[+3(4.50e-15)]_2_[+10(5.64e-12)]_9_[-5(3.35e-06)]_15_\n[-1(5.82e-14)]_4
cg01277910	8.44e-03	13_-[-6(3.62e-05)]_15_[-2(2.23e-05)]_\n32_[-15(4.19e-06)]_84
cg01724041	7.91e-01	116_[+6(4.25e-05)]_18_\n[+2(2.12e-06)]_18
cg02163400	2.83e-01	14_-[-6(4.74e-06)]_19_[+2(6.02e-05)]_\n7_[+2(1.30e-09)]_27_[+6(4.90e-07)]_1_[+11(9.49e-07)]_5_[+11(7.50e-05)]
cg02467054	9.16e-04	47_[+6(9.68e-05)]_6_[+2(1.92e-06)]_\n28_[-4(3.87e-09)]_12_[+6(1.40e-05)]_19
cg02573152	7.18e-30	7_-[-17(1.60e-05)]_7_[+10(3.18e-08)]_\n2_[+8(6.30e-08)]_8_[+9(3.41e-13)]_41_[+29(2.60e-05)]_1_[+1(6.28e-16)]_22
cg02632822	2.58e-31	16_[+15(4.19e-06)]_49_\n[-6(1.74e-06)]_8_[+1(5.11e-21)]_4_[+8(3.66e-07)]_3_[+29(5.98e-06)]_\n[+3(1.17e-09)]_3
cg02907176	3.39e-02	60_-[-6(4.97e-05)]_41_[+2(9.22e-06)]_\n14_[+10(1.21e-08)]_18
cg03147312	9.58e-01	201

cg03532422 6.98e-10 11\_[-11(4.23e-06)]\_40\_\  
 [-2(2.59e-05)]\_36\_[+5(2.90e-06)]\_1\_[-9(1.93e-11)]\_33  
 cg03796003 3.33e-02 107\_[+18(1.23e-09)]\_53\_\  
 [+19(1.53e-07)]\_15  
 cg03983713 6.47e-08 29\_[+8(1.27e-06)]\_87\_\  
 [+12(1.33e-07)]\_30\_[+7(8.37e-08)]\_13  
 cg04039667 3.58e-01 17\_[+6(4.26e-06)]\_7\_[+11(2.37e-06)]\_\  
 141  
 cg04156077 4.24e-30 9\_[-5(5.99e-06)]\_6\_[+28(8.75e-08)]\_\  
 1\_[-13(3.59e-07)]\_1\_[-1(1.92e-13)]\_27\_[+7(9.02e-10)]\_22\_[-3(1.90e-10)]\_17  
 cg04784471 4.11e-01 1\_[+23(8.43e-05)]\_13\_[+6(6.40e-07)]\_\  
 17\_[+11(8.58e-06)]\_56\_[+2(1.00e-05)]\_39  
 cg05004480 4.38e-01 46\_[-6(2.18e-05)]\_31\_[+2(1.91e-05)]\_\  
 75  
 cg05541867 6.67e-03 72\_[-6(6.40e-07)]\_13\_\  
 [+18(1.45e-08)]\_31\_[+13(4.66e-07)]\_36  
 cg05725080 2.52e-02 28\_[-20(1.79e-05)]\_16\_\  
 [+11(2.71e-08)]\_19\_[+11(7.06e-07)]\_[+6(8.68e-06)]\_73  
 cg05834845 8.00e-01 29\_[-11(1.16e-05)]\_81\_\  
 [+2(3.09e-08)]\_48  
 cg06805280 8.84e-01 5\_[+11(7.08e-06)]\_47\_[+2(5.97e-06)]\_\  
 68\_[+11(9.49e-07)]\_23  
 cg06840699 5.60e-03 8\_[+14(9.17e-08)]\_5\_[+21(7.16e-05)]\_\  
 38\_[+6(3.62e-05)]\_112  
 cg07265976 1.65e-03 14\_[-2(1.92e-06)]\_14\_[+6(7.87e-06)]\_\  
 71\_[+12(1.44e-06)]\_38  
 cg07724977 1.57e-07 39\_[+6(6.40e-07)]\_16\_[+6(4.74e-06)]\_\  
 17\_[-5(1.82e-06)]\_25\_[-6(2.18e-05)]\_20\_[+24(3.92e-07)]  
 cg07747690 6.37e-22 10\_[+13(2.05e-07)]\_6\_\  
 [+30(4.19e-06)]\_6\_[+5(4.77e-06)]\_70\_[+1(2.59e-12)]\_10\_[-10(3.23e-10)]\_7  
 cg08034643 9.23e-01 67\_[+6(2.38e-05)]\_10\_\  
 [-23(9.79e-05)]\_15\_[+2(4.15e-06)]\_49  
 cg08590601 5.06e-06 1\_[+4(9.35e-10)]\_10\_[+19(1.53e-07)]\_\  
 107\_[+2(5.48e-08)]\_25  
 cg09368670 1.51e-02 15\_[+6(6.25e-05)]\_107\_\  
 [-12(2.64e-06)]\_4\_[-2(7.43e-07)]\_11  
 cg09588770 6.02e-04 18\_[+16(3.92e-07)]\_59\_\  
 [+12(1.15e-06)]\_37\_[+6(8.39e-05)]\_11\_[-2(4.55e-06)]\_2  
 cg09808690 4.56e-01 46\_[+11(7.84e-07)]\_28\_\  
 [+2(2.34e-06)]\_35\_[+6(1.74e-06)]\_6\_[+11(7.84e-07)]\_7  
 cg10112022 1.21e-01 115\_[+6(4.25e-05)]\_9\_[-2(1.69e-08)]\_\  
 28  
 cg10280383 7.67e-02 23\_[+2(9.22e-06)]\_13\_\  
 [+12(5.25e-06)]\_60\_[-26(1.92e-05)]\_40\_[+14(9.94e-05)]  
 cg10637260 6.28e-11 8\_[+2(1.14e-06)]\_26\_[+20(1.81e-09)]\_\  
 38\_[+5(1.61e-06)]\_21\_[-6(7.87e-06)]\_11\_[+14(9.17e-08)]\_12  
 cg10857807 4.43e-02 36\_[-2(8.47e-06)]\_60\_\

cg10889506	[+11(9.75e-08)]_31_[+6(1.70e-11)]_10	5.52e-01	60_-[-11(7.08e-06)]_14_\
	[+2(7.19e-10)]_19_[+2(8.31e-05)]_37		
cg10990040		9.35e-02	1_-[-4(4.47e-05)]_14_[+12(1.15e-06)]_\ 15_-[-27(5.19e-05)]_128
cg11275803		8.20e-01	34_+[+20(6.22e-05)]_153
cg11847597		8.99e-02	106_+[+23(1.28e-07)]_45_\
	[+2(8.29e-07)]_11		
cg12500857		2.41e-17	24_-[-3(2.23e-11)]_68_-[-7(9.25e-08)]_\ 9_- [+12(2.92e-06)]_17_-[-4(2.05e-12)]_6
cg12509424		2.61e-13	75_+[+5(8.15e-06)]_41_-[-1(8.39e-13)]_\ 16_-[-8(2.32e-07)]_5
cg13233166		9.61e-01	2_-[-2(1.00e-05)]_5_-[-6(2.00e-05)]_6_\
	[ -11(5.39e-05)]_124		
cg13738327		7.65e-02	128_+[+5(2.67e-07)]_29_\
	[+24(4.95e-05)]_23		
cg13752114		8.62e-03	9_- [+2(4.21e-07)]_48_-[-11(1.47e-06)]_\ 41_- [+30(4.19e-06)]_52
cg13936911		2.17e-10	4_- [+3(3.13e-10)]_19_-[-5(5.74e-07)]_\ 16_- [+7(3.28e-08)]_11_- [+12(5.25e-06)]_82
cg14491776		3.35e-01	[+6(1.07e-06)]_44_- [+12(1.78e-08)]_6_\
	[+2(5.97e-06)]_18_- [+2(2.84e-06)]_11_- [+2(3.73e-05)]_2		
cg14685095		1.39e-01	15_- [+21(7.16e-05)]_46_\
	[+2(1.27e-06)]_20_- [+6(2.82e-05)]_20_- [+12(8.04e-05)]_30		
cg16139664		1.84e-08	4_- [-9(4.26e-11)]_36_- [+27(1.57e-06)]_\ 21_- [+28(6.26e-07)]_95
cg16347828		7.57e-01	25_- [+2(4.21e-07)]_108_\
	[+6(2.38e-05)]_19		
cg16456906		7.51e-01	17_- [+7(9.84e-05)]_69_- [+2(4.55e-06)]_\ 72
cg17040924		7.46e-30	5_- [-5(8.66e-07)]_8_-[-1(5.42e-15)]_4_\
	[+3(5.49e-10)]_15_-[-12(1.15e-06)]_28_- [+8(1.16e-07)]_24_-[-16(1.46e-07)]		
cg17775727		3.74e-03	62_- [+18(3.30e-09)]_38_\
	[+2(7.77e-06)]_4_- [+24(2.88e-05)]_44		
cg17862404		6.91e-02	42_-[-13(1.72e-07)]_63_\
	[+2(1.29e-05)]_1_- [+11(3.70e-07)]_39		
cg17891735		9.98e-01	13_- [+2(6.53e-06)]_27_- [+2(9.42e-05)]_\ 27_- [+2(4.60e-05)]_50
cg18255614		5.90e-01	33_- [+6(1.05e-05)]_28_- [+2(1.64e-05)]_\ 91
cg18768400		5.67e-02	43_- [+12(4.25e-06)]_21_\
	[+2(3.78e-06)]_26_- [+6(9.57e-06)]_47		
cg19729672		3.70e-01	[+2(5.63e-05)]_9_- [+11(4.33e-08)]_32_\
	[+2(1.73e-06)]_40_- [+6(6.40e-07)]_28		
cg19801460		1.09e-01	9_- [-6(6.74e-05)]_4_- [+2(1.00e-05)]_7_\
	[+6(7.87e-06)]_28_- [+5(1.08e-05)]_72		
cg19931348		2.92e-20	18_- [-3(1.35e-09)]_3_- [+1(1.05e-12)]_\ \

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11_[-27(1.57e-06)]_25_[+8(5.23e-07)]_8_[-3(5.25e-05)]_18
cg20128772 1.59e-01 160_[-12(1.29e-06)]_8_\
[+22(9.59e-05)]_8
cg20667822 1.11e-16 2_[+7(5.32e-10)]_110_\
[+17(1.60e-05)]_-[-4(3.87e-09)]_19_[+3(1.01e-09)]_1
cg21380181 8.60e-02 30_[+23(1.28e-07)]_23_\
[-25(5.01e-06)]_129
cg21813265 1.27e-07 42_[+26(1.53e-07)]_23_\
[+13(3.27e-08)]_85_[-10(1.49e-08)]_8
cg22040815 6.10e-04 37_[-28(6.96e-05)]_37_\
[+12(2.20e-07)]_3_[+2(7.43e-07)]_48_[+21(7.16e-05)]_17
cg22664157 9.93e-01 [-6(7.13e-06)]_15_[+6(5.37e-05)]_\
144
cg22780612 4.17e-01 17_[+22(4.90e-07)]_174
cg22824635 2.53e-04 49_[+9(1.63e-11)]_85_[+2(2.84e-06)]_\
13
cg22889584 9.99e-01 140_[+11(1.31e-06)]_46
cg22973789 9.34e-01 1_[+18(3.03e-08)]_185
cg24872610 2.02e-20 6_[-10(4.95e-09)]_13_[-9(9.35e-11)]_\
51_[-4(3.60e-09)]_1_[+1(1.11e-11)]_14_[-24(1.46e-07)]_1
cg25208863 9.84e-01 [-11(1.88e-07)]_67_[+6(9.57e-06)]_\
98
cg25613667 3.05e-05 8_[-8(5.23e-07)]_118_[+2(2.07e-05)]_\
[-20(4.33e-09)]_21
cg25917893 4.74e-05 11_[+6(3.83e-06)]_9_[+2(1.40e-07)]_\
25_[+5(5.99e-06)]_45_[+13(1.22e-07)]_38
cg26305881 6.95e-01 45_[+6(2.75e-06)]_46_\
[+11(2.54e-06)]_3_[+2(3.44e-06)]_43
cg26673609 3.68e-02 44_[+12(1.44e-06)]_41_\
[+6(8.68e-06)]_6_[+2(3.78e-06)]_46
cg27099625 1.33e-01 31_[-29(5.98e-06)]_34_\
[+2(3.23e-05)]_27_[+6(7.81e-05)]_52
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Stopped because requested number of motifs (30) found.

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

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