

csDMA: an improved bioinformatics tool for identifying DNA 6mA modifications via Chou's 5-step rule

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MEME - Motif discovery tool

MEME version 5.0.5 (Release date: Mon Mar 18 20:12:19 2019 -0700)

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

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

REFERENCE

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.

TRAINING SET

PRIMARY SEQUENCES= posdata.fa

CONTROL SEQUENCES= negdata.fa

ALPHABET= ACGT

COMMAND LINE SUMMARY

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

command: meme posdata.fa -dna -oc . -nostatus -time 18000 -mod zoops -nmotifs 10 -
minw 6 -maxw 50 -objfun de -neg negdata.fa -revcomp -markov_order 0

model: mod= zoops nmotifs= 10 evt= inf
objective function: em= Differential Enrichment mHG
starts= log likelihood ratio (LLR)

strands: + -

width: minw= 6 maxw= 41
nsites: minsites= 2 maxsites= 2814 wnsites= 0.8
theta: spmap= uni spfuzz= 0.5
em: prior= dirichlet b= 0.01 maxiter= 50
distance= 1e-05
data: n= 115374 N= 2814
sample: seed= 0 hsfrac= 0.5
searchsize= 100000 norand= no csites= -1

Letter frequencies in dataset:

A 0.29 C 0.21 G 0.21 T 0.29

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

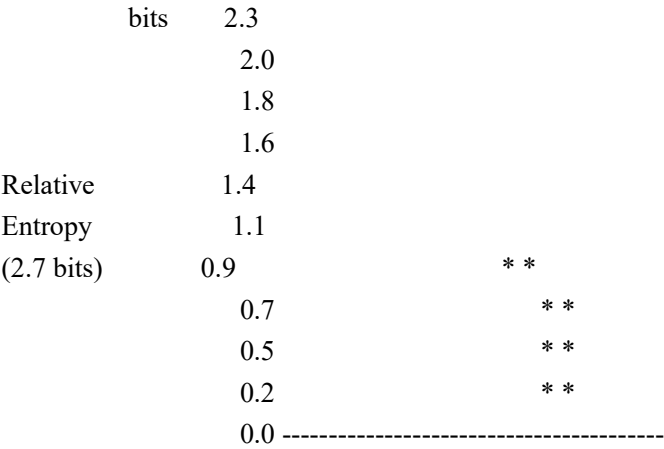
A 0.29 C 0.21 G 0.21 T 0.29

Background model order: 0

MOTIF NNNNNNNHHNHHNHWNTNTNWNNNWNYNNNNNNNNNNNNN
MEME-1 width = 41 sites = 1537 llr = 2837 p-value = 3.3e-018 E-value = 3.3e-018

Motif NNNNNNNHHNHHNHWNTNTNWNNNWNYNNNNNNNNNNNNN
MEME-1 Description

Simplified A 222222222222222322324222322322232223232
pos.-specific C 2232222222222223:3:222223222222222222
probability G 2222222222222222:2:332222222222222222
matrix T 4343333444444443437363344443444333333333



Multilevel consensus TTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTT
CACCAAACAACAACAAATACAGGCACCAACAAAAAAAAAAC
sequence ACAACCCACCACGA G A G CC G GC CCCCCCGCCCA
G GG A G GG G GG

Motif NNNNNNNHHNHHNHWNTNTNWNNNWNYNNNNNNNNNNNNN
MEME-1 position-specific scoring matrix

log-odds matrix: alength= 4 w= 41 n= 2814 bayes= 1.71048 E= 3.3e-018

-37	10	-9	29
-29	10	2	17
-51	26	-15	29
-31	17	-11	21
-27	11	-20	27
-33	10	-5	24
-30	6	-7	25
-30	17	-31	31
-27	4	-32	37
-28	14	-21	27
-37	17	-29	34
-29	1	-27	38
-30	-15	-3	35
-42	21	-24	32
-44	-7	-24	49
-13	-12	-2	20
-48	-16	-22	55
-27	48	-17	-5
18	-1723	-1723	121
-56	34	24	0
60	-1723	-1723	95
-57	0	41	13
-54	9	26	17
-56	9	-11	41
-5	-23	-33	37
-49	11	2	29
-72	45	-47	41
-10	-10	-6	20
-34	-5	-13	38
-58	23	-9	32
-32	0	-11	33
-24	0	-6	24
-14	18	-18	12
-28	0	-5	27
-27	12	-3	17
-25	8	-12	24
-13	-8	-2	19
-24	15	1	10
-20	14	-14	17
-11	1	0	10
-36	12	2	20

 Motif NNNNNNNHHNHHNHWNTNTNWNNNWNYNNNNNNNNNNNNNN
 MEME-1 position-specific probability matrix

letter-probability matrix: alength= 4 w= 41 nsites= 1537 E= 3.3e-018

0.223813	0.224463	0.197788	0.353936
0.236825	0.224463	0.212752	0.325960
0.204294	0.251789	0.188679	0.355237
0.234223	0.236825	0.194535	0.334418
0.240729	0.227066	0.182824	0.349382
0.230319	0.225114	0.202993	0.341574
0.235524	0.218608	0.200390	0.345478
0.234873	0.236825	0.169811	0.358491
0.240078	0.216005	0.167859	0.376057
0.238126	0.230969	0.180872	0.350033
0.225114	0.236174	0.171763	0.366949
0.237476	0.211451	0.173715	0.377358
0.235524	0.188679	0.205595	0.370202
0.217306	0.243331	0.177619	0.361744
0.214053	0.199740	0.178269	0.407938
0.265452	0.193234	0.207547	0.333767
0.207547	0.188029	0.180221	0.424203
0.240078	0.293429	0.186727	0.279766
0.327912	0.000000	0.000000	0.672088
0.196487	0.266103	0.247235	0.290176
0.439818	0.000000	0.000000	0.560182
0.195185	0.209499	0.278465	0.316851
0.199089	0.223162	0.251789	0.325960
0.197137	0.223813	0.194535	0.384515
0.279766	0.178920	0.167209	0.374105
0.206897	0.226415	0.212752	0.353936
0.175667	0.287573	0.151594	0.385166
0.270007	0.195185	0.201041	0.333767
0.229668	0.202342	0.191282	0.376708
0.194535	0.245934	0.197137	0.362394
0.231620	0.209499	0.194535	0.364346
0.245283	0.210150	0.201041	0.343526
0.262850	0.237476	0.184776	0.314899
0.238126	0.209499	0.202993	0.349382
0.240078	0.227716	0.204945	0.327261
0.243331	0.221210	0.192583	0.342876
0.264802	0.198439	0.206897	0.329863
0.245934	0.232921	0.210800	0.310345
0.251789	0.230969	0.189980	0.327261

0.268705 0.210800 0.209499 0.310995
0.226415 0.227716 0.212752 0.333116

Motif NNNNNNNHHNHHNHWNTNTNWNNNWNYNNNNNNNNNNNNNNNN

MEME-1 regular expression

[TCA][TACG][TCA][TCA][TAC][TACG][TACG][TCA][TAC][TAC][TCA][TAC][TAG][TCA][TA][TAG][TA][CTA][TA][TCG][TA][TGC][TGC][TC][TA][TCGA][TC][TAG][TAC][TC][TAC][TACG][TAC][TACG][TACG][TAC][TAG][TACG][TAC][TACG][TCAG]

Time 694.83 secs.

MOTIF TYTTKTWTTTWAARAAA MEME-2 width = 18 sites = 34 llr = 349 p-value = 8.8e-001 E-value = 1.8e+000

Motif TYTTKTWTTTWAARAAA MEME-2 Description

Simplified A ::2:2:63::15675599
pos.-specific C :5::1::1211::1::
probability G 1::142:2222:1:52::
matrix T 95893645886413:21:

bits	2.3				
	2.0				
	1.8				
	1.6				
Relative	1.4	*	*		**
Entropy	1.1	*	*	*	* **
(14.8 bits)	0.9	****	* **		* **

0.7 **** ** ** ** **
0.5 ***** **
0.2 *****
0.0 -----

Multilevel TTTTGTATTTTAAAGAAA
consensus CA TGTA T TAG
sequence A G

Motif TYTTKTWTTTWAARAAA MEME-2 position-specific scoring matrix

log-odds matrix: alength= 4 w= 18 n= 67536 bayes= 11.4821 E= 1.8e+000

-1173	-1173	-125	165
-1173	116	-1173	87
-49	-283	-1173	140
-1173	-1173	-83	160
-49	-283	107	16
-1173	-51	16	109
109	-1173	-1173	40
-13	-1173	16	79
-1173	-1173	-3	145
-1173	-183	-25	140
-230	-25	-25	102
87	-125	-283	28
116	-51	-125	-130
122	-1173	-283	2
70	-1173	133	-1173
87	-125	-3	-72
165	-1173	-1173	-172
170	-1173	-283	-330

Motif TYTTKTWTTTWAARAAA MEME-2 position-specific probability matrix

letter-probability matrix: alength= 4 w= 18 nsites= 34 E= 1.8e+000

0.000000	0.000000	0.088235	0.911765
0.000000	0.470588	0.000000	0.529412
0.205882	0.029412	0.000000	0.764706
0.000000	0.000000	0.117647	0.882353

0.205882	0.029412	0.441176	0.323529
0.000000	0.147059	0.235294	0.617647
0.617647	0.000000	0.000000	0.382353
0.264706	0.000000	0.235294	0.500000
0.000000	0.000000	0.205882	0.794118
0.000000	0.058824	0.176471	0.764706
0.058824	0.176471	0.176471	0.588235
0.529412	0.088235	0.029412	0.352941
0.647059	0.147059	0.088235	0.117647
0.676471	0.000000	0.029412	0.294118
0.470588	0.000000	0.529412	0.000000
0.529412	0.088235	0.205882	0.176471
0.911765	0.000000	0.000000	0.088235
0.941176	0.000000	0.029412	0.029412

Motif TYTTKTWTTTWAARAAA MEME-2 regular expression

T[TC][TA]T[GTA][TG][AT][TAG][TG]TT[AT]A[AT][GA][AG]AA

Time 1154.91 secs.

MOTIF ACCGATCSA MEME-3 width = 9 sites = 22 llr = 208 p-value = 2.8e-002 E-value = 2.9e-002

Motif ACCGATCSA MEME-3 Description

Simplified	A	a::71:2a
pos.-specific	C	:8a3::a4:
probability	G	:2:72::4:
matrix	T	::::9:::

	bits	2.3	*	*
		2.0	*	*
		1.8	*	**
		1.6	***	**
Relative		1.4	****	**
Entropy		1.1	****	**
(13.6 bits)		0.9	*****	*
		0.7	*****	
		0.5	*****	
		0.2	*****	
		0.0	-----	

Multilevel ACCGATCCA

consensus CG G

sequence

Motif ACCGATCSA MEME-3 position-specific scoring matrix

log-odds matrix: alength= 4 w= 9 n= 92862 bayes= 12.9666 E= 2.9e-002

172	-220	-1110	-1110
-1110	196	-21	-1110
-1110	225	-1110	-1110
-1110	60	170	-1110
133	-220	11	-1110
-167	-1110	-1110	165
-1110	225	-1110	-1110
-67	96	96	-1110
178	-1110	-1110	-1110

Motif ACCGATCSA MEME-3 position-specific probability matrix

letter-probability matrix: alength= 4 w= 9 nsites= 22 E= 2.9e-002

0.954545	0.045455	0.000000	0.000000
0.000000	0.818182	0.181818	0.000000
0.000000	1.000000	0.000000	0.000000
0.000000	0.318182	0.681818	0.000000
0.727273	0.045455	0.227273	0.000000
0.090909	0.000000	0.000000	0.909091

0.000000	1.000000	0.000000	0.000000
0.181818	0.409091	0.409091	0.000000
1.000000	0.000000	0.000000	0.000000

Motif ACCGATCSA MEME-3 regular expression

ACC[GC][AG]TC[CG]A

Time 1590.17 secs.

MOTIF AAAAAAAAVMA MEME-4 width = 12 sites = 31 llr = 311 p-value = 9.8e-001 E-value = 3.1e+000

Motif AAAAAAAAVMA MEME-4 Description

Simplified	A	a87a867aa35a
pos.-specific	C	:2:::23::44:
probability	G	::2::2:::3::
matrix	T	::1:2:::1:

	bits	2.3
		2.0
		1.8 * ** *
		1.6 * * ** *
Relative		1.4 * * ** *
Entropy		1.1 ** ** ** *
(14.5 bits)		0.9 ** ** ** *
		0.7 ***** **
		0.5 *****
		0.2 *****

0.0 -----

Multilevel AAAAAAAAAACAA
consensus GC AC
sequence G

Motif AAAAAAAAAVMA MEME-4 position-specific scoring matrix

log-odds matrix: alength= 4 w= 12 n= 84420 bayes= 12.4582 E= 3.1e+000

179	-1160	-1160	-1160
147	-12	-1160	-1160
122	-1160	-12	-117
174	-270	-1160	-1160
147	-1160	-1160	-58
108	-38	11	-1160
122	62	-1160	-1160
179	-1160	-1160	-1160
179	-1160	-1160	-1160
15	100	30	-1160
92	76	-1160	-158
179	-1160	-1160	-1160

Motif AAAAAAAAAVMA MEME-4 position-specific probability matrix

letter-probability matrix: alength= 4 w= 12 nsites= 31 E= 3.1e+000

1.000000	0.000000	0.000000	0.000000
0.806452	0.193548	0.000000	0.000000
0.677419	0.000000	0.193548	0.129032
0.967742	0.032258	0.000000	0.000000
0.806452	0.000000	0.000000	0.193548
0.612903	0.161290	0.225806	0.000000
0.677419	0.322581	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.322581	0.419355	0.258065	0.000000
0.548387	0.354839	0.000000	0.096774
1.000000	0.000000	0.000000	0.000000

Motif AAAAAAAAAVMA MEME-4 regular expression

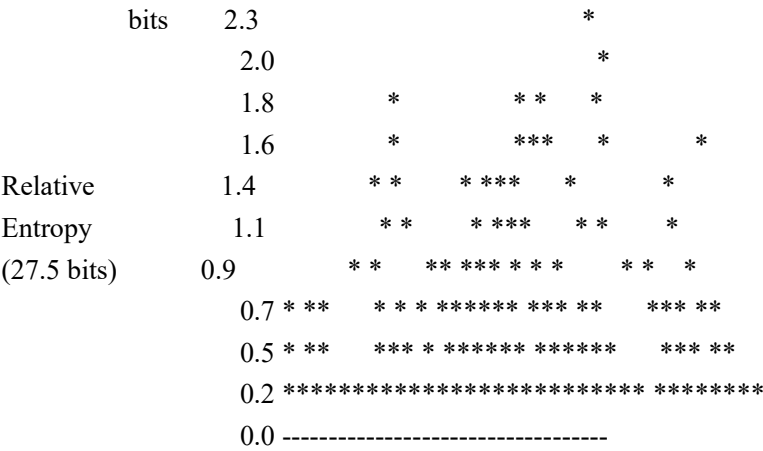
AAAAA[AG][AC]AA[CAG][AC]A

Time 2032.58 secs.

MOTIF SKSRVVMGDSVGVGSVAGGYRSCRGSNVYGBGBGG MEME-5 width =
35 sites = 8 llr = 153 p-value = 9.8e-001 E-value = 3.0e+000

Motif SKSRVVMGDSVGVGSVAGGYRSCRGSNVYGBGBGG MEME-5
Description

Simplified A 11:4444:3:3131:3a1:161:51:3311::11:
pos.-specific C 51413341:63:3363::13:4a::5335:41313
probability G 4555331954464645:99145:484341946466
matrix T :31:111:3:131:.....5::111313:33311



Multilevel CGGGAAAGGCGGGGCGAGGTAGCAGCAGCGCGGGG
consensus GTCACCC AGATACGA CGC G GCAT GTC C

sequence	GG	T	C	C		GC	T	T
						T		

Motif SKSRVVMGDSVGVGVSAGGYRSCRGSNVYGBGBGG MEME-5

position-specific scoring matrix

log-odds matrix: alength= 4 w= 35 n= 19698 bayes= 9.33753 E= 3.0e+000

-121	125	84	-965
-121	-75	125	-21
-965	84	125	-121
37	-75	125	-965
37	25	25	-121
37	25	25	-121
37	84	-75	-121
-965	-75	206	-965
-21	-965	125	-21
-965	157	84	-965
-21	25	84	-121
-121	-965	157	-21
-21	25	84	-121
-121	25	157	-965
-965	157	84	-965
-21	25	125	-965
178	-965	-965	-965
-121	-965	206	-965
-965	-75	206	-965
-121	25	-75	78
111	-965	84	-965
-121	84	125	-965
-965	225	-965	-965
78	-965	84	-121
-121	-965	184	-121
-965	125	84	-121
-21	25	25	-21
-21	25	84	-121
-121	125	-75	-21
-121	-965	206	-965
-965	84	84	-21
-965	-75	157	-21
-121	25	84	-21
-121	-75	157	-121
-965	25	157	-121

Motif SKSRVVMGDSVGVGVSAGGYRSCRGSNVYGBGBGG MEME-5
position-specific probability matrix

letter-probability matrix: alength= 4 w= 35 nsites= 8 E= 3.0e+000

0.125000	0.500000	0.375000	0.000000
0.125000	0.125000	0.500000	0.250000
0.000000	0.375000	0.500000	0.125000
0.375000	0.125000	0.500000	0.000000
0.375000	0.250000	0.250000	0.125000
0.375000	0.250000	0.250000	0.125000
0.375000	0.375000	0.125000	0.125000
0.000000	0.125000	0.875000	0.000000
0.250000	0.000000	0.500000	0.250000
0.000000	0.625000	0.375000	0.000000
0.250000	0.250000	0.375000	0.125000
0.125000	0.000000	0.625000	0.250000
0.250000	0.250000	0.375000	0.125000
0.125000	0.250000	0.625000	0.000000
0.000000	0.625000	0.375000	0.000000
0.250000	0.250000	0.500000	0.000000
1.000000	0.000000	0.000000	0.000000
0.125000	0.000000	0.875000	0.000000
0.000000	0.125000	0.875000	0.000000
0.125000	0.250000	0.125000	0.500000
0.625000	0.000000	0.375000	0.000000
0.125000	0.375000	0.500000	0.000000
0.000000	1.000000	0.000000	0.000000
0.500000	0.000000	0.375000	0.125000
0.125000	0.000000	0.750000	0.125000
0.000000	0.500000	0.375000	0.125000
0.250000	0.250000	0.250000	0.250000
0.250000	0.250000	0.375000	0.125000
0.125000	0.500000	0.125000	0.250000
0.125000	0.000000	0.875000	0.000000
0.000000	0.375000	0.375000	0.250000
0.000000	0.125000	0.625000	0.250000
0.125000	0.250000	0.375000	0.250000
0.125000	0.125000	0.625000	0.125000
0.000000	0.250000	0.625000	0.125000

Motif SKSRVVMGDSVGVGVSAGGYRSCRGSNVYGBGBGG MEME-5
regular expression

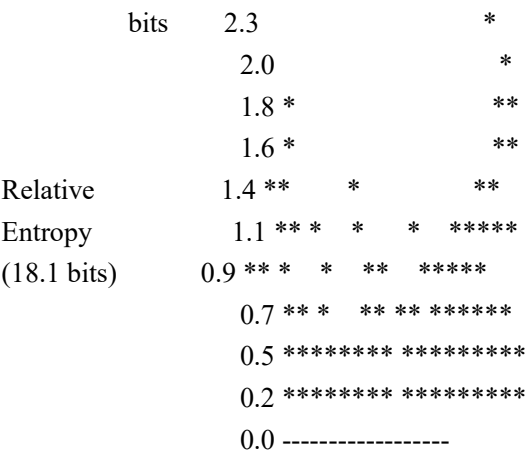
[CG][GT][GC][GA][ACG][ACG][AC]G[GAT][CG][GAC][GT][GAC][GC][CG][GA
C]AGG[TC][AG][GC]C[AG]G[CG][ACGT][GAC][CT]G[CGT][GT][GCT]G[GC]

Time 2462.29 secs.

MOTIF TAAAWTAADKAVTTACAA MEME-6 width = 18 sites = 10 llr = 125
p-value = 1.0e+000 E-value = 4.4e+000

Motif TAAAWTAADKAVTTACAA MEME-6 Description

Simplified A :96851963:732:7:a8
pos.-specific C ::2222:21:33::3a::
probability G ::::1:234:412::::
matrix T a12:361:36::78:::2



Multilevel TAAAATAAATAGTTACAA

consensus	CCTC CGGCAAGC T
sequence	T C GT C

Motif TAAAWTAADKAVTTACAA MEME-6 position-specific scoring matrix

log-odds matrix: alength= 4 w= 18 n= 67536 bayes= 12.7212 E= 4.4e+000

-997	-997	-997	178
163	-997	-997	-153
105	-7	-997	-54
146	-7	-997	-997
78	-7	-997	5
-153	-7	-107	105
163	-997	-997	-153
105	-7	-7	-997
5	-107	51	5
-997	-997	93	105
127	51	-997	-997
5	51	93	-997
-54	-997	-107	127
-997	-997	-7	146
127	51	-997	-997
-997	225	-997	-997
178	-997	-997	-997
146	-997	-997	-54

Motif TAAAWTAADKAVTTACAA MEME-6 position-specific probability matrix

letter-probability matrix: alength= 4 w= 18 nsites= 10 E= 4.4e+000

0.000000	0.000000	0.000000	1.000000
0.900000	0.000000	0.000000	0.100000
0.600000	0.200000	0.000000	0.200000
0.800000	0.200000	0.000000	0.000000
0.500000	0.200000	0.000000	0.300000
0.100000	0.200000	0.100000	0.600000
0.900000	0.000000	0.000000	0.100000
0.600000	0.200000	0.200000	0.000000
0.300000	0.100000	0.300000	0.300000
0.000000	0.000000	0.400000	0.600000
0.700000	0.300000	0.000000	0.000000

0.300000	0.300000	0.400000	0.000000
0.200000	0.000000	0.100000	0.700000
0.000000	0.000000	0.200000	0.800000
0.700000	0.300000	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.800000	0.000000	0.000000	0.200000

Motif TAAAWTAADKAVTTACAA MEME-6 regular expression

TA[ACT][AC][ATC][TC]A[ACG][AGT][TG][AC][GAC][TA][TG][AC]CA[AT]

Time 2877.17 secs.

MOTIF AVCTGRMAMTSATGG MEME-7 width = 15 sites = 16 llr = 199 p-value = 1.0e+000 E-value = 4.5e+000

Motif AVCTGRMAMTSATGG MEME-7 Description

Simplified	A	93:::4584316::1
pos.-specific	C	:4a2:2526141:::
probability	G	:3::a4:::432a9
matrix	T	1::8:::1:71:8::

bits	2.3	* *	*
	2.0	* *	*
	1.8	* *	*
	1.6	* *	**
Relative	1.4	* * *	**
Entropy	1.1	* * * * *	***

(17.9 bits) 0.9 * * * * * * * *

 0.7 * * * * * * * *

 0.5 * * * * * * * * * *

 0.2 * * * * * * * * * *

 0.0 -----

Multilevel ACCTGAAACTGATGG

consensus A GC AACG

sequence G

Motif AVCTGRMAMTSATGG MEME-7 position-specific scoring matrix

log-odds matrix: alength= 4 w= 15 n= 75978 bayes= 12.213 E= 4.5e+000

159	-1064	-1064	-121
11	106	25	-1064
-1064	225	-1064	-1064
-1064	-16	-1064	149
-1064	-1064	225	-1064
59	-16	84	-1064
78	125	-1064	-1064
137	-16	-1064	-221
37	157	-1064	-1064
-21	-175	-1064	124
-121	84	106	-221
111	-75	25	-1064
-1064	-1064	-16	149
-1064	-1064	225	-1064
-121	-1064	206	-1064

Motif AVCTGRMAMTSATGG MEME-7 position-specific probability matrix

letter-probability matrix: alength= 4 w= 15 nsites= 16 E= 4.5e+000

0.875000	0.000000	0.000000	0.125000
0.312500	0.437500	0.250000	0.000000
0.000000	1.000000	0.000000	0.000000
0.000000	0.187500	0.000000	0.812500
0.000000	0.000000	1.000000	0.000000
0.437500	0.187500	0.375000	0.000000
0.500000	0.500000	0.000000	0.000000

0.750000	0.187500	0.000000	0.062500
0.375000	0.625000	0.000000	0.000000
0.250000	0.062500	0.000000	0.687500
0.125000	0.375000	0.437500	0.062500
0.625000	0.125000	0.250000	0.000000
0.000000	0.000000	0.187500	0.812500
0.000000	0.000000	1.000000	0.000000
0.125000	0.000000	0.875000	0.000000

Motif AVCTGRMAMTSATGG MEME-7 regular expression

A[CAG]CTG[AG][AC]A[CA][TA][GC][AG]TGG

Time 3302.72 secs.

MOTIF CTCCCAADGAAARRRTCWYAAR MEME-8 width = 22 sites = 11
llr = 151 p-value = 1.0e+000 E-value = 6.6e+000

Motif CTCCCAADGAAARRRTCWYAAR MEME-8 Description

Simplified	A	::2118642a985541:3:874
pos.-specific	C	7276823:2::1::3726::
probability	G	11:::45:11445:1::236
matrix	T	27131:132::11126254::

bits	2.3		
	2.0		
	1.8	*	
	1.6	*	
Relative	1.4	*	**

Entropy 1.1 * * * * *
 (19.8 bits) 0.9 * * * * *
 0.7 * * * * *
 0.5 * * * * *
 0.2 * * * * *
 0.0 -----

Multilevel CTCCCAAAGAAAAAGTCTCAAG
 consensus T CG GGAC AT GA
 sequence T

Motif CTCCCAADGAAARRRTCWYAAR MEME-8 position-specific scoring matrix

log-odds matrix: alength= 4 w= 22 n= 56280 bayes= 12.5474 E= 6.6e+000

-1010	179	-121	-67
-1010	-21	-121	133
-67	179	-1010	-167
-167	160	-1010	-9
-167	196	-1010	-167
150	-21	-1010	-1010
113	38	-1010	-167
33	-1010	79	-9
-67	-21	111	-67
178	-1010	-1010	-1010
165	-1010	-121	-1010
150	-1010	-121	-167
65	-121	79	-167
91	-1010	79	-167
33	-1010	111	-67
-167	38	-1010	113
-1010	179	-121	-67
-9	-21	-1010	91
-1010	160	-1010	33
150	-1010	-21	-1010
133	-1010	38	-1010
33	-1010	160	-1010

Motif CTCCCAADGAAARRRTCWYAAR MEME-8 position-specific probability

matrix

letter-probability matrix: alength= 4 w= 22 nsites= 11 E= 6.6e+000

0.000000	0.727273	0.090909	0.181818
0.000000	0.181818	0.090909	0.727273
0.181818	0.727273	0.000000	0.090909
0.090909	0.636364	0.000000	0.272727
0.090909	0.818182	0.000000	0.090909
0.818182	0.181818	0.000000	0.000000
0.636364	0.272727	0.000000	0.090909
0.363636	0.000000	0.363636	0.272727
0.181818	0.181818	0.454545	0.181818
1.000000	0.000000	0.000000	0.000000
0.909091	0.000000	0.090909	0.000000
0.818182	0.000000	0.090909	0.090909
0.454545	0.090909	0.363636	0.090909
0.545455	0.000000	0.363636	0.090909
0.363636	0.000000	0.454545	0.181818
0.090909	0.272727	0.000000	0.636364
0.000000	0.727273	0.090909	0.181818
0.272727	0.181818	0.000000	0.545455
0.000000	0.636364	0.000000	0.363636
0.818182	0.000000	0.181818	0.000000
0.727273	0.000000	0.272727	0.000000
0.363636	0.000000	0.636364	0.000000

Motif CTCCCAADGAAARRRTCWYAAR MEME-8 regular expression

CTC[CT]CA[AC][AGT]GAAA[AG][AG][GA][TC]C[TA][CT]A[AG][GA]

Time 3724.89 secs.

MOTIF TGTCHCTDTRCC MEME-9 width = 12 sites = 12 llr = 133 p-value
= 1.0e+000 E-value = 3.8e+000

Motif TGTCHCTDTRCC MEME-9 Description

Simplified A :::3::3:3::
pos.-specific C 1:395a2:::99
probability G :9:::525::
matrix T 91813:838211

	bits	2.3	*
		2.0	*
		1.8	* * *
		1.6	* * *
Relative		1.4	* * *
Entropy		1.1	* * *
(16.0 bits)		0.9	* * *
		0.7	* * *
		0.5	* * *
		0.2	* * *
		0.0	-----

Multilevel TGTCCCTGTGCC
consensus C A A A
sequence T T

Motif TGTCHCTDTRCC MEME-9 position-specific scoring matrix

log-odds matrix: alength= 4 w= 12 n= 84420 bayes= 12.7801 E= 3.8e+000

-1023	-133	-1023	166
-1023	-1023	213	-180
-1023	25	-1023	137
-1023	213	-1023	-180
-21	125	-1023	-21
-1023	225	-1023	-1023
-1023	-33	-1023	152
-21	-1023	125	-21
-1023	-1023	-33	152
20	-1023	125	-80

-1023 213 -1023 -180
-1023 213 -1023 -180

Motif TGTCHCTDTRCC MEME-9 position-specific probability matrix

letter-probability matrix: alength= 4 w= 12 nsites= 12 E= 3.8e+000

0.000000	0.083333	0.000000	0.916667
0.000000	0.000000	0.916667	0.083333
0.000000	0.250000	0.000000	0.750000
0.000000	0.916667	0.000000	0.083333
0.250000	0.500000	0.000000	0.250000
0.000000	1.000000	0.000000	0.000000
0.000000	0.166667	0.000000	0.833333
0.250000	0.000000	0.500000	0.250000
0.000000	0.000000	0.166667	0.833333
0.333333	0.000000	0.500000	0.166667
0.000000	0.916667	0.000000	0.083333
0.000000	0.916667	0.000000	0.083333

Motif TGTCHCTDTRCC MEME-9 regular expression

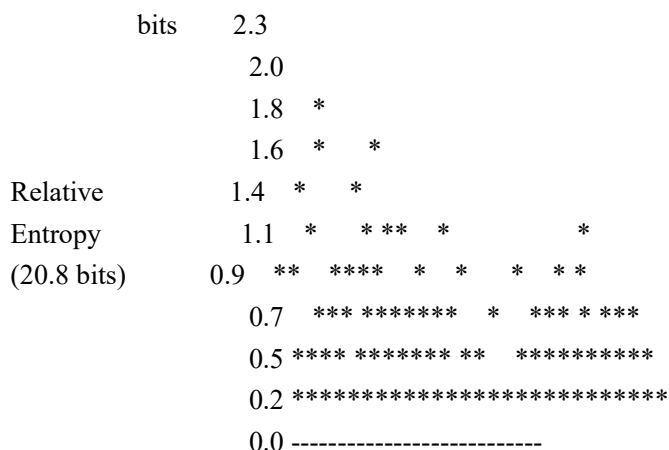
TG[TC]C[CAT]CT[GAT]T[GA]CC

Time 4115.84 secs.

MOTIF MAMAMCWACYTARTAVTARMWGTGAYW MEME-10 width = 27
sites = 13 llr = 187 p-value = 1.0e+000 E-value = 7.0e+000

Motif MAMAMCWACYTARTAVTARMWGTGAYW MEME-10 Description

Simplified A 5a674:6811183284276332226:5
pos.-specific C 4:4248:285:222:31::521:124:
probability G :::212::1:2:4:22224::827222
matrix T 2::2:4:147:261151:25:6::53



Multilevel consensus sequence
AAAAACAACCTAGTAATAACTGTGATA
C C C T TGCAA CGGGAA AACCT
G

Motif MAMAMCWACYTARTAVTARMWGTGAYW MEME-10 position-specific scoring matrix

log-odds matrix: alength= 4 w= 27 n= 42210 bayes= 12.0722 E= 7.0e+000

67	87	-1035	-91
178	-1035	-1035	-1035
108	87	-1035	-1035
125	-45	-45	-1035
41	87	-145	-91
-1035	201	-45	-1035
108	-1035	-1035	41
154	-45	-1035	-1035
-191	187	-145	-191
-191	136	-1035	41
-191	-1035	14	125
141	14	-1035	-1035
8	-45	87	-91
-33	-45	-1035	108

141	-1035	-45	-191
41	55	14	-191
-91	-145	14	89
125	-1035	14	-191
108	-1035	87	-1035
8	136	-1035	-91
8	-45	-1035	89
-91	-145	187	-1035
-33	-1035	-45	108
-33	-145	172	-1035
108	14	-45	-1035
-1035	87	-45	67
89	-1035	-45	8

Motif MAMAMCWACYTARTAVTARMWGTGAYW MEME-10 position-specific probability matrix

letter-probability matrix: alength= 4 w= 27 nsites= 13 E= 7.0e+000

0.461538	0.384615	0.000000	0.153846
1.000000	0.000000	0.000000	0.000000
0.615385	0.384615	0.000000	0.000000
0.692308	0.153846	0.153846	0.000000
0.384615	0.384615	0.076923	0.153846
0.000000	0.846154	0.153846	0.000000
0.615385	0.000000	0.000000	0.384615
0.846154	0.153846	0.000000	0.000000
0.076923	0.769231	0.076923	0.076923
0.076923	0.538462	0.000000	0.384615
0.076923	0.000000	0.230769	0.692308
0.769231	0.230769	0.000000	0.000000
0.307692	0.153846	0.384615	0.153846
0.230769	0.153846	0.000000	0.615385
0.769231	0.000000	0.153846	0.076923
0.384615	0.307692	0.230769	0.076923
0.153846	0.076923	0.230769	0.538462
0.692308	0.000000	0.230769	0.076923
0.615385	0.000000	0.384615	0.000000
0.307692	0.538462	0.000000	0.153846
0.307692	0.153846	0.000000	0.538462
0.153846	0.076923	0.769231	0.000000
0.230769	0.000000	0.153846	0.615385
0.230769	0.076923	0.692308	0.000000

0.615385	0.230769	0.153846	0.000000
0.000000	0.384615	0.153846	0.461538
0.538462	0.000000	0.153846	0.307692

Motif MAMAMCWACYTARTAVTARMWGTGAYW MEME-10 regular expression

[AC]A[AC]A[AC]C[AT]AC[CT][TG][AC][GA][TA]A[ACG][TG][AG][AG][CA][TA]G[TA][GA][AC][TC][AT]

Time 4498.80 secs.

Stopped because requested number of motifs (10) found.

CPU: node058

