

MEME - Motif discovery tool

TRAINING SET

DATAFILE= pasted_sequences

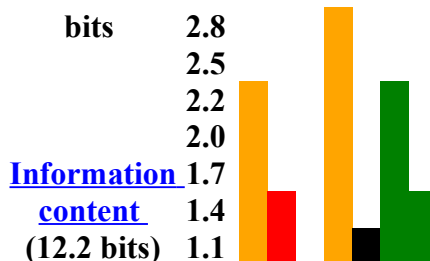
ALPHABET= ACGT

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ab230506b01.r_B01.ab1 50	1.0000	50	ab230506b02.r_B02.ab1	1.0000
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ab230506b05.r_B05.ab1 50	1.0000	69	ab230506b07.r_B07.ab1	1.0000
ab230506b08.r_B08.ab1 50	1.0000	50	ab230506b09.r_B09.ab1	1.0000
ab230506b10.r_B10.ab1 50	1.0000	55	ab230506b11.r_B11.ab1	1.0000
ab230506c01.r_C01.ab1 51	1.0000	50	ab230506c03.r_C03.ab1	1.0000
ab230506c06.r_C06.ab1 49	1.0000	50	ab230506c08.r_C08.ab1	1.0000
ab230506c09.r_C09.ab1 47	1.0000	50	ab230506c12.r_C12.ab1	1.0000
ab230506d01.r_D01.ab1 55	1.0000	50	ab230506d05.r_D05.ab1	1.0000
ab230506d07.r_D07.ab1 50	1.0000	49	ab230506d08.r_D08.ab1	1.0000
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ab230506d11.r_D11.ab1 50	1.0000	50	ab230506d12.r_D12.ab1	1.0000
ab230506e01.r_E01.ab1 50	1.0000	50	ab230506e02.r_E02.ab1	1.0000
ab230506e03.r_E03.ab1 50	1.0000	49	ab230506e04.r_E04.ab1	1.0000
ab230506e05.r_E05.ab1 50	1.0000	65	ab230506e06.r_E06.ab1	1.0000
ab230506e07.r_E07.ab1 50	1.0000	51	ab230506e08.r_E08.ab1	1.0000
ab230506e10.r_E10.ab1 50	1.0000	50	ab230506e11.r_E11.ab1	1.0000
ab230506e12.r_E12.ab1 50	1.0000	50	ab230506f02.r_F02.ab1	1.0000
ab230506f03.r_F03.ab1 50	1.0000	50	ab230506f04.r_F04.ab1	1.0000

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ab230506g03.r_G03.ab1 50	1.0000	50	ab230506g04.r_G04.ab1	1.0000
ab230506g05.r_G05.ab1 50	1.0000	50	ab230506g08.r_G08.ab1	1.0000
ab230506g10.r_G10.ab1 51	1.0000	50	A-1	1.0000
A-2 50	1.0000	49	A-3	1.0000
A-4 49	1.0000	50	A-5	1.0000
A-6 50	1.0000	51	A-7	1.0000
A-8 53	1.0000	50	A-9	1.0000
A-10 50	1.0000	50	A-11	1.0000
A-12 43	1.0000	50	A-14	1.0000
A-15 50	1.0000	50	A-16	1.0000
A03 50	1.0000	50	A04	1.0000
B03 49	1.0000	49	C03	1.0000
C05 50	1.0000	50	D03	1.0000
D04 50	1.0000	65	D05	1.0000
E03 50	1.0000	124	F03	1.0000
G03 50	1.0000	50	G04	1.0000

MOTIF 1 width = 7 sites = 10 llr = 85 E-value = 1.2e+004

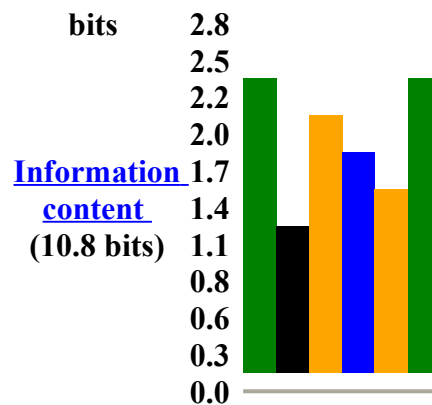
Simplified A 1 a 4 : : : 2
pos.-specific C : : 1 : 1 : :
probability G 9 : 5 a 5 : :
matrix T : : : : 4 a 8



ab230506g05.r_G05.ab1	30	9.15e-05	GCAATTGAAA	T C T C C G C	ATAATGACGA
ab230506b08.r_B08.ab1	30	9.15e-05	AGAATTCCCT	T C T C C G C	GTTACCTACC
ab230506f04.r_F04.ab1	12	1.53e-04	AGTCCTATCT	T T C C C G C	ACGACACCAG
ab230506b07.r_B07.ab1	19	1.53e-04	CCCCATTCAG	T T C C C G C	AACGCAGCTA
A-12	31	1.84e-04	ATGACCCTTA	T C G C C G C	ACATCAGCCG
ab230506b04.r_B04.ab1	41	1.97e-04	CCTTACAGAC	T T G C C G T	AAT
D05	8	2.44e-04	AAGCACG	T C T C C G T	AACTACTTAA
A-5	37	2.44e-04	TTAAAACATC	T T T T C G C	CCGCAA

MOTIF 3 width = 6 sites = 10 llr = 75 E-value = 1.5e+006

Simplified pos.-specific probability matrix
A : 1 : : 4 :
C : : : a : :
G : 4 8 : 6 :
T a 5 2 : : a



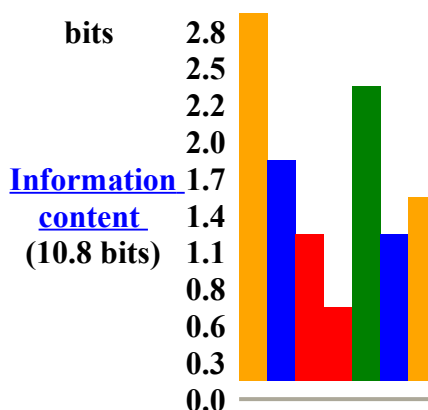
Multilevel consensus sequence
T T G C G T
G T A

NAME	START	P-VALUE	SITES		
E03	95	3.32e-05	ATTCTGAGCT	T G G C G T	AATCATGGTC
D04	17	7.89e-05	CGATGATGAA	T T G C G T	AATACGTAGT
ab230506a07.r_A07.ab1	59	7.89e-05	CAATGATGAA	T T G C G T	AATACGTACC
A-11	34	1.64e-04	TACCCTGCC	T G G C A T	AGACTCCCAC
ab230506a01.r_A01.ab1	34	1.64e-04	ACTAACAACA	T G G C A T	ACCACCCACA
ab230506f02.r_F02.ab1	11	2.80e-04	TGGACCTTAA	T T G C A T	ATTTATATAC
ab230506d12.r_D12.ab1	33	2.80e-04	AAGTATTATC	T T G C A T	CGAAGGTTGG
ab230506b05.r_B05.ab1	63	3.26e-04	GCCACCTGGC	T G T C G T	C
ab230506a09.r_A09.ab1	11	3.89e-04	ATATCCCCAA	T T T C G T	GCCATCCGCG
B03	5	4.74e-04	ATGT	T A G C G T	CAATGCTTCA

MOTIF 4 width = 7 sites = 12 llr = 89 E-value = 6.4e+007

Simplified pos.-specific probability
A : : 8 6 : : 4
C : a : 2 : 8 :
G a : 2 3 : : 6

matrix T : : : : a 3 :

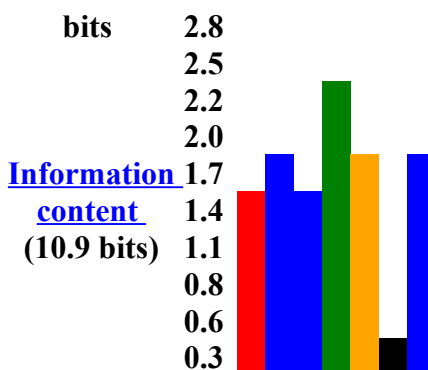


Multilevel consensus sequence
 G C A A T C G
 G T A

NAME	START	P-VALUE	SITES
D04	2	1.83e-05	T G C A G T C G ATGATGAATT
A-14	2	1.83e-05	T G C A G T C G TATACGCACA
A-7	13	6.50e-05	CATTACGTCA G C A A T C G CACGTCCGCA
ab230506e01.r_E01.ab1	2	6.50e-05	A G C A A T C G AAATCATCCC
ab230506g05.r_G05.ab1	20	1.33e-04	ACCCAAACTG G C A A T T G AAATCTCCGC
A-8	42	2.18e-04	TAACCACCGC G C A G T C A CA
ab230506c06.r_C06.ab1	1	3.37e-04	G C A A T C A CCCATCAAAC
ab230506b02.r_B02.ab1	16	3.37e-04	CACCACACCA G C A A T C A ACGCGTTTTT
G04	18	3.54e-04	AGACCCACAC G C G A T T G ACCCAATGTA
ab230506e06.r_E06.ab1	35	3.94e-04	TCCCACATCC G C G C T C G CAAAGCAGT
ab230506a09.r_A09.ab1	28	5.69e-04	CCATCCGCGC G C A A T T A TTTTCACAAA
A-9	17	6.66e-04	CCCTTCAGAC G C A C T C A CTTAACAACA

MOTIF 5 width = 7 sites = 10 llr = 75 E-value = 8.4e+007

Simplified pos.-specific probability matrix
 A a : : : 2 3 :
 C : a 9 : : 4 a
 G : : : : 8 3 :
 T : : 1 a : : :



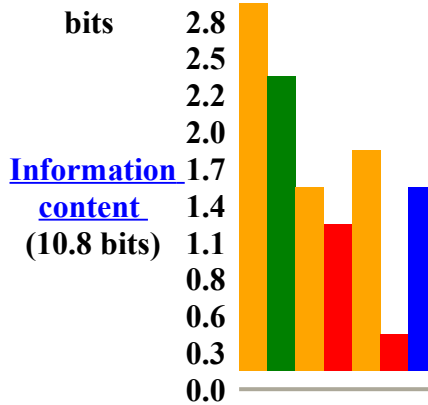
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Multilevel consensus sequence
 A C C T G C C
 A A
 G

NAME	START	P-VALUE	SITES
ab230506e11.r_E11.ab1	7	3.81e-05	ACAACC A C C T G G C AC CAATCAGA
ab230506b05.r_B05.ab1	56	3.81e-05	TGAGTCGGCC A C C T G G C TGTCGTC
ab230506f06.r_F06.ab1	18	1.17e-04	CCATTTAATA A C C T G C C TAAGACGGTC
ab230506a10.r_A10.ab1	31	1.17e-04	TATTCCACTC A C C T G C C CTACGCCCC
ab230506f07.r_F07.ab1	26	2.14e-04	ATTACACCTA A C C T G A C CAGCCCCTAA
ab230506c01.r_C01.ab1	26	2.14e-04	ACTAAAGTAA A C C T G A C CACACCTCCC
ab230506b01.r_B01.ab1	26	2.14e-04	CCAGGGTAAA A C C T G A C TTCACCAACC
ab230506e10.r_E10.ab1	23	3.89e-04	CACAAAACGG A C T T G C C CTCAGCACGC
ab230506e03.r_E03.ab1	33	3.89e-04	ACTCCCATAC A C C T A G C AGACCAATCG
A-2	17	6.56e-04	AAAGTGCACA A C C T A C C CTAACCGCTC

MOTIF 6 width = 7 sites = 12 llr = 90 E-value = 2.0e+007

Simplified pos.-specific probability matrix
 A : : 4 9 : 7 :
 C : : : : : 1 8
 G a : 6 1 6 1 2
 T : a : : 4 2 :



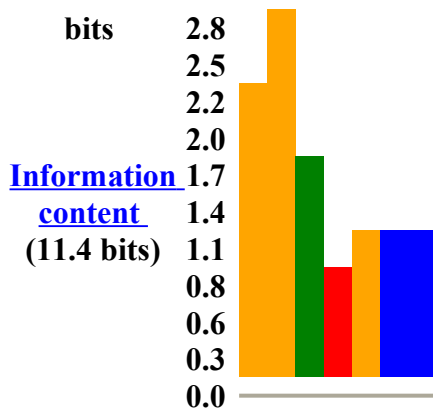
Multilevel consensus sequence
 G T G A G A C
 A T

NAME	START	P-VALUE	SITES
G03	33	6.54e-05	AAATCATCGG G T G A G T C AACGTCAATT
E03	19	6.54e-05	ATTCCCTATA G T G A G T C GTATTACGCA
A-1	38	1.42e-04	CTTCACTTAC G T A A G A C CAAAATC
ab230506d11.r_D11.ab1	10	1.42e-04	AGCTAACAA G T A A G A C AAAAAATCCGC
ab230506d10.r_D10.ab1	43	1.42e-04	AGATAACAAT G T A A G A C T

ab230506a01.r_A01.ab1	19	1.68e-04	AAACAGAACA	G T G G G A C	TAACAACATG
ab230506c03.r_C03.ab1	14	1.82e-04	TCACAAAACC	G T G A T A G	ACAATACACA
ab230506b11.r_B11.ab1	24	1.82e-04	AACAAAATT	G T G A T A G	TAATGCGCCA
ab230506e06.r_E06.ab1	5	2.00e-04	ATGA	G T G A T G C	GCATAACCCT
D04	59	2.98e-04	GATGAATTGC	G T A A T A C	
B03	36	2.98e-04	ACCATCAAAC	G T G A G C C	TAAATGA
ab230506d07.r_D07.ab1	2	2.98e-04	A	G T A A T A C	GGCAGCCACA

MOTIF 7 width = 7 sites = 10 llr = 79 E-value = 4.1e+006

Simplified pos.-specific probability matrix
A : : : 8 1 1 :
C : : 1 : 3 9 6
G 9 a : : 6 : 4
T 1 : 9 2 : : :



Multilevel consensus sequence
G G T A G C C
T C G

NAME	START	P-VALUE	SITES
ab230506d05.r_D05.ab1	8	8.79e-06	TTGAAAA G G T A G C G CCAGAGCCTG
A03	33	2.71e-05	AATAACAAAC G G T A G C C AAACACAACC
A-4	29	4.17e-05	CTCTCCTCAT G G T T G C C ATACCGAGGA
A-16	10	5.99e-05	AATTCGATA G G T A C C G TCATTACAGA
A-10	4	9.80e-05	TTC G G T A C C C GACATCACAT
ab230506a09.r_A09.ab1	58	1.08e-04	CACCGAACCA G G T T C C G CCTCCGCC
ab230506a10.r_A10.ab1	2	1.87e-04	A G G T A A C G CGACAATATT
A-6	35	2.09e-04	CAAACCCAG G G T A G A C AACCTCTGAC
G04	31	2.62e-04	ATTGACCCAA T G T A G C C CTTAACTGAG
ab230506d07.r_D07.ab1	9	2.62e-04	AGTAATAC G G C A G C C ACCTGCTCT

MOTIF 8 width = 7 sites = 10 llr = 75 E-value = 1.9e+008

Simplified pos.-specific probability matrix
A : 9 4 1 : 6 :
C a : 6 : : 2 :
G : 1 : : a : :
T : : : 9 : 2 a

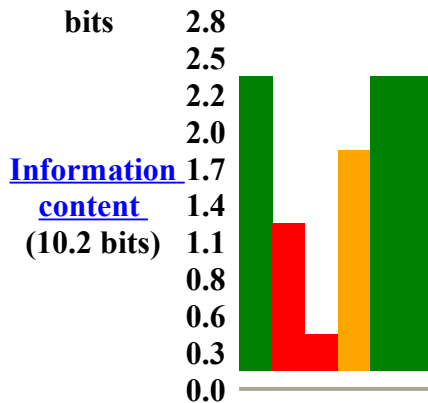
sequence

C

NAME	START	P-VALUE	SITES							
ab230506d11.r_D11.ab1	33	6.16e-05	CCGCATTTAT	A	T	G	G	G	C	CTAAGCCCAC
A-9	45	1.46e-04	TACACTAACC	A	T	G	T	G	C	CGA
ab230506g03.r_G03.ab1	11	1.46e-04	GCCTAGTCAC	A	T	G	T	G	C	ATCCGGACCC
E03	35	2.61e-04	CGTATTACGC	A	A	G	G	G	C	GAATTCGTTT
D03	25	2.61e-04	GCAACAGAAC	A	A	G	G	G	C	CAACACCGCT
ab230506e08.r_E08.ab1	31	2.61e-04	CAGCCTCTAG	A	A	G	G	G	C	ATCTTTGAAC
A-4	6	3.89e-04	TCTAT	A	T	G	C	G	C	GCCTTTTCTC
ab230506b11.r_B11.ab1	33	3.89e-04	TGTGATAGTA	A	T	G	C	G	C	CATGTGAATC
A-2	8	5.46e-04	ATATGAA	A	A	G	T	G	C	ACAACCTACC
ab230506d05.r_D05.ab1	22	5.96e-04	GCGCCAGAGC	C	T	G	G	G	C	ACATGGCACA

MOTIF 10 width = 6 sites = 10 llr = 71 E-value = 1.6e+008

Simplified pos.-specific probability matrix
 A : 9 6 : : :
 C : 1 2 : : :
 G : : : 7 : :
 T a : 2 3 a a

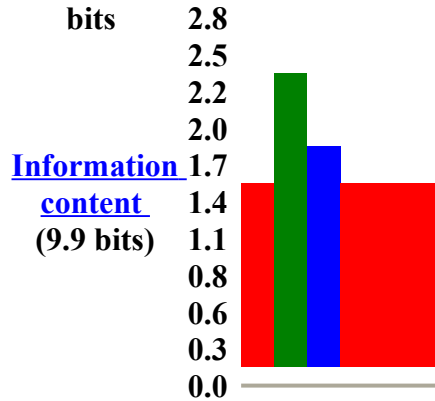


Multilevel consensus sequence
 T A A G T T
 C T
 T

NAME	START	P-VALUE	SITES							
F03	15	1.43e-04	GACAACAATT	T	A	A	G	T	T	AAATCAACAA
A-15	38	1.43e-04	CCATTAGTTG	T	A	A	G	T	T	CCTAAGT
ab230506c12.r_C12.ab1	6	1.43e-04	ACTTA	T	A	A	G	T	T	GAGGTTTTCA
ab230506e01.r_E01.ab1	24	2.20e-04	ATCCCTACAA	T	A	T	G	T	T	ACCATCCAAA
ab230506g08.r_G08.ab1	21	3.37e-04	CCACAGTACC	T	A	C	G	T	T	AATCCAACAT
ab230506f08.r_F08.ab1	21	3.37e-04	CCACAGTACG	T	A	C	G	T	T	AATCCAACAT
ab230506g05.r_G05.ab1	3	5.34e-04	TA	T	A	A	T	T	T	CACCCAAACT
ab230506d09.r_D09.ab1	35	5.34e-04	TTTTAAACCA	T	A	A	T	T	T	AATCCCCTTT
ab230506g01.r_G01.ab1	37	6.40e-04	GTAACCATGT	T	A	T	T	T	T	GCCGGCAC

MOTIF 11 width = 6 sites = 10 llr = 69 E-value = 2.6e+009

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

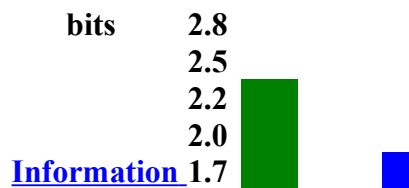


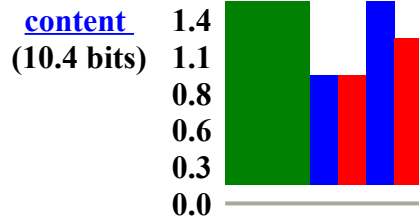
Multilevel consensus sequence A T C A A A

NAME	START	P-VALUE	SITES
B03	29	1.03e-03	CAACACCACC A T C A A A CGTGAGCCTA
ab230506f06.r_F06.ab1	37	1.03e-03	AGACGGTCGA A T C A A A AAGAATC
ab230506e05.r_E05.ab1	21	1.03e-03	GGATAAATGA A T C A A A AACACAACC
ab230506e04.r_E04.ab1	37	1.03e-03	GAAGGTTTCAT A T C A A A ATAGACCC
ab230506e03.r_E03.ab1	7	1.03e-03	ACAACC A T C A A A TGGAACACTC
ab230506d12.r_D12.ab1	18	1.03e-03	CGACTACACC A T C A A A AGTATTATCT
ab230506d08.r_D08.ab1	10	1.03e-03	GTGCCCTAT A T C A A A GTTTCGCTG
ab230506d01.r_D01.ab1	32	1.03e-03	ACAGCAGCCA A T C A A A TGGCAGACAC
ab230506c06.r_C06.ab1	11	1.03e-03	GCAATCACCC A T C A A A CAAACCCGCC
ab230506b08.r_B08.ab1	6	1.03e-03	GTAAC A T C A A A CCATAAACAG

MOTIF 12 width = 7 sites = 10 llr = 72 E-value = 4.1e+009

Simplified pos.-specific probability matrix
 A : : : : 6 : 9
 C : : 3 6 : a :
 G : : : 1 : : :
 T a a 7 3 4 : 1



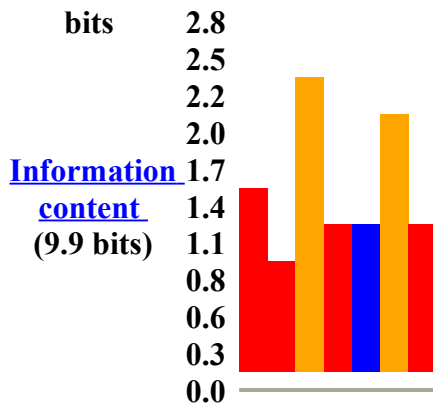


Multilevel consensus sequence
 T T T C A C A
 C T T

NAME	START	P-VALUE	SITES
ab230506d09.r_D09.ab1	8	1.36e-04	GTAAGCA T T T C A C A GCAAGGAAGT
ab230506a09.r_A09.ab1	36	1.36e-04	GCGCAATTAT T T T C A C A AAACGCACCG
ab230506b02.r_B02.ab1	29	1.68e-04	ATCAACGCGT T T T T T C A AACACTGGCA
ab230506c08.r_C08.ab1	24	2.26e-04	TGCAATACAC T T T T A C A CTAAAGGCCG
ab230506a07.r_A07.ab1	2	2.26e-04	C T T T T A C A TAATTGCAAC
ab230506e08.r_E08.ab1	10	2.49e-04	ATGAAACGG T T T G T C A ACGCCAGCCT
A-12	15	3.64e-04	AACACACCCA T T C C T C A TGACCCTTAT
A-8	1	4.97e-04	T T C C A C A CACATATGCC
ab230506a06.r_A06.ab1	5	4.97e-04	AAAA T T C C A C A AAAACACTGC
A-4	16	5.71e-04	ATGCGCGCCT T T T C T C T CCTCATGGTT

MOTIF 13 width = 7 sites = 10 llr = 69 E-value = 1.0e+011

Simplified pos.-specific probability matrix
 A a 8 : 9 1 : 9
 C : 2 : : 9 2 :
 G : : 9 1 : 8 1
 T : : 1 : : : :



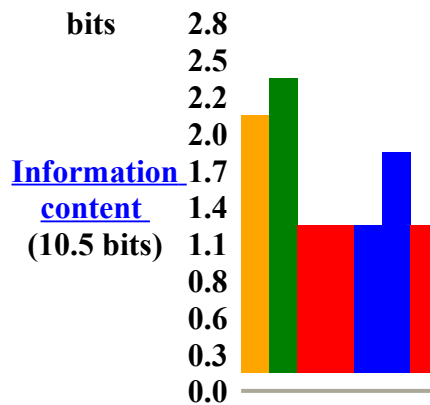
Multilevel consensus sequence
 A A G A C G A
 C C

NAME	START	P-VALUE	SITES
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A-3	14	1.06e-04	GACCGAAACT	A A G A C G A	CCTATAAGCC
ab230506f08.r_F08.ab1	40	1.06e-04	CCAACATAGA	A A G A C G A	TTCG
ab230506g08.r_G08.ab1	40	2.76e-04	CCAACATAGA	A C G A C G A	TTCG
ab230506g04.r_G04.ab1	33	2.76e-04	TACTAGTCCA	A A G G C G A	ATAGGAAACA
ab230506f06.r_F06.ab1	26	2.76e-04	TAACCTGCCT	A A G A C G G	TCGAATCAAA
ab230506e12.r_E12.ab1	7	2.76e-04	CAATAT	A C G A C G A	AGTATTGCGA
A04	12	4.97e-04	GTACTAACAC	A A G A C C A	GACTTTATAG
ab230506g02.r_G02.ab1	43	4.97e-04	AATCCCCTAC	A A G A C C A	
ab230506f07.r_F07.ab1	9	7.11e-04	TCCTCACA	A A G A A G A	ATTACACCTA
ab230506d12.r_D12.ab1	4	8.58e-04	AAC	A A T A C G A	CTACACCATC

MOTIF 14 width = 7 sites = 10 llr = 73 E-value = 2.5e+009

Simplified pos.-specific probability matrix
A : : 9 9 : : 9
C 2 : : : 6 a :
G 8 : 1 : 4 : :
T : a : 1 : : 1



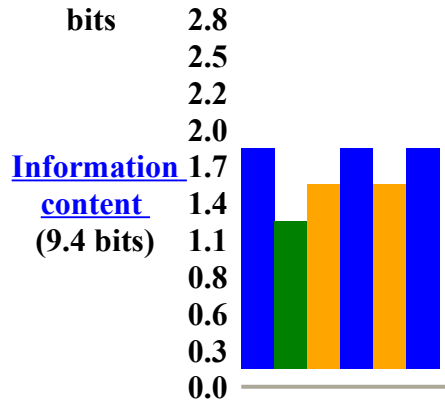
Multilevel consensus sequence
G T A A C C A
C G

NAME	START	P-VALUE	SITES		
ab230506d09.r_D09.ab1	1	5.73e-05	G T A A G C A		TTTCACAGCA
ab230506b11.r_B11.ab1	1	5.73e-05	G T A A G C A		ACTCGCAACA
A-8	31	1.76e-04	AAGTCACAAT	G T A A C C A	CCGCGCAGTC
ab230506g01.r_G01.ab1	27	1.76e-04	CACACTGATA	G T A A C C A	TGTTATTTTG
ab230506e04.r_E04.ab1	7	1.76e-04	AAACGA	G T A A C C A	CCTATAACAA
D04	31	3.07e-04	GTAATACGTA	G T A A G C T	CTGCAGTCGA
ab230506e05.r_E05.ab1	1	3.07e-04		G T G A C C A	CGCGGATAAA
ab230506f03.r_F03.ab1	27	4.36e-04	GAAAAACGTC	G T A T C C A	CAAATAATTC
ab230506c01.r_C01.ab1	42	5.55e-04	CCACACCTCC	C T A A G C A	CA
ab230506f07.r_F07.ab1	39	8.03e-04	TGACCAGCCC	C T A A C C A	TCACT

MOTIF 15 width = 6 sites = 10 llr = 65 E-value = 1.0e+011

Simplified A : : 3 : 3 :

pos.-specific probability matrix C a 4 : a : a
 G : : 7 : 7 :
 T : 6 : : : :

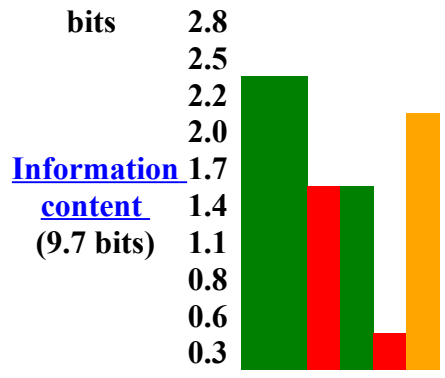


Multilevel consensus sequence C T G C G C
 C A A

NAME	START	P-VALUE	SITES
A-7	41	1.04e-04	ACCCTCAACG C T G C G C ACGG
ab230506c12.r_C12.ab1	28	1.04e-04	TTCATAAGCC C T G C G C AATACACCAC
ab230506f10.r_F10.ab1	23	2.62e-04	CACCCATAAC C C G C G C GAGCGGCTCA
ab230506a09.r_A09.ab1	22	2.62e-04	TTCGTGCCAT C C G C G C GCAATTATTT
ab230506e07.r_E07.ab1	31	7.96e-04	GTCAAACCAA C T A C G C TTTCCGCTTG
ab230506e05.r_E05.ab1	49	7.96e-04	GGCCGTTCGA C T A C G C TAATTATCCC
ab230506a10.r_A10.ab1	38	7.96e-04	CTCACCTGCC C T A C G C CCCCCTC
ab230506a06.r_A06.ab1	18	7.96e-04	CACAAAAACA C T G C A C ACAACTTCCA
F03	33	1.60e-03	ATCAACAAAA C C G C A C TCCCGTGCTA
C03	31	1.60e-03	GAACACACTC C C G C A C GACACCATAG

MOTIF 16 width = 6 sites = 10 llr = 67 E-value = 3.4e+009

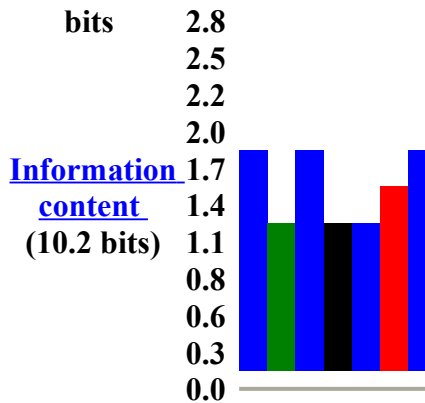
Simplified pos.-specific probability matrix A : : a : 6 :
 C : : : 3 3 2
 G : : : : : 8
 T a a : 7 1 :



ab230506b01.r_B01.ab1	16	1.97e-04	CTACACGAAT	C C A G G G T	AAAACCTGAC
ab230506f10.r_F10.ab1	40	3.92e-04	AGCGGCTCAC	C C A C G G C	AGG
F03	40	4.23e-04	AAACCGCACT	C C C G T G C	TACA
ab230506f02.r_F02.ab1	28	7.36e-04	TTTATATACC	C C C C A G C	TCAACCATTA
ab230506f08.r_F08.ab1	11	9.17e-04	TCCTCAAACA	C C A C A G T	ACGTACGTTA

MOTIF 18 width = 7 sites = 10 llr = 71 E-value = 3.8e+010

Simplified pos.-specific probability matrix
 A : 3 : : : a :
 C a : a 5 8 : a
 G : : : : 2 : :
 T : 7 : 5 : : :



Multilevel consensus sequence
 C T C C C A C
 A T G

NAME	START	P-VALUE	SITES		
ab230506g10.r_G10.ab1	10	1.09e-04	TATAAAATA	C T C T C A C	ATCGCTGACA
ab230506b10.r_B10.ab1	49	1.09e-04	ATGCCCATCA	C T C T C A C	
A-11	43	2.74e-04	CTGGCATAGA	C T C C C A C	C
ab230506e06.r_E06.ab1	24	2.74e-04	ATAACCCTTA	C T C C C A C	ATCCGCGCTC
ab230506e02.r_E02.ab1	15	2.74e-04	ACTAAAACGC	C T C C C A C	CCACTCCAAT
A-6	45	3.26e-04	GGTAGACAAC	C T C T G A C	
A-14	23	4.05e-04	CGCACAATAT	C T C C G A C	TACATCGCCC
C05	9	6.08e-04	ATACATGC	C A C T C A C	GCCAAGAACA
ab230506e03.r_E03.ab1	18	6.08e-04	TCAAATGGAA	C A C T C A C	TCCATACAC
ab230506a01.r_A01.ab1	42	9.13e-04	CATGGCATAC	C A C C A C	AA

MOTIF 19 width = 7 sites = 10 llr = 73 E-value = 1.1e+009

Simplified pos.-specific probability matrix
 A : 7 a 1 : : :
 C 1 : : : : 5 a
 G 7 : : : : 1 5 :
 T 2 3 : 9 9 : :

bits 2.8

NAME	START	P- VALUE	SITES
A-9	33	1.03e-03	ACTTAACAAC A A T A C A CTAACCATGT
A-4	45	1.03e-03	CATACCGAGG A A T A C A
ab230506e07.r_E07.ab1	9	1.03e-03	AAGAAAAA A A T A C A GAACAAGTCA
ab230506c12.r_C12.ab1	34	1.03e-03	AGCCCTGCGC A A T A C A CCACTGAT
ab230506c08.r_C08.ab1	17	1.03e-03	AGAGAAATGC A A T A C A CTTTTACTACT
ab230506c03.r_C03.ab1	23	1.03e-03	CGTGATAGAC A A T A C A CAAACTTGAG
ab230506a12.r_A12.ab1	28	1.03e-03	CTAACCCAAC A A T A C A AACCAATTAC
G04	2	1.86e-03	A A A T A C C AGACCCACAC
ab230506g04.r_G04.ab1	3	1.86e-03	TA A A T A C C CAAGCAGCAA
ab230506e02.r_E02.ab1	32	1.86e-03	CCACTCCAAT A A T A C C GACACAAC TA