

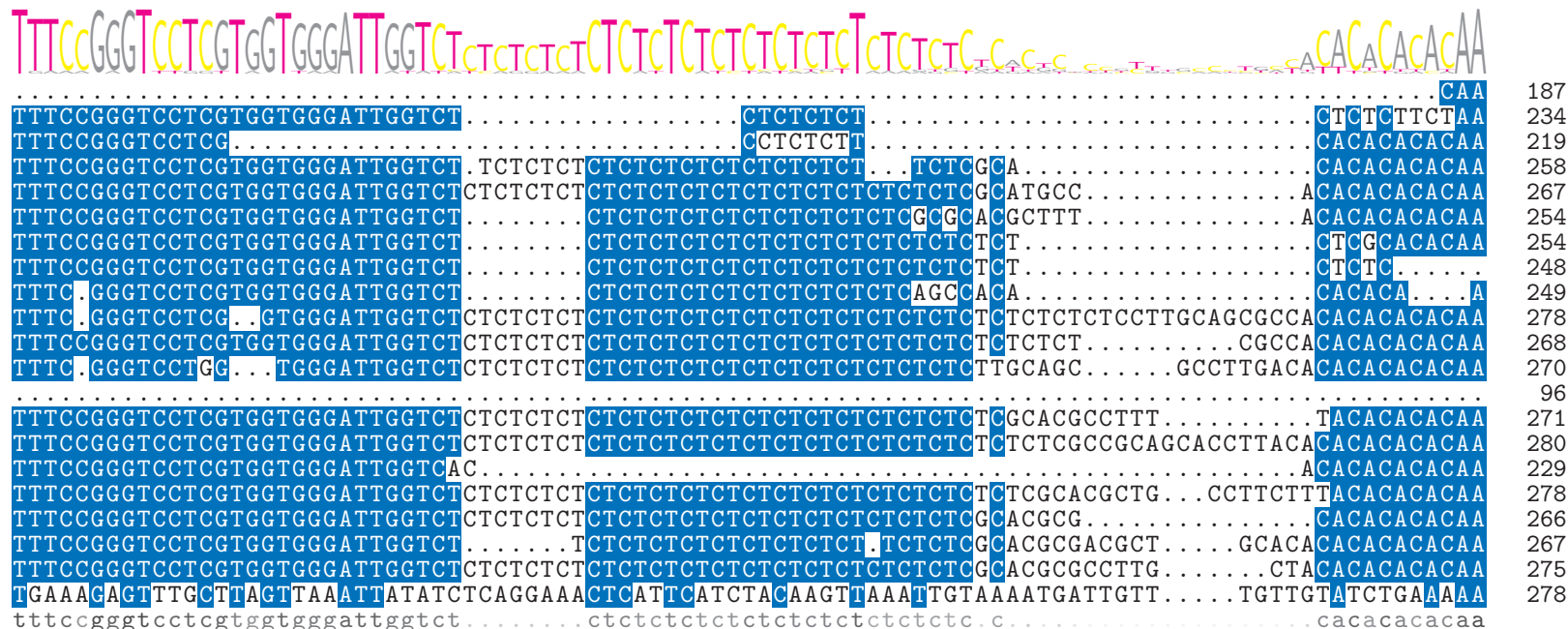
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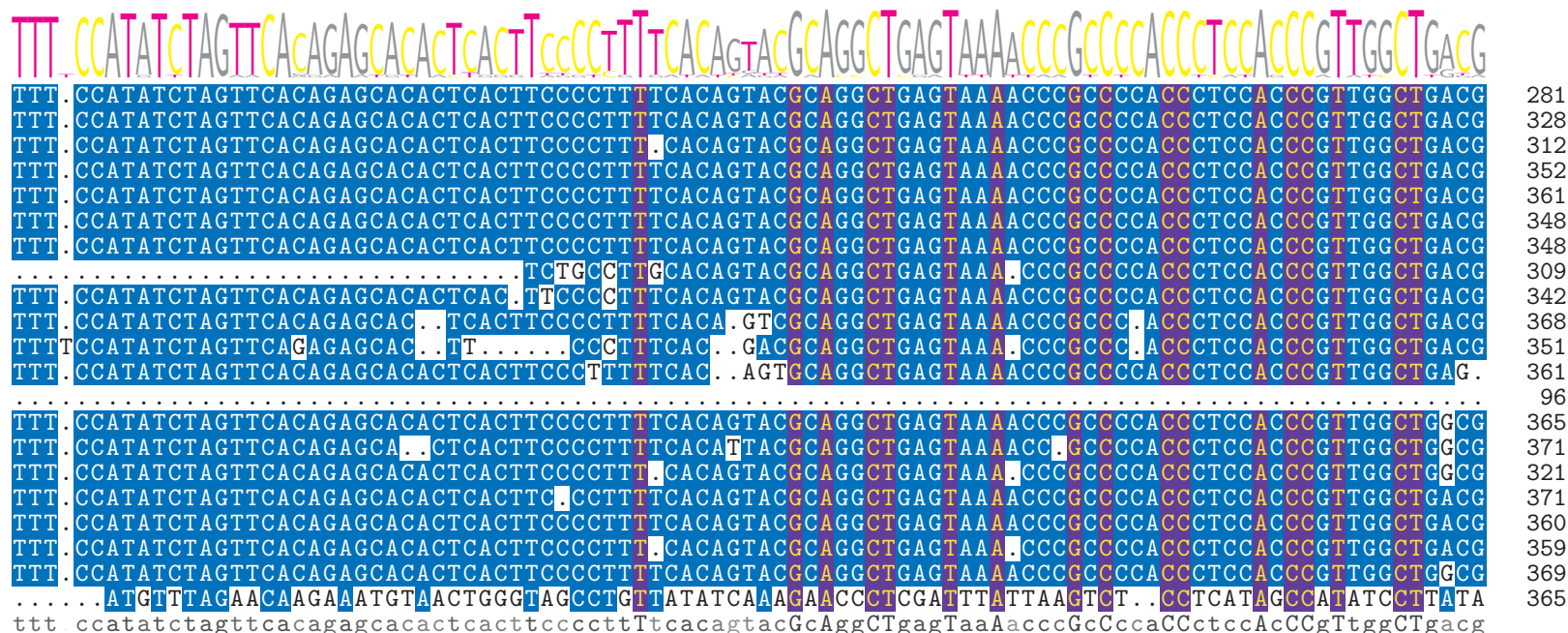
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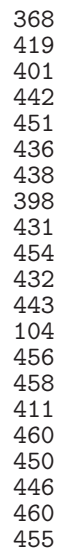
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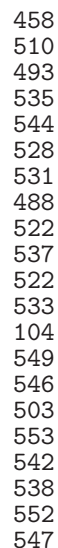
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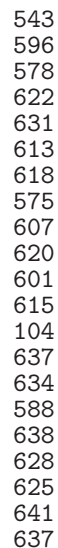
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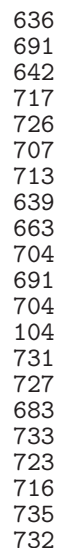
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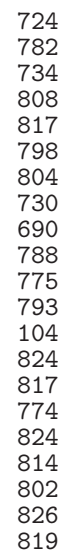
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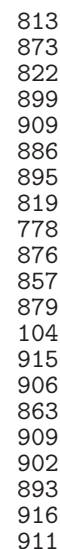
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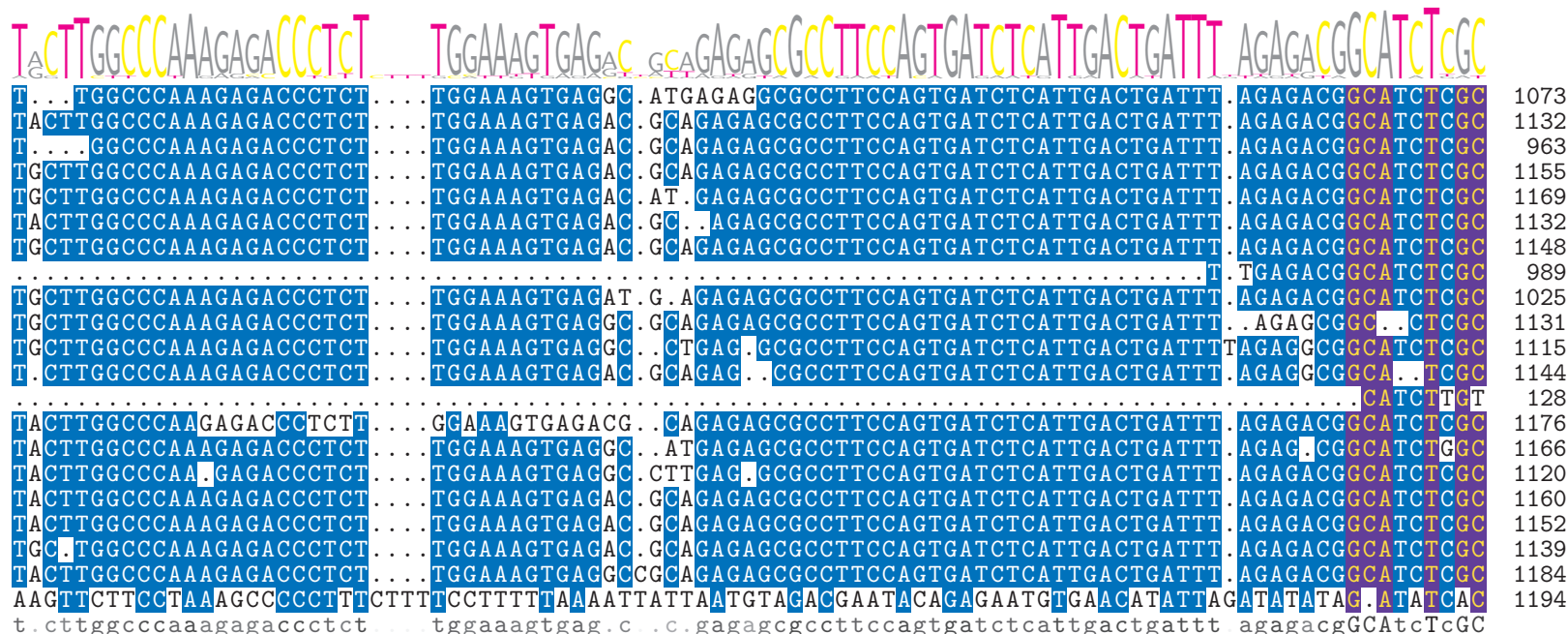


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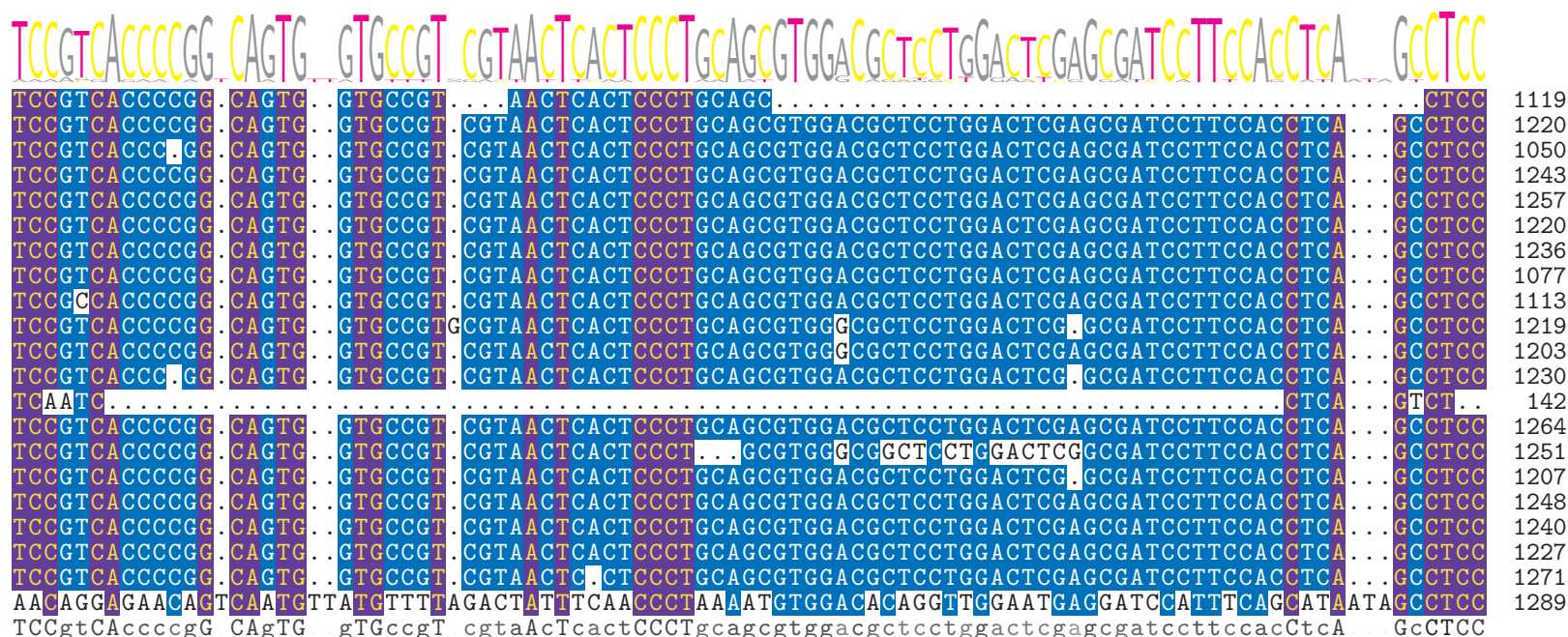
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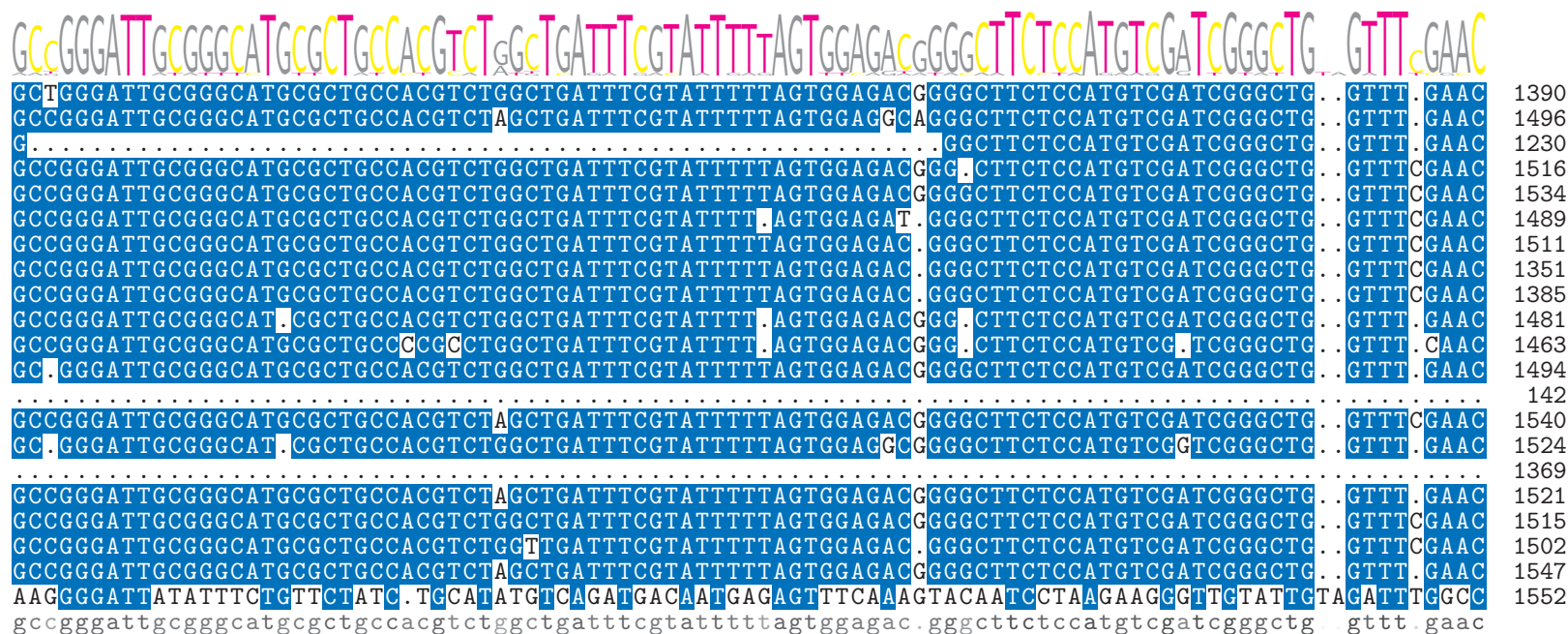
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tig00008216:94751-135048(-)	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCA	TTCTGTCATCGGCCTCC	TGAGTA	1197	
tig00002380:120727-159743()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1424	
tig00008216:53978-94751(-)	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1441	
tig00002380:1146-40745()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGA...TTCTGTCATCGGCCTCC	TGAGTA	1398	
tig00008411:94672-134529()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1419	
tig00008411:217104-257759()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1259	
tig00008411:257759-297618()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1293	
tig00002380:80433-120727()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GATTCTCTGTCATCGGCCTCC	TGAGTA	1392	
tig00008215:19898-58526(-)	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1374	
tig00008215:58526-97877(-)	GGCCTAGACTGCAGT	GCGGTGGCG...ATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1403	
tig00008216:21673-53978(-)					142	
tig00008411:14398-55544()	GGC...TAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1447	
tig00008215:97877-137448(-)	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1434	
tig00008411:55544-94672()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCT		1369	
tig00002380:40745-80433()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1429	
tig00008411:176298-217104()	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1422	
tig00008215:0-19898(-)	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCA	TGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1410
tig00008216:0-21673(-)	GGCCTAGACTGCAGT	GCGGTGGCGCGATCTTGGCTCACCGCAACCTCTGCCTCCCGGTTTCAA	GCGATTCTCTGTCATCGGCCTCC	TGAGTA	1455	
tig00008411:297618-338078()	TTAAATAG...TGGAATCTTATG	...TCAGGGATTACTGATGTTTCAGCAAGCTAAATTCGTAC	CAGGGAGACAATGTAAACATTT	...AGA	1458	
consensus	ggccTAGacTGcagT	gcggTGGcgcgaTcTtGGcTcACcgcaacctctgcctcccggtttcaa	gcgattctcCtgcacTcggcctcc	tgagta		

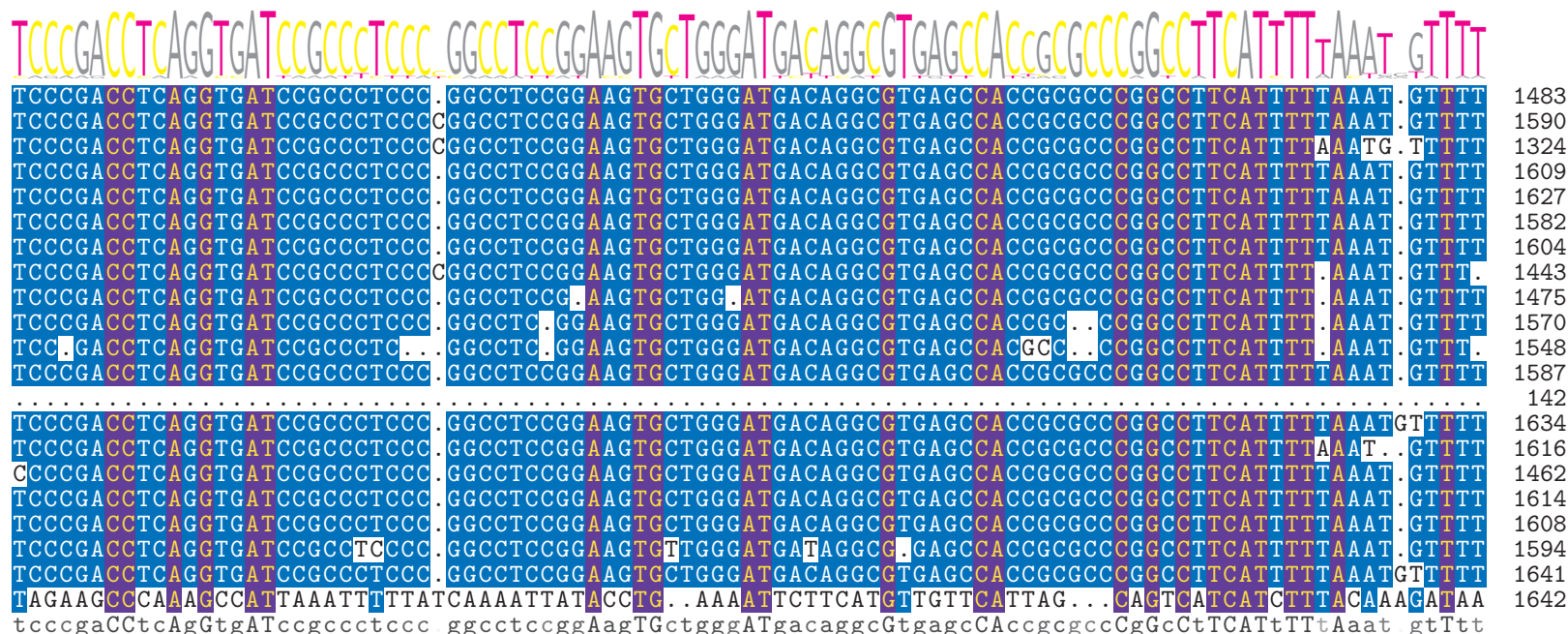
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consensus



logo

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consensus

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 CCCACAGACGGG.TCTCATCATTTCTTTGCAACCCCTCCTGCCCGGGCTCTCAAAGTgctTGGCGTG.CGGG..TG.AGCCACTCGC...GG 1631
 CCCACAGACGGGGTCTCATCATTTCTTTGCAACCCCTCCTGCCCGGGCTCTCAAAGTgctTGGCGTG.CAGGCGTG.AGCCACTCGCCT..GG 1675
 ..GTCTCA.. 148
 CCCACAGACGGGGTCTCATCATTTCTTTGCAACCCCTCCTGCCCGGGCTCTCAAAGTgctTGGCGTGA.CGGGCGTG.AGCCACTGCGCCTGGA 1724
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 CCCACAGACGGGGTCTCATCATTTCTTTGCAACCCCTCCTGCCCGGGCTCTCAAAGTgC.CGGCGTGA.GCAGCGTG.AGCCACTGCGCCTGGA 1732
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 cccAcAgAcgGggTCTcATtTtctTtGCAAcCctCctgCCcgggctTcTcAaagTgctGgCgtga.cgggcgTgagccactgcgCctgga

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 tig00008215:0-19898(-)
 tig00008216:0-21673(-)
 tig00008411:297618-338078()
 consensus

Sequence	Position	Count
CTCCGGGGAATGACTCACGA	1	16
CTCCGGGGAATGACTCACGA	2	16
CTCCGGGGAATGACTCACGA	3	16
CTCCGGGGAATGACTCACGA	4	16
CTCCGGGGAATGACTCACGA	5	16
CTCCGGGGAATGACTCACGA	6	16
CTCCGGGGAATGACTCACGA	7	16
CTCCGGGGAATGACTCACGA	8	16
CTCCGGGGAATGACTCACGA	9	16
CTCCGGGGAATGACTCACGA	10	16
CTCCGGGGAATGACTCACGA	11	16
CTCCGGGGAATGACTCACGA	12	16
CTCCGGGGAATGACTCACGA	13	16
CTCCGGGGAATGACTCACGA	14	16
CTCCGGGGAATGACTCACGA	15	16
CTCCGGGGAATGACTCACGA	16	16

The sequence logo displays the information content of each position in the 16bp motif. The y-axis represents the information content in bits, ranging from 0 to 2.0. The x-axis represents the 16 positions of the motif. The motif is CTCCGGGGAATGACTCACGA. The logo shows high conservation for the first 10 positions, with the 11th position (A) being the most conserved. The last 6 positions (GACTCAG) show lower conservation, with the 16th position (G) being the least conserved.

logo

tig00002380:159743-198526()	T.....C	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGCG...AGGCGAG	1725
tig00008411:134529-176298()	T.....C	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGGCGAGGGCGAG	1855
tig00008216:94751-135048(-)	TCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGG...GGCG...AGGCGAG	1544
tig00002380:120727-159743()	T.....C	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGGCG...GAGGCGAG	1855
tig00008216:53978-94751(-)	T.....C	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGGCG...GAGGCGAG	1872
tig00002380:1146-40745()	TCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGGCG...AGGCGAG	1820
tig00008411:94672-134529()	TT.....C	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGGCG...GAGGCGAG	1852
tig00008411:217104-257759()	C.....	TTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGG...GCCGCGAG	1676
tig00008411:257759-297618()	T.....	TTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGG.....GCGAG	1702
tig00002380:80433-120727()	C.....	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTT...TTTCAGGCGGAGTCTCGCTCTGGCAGGCGAGG.CG.....	1815
tig00008215:19898-58526(-)	C.....	TTTCTTGA...ATTATCTTATGATT	ATTGTGTACTTA...TTTCAGACGGAGTCTCGCTCTGGGCGG.AGGC.TG.....	1777
tig00008215:58526-97877(-)	C.....	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGTGAAGTCTCGCTCTGGCGGGCGGGG.GGC...AG	1840
tig00008216:21673-53978(-)			148
tig00008411:14398-55544()	C.....	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGAGC.GGGGGCGAG	1892
tig00008215:97877-137448(-)		TTTGTGTACTTATTTT.....	1696
tig00008411:55544-94672()	T.....	TCTTGATGAATTATCTTATGATT	ATTGTGTACTTA...TTTCAGACGGAGTCTCGCTCTGGGCGGGGCG...GAGGCGA.	1693
tig00002380:40745-80433()	T.....C	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGGCG.....GAG	1849
tig00008411:176298-217104()	C.....	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGGCGGAGGGCGAG	1861
tig00008215:0-19898(-)	TT.....C	TTTCTTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGC...CTGGGCGGGGCG.....GAG	1839
tig00008216:0-21673(-)	CTTTCTGTCTTTCA	TTTATTGATGAATTATCTTATGATT	ATTGTGTACTTATTTTCAGACGGAGTCTCGCTCTGGGCGGGGCGGGGGCGGAG	1918
tig00008411:297618-338078()	CAGCACATAAACAGATC	CAAAAGACAAAAACACATGATT	ATCTCAATAGATG...CAGAAAAGGCCTTTGACAAAATTCAACAACACTTCAT	1903
consensus	tttcttgatgaattatcttatgattt	aTtTgtgTActTattttcagacggagtctcgctctgggcgggg.....ggcgag	

logo

tig00002380:159743-198526()	GCGAGG....	CACAGCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1810	
tig00008411:134529-176298()	GGCGAA....	CACAGCGCATCGCTTT....	GGAAGCCG...GCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1938	
tig00008216:94751-135048(-)	GC.....	CACAGCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1625	
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tig00002380:1146-40745()	G.....	CACAGCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1900	
tig00008411:94672-134529()	GCGAGG....	CACAGCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1937	
tig00008411:217104-257759()	GCGAGG....	CACAGCGCATCGCTTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1762	
tig00008411:257759-297618()	GCGAGG....	CACAGCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1787	
tig00002380:80433-120727()	GCGAA....	CA...GCGCTTCGCTTT....	GAGCGCA...GCAGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1894	
tig00008215:19898-58526(-)	GCGAG....	CA...GC...ATCGCTTT....	GGAAGGTG...GCAGCCTTTCAAAGCCCCATTTCATATGCACAGAGCCT	TATTCCCTTCCTGG	1854	
tig00008215:58526-97877(-)	GCGAG....	CACAGCGCATCGCTTT....	G...AGCGC...GCAGCCTTTCAAAGCCCCATTTC...ATGCACAGAGCCT	TATTCCCTTCCTGG	1917	
tig00008216:21673-53978(-)					148	
tig00008411:14398-55544()	GCGAG....	CGGC	GCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	T...ATTCCCTTCCTGG	1975
tig00008215:97877-137448(-)			TCAGGCGGAATA	T...TCCCTTCCTGG	1721	
tig00008411:55544-94672()	...AGA....	CACAGCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1775	
tig00002380:40745-80433()	GCGAGG....	CGAGCGAGCTCGCGGCT....	GGAAGCCGC...AACGCCTTCAAA.....CACAGAGCCT	TATTCCCTTCCTGG	1917	
tig00008411:176298-217104()	GCGAG....	CACAGCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1945	
tig00008215:0-19898(-)	GCGAG....	CACAGCGCATCGCTTT....	GGAAGCCATGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	1923	
tig00008216:0-21673(-)	GCGAGGCGAG	CACAGCGCATCGCTTT....	GGAAGCCGCGGCAACGCCTTTCAAAGCCCCATTTCGTATGCACAGAGCCT	TATTCCCTTCCTGG	2006	
tig00008411:297618-338078()	GCTAAAAACTCT	CAATAAATAGGTGTCGAT	GGGACATATCTCAAAATAATAAGAGCTATCTATGACAAACCCACAGCCAA	TATCATAC	1998	
consensus	gcgag.	cacagcgcatcgcttt	ggaagccgcgggcaacgcctttcaaagccccatttcgtatgcacagagcct	TattccctTcctgG		