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 tig00008216:53978-94751(-)
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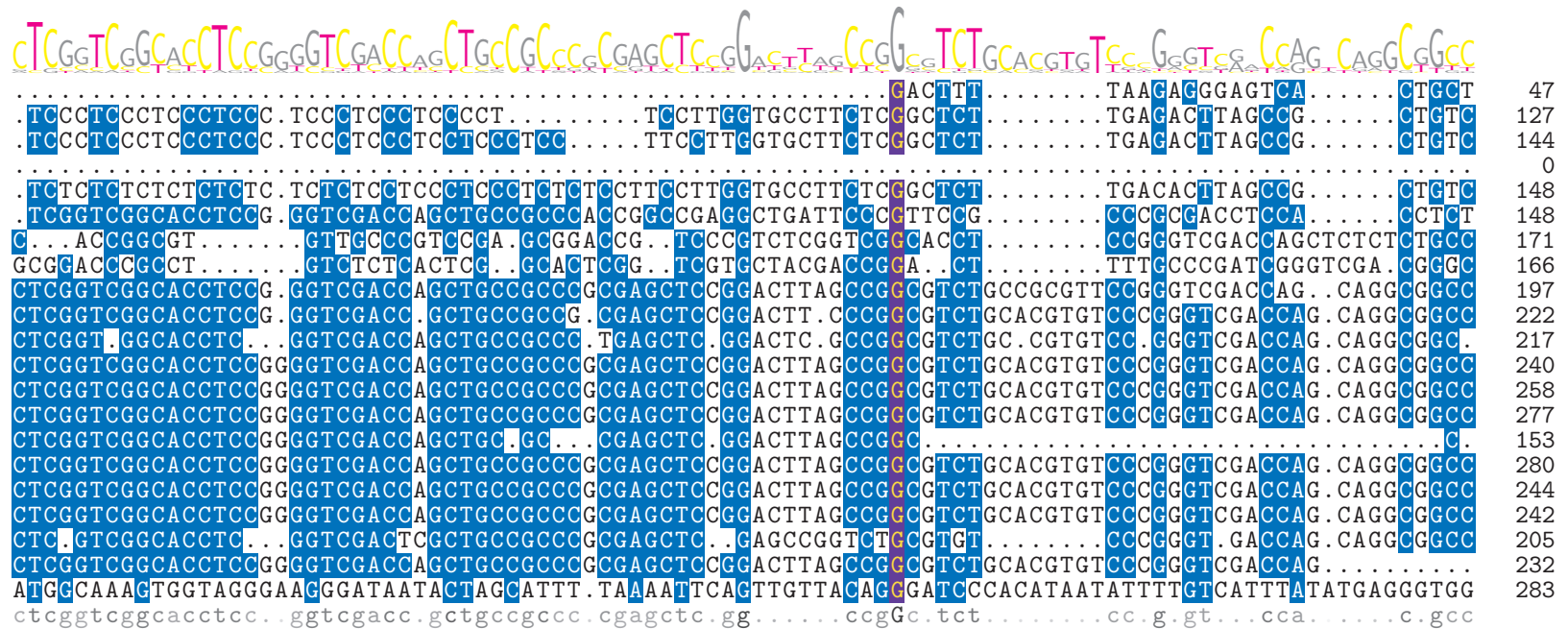
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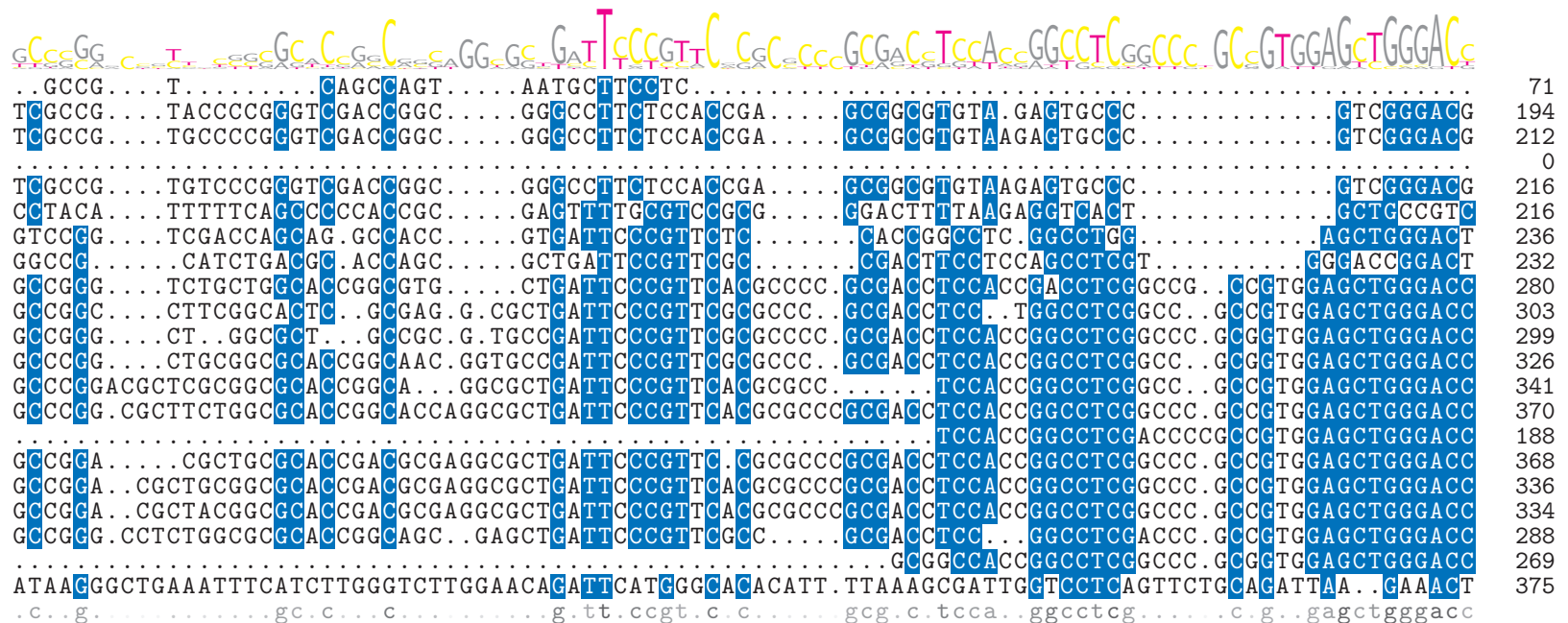
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consensus

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 tig00008411:297618-338078()
 consensus



<p> AGCGGACGCGCGTCCCCGTCTCG GTCGGCAC </p>		71
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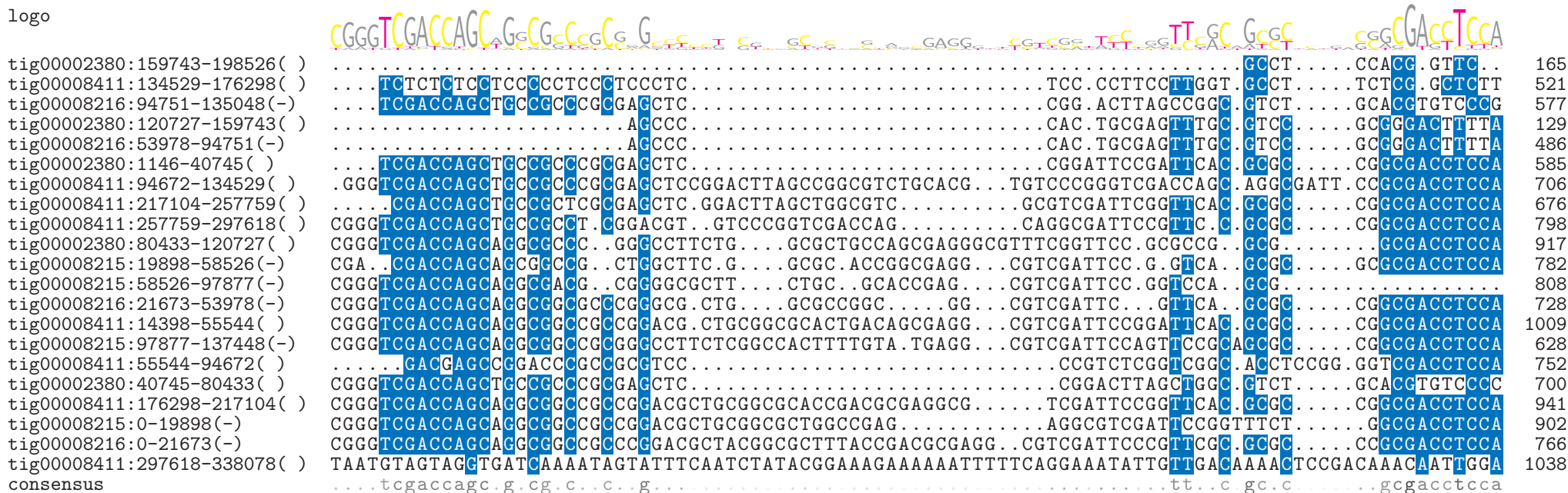
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consensus c g . . gct.tct cg.c..tc. g. . . . c. cg..c. c.t.t. cgt.	

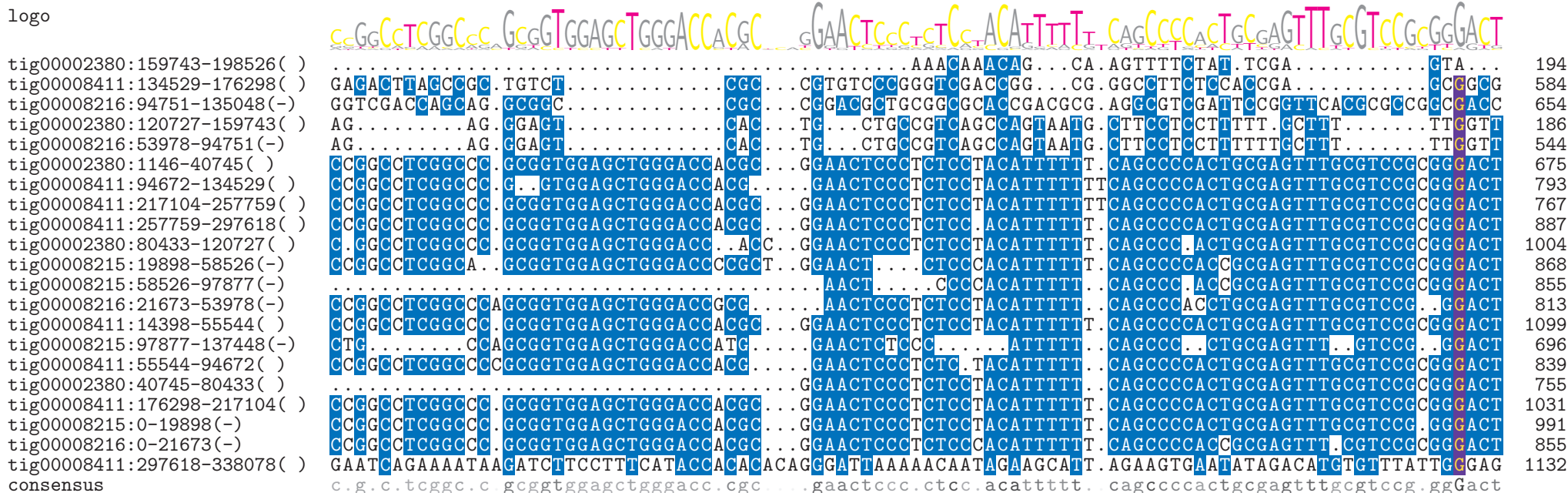
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consensus		

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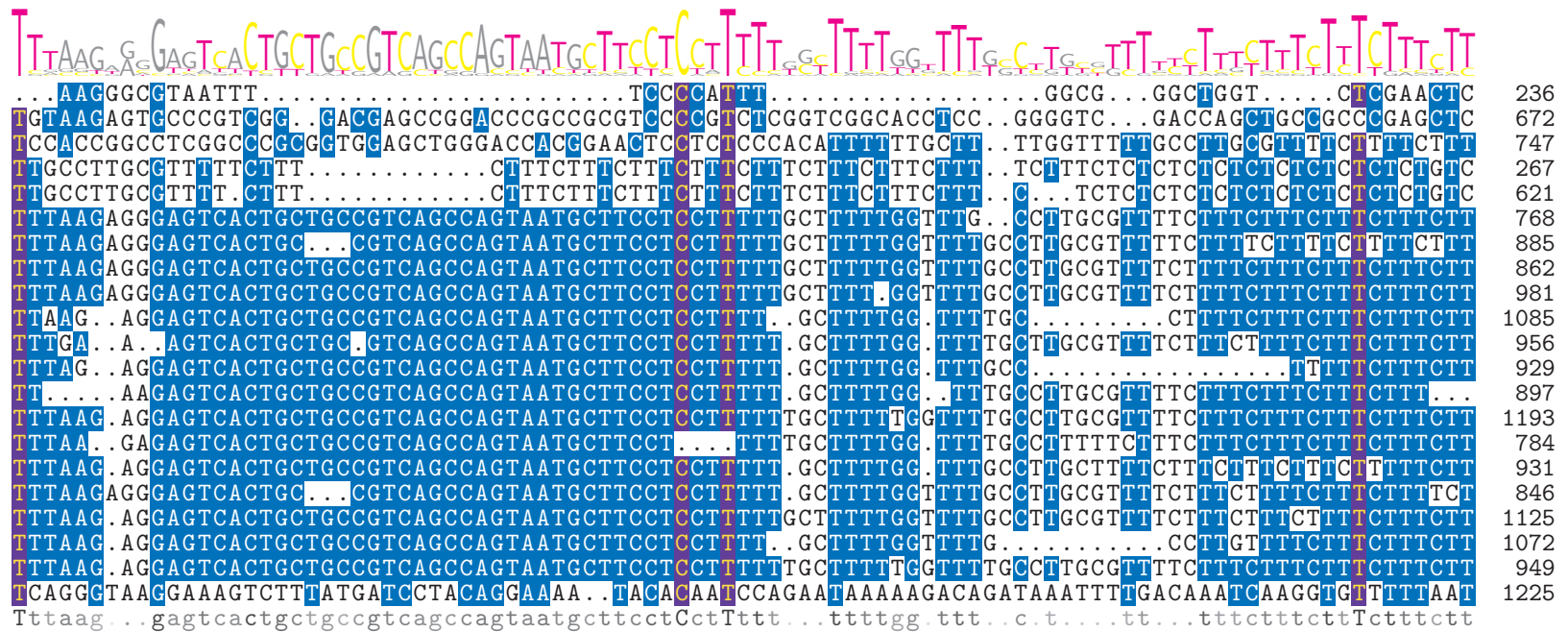
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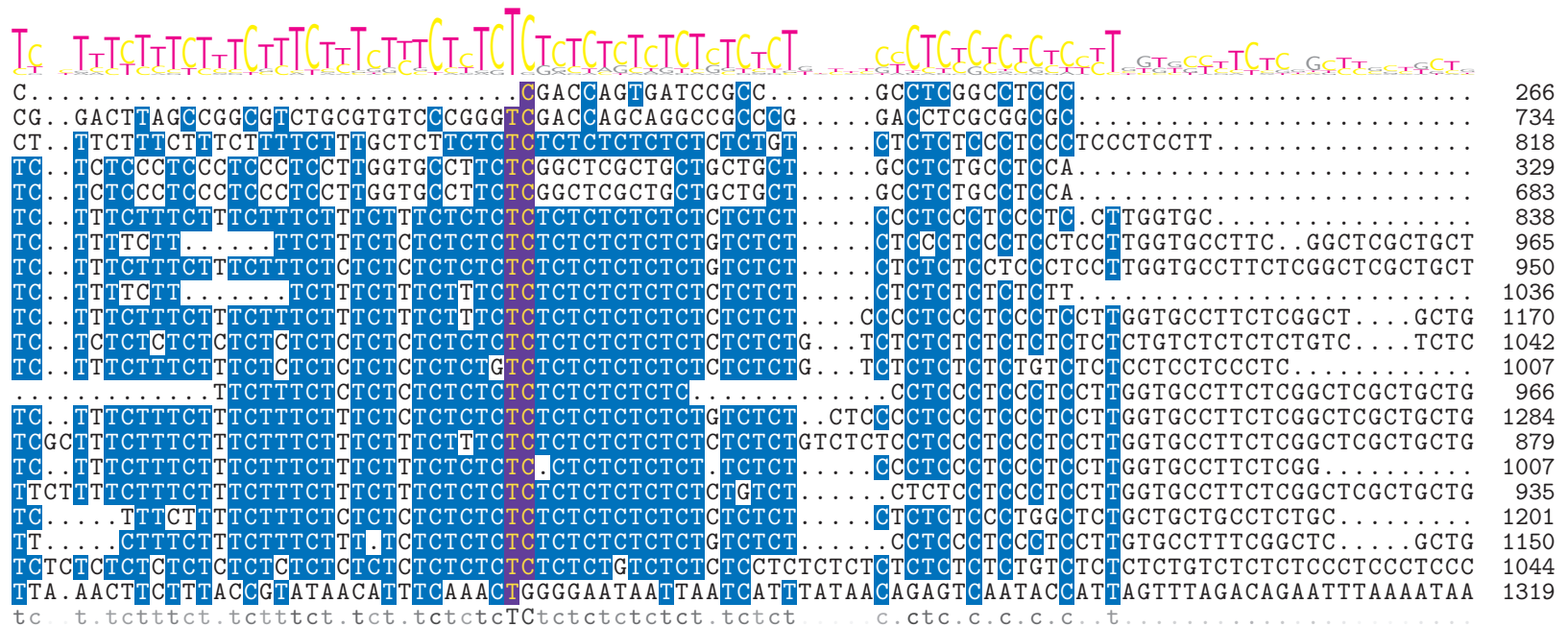
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consensus



Logo

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 tig00008215:58526-97877(-) ACTCCCgACC TAGTGATCcGCCC GCCTCGGCC TCCCAAG... CGATTCCCTTCCTTTTT 1145
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 tig00008411:297618-338078() AATGcAGTcAA TAATAAGTcAACA TGTTcAGTcTACCAAATCGTGTATAAAATTAAGAAAAATGATTATTTCTAGTTTAgCTAcAcTGAAAATTGGA 1502
 consensus actcccGACC tagtgatcGccc gcctcgGCC TcccaagactgctgggagttacagatgtgagccaccatgcccgGCCgattcccttcctTTTT

[illegible]

Logo

Sequence logo showing nucleotide conservation across 1670 sequences. The y-axis represents information content in bits. The x-axis shows positions from 1 to 25. The logo is color-coded: A (green), C (blue), G (red), T (orange). Below the logo, the consensus sequence is shown: CCGC.CCGCCTCGGCCTCCC.AAA.GACTGCTGG...GGTACAGATGTTGAGCCACCATGCCCGGCCGATTCCTTCCCTTT. The sequences are aligned in blocks of 10, with the first block starting at position 1 and the last block ending at position 25. The sequences are numbered on the right from 1 to 1670.

logo

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tig00008216:94751-135048(-)	CGAAGCCCCATTTCATTTCACATACACGTGTATGTATATCCTTCCTCCCTTC	CTTCATTcATTAT	TTATTAATAATTTT	CGTTTATTTA	1246
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tig00008215:19898-58526(-)	.GAAGCCCCATTTCATTTCACATACACGTGTATGTATATCCTTCCTCCCTTC	CTTCATTcATTAT	TTATTAATAATTTT	CGTTTATTTA	1425
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tig00008216:0-21673(-)	CGAAGCCCCATTTCATTTCACATACACGTGTATGTATATCCTTCCTCCCTTC	CTTCATTcATTAT	TTATTAATAATTTT	CGTTTATTTA	1499
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tig00008216:94751-135048(-)	TTTTCTTTT.C	TTTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1339
tig00002380:120727-159743()	TTTTCTTTT.CT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	850
tig00008216:53978-94751(-)	TTTTCTTTT.CT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1200
tig00002380:1146-40745()	TTTCTTTCT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1297
tig00008411:94672-134529()	TTTTTCTT.....TTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1467	
tig00008411:217104-257759()	TTTTCTTTTCT	TTTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1394
tig00008411:257759-297618()	TTTTCTTTT.CT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1463
tig00002380:80433-120727()	TTTCTTTTCT	TTTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1694
tig00008215:19898-58526(-)	TTTCTTTCT	TTTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1515
tig00008215:58526-97877(-)	CTTTTCTTT	TTTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1427
tig00008216:21673-53978(-)	TTTTCTTTT.CT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1503
tig00008411:14398-55544()	TTTTCTTTTCT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1833
tig00008215:97877-137448(-)	TTTTCTTTT.CT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1275
tig00008411:55544-94672()	TTTCTTTCT	TTTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1308
tig00002380:40745-80433()	TTTTCTTTT.....TTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1417	
tig00008411:176298-217104()	TTTTCTTTTCT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1726
tig00008215:0-19898(-)	TTTTTCTTT	TTTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGCGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1631
tig00008216:0-21673(-)	TTTTCTTTT.CT	TTTGGGGCCGGCCCGCCTGGTCTTCTGTCTCTGGCTCTG	TGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT	1593
tig00008411:297618-338078()	ATTTTCTTTCTTTCTTTATGTTGAATATGCACACTTTTAAAAATAAACTTTAAACGTAATTTTACATCA.AAACAAACAGTAATACTG.....CAT	1846		
consensus	tTTTctTtt.....tttggGGccGGCCcGCCTGGTCTTCTGTCTCTGcgCTCTGgTGACCTCAGCCTCCCAAATAGCTGGGACTACAGGGATCTCTT			

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tig00002380:159743-198526()	AAGCCCGGA..GGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTA.....AGGCAGAG..	608
tig00008411:134529-176298()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TGGGGGTGGGGGTGGGGGTGAGA..	1289
tig00008216:94751-135048(-)	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAG.....AG..	1394
tig00002380:120727-159743()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TGGGGTGCGGTGGGGTGGGGTGGGG	944
tig00008216:53978-94751(-)	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TGGGGTGCGGTGGGGTGGGGTGGGG	1294
tig00002380:1146-40745()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TGGGGTGCGGTGGGGTGGGGTGGGG	1391
tig00008411:94672-134529()	AAGCCCGGGAGGGAG..GTTAACGTGGGCTGTGATCGCACACTTCCAC..CCAGCTTACGTGGGCTGCGG..GGT....GGGGTGGGTGGGGTGGG..	1554
tig00008411:217104-257759()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TG....GGGTGGGGTGGGGTGGGG	1483
tig00008411:257759-297618()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TGGGGTGCGGTGGGGTGGGGTGGGG	1557
tig00002380:80433-120727()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATC...ACACTTCCACTCCAGCTTACGTGGGGCTGGGGTGGGGTGCGGTGGGGTGGGGTGGGG	1787
tig00008215:19898-58526(-)	AAGCCCGGGAGG..AGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTT..CGTGGGCTGCGGGGTGGGGTGCGGTGGG..TGGGTGGGT	1606
tig00008215:58526-97877(-)	AAGCCCGGGAGGGAGAGTTA..GTGGCTGTGATCGCACACTTCCAC..CCAGCTTACGTGGGCTGCGG..TGGGGTGCGGTGGGGTGGGGTGGGG	1518
tig00008216:21673-53978(-)	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TGGGGTGCGGTGGGGTGGGGTGGGG	1597
tig00008411:14398-55544()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TGGGGTGCGGTGGGGTGGGGTGGGG	1927
tig00008215:97877-137448(-)	AAGCC..GGGAGGAGAGTTAGCGTGGGCTGTGATCGCACACTTCCACTCCAGCTTCTGTGGGCTGCGG..TG.....	1344
tig00008411:55544-94672()	AA.....TTGC.....	1314
tig00002380:40745-80433()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG.....GGTGGGGTGGGGTGGGG	1504
tig00008411:176298-217104()	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGGTGGGGTGCGGTGGGGTGGGGTGGGG	1821
tig00008215:0-19898(-)	AAGCCCGGGAGGGAGAGTTAA..TGGGCTGTGATCGCACACTTCCACTCCAGCTTAC..GGGCTGCGG....GGTGGGGTGGGGTGGGGTGGGG	1717
tig00008216:0-21673(-)	AAGCCCGGGAGGGAGAGTTAACGTGGGCTGTGATCGCACACTTCCACTCCAGCTTACGTGGGCTGCGG..TGGGGTGCGGTGGGGTGGGGTGGGG	1687
tig00008411:297618-338078()	ATGC....AATGGTGATGT..ATAATGGATTTTTTTAGAGATAATTTGTAAATGTTTTTCAACAACAATGTGTCACTAAAAATAGAAAAAATTAGCTGGGC	1935
consensus	AAGCcgggagGgaGagGTTaacgTGGGcTGTGaTcgCAcAcTTccActccagcttacgtgggctgCGg.tg.g...ggg.ggggtggggTggg.	

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tig00002380:159743-198526()	AAACGATTGATTGCGATCTCAATTGCCTTTTAGCTTCATTTCATACCCTGTTATTT..GCTCGTTT..ATTG	675
tig00008411:134529-176298()	AAACGATTGATTGCGATCTCAATTGCCTTTTAGCTTCATTTCATACCCTGTTATTT..GCTCGTTT..ATTG	1356
tig00008216:94751-135048(-)	AAACGATTGATTGCGATCTCAATTGCCTTTTAGCTTCATTTCATACCCTGTTATTT..GCTCGTTT..ATTG	1461
tig00002380:120727-159743()	TG....CAG.....AGA	1019
tig00008216:53978-94751(-)	TGGGGTGCA.....AGA	1374
tig00002380:1146-40745()	GC.....A.....GAG	1464
tig00008411:94672-134529()	TGGGGTGCA.....GAG	1633
tig00008411:217104-257759()	TGGGGTGT.....GAG	1561
tig00008411:257759-297618()	TGGGGTGCA.....GAG	1636
tig00002380:80433-120727()	TGCAG.....AGA	1862
tig00008215:19898-58526(-)	GGGTG.....CAG	1681
tig00008215:58526-97877(-)	TGGGG.....TGC	1593
tig00008216:21673-53978(-)	TGCAG.....AGA	1672
tig00008411:14398-55544()	TGGGGTGGGGTGGGGTGGGGTGCAGA	2020
tig00008215:97877-137448(-)A.....TCTCAATTGCCTTTAGCTTCATTTCATACCCTGTTATTT..GCTCGTTT..ATTG	1396
tig00008411:55544-94672()CTTTTAGCTTCATTTCATACCCTGTTATTT..GCTCGTTT..ATTG	1356
tig00002380:40745-80433()	TGCAG.....AGA	1581
tig00008411:176298-217104()	TGCAG.....A	1894
tig00008215:0-19898(-)	GTGCA.....GAG	1792
tig00008216:0-21673(-)	TGCAG.....AGA	1762
tig00008411:297618-338078()	GCTGT.....GGTGGGGCCGTGAATCCAGCTTACTTGGGAGGCCAAGGCAGGAGAATCACATTGAACCCGGGAGGTAG	2008
consensus	.g.....aaacgattgattgCGaTCTCAaTgCcTTTTAGCTTCATTTCATACCCTGTTATTT..GCTCGTTT..ATTG	