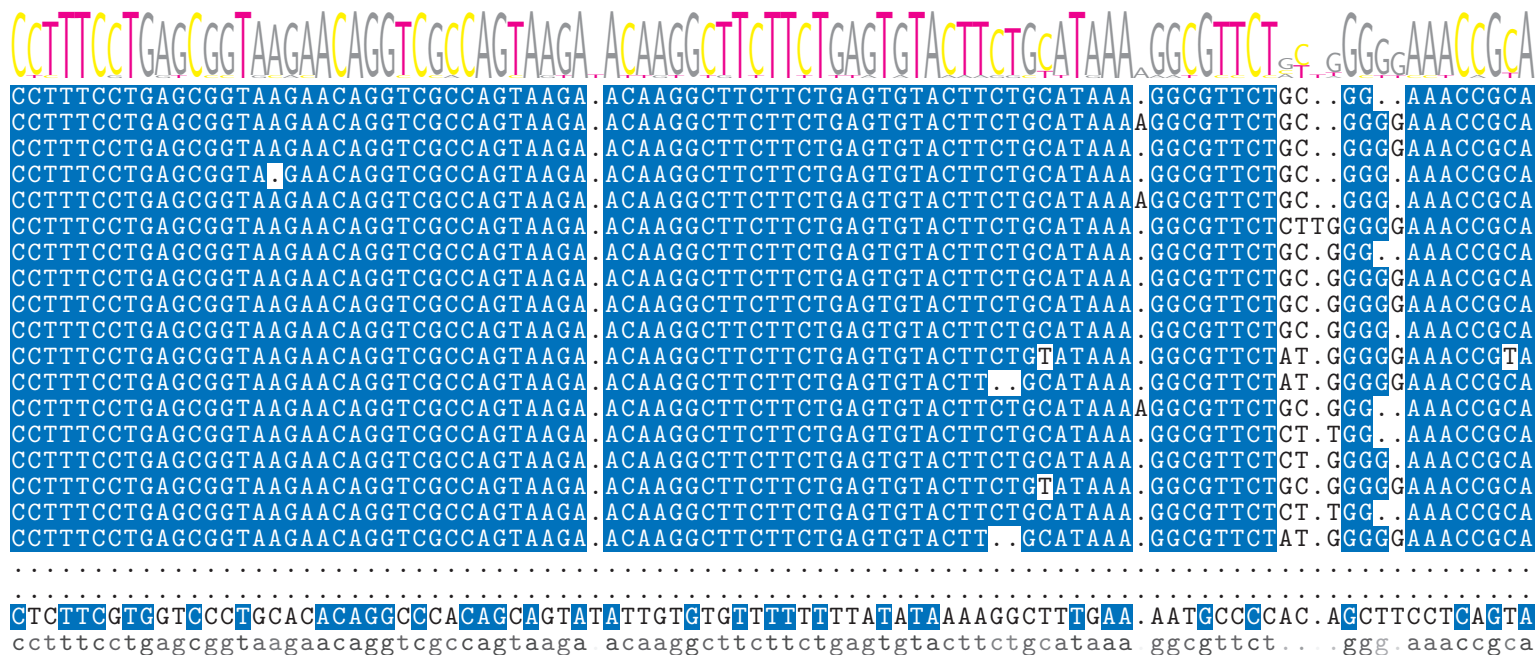


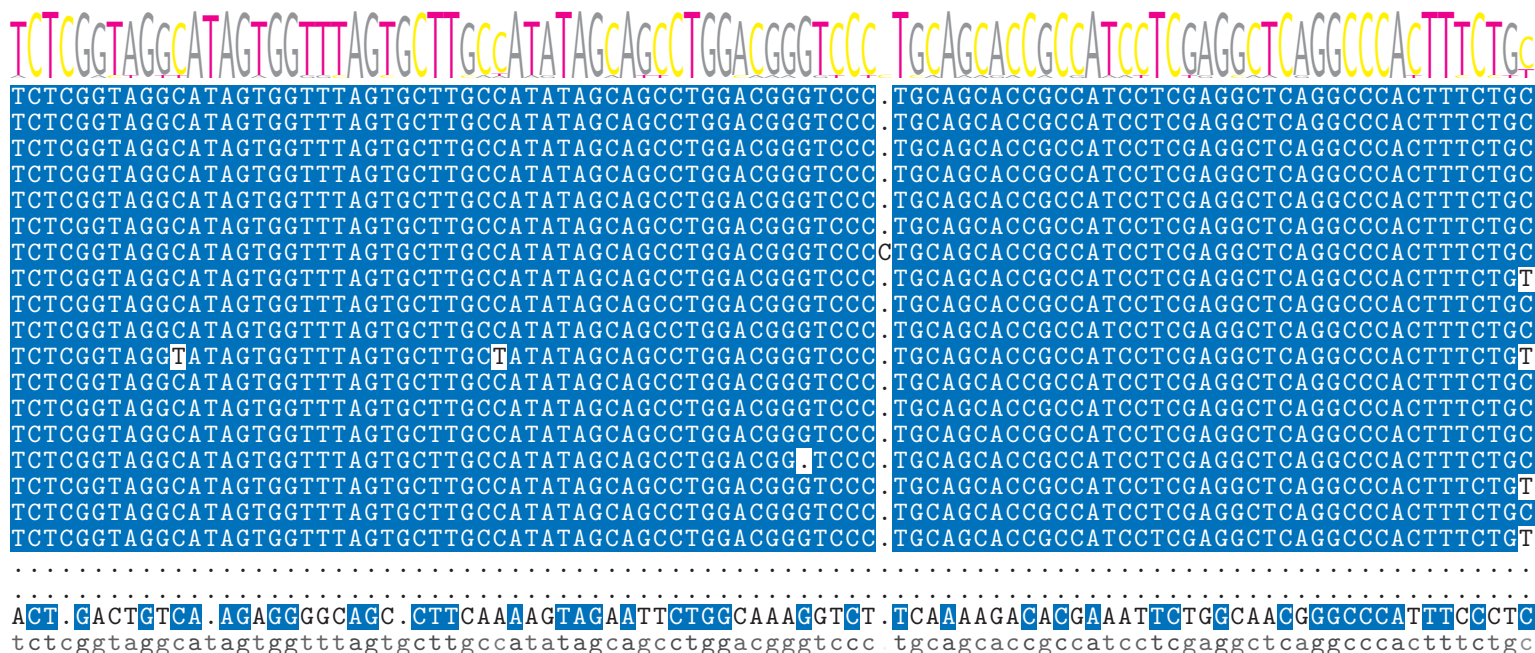
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tig00008411:297618-338078( )  
consensus



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consensus



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tig00008411:134529-176298( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	274
tig00008216:94751-135048(-)	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	273
tig00002380:120727-159743( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	270
tig00008216:53978-94751(-)	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	272
tig00002380:1146-40745( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	276
tig00008411:94672-134529( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	273
tig00008411:217104-257759( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	279
tig00008411:257759-297618( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	277
tig00002380:80433-120727( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	276
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tig00008215:58526-97877(-)	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	274
tig00008216:21673-53978(-)	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	272
tig00008411:14398-55544( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	273
tig00008215:97877-137448(-)	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	268
tig00008411:55544-94672( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	278
tig00002380:40745-80433( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	262
tig00008411:176298-217104( )	AGTGCCACAGGCACCCCCC	ATAGCGGCTCC	GGCCCCGGCCAGCCC	GGCTCATTTAAAGGCACCAGCCGCCGTTACCGGGGG		ATGGGG	278
tig00008215:0-19898(-)							0
tig00008216:0-21673(-)							0
tig00008411:297618-338078( )	CCGCCTTGCTCTTCTGGATGCATCCATTCTCTCCACAGCATAGTC	TTTTTCTTC	CACCTCCACTGTAGAGACTGTCTCTCTAGTGGCAACAGTG				278
consensus	agtgccacaggcac.cccccc	atagcggctcc	ggccccggccagccc	ggctcatTTAAAGGCACCAGCCGCCGTTACCGGGGG		atgggg	

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tig00002380:120727-159743( )	GAGTCCGAGACAGAATGACTTCTTTATCCTGCTGACTCTGAAAAGCCC	GGCGCCTTGTGATCCATTGCAAACCGAGAGTCACCTCGTGTTT	AG	362
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tig00002380:40745-80433( )	AGTCCGAGACAGAATGACTTCTTTATCCTGCTGACTCTGAAAAGCCC	GGCGCCTTGTGATCCATTGCAAACCGAGAGTCACCTCGTGTTT	AG	353
tig00008411:176298-217104( )	GAGTCCGAGACAGAATGACTTCTTTATCCTGCTGACTCTGAAAAGCCC	GGCGCCTTGTGATCCATTGCAAACCGAGAGTCACCTCGTGTTT	AG	371
tig00008215:0-19898(-)				0
tig00008216:0-21673(-)				0
tig00008411:297618-338078( )	ACTTGAGTGTATGCGGAAATTTCTTTCCAAAGCCTGTTGAGAAAGCGTCCTCTGCTGCTTCTTTTGGCCACC	TCCTGCATGGTA	AG	367
consensus	agtccgagacagaatgacttctttatcctgctgactctgaaaagccc	ggcgcccttgtgatccattgcaaaccgagagtcacctcgtgttt	ag	

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tig00008216:94751-135048(-)	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTGGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	458
tig00002380:120727-159743( )	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	453
tig00008216:53978-94751(-)	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTGGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	457
tig00002380:1146-40745( )	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	460
tig00008411:94672-134529( )	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	456
tig00008411:217104-257759( )	AACACGGATCCACGCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGTAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	461
tig00008411:257759-297618( )	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	462
tig00002380:80433-120727( )	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	460
tig00008215:19898-58526(-)	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGTAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	460
tig00008215:58526-97877(-)	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGTAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	456
tig00008216:21673-53978(-)	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	454
tig00008411:14398-55544( )	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	458
tig00008215:97877-137448(-)	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	447
tig00008411:55544-94672( )	AACACGGATCCACGCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGTAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	459
tig00002380:40745-80433( )	AACACGGATCCACTCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGCAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	443
tig00008411:176298-217104( )	AACACGGATCCACGCCCAA	GTTTCAGTGGGGG	..ATGTGAGGGG	TGTGGTAGGTAGGACGAAGGACTCTCTTCCTTCTGATTTCGGTCTGCACAG	462
tig00008215:0-19898(-)	.....	.....	.....	.....	0
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consensus	aacacggatccactcccaa	gttcagtggggg	atgtgagggg	tgtggcaggtaggacgaaggactctcttccttctgatttcggtctgcacag	

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tig00008411:134529-176298( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		551
tig00008216:94751-135048(-)	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		549
tig00002380:120727-159743( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		544
tig00008216:53978-94751(-)	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		548
tig00002380:1146-40745( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		551
tig00008411:94672-134529( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		547
tig00008411:217104-257759( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		552
tig00008411:257759-297618( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		553
tig00002380:80433-120727( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		551
tig00008215:19898-58526(-)	TGGGGCCTAGG	GTTGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		548
tig00008215:58526-97877(-)	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		547
tig00008216:21673-53978(-)	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		545
tig00008411:14398-55544( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		549
tig00008215:97877-137448(-)	TGGGGCCTAGG	GCTGGAGCTCTCTCTGTCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAAGCGCGGG	CCTTG	G		535
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tig00002380:40745-80433( )	TGGGGCCTAGG	GCTGGAGCTCTCTCCGTGCGGACCGCTGACTCCCTCTACCTTGGGTTCCCTCGGCCCCACCC	TGGAACGCGCGGG	CCTTG	G		535
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tig00008216:0-21673(-)	.....	.....	.....	.....	.....	.....	0
tig00008411:297618-338078( )	GAAACATCATGCATC	GGAGCAGCATGGG	GACAGGG	GCTGGCCAGCTGGGC	...AGGTCTCACA	CTGACACTCAGACTCCACGATATC	549
consensus	tggggcctagg	gctggagctctctccgtgcggaccgctgactccctctaccttggggttccctcgggccccacc	tggagcgccggg	ccttg	g		

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consensus

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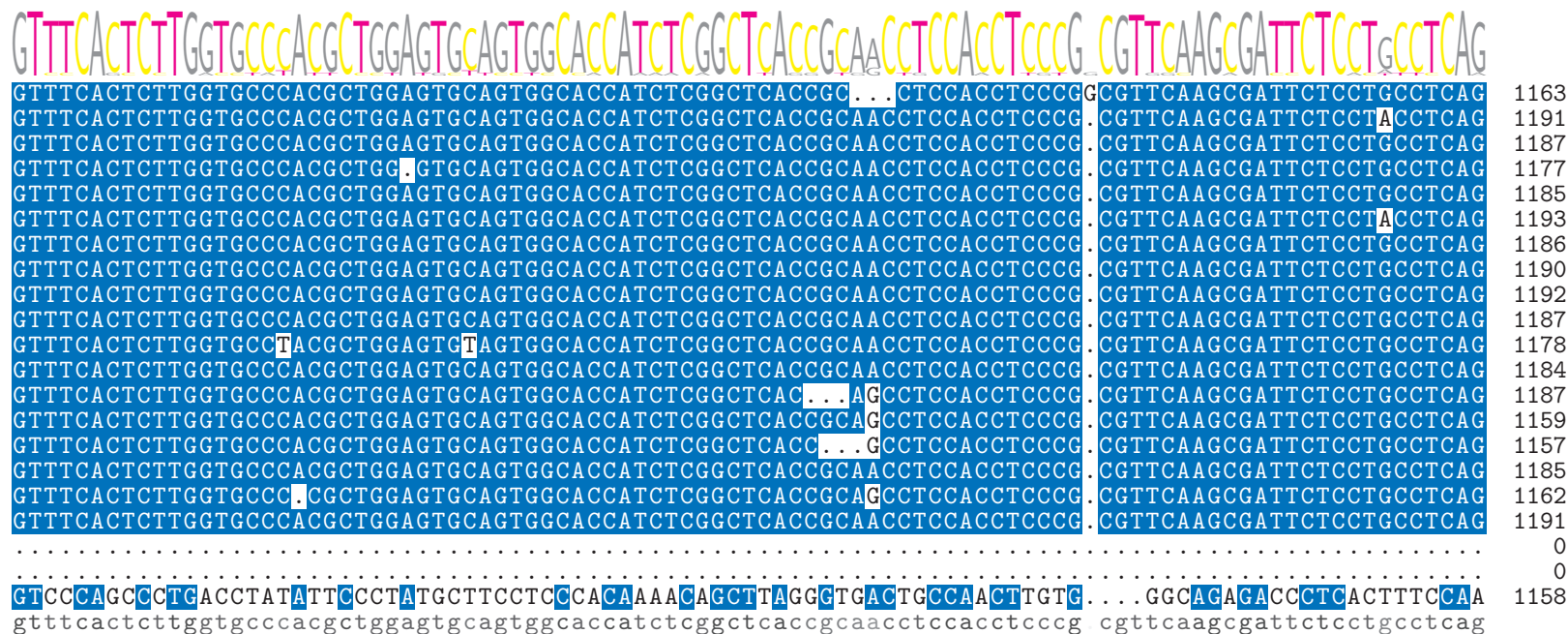
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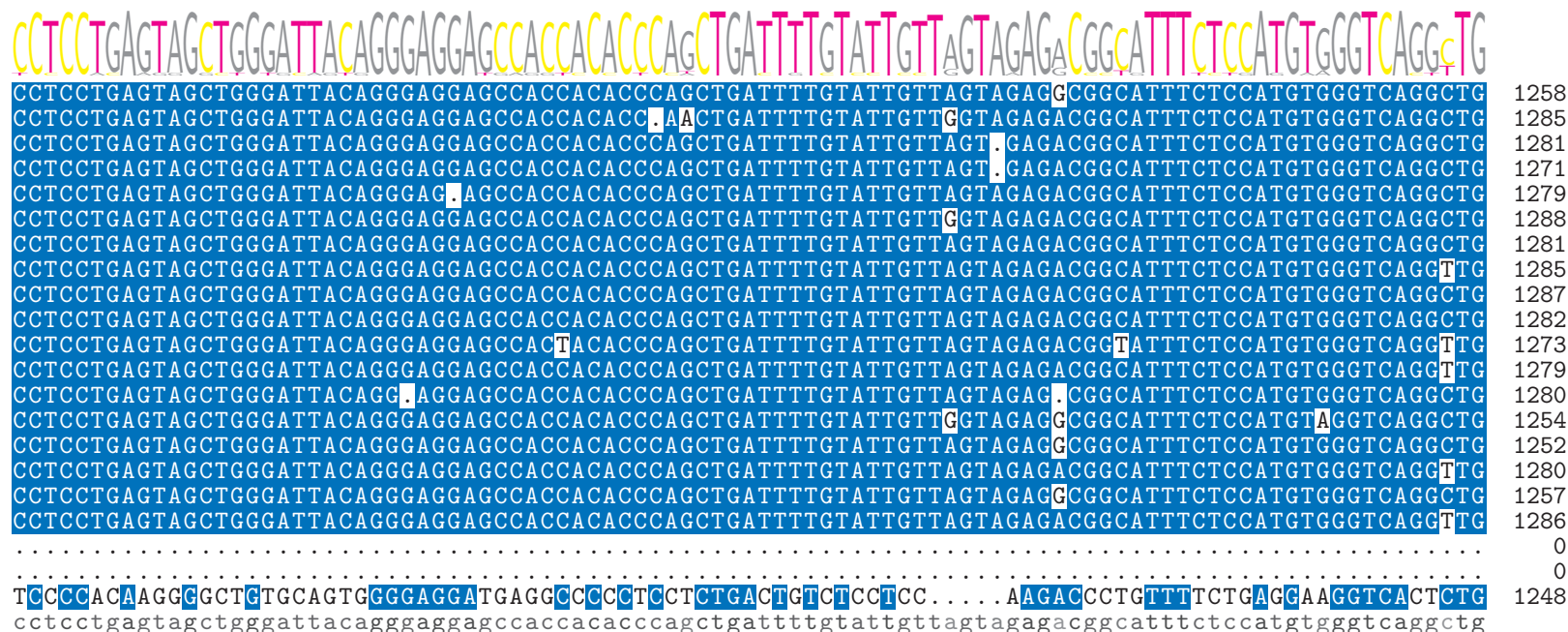
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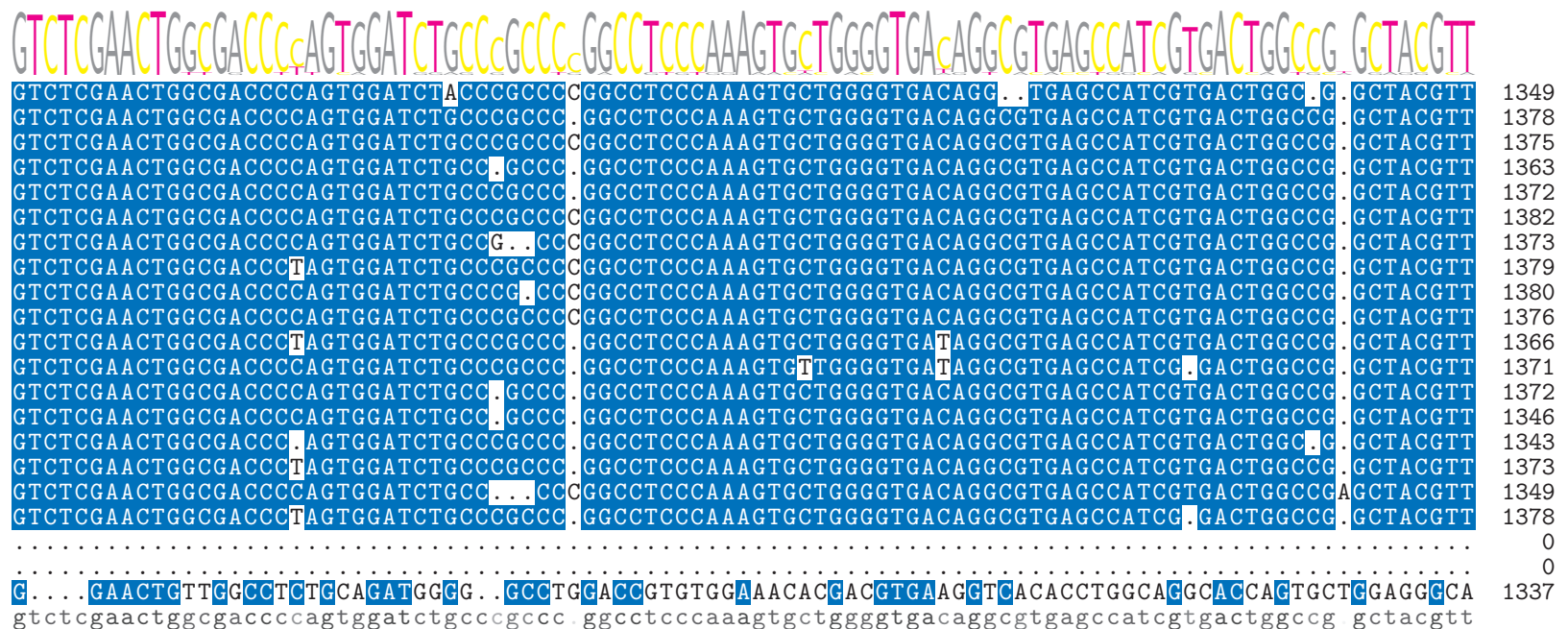
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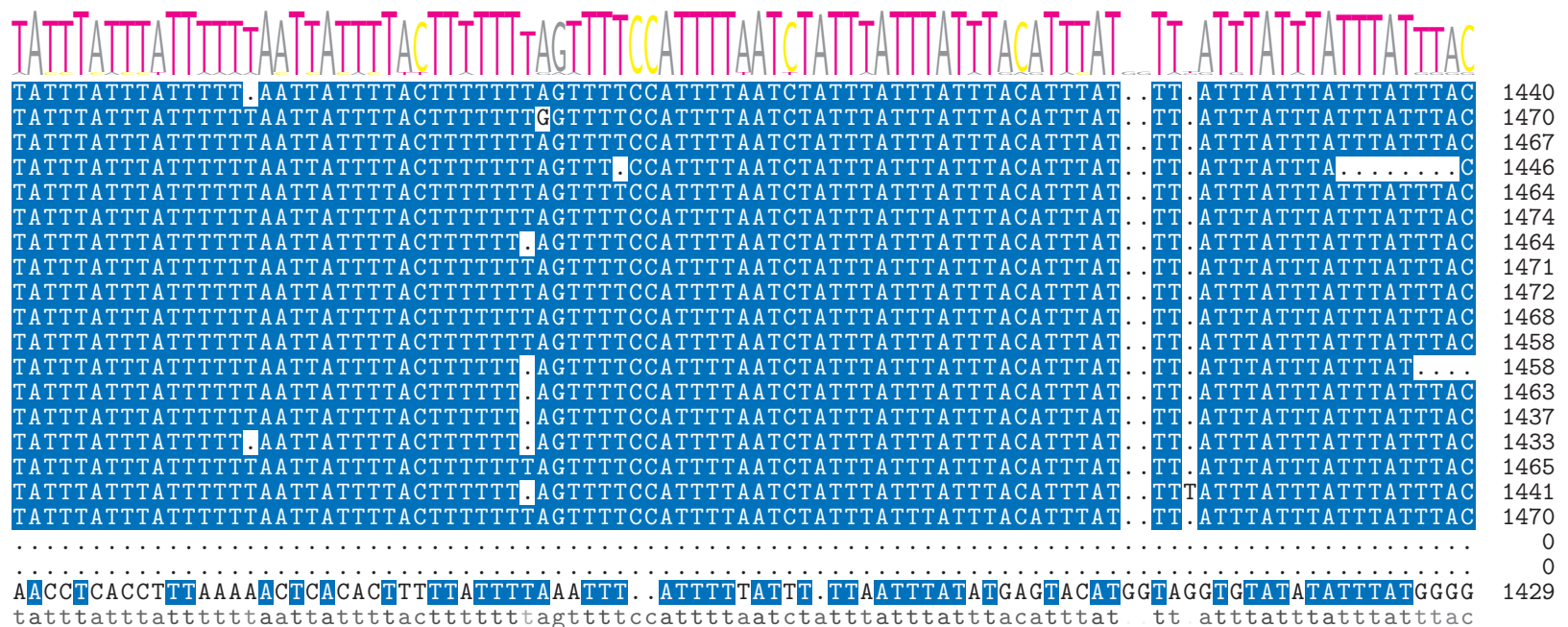
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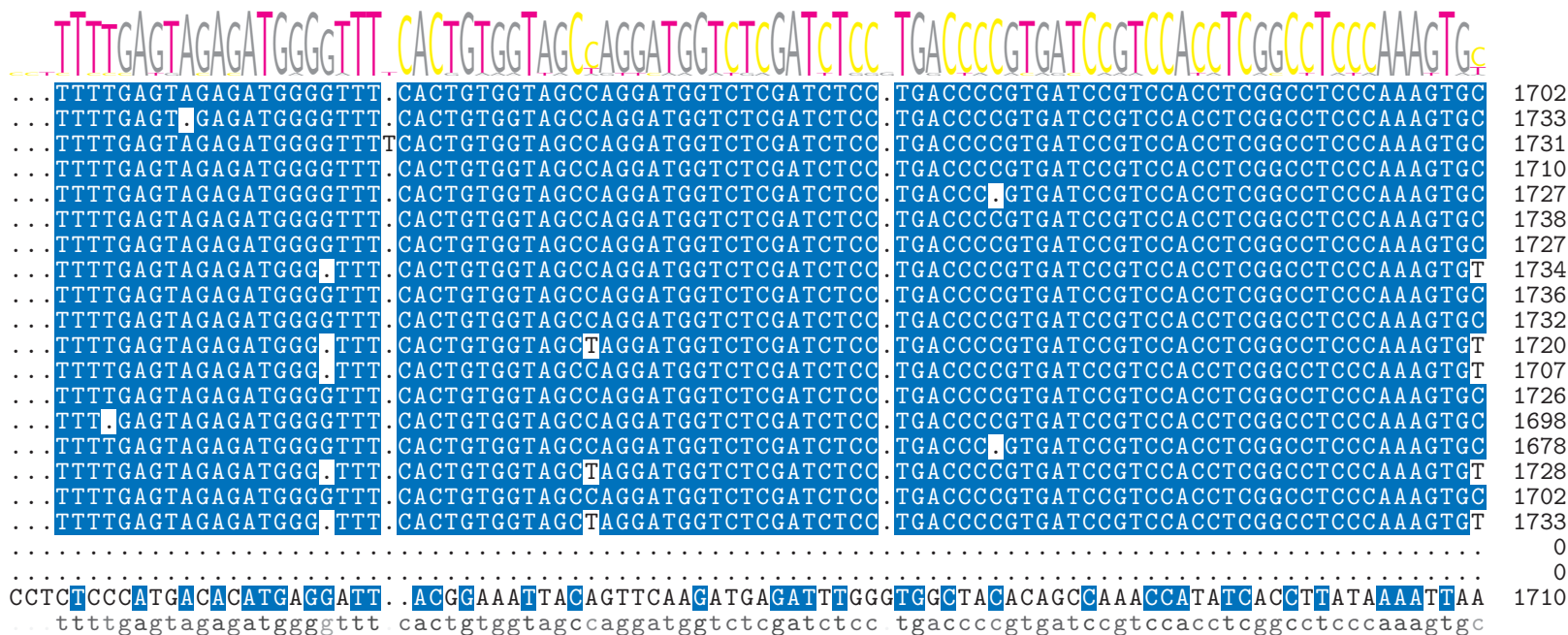
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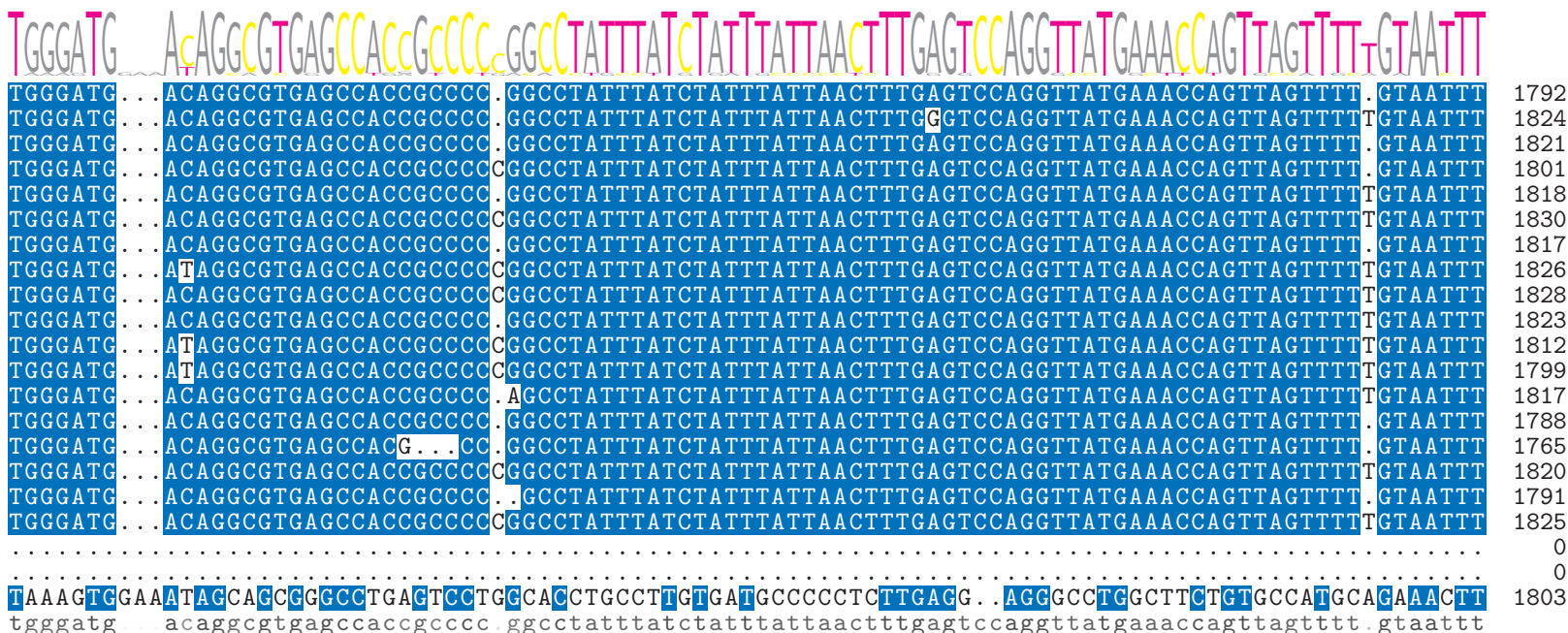
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