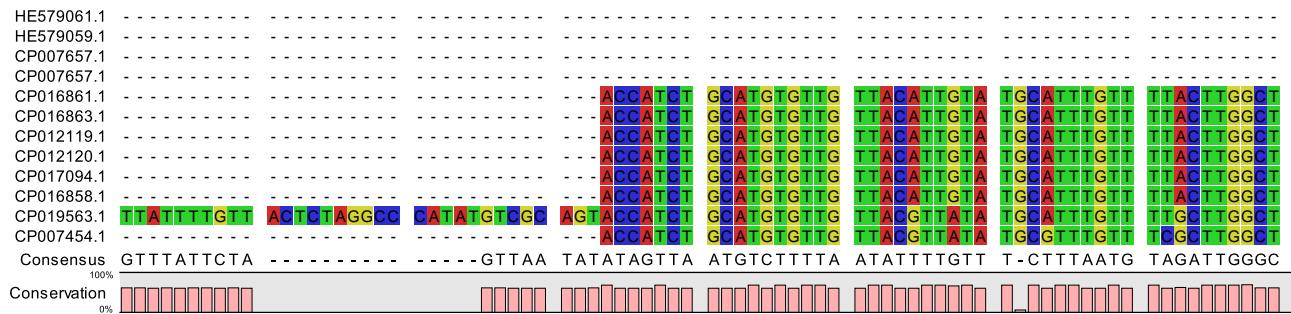
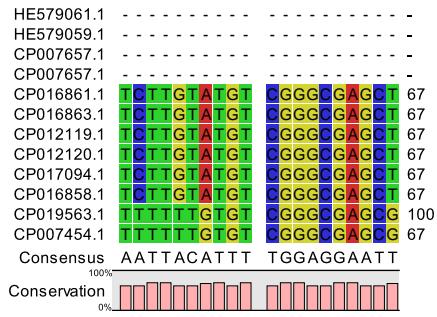


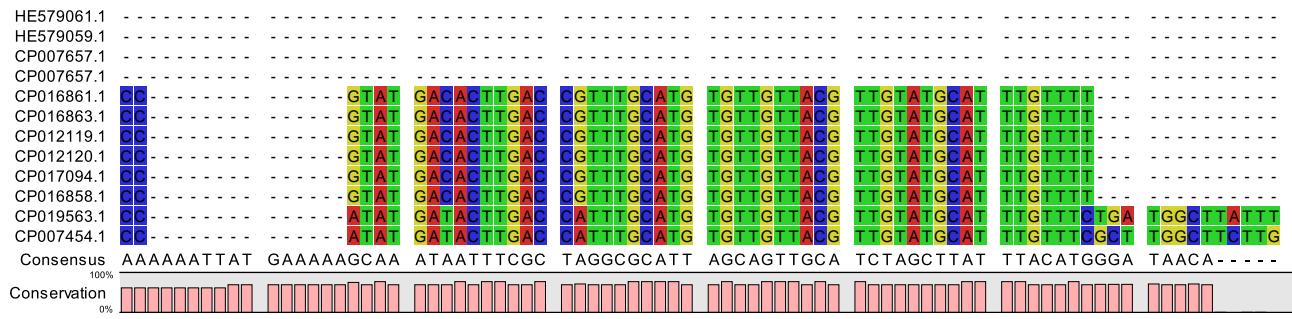
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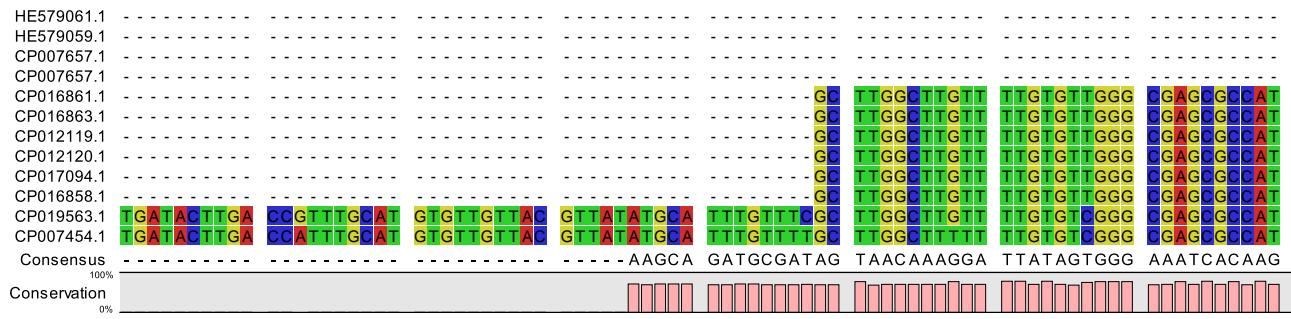


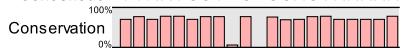
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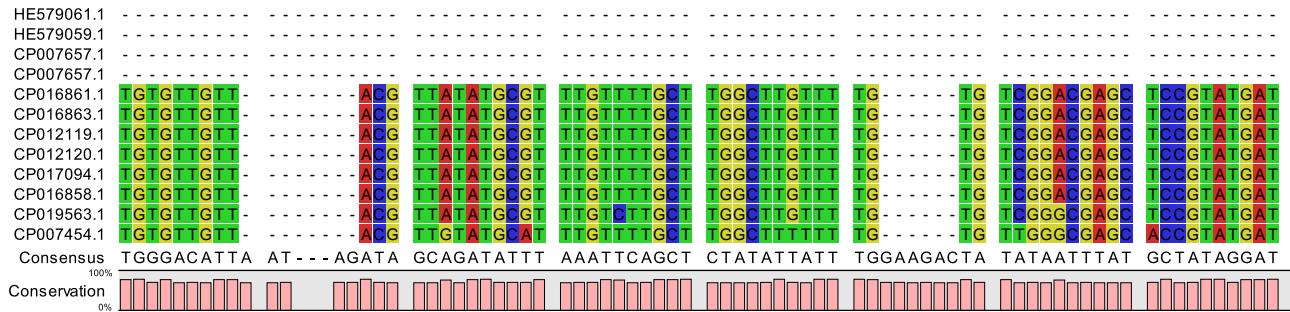
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0%
Conservation

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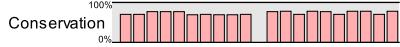
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 Conservation 100%
 0%

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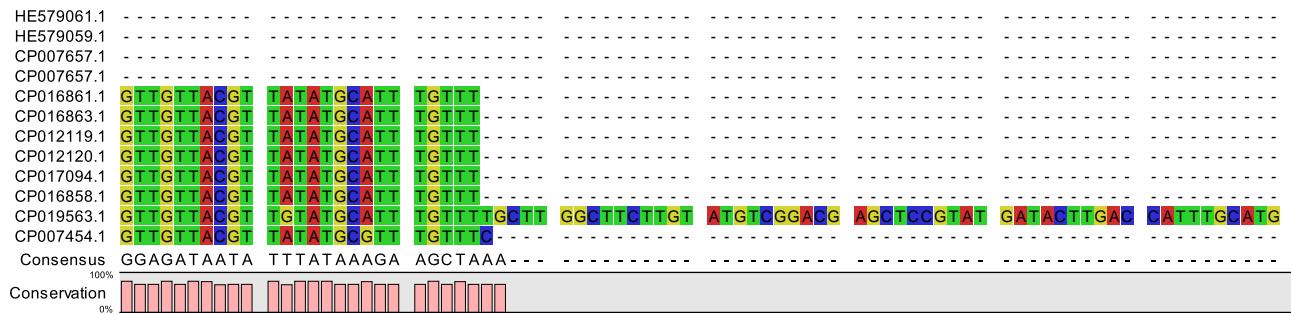
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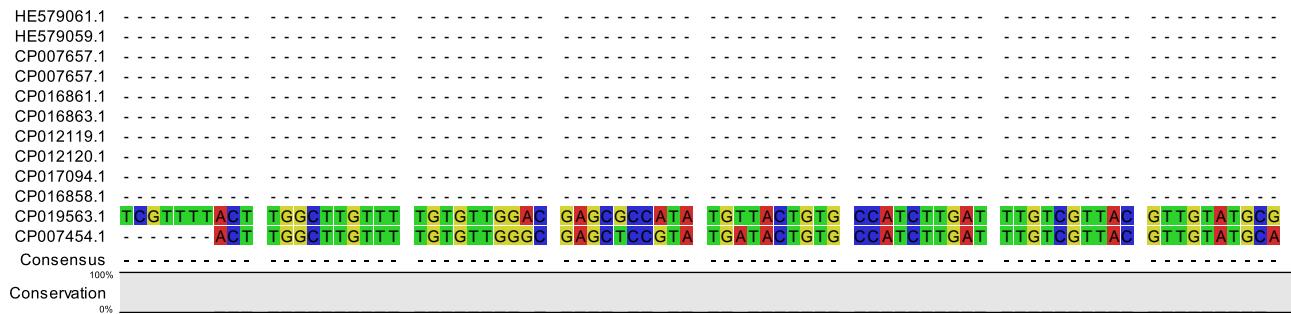
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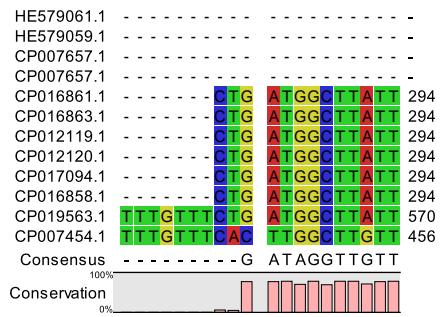


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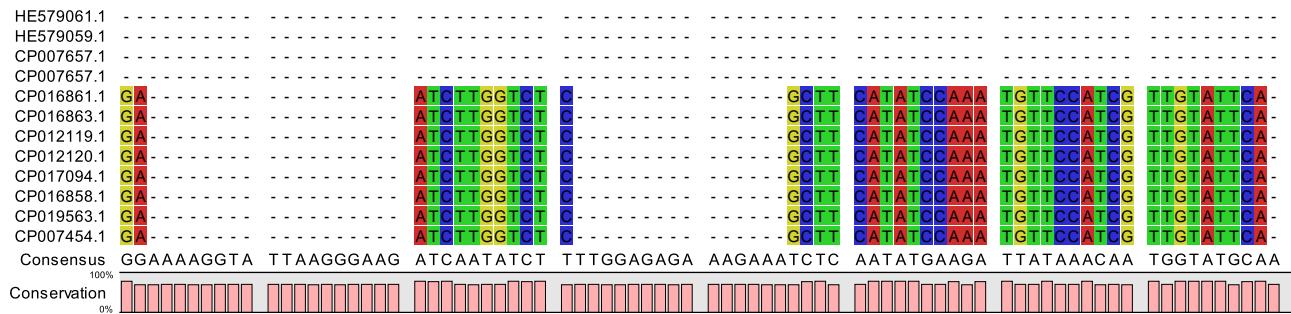
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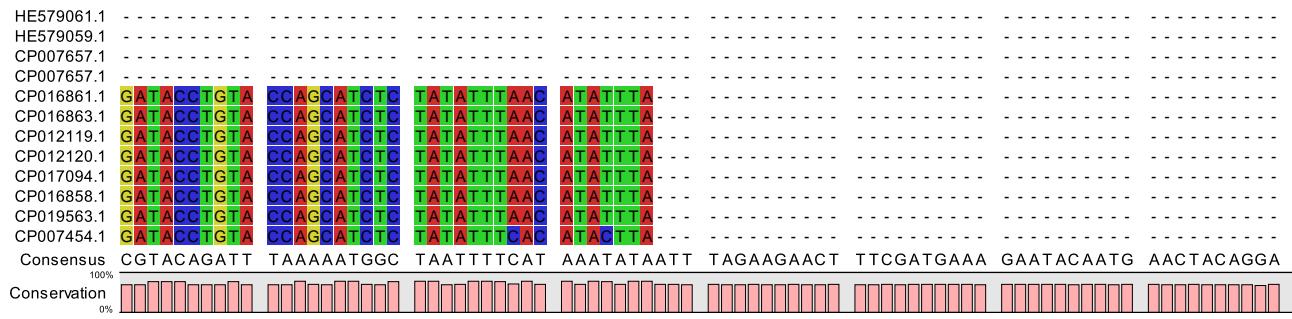


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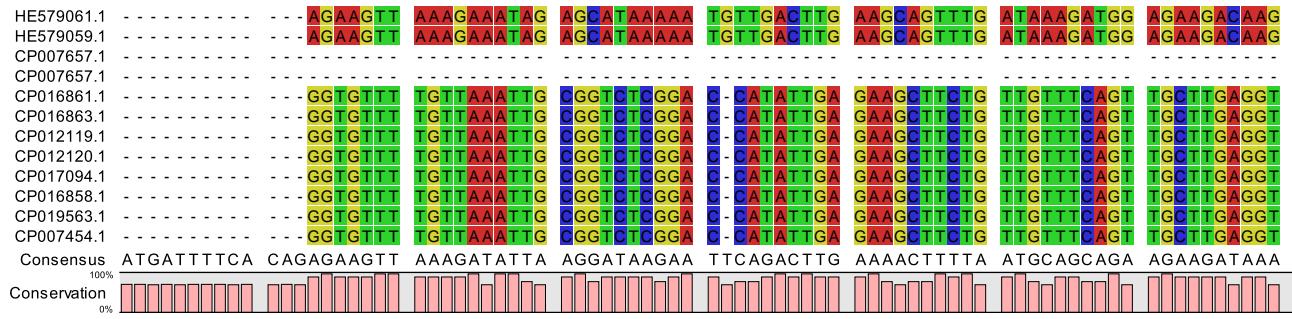


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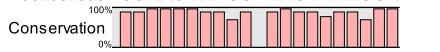
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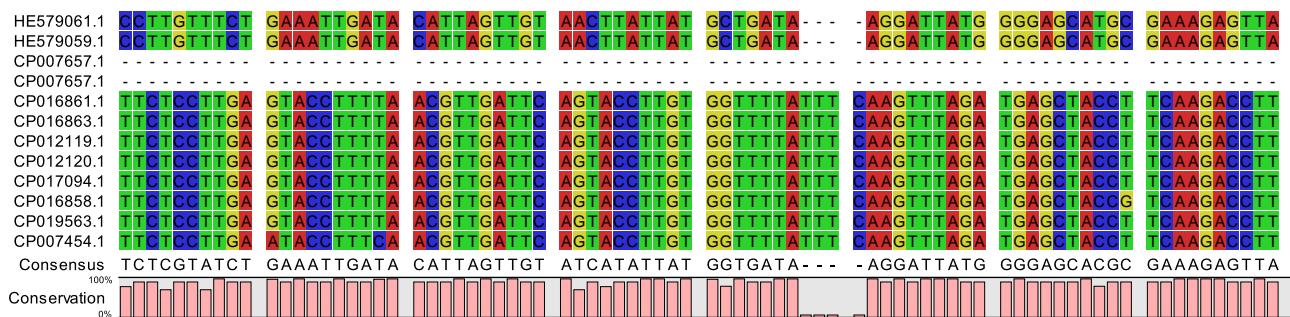
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CP010296.1	G	C	A	T
CP010295.1	G	C	A	T
CP007690.1	G	C	A	T
CP007176.1	G	C	A	T
CP000730.1	G	C	A	T
CP00255.1	G	C	A	T
CP007539.1	G	C	A	T
CP007657.1	G	C	A	T
AP014921.1	G	C	A	T
AB436955.1	G	C	A	T
AB489885.1	G	C	A	T
AB489873.1	G	C	A	T
AB489883.1	G	C	A	T
AB489874.1	G	C	A	T
LT615218.1	G	C	A	T
AB436976.1	G	C	A	T
AB489892.1	G	C	A	T
AJ306908.1	G	C	A	T
CP015646.1	G	C	A	T
AB488510.1	G	C	A	T
EU105387.1	G	C	A	T
AB436975.1	G	C	A	T
AB488499.1	G	C	A	T
AJ309189.1	G	C	A	T
FR821779.1	G	C	A	T
CP012593.1	G	C	A	T
CP012692.1	G	C	A	T
CP013955.1	G	C	A	T
CP013953.1	G	C	A	T
CP014064.1	G	C	A	T
LT09690.1	G	C	A	T
AP017320.1	G	C	A	T
CP010890.1	G	C	A	T
CP001844.2	G	C	A	T
CP001781.1	G	C	A	T
AB488501.1	G	C	A	T
AB489898.1	G	C	A	T
HE579073.1	G	C	A	T
HE579071.1	G	C	A	T
HE579069.1	G	C	A	T
HE579065.1	G	C	A	T
HE579063.1	G	C	A	T



HE579061.1	G C A A C T T A A G	A A G T T T A T G A	87
HE579059.1	G C A A C T T A A G	A A G T T T A T G A	87
CP007657.1	- - - - -	- - - - -	-
CP007657.1	- - - - -	- - - - -	-
CP016861.1	T T A A C T T C A A	T A T C A C T T G A	465
CP016863.1	T T A A C T T C A A	T A T C A C T T G A	465
CP012119.1	T T A A C T T C A A	T A T C A C T T G A	465
CP012120.1	T T A A C T T C A A	T A T C A C T T G A	465
CP017094.1	T T A A C T T C A A	T A T C A C T T G A	465
CP016858.1	T T A A C T T C A A	T A T C A C T T G A	465
CP019563.1	T T A A C T T C A A	T A T C A C T T G A	741
CP007454.1	T T A A C T T C A A	T A T C A C T T G A	627
Consensus	G C A A C T A A G G	A A G T A T A C G A	



The chart shows a single horizontal bar at the 100% conservation level, spanning the entire width of the alignment.

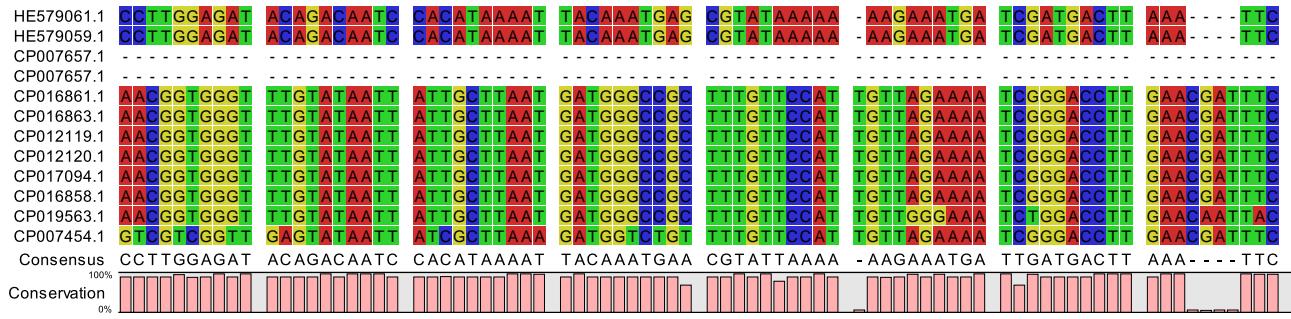


HE579061.1	C GAG CAAAAAC	TGGACTTAAT	183
HE579059.1	GAGCAAAAC	TGGACTTAAT	183
CP007657.1	- - - - -	- - - - -	-
CP007657.1	- - - - -	- - - - -	-
CP016861.1	C - - TAAAAAT	AGGGTTTCGTT	562
CP016863.1	C - - TAAAAAT	AGGGTTTCGTT	562
CP012119.1	C - - TAAAAAT	AGGGTTTCGTT	562
CP012120.1	C - - TAAAAAT	AGGGTTTCGTT	562
CP017094.1	C - - TAAAAAT	AGGGTTTCGTT	562
CP016858.1	C - - TAAAAAT	AGGGTTTCGTT	562
CP019563.1	C - - TAAAAAT	AGGGTTTCGTT	838
CP007454.1	C - - TAAAAAT	AGGGTTTCGGT	724
Consensus	CGAGCAAAAC	TGGACTTAAT	

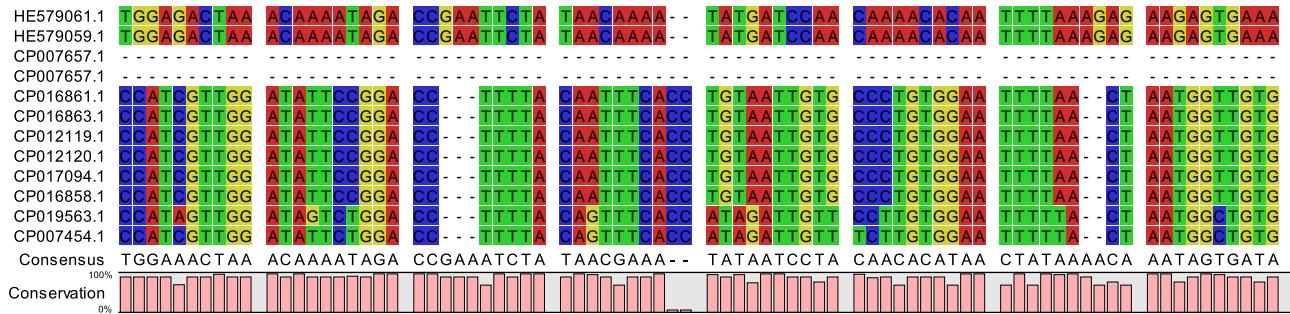


The conservation logo consists of 10 vertical bars, each representing a position in the sequence. The bars are colored red, indicating 100% conservation across all 10 entries.

	1,100			
CP007670.1	A	ATT	ATT	GAT
CP003033.1	A	ATT	ATT	GAT
CP018205.1	A	ATT	ATT	GAT
AP017377.1	A	ATT	ATT	GAT
LT598688.1	A	ATT	ATT	GAT
CP007676.1	A	ATT	ATT	GAT
CP007672.1	A	ATT	ATT	GAT
CP007674.1	A	ATT	ATT	GAT
CP011526.1	A	ATT	ATT	GAT
HF937103.1	A	ATT	ATT	GAT
AP009351.1	A	ATT	ATT	GAT
CP000046.1	A	ATT	ATT	GAT
CP000253.1	A	ATT	ATT	GAT
AC025591.8	A	ATT	ATT	GAT
LT671859.1	A	ATT	ATT	GAT
CP007499.1	A	ATT	ATT	GAT
X17679.1	A	ATT	ATT	GAT
CP007657.1	A	ATT	ATT	GAT
CP014444.1	A	ATT	ATT	GAT
CP014441.1	A	ATT	ATT	GAT
CP014438.1	A	ATT	ATT	GAT
CP014435.1	A	ATT	ATT	GAT
CP014432.1	A	ATT	ATT	GAT
CP014429.1	A	ATT	ATT	GAT
CP014426.1	A	ATT	ATT	GAT
CP014423.1	A	ATT	ATT	GAT
CP014420.1	A	ATT	ATT	GAT
CP014415.1	A	ATT	ATT	GAT
CP014412.1	A	ATT	ATT	GAT
CP014409.1	A	ATT	ATT	GAT
CP014407.1	A	ATT	ATT	GAT
CP014402.1	A	ATT	ATT	GAT
CP014397.1	A	ATT	ATT	GAT
CP014392.1	A	ATT	ATT	GAT
CP014387.1	A	ATT	ATT	GAT
CP014384.1	A	ATT	ATT	GAT
CP014381.1	A	ATT	ATT	GAT
CP014371.1	A	ATT	ATT	GAT
CP014368.1	A	ATT	ATT	GAT
CP014365.1	A	ATT	ATT	GAT
CP014362.1	A	ATT	ATT	GAT
CP014376.1	A	ATT	ATT	GAT
CP009423.1	A	ATT	ATT	GAT
CP016855.1	A	ATT	ATT	GAT
CP013231.1	A	ATT	ATT	GAT
CP010300.1	A	ATT	ATT	GAT
CP010299.1	A	ATT	ATT	GAT
CP010298.1	A	ATT	ATT	GAT
CP010297.1	A	ATT	ATT	GAT
CP010296.1	A	ATT	ATT	GAT
CP010295.1	A	ATT	ATT	GAT
CP007690.1	A	ATT	ATT	GAT
CP007176.1	A	ATT	ATT	GAT
CP000730.1	A	ATT	ATT	GAT
CP000255.1	A	ATT	ATT	GAT
CP007539.1	A	ATT	ATT	GAT
CP007657.1	A	ATT	ATT	GAT
AP014921.1	A	ATT	ATT	GAT
AB436955.1	A	ATT	ATT	GAT
AB489885.1	A	ATT	ATT	GAT
AB489873.1	A	ATT	ATT	GAT
AB489883.1	A	ATT	ATT	GAT
AB489874.1	A	ATT	ATT	GAT
LT615218.1	A	ATT	ATT	GAT
AB436976.1	A	ATT	ATT	GAT
AB489892.1	A	ATT	ATT	GAT
AJ306908.1	A	ATT	ATT	GAT
CP015646.1	A	ATT	ATT	GAT
AB488510.1	A	ATT	ATT	GAT
EU105387.1	A	ATT	ATT	GAT
AB436975.1	A	ATT	ATT	GAT
AB488499.1	A	ATT	ATT	GAT
AJ309189.1	A	ATT	ATT	GAT
FR821779.1	A	ATT	ATT	GAT
CP012593.1	A	ATT	ATT	AGAT
CP012692.1	A	ATT	ATT	AGAT
CP013955.1	A	ATT	ATT	AGAT
CP013953.1	A	ATT	ATT	AGAT
CP014064.1	A	ATT	ATT	AGAT
LT009690.1	A	ATT	ATT	AGAT
AP017320.1	A	ATT	ATT	AGAT
CP010890.1	A	ATT	ATT	AGAT
CP001844.2	A	ATT	ATT	AGAT
CP001781.1	A	ATT	ATT	AGAT
AB488501.1	A	ATT	ATT	AGAT
AB489898.1	A	ATT	ATT	AGAT
HE579073.1	A	ATT	ATT	AGAT
HE579071.1	A	ATT	ATT	AGAT
HE579069.1	A	ATT	ATT	AGAT
HE579065.1	A	ATT	ATT	AGAT
HE579063.1	A	ATT	ATT	AGAT



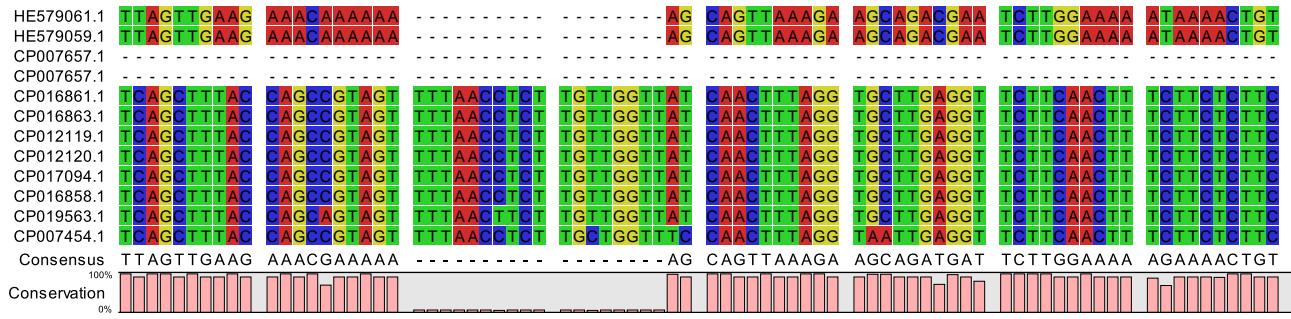
HE579061.1	AATTATAGAT	GATTTCTTTA	278
HE579059.1	AATTATAGAT	GATTTCTTTA	278
CP007657.1	- - - - -	- - - - -	-
CP007657.1	- - - - -	- - - - -	-
CP016861.1	ACCTTGTACC	GT TTT ATTTT	662
CP016863.1	ACCTTGTACC	GT TTT ATTTT	662
CP012119.1	ACCTTGTACC	GT TTT ATTTT	662
CP012120.1	ACCTTGTACC	GT TTT ATTTT	662
CP017094.1	ACCTTGTACC	GT TTT ATTTT	662
CP016858.1	ACCTTGTACC	GT TTT ATTTT	662
CP019563.1	ACCTTGTACC	GT TTT ATTTT	938
CP007454.1	ACCTTGTACC	GT TTT ATTTT	824
Consensus	AATTATTGAT	GATTTCTTTA	
Conservation			

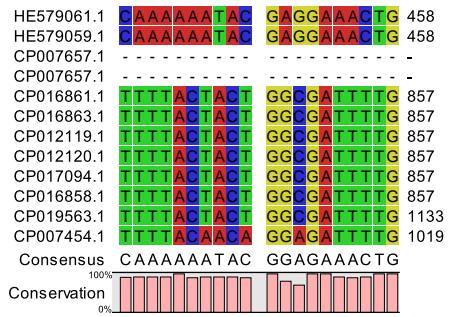


HE579061.1	A	T	A	A	A	C	G	T	A	A	A	T	A	A	376
HE579059.1	A	T	A	A	A	C	C	T	A	A	A	T	A	A	376
CP007657.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CP007657.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CP016861.1	C	A	A	C	T	G	G	T	T	G	T	T	T	C	757
CP016863.1	C	A	A	C	T	G	G	T	T	G	T	T	T	C	757
CP012119.1	C	A	A	C	T	G	G	T	T	G	T	T	T	C	757
CP012120.1	C	A	A	C	T	G	G	T	T	G	T	T	T	C	757
CP017094.1	C	A	A	C	T	G	G	T	T	G	T	T	T	C	757
CP016858.1	C	A	A	C	T	G	G	T	T	G	T	T	T	C	757
CP019563.1	C	C	A	C	T	G	G	T	T	G	T	T	T	C	1033
CP007454.1	C	C	A	C	T	G	G	T	T	G	T	T	T	C	919
Consensus	A	T	A	A	A	C	C	T	T	G	T	T	T	A	A

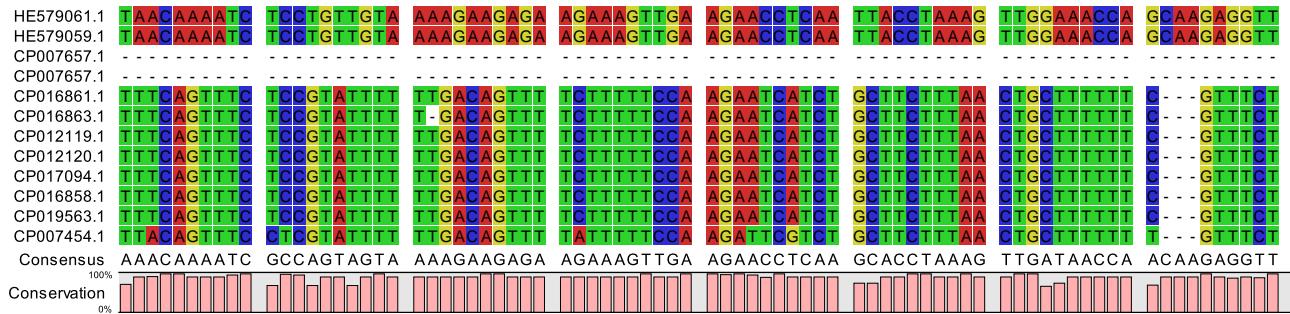


The sequence logo at the bottom shows a red bar extending from the bottom to the top of the chart, indicating 100% conservation for every position.



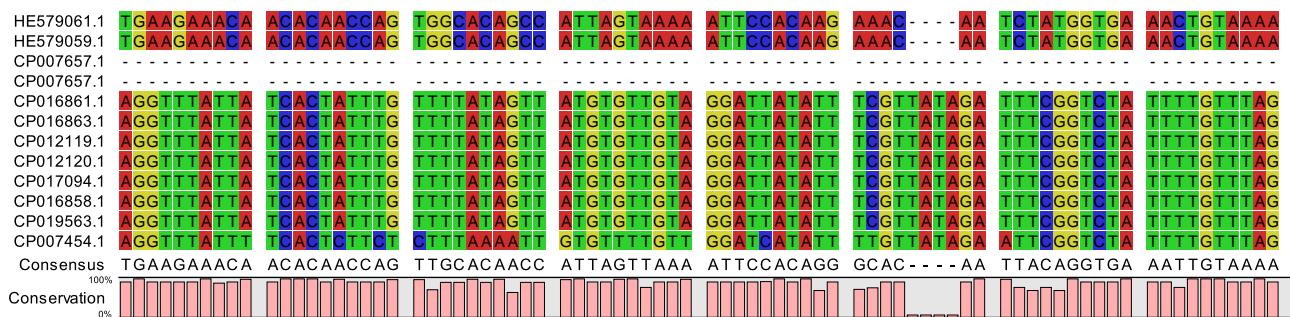


				1,400
CP007670.1	AAAAACTA ^G G	CTGGTAAAGC	1129	
CP003033.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP018205.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
AP017377.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
LT598688.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007676.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007672.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007674.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP011526.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
HF937103.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
AP009351.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP000046.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP000253.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
AC025591.8	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
LT671859.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007499.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
X17679.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007657.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014444.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014441.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014438.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014435.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014432.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014429.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014426.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014423.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014420.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014415.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014412.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014409.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014407.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014402.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014397.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014392.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014387.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014384.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014381.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014371.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014368.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014365.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014362.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP014376.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP009423.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP016855.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP013231.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP010300.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP010299.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP010298.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP010297.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP010296.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP010295.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007690.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007176.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP000730.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP000255.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007539.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
CP007657.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
AP014921.1	AAA ^A CTA ^G G	CTGGTAAAGC	1129	
AB436955.1	AAA ^A CTA ^G G	CTGGTAAAGC	1037	
AB489885.1	AAA ^A CTA ^G G	CTGGTAAAGC	1037	
AB489873.1	AAA ^A CTA ^G G	CTGGTAAAGC	1037	
AB489883.1	AAA ^A CTA ^G G	CTGGTAAAGC	1037	
AB489874.1	AAA ^A CTA ^G G	CTGGTAAAGC	1037	
LT615218.1	AAA ^A CTA ^T G	CTGGTAAAGC	1129	
AB436976.1	AAA ^A CTA ^T G	CTGGTAAAGC	1129	
AB489892.1	AAA ^A CTA ^T G	CTGGTAAAGC	1037	
AJ306908.1	AAA ^A CTA ^C AG	TTGATAAAGC	1129	
CP015646.1	AAA ^A CTA ^C AG	TTGATAAAGC	1129	
AB488510.1	AAA ^A CTA ^C GG	CTGGTAAAGC	1037	
EU105387.1	AAA ^A CTA ^C GG	CTGGTAAAGC	1069	
AB436975.1	GAAA ^A CTA ^C AG	TTGATAAAGC	1129	
AB488499.1	GAAA ^A CTA ^C AG	TTGATAAAGC	1037	
AJ309189.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	953	
FR821779.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	1114	
CP012593.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
CP012692.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
CP013955.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
CP013953.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
CP014064.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
LT009690.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
AP017320.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
CP010890.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
CP001844.2	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
CP001781.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
AB488501.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
AB489898.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
HE579073.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
HE579071.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
HE579069.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
HE579065.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	
HE579063.1	GAAA ^A CTA ^C GG	CTGGTAAAGC	558	

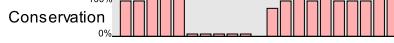


HE579061.1	AAA A C T A C G	C T G G T A A A G C	558
HE579059.1	AAA A C T A C G	C T G G T A A A G C	558
CP007657.1	- - - - -	- - - - -	-
CP007657.1	- - - - -	- - - - -	-
CP016861.1	T C A A C T A A T T	T A T C A A A A T T	954
CP016863.1	T C A A C T A A T T	T A T C A A A A T T	953
CP012119.1	T C A A C T A A T T	T A T C A A A A T T	954
CP012120.1	T C A A C T A A T T	T A T C A A A A T T	954
CP017094.1	T C A A C T A A T T	T A T C A A A A T T	954
CP016858.1	T C A A C T A A T T	T A T C A A A A T T	954
CP019563.1	T C A A C T A A T T	T A T C A A A A T T	1230
CP007454.1	T C A A C T A A T T	T A T C A A A A T T	1116
Consensus	AAA A C T A C G	C T G G T A A A G C	
Conservation			

			1,500
CP007670.1	GGTCC	GGAAATATCCA	1220
CP003033.1	GGTCC	GGAAATATCCA	1220
CP018205.1	GGTCC	GGAAATATCCA	1220
AP017377.1	GGTCC	GGAAATATCCA	1220
LT598688.1	GGTCC	GGAAATATCCA	1220
CP007676.1	GGTCC	GGAAATATCCA	1220
CP007672.1	GGTCC	GGAAATATCCA	1220
CP007674.1	GGTCC	GGAAATATCCA	1220
CP011526.1	GGTCC	GGAAATATCCA	1220
HF937103.1	GGTCC	GGAAATATCCA	1220
AP009351.1	GGTCC	GGAAATATCCA	1220
CP000046.1	GGTCC	GGAAATATCCA	1220
CP000253.1	GGTCC	GGAAATATCCA	1220
AC025591.8	GGTCC	GGAAATATCCA	1220
LT671859.1	GGTCC	GGAAATATCCA	1220
CP007499.1	GGTCC	GGAAATATCCA	1220
X17679.1	GGTCC	GGAAATATCCA	1220
CP007657.1	GGTCC	GGAAATATCCA	1220
CP014444.1	GGTCC	GGAAATATCCA	1220
CP014441.1	GGTCC	GGAAATATCCA	1220
CP014438.1	GGTCC	GGAAATATCCA	1220
CP014435.1	GGTCC	GGAAATATCCA	1220
CP014432.1	GGTCC	GGAAATATCCA	1220
CP014429.1	GGTCC	GGAAATATCCA	1220
CP014426.1	GGTCC	GGAAATATCCA	1220
CP014423.1	GGTCC	GGAAATATCCA	1220
CP014420.1	GGTCC	GGAAATATCCA	1220
CP014415.1	GGTCC	GGAAATATCCA	1220
CP014412.1	GGTCC	GGAAATATCCA	1220
CP014409.1	GGTCC	GGAAATATCCA	1220
CP014407.1	GGTCC	GGAAATATCCA	1220
CP014402.1	GGTCC	GGAAATATCCA	1220
CP014397.1	GGTCC	GGAAATATCCA	1220
CP014392.1	GGTCC	GGAAATATCCA	1220
CP014387.1	GGTCC	GGAAATATCCA	1220
CP014384.1	GGTCC	GGAAATATCCA	1220
CP014381.1	GGTCC	GGAAATATCCA	1220
CP014371.1	GGTCC	GGAAATATCCA	1220
CP014368.1	GGTCC	GGAAATATCCA	1220
CP014365.1	GGTCC	GGAAATATCCA	1220
CP014362.1	GGTCC	GGAAATATCCA	1220
CP014376.1	GGTCC	GGAAATATCCA	1220
CP009423.1	GGTCC	GGAAATATCCA	1220
CP016855.1	GGTCC	GGAAATATCCA	1220
CP013231.1	GGTCC	GGAAATATCCA	1220
CP010300.1	GGTCC	GGAAATATCCA	1220
CP010299.1	GGTCC	GGAAATATCCA	1220
CP010298.1	GGTCC	GGAAATATCCA	1220
CP010297.1	GGTCC	GGAAATATCCA	1220
CP010296.1	GGTCC	GGAAATATCCA	1220
CP010295.1	GGTCC	GGAAATATCCA	1220
CP007690.1	GGTCC	GGAAATATCCA	1220
CP007176.1	GGTCC	GGAAATATCCA	1220
CP000730.1	GGTCC	GGAAATATCCA	1220
CP000255.1	GGTCC	GGAAATATCCA	1220
CP007539.1	GGTCC	GGAAATATCCA	1220
CP007657.1	GGTCC	GGAAATATCCA	1220
AP014921.1	GGTCC	GGAAATATCCA	1220
AB436955.1	GGTCC	GGAAATATCCA	1128
AB489885.1	GGTCC	GGAAATATCCA	1128
AB489873.1	GGTCC	GGAAATATCCA	1128
AB489883.1	GGTCC	GGAAATATCCA	1128
AB489874.1	GGTCC	GGAAATATCCA	1116
LT615218.1	GGTCC	AGACTATCCA	1220
AB436976.1	GGTCC	AGACTATCCA	1220
AB489892.1	GGTCC	AGACTATCCA	1128
AJ306908.1	GGTCC	AGACTATCCA	1220
CP015646.1	GGTCC	AGACTATCCA	1220
AB488510.1	GGTCC	GGAAATATCCA	1128
EU105387.1	GGTCC	GGAAATATCCA	1160
AB436975.1	GGTCC	CGACTATCTA	1220
AB488499.1	GGTCC	CGACTATCTA	1128
AJ309189.1	GGTCC	GGAAATATCCA	1044
FR821779.1	GGTCC	CGACTATCTA	1205
CP012593.1	GGTCC	AGAAATATCCA	649
CP012692.1	GGTCC	AGAAATATCCA	649
CP013955.1	GGTCC	AGAAATATCCA	649
CP013953.1	GGTCC	AGAAATATCCA	649
CP014064.1	GGTCC	AGAAATATCCA	649
LT009690.1	GGTCC	AGAAATATCCA	649
AP017320.1	GGTCC	AGAAATATCCA	649
CP010890.1	GGTCC	AGAAATATCCA	649
CP001844.2	GGTCC	AGAAATATCCA	649
CP001781.1	GGTCC	AGAAATATCCA	649
AB488501.1	GGTCC	AGAAATATCCA	649
AB489898.1	GGTCC	AGAAATATCCA	649
HE579073.1	GGTCC	AGAAATATCCA	649
HE579071.1	GGTCC	AGAAATATCCA	649
HE579069.1	GGTCC	AGAAATATCCA	649
HE579065.1	GGTCC	AGAAATATCCA	649
HE579063.1	GGTCC	AGAAATATCCA	649

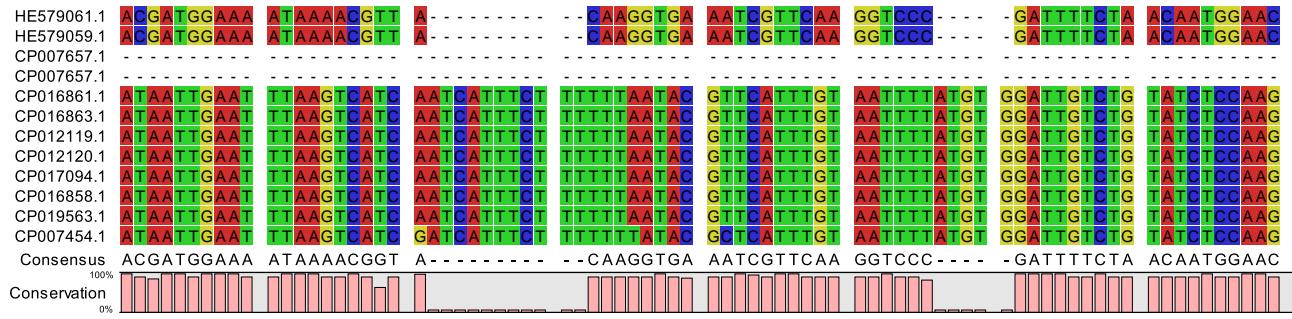


HE579061.1	GGTCC	- - -	AGAATATCCA	649
HE579059.1	GGTCC	- - -	AGAATATCCA	649
CP007657.1	- - - - -	- - - - -	- - - - -	
CP007657.1	- - - - -	- - - - -	- - - - -	
CP016861.1	TTTCCATAAA	GAAATCATCA	1054	
CP016863.1	TTTCCATAAA	GAAATCATCA	1053	
CP012119.1	TTTCCATAAA	GAAATCATCA	1054	
CP012120.1	TTTCCATAAA	GAAATCATCA	1054	
CP017094.1	TTTCCATAAA	GAAATCATCA	1054	
CP016858.1	TTTCCATAAA	GAAATCATCA	1054	
CP019563.1	TTTCCATAAA	GAAATCATCA	1330	
CP007454.1	TCTCCATAAA	GAAATCATCT	1216	
Consensus	GGTCC	- - -	GGAATATCCA	



The chart shows a single row of bars representing conservation levels for each position in the alignment. The y-axis is labeled 'Conservation' with ticks at 0% and 100%. The x-axis represents the positions from 1 to 1216. All bars are filled with a light red color, indicating 100% conservation across all 100% of the alignment.

			1,600
CP007670.1	AAAGGGCCC	ATCATTAAAGC	1304
CP003033.1	AAAGGGCCC	ATCATTAAAGC	1304
CP018205.1	AAAGGGCCC	ATCATTAAAGC	1304
AP017377.1	AAAGGGCCC	ATCATTAAAGC	1304
LT598688.1	AAAGGGCCC	ATCATTAAAGC	1304
CP007676.1	AAAGGGCCC	ATCATTAAAGC	1304
CP007672.1	AAAGGGCCC	ATCATTAAAGC	1304
CP007674.1	AAAGGGCCC	ATCATTAAAGC	1304
CP011526.1	AAAGGGCCC	ATCATTAAAGC	1304
HF937103.1	AAAGGGCCC	ATCATTAAAGC	1304
AP009351.1	AAAGGGCCC	ATCATTAAAGC	1304
CP000046.1	AAAGGGCCC	ATCATTAAAGC	1304
CP000253.1	AAAGGGCCC	ATCATTAAAGC	1304
AC025591.8	AAAGGGCCC	ATCATTAAAGC	1304
LT671859.1	AAAGGGCCC	ATCATTAAAGC	1304
CP007499.1	AAAGGGCCC	ATCATTAAAGC	1304
X17679.1	AAAGGGCCC	ATCATTAAAGC	1304
CP007657.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014444.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014441.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014438.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014435.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014432.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014429.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014426.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014423.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014420.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014415.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014412.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014409.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014407.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014402.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014397.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014392.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014387.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014384.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014381.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014371.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014368.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014365.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014362.1	AAAGGGCCC	ATCATTAAAGC	1304
CP014376.1	AAAGGGCCC	ATCATTAAAGC	1304
CP009423.1	AAAGGGCCC	ATCATTAAAGC	1304
CP016855.1	AAAGGGCCC	ATCATTAAAGC	1304
CP013231.1	AAAGGGCCC	ATCATTAAAGC	1304
CP010300.1	AAAGGGCCC	ATCATTAAAGC	1304
CP010299.1	AAAGGGCCC	ATCATTAAAGC	1304
CP010298.1	AAAGGGCCC	ATCATTAAAGC	1304
CP010297.1	AAAGGGCCC	ATCATTAAAGC	1304
CP010296.1	AAAGGGCCC	ATCATTAAAGC	1304
CP010295.1	AAAGGGCCC	ATCATTAAAGC	1304
CP007690.1	AAAGGGCCC	ATCATTAAAGC	1304
CP007176.1	AAAGGGCCC	ATCATTAAAGC	1304
CP000730.1	AAAGGGCCC	ATCATTAAAGC	1304
CP000255.1	AAAGGGCCC	ATCATTAAAGC	1304
CP007539.1	AAAGGGCCC	ATCATTAAAGC	1303
CP007657.1	AAAGGGCCC	ATCATTAAAGC	1304
AP014921.1	AAAGGGCCC	ATCATTAAAGC	1304
AB436955.1	AAAGGGCCC	ATCATTAAAGC	1212
AB489885.1	AAAGGGCCC	ATCATTAAAGC	1212
AB489873.1	AAAGGGCCC	ATCATTAAAGC	1212
AB489883.1	AAAGGGCCC	ATCATTAAAGC	1212
AB489874.1	AAAGGGCCC	ATCATTAAAGC	1200
LT615218.1	AAAGGGCCC	ATCATTAAAGC	1304
AB436976.1	AAAGGGCCC	ATCATTAAAGC	1304
AB489892.1	AAAGGGCCC	ATCATTAAAGC	1212
AJ306908.1	AAAACAGACC	ATCTTTAAGC	1304
CP015646.1	AAAACAGACC	ATCTTTAAGC	1304
AB488510.1	AAAGGGCCC	ATCATTAAAGC	1212
EU105387.1	AAAGGGCCC	ATCATTAAAGC	1244
AB436975.1	AAAACAGACC	ATCTTTAAGC	1304
AB488499.1	AAAACAGACC	ATCTTTAAGC	1212
AJ309189.1	AAAGGGCCC	ATCATTAAAGC	1128
FR821779.1	AAAACAGACC	ATCTTTAAGC	1289
CP012593.1	AAAACAGACC	ATCTTTAAGC	733
CP012692.1	AAAACAGACC	ATCTTTAAGC	733
CP013955.1	AAAACAGACC	ATCTTTAAGC	733
CP013953.1	AAAACAGACC	ATCTTTAAGC	733
CP014064.1	AAAACAGACC	ATCTTTAAGC	733
LT009690.1	AAAACAGACC	ATCTTTAAGC	733
AP017320.1	AAAACAGACC	ATCTTTAAGC	733
CP010890.1	AAAACAGACC	ATCTTTAAGC	733
CP001844.2	AAAACAGACC	ATCTTTAAGC	733
CP001781.1	AAAACAGACC	ATCTTTAAGC	733
AB488501.1	AAAACAGACC	ATCTTTAAGC	733
AB489898.1	AAAACAGACC	ATCTTTAAGC	733
HE579073.1	AAAACAGACC	ATCTTTAAGC	733
HE579071.1	AAAACAGACC	ATCTTTAAGC	733
HE579069.1	AAAACAGACC	ATCTTTAAGC	733
HE579065.1	AAAACAGACC	ATCTTTAAGC	733
HE579063.1	AAAACAGACC	ATCTTTAAGC	733

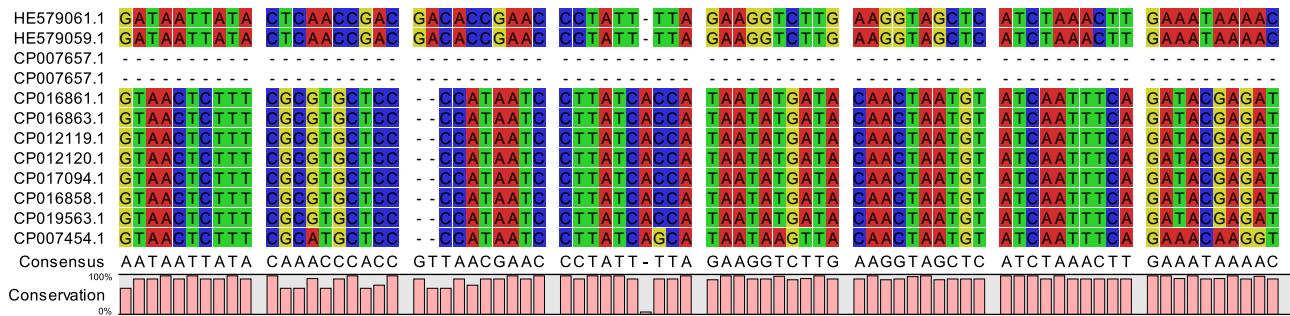


HE579061.1	AAAAACAGACC	ATCTTTAAGC	733
HE579059.1	AAAACAGACC	ATCTTTAAGC	733
CP007657.1	- - - - -	- - - - -	
CP007657.1	- - - - -	- - - - -	
CP016861.1	GATTAAAGTCC	AGTTTTGCTC	1154
CP016863.1	GATTAAAGTCC	AGTTTTGCTC	1153
CP012119.1	GATTAAAGTCC	AGTTTTGCTC	1154
CP012120.1	GATTAAAGTCC	AGTTTTGCTC	1154
CP017094.1	GATTAAAGTCC	AGTTTTGCTC	1154
CP016858.1	GATTAAAGTCC	AGTTTTGCTC	1154
CP019563.1	GATTAAAGTCC	AGTTTTGCTC	1430
CP007454.1	GATTAAAGTCC	AGTTTTGCTC	1316
Consensus	AAAGCGGGCCC	ATCATTAAGC	



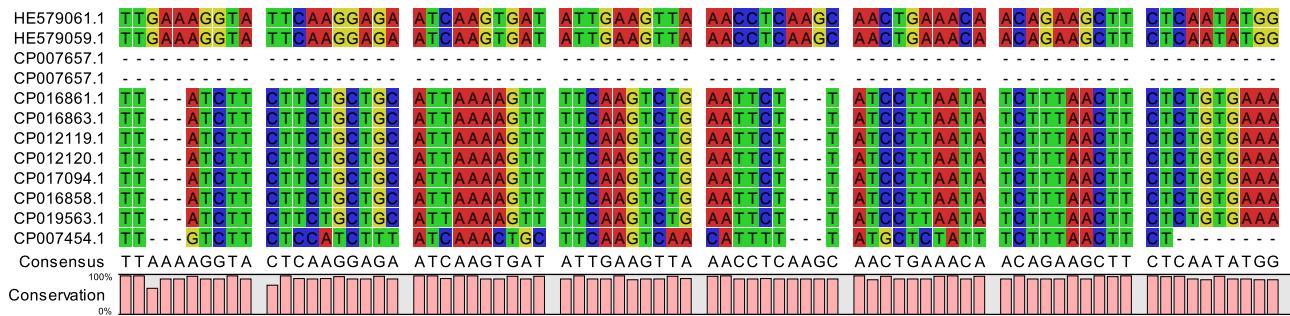
The chart shows a single row of bars representing 100% conservation across all positions of the sequence. The y-axis is labeled 'Conservation' with ticks at 0% and 100%. The x-axis represents the sequence positions.

				1,700
CP007670.1	CACAAGGTAC	TGAATCAACG	1403	
CP003033.1	CACAAGGTAC	TGAATCAACG	1403	
CP018205.1	CACAAGGTAC	TGAATCAACG	1403	
AP017377.1	CACAAGGTAC	TGAATCAACG	1403	
LT598688.1	CACAAGGTAC	TGAATCAACG	1403	
CP007676.1	CACAAGGTAC	TGAATCAACG	1403	
CP007672.1	CACAAGGTAC	TGAATCAACG	1403	
CP007674.1	CACAAGGTAC	TGAATCAACG	1403	
CP011526.1	CACAAGGTAC	TGAATCAACG	1403	
HF937103.1	CACAAGGTAC	TGAATCAACG	1403	
AP009351.1	CACAAGGTAC	TGAATCAACG	1403	
CP000046.1	CACAAGGTAC	TGAATCAACG	1403	
CP000253.1	CACAAGGTAC	TGAATCAACG	1403	
AC025591.8	CACAAGGTAC	TGAATCAACG	1403	
LT671859.1	CACAAGGTAC	TGAATCAACG	1403	
CP007499.1	CACAAGGTAC	TGAATCAACG	1403	
X17679.1	CACAAGGTAC	TGAATCAACG	1403	
CP007657.1	CACAAGGTAC	TGAATCAACG	1403	
CP014444.1	CACAAGGTAC	TGAATCAACG	1403	
CP014441.1	CACAAGGTAC	TGAATCAACG	1403	
CP014438.1	CACAAGGTAC	TGAATCAACG	1403	
CP014435.1	CACAAGGTAC	TGAATCAACG	1403	
CP014432.1	CACAAGGTAC	TGAATCAACG	1403	
CP014429.1	CACAAGGTAC	TGAATCAACG	1403	
CP014426.1	CACAAGGTAC	TGAATCAACG	1403	
CP014423.1	CACAAGGTAC	TGAATCAACG	1403	
CP014420.1	CACAAGGTAC	TGAATCAACG	1403	
CP014415.1	CACAAGGTAC	TGAATCAACG	1403	
CP014412.1	CACAAGGTAC	TGAATCAACG	1403	
CP014409.1	CACAAGGTAC	TGAATCAACG	1403	
CP014407.1	CACAAGGTAC	TGAATCAACG	1403	
CP014402.1	CACAAGGTAC	TGAATCAACG	1403	
CP014397.1	CACAAGGTAC	TGAATCAACG	1403	
CP014392.1	CACAAGGTAC	TGAATCAACG	1403	
CP014387.1	CACAAGGTAC	TGAATCAACG	1403	
CP014384.1	CACAAGGTAC	TGAATCAACG	1403	
CP014381.1	CACAAGGTAC	TGAATCAACG	1403	
CP014371.1	CACAAGGTAC	TGAATCAACG	1403	
CP014368.1	CACAAGGTAC	TGAATCAACG	1403	
CP014365.1	CACAAGGTAC	TGAATCAACG	1403	
CP014362.1	CACAAGGTAC	TGAATCAACG	1403	
CP014376.1	CACAAGGTAC	TGAATCAACG	1403	
CP009423.1	CACAAGGTAC	TGAATCAACG	1403	
CP016855.1	CACAAGGTAC	TGAATCAACG	1403	
CP013231.1	CACAAGGTAC	TGAATCAACG	1403	
CP010300.1	CACAAGGTAC	TGAATCAACG	1403	
CP010299.1	CACAAGGTAC	TGAATCAACG	1403	
CP010298.1	CACAAGGTAC	TGAATCAACG	1403	
CP010297.1	CACAAGGTAC	TGAATCAACG	1403	
CP010296.1	CACAAGGTAC	TGAATCAACG	1403	
CP010295.1	CACAAGGTAC	TGAATCAACG	1403	
CP007690.1	CACAAGGTAC	TGAATCAACG	1403	
CP007176.1	CACAAGGTAC	TGAATCAACG	1403	
CP000730.1	CACAAGGTAC	TGAATCAACG	1403	
CP000255.1	CACAAGGTAC	TGAATCAACG	1403	
CP007539.1	CACAAGGTAC	TGAATCAACG	1402	
CP007657.1	CACAAGGTAC	TGAATCAACG	1403	
AP014921.1	CACAAGGTAC	TGAATCAACG	1403	
AB436955.1	CACAAGGTAC	TGAATCAACG	1311	
AB489885.1	CACAAGGTAC	TGAATCAACG	1311	
AB489873.1	CACAAGGTAC	TGAATCAACG	1311	
AB489883.1	CACAAGGTAC	TGAATCAACG	1311	
AB489874.1	CACAAGGTAC	TGAATCAACG	1299	
LT615218.1	CACAAGGTAC	TGAATCAACG	1403	
AB436976.1	CACAAGGTAC	TGAATCAACG	1403	
AB489892.1	CACAAGGTAC	TGAATCAACG	1311	
AJ306908.1	CACAAGGTAC	TGAATCAACG	1403	
CP015646.1	CACAAGGTAC	TGAATCAACG	1403	
AB488510.1	CACAAGGTAC	TGAATCAACG	1311	
EU105387.1	CACAAGGTAC	TGAATCAACG	1343	
AB436975.1	CACAAGGTAC	TGAATCAACG	1403	
AB488499.1	CACAAGGTAC	TGAATCAACG	1311	
AJ309189.1	CACAAGGTAC	TGAATCAACG	1227	
FR821779.1	CACAAGGTAC	TGAATCAACG	1388	
CP012593.1	CACAAGGTAC	TGAATCAACG	832	
CP012692.1	CACAAGGTAC	TGAATCAACG	832	
CP013955.1	CACAAGGTAC	TGAATCAACG	832	
CP013953.1	CACAAGGTAC	TGAATCAACG	832	
CP014064.1	CACAAGGTAC	TGAATCAACG	832	
LT009690.1	CACAAGGTAC	TGAATCAACG	832	
AP017320.1	CACAAGGTAC	TGAATCAACG	832	
CP010890.1	CACAAGGTAC	TGAATCAACG	832	
CP001844.2	CACAAGGTAC	TGAATCAACG	832	
CP001781.1	CACAAGGTAC	TGAATCAACG	832	
AB488501.1	CACAAGGTAC	TGAATCAACG	832	
AB489898.1	CACAAGGTAC	TGAATCAACG	832	
HE579073.1	CACAAGGTAC	TGAATCAACG	832	
HE579071.1	CACAAGGTAC	TGAATCAACG	832	
HE579069.1	CACAAGGTAC	TGAATCAACG	832	
HE579065.1	CACAAGGTAC	TGAATCAACG	832	
HE579063.1	CACAAGGTAC	TGAATCAACG	832	



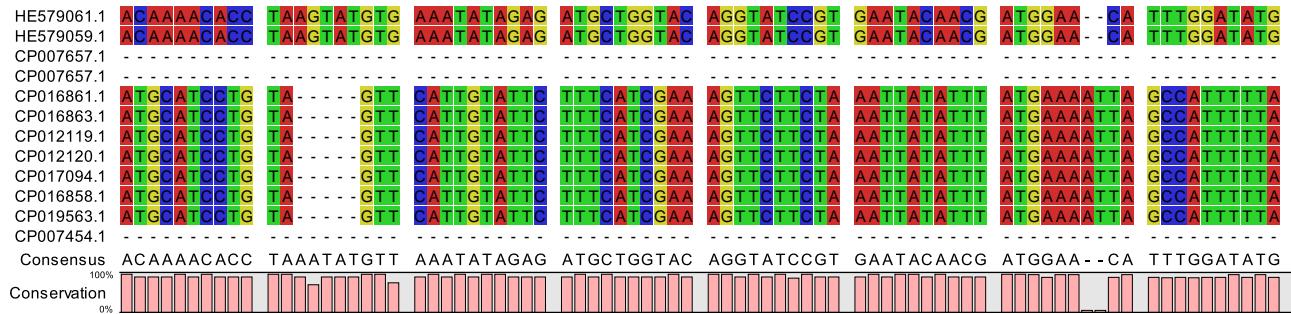
HE579061.1	CACAAGGTAC	TGAATCAACG	832
HE579059.1	CACAAGGTAC	TGAATCAACG	832
CP007657.1	- - - - -	- - - - -	
CP007657.1	- - - - -	- - - - -	
CP016861.1	CGTATACTTC	TTTAGTTGCT	1252
CP016863.1	CGTATACTTC	TTTAGTTGCT	1251
CP012119.1	CGTATACTTC	TTTAGTTGCT	1252
CP012120.1	CGTATACTTC	TTTAGTTGCT	1252
CP017094.1	CGTATACTTC	TTTAGTTGCT	1252
CP016858.1	CGTATACTTC	TTTAGTTGCT	1252
CP019563.1	CGTATACTTC	TTTAGTTGCT	1528
CP007454.1	CATAAACTTC	TTTAGTTGCC	1414
Consensus	CACAAGGTAC	TGAATCAACG	
Conservation			

				1,800
CP007670.1	T CCG - -	AGA	CCGCAATT T A	1500
CP003033.1	T CCG - -	AGA	CCGCAATT T A	1500
CP018205.1	T CCG - -	AGA	CCGCAATT T A	1500
AP017377.1	T CCG - -	AGA	CCGCAATT T A	1500
LT598688.1	T CCG - -	AGA	CCGCAATT T A	1500
CP007676.1	T CCG - -	AGA	CCGCAATT T A	1500
CP007672.1	T CCG - -	AGA	CCGCAATT T A	1500
CP007674.1	T CCG - -	AGA	CCGCAATT T A	1500
CP011526.1	T CCG - -	AGA	CCGCAATT T A	1500
HF937103.1	T CCG - -	AGA	CCGCAATT T A	1500
AP009351.1	T CCG - -	AGA	CCGCAATT T A	1500
CP000046.1	T CCG - -	AGA	CCGCAATT T A	1500
CP000253.1	T CCG - -	AGA	CCGCAATT T A	1500
AC025591.8	T CCG - -	AGA	CCGCAATT T A	1500
LT671859.1	T CCG - -	AGA	CCGCAATT T A	1500
CP007499.1	T CCG - -	AGA	CCGCAATT T A	1500
X17679.1	T CCG - -	AGA	CCGCAATT T A	1500
CP007657.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014444.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014441.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014438.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014435.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014432.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014429.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014426.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014423.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014420.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014415.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014412.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014409.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014407.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014402.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014397.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014392.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014387.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014384.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014381.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014371.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014368.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014365.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014362.1	T CCG - -	AGA	CCGCAATT T A	1500
CP014376.1	T CCG - -	AGA	CCGCAATT T A	1500
CP009423.1	T CCG - -	AGA	CCGCAATT T A	1500
CP016855.1	T CCG - -	AGA	CCGCAATT T A	1500
CP013231.1	T CCG - -	AGA	CCGCAATT T A	1500
CP010300.1	T CCG - -	AGA	CCGCAATT T A	1500
CP010299.1	T CCG - -	AGA	CCGCAATT T A	1500
CP010298.1	T CCG - -	AGA	CCGCAATT T A	1500
CP010297.1	T CCG - -	AGA	CCGCAATT T A	1500
CP010296.1	T CCG - -	AGA	CCGCAATT T A	1500
CP010295.1	T CCG - -	AGA	CCGCAATT T A	1500
CP007690.1	T CCG - -	AGA	CCGCAATT T A	1500
CP007176.1	T CCG - -	AGA	CCGCAATT T A	1500
CP000730.1	T CCG - -	AGA	CCGCAATT T A	1500
CP000255.1	T CCG - -	AGA	CCGCAATT T A	1500
CP007539.1	T CCG - -	AGA	CCGCAATT T A	1499
CP007657.1	T CCG - -	AGA	CCGCAATT T A	1500
AP014921.1	T CCG - -	AGA	CCGCAATT T A	1500
AB436955.1	T CCG - -	AGA	CCGCAATT T A	1408
AB489885.1	T CCG - -	AGA	CCGCAATT T A	1408
AB489873.1	T CCG - -	AGA	CCGCAATT T A	1408
AB489883.1	T CCG - -	AGA	CCGCAATT T A	1408
AB489874.1	T CCG - -	AGA	CCGCAATT T A	1396
LT615218.1	T CCG - -	AGA	CCGCAATT T A	1500
AB436976.1	T CCG - -	AGA	CCGCAATT T A	1500
AB489892.1	T CCG - -	AGA	CCGCAATT T A	1408
AJ306908.1	A GCG - -	AGA	CCGCAATT T A	1500
CP015646.1	A GCG - -	AGA	CCGCAATT T A	1500
AB488510.1	T CCG - -	AGA	CCGCAATT T A	1408
EU105387.1	T CCG - -	AGA	CCGCAATT T A	1440
AB436975.1	T CCG - -	AGA	CCTCAATT T A	1500
AB488499.1	T CCG - -	AGA	CCTCAATT T A	1408
AJ309189.1	T CCG - -	AGA	CCGCAATT T A	1324
FR821779.1	T CCG - -	AGA	CCGCAATT T A	1485
CP012593.1	T CCG - -	AGA	CCGCAATT T A	929
CP012692.1	T CCG - -	AGA	CCGCAATT T A	929
CP013955.1	T CCG - -	AGA	CCGCAATT T A	929
CP013953.1	T CCG - -	AGA	CCGCAATT T A	929
CP014064.1	T CCG - -	AGA	CCGCAATT T A	929
LT009690.1	T CCG - -	AGA	CCGCAATT T A	929
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HE579073.1	T CCG - -	AGA	CCGCAATT T A	929
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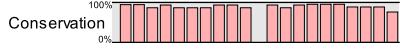
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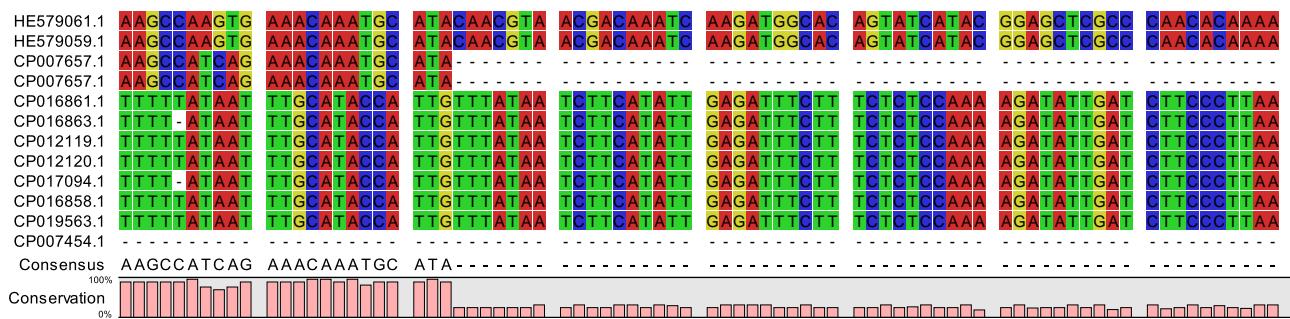
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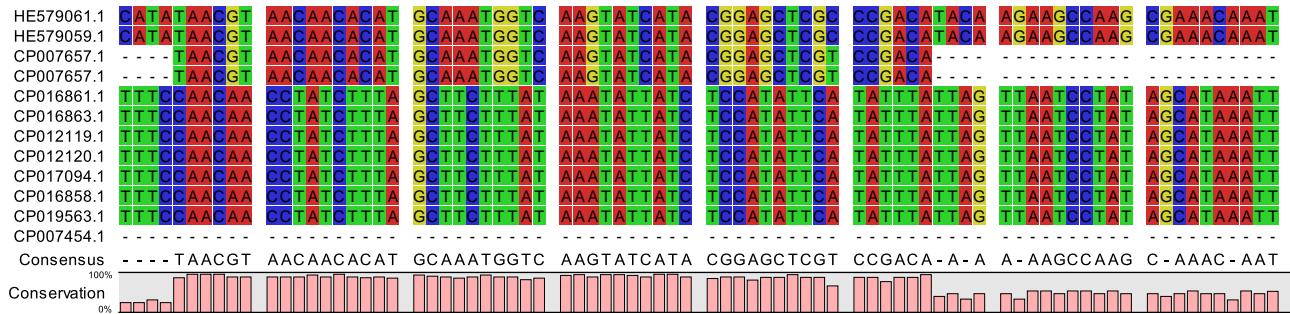
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CP016863.1	TAC - - - - -	CT	1524
CP012119.1	TAC - - - - -	CT	1526
CP012120.1	TAC - - - - -	CT	1526
CP017094.1	TAC - - - - -	CT	1525
CP016858.1	TAC - - - - -	CT	1526
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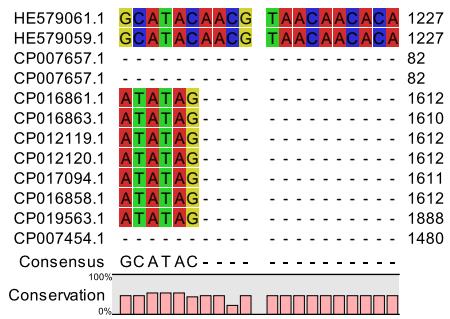
Consensus - - - - -

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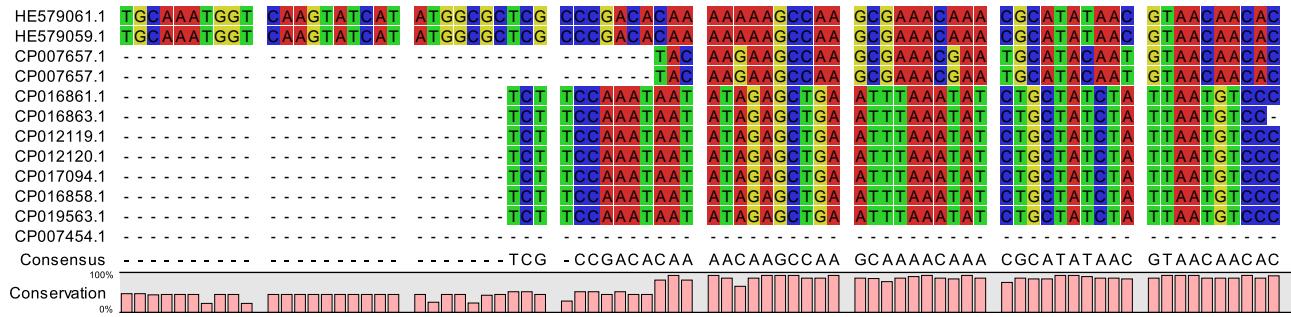
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CP018205.1	G C A T A C A A A T G	T A A C A A C A C A	1717
AP017377.1	G C A T A C A A A T G	T A A C A A C A C A	1717
LT598688.1	G C A T A C A A A T G	T A A C A A C A C A	1717
CP007676.1	G C A T A C A A A T G	T A A C A A C A C A	1717
CP007672.1	G C A T A C A A A T G	T A A C A A C A C A	1717
CP007674.1	G C A T A C A A T G	T A A C A A C A C A	1717
CP011526.1	G C A T A C A A A T G	T A A C A A C A C A	1717
HF937103.1	G C A T A C A A A T G	T A A C A A C A C A	1717
AP009351.1	G C A T A C A A A T G	T A A C A A C A C A	1717
CP000046.1	G C A T A C A A A T G	T A A C A A C A C A	1717
CP000253.1	G C A T A C A A A T G	T A A C A A C A C A	1717
AC025591.8	G C A T A C A A A T G	T A A C A A C A C A	1717
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CP007499.1	G C A T A C A A A T G	T A A C A A C A C A	1717
X17679.1	G C A T A C A A A T G	T A A C A A C A C A	1717
CP007657.1	G C A T A C A A A T G	T A A C A A C A C A	1717
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AB436976.1	G C A T A C A A A C G	T A A C A A C A C A	1798
AB489892.1	G C A T A C A A A C G	T A A C A A C A C A	1706
AJ306908.1	G C A T A C A A A T G	T A A C A A C A C A	1798
CP015646.1	G C A T A C A A A T G	T A A C A A C A C A	1798
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CP013955.1	G C A T A C A A A C G	T A A C A A C A C A	1227
CP013953.1	G C A T A C A A A C G	T A A C A A C A C A	1227
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CP010890.1	G C A T A C A A A C G	T A A C A A C A C A	1227
CP001844.2	G C A T A C A A A C G	T A A C A A C A C A	1227
CP001781.1	G C A T A C A A A C G	T A A C A A C A C A	1227
AB488501.1	G C A T A C A A A C G	T A A C A A C A C A	1227
AB489898.1	G C A T A C A A A C G	T A A C A A C A C A	1227
HE579073.1	G C A T A C A A A C G	T A A C A A C A C A	1227
HE579071.1	G C A T A C A A A C G	T A A C A A C A C A	1227
HE579069.1	G C A T A C A A A C G	T A A C A A C A C A	1227
HE579065.1	G C A T A C A A A C G	T A A C A A C A C A	1227
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CP003033.1	A TGG AAA CGG	CC AAG TAT CA	1817	
CP018205.1	A TGG AAA CGG	CC AAG TAT CA	1817	
AP017377.1	A TGG AAA CGG	CC AAG TAT CA	1817	
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CP007676.1	A TGG AAA CGG	CC AAG TAT CA	1817	
CP007672.1	A TGG AAA CGG	CC AAG TAT CA	1817	
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HF937103.1	A TGG AAA CGG	CC AAG TAT CA	1817	
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CP000046.1	A TGG AAA CGG	CC AAG TAT CA	1817	
CP000253.1	A TGG AAA CGG	CC AAG TAT CA	1817	
AC025591.8	A TGG AAA CGG	CC AAG TAT CA	1817	
LT671859.1	A TGG AAA CGG	CC AAG TAT CA	1817	
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CP007657.1	- - - GAAA CGG	CC AAG TAT CA	1736	
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CP007657.1	- - - GAAA CGG	CC AAG TAT CA	1736	
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AB436955.1	A TGG AAA CGG	CC AAG TAT CA	1725	
AB489885.1	A TGG AAA CGG	CC AAG TAT CA	1725	
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AB489883.1	A TGG AAA CGG	CC AAG TAT CA	1644	
AB489874.1	A TGG AAA CGG	CC AAG TAT CA	1632	
LT615218.1	A TG AAA CGG	CC AAG TAT CA	1898	
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AB489892.1	A TGC AAA CGG	CC AAG TAT CA	1806	
AJ306908.1	A TGC AAA CGG	TCA AAG TAT CA	1898	
CP015646.1	A TGC AAA CGG	TCA AAG TAT CA	1898	
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EU105387.1	- - - - -	- - - - -	1520	
AB436975.1	A TG AAA TGG	CC AAG TAT CA	1898	
AB488499.1	A TGC AAA TGG	CC AAG TAT CA	1806	
AJ309189.1	- - - - -	- - - - -	1386	
FR821779.1	A TG AAA CGG	CC AAG TAT CA	1883	
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CP012692.1	A TG AAA CGG	TCA AAG TAT CA	1327	
CP013955.1	A TGC AAA TGG	TCA AAG TAT CA	1327	
CP013953.1	A TG AAA CGG	TCA AAG TAT CA	1327	
CP014064.1	A TGC AAA TGG	TCA AAG TAT CA	1327	
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AB489898.1	A TGC AAA TGG	TCA AAG TAT CA	1327	
HE579073.1	A TG AAA TGG	TCA AAG TAT CA	1327	
HE579071.1	A TG AAA TGG	TCA AAG TAT CA	1327	
HE579069.1	A TGC AAA TGG	TCA AAG TAT CA	1327	
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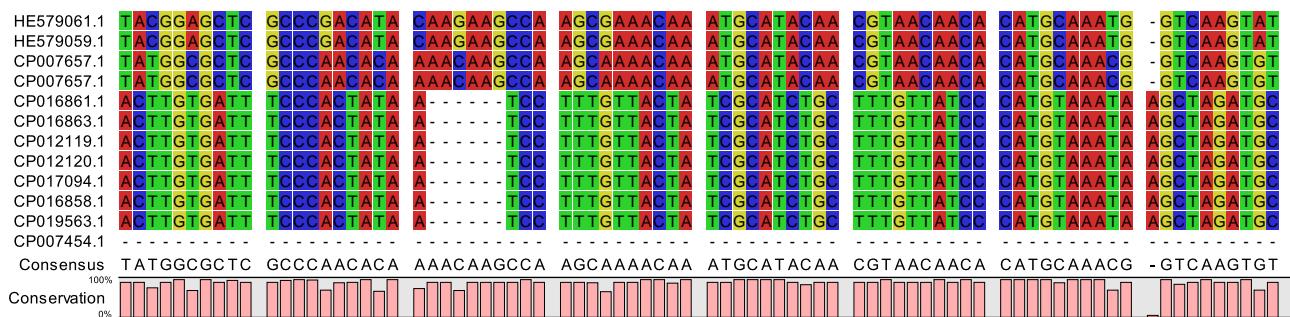


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CP007657.1	A T G G A A A C G G	C C A A G T A T C A	145
CP016861.1	A T T T T T T A C T C	C C A - G C A T T A	1684
CP016863.1	A T T T T T T A C T C	C C A - G C A T T A	1681
CP012119.1	A T T T T T T A C T C	C C A - G C A T T A	1684
CP012120.1	A T T T T T T A C T C	C C A - G C A T T A	1684
CP017094.1	A T T T T T T A C T C	C C A - G C A T T A	1683
CP016858.1	A T T T T T T A C T C	C C A - G C A T T A	1684
CP019563.1	A T T T T T T A C T C	C C A - G C A T T A	1960
CP007454.1	- - - - -	- - - - -	1480

Consensus ATGGAAACGG CCAAGTATCA



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CP003033.1	CAT	A	GG	GCG
CP018205.1	CAT	A	GG	AGC
AP017377.1	CAT	A	GG	GAG
LT598688.1	CAT	A	GG	AGO
CP007676.1	CAT	A	GG	GAGC
CP007672.1	CAT	A	GG	GAGC
CP007674.1	CAT	A	GG	GAGU
CP011526.1	CAT	A	GG	GAGC
HF937103.1	CAT	A	GG	AGG
AP009351.1	CAT	A	GG	GAGC
CP000046.1	CAT	A	GG	GAGC
CP000253.1	CAT	A	GG	GAGC
AC025591.8	CAT	A	GG	GAGC
LT671859.1	CAT	A	GG	GAGC
CP007499.1	CAT	A	GG	GAGC
X17679.1	CAT	A	GG	AGG
CP007657.1	CAT	A	GG	GAGC
CP014444.1	CAT	A	GG	GAGC
CP014441.1	CAT	A	GG	GAGC
CP014438.1	CAT	A	GG	GAGC
CP014435.1	CAT	A	GG	GAGC
CP014432.1	CAT	A	GG	GAGC
CP014429.1	CAT	A	GG	GAGC
CP014426.1	CAT	A	GG	GAGC
CP014423.1	CAT	A	GG	GAGC
CP014420.1	CAT	A	GG	GAGC
CP014415.1	CAT	A	GG	GAGC
CP014412.1	CAT	A	GG	GAGC
CP014409.1	CAT	A	GG	GAGC
CP014407.1	CAT	A	GG	GAGC
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CP013231.1	CAT	A	GG	GAGC
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CP000255.1	CAT	A	GG	GAGC
CP007539.1	CAT	A	GG	GAGC
CP007657.1	CAT	A	GG	GAGC
AP014921.1	CAT	A	GG	GAGC
AB436955.1	CAT	A	GG	GAGC
AB489885.1	CAT	A	GG	GAGC
AB489873.1	CAT	A	GG	GAGC
AB489883.1	CAT	A	GG	GAGC
AB489874.1	CAT	A	GG	GAGC
LT615218.1	CAT	A	TGG	CG
AB436976.1	CAT	A	TGG	GC
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AJ306908.1	CAT	A	TGG	GC
CP015646.1	CAT	A	TGG	GC
AB488510.1	-	-	-	-
EU105387.1	-	-	-	1520
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AB488499.1	CAT	A	TGG	GC
AJ309189.1	-	-	-	1386
FR821779.1	CAT	A	GGT	GC
CP012593.1	CAT	A	GG	GC
CP012692.1	CAT	A	GG	GC
CP013955.1	CAT	A	GG	GC
CP013953.1	CAT	A	GG	GC
CP014064.1	CAT	A	GG	GC
LT009690.1	CAT	A	GG	GC
AP017320.1	CAT	A	GG	GC
CP010890.1	CAT	A	GG	GC
CP001844.2	CAT	A	GG	GC
CP001781.1	CAT	A	GG	GC
AB488501.1	CAT	A	GG	GC
AB489898.1	CAT	A	GG	GC
HE579073.1	CAT	A	GG	GC
HE579071.1	CAT	A	GG	GC
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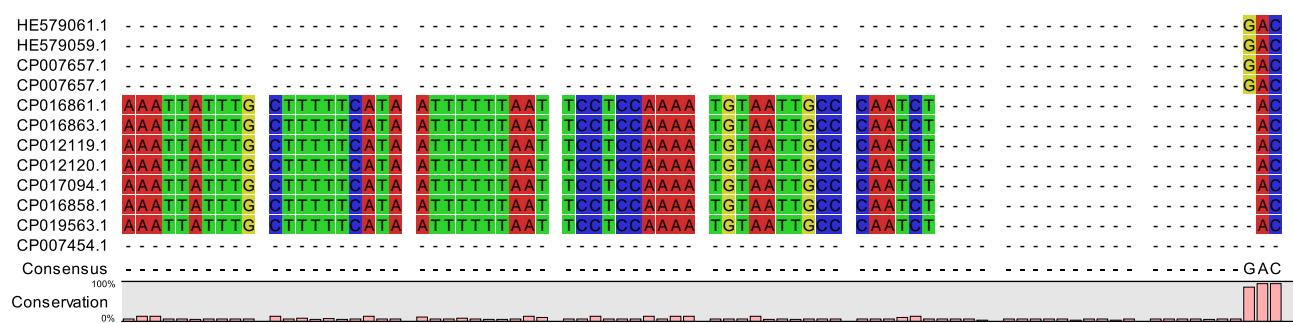
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CP007657.1	CATATGGAGC	TGCCCC	- - -	240
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CP016861.1	AACTGCTAAT	GCGCC	TAGCG	1778
CP016863.1	AACTGCTAAT	GCGCC	TAGCG	1775
CP012119.1	AACTGCTAAT	GCGCC	TAGCG	1778
CP012120.1	AACTGCTAAT	GCGCC	TAGCG	1778
CP017094.1	AACTGCTAAT	GCGCC	TAGCG	1777
CP016858.1	AACTGCTAAT	GCGCC	TAGCG	1778
CP019563.1	AACTGCTAAT	GCGCC	TAGCG	2054
CP007454.1	- - -	- - -	- - -	1480

Consensus CATACGGAGC TCGCCC - - -



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CP018205.1	- - -	- - -	- - -	GAC				
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HF937103.1	- - -	- - -	- - -	GAC				
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AC025591.8	- - -	- - -	- - -	GAC				
LT671859.1	- - -	- - -	- - -	GAC				
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X17679.1	- - -	- - -	- - -	GAC				
CP007657.1	- - -	- - -	- - -	GAC				
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CP014435.1	- - -	- - -	- - -	GAC				
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CP014426.1	- - -	- - -	- - -	GAC				
CP014423.1	- - -	- - -	- - -	GAC				
CP014420.1	- - -	- - -	- - -	GAC				
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CP014387.1	- - -	- - -	- - -	GAC				
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CP014371.1	- - -	- - -	- - -	GAC				
CP014368.1	- - -	- - -	- - -	GAC				
CP014365.1	- - -	- - -	- - -	GAC				
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CP009423.1	- - -	- - -	- - -	GAC				
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CP010297.1	- - -	- - -	- - -	GAC				
CP010296.1	- - -	- - -	- - -	GAC				
CP010295.1	- - -	- - -	- - -	GAC				
CP007690.1	- - -	- - -	- - -	GAC				
CP007176.1	- - -	- - -	- - -	GAC				
CP000730.1	- - -	- - -	- - -	GAC				
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CP007539.1	- - -	- - -	- - -	GAC				
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AP014921.1	- - -	- - -	- - -	GAC				
AB436955.1	- - -	- - -	- - -	GAC				
AB489885.1	- - -	- - -	- - -	GAC				
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AB489883.1	- - -	- - -	- - -	GAC				
AB489874.1	- - -	- - -	- - -	GAC				
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AB489892.1	C A A A A T A A G C	C A T C A G A A A C	A A A T G C A T A O	A A C G T T A A C A A	C A C A T G C A A A	T G G T C A A G T A	T C A T A T T G G G G	C T C G C C C G A C
AJ306908.1	C A A A A C A A G C	C A A G C G A A A C	A A A C G C A T A T	A A C G T T A A C A A	C A C A T G C A A A	T G G T C A A G T G	T C A T A C G G G G	C T C G C C C G A C
CP015646.1	C A A A A C A A G C	C A A G C G A A A C	A A A C G C A T A T	A A C G T T A A C A A	C A C A T G C A A A	T G G T C A A G T G	T C A T A C G G G G	C T C G C C C G A C
AB488510.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
EU105387.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
AB436975.1	C A A A A C A A G C	C A A G T G A A A C	G A A C G C A T A T	A A C G T T A A C A A	C A C A C G G A A A	T G G C C A A G T A	T C A T A T T G G G G	C T C G C C C A A C
AB488499.1	C A A A A C A A G C	C A A G T G A A A C	G A A C G C A T A T	A A C G T T A A C A A	C A C A C G G A A A	T G G C C A A G T A	T C A T A T T G G G G	C T C G C C C A A C
AJ309189.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
FR821779.1	C A A A A C A A G C	C A A A C A A A A C	A A A C G G A G T A T	A A C G T T A A C A A	C A C A T G C A A A	C G G C C A A G T G	T C A T A C G G A G	C T C G T C C G A C
CP012593.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
CP012692.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
CP013955.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
CP013953.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
CP014064.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
LT009690.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
AP017320.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
CP010890.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
CP001844.2	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
CP001781.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
AB488501.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
AB489898.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
HE579073.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
HE579071.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
HE579069.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
HE579065.1	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
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CP018205.1	A T A C A A G A A G	CC A A G T A A - A	1934	
AP017377.1	A T A C A A G A A G	CC A A G T A A - A	1934	
LT598688.1	A T A C A A G A A G	CC A A G T A A - A	1934	
CP007676.1	A T A C A A G A A G	CC A A G T A A - A	1934	
CP007672.1	A T A C A A G A A G	CC A A G T A A - A	1934	
CP007674.1	A T A C A A G A A G	CC A A G T A A - A	1934	
CP011526.1	A T A C A A G A A G	CC A A G T A A - A	1934	
HF937103.1	A T A C A A G A A G	CC A A G T A A - A	1934	
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CP000046.1	A T A C A A G A A G	CC A A G T A A - A	1934	
CP000253.1	A T A C A A G A A G	CC A A G T A A - A	1934	
AC025591.8	A T A C A A G A A G	CC A A G T A A - A	1934	
LT671859.1	A T A C A A G A A G	CC A A G T A A - A	1934	
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X17679.1	A T A C A A G A A G	CC A A G T A A - A	1934	
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CP014444.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP014441.1	A T A C A A G A A G	CC A A G T A A - A	1853	
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CP014435.1	A T A C A A G A A G	CC A A G T A A - A	1853	
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CP014420.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP014415.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP014412.1	A T A C A A G A A G	CC A A G T A A - A	1853	
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CP014407.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP014402.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP014397.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP014392.1	A T A C A A G A A G	CC A A G T A A - A	1853	
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CP014368.1	A T A C A A G A A G	CC A A G T A A - A	1853	
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CP014362.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP014376.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP009423.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP016855.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP013231.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP010300.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP010299.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP010298.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP010297.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP010296.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP010295.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP007690.1	A T A C A A G A A G	CC A A G T A A - A	1853	
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CP000255.1	A T A C A A G A A G	CC A A G T A A - A	1853	
CP007539.1	A T A C A A G A A G	CC A A G T A A - A	1933	
CP007657.1	A T A C A A G A A G	CC A A G T A A - A	1853	
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AB436955.1	A T A C A A G A A G	CC A A G T A A - A	1842	
AB489885.1	A T A C A A G A A G	CC A A G T A A - A	1842	
AB489873.1	A T A C A A G A A G	CC A A G T A A - A	1842	
AB489883.1	A T A C A A G A A G	CC A A G T A A - A	1761	
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AB489892.1	A C A A A A A A A G	CC A A G C A A - A	2004	
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CP015646.1	A C A A A A C A A G	CC A A G T A A - A	2096	
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EU105387.1	- - - - -	- - - - -	1520	
AB436975.1	A C A A A A C A A A	CC A A G T A A - A	2096	
AB488499.1	A C A A A A C A A A	CC A A G T A A - A	2004	
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FR821779.1	A T A C A A G A A G	CC A A G C G A - A	2081	
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CP013955.1	A C A A A A A A A A G	CC A A G C G A - A	1444	
CP013953.1	A C A A A A A A A G	CC A A G C G A - A	1444	
CP014064.1	A C A A A A A A A G	CC A A G C G A - A	1444	
LT009690.1	A C A A A A A A A G	CC A A G C G A - A	1444	
AP017320.1	A C A A A A A A A G	CC A A G C G A - A	1444	
CP010890.1	A C A A A A A A A G	CC A A G C G A - A	1444	
CP001844.2	A C A A A A A A A G	CC A A G C G A - A	1444	
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HE579065.1	A C A A A A A A A G	CC A A G C G A - A	1444	
HE579063.1	A C A A A A A A A G	CC A A G C G A - A	1444	



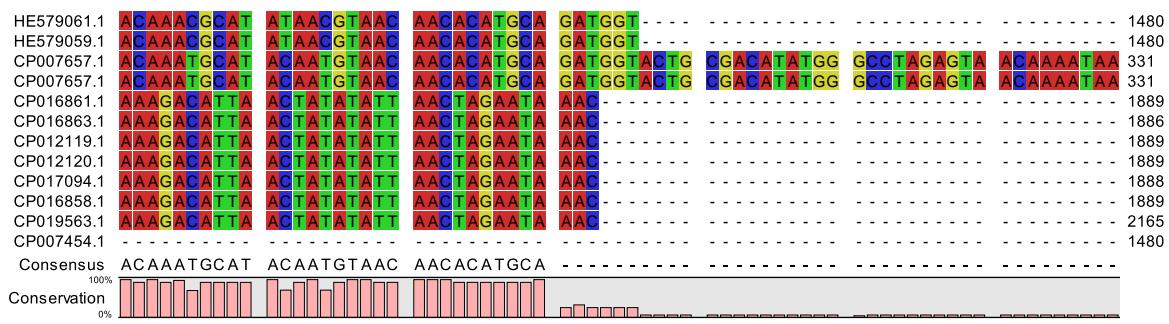
HE579061.1	A C A A A A A A G	C C A A G C G A - A	1444
HE579059.1	A C A A A A A A G	C C A A G C G A - A	1444
CP007657.1	A T A C A A G G A G	C C A A G T A A - A	262
CP007657.1	A T A C A A G G A G	C C A A G T A A - A	262
CP016861.1	A T T A A A G G A A A	C A A A A T A T T A	1856
CP016863.1	A T T A A A G G A A A	C A A A A T A T T A	1853
CP012119.1	A T T A A A G G A A A	C A A A A T A T T A	1856
CP012120.1	A T T A A A G G A A A	C A A A A T A T T A	1856
CP017094.1	A T T A A A G G A A A	C A A A A T A T T A	1855
CP016858.1	A T T A A A G G A A A	C A A A A T A T T A	1856
CP019563.1	A T T A A A G G A A A	C A A A A T A T T A	2132
CP007454.1	- - - - -	- - - - -	1480

Consensus ATACAAGAAG CCAAGTAA- A



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CP018205.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
AP017377.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
LT598688.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
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CP007674.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
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AP009351.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP000046.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP000253.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
AC025591.8	ACAAATGCA	ACAAATGAA	ACACATGCA	-
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CP007499.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
X17679.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP007657.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
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CP014429.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014426.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014423.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014420.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014415.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014412.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014409.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014407.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014402.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014397.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014392.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014387.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014384.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014381.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014371.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014368.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014365.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014362.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP014376.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP009423.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP016855.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP013231.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP010300.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP010299.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP010298.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP010297.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP010296.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP010295.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP007690.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP007176.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP000730.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
CP000255.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
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CP007657.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
AP014921.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
AB436955.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
AB489885.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
AB489873.1	ACAAATGCA	ACAAATGAA	ACACATGCA	-
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AC306908.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGTACTC
CP015646.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGTACTC
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EU105387.1	-	-	-	-
AB436975.1	ACAAGTCAT	ATAACGTAA	ACACATGCA	-
AB488499.1	ACAAGTCAT	ATAACGTAA	ACACATGCA	-
AJ309189.1	-	-	-	-
FR821779.1	ACAAATGCA	ATAACGTAA	ACACATGCA	GATGGTACTC
CP012593.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
CP012692.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
CP013955.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
CP013953.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
CP014064.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
LT009690.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
AP017320.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
CP010890.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
CP001844.2	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
CP001781.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
AB488501.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
AB489898.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
HE579073.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
HE579071.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
HE579069.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
HE579065.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT
HE579063.1	ACAAACGCA	ATAACGTAA	ACACATGCA	GATGGT

CP007670.1
CP003033.1
CP018205.1
AP017377.1
LT598688.1
CP007676.1
CP007672.1
CP007674.1
CP011526.1
HF937103.1
AP009351.1
CP000046.1
CP000253.1
AC025591.8
LT671859.1
CP007499.1
X17679.1
CP007657.1
CP014444.1
CP014441.1
CP014438.1
CP014435.1
CP014432.1
CP014429.1
CP014426.1
CP014423.1
CP014420.1
CP014415.1
CP014412.1
CP014409.1
CP014407.1
CP014402.1
CP014397.1
CP014392.1
CP014387.1
CP014384.1
CP014381.1
CP014371.1
CP014368.1
CP014365.1
CP014362.1
CP014376.1
CP009423.1
CP016855.1
CP013231.1
CP010300.1
CP010299.1
CP010298.1
CP010297.1
CP010296.1
CP010295.1
CP007690.1
CP007176.1
CP000730.1
CP000255.1
CP007539.1
CP007657.1
AP014921.1
AB436955.1
AB489885.1
AB489873.1
AB489883.1
AB489874.1
LT615218.1
AB436976.1
AB489892.1
AJ306908.1
CP015646.1
AB488510.1
EU105387.1
AB436975.1
AB488499.1
AJ309189.1
FR821779.1
CP012593.1
CP012692.1
CP013955.1
CP013953.1
CP014064.1
LT009690.1
AP017320.1
CP010890.1
CP001844.2
CP001781.1
AB488501.1
AB489898.1
HE579073.1
HE579071.1
HE579069.1
HE579065.1
HE579063.1



HE579061.1
HE579059.1
CP007657.1
CP007657.1
CP016861.1
CP016863.1
CP012119.1
CP012120.1
CP017094.1
CP016858.1
CP019563.1
CP007454.1
Consensus 100%
Conservation 0%