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NC_001488 CAATTGGGGGCTCGTCCGGG-----ATTTGAATTCTCCAT-----TCTCACA-----TTATGGGACAAATCCACGGGCT-T-T- 67
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AF139382 CAATTGGGGGCTCGTCCGGG-----ATCTGAATTCTCCAT-----TCTCACA-----TTATGGGACAAATCCACGGGCT-T-T- 67
AF326584 CAATTGGGGGCTCGTCCGGG-----ATCTGAATTCTCCAT-----TCTCACA-----TTATGGGACAAATCCACGGGCT-T-T- 67
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L11456 CAAGTGGGGGCTCGTCCGGG-----ATTTGAAC-CCGGGACC-----TCTCGCA-----TTATGGGGCAAATCCACGGGCT-T-T- 67
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ruler 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100



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AF139382 -C-CCCAACTCCAATACCCAAAGCC-CCCAGGGGGCTATCGACCCACCA--CTGGCTTAACTTTCTCCAGGCTGCTTATCGCTTGAGCCTG-GGCCCTC 161
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NC_001488 CGATTTGACTTCCAGCAGCTACGACGCTTTCTAAAACTAGCCCT-TAAAAAGCCCATTTGGCTAAATCCTATTGACTACTCGCTTTTAG----CTAGCC 256
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AF139382 CGATTTGACTTTTCCAGCAGCTACGACGCTTTCTGAAATTAGCCCT-TAAAAAGCCCATTTGGCTAAATCCTATTGACTACTCGCTTTTAG----CTAGCC 256
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K02120 TCCTAGCGATTTT-ACCGATTTAAAAAATTACATCCATTGGTTTCATAAGACCCAGA-----AAAAACCATGGACT-TTCACTTCTGGTGGCCCCGCC 288
D00647 CCCCAGCGATTTT-ACCGATTTAAAAAATTACATCCATTGGTTTCATAAGACCCAGA-----AAAAACCATGGACT-TTCACTTCTGGTGGCCCCGCC 288
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NC_001488 ACACCTATCTG-----CCC-TACT-ACTACTCCTCCGCCACC-----TCCCCCCCCTTCCCCGGAGGCCCATGTTCCCCCCCCTTACGTGGAACCCACCA 439
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AF139382 ACACCTATCTG-----CCC-TACT-ACTACTCCTCCGCCACC-----TCCCCCCCCTTCCCCGGAGGCCCATGTTCCCCCCCCTTACGTGGAACCCACCA 439
AF326584 ACACCTATCTG-----CCC-TACT-ACTACTCCTCCGCCACC-----TCCCCCCCCTTCCCCGGAGGCCCATGTTCCCCCTCCTTACGCGGAACCCACCA 439
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L02534 TCATCCC-CCA-----CCC-ACG-ACCCCC-----CAGATTCGATCCACAGATCCCCCCTCCCTATGTTGAGCCTACAG 428
Z46900 TCACCTC-CCA-----CCC-ACA-GCCCC-----CAGATTCGGATCCGCAAATCCCCCCTCCCTACATTGAGCCTACGG 423
AY590142 GCCTCTC-CCAACACTGCCC-CCA-GCTCCCAGTTTCCCGCTGAAACTAGTCTAATGCGCTCTGACCTCCACATCCCACCCCCCTATGCGGAGCCCTCTG 466
AF033818 GCATCAGCC-----CCAGAAGAACA-----ACCCCCCCTTATG-----A 410
NC_001414 GCATCAGCC-----CCAGAAGAACA-----ACCCCCCCTTATG-----A 410
K02120 GCATCGGCC-----CCAGAAGAACA-----ACCCCCCCTTATG-----A 410
D00647 GCATCGGCC-----CCAGAAGAACA-----ACCCCCCCTTATG-----A 410
AF257515 GCATCGGCC-----CCAGAAGAACA-----ACCCCCCCTTATG-----A 410
ruler .....410.....420.....430.....440.....450.....460.....470.....480.....490.....500

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M10060	CCACG-CAATGCTTC-CCTATCTTACATCCCCAGGAGCCCCTCAGCTCATAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
NC_001488	CCACG-CAATGCTTC-CCTATCTTACATCCCCAGGAGCCCCTCAGCTCATAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
AF412314	CCACG-CAATGCTTC-CCTATCTTACATCCCCAGGAGCCCCTCAGCTCATAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
AF139382	CCACG-CAATGCTTC-CCTATCTTACATCCCCAGGAGCCCCTCAGCTCACAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
AF326584	CCACG-CAATGCTTC-CCTATCTTACATCCCCAGGAGCCCCTCAGCTCACAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
AF326583	CCACG-CAATGCTTC-CCTATCTTACATCCCCAGGAGCCCCTCAGCTCACAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
L20734	CCACA-CAATGCTTT-CCTATCTTACATCCCCCTGGAGCCCCTCAGCTCACAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
Y13051	CCACA-CAATGCTTT-CCTATCTTACATCCCCCTGGAGCCCCTCAGCTCACAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
L11456	CCACA-CAATGCTTT-CCTATCTTACATCCCCCTGGAGCCCCTCAGCTCACAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
X89270	CCACG-AAATGCTTT-CCTATCTTACATCCCCCTGGAGCCCCTCAGCTCATAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	536
AF074965	CCACG-CAATGCTTT-CCTATCTTACATCCCCCTGGAGCCCCTCAGATCACAGGCCCTGGCAGATGAAAAGACTTACAGGCC-ATCAAGCAGGAGGTCAG	471
Y14365	CCACA-CAATGCTTT-CCCATAATTACATCCCCCTGGGGCCCCTCAGCTCACAGGCCCTGGCAAATGAAAAGACTTACAAGCC-ATCAAAACAGGAGGTCAG	536
Y14570	CTACC-CATTGCCTT-CCCATACTACACCCACATGGGGCCCCTCGGCTCACAGCCCTTGGCAAATGAAAAGACTGCAGGCC-ATCAAGCAGGAGGTCAG	533
NC_001815	CTACC-CATTGCCTT-CCCATACTACACCCACATGGGGCCCCTCGGCTCACAGCCCTTGGCAAATGAAAAGACTGCAGGCC-ATCAAGCAGGAGGTCAG	533
U90557	CTACC-CATTGCCTT-CCCATACTACATCCACATGGGGTCCCTCGGCTCACAGGCCATGGCAAATGAAAAGACTGCAGGCC-ATCAAAACAGGAGGTCAG	534
Y07616	GCACCTCAGTGCCTC-CCTGTCTTACACCCCATGGGGCCCAGCCGCTCATCGCCCTTGGCAGATGAAAAGATCTCCAGGCT-ATCAAGCAGGATGTCAG	513
AY217650	GCACCTCAGTGCCTC-CCTGTCTTACACCCCATGGGGCCCAGCCGCTCATCGCCCTTGGCAGATGAAAAGATCTCCAGGCT-ATCAAAACAGGAAGTCAG	513
AF517775	GCACCTCAGTGCCTC-CCTGTCTTCCACCCACAGGGGCCCCAGCCGCCCATCGCCCTTGGCAAATGAAAAGATCTCCAAGCT-ATTAACAGGAAGTCAG	512
AY22339	ACATCCCAGTGCCTC-CCTGTCTTACACCCCATGGGGCCCAGCCGCTTCCATCGCCCTTGGCAAATGAAAAGATCTCCAAGCT-ATTAACAGGAAGTCAG	512
NC_003323	GAACCTCAGTGCCTC-CCTGTCTTACACCCCATGGGGCCCAGCCACTCCCGCCCTGGCAAATGAAAAGATCTCCAAGCT-ATCAAGCAGGAAGTTAG	513
L36905	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
AF139170	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
AF042071	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
L03561	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
AF259264	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
AY563953	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
AY563954	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
U19949	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
J02029	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
D13748	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
AF033817	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
NC_001436	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACATGGTGCCCTCCCAACCACCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
AF074966	CCCCT-CAAGTCCTT-CCAGTCATGCATCCACATGGGGTCTCTCCAGCCATCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
NC_000858	CCCCT-CAAGTCCTT-CCAGTCATGCATCCACATGGGGTCTCTCCAGCCATCGCCCATGGCAAATGAAAAGACTACAGGCC-ATTAAGCAAGAAGTC--	519
L02534	CCCCC-CAAGTCCTT-CCAGTCATGCACCCACACGGTGTCCCTCCCACGCACCGCCCGTGGCAAATGAAAAGACTACAGGCC-ATTAAGCAGGAAGTC--	524
Z46900	CCCCC-CAGGTCCTT-CCAGTCATGCACCCGCATGGTGCCCTCCTAGCCACCGTCCATGGCAAATGAAAAGACTACAGGCC-ATTAACAGGAGGTC--	518
AY590142	CTCCC-CAAGTCCTC-CCAGTTGTACACCCACAGGGGCCCCGCCAACCCCGCCCTTGGCAGATGAAAAGACTCCAAGCC-ATAAAGCAGGAGGTA--	561
AF033818	CCCCCCCGCCATTTTGCCAATTAT--ATCTGAAGGAAATCGCAACCG--CCATCGCGCTTGGGCACCTCCGAGAATTACAAGAT-ATTAAGCAAGAAGTGA	506
NC_001414	CCCCCCCGCCATTTTGCCAATTAT--ATCTGAAGGAAATCGCAACCG--CCATCGCGCTTGGGCACCTCCGAGAATTACAAGAT-ATTAAGCAAGAAGTGA	506
K02120	CCCCCCCGCCATTTTGCCAATTAT--ATCTGAAGGAAATCGCAACCG--CCATCGTGCTTGGGCACCTCCGAGAATTACAAGAT-ATCAAGCAAGAAGTGA	506
D00647	CCCTCCCGCTGTTTTACCAATCAT--ATCTGAAGGAAATCGCAACCG--CCACCGCGCTTGGGCACCTCCGAGAATTACAAGAT-ATTAAGCAAGAAGTGA	506
AF257515	CCCCCCCCTGTTTTGCCAATCAT--ATCTGAAGGAAATCGTAACCG--CCATCGCGCTTGGGCACCTCCGAGAAGTACAAGAT-ATCAAGCAAGAAGTGA	506

ruler 510.....520.....530.....540.....550.....560.....570.....580.....590.....600



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 M10060 CTCCT---CTGCTCTTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 NC_001488 CTCCT---CTGCTCTTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 AF412314 CTCCT---CTGCTCCGGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 AF139382 CTCCT---CTGCTCCTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 AF326584 CTCCT---CTGCTCCTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 AF326583 CTCCT---CTGCTCCTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 L20734 CTCCT---CTGCCCTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 Y13051 CTCCT---CTGCCCTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 L11456 CTCCT---CTGCCCTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 X89270 CTCCT---CTGCCCTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 631
 AF074965 CTCCT---CTGCCCTGGCAGCCCCAGTTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGACTTACAAGATCTCCTCC 566
 Y14365 CTCCT---CTGCCCTGGCAGCCCCAATTC--ATGCAGACCCGCCGGCTGGCGGTACAACAGTTTGACCCCAACCGCCAAGGATTTGCAAGATCTCCTCC 631
 Y14570 CACCT---CAGCCCCGGGAGTCCCCAGTTC--ATGCAAACAGTCCGGCTCGCAATTGAGCAATTCGACCCCAACCGCCAAGGACTTACAAGATCTCCTGC 628
 NC_001815 CACCT---CAGCCCCGGGAGTCCCCAGTTC--ATGCAAACAGTCCGGCTCGCAATTGAGCAATTCGACCCCAACCGCCAAGGACTTACAAGATCTCCTGC 628
 U90557 TACCT---CGGCCCTGGGAGTCCCCAGTTC--ATGCAAACAGTCCGGCTCGCAATTGAGCAATTCGACCCCAACCGCCAAGGACTTACAAGATCTCCTGC 629
 Y07616 CTCTT---CCGCCCTGGCAGCCTCCAATTC--ATGCAGACTGTCCGGCTAGCTGTTCAACAATTTGACCCCAACCGCAAAGATCTTCACGACCTCCTAC 608
 AY217650 CTCTT---CCGCCCAGGCAGCCCCAATTC--ATGCAGACTGTCCGGCTAGCCGTTGAGCAATTTGACCCCAACCGCAAAGATCTTCACGACCTCCTAC 608
 AF517775 CTCTT---CCGCCCTGGTAGCCCCAGTTC--ATGCAGACTGTCCGGCTTAGCTGTCCAGCAATTTGACCCCAACCGCAAAGGATCTCCAGATCTCCTAC 607
 AY222339 CTCTT---CCGCCCTGGTAGCCCCAGTTC--ATGCAGACTGTCCGGCTTAGCTGTCCAGCAATTTGACCCCAACCGCAAAGATCTTCACGATCTCCTAC 607
 NC_003323 TTCTT---CCGCCCTGGCAGCCCCAGTTC--ATGCAGACCCGTCCGGCTAGCTGTCCAGCAATTTGACCCCAACCGCAAAGATCTCCATGATCTCCTAC 608
 L36905 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 AF139170 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 AF042071 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 L03561 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 AF259264 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 AY563953 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 AY563954 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 U19949 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 J02029 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 D13748 -TCCCAAGCGGCCCTGGAAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 AF033817 -TCCCAAGCGGCCCTGGAAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 NC_001436 -TCCCAAGCGGCCCTGGAAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 AF074966 -TCCCAAGCAGCCCCGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 NC_000858 -TCCCAAGCAGCCCCGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 616
 L02534 -TCCCAAGCAGCCCCGGGAGCCCCAGTTT--ATGCAGACCATCCGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 621
 Z46900 -TCCCAAGCAGCCCCTGGGAGCCCCAGTTT--ATGCAAACCTGTGAGGCTTGCAGTGCAGCAGTTTGACCCCAACCGCAAAGACCTCCAAGACCTCCTGC 615
 AY590142 -TCCCAAGCCGCTCCGGGAAGCCCCAGTTC--ATGCAAACCGTTAGGCTAGCGGTACAACAATTCGATCCCCTGACCCCAAGGATCTGCAGGATCTCCTGC 658
 AF033818 AAATAA---GGCACC GGGT---TCGCAAGTATGGATACAAACACTACGACTTGCAATCTTACAGGCCGACCCCTACTCCTGCTGACCTAGAACAACCTTTGCC 601
 NC_001414 AAATAA---GGCACC GGGT---TCGCAAGTATGGATACAAACACTACGACTTGCAATCTTACAGGCCGACCCCTACTCCTGCTGACCTAGAACAACCTTTGCC 601
 K02120 AAATAA---GGCACC GGGT---TCGCAAGTATGGATACAAACACTACGACTTGCAATCTTACAGGCCGACCCCTACTCCTGCTGACCTAGAACAACCTTTGCC 601
 D00647 AAATAA---GGCACC GGGG---TCGCAAGTATGGATACAAACGCTACGACTTGCAATCTTGCAGGCCGACCCCTACCCCTGCTGACCTAGAACAGCTTTGCC 601
 AF257515 AAATAA---GGCACC GGGT---TCGCAAGTATGGATACAAACACTACGACTTGCAATCTTGCAGGCCGACCCCTACTCCTGCTGACCTAGAACAACCTTTGCC 601

ruler610.....620.....630.....640.....650.....660.....670.....680.....690.....700



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M10060	AGTACCTATGCTCCTCCCTCGTAGTTT	---	C---	CTTACACCATCAGCAGCTTAACACACTAATTACCGAGGCTGAGAC	---	CCGC	GGGATGACAGGCTAC	723										
NC_001488	AGTACCTATGCTCCTCCCTCGTAGTTT	---	C---	CTTACACCATCAGCAGCTTAACACACTAATTACCGAGGCTGAGAC	---	CCGC	GGGATGACAGGCTAC	723										
AF412314	AGTACCTATGCTCCTCCCTCGTAGTTT	---	C---	CTTACACCATCAGCAGCTTAACACACTAATTACCGAGGCTGAGAC	---	CCGC	GGGATGACAGGCTAC	723										
AF139382	AGTACCTATGCTCCTCCCTCGTAGTTT	---	C---	CTTACACCATCAGCAGCTCAACACACTAATTACCGAAGCTGAGAC	---	CCGC	GGGATGACAGGCTAC	723										
AF326584	AGTACCTATGCTCCTCCCTCGTAGTTT	---	C---	CTTACACCATCAGCAGCTCAACACACTAATTACCGAGGCTGAGAC	---	CCGC	GGGATGACAGGCTAC	723										
AF326583	AGTACCTATGCTCCTCCCTCGTAGTTT	---	C---	CTTACACCATCAGCAGCTCAACACACTAATTACCGAGGCTGAGAC	---	CCGC	GGGATGACAGGCTAC	723										
L20734	AGTACCTATGCTCCTCCCTCGTGGTTT	---	C---	CTTACACCATCAGCAGCTCAACACACTAATCACCGAGGCTGAGAC	---	TCGC	GGGGTGACAGGCTAC	723										
Y13051	AGTACCTATGCTCCTCCCTCGTGGTTT	---	C---	CTTACACCATCAGCAGCTCAACACACTAATTACCGAGGCTGAGAC	---	TCGC	GGGGTGACAGGCTAC	723										
L11456	AGTACCTGTGCTCCTCCCTCGTGGTTT	---	C---	CTTACACCATCAGCAGCTCAACACACTAATCACCGAGGCTGAGAC	---	TCGC	GGGGTGACAGGCTAC	723										
X89270	AGTACCTATGCTCCTCCCTCGTGGTTT	---	C---	CTTACACCATCAGCAGCTCAACACACTAATCACCGAGGCTGAGAC	---	TCGC	GGGGTGACAGGCTAC	723										
AF074965	AGTACCTGTGCTCCTCCCTCGTGGTTT	---	C---	CTTACACCATCAGCAGCTCAACACACTAATCACCGAGGCTGAGAC	---	TCGC	GGGGTGACAGGCTAC	658										
Y14365	AGTACCTATGCTCCTCTCTCGTGGTCT	---	C---	CCTACACCATCAGCAGCTCAACACACTAATCACCGAGGCTGAGAC	---	CCGC	GGGATGGCAGGCTAT	723										
Y14570	AGTACCTCTGCTCCTCCCTAGTCTGTCT	---	C---	CCTTACCATCAACAATTCCATACCCTGATTACCGAAGCTGAAAC	---	CCGGG	AATGACAGGTTAT	720										
NC_001815	AGTACCTCTGCTCCTCCCTAGTCTGTCT	---	C---	CCTTACCATCAACAATTCCATACCCTGATTACCGAAGCTGAAAC	---	CCGGG	AATGACAGGTTAT	720										
U90557	AGTACCTCTGCTCCTCCCTAGTCTGTCT	---	C---	CCTTACCATCAACAATTCCATACCCTAATTACCGAGGCTGAAAC	---	CAGGG	AATGACAGGTTAT	721										
Y07616	AGTACCTATGCTCCTCACTAGTTGCCT	---	C---	TTACTTACATCATCAGCAGCTTGAGACCCCTCATAGCTCAGGCAGAAAC	---	TCAAG	TATAACAGGATAC	703										
AY217650	AGTACCTATGCTCCTCCCTAGTTGCCT	---	C---	CTTACACCATCAGCAGCTTGAGACCCCTCATAGCTCAGGCAGAAAC	---	TCAAG	TATAACAGGATAT	700										
AF517775	AGTACCTATGCTCCTCATTAGTGCCT	---	C---	CCTGCACCATCAGCAGCTTGAGACCCCTCATAGCTCAGGCAGAAAC	---	CCAAG	TATAACAGGATAT	699										
AY222339	AGTACCTATGCTCCTCACTAGTTGCCT	---	C---	CCTACACCATCAACAATTGAGACCCCTCATAGCCAGGCAGAGAC	---	CCAAG	TATAACAGGTTAT	699										
NC_003323	AGTACTTATGCTCCTCGCTAGTTACCT	---	C---	CCTGCACCATCAGCAACTTGAGACTCTCATAGCCAGGCAGAAAC	---	CCAAG	TATAACAGGTTAT	700										
L36905	AGTACCTTTGCTCCTCCCTCGTGGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGAG	GTTATTACAGGTTAT	708										
AF139170	AGTACCTTTGCTCCTCCCTCGTGGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGAG	GTTATTACAGGTTAT	708										
AF042071	AGTACCTTTGCTCCTCCCTCGTGGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGAG	GTTATTACAGGTTAT	708										
L03561	AGTACCTTTGCTCCTCCCTCGTGGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGAG	GTTATTACAGGTTAT	708										
AF259264	AGTACCTTTGCTCCTCCCTCGTGGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGGG	GTTATTACAGGTTAT	708										
AY563953	AGTACCTTTGCTCCTCCCTCGTGGCCT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGAG	GTTATTACAGGTTAT	708										
AY563954	AGTACCTTTGCTCCTCCCTCGTGGCCT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGAG	GTTATTACAGGTTAT	708										
U19949	AGTACCTTTGCTCCTCCCTCGTGGCCT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGAG	GTTATTACAGGTTAT	708										
J02029	AGTACCTTTGCTCCTCCCTCGTGGCCT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	CCGAG	GTTATTACAGGTTAT	708										
D13748	AGTACCTTTGCTCCTCCCTCGTGGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	TCGAG	GTTATTACAGGTTAT	708										
AF033817	AGTACCTTTGCTCCTCCCTCGTGGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	TCGAG	GTTATTACAGGTTAT	708										
NC_001436	AGTACCTTTGCTCCTCCCTCGTGGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	TCGAG	GTTATTACAGGTTAT	708										
AF074966	AGTACCTTTGCTCCTCCCTCGTGGCCT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	TCGAG	GTTATTACAGGTTAT	708										
NC_000858	AGTACCTTTGCTCCTCCCTCGTGGCCT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCCGAAAC	---	TCGAG	GTTATTACAGGTTAT	708										
L02534	AGTACCTTTGCTCCTCCCTAGTAGCTT	---	C---	CCTCCATCACCAGCAGCTAGATAGCCTTATATCAGAGGCTGAGAC	---	TCGAG	GTTATTACAGGATAT	713										
Z46900	AATACCTTTGCTCCTCCCTGGTGGCTT	---	C---	CCTCCATCACCAACAGCTAGATAGCCTTATGTGAGAAAGCCGAGAC	---	TCGAG	GTTATTACAGGCTAT	707										
AY590142	AGTATCTATGTTCCCTTAATAGCCT	---	C---	CCTCCACCATCAACAGCTAGATAGCCTCATCTCAGAGGCAGAAAC	---	CCGAG	GAATTACCGGATAC	750										
AF033818	AATATAT-TGCT--TCCCCGGTTCGATCAAACG-GCCCACATGACCAGC--CTAACGGCAGCAATAGCCCGCTGAAGCGGCCAATACCCTCCAGGGTTT							695										
NC_001414	AATATAT-TGCT--TCCCCGGTTCGATCAAACG-GCCCACATGACCAGC--CTAACGGCAGCAATAGCCCGCTGAAGCGGCCAATACCCTCCAGGGTTT							695										
K02120	AATATAT-TGCT--TCCCCGGTTCGATCAAACG-GCCCACATGACCAGC--CTAACGGCAGCAATAGCCCGCTGAAGCGGCCAATACCCTCCAGGGTTT							694										
D00647	AATATAT-TGCT--TCCCCGGTTCGATCAAACG-GCCCACATGACCAGC--CTAACGGCAGCAATAGCCG---CTGAAGCGGC-AATACCCTCCAGGGTTT							691										
AF257515	AATATAT-TGCT--TCCCCGGTTCGATCAAACG-GCCCACATGACTAGC--CTAACGGCAGCAATAGCTGCCGCTGAAGCGGCCAATACCCTCCAGGGTTT							695										

ruler710.....720.....730.....740.....750.....760.....770.....780.....790.....800




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M10060 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCAGCA---AGGT-CTTAGACGGGAGTACCAGAATCTTTGGCTGGCTGCTTTCT 817
NC_001488 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCAGCA---AGGT-CTTAGACGGGAGTACCAGAATCTTTGGCTGGCTGCTTTCT 817
AF412314 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCAGCA---AGGT-CTTAGACGGGAGTACCAGAATCTTTGGCTGGCTGCTTTCT 817
AF139382 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCAGCA---AGGT-CTTAGACGGGAGTACCAGAACCTTTGGCTGGCTGCTTTCT 817
AF326584 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCAGCA---AGGT-CTTAGACGGGAGTACCAGAACCTTTGGCTGGCTGCTTTCT 817
AF326583 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCAGCA---AGGT-CTTAGACGGGAGTACCAGAACCTTTGGCTGGCTGCTTTCT 817
L20734 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCCAACA---AGGT-CTTAGACGGGAGTACCAGAACCTTTGGCTGGCTGCTTTCT 817
Y13051 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCCAACA---AGGT-CTTAGACGGGAATACCAGAACCTTTGGCTGGCTGCTTTCT 817
L11456 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCCAACA---AGGT-CTTAGACGGGAATACCAGAACCTTTGGCTGGCTGCTTTCT 817
X89270 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCTAATAACCCCGCCCAACA---AGGT-CTTAGACGGGAATACCAGAACCTTTGGCTGGCTGCTTTCT 817
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Y14365 -AA- CCCCATGGCAGGGCCCCTAAGAATGCAGGCCAATAACCCCGCCAGCA---AGGT-CTTAGACGGGAGTACCAGAACCTTTGGCTGGCCGCTTTCT 817
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Z46900 TCGAGGACACACCAATAGTCCCTC-TAGGAGATATGCTGCGGGCTTGT-CAGGCTTGGACACCCCAAGACAAAAAC-----CA 1071
AY590142 CAGGGGGCATACTAACAGCCCC-TGGGAGACATGTTGCGAGCCTGC-CAGGCTGGGCCCCTAAGGACAAAGC-----CA 1114
AF033818 GCGGGG-CCTAGTGGCCGCCCCGGTGGGACAAAAACTGCAGGCTTGTGCACA-TTGGGCCCCAAGGTT-AAAACAGCCTGCAATCCTCGTCCACACCCCA 1083
NC_001414 GCGGGG-CCTAGTGGCCGCCCCGGTGGGACAAAAACTGCAGGCTTGTGCACA-TTGGGCCCCAAGGTT-AAAACAGCCTGCAATCCTCGTCCACACCCCA 1083
K02120 GCGAGG-CC-AGTGGCCGC---GGTGGGCAAAAACTGCAGGCTTGTGCACAATTTGGGCCCCAAGAATGAAACAGCCTGCACTTCTCGTCCACACCCCA 1080
D00647 GCGGGG-CCTAGTGGCCGCCCCGGTGGGACAAAAACTGCAGGCTTGTGCACA-CTGGGCCCCAAGACT-AAAACAGCCTGCAATCCTCGTCCACACCCCA 1080
AF257515 GCGGGG-CCTAGTGGCCGCCCCGGTGGGCAAAAACTGCAGGCTTGTGCACA-TTGGGCCCCAAGATC-AAAACAGCCTGCGATCCTCGTCCACACCCCA 1083
ruler .....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200

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		*		*	*	***		*		**	**	*	**	*	*	*	*	*	**	**	***	*	**	*
M10060	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGG	TAGGACACTGGAGT	CGGGACTG	---	1172								
NC_001488	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGG	TAGGACACTGGAGT	CGGGACTG	---	1172								
AF412314	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGG	TAGGACACTGGAGT	CGGGACTG	---	1172								
AF139382	AGGTCCTTGTGGTCCAA	CCACGGAAG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGAT	TAGGACACTGGAGT	CGGGACTG	---	1172								
AF326584	AGGTCCTTGTGGTCCAA	CCACGGAAG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGAT	TAGGACACTGGAGT	CGGGACTG	---	1172								
AF326583	AGGTCCTTGTGGTCCAA	CCACGGAAG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGAT	TAGGACACTGGAGT	CGGGACTG	---	1172								
L20734	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGAT	TAGGACACTGGAGT	CGGGACTG	---	1172								
Y13051	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAAA	TAGGACACTGGAGT	CGGGACTG	---	1172								
L11456	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGG	TAGGACACTGGAGT	CGGGACTG	---	1172								
X89270	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGAT	TAGGACACTGGAGT	CGGGACTG	---	1172								
AF074965	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTGTGGCAAGG	TAGGACACTGGAGT	CGGGACTG	---	1107								
Y14365	AGGTCCTTGTGGTCCAA	CCACGGAGG	CCCCCCCC	CACA	---	C	---	---	---	AGCCC	TGCTTT	CGTTTTTGGCAAGG	TAGGACACTGGGT	CGGGACTG	---	1172								
Y14570	GGGTCCTCGTCTCCAA	CCAGGAAAG	CCCCG	GCCACG	---	C	---	---	---	AGCCC	TGCTTC	CGCTGCGGGAAAA	CAGGGCATTGGAG	CCGAGACTG	---	1169								
NC_001815	GGGTCCTCGTCTCCAA	CCAGGAAAG	CCCCG	GCCACG	---	C	---	---	---	AGCCC	TGCTTC	CGCTGCGGGAAAA	CAGGGCATTGGAG	CCGAGACTG	---	1169								
U90557	GGGTCCTCGTCTCCAA	TCAGGAAAG	CCCCG	GCCACG	---	C	---	---	---	AGCCC	TG	TTCCGCTGTGGAAA	GGCAGGGCATTGGAG	CCGAGACTG	---	1168								
Y07616	AAATACTGATGATACAG	CCTAAAAAGACT	TCC	TCCCCGAAC	---	C	---	---	---	AGCCG	TGCTTC	CGCTGCGGGCAAG	CGGGCCATTGGAG	CAGGGACTG	---	1155								
AY217650	AAATACTAATGATACAG	CCTAAAAAGACT	TCC	TCCCCGAAC	---	C	---	---	---	AGCCA	TGCTTC	CGCTGCGGGCAGG	CAGGTTCATTGGAG	CAGAGACTG	---	1152								
AF517775	AAATACTGATGATACAA	CCTAAAAAGACT	TCC	TCCCCAAAC	---	C	---	---	---	AACCA	TGCTTC	CGCTGCGGGCAAG	TAGGTTCATTGGAG	CAGAGATTG	---	1151								
AY222339	AAGTACTAATAATACAA	CCTAAAAAGACT	TCC	TCCCCAAAC	---	C	---	---	---	AACCA	TGTTTC	CGCTGCGGACAAG	TAGGTTCATTGGAG	CAGAGATTG	---	1151								
NC_003323	AAATACTAATGATACAA	CCTAAAAAGACT	TCC	TCCCCAAAC	---	C	---	---	---	AACCA	TGCTTC	CGCTGTGGCAAG	CAGGTTCATTGGAG	CAGAGATTG	---	1152								
L36905	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
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AF042071	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGAGACTG	---	1157								
L03561	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
AF259264	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
AY563953	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
AY563954	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
U19949	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
J02029	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
D13748	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
AF033817	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
NC_001436	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAGT	CGGGACTG	---	1157								
AF074966	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGTTC	ACTGGAGCCGAGACTG	---	1157								
NC_000858	AAGTGTTAGTTGTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGTTC	ACTGGAGCCGAGACTG	---	1157								
L02534	AGGTGTTAGTCTCCAG	CCTAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCG	TGCTTC	CGGTGCGGGAAAG	CAGGCCACTGGAG	CCGAGACTG	---	1162								
Z46900	AAGTGCTAGTTATCCAG	CCAAAAAACCCCC	CCC	AAAT	---	C	---	---	---	AGCCA	TGTTTC	CGGTGCGGAAAAG	CAGGCCACTGGAG	CCGGGACTG	---	1156								
AY590142	AGGTACTAGTAGTCCAG	CCAAAAAGCCTCC	CCC	AAAT	---	C	---	---	---	AACCT	TGCTTC	CGGATGCGGGAAAG	CTGGCCATTGGAG	CCGAGACTG	---	1199								
AF033818	GGGCCCAAGATGCCCGGG	CCTCGGCAACCGG	CCCC	AAAAGGCC	CCCC	GGGACCA	---	---	---	TGCTAT	CGATGCCTCAA	AAGAAGGCCATTGGG	CCCGGGACTGT	---	1182									
NC_001414	GGGCCCAAGATGCCCGGG	CCTCGGCAACCGG	CCCC	AAAAGGCC	CCCC	GGGACCA	---	---	---	TGCTAT	CGATGCCTCAA	AAGAAGGCCATTGGG	CCCGGGACTGT	---	1182									
K02120	GGGCCCAAGATGCCCGGG	CCTCGGCAACCGG	CCCC	AAAAGGCC	TCCCC	GGACCA	---	---	---	TGCTAT	CGATGCCTCAA	AAGAAGGCCATTGGG	CCCGGGATTGT	---	1179									
D00647	GGGCCCAAGATGCCCGGG	CCTCGGCAACCGG	CCCC	AAAAGGCC	CCCC	GGGACCA	---	---	---	TGCTAT	CGATGCCTCAA	AAGAAGGCCATTGGG	CCCGGGACTGT	---	1179									
AF257515	GGGCCCAAGATGCCCGGG	CCCCGGCAACCGG	CCCC	AAAAGGCC	CCCC	AGGACCA	---	---	---	TGCTAT	CGATGCCTCAA	AAGAAGGCCATTGGG	CCCGGGACTGT	---	1182									

ruler1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300



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M10060 --TACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGGGACTGCCACAACCTCAAACCCC--CTCAGGA-- 1265
 NC_001488 --TACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGGGACTGCCACAACCTCAAACCCC--CTCAGGA-- 1265
 AF412314 --TACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGGGACTGCCACAACCTCAAACCCC--CTCAGGA-- 1265
 AF139382 --TACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGGGACTGCCACAACCTCAAACCCC--CTCAGGA-- 1265
 AF326584 --TACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGAACCTTCTCACTGGAAAAGGGACTGCCACAACCTCAAACCCC--CTCAGGA-- 1265
 AF326583 --TACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGGGACTGCCACAACCTCAAACCCC--CTCAGGA-- 1265
 L20734 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAGGATCCTTCTCATTGGAAAAGGGACTGCCACAGCTTAAACCCC--CTCAGGA-- 1265
 Y13051 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCATTGGAAAAGGGACTGCCACAGCTTAAACCCC--CTCAGGA-- 1265
 L11456 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAGGATCCTTCTCACTGGAAAAGGGACTGCCACAGCTTAAACCCC--CTCAGGA-- 1265
 X89270 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAGGATCCTTCTCACTGGAAAAGGGACTGCCACAACCCAAACCCC--CTCAGGA-- 1265
 AF074965 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAGGATCCTTCTCACTGGAAAAGGGACTGCCACAGCTTAAACCCC--CTCAGGA-- 1200
 Y14365 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGAGACTGCCACAGCTTAAACCCC--CTCAGGA-- 1265
 Y14570 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGAGACTGCCACAGCTTAAACCCC--CTCAGGA-- 1262
 NC_001815 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGAGACTGCCACAGCTTAAACCCC--CTCAGGA-- 1262
 U90557 --CACCCAG--CCAC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGAGACTGCCACAGCTTAAACCCC--CTCAGGA-- 1261
 Y07616 --TAAACAG--CCCC--GGCCCCCTCCAGGCCCTTGCCCCCTATGCCAGGATCCCGCCCCTGGAAGCGGGACTGCCACAGTTAAAAGCGGACACCAA-- 1248
 AY217650 --TAAACAG--CCCC--GGCCCCCTCCAGGCCCTTGCCCCCTATGCCAGGATCCCGCCCCTGGAAGCGGGACTGCCACAGTTAAAAGCGAGACACCAA-- 1245
 AF517775 --TAAACAG--CCTC--GGCCCCCTCCAGGCCCTTGCCCCCTATGTCAGGACCCCGCCCCTGGAAGCGGGACTGTCACAAATTAATAAGCAGACACCAA-- 1244
 AY22339 --TAAACAG--CCTC--GGCCCCCTCCAGGCCCTTGCCCCCTATGTCAGGACCCCGCCCCTGGAAGCGGGACTGTCACAAATTAATAAGCAGACACCAA-- 1244
 NC_003323 --TAAACAG--CCCC--GACCCCCCTCCGGGCCCTGCCCCCTATGTCAGGACCCCGCCCCTGGAAGCGGGACTGCCACAGTTAAAAGCAGATACCAA-- 1245
 L36905 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 AF139170 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 AF042071 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
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 AF259264 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 AY563953 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 AY563954 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 U19949 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 J02029 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 D13748 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 AF033817 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 NC_001436 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1252
 AF074966 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1249
 NC_000858 --CACTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGAGACTGCCCCCCGCTAAAAGCCCCTATCCCAG 1249
 L02534 --CGCTCAG--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGGGACTGTCCTCGCCTAAAAGCCCCTATCCCAG 1257
 Z46900 --CACTCAA--CCTC--GTCCCCCCCCGGGCCATGCCCCCTATGTCAAGACCCAACCTCACTGGAAGCGGGACTGTCCTCGCCTAAAAGCCCCTATCCCAG 1251
 AY590142 --CACCCAG--CCTC--GCCCCCTCCTGGCCCCTGCCCCCTATGCCAAGATCCTTCTCACTGGAAAAGGGACTGCCACAACCTCAAACCCC--CTCAGGA-- 1292
 AF033818 CCCACCAAGACCACCGGCCCCCTCCGGGACCTTGTCCCATATGTAAAAGATCCTTCCCATTTGGAAAAGGGACTGTCCAACCCCTCAAATCAAAAAACTAA-- 1281
 NC_001414 CCCACCAAGACCACCGGCCCCCTCCGGGACCTTGTCCCATATGTAAAAGATCCTTCCCATTTGGAAAAGGGACTGTCCAACCCCTCAAATCAAAAAACTAA-- 1281
 K02120 CCTACCAAGGCCACCGGCCCCCTCCGGGACCTTGTCCCATATGTAAAAGATCCTTCCCATTTGGAAAAGGGACTGTCCAACCCCTCAAATCAAAAAACTAA-- 1278
 D00647 CCCACCAAAACCACCGGCCCCCTCCGGGACCTTGTCCCATATGTAAAAGATCCTTCCCATTTGGAAAAGGGACTGTCCAACCCCTCAAATCAAAAAACTAA-- 1278
 AF257515 CCCACCAAGACCACCGGCCCCCTCCGGGACCTTGTCCCATATGTAAAAGATCCTTCCCATTTGGAAAAGGGACTGTCCAACCCCTCAAATCAAAAAACTAA-- 1281

ruler1310.....1320.....1330.....1340.....1350.....1360.....1370.....1380.....1390.....1400




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      *      *      *      *      **      *      *      **
M10060 -----GGAAGGGGAACCCCTCCTGTTGGATCTCCCTTCC-----ACCTCAGGCCTACTGAGGAAAAAACTC-CTTAAGGGGGGAGATCTAATCTC 1351
NC_001488 -----GGAAGGGGAACCCCTCCTGTTGGATCTCCCTTCC-----ACCTCAGGCCTACTGAGGAAAAAACTC-CTTAAGGGGGGAGATCTAATCTC 1351
AF412314 -----GGAAGGGGAACCCCTCCTGTTGGATCTCCCTTCC-----ACCTCAGGCCTACTGAGGAAAAAACTC-CTTAAGGGGGGAGATCTAATCTC 1351
AF139382 -----GGAAGGGGAACCCCTCCTGTTGGATCTCTCTTCC-----ACCTCAGGCATTACTGAGGAAAAAACTC-CTTAGGGGGGGAGATCTAATCTC 1351
AF326584 -----GGAAGGGGAACCCCTCCTGTTGGATCTCCCTTCC-----ACCTCAGGCCTACTGAGGAAAAAACTC-CTTAAGGGGGGAGATCTAATCTC 1351
AF326583 -----GGAAGGGGAACCCCTCCTGTTGGATCTCTCTTCC-----ACCTCAGGCCTACTGAGGAAAAAACTC-CTTAGGGGGGGGAGATCTAATCTC 1351
L20734 -----GGAAGGGGAACCCCTCCTGTTGGATCTCTCCTCC-----ACCTCAGGTACTACTGAGGAAAAAACTC-CTTAGGGGGGGGAGATCTAATCTC 1351
Y13051 -----GGAAGGGGAACCCCTCCTGTTGGATCTCTCCTCC-----ACCTCAGGTACTACTGAGGAAAAAACTC-CTTAGGGGGGGGAGATCTAATCTC 1351
L11456 -----GGAAGGGGAACCCCTCCTGTTGGATCTCTCCTCC-----ACCTCAGGTACTACTGAGGAAAAAACTC-CTTAGGGGGGGGAGATCTAATCTC 1351
X89270 -----GGAAGGGGAACCCCTCCTGTTGGATCTCTCCTCC-----ACCTCAGGCCTACTGAGGAAAAAACTC-CTTAAGGGGGGAGATCTAATCTC 1351
AF074965 -----GGAAGGGGAACCCCTCCTGTTGGATCTCTCCTCC-----ACCTCAGGTACTACTGAGGAAAAAACTC-CTTAGGGGGGGGAGATCTAATCTC 1286
Y14365 -----GGAAGGGGAACCCCTCCTGTTAGATCTCTCCTCC-----ACCTCAAATACTACTGAGGAAAAAACTC-CTTGGGGGGGGGAGATCTAATCTC 1351
Y14570 -----GGAGGAGGAACCCCTCCTGCTGGACCTGCCCTCG--GATGCCAT-TGCCACCGAGGAAAAAACTC-CCTGGGGGGGGGAGATGTAATCTC 1348
NC_001815 -----GGAGGAGGAACCCCTCCTGCTGGACCTGCCCTCG--GATGCCAT-TGCCACCAGGAAAAAACTC-CCTGGGGGGGGGAGATGTAATCTC 1348
U90557 -----GGAGGAGGAACCCCTCCTGCTGGACCTGCCCTCA--GATGCCGT-TGCCACCAGGAAAAAACTC-CCTAGGGGGGGGAGATCTAATCTC 1347
Y07616 -----GGGCAACGAAAACCTACTCCTAGACTTGCCCTGTGAAACATCCAATGCCCGGGAGCGAAAAAACTC-CTCGGGGGGGGAGGACTAACCTC 1337
AY217650 -----AGGCAACGAAAACCTACTTCTAGACTTGCCCTGTGAAACCTCCAATGCCCGGGAGCGAAAAAACTC-CTCGGGGGGGGAGGACTAACCTC 1334
AF517775 -----AGGCAGTGAAGACCTACTCTTAGACCTGCCCTGTGAGGCACCCAACGCCCGGGAGCGAAAAAACTC-CTCGGGGGGGGAGGACTAACCTC 1333
AY22339 -----AGGCAGTGAAGACCTACTCTTAGACCTACCCTGTGAAAGCACCCGACGTCCGGGAGCAAAAAAACTC-CTCGGGGGGGGAGGACTAACCTC 1333
NC_003323 -----AGGCAGTGAAGACCTACTCCTAGACCTGCCCTGTGAAAGCTCCCATGTCCGGAGCAAAAAAACTC-CTCAGGGGGGGGAGGACTAACCTC 1334
L36905 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCACT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
AF139170 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCACT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGG----- 1330
AF042071 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCACT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
L03561 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCGCT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
AF259264 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCGCT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
AY563953 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCGCT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
AY563954 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCGCT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
U19949 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCGCT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
J02029 AACCAGAGCCAGAGGAAGATGCCCTCCTATTAGACCTCCCCGCT--GACATCCCACACCC-----AAAAAACTT-CATAGGGGGGGGAGGTTTAACTC 1342
D13748 AACCAGAGCCAGAGGAGGATGCCCTCCTATTAGATCTCCCCGCC--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
AF033817 AACCAGAGCCAGAGGAGGATGCCCTCCTATTAGATCTCCCCGCC--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1342
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AF074966 ACCCAGAGCCAGAGGAGGATGCCCTCCTATTAGACCTCCCCACT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGCTAACCCTC 1339
NC_000858 ACCCAGAGCCAGAGGAGGATGCCCTCCTATTAGACCTCCCCACT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGCTAACCCTC 1339
L02534 AACCAGAGCCAGAGGAAGATGCCCTCCTACTAGACCTCCCCGCT--GACATCCCGCATCC-----AAAAAACTC-CATAGGGGGGGGAGGTTTAACTC 1347
Z46900 AACCAGAGCCAGAAGAAGACGCCCTCCTATTAGACCTCCCCACT--GACATCCCACACCC-----AAAAAACTC-CATAGGGGGGGGAGGCTAACCCTC 1341
AY590142 ----AGAGCCAGAGGAGGAAGCCCTTCTACTAGACCTCCCTGCG--GATGTGTCTTACCA-----AAAAAACTT-GATAGGGGGGGGAGGCTTAACTC 1378
AF033818 -----TAGAGGGGGGGAC-----TTAGCGCCCCCAA-----CCGTAACCCCTAT-----AACAGATCCTCTTAGTGAGGCCGAATTAGAATG 1354
NC_001414 -----TAGAGGGGGGGAC-----TTAGCGCCCCCAA-----CCGTAACCCCTAT-----AACAGATCCTCTTAGTGAGGCCGAATTAGAATG 1354
K02120 -----TAGAGGGGGGGAC-----TTAGCGCCCCCAA-----CCATAACACCTAT-----AACGGATTCTCTTAGTGAGGCCGAATTAGAATG 1351
D00647 -----TAGAGGGGGGGAC-----CTAGCGCCCCCAA-----TCATAACACCTAT-----AACAGATTCTCTCAGTGAGGCCGAATTAGAATG 1351
AF257515 -----TAGAGGGGGGGAC-----TAAGCGCCCCCAA-----CTACAACACCTAT-----AACAGATTCTCTTAGTGAGGCCGAATTAGAATG 1354
ruler .....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500

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Accession	Sequence	Position
M10060	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CGATACTCCCACATCATCCCCCTGCGGCAGCAACAGCAACCAATT---CTAGGG	1424
NC_001488	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CGATACTCCCACATCATCCCCCTGCGGCAGCAACAGCAACCAATT---CTAGGG	1424
AF412314	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CGATACTCCCACATCATCCCCCTGCGGCAGCAACAGCAACCAATT---CTAGGG	1424
AF139382	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CGATACTCCCACATCATCCCCCTGCGGCAGCAACCAACCAACCAATT---CTAGGG	1424
AF326584	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CGATACTCCCACATCATCCCCCTGCGGCAGCAACCAACCAACCAATT---CTAGGG	1424
AF326583	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CGATACTCCCACATCATCCCCCTGCGGCAGCAACAGCAACCAATT---CTAGGG	1424
L20734	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CAATACTCCCACATCATCCCCCTGCGGCAACAACAACAACCAATT---CTAGGA	1424
Y13051	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CAATACTCCCACATCATCCCCCTGCGGCAACAACAACAACCAATT---CTAGGA	1424
L11456	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CAATACTCCCACATCATCCCCCTGCGGCAACAACAACAACCAATT---CTAGGA	1424
X89270	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CAATACTCCCACATCGTTCCCTGCGGCAACAACAACAACCAATT---CTAGGA	1424
AF074965	CCCCCA---TCCCGAT---CAAGAC---ATCT-----CAATACTCCCACATCATCCCCCTGCGGCAACAACAACAACCAATT---CTAGGA	1359
Y14365	CCCCCA---TCCCGAT---AAAAAC---TTCT-----CAATACTCCCACATCATCCCCCTGCGAGCAGCAACAACAACCGATT---CTAGGG	1424
Y14570	CCCCC-----AACAA---ATCT-----CAATGCTCCCTGTCATTCCGTTAGAGCAACAGCACCAGCCCCTT---CTAGAC	1412
NC_001815	CCCCC-----AACAA---ATCT-----CAATGCTCCCTGTCATTCCGTTAGAGCAACAGCACCAGCCCCTT---CTAGAC	1412
U90557	CCCCC-----AACAA---ATCT-----CACTGCTCCCTCTCATTCTTTAGAGCAACAGCAGCAGCCCCTT---CTAGAC	1411
Y07616	CCCCC-----GA---ACC-----GTACTACCTCTTATGCCTTTTGTCTCAACAGAAACAGCCTATC---TTGCAT	1395
AY217650	CCCCC-----GA---ACC-----ATACTACCTCTGATACCTTTTGTCTCAACAAAAACAGCCTATC---TTGCAT	1392
AF517775	CCCCC-----GA---ACC-----ATACTACCCCTGATACCTTTTGTCCAGAGAGAAGCAGCCTATC---CTGCAT	1391
AY22339	CCCCC-----GA---ACC-----ATACTACCCCTTATACCTCTGTCCCAACAGAAACAGCCTATT---CTACAT	1391
NC_003323	CCCCC-----GA---ACC-----ATACTACCCCTCATAACCCTTGTCCCAACAAAGGCAACCTATC---CTACAT	1392
L36905	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCCAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
AF139170	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCCAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1424
AF042071	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCCAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
L03561	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCCAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
AF259264	CCCCC---CCACATTACGGCAA---GTCCTTCCTAACCAAGACCCAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
AY563953	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCAAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCTTAATTA---AA	1436
AY563954	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCAAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCTTAATTA---AA	1436
U19949	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCCAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
J02029	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCCAGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
D13748	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCAACATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
AF033817	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCAACATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
NC_001436	CCCCC---CCACATTACAGCAA---GTCCTTCCTAACCAAGACCAACATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGTGGCCCGTAATTA---AA	1436
AF074966	CCCCC---CCACATTACGGCAA---GTCCTTCCTAACCAAGGCCCGGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGCGGCCATAATTA---AG	1433
NC_000858	CCCCC---CCACATTACGGCAA---GTCCTTCCTAACCAAGGCCCGGCATCTATTCTGCCAGTTATACCATTAGATCCCGCCCGCGGCCATAATTA---AG	1433
L02534	CCCCC---CCACGTTGCAGCAA---GTCCATCCGAATAAAGACCCGGCATCCATTCTACCAGTTATACCATTAGATCCCGCCCGGGCCCTTAATTA---AG	1441
Z46900	CCCCC---TCACGTCACGGCAG---GACCATTCCAACGGAGACCCAGCACATATTCTGCCAGTAATACCATTAGATCCCGCCCGGGCG---CCCCTAATTA---AG	1434
AY590142	CCCCC---AACCAGAAAT---CGGCCGTGCCCGTCT---CCG---GACCCGCCA---CCATTTTGCCAGTTATACCATTGGACCCTAAACAGCGGCCTTAATTA---AG	1469
AF033818	CC-----TACTTTCTATTCTCTGGCTCGCAGCCGTCCCTCCGTGGCTGTAT	1401
NC_001414	CC-----TACTTTCTATTCTCTGGCTCGCAGCCGTCCCTCCGTGGCTGTAT	1401
K02120	CT-----TACTTTCTATTCTCTGGCTCGCAGCCGTCCCTCCGTGGCTGTAT	1398
D00647	CT-----TACTTTCTATTCTCTGGCTCGCAGCCGTCCCTCCGTGGCTGTAT	1398
AF257515	CC-----TACTTTCCATTCTCTGGCCCGCAGCCGCCCTCCGTGGCTGTAT	1401



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M10060	GTGCCCGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGATCCTAGGC	GCCAGTGGG	CAAA	CCAAC	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
NC_001488	GTGCCCGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGATCCTAGGC	GCCAGTGGG	CAAA	CCAAC	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
AF412314	GTGCCCGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGATCCTAGGC	GCCAGTGGG	CAAA	CCAAC	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
AF139382	GTGCCCGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGGTCTTAGGC	GCCAGTGGG	CAAA	CCAAT	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
AF326584	GTGCCCGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGATCCTAGGC	GCCAGTGGG	CAAA	CCAAC	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
AF326583	GTGCCCGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGGTCTTAGGC	GCCAGTGGG	CAAA	CCAAT	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
L20734	GTGCCTGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGGTCTTAGGC	GCCAGTGGG	CAAA	CTAAT	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
Y13051	GTGCCTGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGGTCTTAGGC	GCCAGTGGG	CAAA	CTAAT	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
L11456	GTGCCTGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGGTCTTAGGC	GCCAGTGGG	CAAA	CTAAT	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
X89270	GTGCCTGGGCCGGTA-AAGC-TCCACGA	---	CACCC	TGGTCTTAGGC	GCCAGTGGG	CAAA	CTAAT	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
AF074965	GTGCCTGGGCCGGTA-AAAC-TCCACGA	---	CACCC	TGGTCTTAGGC	GCCAGTGGG	CAAA	CTAAT	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1543										
Y14365	GTGCCTGGGCCGGTA-AAGC-TCCACGA	---	CACCC	AAGTCTTGGG	GCCAGTGGG	CAAA	CTAAC	ACCCAGTTCAAAC	TCCTCCAAAC	CCCCCTACACA	1608										
Y14570	GCCCCGAGTCAGTA--AGTGTTCCTGA	---	TACAAC	GGTTCCTGGG	GCTGGCGGAC	GAGACC	AGCTCCC	AGTTCAAAC	TCCTTCAAT	CCCCCTGTGCG	1596										
NC_001815	GCCCCGAGTCAGTA--AGTGTTCCTGA	---	TACAAC	GGTTCCTGGG	GCTGGCGGAC	GAGACC	AGCTCCC	AGTTCAAAC	TCCTTCAAT	CCCCCTGTGCG	1596										
U90557	GCCCCGAGTCAGAA--GGT--CTCTGA	---	CACAAC	GGTTCCTAGG	GCTGGCGGT	CAGACC	AGCTCCC	AGTTCAAAC	TCCTCCGAT	CCCCCTGTGCG	1593										
Y07616	GTGCCCTC--CGATTCCAACCTCCAGGA	---	CACCACC	TCTTAGGC	GCCAGGCGGAC	CAAGCGC	CAACAAGTTAAGAT	TCCTGCCT	CATCCC	CGTCCATA	1579										
AY217650	GTGCCCTC--CGATTCCAACCTCCAGGA	---	CACCACC	TCTTAGGC	GCCAGGCGGAC	CAAGTG	CAACAAGTTAAGG	TCCTGCC	CATCCC	CGTCCATA	1576										
AF517775	GTGCCCTC--CTGACTCTAATCTCCAGGA	---	CACCAC	TGTCTTAGGT	GCCAGGCGGAC	CAAGTG	CTAACAAAGTTCAAGAT	TCTGCC	CGTCCC	CGTCCATA	1575										
AY22339	GTGCCCTC--CTGACTCCAACCTCCAGGA	---	TACCAC	TCTTAGGT	GCCAGGCGGAC	CAAGTG	CAACAAGTTCAAAAT	TCTACC	CGTCCC	CGTCCATA	1575										
NC_003323	GTGCCCTC--CTGACTCCAACCTCCAGGA	---	CACCAC	TGTCTTAGGC	GCCAGGCGGAC	CAAGTG	CAACAAGTTAAGAT	TCCTGC	CTCC	CGTCCATA	1576										
L36905	GTTCTCAAG--TAATACTCCCCCTCAGAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTACTAA	1620										
AF139170	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1608										
AF042071	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
L03561	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
AF259264	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
AY563953	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
AY563954	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
U19949	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
J02029	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	TACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
D13748	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	CACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
AF033817	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	CACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
NC_001436	GTTCTCAAG--TAATACTCCCCCTCAAAAA	---	CACAT	CCGTATTAGGGG	CAGGGGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1620										
AF074966	GTTCTCAAG--TAATACTCCCCCTCAAAGA	---	CACAT	CCGTATTAGGGG	CAGGAGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1617										
NC_000858	GTTCTCAAG--TAATACTCCCCCTCAAAGA	---	CACAT	CCGTATTAGGGG	CAGGAGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1617										
L02534	ATTCTCAAG--TGACACTCCCCCTTAAAGA	---	CACAT	CCGTATTAGGGG	CAGGAGG	CAAA	CCAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGTGCTAA	1625										
Z46900	ATTCTCAAA--TAACACCCCCCTTAAAAA	---	CACAT	CTGTACTAGGGG	CAGGAGG	CAAA	CTAAGATCACTTTAAG	CTCACCT	CCCTT	CCTGGTGCTAA	1618										
AY590142	GTTTCCGGA--AAATACCCCCCTTAAAAA	---	CACCG	CAGTTGTAGGAG	CAGGAGG	CAAA	CTAAGATCAGTTTAAAT	TCGCT	CCCTT	CCTGGTGCTAA	1653										
AF033818	GCTGGTTCGAGATTACCCAC	----	GGAT	CCCCGCGCGGTGCTCGGAG	CAGGGGGAGT	CTCCCG	GAAACAGATACAATTGG	CTACA	AGGCCCT	CTGAC	1585										
NC_001414	GCTGGTTCGAGATTACCCAC	----	GGAT	CCCCGCGCGGTGCTCGGAG	CAGGGGGAGT	CTCCCG	GAAACAGATACAATTGG	CTACA	AGGCCCT	CTGAC	1585										
K02120	GCTGGTTCGAGATTACCCAC	----	GGAT	CCCCGCGCGGTGCTCGGAG	CAGGGGGAGT	CTCCCG	GAAACAGATACAATTGG	CTACA	AGGCCCT	CTGAC	1582										
D00647	GCTGGTTCGAGATTACCCAC	----	GGAC	CCCCGCGCGGTACTCGGAG	CAGGAGGAAT	CTCCCG	GAAACAGATACAATTGG	CTACA	AGGCCCT	CTGAC	1582										
AF257515	GCTGGTTCGAGAATAACCCAC	----	GGAC	CCCCGCGCGAGTCTCGGAG	CAGGGGGGAAT	CTCCCG	GAAACAGATACAATTGG	CTACA	AGGCCCT	CTGAC	1585										
ruler1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800																				



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M10060 TATTCTTGCCCTT----CCGAAGGTCCCCGTTATCCTTTCTCCTG-----CCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGGGACGCC 1698
NC_001488 TATTCTTGCCCTT----CCGAAGGTCCCCGTTATCCTTTCTCCTG-----CCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGGGACGCC 1698
AF412314 TATTCTTGCCCTT----CCGAAAGTCCCCGTTATCCTTTCTCCTG-----CCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGGGACGCC 1698
AF139382 TATTCTTGCCCTT----CCGAAAGTCCCCGTTATCCTTTCTCCTG-----CCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGGGACGCC 1698
AF326584 TATTCTTGCCCTT----CCGAAGGTCCCCGTTATCCTTTCTCCTG-----CCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGGGACGCC 1698
AF326583 TATTCTTGCCCTT----CCGAAAGTCCCCGTTATCCTTTCTCCTG-----CCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGGGACGCC 1698
L20734 TATTCTTACCCTT----CCGAAAGTCCCCGTTATCTTCCCTCCTG-----TCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGAGACGCC 1698
Y13051 TATTCTTACCCTT----CCGAAAGTCCCCGTTATCTTCCCTCCTG-----TCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGAGACGCC 1698
L11456 TATTCTTACCCTT----CCGAAAGTCCCCGTTATCTTCCCTCCTG-----TCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGAGACGCC 1698
X89270 TATTCTTACCCTT----CCGAAAGTCCCCGTTATCTTCCCTCCTG-----TCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGGGACGCC 1698
AF074965 TATTCTTACCCTT----CCGAAAGTCCCCGTTATCTTCCCTCCTG-----TCTCTTAGACACCCACAACAAATGGACCATCATT--GGAAGAGACGCC 1633
Y14365 TATTCTTACCCTT----CCGAAAGTCCCCGTTATCTTCCCTCCTG-----TCTCTTAGACACCCACAACAAATGGACCATCATT--GGGAGGGATGCC 1698
Y14570 TCTACCTACCCTT----CCGGAGGGCCCTGTTACCCTCCCATCATG-----CCTTGTAGACACCAATAGCAAATGGGCCATTATT--GGCCGTGATATCC 1686
NC_001815 TCTACCTACCCTT----CCGGAGGGCCCTGTTACCCTCCCATCATG-----CCTTGTAGACACCAATAGCAAATGGGCCATTATT--GGCCGTGATATCC 1686
U90557 TCTACCTGCCCTT----CCGGAAAGGCCCCCGTTACTCTCCCGTCATG-----CCTTCTAGACACCGATAATAAATGGGCCATTATT--GGCCGTGATATCC 1683
Y07616 TCCATTTGCCCTT----CCGAAGGCAGCCAGTAACCTTAACTTTG-----CCTAATCGACACCAACAACCAATGGGCCAT--ATTAGGACGAGATGCC 1669
AY217650 TCCATTTGCCCTT----CCGAAGGCAGCCAGTAACCTTAACTTTG-----CCTAATCGACACCAACAACCAATGGGCCAT--ATTAGGACGAGATGCC 1666
AF517775 TCCATTTGCCCTT----CCGAAGAGCAGCCAGTGACCTGACCTCTTG-----TCTAATCGATGTTAACAACCAAGTGGCCAT--ATTAGGGCGGGACGCC 1665
AY22339 TCCACTTGCCCTT----CCGAAGACAGCCAGTGACCTAACCCTTTG-----CCTAATCGATATTAACAACCAATGGACCAT--ATTAGGACGGGACGCC 1665
NC_003323 TCCACTTGCCCTT----CCGGAAACGGCCAGTAACCTTAACTTTG-----CCTAATTGATACCTAACGATCAGTGGACTAT--ACTAGGACGGGATGCTC 1666
L36905 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
AF139170 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1698
AF042071 TACGCCTCCCTTT----CCGGACAACGCCTATTATTTTAAACATCGTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
L03561 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
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AY563953 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
AY563954 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
U19949 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
J02029 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
D13748 TACGCCTCCCTTT----CCGGACGACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
AF033817 TACGCCTCCCTTT----CCGGACGACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
NC_001436 TACGCCTCCCTTT----CCGGACGACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1710
AF074966 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCGAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1707
NC_000858 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTTGATACCGAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1707
L02534 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTCGATACCAAAAAACAACGGGCCATCATA--GGTCGTGATGCCT 1715
Z46900 TACGCCTCCCTTT----CCGGACAACGCCTATTGTTTAAACATCTTG-----CCTAGTCGATACCAAAAAACAACGGGCCATCATA--GGTCGTGACGCCT 1708
AY590142 TTCACCTCCCTTT----CCGGACGACACCCATTGTTTAACTCATG-----CCTTATAGATACCGAAAAACAACGGGTCATAATT--GGCCGCGACGCC 1743
AF033818 ----CCTGGCTCTAAAACAGAGGGTCCCTTTA----TCACCATCCCAAAAATTTTAGTTGACACTTTCGATAAATGGCAAATTTTA--GGACGGGACGTCC 1677
NC_001414 ----CCTGGCTCTAAAACAGAGGGTCCCTTTA----TCACCATCCCAAAAATTTTAGTTGACACTTTCGATAAATGGCAAATTTTA--GGACGGGACGTCC 1677
K02120 ----CCTGGCTCTAAAACAGAGGGTCCCTTTA----TCACCATCCCAAAAATTTTAGTTGACACTTTCGATAAATGGCAAATTTTA--GGACGGGACGTCC 1674
D00647 ----CCTGGCTCTAAAACAGAGGGTCCCTTTA----TCACCATCCCAAAAATTTTAGTTGACACTTTCGATAAATGGCAAATTTTA--GGACGGGACGTCT 1674
AF257515 ----CCTGGCTATAAAAACAGAGGGTCCCTTTA----TCACCATCCCAAAAATTTTAGTTGACACTTTCGACAAAATGGCAAATTTTA--GGACGGGACGCCT 1677
ruler .....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900

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M10060 TACAACAATGCC-AGGGGCTTCTATAACC--TCCCAGACGAC-----CCCAGCCCCC-----ACCAAT-TGC--T 1756
 NC_001488 TACAACAATGCC-AGGGGCTTCTATAACC--TCCCAGACGAC-----CCCAGCCCCC-----ACCAAT-TGC--T 1756
 AF412314 TACAACAATGCC-AGGGGCTTCTATAACC--TCCCAGACGAC-----CCCAGCCCCC-----ACCAAT-TGC--T 1756
 AF139382 TACAACAATGCC-AGGGGCTTCTATAACC--TTCCAGACGAC-----CCCAGCCCCC-----ACCAAT-TGC--T 1756
 AF326584 TACAACAATGCC-AGGGGCTTCTATAACC--TTCCAGACGAC-----CCCAGCCCCC-----ACCAAT-TGC--T 1756
 AF326583 TACAACAATGCC-AGGGGCTTCTATAACC--TTCCAGACGAC-----CCCAGCCCCC-----ACCAAT-TGC--T 1756
 L20734 TACAACAATGCC-AGGGGCTTCTATAACC--TTCCAGACGAT-----CCCAGCCCCC-----ATCAAT-TGC--T 1756
 Y13051 TACAACAATGCC-AGGGGCTTCTATAACC--TTCCAGACGAT-----CCCAGCCCCC-----ATCAAT-TGC--T 1756
 L11456 TACAACAATGCC-AGGGGCTTCTATAACC--TTCCAGACGAT-----CCCAGCCCCC-----ACCAAT-TGC--T 1756
 X89270 TACAACAATGCC-AGGGGCTTCTATAACC--TTCCAGACGAT-----CCCAGCCCCC-----ACCAAT-TGC--T 1756
 AF074965 TACAACAATGCC-AGGGGCTTCTATAACC--TTCCAGACGAT-----CCCAGCCCCC-----ACCAAT-TGC--T 1691
 Y14365 TGCAACAATGCC-AGGGACTTCTATAACC--TCCCAGACGAT-----CCCAGCCCCCGGT-----GCTCCCACCAAT-TGC--T 1765
 Y14570 TCCAGAAATGCC-AGAGTGTCTGTACC--TTCCGGAGGACAATCTGTGCAAGGGTACCCCCGGTCCCCGATGGAATAACTCCTCCCCGAT-TAT--T 1780
 NC_001815 TCCAGAAATGCC-AGAGTGTCTGTACC--TTCCGGAGGACAATCTGTGCAAGGGTACCCCCGGTCCCCGATGGAATAACTCCTCCCCGAT-TAT--T 1780
 U90557 TCCAGCAATGCC-AGAGTGTCTGTACC--TCCCGGAGGACAATCTCTGCAAGGTACCCCCGGCCCTCCGGCAGAATGAATTCCCCCGAC-TAT--T 1777
 Y07616 TACAACAATGTC-AGAGTTCCCTTTATC--TTGCTGA-----CCAACCCCC-----GGAGGTCC--T 1721
 AY217650 TACAACAATGTC-AGAGTTCCCTCTATC--TTGCTGA-----CCAACCCCC-----GGAGATCC--T 1718
 AF517775 TACAACAGTGTC-AGGGCTCCCTCTATC--TGGCTGA-----CCAGCCCTC-----GAGTGTCC--T 1717
 AY222339 TACAACAGTGTC-AGGGCTCCCTCTATC--TGGCGGA-----CCAACCTC-----AAATGTCC--T 1717
 NC_003323 TGCAACAGTGTC-AAAGCTCCCTCTACC--TTGCTGA-----CCAACCTC-----AAGTGTTT--T 1718
 L36905 TACAACAATGCC-AAGGCGCCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----TGTAAT--CT-T 1768
 AF139170 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----TGTAAT--CT-T 1756
 AF042071 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----TGTAAT--CT-T 1768
 L03561 TACAACAATGCC-AGGGCGTCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----TGTAAT--CT-T 1768
 AF259264 TACAACAATGCC-AGGGCGTCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----TGTAAT--CT-T 1768
 AY563953 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----TGTTAT--CT-T 1768
 AY563954 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----TGTTAT--CT-T 1768
 U19949 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AAGGCCGCC-----TGTAAT--CT-T 1768
 J02029 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AAGGCCGCC-----TGTAAT--CT-T 1768
 D13748 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AAGGCCGCC-----TGTAAT--CT-T 1768
 AF033817 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AAGGCCGCC-----TGTAAT--CT-T 1768
 NC_001436 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AAGGCCGCC-----TGTAAT--CT-T 1768
 AF074966 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----AGTAAT--CC-T 1765
 NC_000858 TACAACAATGCC-AAGGCGTCTGTACC--TCCCTGAGGCAA-----AGGGCCGCC-----AGTAAT--CC-T 1765
 L02534 TACAGCAATGCC-AAGGCGTTCTGTATC--TTCCCTGAGGCAA-----AAGGCCGCC-----TGTAAT--TCT-T 1774
 Z46900 TACAACAATGCC-AAGGCGTCTATATC--TTCCCGAGGCAA-----GGGGCCGTC-----TGTCAT--CT-T 1766
 AY590142 TACAGCAATGCC-AAGGGGCCCTATAACC--TCCCTGAGGCAAG--TCGCCCACC-----ACTAAT--AC--T 1801
 AF033818 TCTCCC---GCCTACAGGCCTCTATCTCCATACCTGAGGAGGT--ACGCCCCCC-----CATGGTAGGCG--T 1738
 NC_001414 TCTCCC---GCCTACAGGCCTCTATCTCCATACCTGAGGAGGT--ACGCCCCCC-----CATGGTAGGCG--T 1738
 K02120 -CTCCC---GCCTACAGGCTTCTATCTCCATACCTGAGGAAGT-----ACGCCCCCC-----TGTTGGTAGGCG--T 1734
 D00647 -CTCCC---GCCTACAGGCTTCTATCTCCATACCTGAGGAAGT-----ACACCCCCC-----TGTTGGTAGGCG--T 1734
 AF257515 -CTCCC---GGCTACAGGCTTCTATCTCCATACCTGAGGAAGT-----ACCCCCCCC-----TGTTGGTAGGCG--T 1737

ruler1910.....1920.....1930.....1940.....1950.....1960.....1970.....1980.....1990.....2000



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M10060	GCCAA-T--AGCCACTCCAAACACCATAGGCCTCGAACACCTTCCCCACCTCCCCAAGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
NC_001488	GCCAA-T--AGCCACTCCAAACACCATAGGCCTCGAACACCTTCCCCACCTCCCCAAGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
AF412314	GCCAA-T--AGCCACTCCAAACACCATAGGCCTCGAACACCTTCCCCACCTCCCCAAGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
AF139382	GCCAA-T--AGCCACCCCAAACACCATAGGCCTCGAACACCTTCCCCACCTCCCCAAGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
AF326584	GCCAA-T--AGCCACCCCAAACACCATAGGCCTCGAACACCTTCCCCACCTCCCCAAGTGGACCAATTTTC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
AF326583	GCCAA-T--AGCCACCCCAAACACCATAGGCCTCGAACACCTTCCCCACCTCCCCAAGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
L20734	GCCAA-T--AGCCACTCCACACACCATAGGCCTCGAACACCTTCCCCACCGCCCCAGGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
Y13051	GCCAA-T--AGCCACTCCACACACCATAGGCCTCGAACACCTTCCCCACCGCCCCAGGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
L11456	GCCAA-T--AGCCACTCCACACACCATAGGCCTCGAACACCTTCCCCACCGCCCCAGGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
X89270	GCCAA-T--AGCCACTCCACACACCATAGGCCTCGAACACCTTCCCCACCGCCCCAGGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1852
AF074965	GCCAA-T--ATCCACTCCACACCCCATAGGCTTCGAACACCTTCCCCACCGCCGCAGGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1787
Y14365	GCCAA-T--AGCCACTCCAAACACCATAGGCCTCGAACACCTTCCCCACCTCCCCAGGTGGACCAATTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTA	1861
Y14570	ACCCG-T--GACCACCCCAATGTCATTGGCCTTGAGCACTTCCCAACCCCCACAGATAGATCAGTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTG	1876
NC_001815	ACCCG-T--GACCACCCCAATGTCATTGGCCTTGAGCACTTCCCAACCCCCACAGATAGATCAGTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTG	1876
U90557	ACCCG-T--GGCCACCCCAAGTGTATCGGCCTTGAGCACTTCCCAACCCCCACAGATAGATCAGTTCC--TTTAAACCTGAGCGCCTCCAGGCCTTG	1874
Y07616	CCCCG-TTCAAACAC-CCAAGC-TCATTGGGCTAGAACACCTGCCTCCGCCCCGGAAATCTCGCAGTTCC--GTTAAACCGGAACGCCTCCAGGCCTTG	1817
AY217650	CCCCG-TTCAAACAC-CCAAGC-TTATTGGTTTAGAGCACCTGCCCCCGCCCCGGAGGTCTCGCAGTTCC--GTTAAACCGAAGCGCCTCCAGGCCTTG	1814
AF517775	CCCTG-TTCAGACAC-CCAAGC-TTATCGGATTAGAACACCTTCCCCGCCCCGGAAATCTCTCAGTTCC--GTTAAACCGGAGCGCCTCCAGGCCTTG	1813
AY222339	TCCTG-TCCAAACAC-CCAAGC-TTATTGGATTAGAACACCTTCCCCGCCCCAGAAATTTCTCAGTTCC--GTTAAACCGGAGCGCCTCCAGGCCTTG	1813
NC_003323	CCCTG-TCCAAACAC-CCAAGC-TTATTGGTTAGAACATCTTCCCCGCCCCGGAGGTCTCGCAGTTCC--GTTAAACCGGAGCGCCTCCAGGCCTTG	1814
L36905	GCCAA-TACAGGCGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
AF139170	GCCAA-TACAGGCGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1852
AF042071	GCCAA-TACAGGCGC--CAGCGTCCTTGGGCTAGAACATCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
L03561	GCCAA-TACAGGCGC--CAGCGTCCTTGGACTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
AF259264	GCCAA-TACAGGCGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATTAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
AY563953	GCCAA-TACAGGCGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
AY563954	GCCAA-TACAGGCGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
U19949	GCCAA-TACAGGCGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
J02029	GCCAA-TACAGGCGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
D13748	GCCAA-TACAGGCGC--CAGCTGTCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
AF033817	GCCAA-TACAGGCGC--CAGCTGTCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
NC_001436	GCCAA-TACAGGCGC--CAGCTGTCTTGGGCTAGAACACCTCCCAAGGCCCCCCGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1864
AF074966	GCCTA-TACAGGTGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCACCTGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1861
NC_000858	GCCTA-TACAGGTGC--CAGCGTCCTTGGGCTAGAACACCTCCCAAGGCCACCTGAAATCAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1861
L02534	GCCAA-TACAGGCGC--CAGCGTCCTTGGACTAGAACACCTCCCAAGGCCCCCAGAAATTAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1870
Z46900	ACCAA-TACAGACGC--CAGCGTCCTTGGGCTAGAGCACCTCCCGAAGGCCCCCCGAAATTAGCCAGTTCC--TTTAAACCGAAGCGCCTCCAGGCCTTG	1862
AY590142	GCCAG-TTCAAGGCGC--CGGCCATGTAGGCCTCGAGCATTTCACAAAACCCCCGAAATCAGCCAGTTTCC--TTTAAACCTGAACGCCTCCAGGCCTTG	1897
AF033818	CCTAGAT---GCCCCCAGCCACATTGGATTAGAACATTTGCCCGTCCCACCTGAGGTACCTCAATTCC--TTTAAACTAGAACGCCTCCAGGCCTTG	1834
NC_001414	CCTAGAT---GCCCCCAGCCACATTGGATTAGAACATTTGCCCGTCCCACCTGAGGTACCTCAATTCC--TTTAAACTAGAACGCCTCCAGGCCTTG	1834
K02120	CTTGGAT---ACCCCCGAGCCACATTGGATTAGAACATCTGCCCCCCACCTGAGGTGCCTCAATTCC--TTTAAACTAGAACGCCTCCAGGCCTTG	1830
D00647	CTTAGAT---GCCCCCAGCCACATTGGATTAGAACATTTGCCCCCCACCTGAGGTACCTCAATTCC--TTTAAACTAGAACGCCTCCAGGCCTTG	1830
AF257515	CTTGGAT---GCCCCCAGCCACATTGGATTAGAACATCTGCCCCCCACCTGAGGTACCTCAATTCC--TTTAAACTAGAACGCCTCCAGGCCTTG	1833

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