

Thu Oct 27, 2022 10:53 JST

CG6084(RA) CDS\_WT.ape from 1 to 951

Alignment to

CG6084 (RA)CDS\_10-1 allele.ape-- Matches:948; Mismatches:2; Gaps:3; Unattempted:0

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      *      *      *      *      *      *      *      *      *      *
1>ATGGCTGTACCGAACGTTAAATTCACAACCGCAAGGAAGTCCAATCATTGGACTGGGAACCTGGGGCAGCCCCAAGGGTCAGGTC-A-CCGAGGCTGT>98
1>|||||                                     # #|
1>ATGGCTGTACCGAACGTTAAATTCACAACCGCAAGGAAGTCCAATCATTGGACTGGGAACCTGGGGCAGCCCCAAGGGTCAGGTCTTGTCAGGCTGT>99

      *      *      *      *      *      *      *      *      *      *
99>CAAAGTTGCCATTGATGCCGATACAGGCACATTGACTGTGCTATGTATACAAAACGAGGATGAGGTCGGAGATGGTGTGAGGCCAAGATCAAGGAG>198
100>|||||
100>CAAAGTTGCCATTGATGCCGATACAGGCACATTGACTGTGCTATGTATACAAAACGAGGATGAGGTCGGAGATGGTGTGAGGCCAAGATCAAGGAG>199

      *      *      *      *      *      *      *      *      *      *
199>GGCGTTGTCAAGCGTGAGGATCTGTTTCATCACCAGCAAACCTGTGGAACACTTTCCATCGCCCGGATCTTGTCAAGTCGGCATTGGAGAACACATTGAGCT>298
200>|||||
200>GGCGTTGTCAAGCGTGAGGATCTGTTTCATCACCAGCAAACCTGTGGAACACTTTCCATCGCCCGGATCTTGTCAAGTCGGCATTGGAGAACACATTGAGCT>299

      *      *      *      *      *      *      *      *      *      *
299>CCCTGAAGCTGAAGTACCTCGATCTGTACCTTATCCACTGGCCCATGGGCTACAAGAGGGATGCGATCTGTTCCCCACCGACAAGGATGGCAAGACGCT>398
300>|||||
300>CCCTGAAGCTGAAGTACCTCGATCTGTACCTTATCCACTGGCCCATGGGCTACAAGAGGGATGCGATCTGTTCCCCACCGACAAGGATGGCAAGACGCT>399

      *      *      *      *      *      *      *      *      *      *
399>GTACTCGCCGGTTGATTACGTCGACACGTGGAAGGCCATGGAGAAGTTGGTGGAAAGAGGGTCTGGTCAAGTCCATTGGTGTTCCTCAACTTCAACAGAAGG>498
400>|||||
400>GTACTCGCCGGTTGATTACGTCGACACGTGGAAGGCCATGGAGAAGTTGGTGGAAAGAGGGTCTGGTCAAGTCCATTGGTGTTCCTCAACTTCAACAGAAGG>499

      *      *      *      *      *      *      *      *      *      *
499>CAGATCGAGCGCGTGCCTGAGGTGGCCACTATTCCACCAGTAACCAATCAGATTGAGTGCCATCCATATCTGACCCAGAAGAAGCTGATTGACTTCTGCA>598
500>|||||
500>CAGATCGAGCGCGTGCCTGAGGTGGCCACTATTCCACCAGTAACCAATCAGATTGAGTGCCATCCATATCTGACCCAGAAGAAGCTGATTGACTTCTGCA>599

      *      *      *      *      *      *      *      *      *      *
599>AGTCAAAGGACATTACAATCACTGCCTACAGTCCCTTGGGATCTCCAACCGCCCATGGGCCAAGGCTGGTGATCCGGTCATCCTAGAGGAGGCTAAGAT>698
600>|||||
600>AGTCAAAGGACATTACAATCACTGCCTACAGTCCCTTGGGATCTCCAACCGCCCATGGGCCAAGGCTGGTGATCCGGTCATCCTAGAGGAGGCTAAGAT>699

      *      *      *      *      *      *      *      *      *      *
699>CAAGGAAATGCGCTAAGAAGAAGAAGACCCCTGGACAGATCCTTATTCGATACCAGGTTTCAGCGTGCCAACATTGTTATCCCAAATCTGTGACCAAG>798
700>|||||
700>CAAGGAAATGCGCTAAGAAGAAGAAGACCCCTGGACAGATCCTTATTCGATACCAGGTTTCAGCGTGCCAACATTGTTATCCCAAATCTGTGACCAAG>799

      *      *      *      *      *      *      *      *      *      *
799>GACCGCATCGAGTCCAACCTCCAGGCTTCGACTTCGAACTGACACCTGAGGAAATCGAAATCATCGAAAGCTTCGAGTGCAACGGCCGCTTGTTCCTCC>898
800>|||||
800>GACCGCATCGAGTCCAACCTCCAGGCTTCGACTTCGAACTGACACCTGAGGAAATCGAAATCATCGAAAGCTTCGAGTGCAACGGCCGCTTGTTCCTCC>899

      *      *      *      *      *      *
899>TACTCAACCAATACGGTCACCTCACCACCTTTCGAGAAGGACGAATACTAG>951
900>|||||
900>TACTCAACCAATACGGTCACCTCACCACCTTTCGAGAAGGACGAATACTAG>952
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