

nrxn1A.ape
Alignment to
1A_Full1_32-2R_215.txt-- Matches:274; Mismatches:4; Gaps:103; Unattempted:0

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      *      *      *      *      *      *      *      *
1>~GCATAGA-CTTCGAGTGTTCATGTTGTTTCATAAATGAACATTGGGATGCAAGAATTGATAATAGTCTTGTATAGTAACCGATGCCATGTTTGAATGCTG>98
280<AGCATAGACCTCGAGTGTTCATGTTGTTTCATAAATGAACATTGGGATGCAAGAATTGATAATAGTCTTGTATAGTAACCGATGCCATGTTTGAATGCTG<181

      *      *      *      *      *      *      *      *
99>CACCACATTTTGACAGATAAACCTTTTTTCATTTCCCTTTCTTTCTTTTGGATACGCATGACCGGTTCACTCATATATGTAATGTTGACTAATAGG>198
180<CACCACATTTTGACAGATAAACCTTTTTTCATTTCCCTTTCTTTCTTTTGGATACGCATGACCGGTTCACTCATATATGTAATGTTGACTAATAGG<81

      *      *      *      *      *      *      *      *
199>AGCTCATTCCTTCGTAAATAGCTTTGAAGCACAGCAATGAAACAGAGAAGACCATACTGGCAATTTAGCTGGAAATAGnnnnnnnnnnnnnnnnCCGGGGCC>298
80<AGCTCATTCCTTCGTAAATAGCTTTGAAGCACAGCAATGAAACAG-----<36

      *      *      *      *      *      *      *      *
299>ATTCGGAATAGATTGAGGAAAACTCCATGCACGTAAAGTATCTTATTACATGTTTATATACGGTGCAAAGACTATCTGTG>379
35<-----GAAAAACTCCATGCACGTAAAGTATC-----CAAACCCE-C-C<1
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