

nrxn2a.ape  
Alignment to  
2A\_Full\_41-3\_F\_219.txt-- Matches:288; Mismatches:1; Gaps:192; Unattempted:0  
2A\_Full\_41-3\_R\_210.txt-- Matches:288; Mismatches:5; Gaps:185; Unattempted:0

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      *      *      *      *      *      *      *      *
1>~GCTACAT-GTGTGAACATGCCCTACATTTGTAAGTCTGTAATTGGCAAGGATTCCTTGAGCTAAATTAACATTATCTTTTCTTTTCACCTTCAGGCATT>98
1>-----TGC-----TGTAG-----TGGCAGGATTCAGAGCTAAATTAACATTATCTTTTCTTTTCACCTTCAGGCATT>64
295<TGCTACAAGGSGGAACATGCCCTACATTTGTAAGTCTGTAATTGGCAAGGATTCAGAGCTAAATTAACATTATCTTTTCTTTTCACCTTCAGGCATT<196

      *      *      *      *      *      *      *      *
99>CAAAGAAGGATTTCTAACAGTGACGGCTTGCCGGTGGAATGCAGGTGCACCTTCTTCTGAAATAAGCTGAGGATTCCTGGGTGGAAGAGAAATCATGTTTT>198
65>CAAAGAAGGATTTCTAACAGTGACGGCTTGCCGGTGGAATGCAGGTGCACCTTCTTCTGAAATAAGCTGAGGATTCCTGGGTGGAAGAGAAATCATGTTTT>164
195<CAAAGAAGGATTTCTAACAGTGACGGCTTGCCGGTGGAATGCAGGTGCACCTTCTTCTGAAATAAGCTGAGGATTCCTGGGTGGAAGAGAAATCATGTTTT<96

      *      *      *      *      *      *      *      *
199>TGACCTACTATCTACAAAACGAAAATACAACCGCAGCAGTAATCCTACTTTCACCAGAGGGTGAGATGCATAAATCGGTCTTTTAACATnnnnnnnnnn>298
165>TGACCTACTATCTACAAAACGAAAATACAACCGCAGCAGTAATCCTACT----->214
95<TGACCTACTATCTACAAAACGAAAATACAACCGCAGCAGTAATCCTACT-----<46

      *      *      *      *      *      *      *      *
299>nnnAAGGCTCTTATCAGGTGGATCAAAGCCGCAACTCCGGCTCTGAAAGCAACGGTGCCGTAGTGAAGGAGAAAACGCCGAGTACGACTGCCGCCGTGGC>398
214>----->214
46<-----<46

      *      *      *      *      *      *      *      *
399>TAAACACCACCAAGGGCAAGAAGACAAAGACAAGGAGTATTACGTCTGAGAAAGACAGAGGAGAAGGTA-CTGATG~~~~>476
215>TAAACACCACCAAGGGCAAGAAGACAAAGACAAGGAGTATTACGTCTGAGAAAGACAGAGGAGA-STAGCTGATGAAGT>294
45<TAAACACCACCAAGGGCAAGAAGACAAAGACAAGGAGTAT-----AT~~~~<1
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