

nrxn2b_tmr.ape
Alignment to
2B_TMR_7-3F_211.txt-- Matches:241; Mismatches:1; Gaps:286; Unattempted:0
2B_TMR_7-3R_212.txt-- Matches:250; Mismatches:0; Gaps:283; Unattempted:0

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      *      *      *      *      *      *      *      *
1>---GCTCAAACCGGGCATCAA-TGCGCCCAACAT-CCCCGCGGGTAAATGAACACTCGAGATCAGGTGCTGCTGCCGCCCTGCTCAGCCCTCGGGGCGACA>95
1>-----T-CCGCGGTTAAATGACACTCGAGATCAGGTGCTGCTGCCGCCCTGCTCAGCCCTCGGGGCGACA>62
255<TTGGCTCAAACCGGGCATCAAATGCGCCCAACATCCCCGCGGGTAAATGAACACTCGAGATCAGGTGCTGCTGCCGCCCTGCTCAGCCCTCGGGGCGACA<156
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      *      *      *      *      *      *      *      *
96>CTGATCACAGCGGGCGGCATCGACACATCCCAGGTATAACATATCCCCCTAATTTCCCCCATGTGCCCACTACAGACCCCTCATCGCCGGACCGAGGGCC>195
63>CTGATCACAGCGGGCGGCATCGACACATCCCAGGTATAACATATCCCCCTAATTTCCCCCA----->123
155<CTGATCACAGCGGGCGGCATCGACACATCCCAGGTATAACATATCCCCCTAATTTCCCCCATGTGCCCACTACAGACCCCTCATCGCCGGACCGAGGGCC<56
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      *      *      *      *      *      *      *      *
196>GCC TGGAGCGTGGAGGTGATCCGAGAGTCCAGCAGTACCACGGGTATGGTGGTGGGCATCGTGGCAGCGGCTGCCCTCTGCATCCTCATCTGCTGTAC>295
123>----->123
55<GCCTGGAGCGTGGAGGTGATCCGAGAGTCCAGCAGTACCACGGGT-----TA<8
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      *      *      *      *      *      *      *      *
296>GCCATGTACAAGTACCGCAACCGCGACGAAGGCTCCTACCAGTGGACCAGAGCCGCAATTACATTAGCAATTCAGCCACGCAAAGCAATGGCGCCCTAG>395
123>----->123
7<-----GCT-----CAA-----<2
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      *      *      *      *      *      *      *      *
396>TGAAGGAGAAACAGCCCGGCGCTGCCAAGACGGGCACCAAGAGCAAGAAAAACAAAGACAAGGAGTATTACGTCTGAGCACGGCCCCCTAGGGGGACCCGA>495
124>---GGAGAAACAGCCCGGCGCTGCCAAGACGGGCACCAAGAGCAAGAAAAACAAAGACAAGGAGTATTACGTCTGAGCACGGCCCCCTAGGGGGACCCGA>219
2<-----<2
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      *      *      *      *
496>GGGGAGAAGGAGAGAGATAGGATGAGGACTGGA>528
220>GGGGAGAAGGAGAGAGATAGC-----GA>242
1<-----A<1
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