

nrxn1A.ape
Alignment to
1A_TMR_F8_2F_179.txt-- Matches:165; Mismatches:2; Gaps:209; Unattempted:0
1A_TMR_F8_2R_180.txt-- Matches:168; Mismatches:2; Gaps:203; Unattempted:0

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      *      *      *      *      *      *      *      *      *      *
1>nnataaacgtctctctcttctccnnagtactccttgctccttggtctcttaaacgtctctctcttctccctttctgtctacagctcaccaccacttcccgag>100
1>-----CCT-----ACCCACCACCTTCCGAG>19
170<-----TCATAACGCTCTCCTTTCTCCCTTTCTGTCTACAGCTCACCCACCACCTTCCCGAG<114
```

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      *      *      *      *      *      *      *      *      *      *
101>gccaagggttacccgagcccagaggtgattcgggagtcagcagcaccacgggcatggtcgtagcatcgttgccagccgctgcactctgcacctaacc>200
20>GCAAGGGTTACCCGAGCCCAGA----->41
113<GCCAAGGGTTACCCGAGCCCAGA-----<91
```

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      *      *      *      *      *      *      *      *      *      *
201>tgtctacgccatgtacaaatacacaaaaccgacgaagggctcttaccacgtggacgagagtcgtaactacattagtaattctgccacgcagcccaatgg>300
42>-----CACGTGGACGAGAGTCGTAACCTACATTAGTAATTCTGCCACGC-----GCCCAATGG>94
90<-----CACGTGGACGAGAGTCGTAACCTACATTAGTAATTCTGCCACGCAGCCCAATGG<38
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      *      *      *      *      *      *      *
301>agctgccgtcaaagaaaagcccatcgccgtgccccaaaaataaaaaagataaaaaagaacaaggacaaggaggtac~~~>373
95>AGCTGCCGTCAAAGAAAAGCCCATCGGCGTGCCCCAAAAATAAAAAAGATAAAAAAGACAAGACAAGGAGTACAAA>170
37<AGCTGCCGTCAAAGAAAAGCCCATCGCTCCCA-----ACAA-----A~~~~~<1
```