

nrxn3b-tmr region.ape
Alignment to
3B_TMR_20-4F_207.txt-- Matches:152; Mismatches:3; Gaps:352; Unattempted:0
3B_TMR_20-4R_208.txt-- Matches:153; Mismatches:1; Gaps:353; Unattempted:0

* * * * *
1>---CCAAAATCCCAGCAGGGAAAAATGAATAACCGCGAGGTCAAACCCCAACCG-GATATAGTGCTGCTGCCGCTCCCCACGTCTTTCGATATGGATGGCA>96
1>-----GGA---GA---C-----ACCTACCGGATATAGTGCTGCTGCCGCTCCCCACGTCTTTCGATATGGATGGCA>63
157<AGTCCAAAATCCCAGCAGGGAAAAATGAATAACCGCGAGGTCAAACCCCAACCG-GATATAGTGCTGCTGCCGCTCCCCACGTCTTTCGATATGGATGGCA<59

* * * * *
97>CCAAACCGAAGGGGCCGTACATCACACAGCCCATGTTGCGGACCATCCCCAGTGCCCTACCCACTGTGCCAGGTATCAGGAGAGTGCCCCCTGGTGCCTC>196
64>CCAAACC----->70
58<CCAAACC-----<52

* * * * *
197>GGAGGTAATACGAGAGTCCAGCAGCACTACGGGCATGGTGGTGGGTATCGTTTCTGCTGCTGCTCTTTCATTCTCATCTTCTCTATGCCATGTACAAA>296
70>----->70
52<-----<52

* * * * *
297>TACAGAAACAGGGACGAGGGTTCCTATCAGGTAGATGAAACCCGGAACACATCAGTAATTCGGCACAGAATAACGGCACAGTAGTGAAAGACAAACAGC>396
70>----->70
52<-----<52

* * * * *
397>CCAGCACTAAAGGTGCCAGTAACAAGAGACCCAAAGACAAGGACAAGGAATACTATGTATAAAAGAACATTCCAATGACAAAACACAGAGACAGAGCAAC>496
71>-----CAAGAGACCCAAAGACAAGGACAAGGAATACTATGTATAAAAGAACATTCCAATGACAAAACACAGAGACAGAGCAAC>148
51<-----CAAGAGACCCAAAGACAAGGACAAGGAATACTATGTATAAAAGAACATTCCAATGACAAAACACAGAGACAGAGCAAC>1

*
497>ATCTGAGA~~>504
149>ATCTGAGAGG>158
1<~~~~~<1