L270R MGA Most Frequent Non-T Mismatch Alignments

This document contains alignments between the expected non-T amplicon sequence and the top ten most frequent sequences that did not pass the T-strip filter. Percentages are relative to the total number of Non-T mismatches (19), not the total number of input sequences. Nucleotides are highlighted relative to the expected amplicon non-T sequence.

Expected Amplicon non-T Sequence:

AAGAAAGGAAAACAAAGAAAGGGG-A-AAGAGG-CGAG-AGCGGGAGAG

13 (68.42%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGG-A-AAGAGG-CGAG-CGCGGGAGAG

1 (5.26%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGCGGA-AAGAGG-CGAG-AGCGGGAGAG

1 (5.26%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGG-AAANGAGG-CGAG-AGCGGGAGAG

1 (5.26%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGG-A-AAGANGCNGAG-AGCGGGAGAG

1 (5.26%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGG-A-AAGAGG-CGAGACGCGGGAGAG

1 (5.26%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGG-G-A-AAGAGG-CGAG-AGCGGGAGAG

1 (5.26%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGG-A-AAGAGG-CGA--CGCGGGAGAG