WT 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 (17), not the total number of input sequences. Nucleotides are highlighted relative to the expected amplicon non-T sequence.

Expected Amplicon non-T Sequence:

AAGAAAGGAAAACAAAGAAAGGGGA-AAGAG-GCGAG-AGCGGGAGAG

10 (58.82%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGGA-AAGAG-GCGAG-CGCGGGAGAG

2 (11.76%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGGA-AAGAG-GCGA--CGCGGGAGAG

1 (5.88%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGGNAAAGAGGGNGAG-AGCGGGAGAG

1 (5.88%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGGA-AAGAG-GCGAGNAGCGGGAGAG

1 (5.88%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGGA-AAGACGGCGAG-AGCGGGAGAG

1 (5.88%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAGAGGGGA-AAGAG-GCGAG-AGCGGGAGAG

1 (5.88%) Non-T Mismatches:   
AAGAAAGGAAAACAAAGAAAGGGGA-AAGAG-GCGAG-GGCGGGAGAG