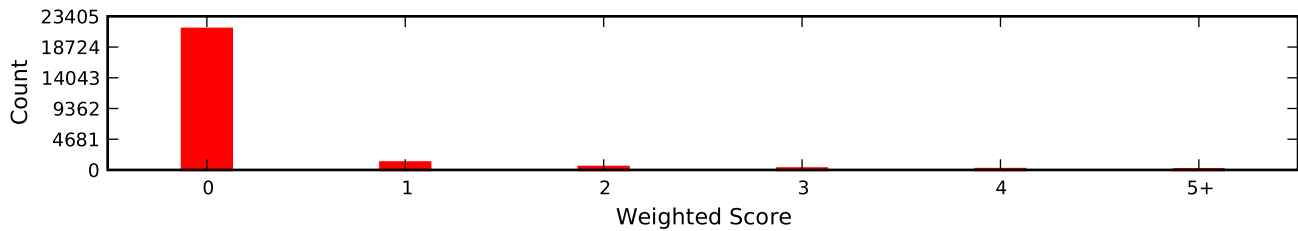
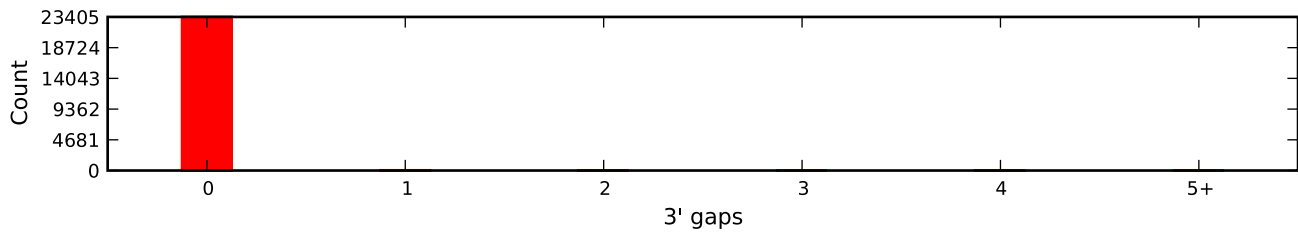
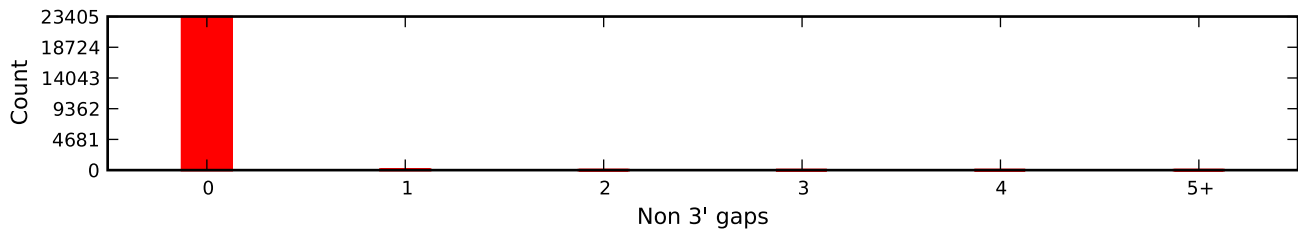
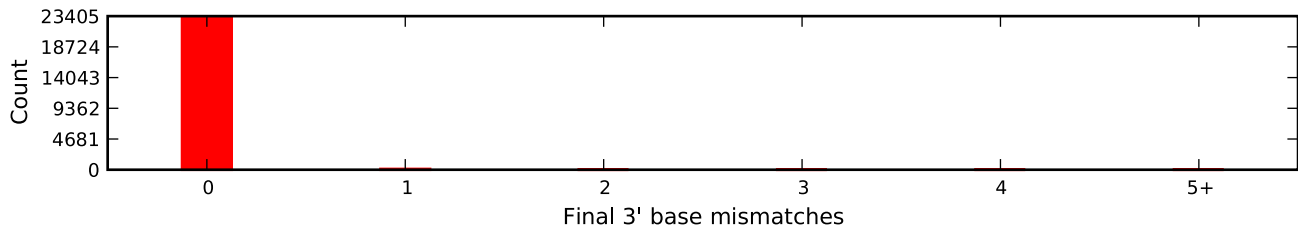
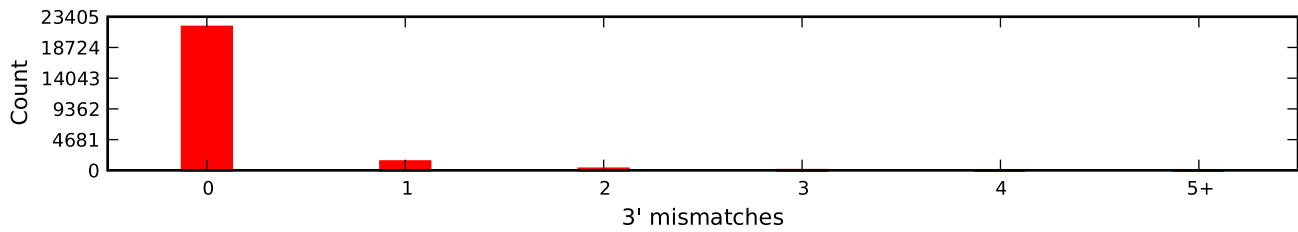
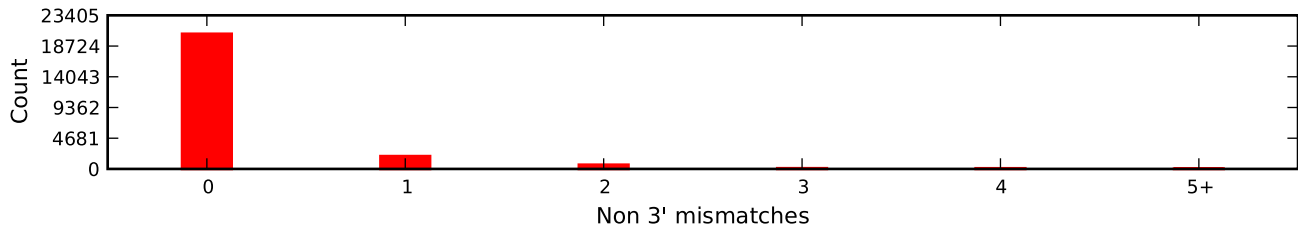


338r; Degeneracy: 1; GC content 0.67 - 0.67

5'-GCTGCCTCCCGTAGGAGT-3'
Sequences tested: bacterial_v16.fasta



3' length: 5 nucleotides

Weighted score = non-3' mismatches * 0.40 + 3' mismatches * 1.00 + non 3' gaps * 1.00 + 3' gaps * 3.00

An additional 3.00 penalty is assigned if the final 3' base mismatches

Weighted score is rounded to the nearest whole number in this graphical display