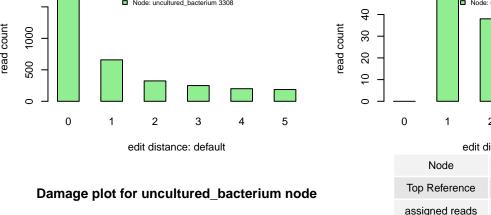
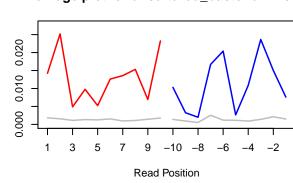
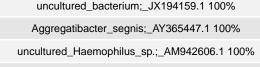
## Node: uncultured\_bacterium 3308

0101\_S0\_L000\_R1\_000.fastq.merged.prefixed.hg19ur0101\_S0\_L000\_R1\_000.fastq.merged.prefixed.hg19ur





C2T/G2A rate



Aggregatibacter\_segnis;\_GU727818.1 100%

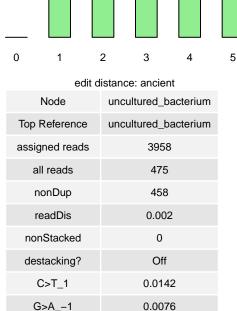
laemophilus\_genomosp.\_P2\_oral\_clone\_MB3\_C24;\_DQ003621.1 100%

uncultured\_Haemophilus\_sp.;\_AM420165.1 100%

uncultured\_Haemophilus\_sp.;\_AM420226.1 100%
uncultured\_Haemophilus\_sp.;\_FJ976274.1 100%

uncultured\_Haemophilus\_sp.;\_AY807017.1 100%

Aggregatibacter\_sp.\_oral\_taxon\_G01;\_GU431918.1 100%



mean length (sd)

69 (21.545)