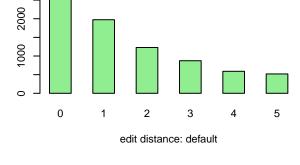
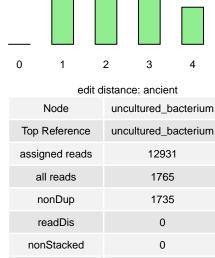
Node: uncultured_bacterium 2251 Node: uncultured_bacterium 8035 9 ead count

400

200

0101_S0_L000_R1_000.fastq.merged.prefixed.hg19ur0101_S0_L000_R1_000.fastq.merged.prefixed.hg19ur





Off

0.2544

0.2823

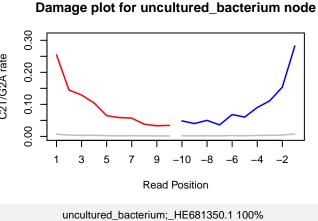
63 (25.518)

destacking?

C>T_1

G>A_-1

mean length (sd)



Clostridiales_bacterium_oral_taxon_G74;_GU432185.1 100%

ostreptococcaceae_bacterium_canine_oral_taxon_030;_JN713194.1 100% tostreptococcaceae_bacterium_feline_oral_taxon_028;_KM461989.1 100%

actinomyces_genomosp._P1_oral_clone_MB6_C03;_DQ003632.1 100% uncultured_Actinomyces_sp.;_FJ976431.1 100% uncultured_Actinomyces_sp.;_JQ406543.1 100%

uncultured_Actinomyces_sp.;_AM420166.1 100%

uncultured_Actinomyces_sp.;_FJ976253.1 100%

Actinomyces;_NR_025633.1 100%