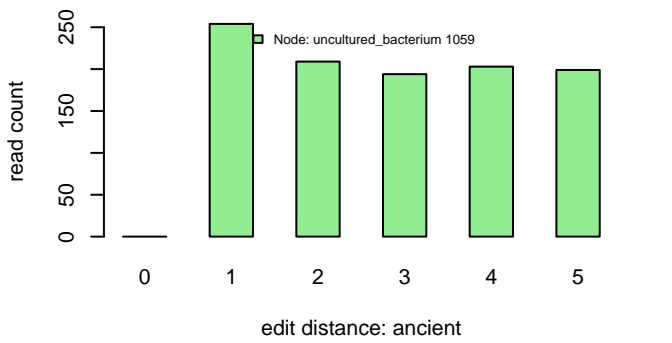
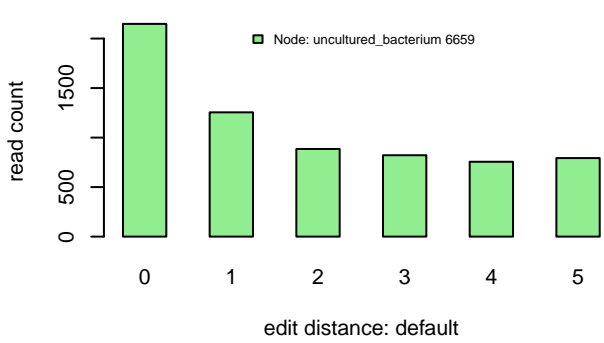
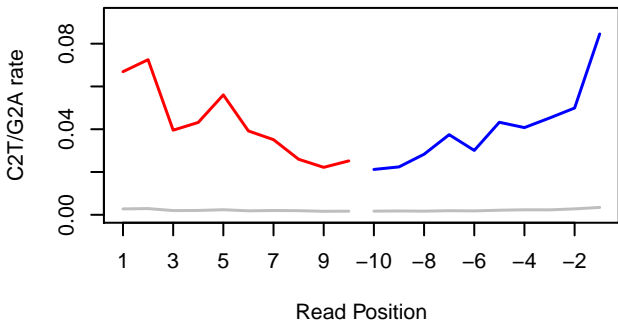


0101_S0_L000_R1_000.fastq.merged.prefixed.hg19ur0101_S0_L000_R1_000.fastq.merged.prefixed.hg19ur



Damage plot for uncultured_bacterium node



Node	uncultured_bacterium
Top Reference	uncultured_bacterium
assigned reads	17716
all reads	736
nonDup	720
readDis	0.006
nonStacked	2
destacking?	Off
C>T_1	0.0669
G>A_-1	0.0845
mean length (sd)	69 (25.985)

uncultured_bacterium;_KF312328.1 100%
actinomyces_genomosp._P1_oral_clone_MB6_C03;_DQ003632.1 100%
Eubacterium_sp._oral_clone_FX028;_AY134903.1 100%
Eubacterium_sp._oral_taxon_B60;_GU429169.1 100%
uncultured_Actinomyces_sp.;_JQ406543.1 100%
uncultured_Actinomyces_sp.;_FJ976431.1 100%
Actinomyces;_NR_025633.1 100%
uncultured_Actinomyces_sp.;_AM420166.1 100%
uncultured_Candidatus_Saccharibacteria_bacterium;_GU227159.1 100%
TM7_phylum_sp._canine_oral_taxon_308;_JN713475.1 100%