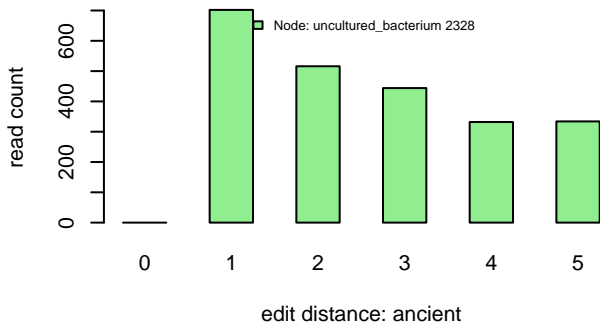
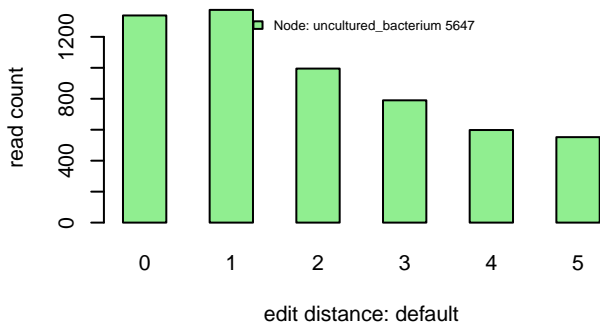
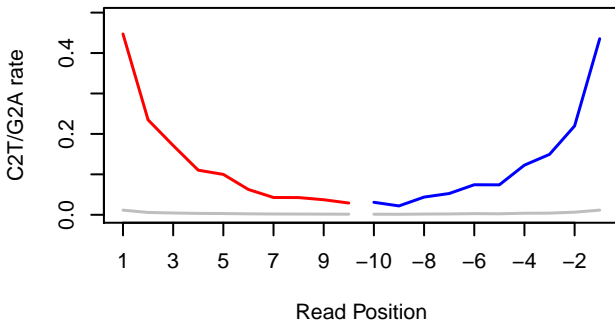


0101_S0_L000_R1_000.fastq.merged.prefixed.hg19ur0101_S0_L000_R1_000.fastq.merged.prefixed.hg19ur



Damage plot for uncultured_bacterium node



Node	uncultured_bacterium
Top Reference	uncultured_bacterium
assigned reads	6687
all reads	349
nonDup	340
readDis	0.029
nonStacked	5
destacking?	Off
C>T_1	0.4472
G>A_-1	0.4354
mean length (sd)	48 (14.496)

uncultured_bacterium;_KF312316.1 100%
actinomyces_genomosp._P1_oral_clone_MB6_C03;_DQ003632.1 100%
Methanobrevibacter_millerae;_CP011266.1 100%
uncultured_Actinomyces_sp.;_JQ406543.1 100%
uncultured_Actinomyces_sp.;_FJ976431.1 100%
TM7_phylum_sp._oral_clone_CW040;_AF385506.1 100%
uncultured_Candidatus_Saccharibacteria_bacterium;_FJ976240.1 100%
Clostridiales_bacterium_oral_taxon_G74;_GU432185.1 100%
uncultured_Actinomyces_sp.;_AM420166.1 100%
Actinomyces;_NR_025633.1 100%