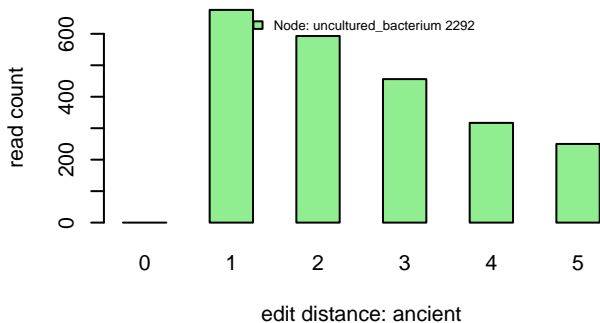
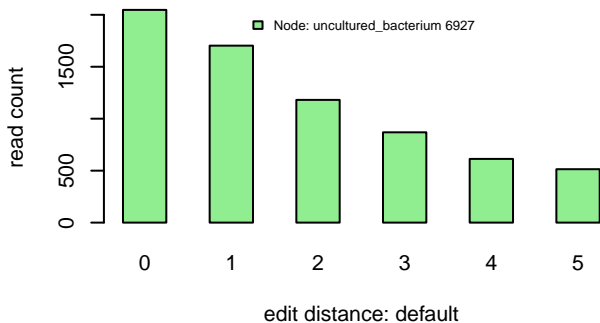
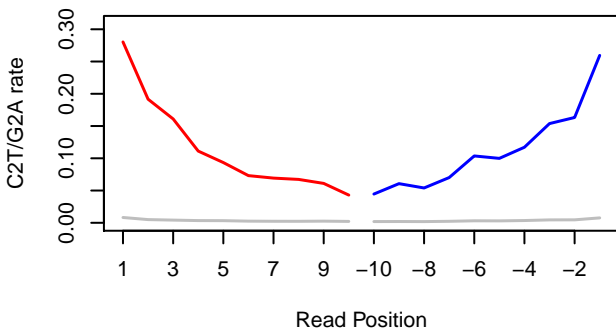


0101_S0_L000_R1_000.fastq.merged.prefixed.hg19ur0101_S0_L000_R1_000.fastq.merged.prefixed.hg19ur



Damage plot for uncultured_bacterium node



uncultured_bacterium;_GU925200.1 100%
[Eubacterium]_yurii_subsp._schtitka;_NR_115260.1 100%
[Eubacterium]_yurii_subsp._yurii;_NR_104843.1 100%
uncultured_bacterium;_GU925200.1 100%
[Eubacterium]_yurii_subsp._margaretiae_ATCC_43715;_NR_115259.1 100%
Eubacterium_sp._oral_strain_A03MT;_AF287765.1 100%
Peptostreptococcaceae_bacterium_AS15;_HQ616364.1 100%
Eubacterium_sp._oral_clone_OH3A;_AY947497.1 100%
[Eubacterium]_yurii_subsp._yurii;_L34629.2 100%
uncultured_Eubacterium_sp.;_AM420118.1 100%
uncultured_Eubacterium_sp.;_AM420046.1 100%

Node	uncultured_bacterium
Top Reference	uncultured_bacterium
assigned reads	8078
all reads	110
nonDup	108
readDis	0.011
nonStacked	1
destacking?	Off
C>T_1	0.2803
G>A_-1	0.2595
mean length (sd)	50 (13.703)