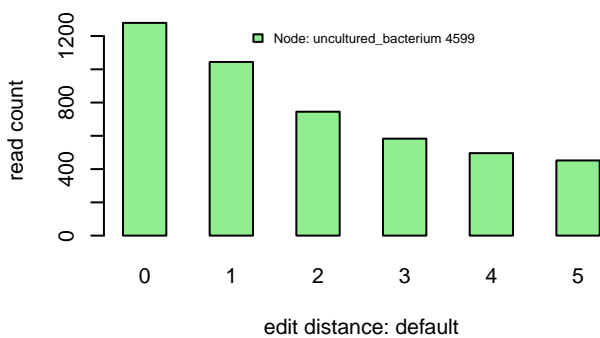
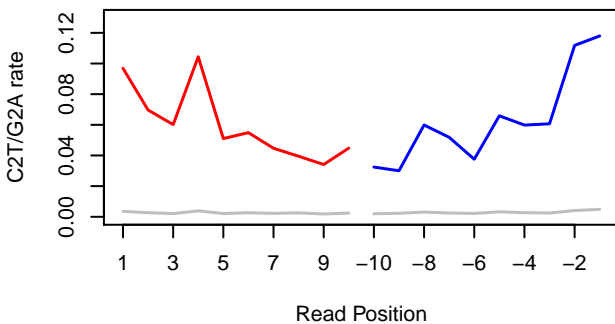


0101\_S0\_L000\_R1\_000.fastq.merged.prefixed.hg19ur0101\_S0\_L000\_R1\_000.fastq.merged.prefixed.hg19ur



### Damage plot for uncultured\_bacterium node



Node	uncultured_bacterium
Top Reference	uncultured_bacterium
assigned reads	5522
all reads	262
nonDup	256
readDis	0.001
nonStacked	0
destacking?	Off
C>T_1	0.0969
G>A_1	0.118
mean length (sd)	50 (17.271)

uncultured\_bacterium;\_JQ696889.1 100%

Bacteroidetes\_bacterium\_Oral\_Taxon\_274;\_FJ577256.2 100%

uncultured\_Bacteroidales\_bacterium;\_FJ976400.1 100%

uncultured\_Porphyromonadaceae\_bacterium;\_AM420225.1 100%

Bacteroidetes\_bacterium\_oral\_taxon\_274;\_GU409193.1 100%

Bacteroidetes\_bacterium\_oral\_taxon\_274;\_GU409196.1 100%

Bacteroidetes\_bacterium\_oral\_taxon\_274;\_GU409198.1 100%

Bacteroides-like\_sp.\_oral\_clone\_AU126;\_AY005072.1 100%

Bacteroidetes\_bacterium\_oral\_taxon\_274;\_GU409195.1 100%

Bacteroidetes\_bacterium\_oral\_taxon\_274;\_GU409197.1 100%