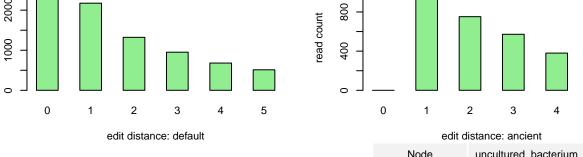
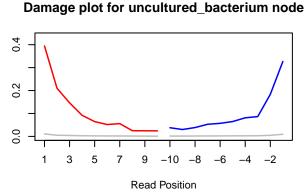
Node: uncultured_bacterium 8293 Node: uncultured_bacterium 3072

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





C2T/G2A rate

uncultured_bacterium;_FM873256.1 100%
Actinomyces_naeslundii;_JF496733.1 100%
Actinomyces oris: GQ421315.1 100%

Actinomyces_oris;_GQ421315.1 100%	
Actinomyces_sporal_taxon_170;_HM596278.1 1009	6

Actinomyces_oris;_AJ234052.1 100%

Actinomyces oris: GQ421309.1 100%

Actinomyces_massiliensis_4401292;_NR_044288.1 100%

Actinomyces_oris;_GQ421316.1 100%

uncultured_Candidatus_Saccharibacteria_bacterium;_FJ976257.1 100%

Actinomyces	oris;_GQ421320.1	100%

0	1	2	3	4	
	edit distance: ancient				
Node			uncultured_bacterium		
Top Reference		ce ur	uncultured_bacterium		
assigned reads		ds	9441		
all reads			340		
nonDup			329		
readDis			0.015		
nonStacked		i	2		
destacking?			Off		
C>T_1			0.3945		
G	6>A1		0.3269		
mean length (sd)		sd)	53 (19.061)		