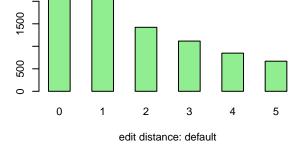
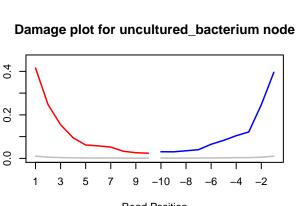
Node: uncultured_bacterium 8578 Node: uncultured_bacterium 3498 read count ead count

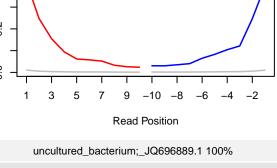
400

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





C2T/G2A rate



actinomyces_genomosp._P1_oral_clone_MB6_C03;_DQ003632.1 100%

incultured_Candidatus_Saccharibacteria_bacterium;_FJ976240.1 100% TM7_phylum_sp._oral_clone_CW040;_AF385506.1 100% ostreptococcaceae_bacterium_canine_oral_taxon_030;_JN713194.1 100%

_	_	_	_	_	~
uncultured_rumen_	_bacteriu	m;_E	U3814	36.1	100%

Clostridiales_bacterium_oral_taxon_G74;_GU432185.1 100	%
uncultured_Actinomyces_sp.;_JQ406543.1 100%	

uncultured_Actinomyces_sp.;_FJ976431.1 100% uncultured_rumen_bacterium;_EU381612.1 100% 0 2 3 edit distance: ancient Node uncultured_bacterium Top Reference uncultured_bacterium assigned reads 13578 all reads 401 nonDup 396 readDis 0.002 nonStacked 0

Off

0.4156

0.3958

47 (15.019)

destacking?

C>T_1

G>A_-1

mean length (sd)