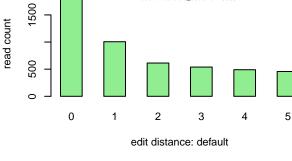
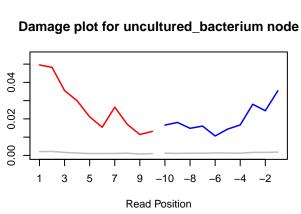
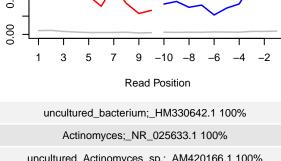
150 ■ Node: uncultured_bacterium 5065 Node: uncultured_bacterium 601 ead count 100

20

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







Actinomyces;_NR_025633.1 100%	
uncultured_Actinomyces_sp.;_AM420166.1	100%

uncultured_Actinomyces_sp.;_FJ976431.1 100% actinomyces_genomosp._P1_oral_clone_MB6_C03;_DQ003632.1 100%

uncultured_Actinomyces_sp.;_JQ406543.1 100%

Actinomyces_genomosp._C1;_AY278610.1 100% uncultured_Actinomyces_sp.;_FJ976446.1 100%

uncultured_Actinomyces_sp.;_GU227166.1 100% incultured_Candidatus_Saccharibacteria_bacterium;_FJ976255.1 100%

0	1	2	2	3	4	5		
	edit distance: ancient							
Node			uncultured_bacterium			m		
Top Reference			uncultured_bacterium			m		
assigned reads			6720					
all reads			285					
ı	nonDup		282					
1	readDis		0.004					
nonStacked			0					
de	stacking?	,	Off					
	C>T_1		0.0495					

0.0354

65 (24.563)

G>A_-1

mean length (sd)