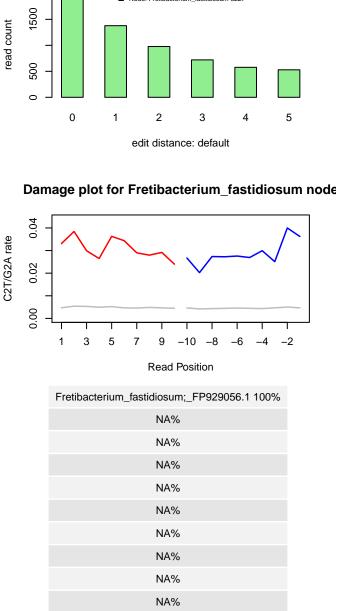
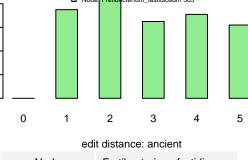
S0_L001_R1_001.fastq.combined.fq.prefixed.extractuS0_L001_R1_001.fastq.combined.fq.prefixed.extractu

read count

40 60

0 20





| edit distance: ancient | |
|------------------------|----------------------------|
| Node | Fretibacterium_fastidiosum |
| Top Reference | Fretibacterium_fastidiosum |
| assigned reads | 426328 |
| all reads | 10000 |
| nonDup | 9903 |
| readDis | 0.542 |
| nonStacked | 3446 |
| destacking? | Off |
| C>T_1 | 0.0331 |
| G>A1 | 0.0362 |
| mean length (sd) | 106 (40.524) |
| | |