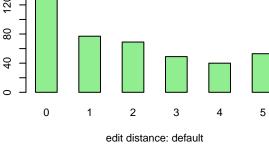
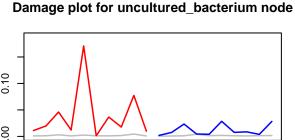
■ Node: uncultured bacterium 41 Node: uncultured_bacterium 434 120 read count read count

 ∞

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





C2T/G2A rate

0.10 0.00 3 5 -10 Read Position uncultured_bacterium;_JQ972699.1 100%

| uncultured_Firmicules_bacterium;_EF651196.1 100% | | | | | | |
|--|------------|--|--|--|--|--|
| uncultured_Epsilonproteobacteria_bacterium;_AY1543 | 389.1 100% | | | | | |

TM7_phylum_sp._oral_clone_FR058;_AF432141.1 100% TM7_phylum_sp._oral_taxon_350;_GU410604.1 100%

TM7_phylum_sp._oral_taxon_350;_GU410603.1 100%

TM7_phylum_sp._oral_taxon_A56;_GU428816.1 100%

uncultured_eubacterium_WJGRT-1;_AF175579.1 100%

| 0 | 1 | : | 2 | 3 | | 4 | | 5 |
|------------------------|---|----------------------|----------------------|---|-----|---|---|---|
| edit distance: ancient | | | | | | | | |
| Node | | | uncultured_bacterium | | | | m | |
| Top Reference | | uncultured_bacterium | | | | m | | |
| assigned reads | | 603 | | | | | | |
| all reads | | 17 | | | | | | |
| nonDup | | 11 | | | | | | |
| readDis | | 0.314 | | | | | | |
| nonStacked | | | 4 | | | | | |
| destacking? | | | | C | Off | | | |

0.011

0.0283

63 (22.576)

C>T_1

G>A_-1

mean length (sd)

ncultured_Candidatus_Saccharibacteria_bacterium;_GU227163.1 100%

ncultured_Candidatus_Saccharibacteria_bacterium;_GU480932.1 100%