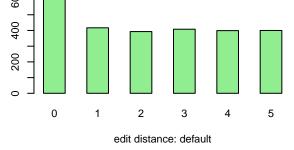
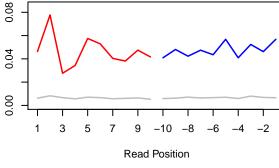
## 9 50 ■ Node: Streptococcus\_intermedius 2694 intermedius 226 ead count 30

0101\_S0\_L000\_R1\_000.fastq.merged.prefixed.hg19ur0101\_S0\_L000\_R1\_000.fastq.merged.prefixed.hg19ur







C2T/G2A rate

Streptococcus\_intermedius\_C270;\_CP003858.1 100% Streptococcus\_intermedius\_B196;\_CP003857.1 100%

Streptococcus\_intermedius;\_CP020433.1 100%

Streptococcus\_intermedius\_JTH08;\_AP010969.1 100%

Streptococcus\_troglodytae;\_AP014612.1 003%

Streptococcus\_merionis;\_LT906439.1 002%

Streptococcus\_sanguinis\_SK36;\_CP000387.1 001% reptococcus\_constellatus\_subsp.\_pharyngis\_C1050;\_CP003859.1 001% 0 2 3 edit distance: ancient

Node	Streptococcus_intermedius
Top Reference	Streptococcus_intermedius
assigned reads	4195
all reads	2460
nonDup	2348
readDis	0.395
nonStacked	842
destacking?	Off
C>T_1	0.0464
G>A1	0.0568
mean length (sd)	59 (18.985)

treptococcus\_constellatus\_subsp.\_pharyngis\_C232;\_CP003800.1 001%

Streptococcus\_sp.\_NPS\_308;\_AP017652.1 001%