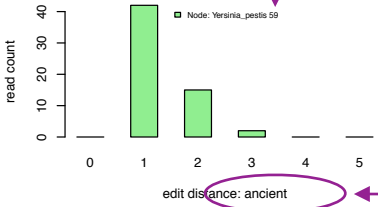
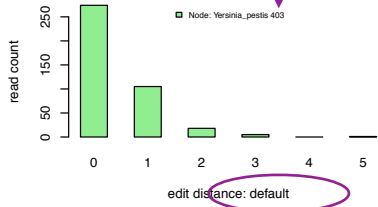


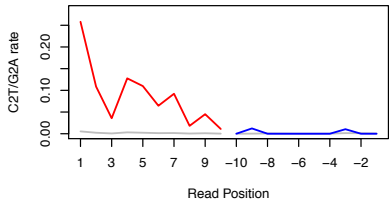
All reads assigned to node (possible across multiple references)

All reads assigned to node that carry signs of damage  
(possible across multiple references)

5000\_dentine\_UDGno\_5m\_LP39.10\_pB\_I5.fa.gz\_yers5000\_dentine\_UDGno\_5m\_LP39.10\_pB\_I5.fa.gz\_yers



Damage plot for Yersinia\_pestis node



Node	Yersinia_pestis
Top Reference	Yersinia_pestis_CO92
all reads	348
nonDup	348
readDis	0.973
nonStacked	336
destacking?	On
C>T_1	0.2581
G>A_1	0
mean length (sd)	39 (8.211)

- Indicator default or ancient data used
- Node analysed
- Reference genome with most assigned reads
- Info about alignments to top reference genome:
  - all reads assigned in total
  - all reads after duplicate removal (same 3' & 5')
  - distribution of reads across reference genome (sum(covered bases)/sum(length all aligned reads) )
  - all reads without any stacking (overlap 1b or more)
  - are stacking reads removed?
- Damage terminal bases
  - 5' prime
  - 3' prime
- Read length distribution: mean (standard deviation)

Damage plot  
Based on all alignments assigned to interrogated node (plotted in figure title)

Top 10 Reference Genomes assigned to interrogated node.  
% of reads aligned are indicated relative to best reference genome.

Yersinia_pestis_CO92:_AL590842.1	100%
Yersinia_pestis:_CP009492.1	099%
Yersinia_pestis:_CP016273.1	099%
Yersinia_pestis_A1122:_CP002956.1	099%
Yersinia_pestis_A1122:_CP009840.1	099%
Yersinia_pestis:_CP009785.1	099%
Yersinia_pestis:_CP009844.1	099%
Yersinia_pestis:_CP009723.1	098%
Yersinia_pestis_Z176003:_CP001593.1	098%
Yersinia_pestis_D182038:_CP001589.1	097%