

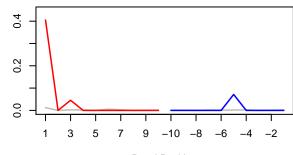
0

C2T/G2A rate

2 3

edit distance: default

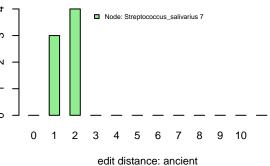
Damage plot for Streptococcus_salivarius node



Read Position

Streptococcus_salivarius;_NZ_CP066093.1 100%	
Streptococcus_salivarius_CCHSS3;_NC_015760.1 012%	
Streptococcus_salivarius_57.l;_NC_017594.1 012%	
NA%	

Pool-3-043-AZP-228_S47.unmapped.rma6



read count

10

Node	Streptococcus_salivarius
Top Reference	Streptococcus_salivarius
all reads	29
nonDup	26
readDis	0.916
nonStacked	24
destacking?	Off
C>T_1	0.4054
G>A1	0
mean length (sd)	66 (19.632)