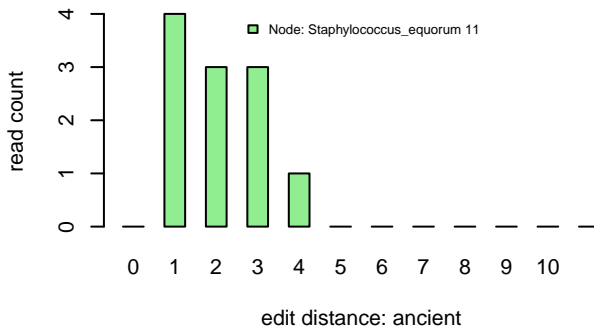


Pool-3-045-AZP-230_S49.unmapped.rma6



Line graph showing the C2T/G2A rate (Y-axis, 0.00 to 0.30) versus Read Position (X-axis, 1 to -2). The red line represents the C2T/G2A rate for the 1000 Genomes dataset, showing a high rate (up to 0.30) for positions 1-10, then dropping to near zero. The blue line represents the C2T/G2A rate for the 1000 Genomes dataset, showing a low rate (near 0.00) for positions 10-20. The grey shaded area represents the background rate.

Node	Staphylococcus_equorum
Top Reference	NA
all reads	39
nonDup	36
readDis	0.697
nonStacked	22
destacking?	Off
C>T_1	0.1437
G>A_-1	0
mean length (sd)	60 (16.805)

[illegible]