

Pool-1-031-AZP-110_S31.unmapped.rma6

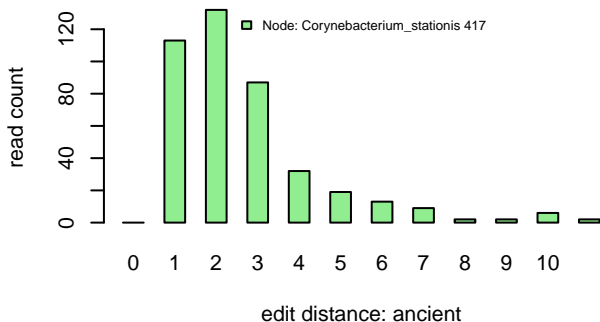


Figure 1: C2T/G2A rate vs Read Position for the 1000 Genomes dataset. The red line shows a high C2T/G2A rate on the positive strand, starting at ~0.14 at position 1 and dropping to ~0.01 by position 10. The blue line shows a low C2T/G2A rate on the negative strand, starting at ~0.005 at position -10 and fluctuating slightly around 0.01. A grey line at the bottom represents the background rate.

Node	Corynebacterium_stationis
Top Reference	Corynebacterium_stationis
all reads	4588
nonDup	3852
readDis	0.838
nonStacked	2712
destacking?	Off
C>T_1	0.1504
G>A_1	0.0128
mean length (sd)	67 (16.013)

[illegible]