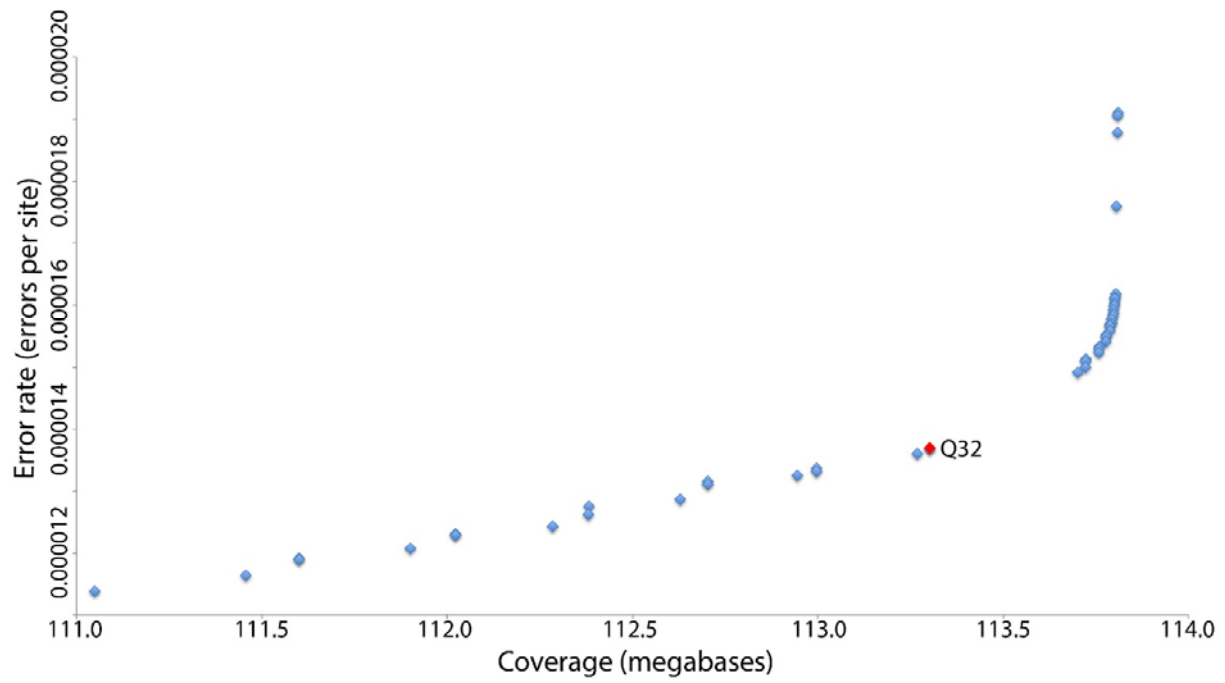Figure S4

Figure S4 Evaluation of the tradeoff between genomic coverage and error rate for the diploid caller of the Unified Genotyper; quality values ranged from 10 to 100. Resequenced genomes from the reference strain (y^1 cn^1 bw^1 sp^1) were modified to simulate realistic levels of variation. We chose a cutoff of Q32 (red) to maximize coverage and minimize error.