

SUPPLEMENTARY FIGURES

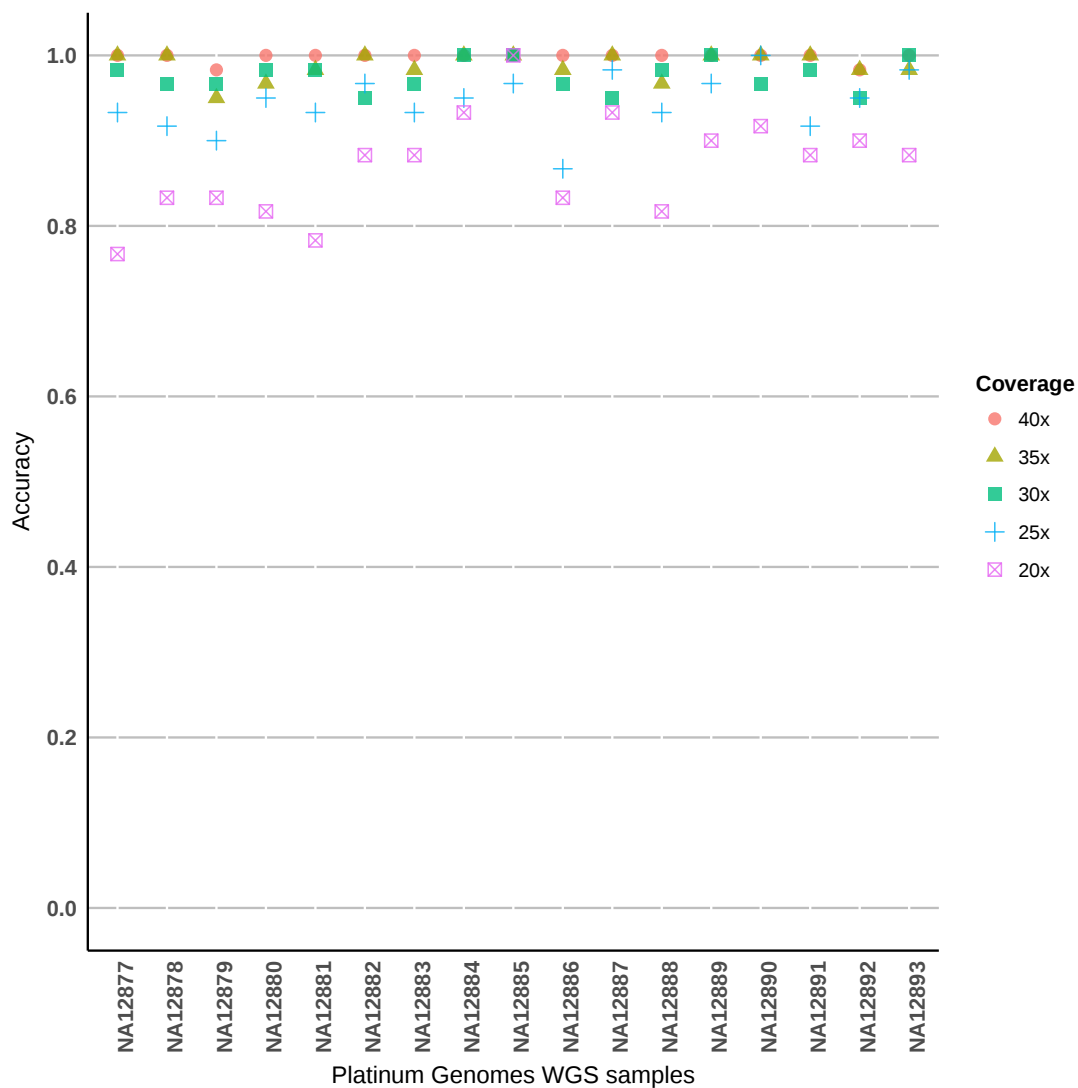


Figure S1. Sample-specific typing accuracy of Kourami across varying coverages for 17 Platinum Genomes. Each data point represents the fraction of correct calls across 5 replicates. The total number of calls is 60 (5 replicates $\times$ 12 calls) per data point.

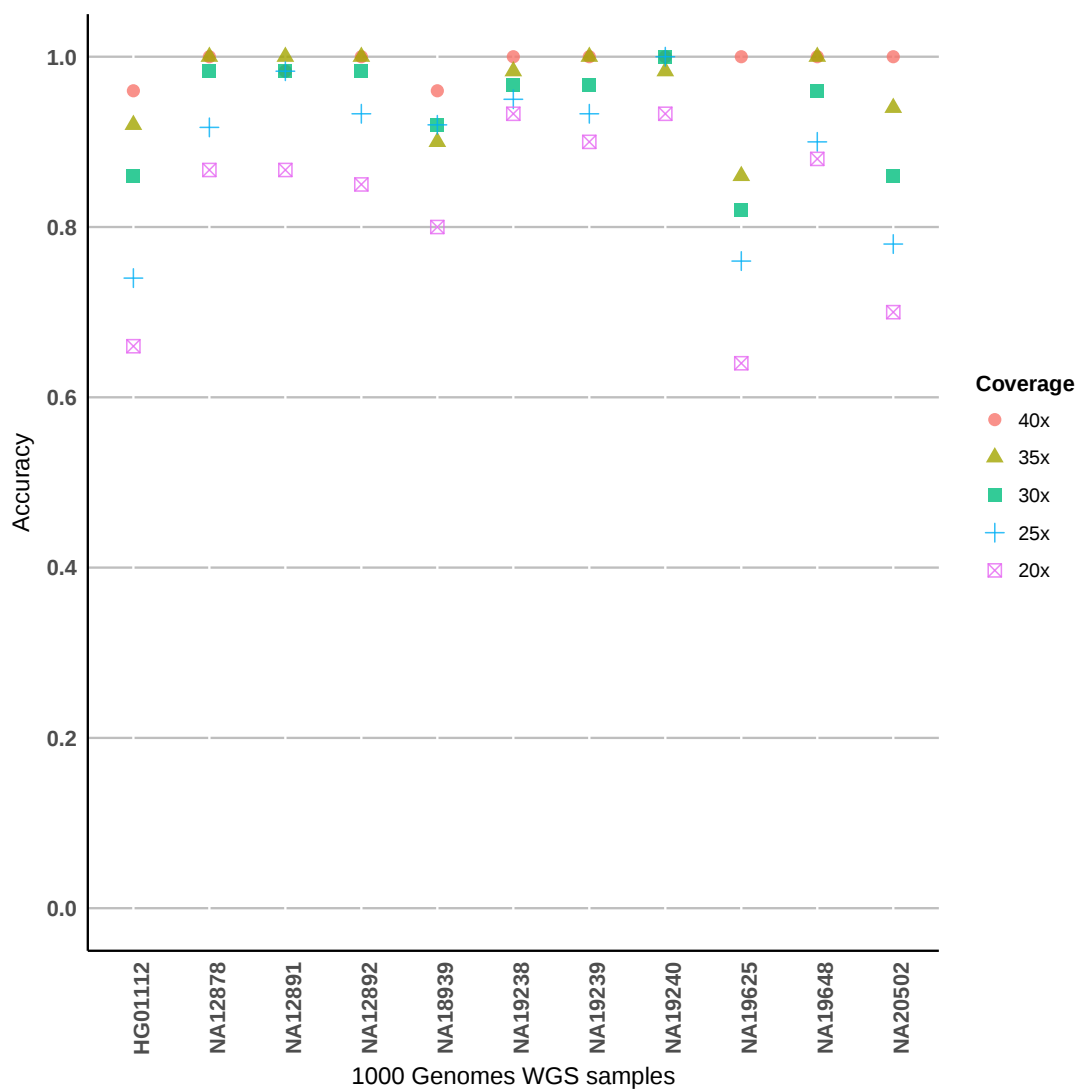


Figure S2. Sample-specific typing accuracy of Kourami across varying coverages for 11 samples from 1000 Genomes. Each data point represents the fraction of correct calls across 5 replicates. The total number of calls is 60 (5 replicates $\times$ 12 calls) for the Utah resident trio and 50 (5 replicates $\times$ 10 calls) for the Yoruban trio per data point.

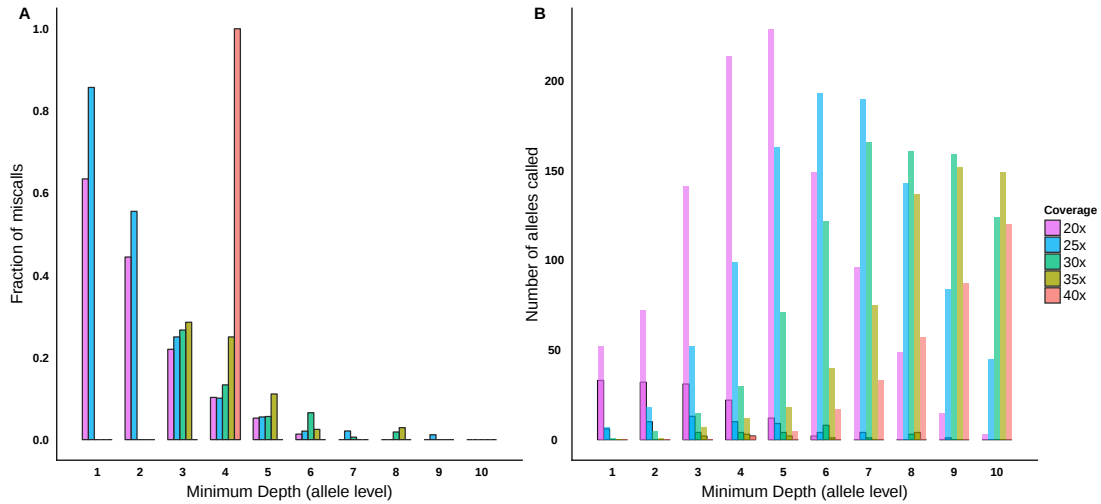


Figure S3. Incorrect calls at allele-specific minimum depths across varying coverages for 17 Platinum Genomes. Panel A shows the fraction of incorrect calls at varying allele-specific minimum depths across varying coverages. Panel B shows the total number of incorrect calls (black border) in front of the total number of alleles (no border, lighter shade) called at varying allele-specific minimum depths across varying coverages. The high peak at 40x coverage for minimum depth of 4 is caused by the small number of total calls made (see the corresponding bar on Panel B). Minimum depths on the x-axis are only shown up to 10 as the calls with larger minimum depths are all correct.

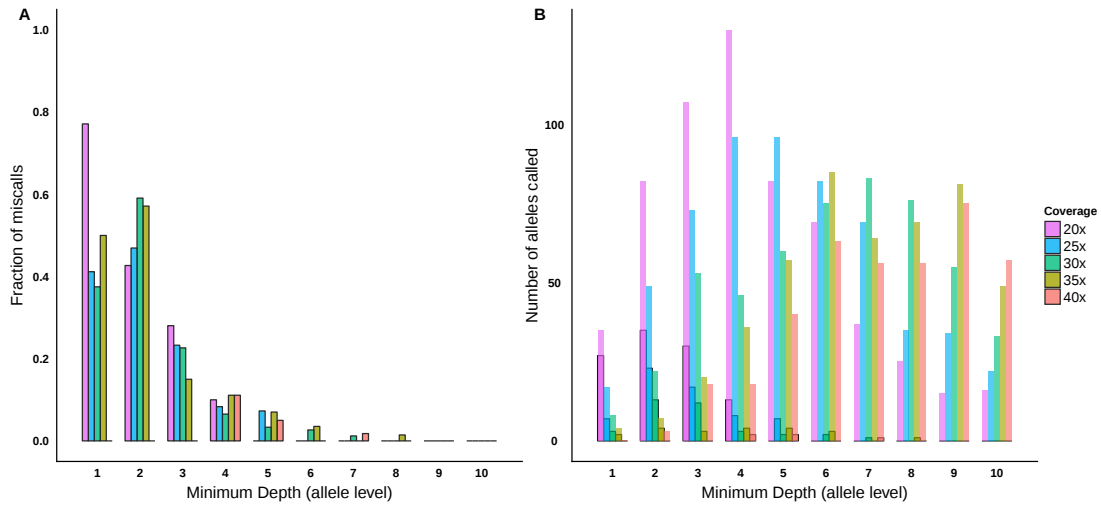


Figure S4. Incorrect calls at allele-specific minimum depths across varying coverages for 11 samples from 1000 Genomes. Panel A shows the fraction of incorrect calls at varying allele-specific minimum depths across varying coverages. Panel B shows the total number of incorrect calls (black border) in front of the total number of alleles (no border, lighter shade) called at varying allele-specific minimum depths across varying coverages. Minimum depths on the x-axis are only shown up to 10 as the calls with larger minimum depths are all correct.