

S1 Table. Post-QC sequencing call concordance between replicates.

Variant Type	Variants (mean)	Call concordance
All Variants	4,284,228	0.9985
SNPs	3,793,694	0.9997
Common SNPs (MAF > 0.05)	3,244,661	0.9997
Low Frequency SNPs (0.01 > MAF ≤ 0.05)	383,918	0.9995
Rare SNPs (MAF ≤ 0.01)	165,115	0.9995
InDels	490,534	0.9892
Common InDels (MAF > 0.05)	428,621	0.9896
Low Frequency InDels (0.01 > MAF ≤ 0.05)	39,572	0.9845
Rare InDels (MAF ≤ 0.01)	22,340	0.9911

Variant call concordance between three pairs of replicate samples, by variant type and cohort allele frequency. SNPs, single nucleotide polymorphisms; MAF, minor allele frequency; InDels, insertions and deletions.