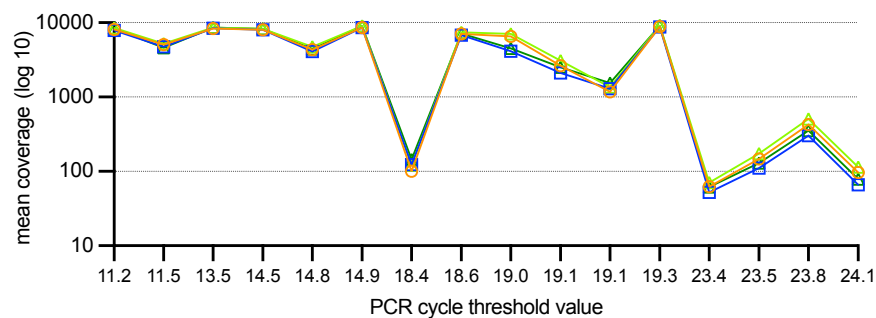
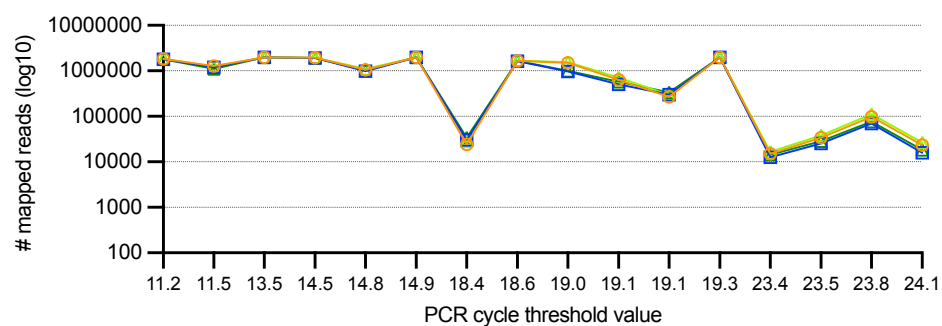
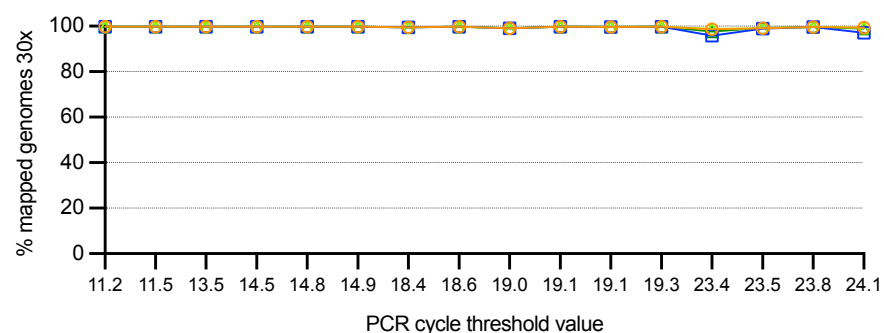
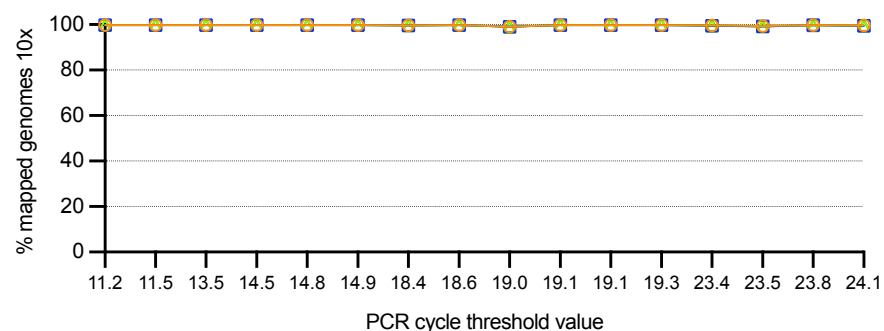
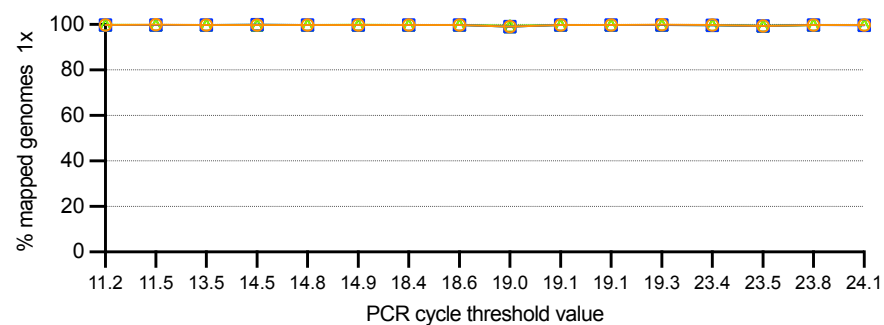




- standard SPRI and 1x reaction volume
- standard SPRI and 1.6x reaction volume
- △— stringent SPRI and 1.6x reaction volume
- △— stringent SPRI and 1x reaction volume

Figure S9 - Correlation between Ct value and reference mapping performance metrics

Relationship between PCR cycle threshold (Ct) values and sequencing outcomes for 16 SARS-CoV-2-positive clinical samples from the Pilot 3 study, processed with the in-house RVI-seq bait capture method. Pilot 3 evaluated two solid-phase reversible immobilisation (SPRI) bead conditions, standard SPRI and stringent SPRI in combination with two cDNA synthesis reaction volumes (1× and 1.6×). Sequencing performance metrics include the proportion of the genome covered at 1×, 10×, and 30× depth, total mapped reads, and mean coverage.