

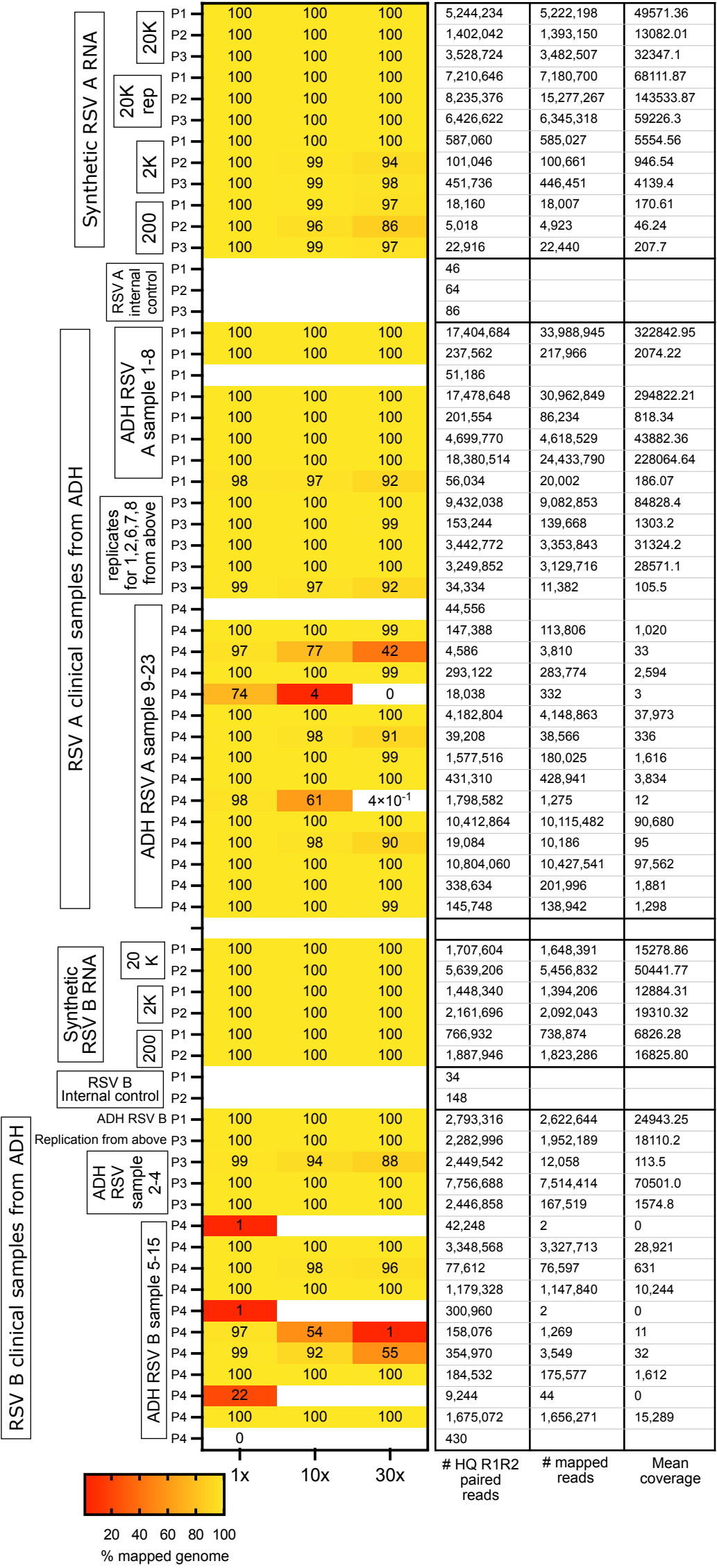


Figure S11 - Validation of synthetic and clinical RSV A and B samples

High-quality paired-end reads (minimum read length ≥70 bp) were mapped to a panel of RSV A and B reference genomes using minimap2. The mapping results using reference strains RSV A_EPI_ISL_412866 and RSV B_EPI_ISL_1653999 are shown here. Mapping results are shown for both synthetic and clinical samples at 1×, 10×, and 30× depth. The number of high-quality forward (R1) and reverse (R2) reads, mapped reads, and mean coverage are summarised in adjacent tables. Genome coverage proportions were calculated with Qualimap and visualised as heat maps. Abbreviations: P1–P4 = 96-well production plates 1–4; ADH = Addenbrooke's Hospital, Cambridge; RSV = respiratory syncytial virus.