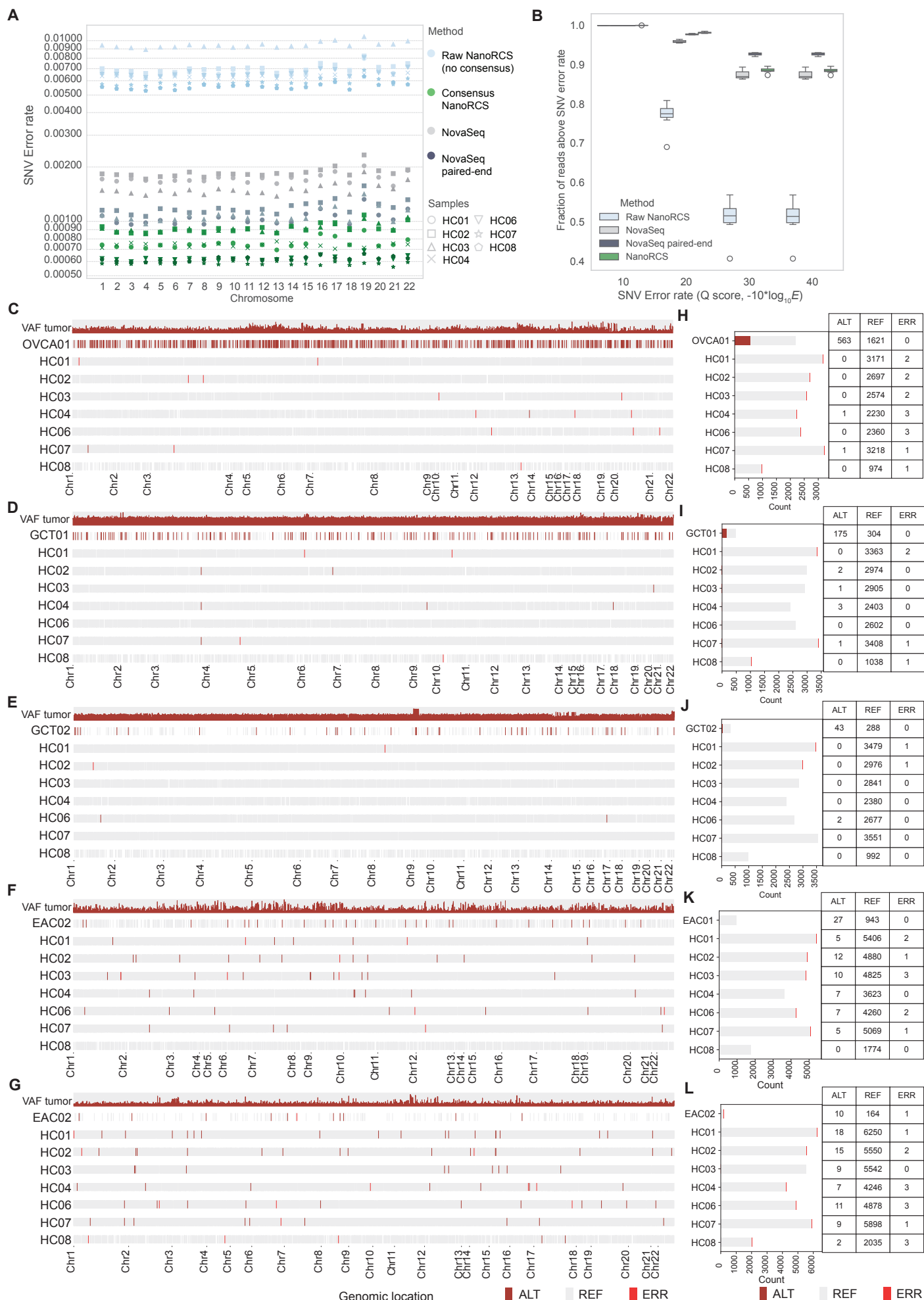




Supplementary Figure S2. NanoRCS enables confident SNV detection on Nanopore.

(A) Single-nucleotide error rate per chromosome in cfDNA of seven healthy controls using different sequencing methods. (B) Fraction of reads with read quality of at least phred score of 30, 40, 50, 60 (equivalent to SNV error rate of 1 in 103, 1 in 104, 1 in 105 bases) in different sequencing methods. (C-G) SNV observations in the five liquid biopsy samples with known tumor somatic SNV profile. For each panel, the top row shows the VAF of detected mutations in the tumor biopsy, the second row represents the MUT or REF allele observations in the liquid biopsy of the corresponding patient, and the bottom seven rows represent the observations in seven healthy controls (not downsampled). (H-L) Raw counts of SNV observations corresponding to the data shown in (C-G).