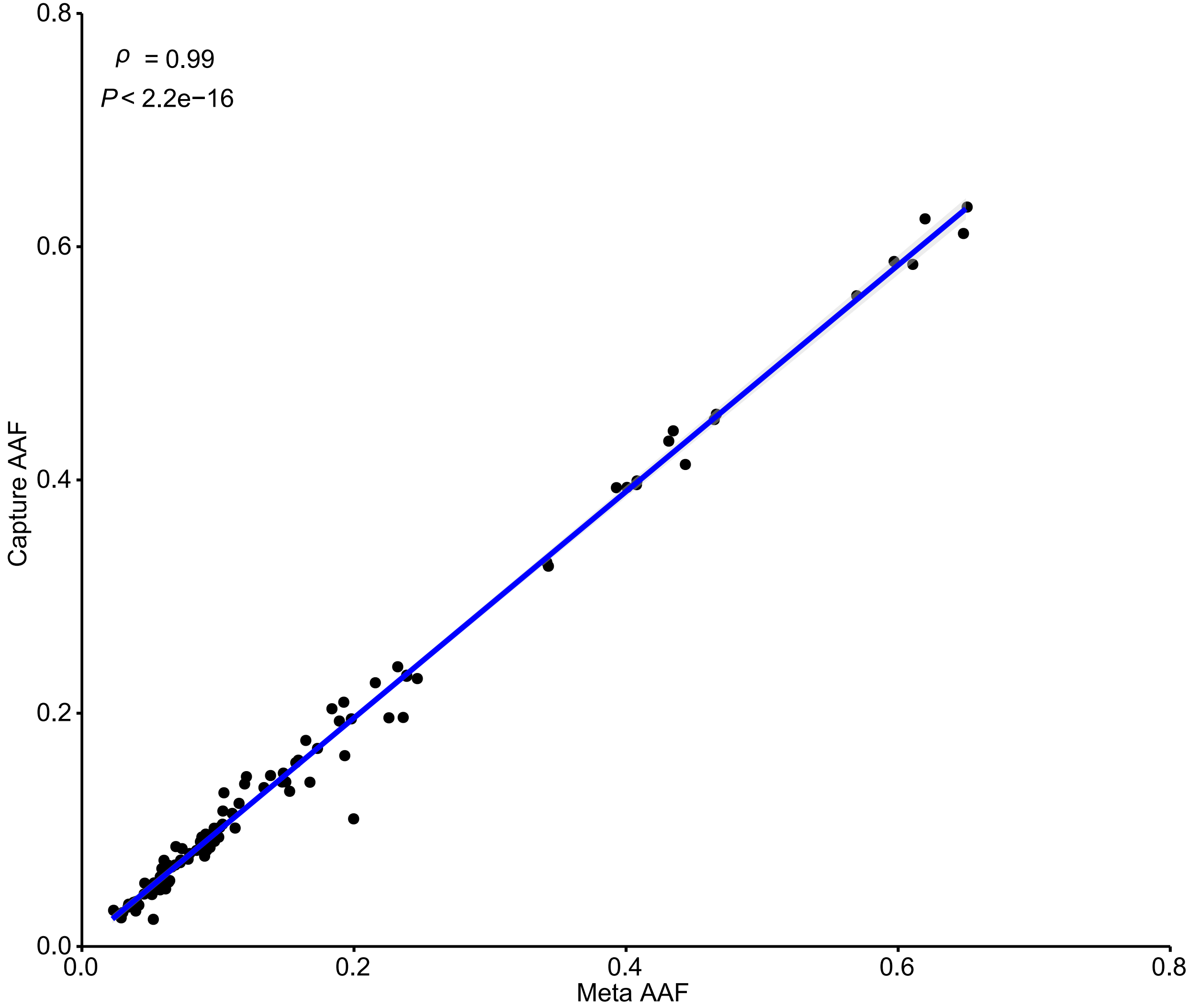

Fig. S1 Correlation of estimated alternative allele frequencies between metatranscriptomic and hybrid capture data.

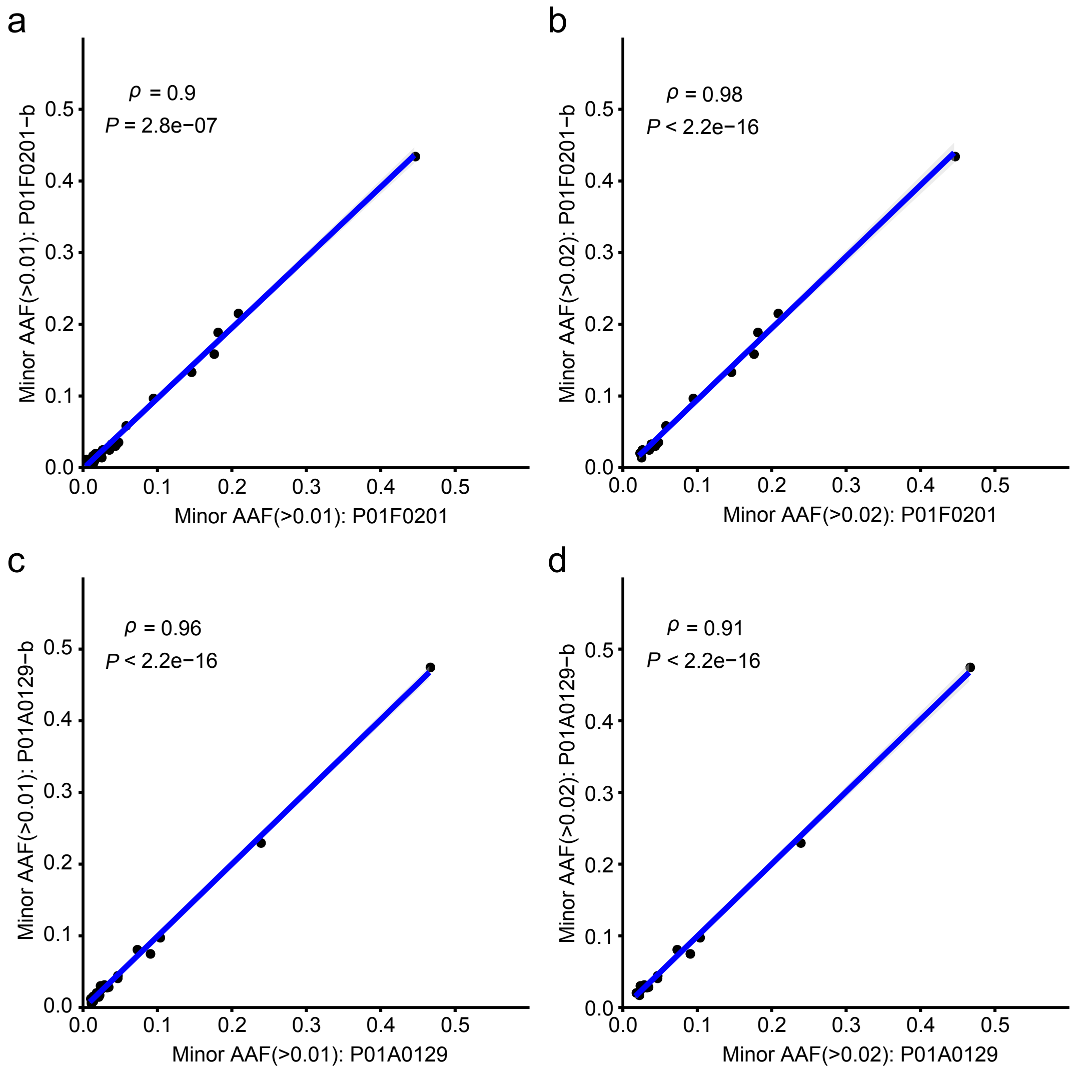

Fig. S2 Correlation of estimated minor alternative allele frequencies between biological replicates.

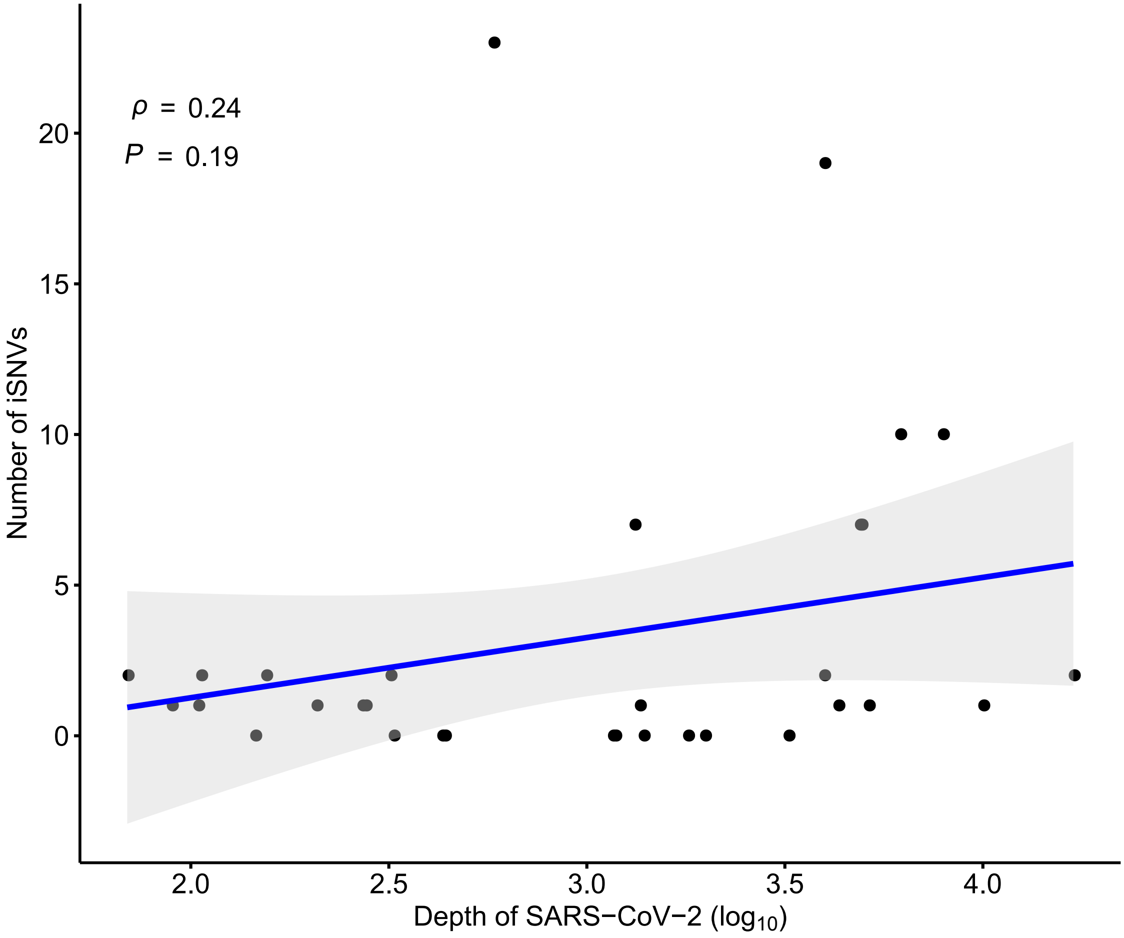

Fig. S3 Correlation between sequencing depth and detected iSNVs.

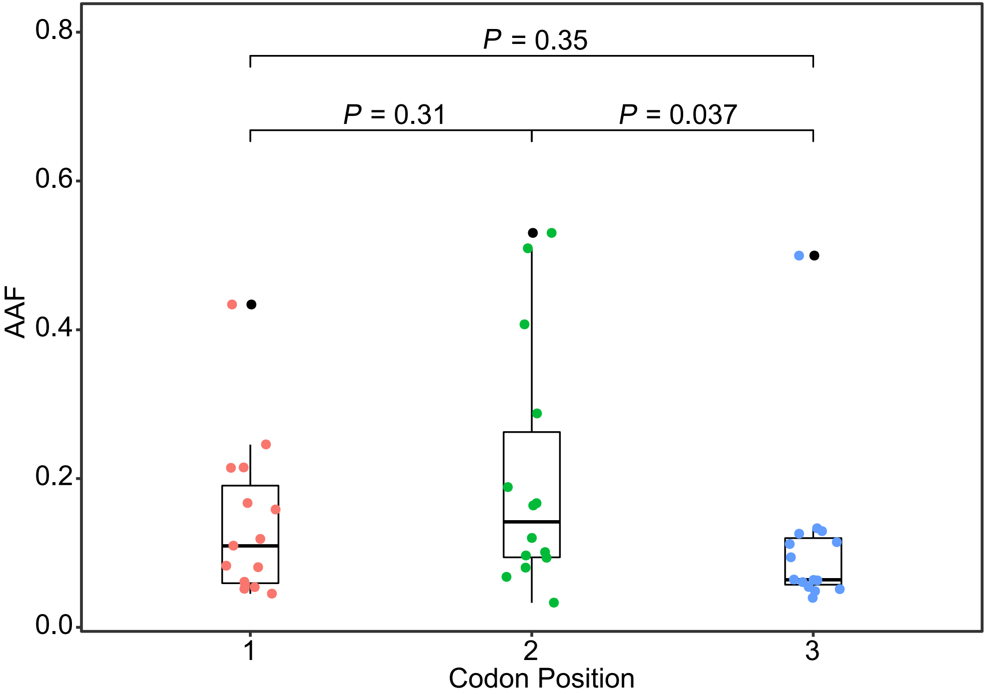

Fig. S4 Number of iSNV among three codon positions.

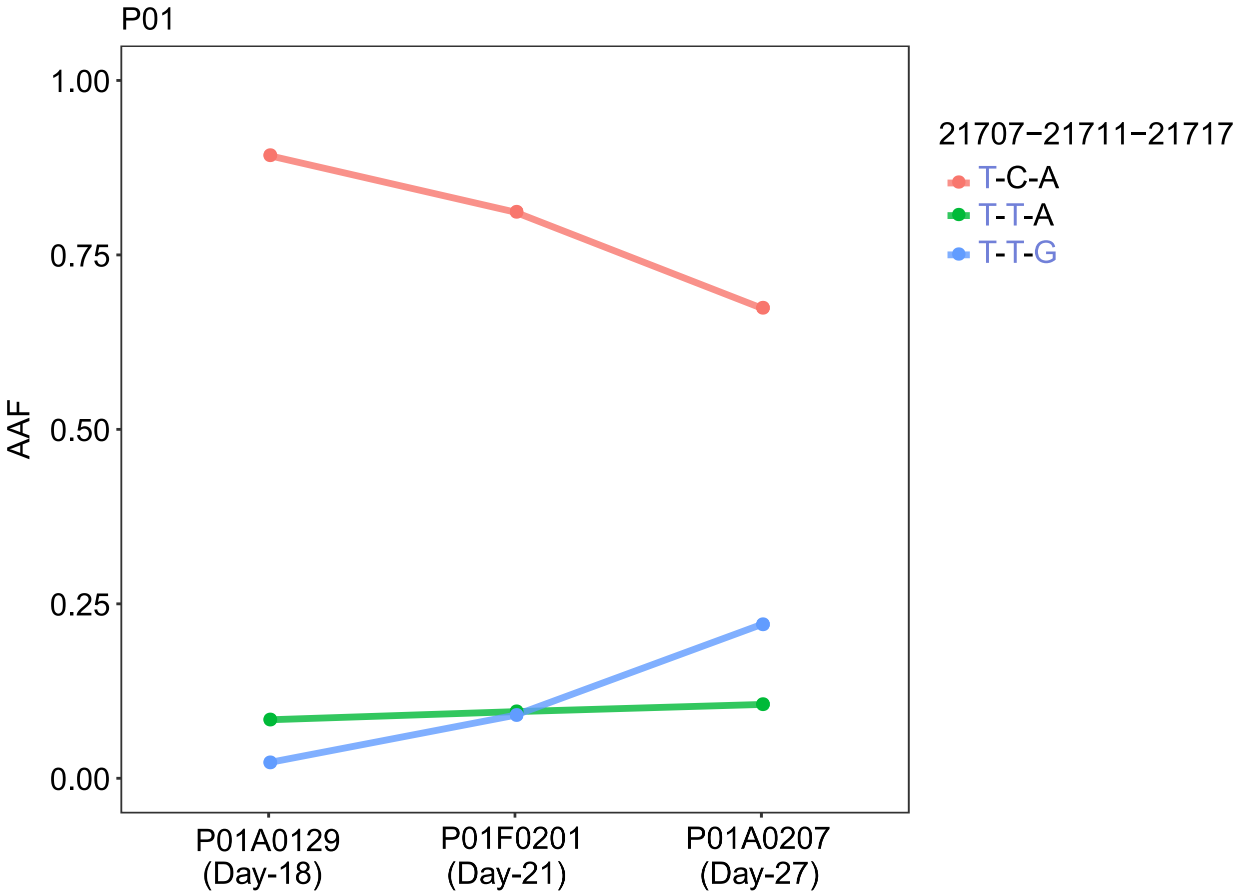

Fig. S5 Haplotype frequency of proximal iSNVs within the gastrointestinal tract of patient P01