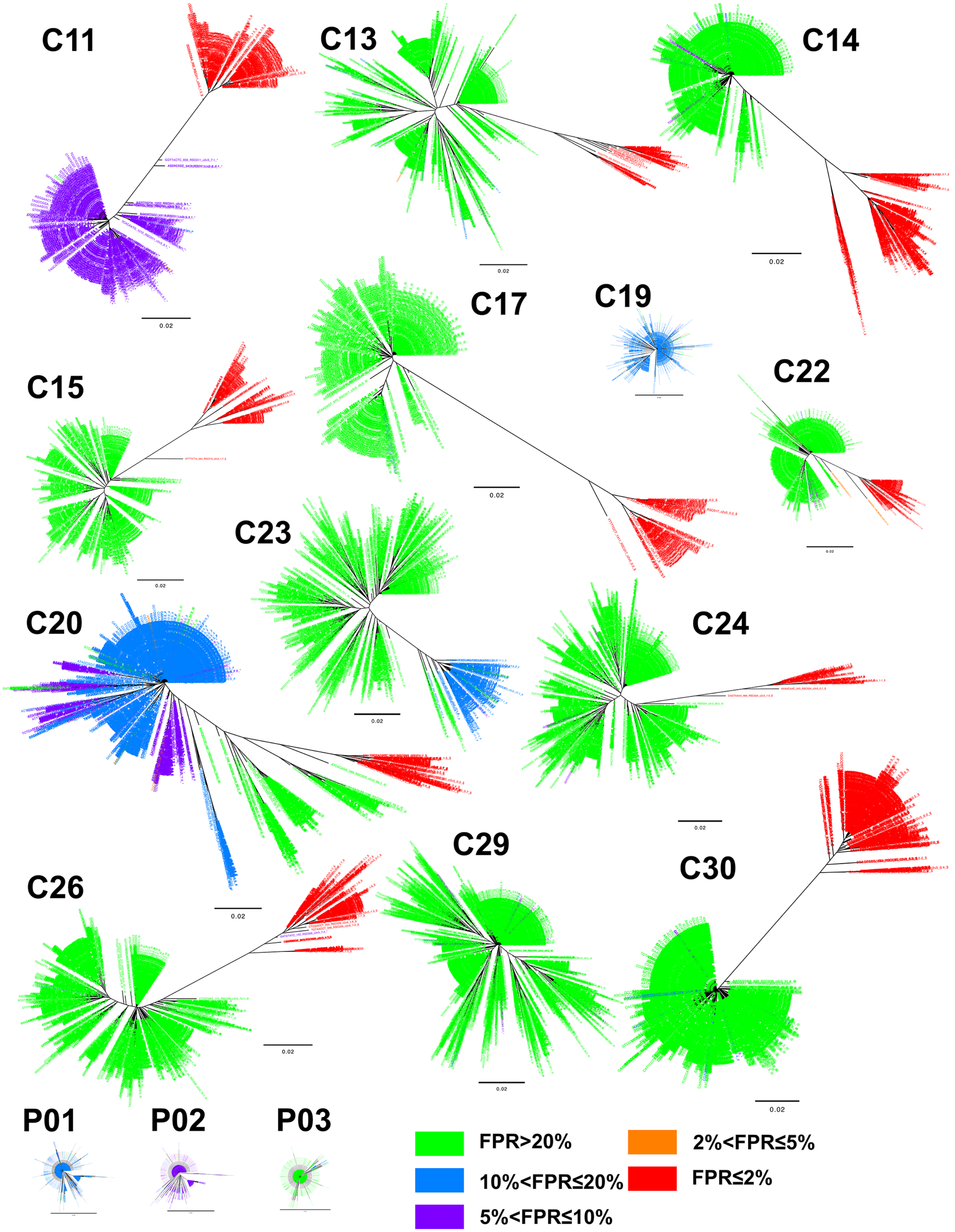
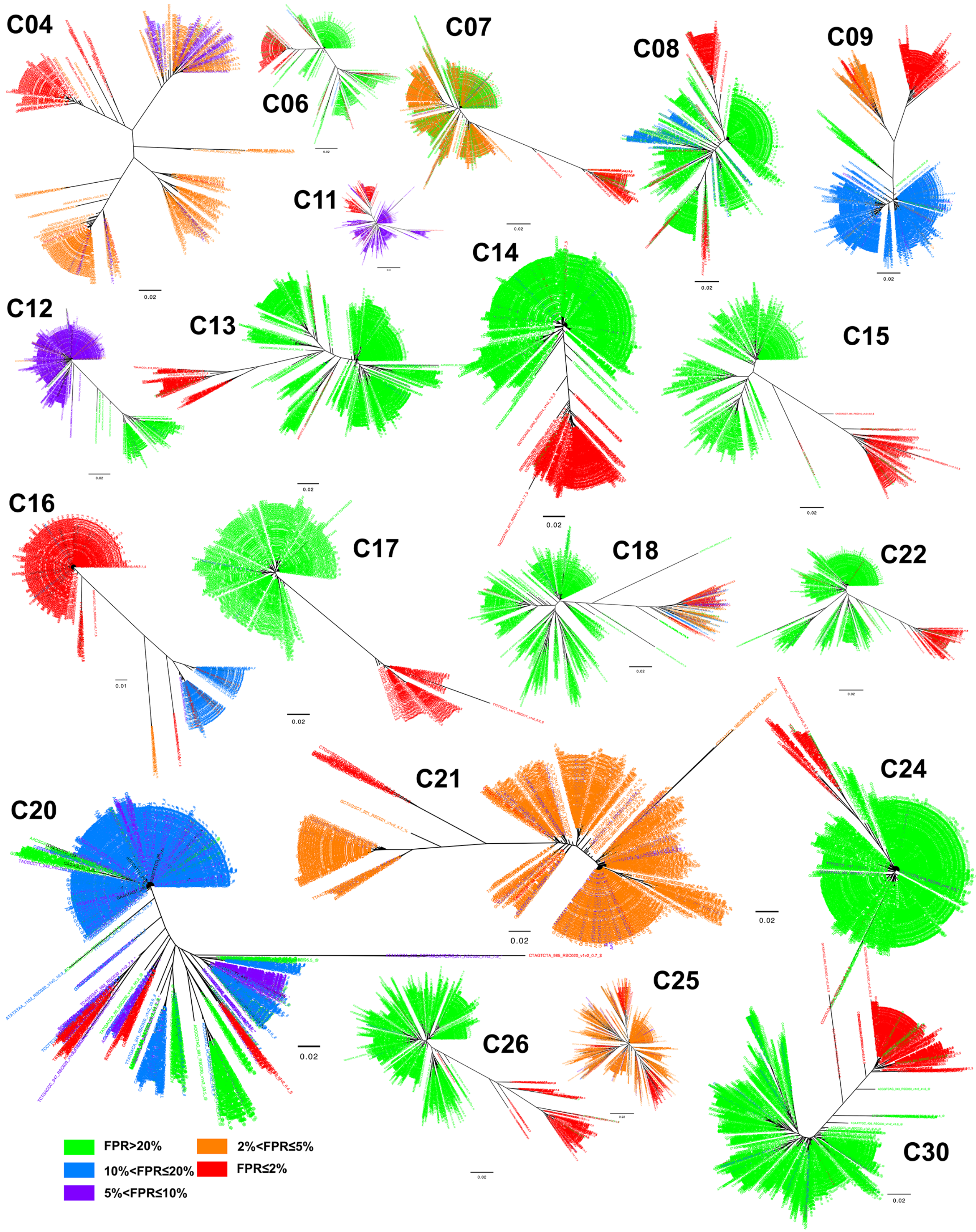


Supplementary Figure 1 Phylogenetic trees of C2/V3 region of study samples showing different level of Geno2pheno$_{[CORECEPTOR]}$ false positive rate (FPR) among viral population. Color of taxa names indicates level of FPR: red, FPR ≤ 2%; orange, FPR 2-5%; purple, FPR 5-10%; blue, FPR 10-20%; green, FPR > 20%. The unit of the scale bar of the phylogenetic trees is nucleotide substitutions per site.



Supplementary Figure 2 Phylogenetic trees of C1/V2 region of study samples with mixed X4/R5 variants, showing different level of Geno2pheno$_{\text{[CORECEPTOR]}}$ false positive rate (FPR) among viral population based on the corresponding C2/V3 sequences. Color of taxa names indicates level of FPR: red, FPR ≤ 2%; orange, FPR 2-5%; purple, FPR 5-10%; blue, FPR 10-20%; green, FPR > 20%. The unit of the scale bar of the phylogenetic trees is nucleotide substitutions per site.