Supplementary Material. Definition of quasispecies complexity indices

Number of haplotypes (nHpl) is defined as the number of unique sequences in a set of all reads (sequences obtained by next-generation sequencing).

Number of mutations (nMuts) is the number of different mutations observed in the multiple sequence alignment of all haplotypes with respect to the dominant or master haplotype.
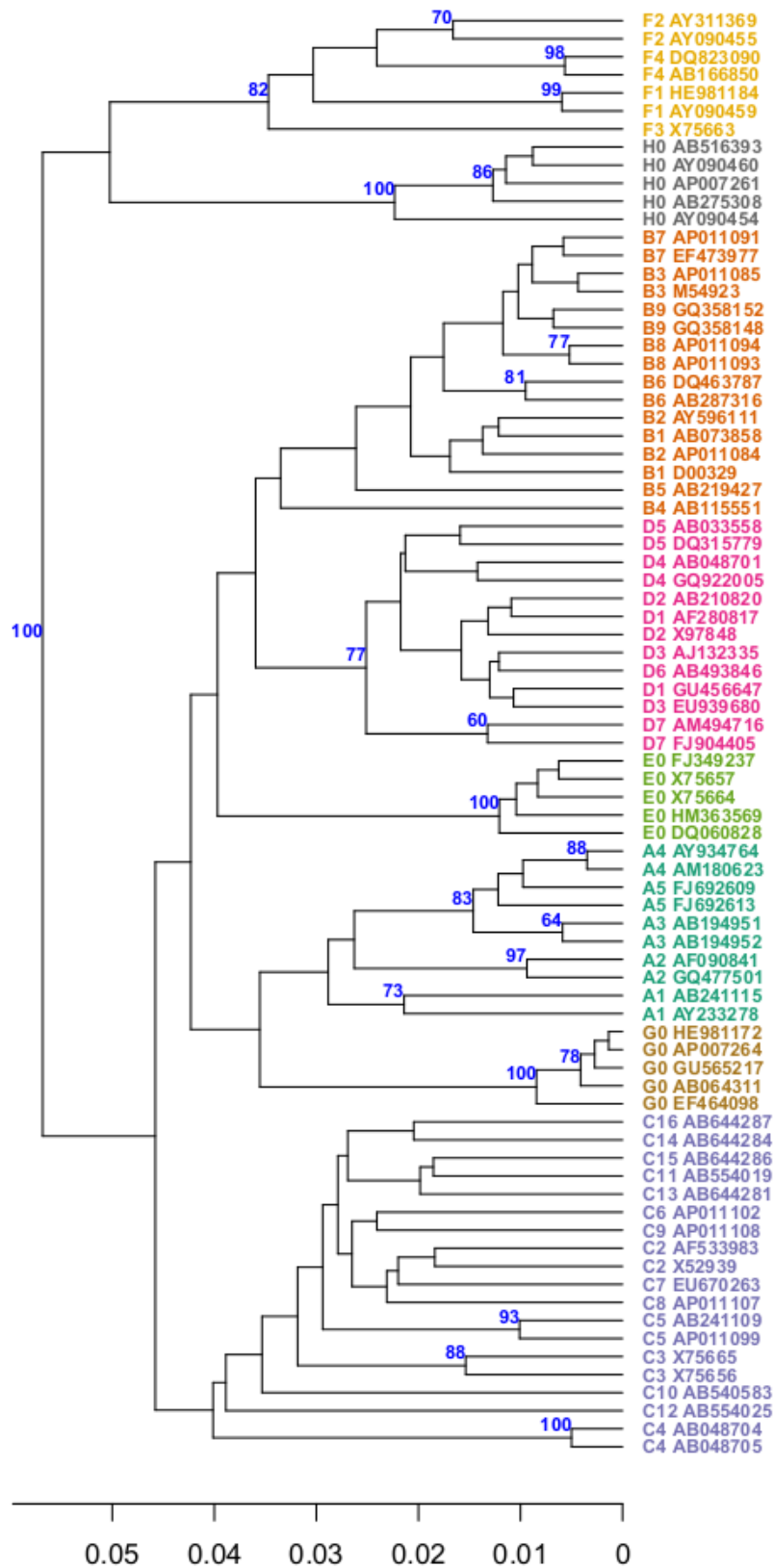
Hill numbers represent the effective number of species, with an exponent of order q, 'the order' of the diversity measure, which influences the sensitivity of the diversity index with respect to the rare haplotypes in the quasispecies. To characterize species diversity, we used the exponential of Shannon's entropy index (q=1) and the inverse of Simpson's index (q=2). These numbers are favored because they exhibit the doubling property, are less prone to saturation, and have common units with an intuitive meaning: number of equally abundant haplotypes that show the same diversity measures as the sample being examined.

Mutation frequency (Mf) is the fraction of nucleotides in the quasispecies that differ with respect to those of the most abundant haplotype in the sample.

Nucleotide diversity (Pi) is expressed as the mean fraction of different nucleotides between all pairs of molecules in the sample.

The equations used to calculate these indices can be found at: Gregori J, Perales C, Rodriguez-Frias F, Esteban JI, Quer J, Domingo E. Viral quasispecies complexity measures. *Virology* [Internet] 2016 [cited 2018 Jan 26];**493**:227–37 [DOI: 10.1016/j.virol.2016.03.017]

Supplementary Figure 1. Phylogenetic analysis of HBV genotyping reference sequences extracted from nucleotides 1255 to 1611 of GenBank full-length hepatitis B virus genomes. The UPGMA trees were designed to visualize the genetic distances between sequences (blue numbers).

Supplementary Figure 2. Phylogenetic analysis of HDV genotyping reference sequences extracted from nucleotide 910 to 1270 of GenBank full-length hepatitis delta virus genomes. The UPGMA trees were designed to visualize the genetic distances between sequences (blue numbers).