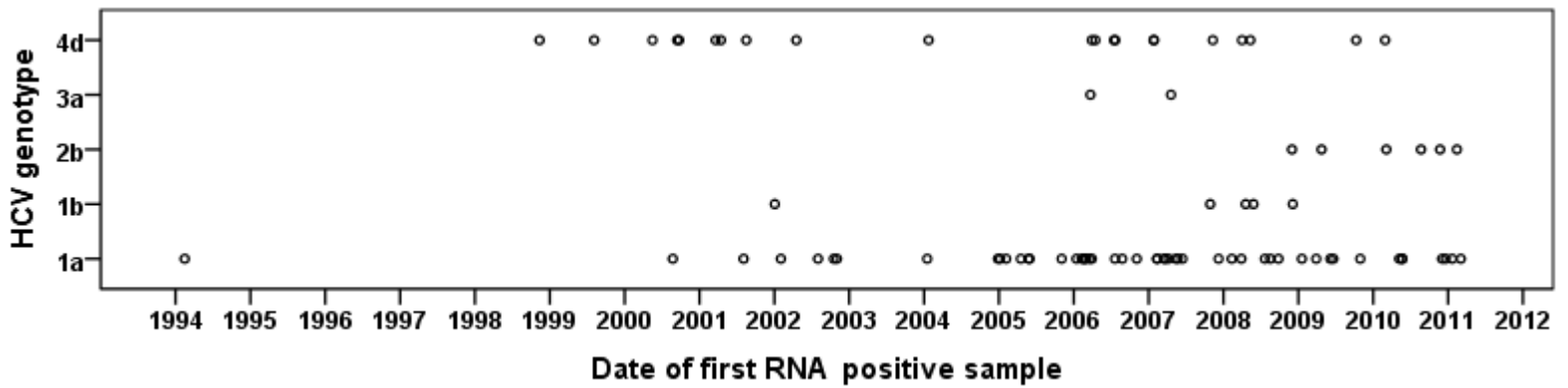


SUPPLEMENT FIGURE LEGENDS

Supplement figure 1. Date of first HCV RNA positive sample. First HCV RNA positive samples from all primary infections are depicted with open bullets. Genotypes are indicated on the y-axis.



6

7 **Supplement figure 2. Maximum likelihood phylogeny of HCV genotype 1a.** ML-tree of all

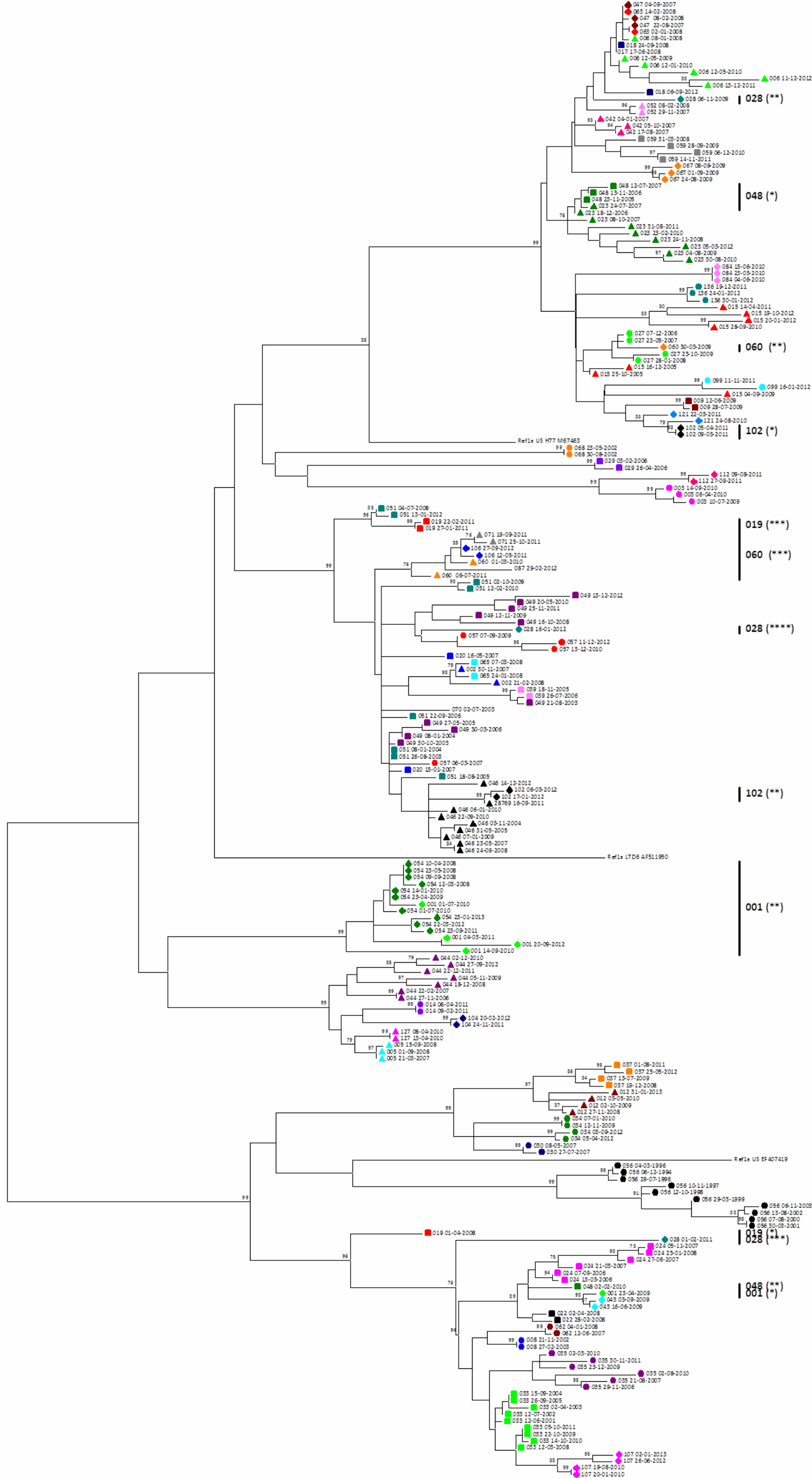
8 E2/HVR1 HCV-1a sequences. Bootstrap values ≥ 75 indicative of well-supported clades are

9 shown. Symbols are patient specific. Tip labels denote patient code followed by sampling date.

10 Multiple HCV-1a infections in the same patients are indicated on the right of the phylogenetic

11 tree. Number of asterisks behind patient code indicates the number of infection.

12



Supplement figure 3. Maximum likelihood phylogeny of HCV genotype 4d. ML-tree of all

E2/HVR1 HCV-4d sequences. Bootstrap values ≥ 75 indicative of well-supported clades are

shown. Symbols are patient specific.

