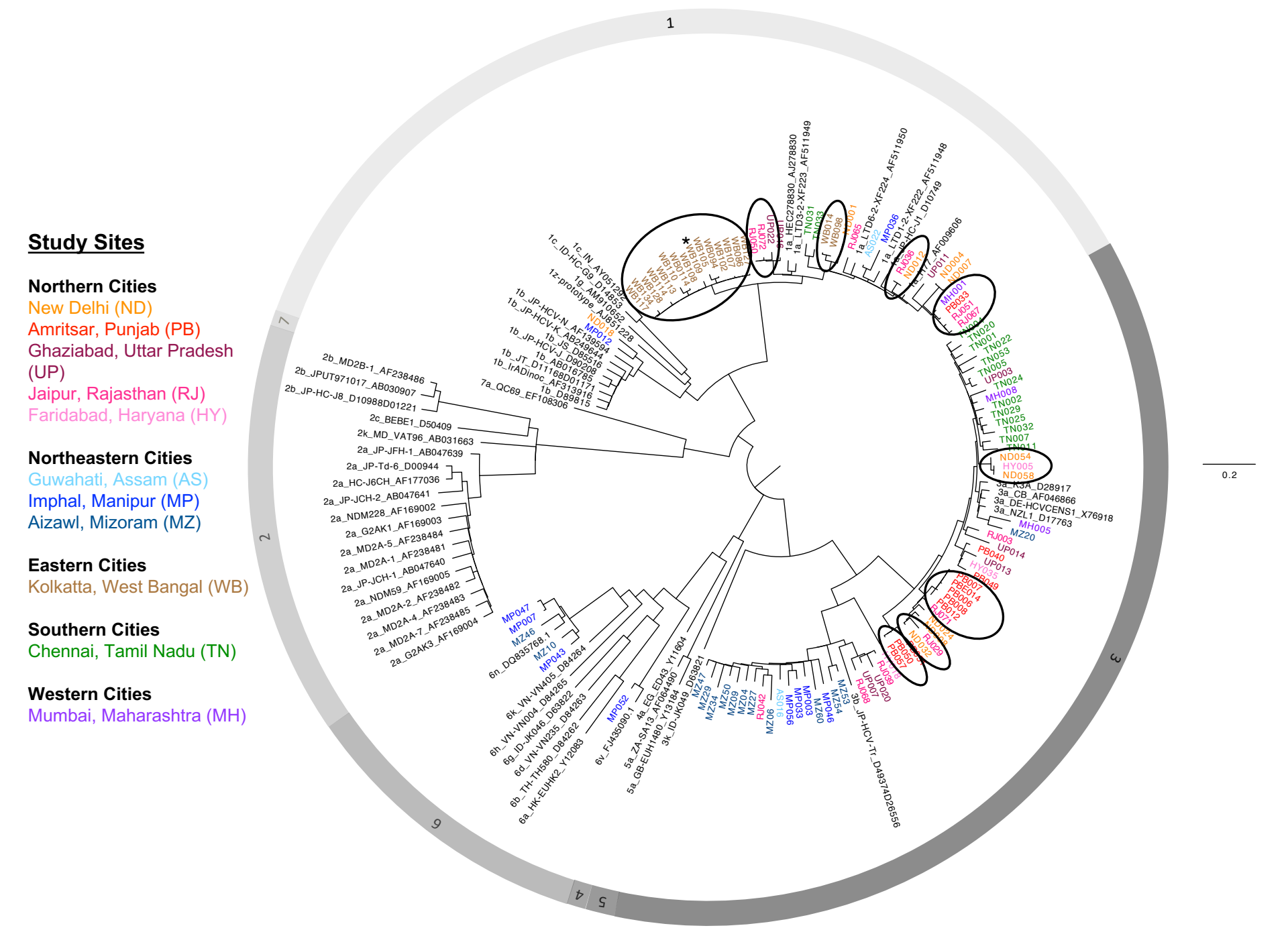
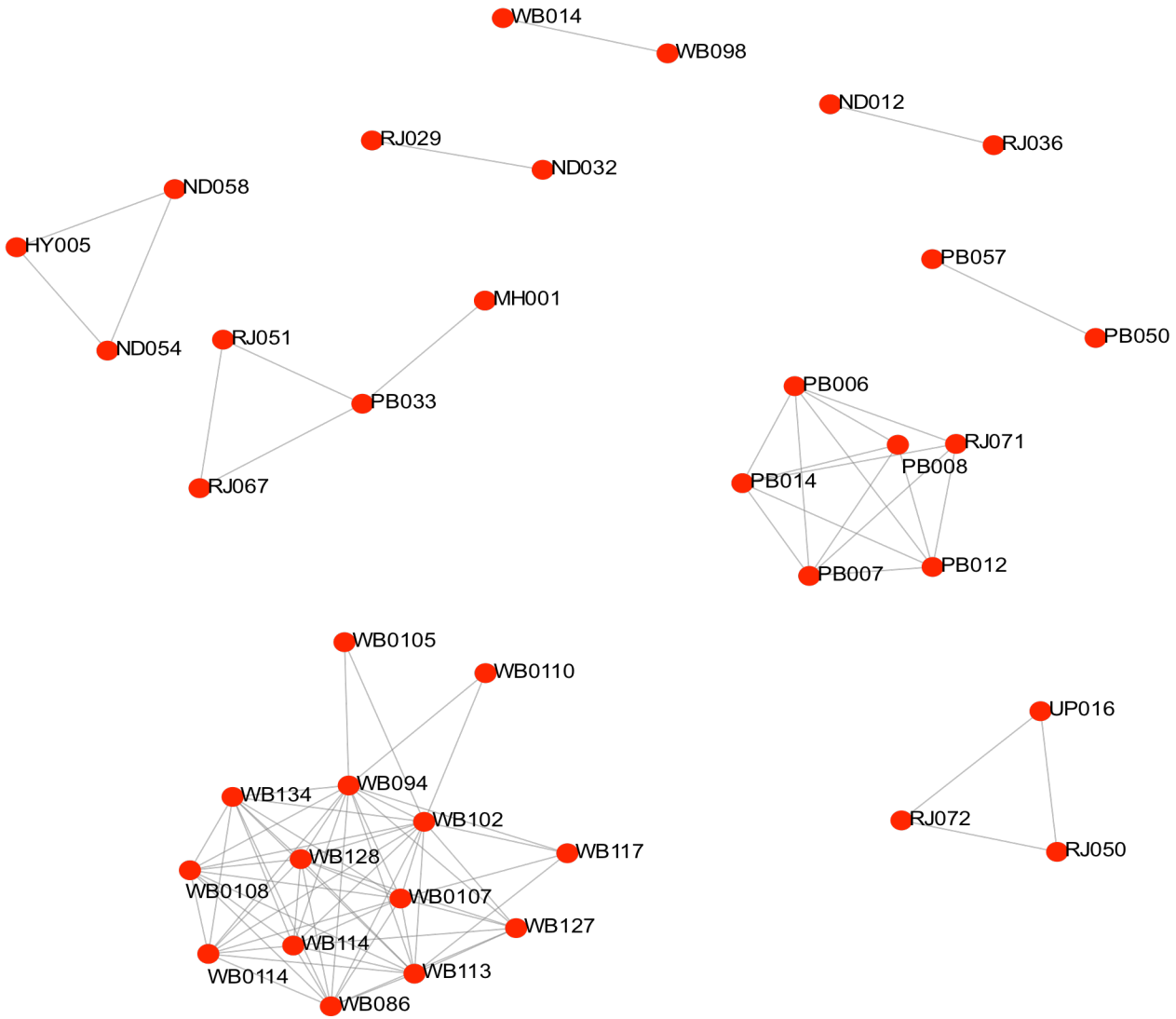


Online Resource 2. Phylogenetic tree of HCV sequences from 105 participants in 8 study sites with clusters designation. Phylogenetic tree was inferred by maximum-likelihood reconstruction with 1000 bootstrap replicates based on the nucleotide alignment of the core/E1 sequences as implemented in the MEGA version 6 package. Clusters were determined using a genetic distance threshold of 4% using MicrobeTRACE v1.9



Online Resource 3. Genetic clusters identified using a genetic distance threshold of 4% (MicrobeTRACE version 1.9)