Supplemental Data

Supplemental Data: **Reconstructed most recent common ancestor to hepatitis C virus genotype 1a.** Sequence was reconstructed by maximum-likelihood phylogenetic analysis of codons 9 through 174 of non-structural protein 3 (NS3).

CAGACAAGGGGCTCTCTAGGGTATAATCACCAGCCTGAACCGCCGCCGCCACAAAAA
CCAAGTGGAGGGTGAGGTCCAGATTGTGTACAATGCTGCCGAGACCTCCTGGCAAC
ATGCATCAATGGGGTGTGCTGGACTGTCTACCACGCGGCGGAACGAGGACCACCATCG
CATCACCCCAAGGGTCCTTATCCAGATGTATACCAATGTAAGCACAAGACCTCGTAG
GCTGCCGGCCTCCTCAAGGGTCCCCGCTCATGGACACCCTGCACTTCGCGGCTCCTCGG
ACCTTTACTTGGTGCTACGGACAGCCGATTCGCTATTCCCGTGCGCCGCCGCGGGGTGATA
GCAGGGGCACCTGCTTTTGCCGCCCCGGCCTTTCTTACTTGAAGGGCTCTTCGGG
GTCCGCTGTGCTGCCCGCGGGACACGGCGTAGGGCATATTCCAGGGCCGGCGGTTGCA
CCCGTGGAGTGGCTAAGGGCCTGGAACCTTTATCCCTGTGGAGAGC
Supplemental Figure Legends

Figure S1: Kernel density of pairwise distances of publicly available NS3 sequences. A kernel density is similar to a histogram, but normalized and smoothed. We took the spike on the left tail to indicate clonal sequences from within the same individual. The cutoff of 0.04 used to filter out these sequences is indicated by a dotted line.

Figure S2: Hepatitis C virus lineages carrying known drug resistance mutations in non-structural protein 3 in a global phylogeny. None of these mutations has a deep common origin, in contrast to Q80K.