Supplemental Data

Figure S1. Highlighter plot of 5' half genome sequences from Donor A, Recipient AK1, and Recipient AK2

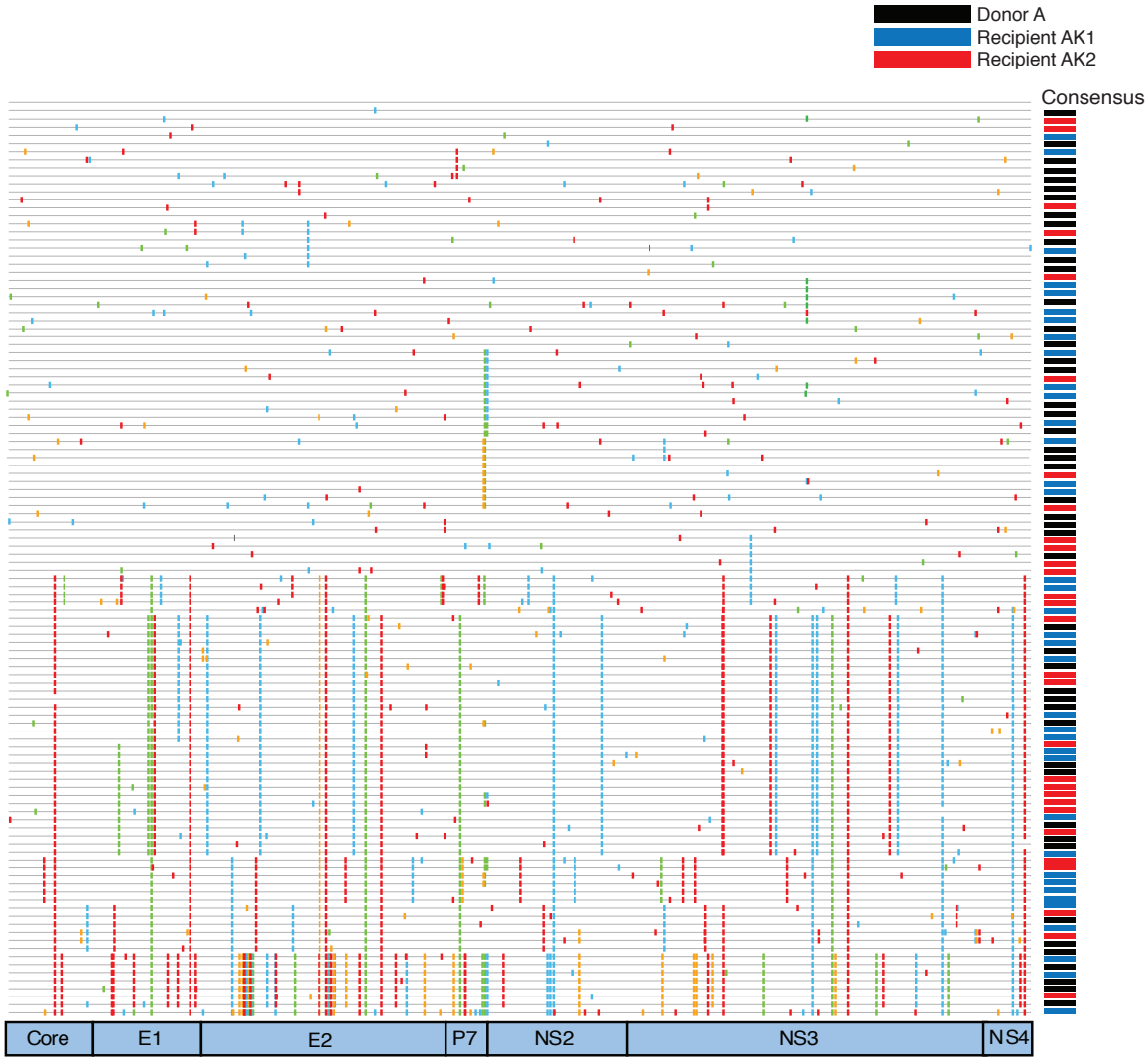
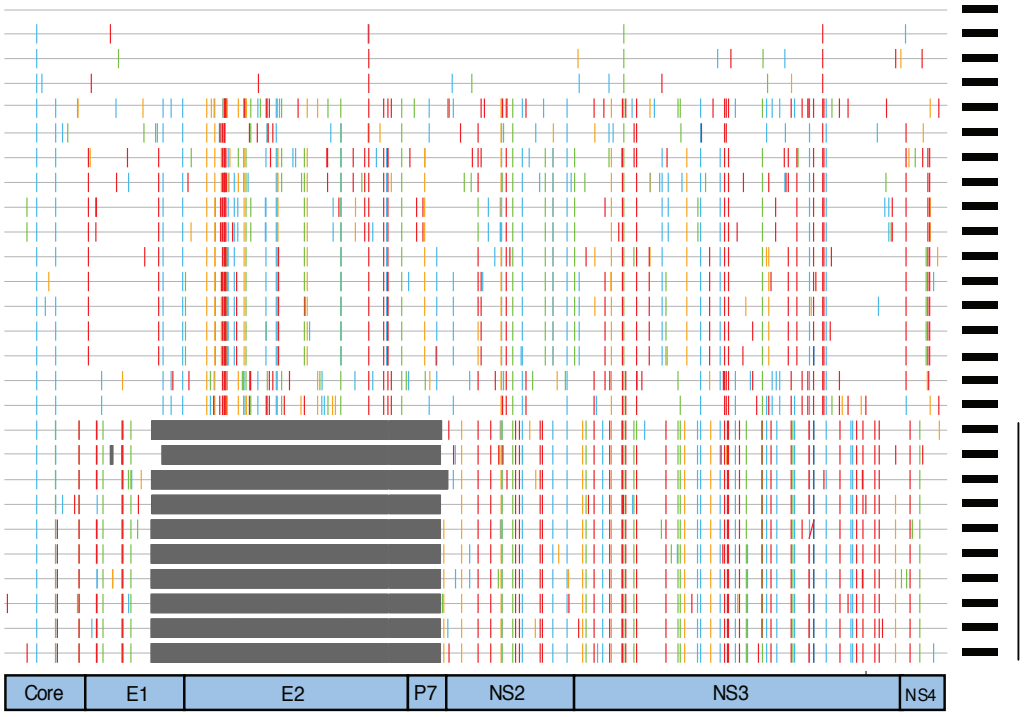


Figure S1. The consensus of all displayed sequences is shown at the top, with individual sequences displayed as horizontal lines below, labeled by color-coded bars. Each nucleotide difference from the consensus sequence is shown as a colored tic (green: A, red: T, blue: C, yellow: G). Viral sequences from the donor and two recipients are interspersed throughout the lineages.

Figure S2. Highlighter plot of 5' half genome sequences from Donor D and the Donor D 'deleted lineage'

A.



B.

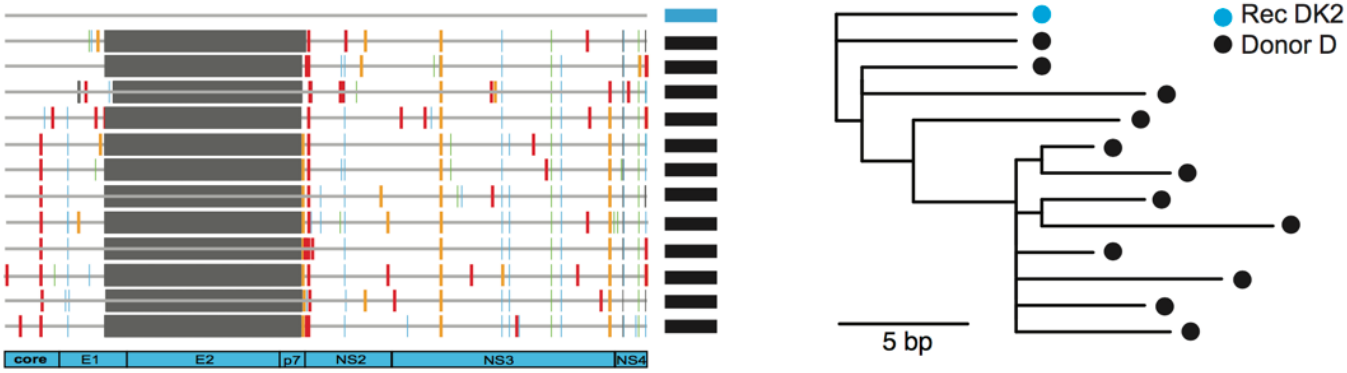


Figure S2. Highlighter plot of 5' half genome sequences from Donor D (A), demonstrating the lineage with E1E2 deletion. Highlighter plot and phylogenetic tree (B) of the deleted lineage from Donor D and Recipient DK2. Notably, the sequence from Recipient DK2 encodes an intact 5' half genome.

Table S1. Geneological Sorting Indices

GSI value (p value) are presented comparing sequences from the indicated donor to the indicated recipient across each row.

Donor **GSI value (p value)**	**Recipient** **GSI value (p value)**
Donor A 0.151 (p=0.144)	Rec AK1 0.060 (p=0.962)
Donor A 0.113 (p=0.401)	Rec AK2 0.071 (p=0.978)
Donor B 0.115 (p=0.494)	Rec BK 0.165 (p=0.080)
Donor C 0.109 (p=0.563)	Rec CK 0 (p=1)
Donor D 0.225 ***(p=0.014)****	Rec DK1 0.271 ***(p=0.001)****
Donor D 0.453 ***(p=0.0001)****	Rec DK2 0.248 ***(p=0.0096)****
Donor D 0.212 (p=0.089)	Rec DH 0 (p=1)
Donor D (excluding E1E2-deleted sequences) 0.116 (p=0.743)	Rec DK1 (excluding E1E2-deleted sequences) 0 (p=1)
Donor D (excluding E1E2-deleted sequences) 0.186 (p=0.165)	Rec DK2 (excluding E1E2-deleted sequences) 0.066 (0.592)
Donor D (excluding E1E2-deleted sequences) 0.2 (p=0.3167)	Rec DH (excluding E1E2-deleted sequences) 0 (p=1)

The GSI tests the phylogenetic similarities of two sequence groups with the null hypothesis that the virus populations were the same; GSI values range from 0 (complete interspersion) to 1 (complete monophyly) with statistical significance indicating greater than random segregation between groups.

Table S2. Donor Clinical Data

Donor ID	Sex	Ethnicity	Age (years)	Risk for HCV	HCV genotype	Reported mechanism and cause of death
A	Male	Caucasian	46	Injection drug use	1a	Cardiovascular; Anoxia
B	Male	Caucasian	25	Injection drug use	1a	Drug intoxication; Anoxia
C	Male	Caucasian	29	Injection drug use	1a	Drug intoxication; Anoxia
D	Male	Caucasian	37	Injection drug use	1a	Drug intoxication; Anoxia

Supplemental Methods.

Sequencing primers. The primers were as follows: (i) first-round sense primer 1aCore.F1 (5'-ATGAGCACGAATCCTAAACCTCAAAGA-3'; nucleotides [nt] 342-368, H77), (ii) first-round antisense primer 1aNS4A.R1 (5'-GCACTCTTCCATCTCATCGAACTC-3'; nt 5451-5474, H77), (iii) second-round sense primer 1aCore.F2 (5'-TCAAAGAAAAACCAAACGTAACACCAACCG-3'; nt 362-391, H77), (iv) second-round antisense primer 1aNS4A.R2 (5'-AGGTGCTCGTGACGACCTCCAGG-3'; nt 5297-5319, H77)

Geneological Sorting Indices. To assess similarities between sampled virus populations, within-person maximum likelihood phylogenies of combinations of donor and recipient sequences were inferred using PhyML version 3.0 and GSI values were calculated using the genealogical Sorting R package (http://molecularevolution.org/software/phylogenetics/gsi/download) (27). Statistical significance was assessed by randomly permuting character states across the tips of the tree 10,000 times. Non-significant values indicate the absence of compartmentalization (p values were corrected for multiple tests).