Supplemental Table 1. Identified resistance-associated mutations in HCV genotype 1b.

Mutation	Region					
	NS3			NS5A		NS5B
	T54S[1]	Y56F[2]	D168E[3]	L31M[4]	Y93H[5]	S556G[6]
Cluster A (n=7)	0	0	0	0	0	1 (14.3)
Cluster B (n=24)	0	24 (100)	0	0	0	24 (100)
Others (n=28)	1 (3.6)	12 (42.9)	1 (3.6)	1 (3.6)	1 (3.6)	2 (6.9)
Total (n=59)	1 (1.7)	36 (61.0)	1 (1.7)	1 (1.7)	1 (1.7)	28 (47.5)

[1]Boceprevir and telaprevir-resistance-associated mutations [refs. 24, 27-29].

[2]Grazoprevir-resistance-associated mutations [ref. 30].

[3]Asunaprevir-, simeprevir-, pariteprevir- and grazoprevir-resistance-associated mutations [refs. 24, 31].

[4]Daclatasvir-, ombitasvir-, elbasvir- and ledipasvir-resistance-associated mutations [refs. 24, 30-34].

[5]Daclatasvir, ombitasvir, elbasvir, ledipasvir and velpatasvir resistance-associated mutations [refs. 24, 30-37].

[6]Dasabuvir resistance-associated mutations [refs. 24, 31, 38].

Supplemental Table 2. Identified resistance-associated mutations in HCV genotype 1a.

Mutation	Region		
	NS3		NS5A
	V55A[1]	Q80K[2]	Q30H[3]
1a (n=4)	1 (25)	1 (25)	1 (25)

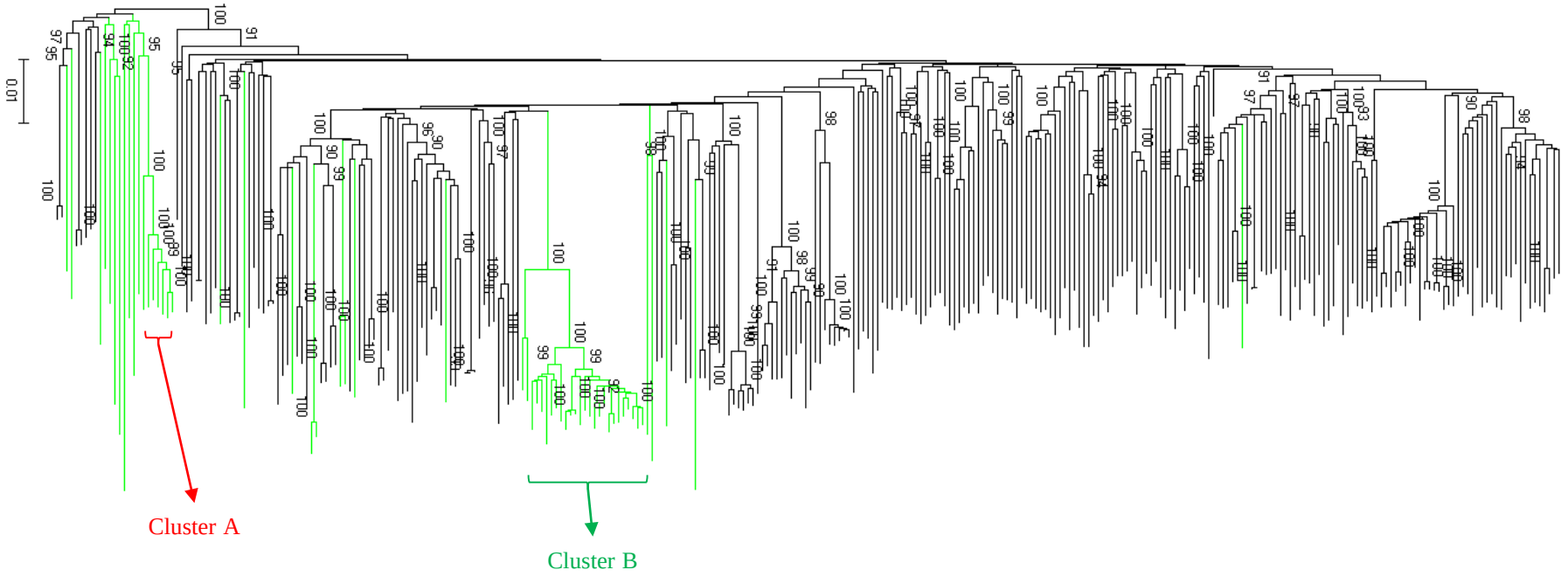
[1]Boceprevir- and telaprevir-resistance-associated mutation [refs. 24, 28, 39].

[2]Simeprevir-, asunaprevir- and paritaprevir-resistance-associated mutation [refs. 24, 31, 40, 41].

[3]Daclatasvir-, elbasvir-, ledipasvir- and ombitasvir-resistance-associated mutation [refs. 24, 29-32, 34, 36, 37].

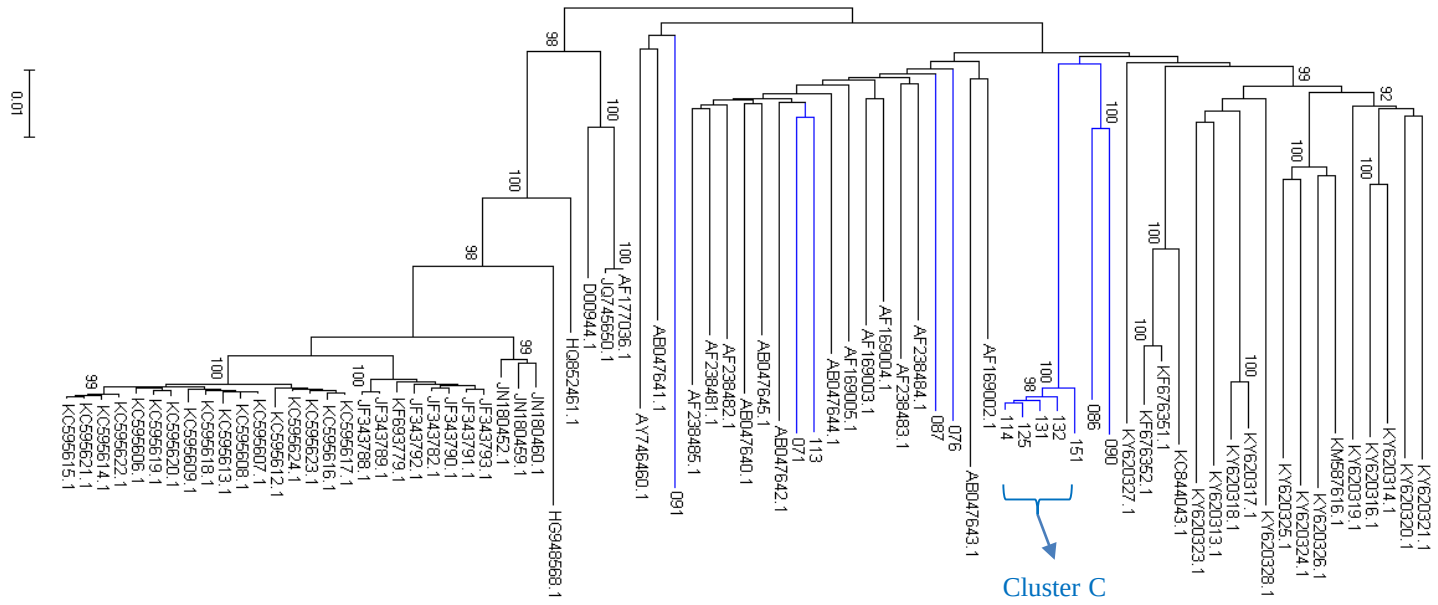
Supplemental Figure 1. Phylogenetic tree for HCV genotype 1b.

The tree was consructed using 59 HCV genotype 1b full-genome sequences derived from the study patients (green branches) and 255 reference sequences highly similar to one of the clustered cohort sequence (#025) selected by BLAST (black branches).

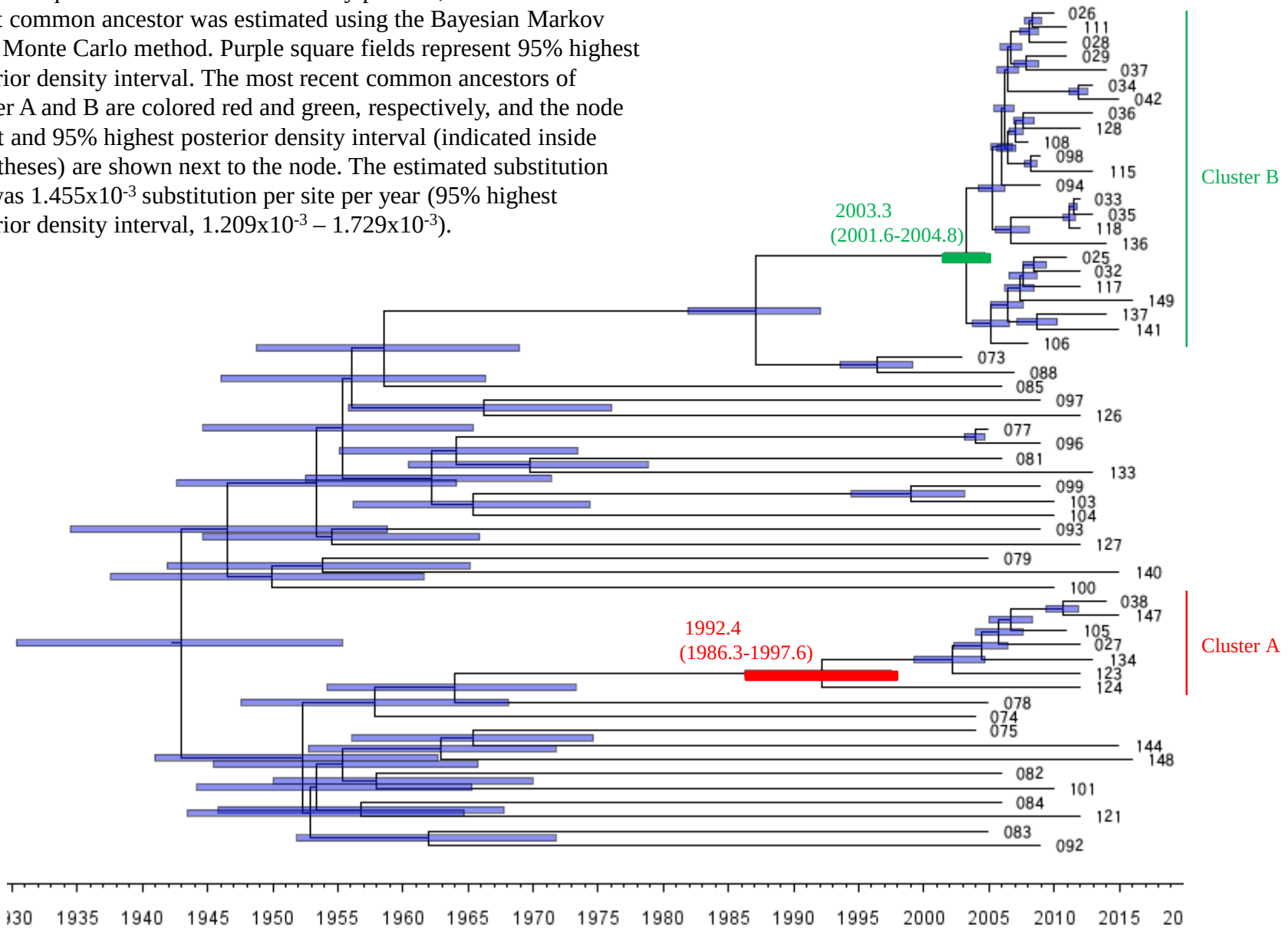


Supplemental Figure 2. Phylogenetic tree for HCV genotype 2a.

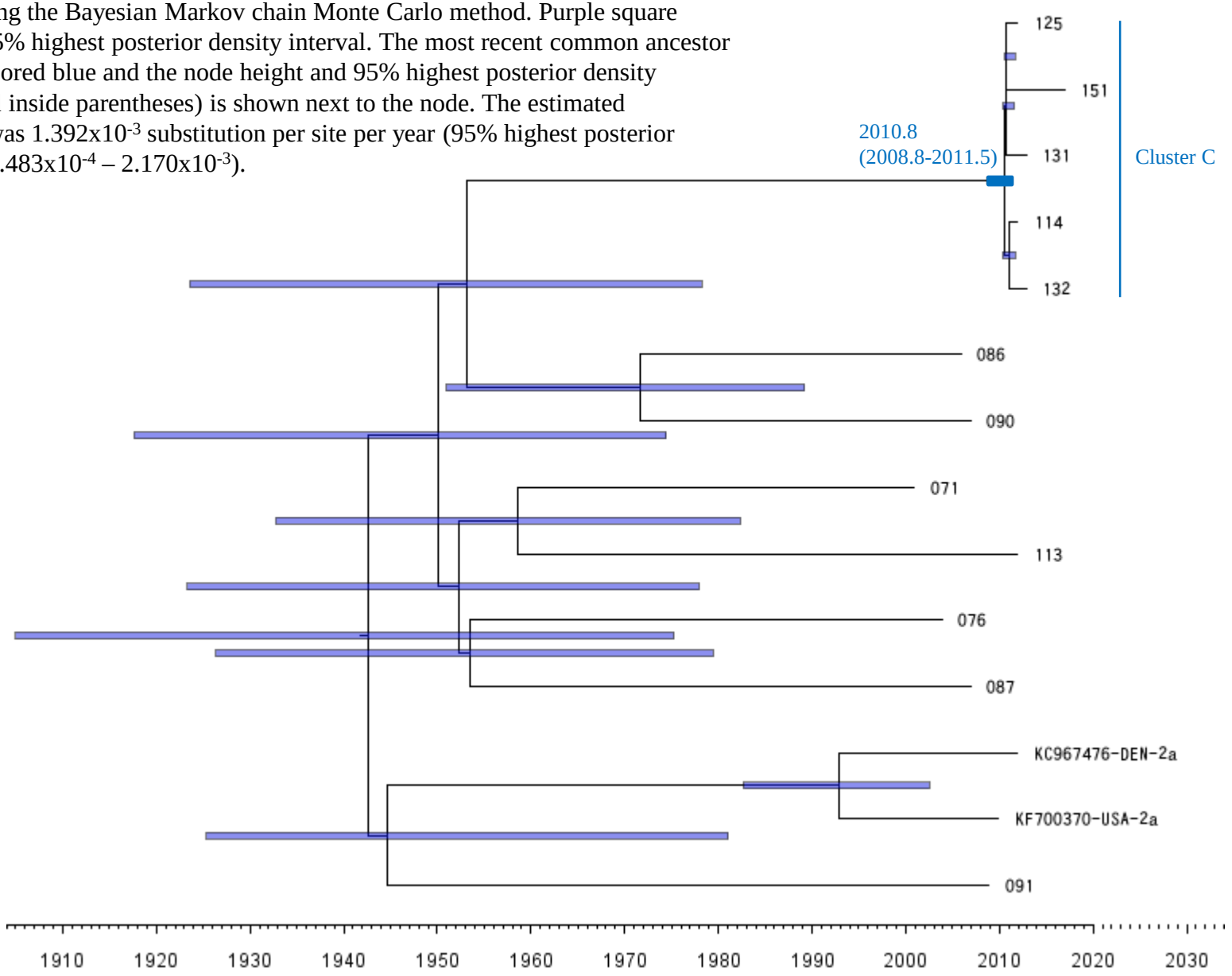
The tree was consructed using 12 HCV genotype 2a full-genome sequences derived from the study patients (blue branches) and 67 reference sequences highly similar to one of the clustered cohort sequence (#125) selected by BLAST (black branches).



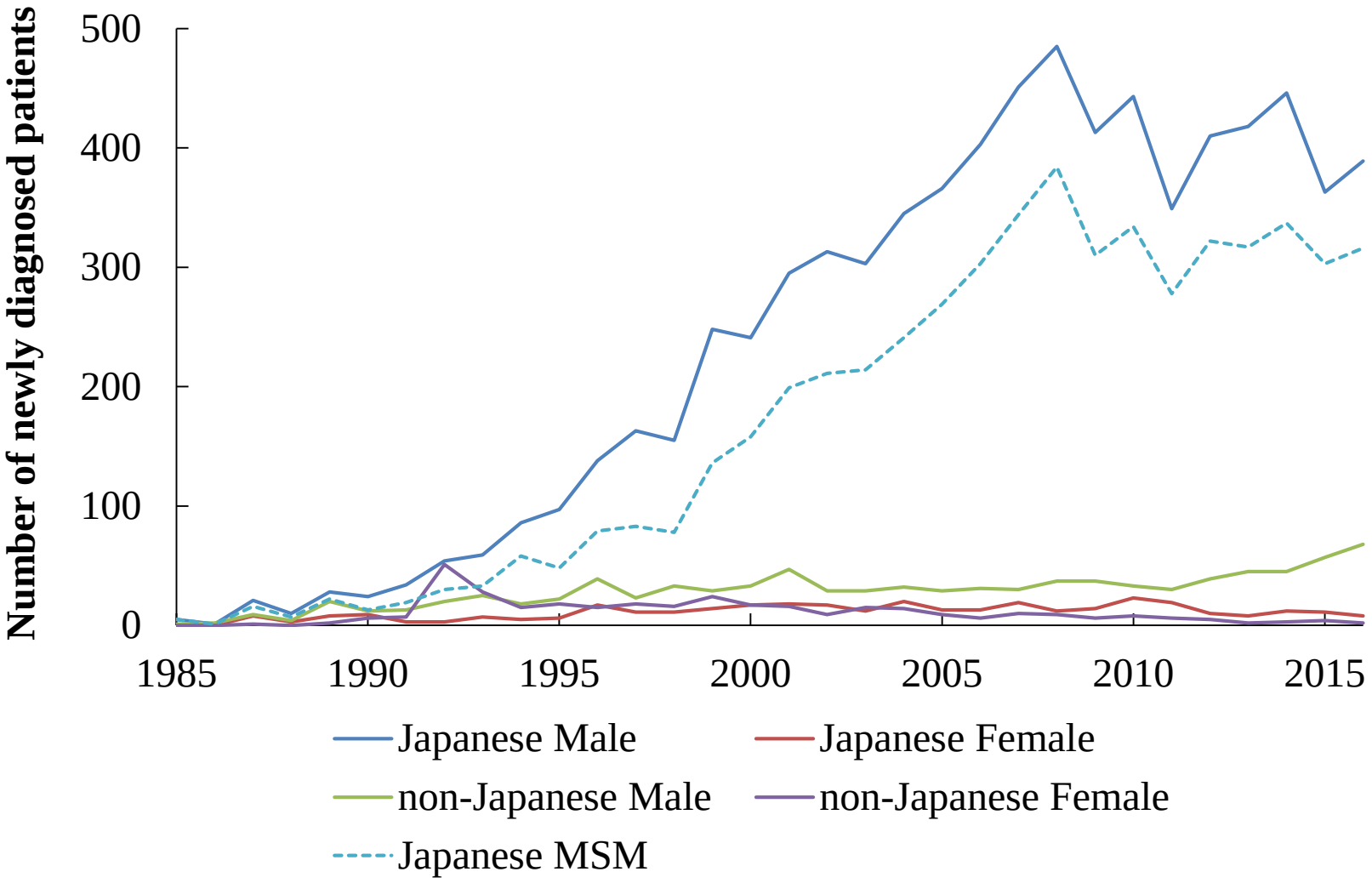
Supplemental Figure 3. Maximum clade credibility tree of HCV genotype 1b full-genome sequences. Using 59 HCV genotype 1b full-genome sequences derived from the study patients, the time to the most recent common ancestor was estimated using the Bayesian Markov chain Monte Carlo method. Purple square fields represent 95% highest posterior density interval. The most recent common ancestors of Cluster A and B are colored red and green, respectively, and the node height and 95% highest posterior density interval (indicated inside parentheses) are shown next to the node. The estimated substitution rate was 1.455×10^{-3} substitution per site per year (95% highest posterior density interval, $1.209 \times 10^{-3} – 1.729 \times 10^{-3}$).



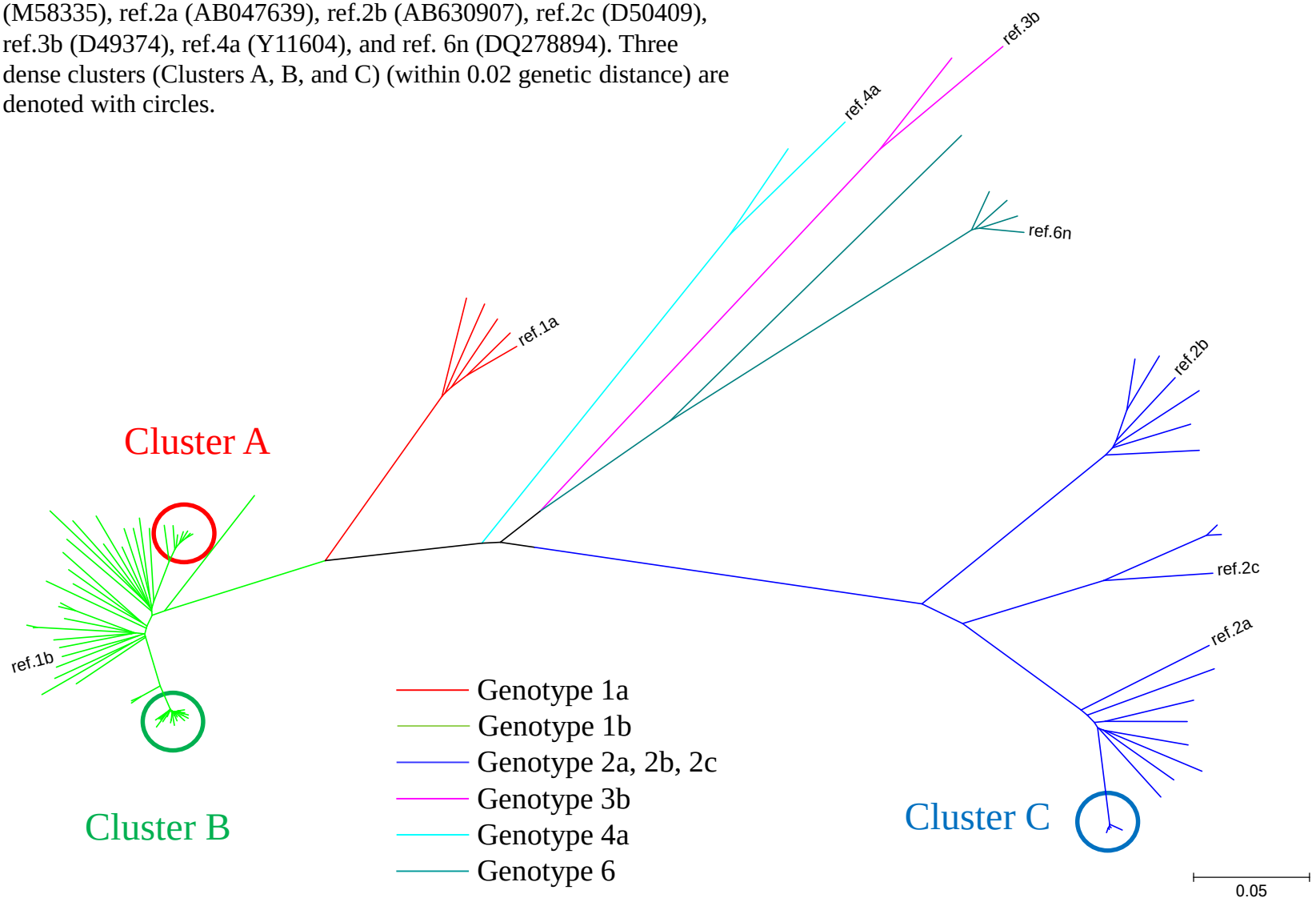
Supplemental Figure 4. Maximum clade credibility tree of HCV genotype 2a full-genome sequences. Using 12 HCV genotype 2a full-genome sequences derived from the study patients and 2 reference sequences, the time to the most recent common ancestor was estimated using the Bayesian Markov chain Monte Carlo method. Purple square fields represent 95% highest posterior density interval. The most recent common ancestor of Cluster C is colored blue and the node height and 95% highest posterior density interval (indicated inside parentheses) is shown next to the node. The estimated substitution rate was 1.392×10^{-3} substitution per site per year (95% highest posterior density interval, $7.483 \times 10^{-4} – 2.170 \times 10^{-3}$).



Supplemental Figure 5. Annual number of newly diagnosed HIV-1-infected cases in Tokyo. Newly diagnosed cases were categorized by their gender and nationality (Japanese or non-Japanese) and their annual numbers are shown with solid lines. Additionally, the number of MSM cases are also shown with dotted line.



Supplemental Figure 6. Phylogenetic tree of HCV full-genome. Eighty-eight HCV sequences derived from HIV-1-coinfected patients were used and one referential sequence for each genotype was selected from Hepatitis Virus Database Server [18]; ref.1a (M62321), ref.1b (M58335), ref.2a (AB047639), ref.2b (AB630907), ref.2c (D50409), ref.3b (D49374), ref.4a (Y11604), and ref. 6n (DQ278894). Three dense clusters (Clusters A, B, and C) (within 0.02 genetic distance) are denoted with circles.



Supplemental Figure 7. Phylogenetic tree of HCV NS5B fragment. Eighty-eight HCV sequences derived from HIV-1-coinfected patients were used and one referential sequence for each genotype was selected from Hepatitis Virus Database Server [18]; ref.1a (M62321), ref.1b (M58335), ref.2a (AB047639), ref.2b (AB630907), ref.2c (D50409), ref.3b (D49374), ref.4a (Y11604), and ref. 6n (DQ278894). *Circles*: three dense clusters (Clusters A, B, and C) within 0.02 genetic distance.