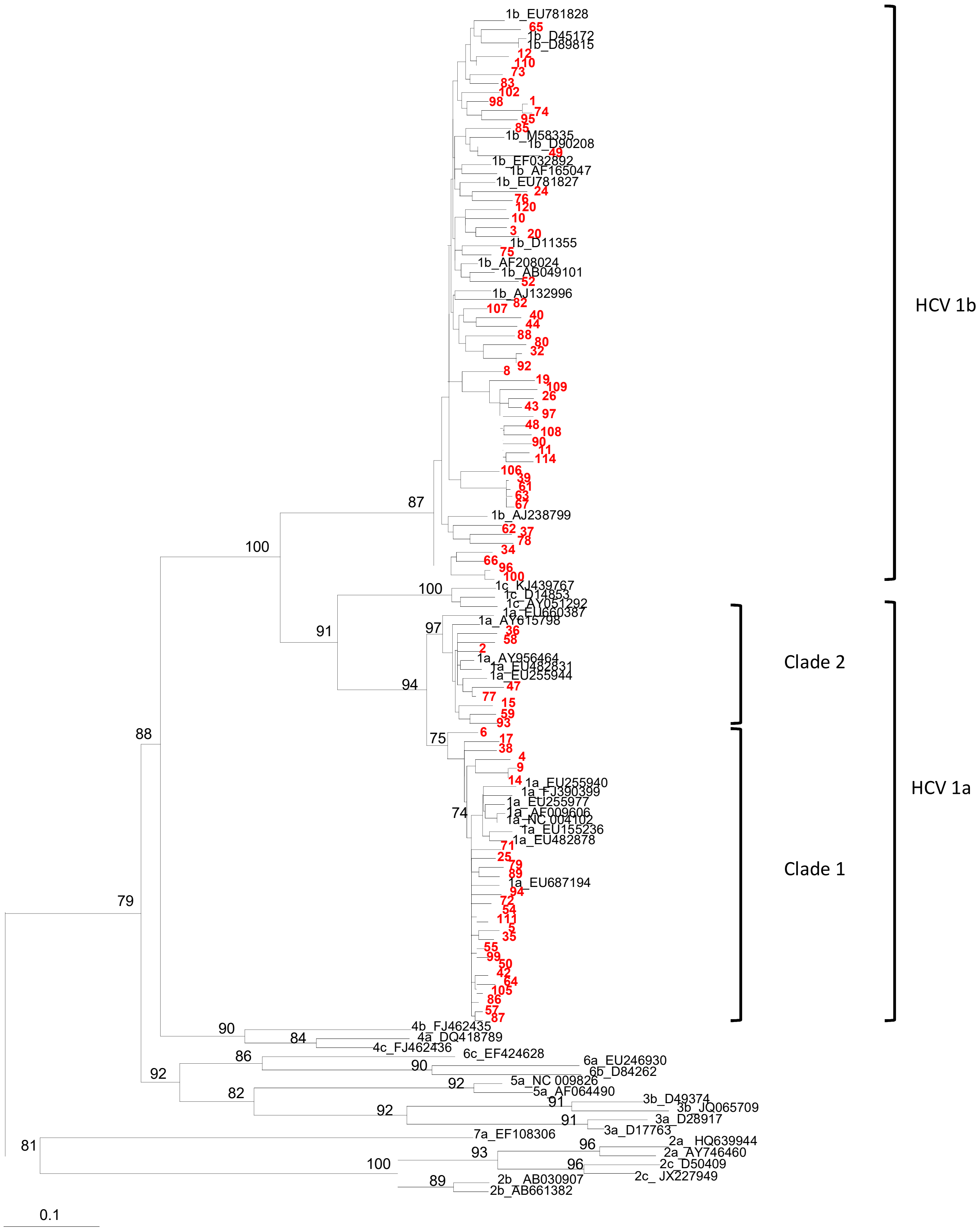
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100
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1c_AY051292
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100
1a_AY615798
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91
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77
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1a_EU687194
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3b_D49374
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3b_JQ065709
92
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3a_D28917
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2a_HQ639944
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100
96
2c_D50409
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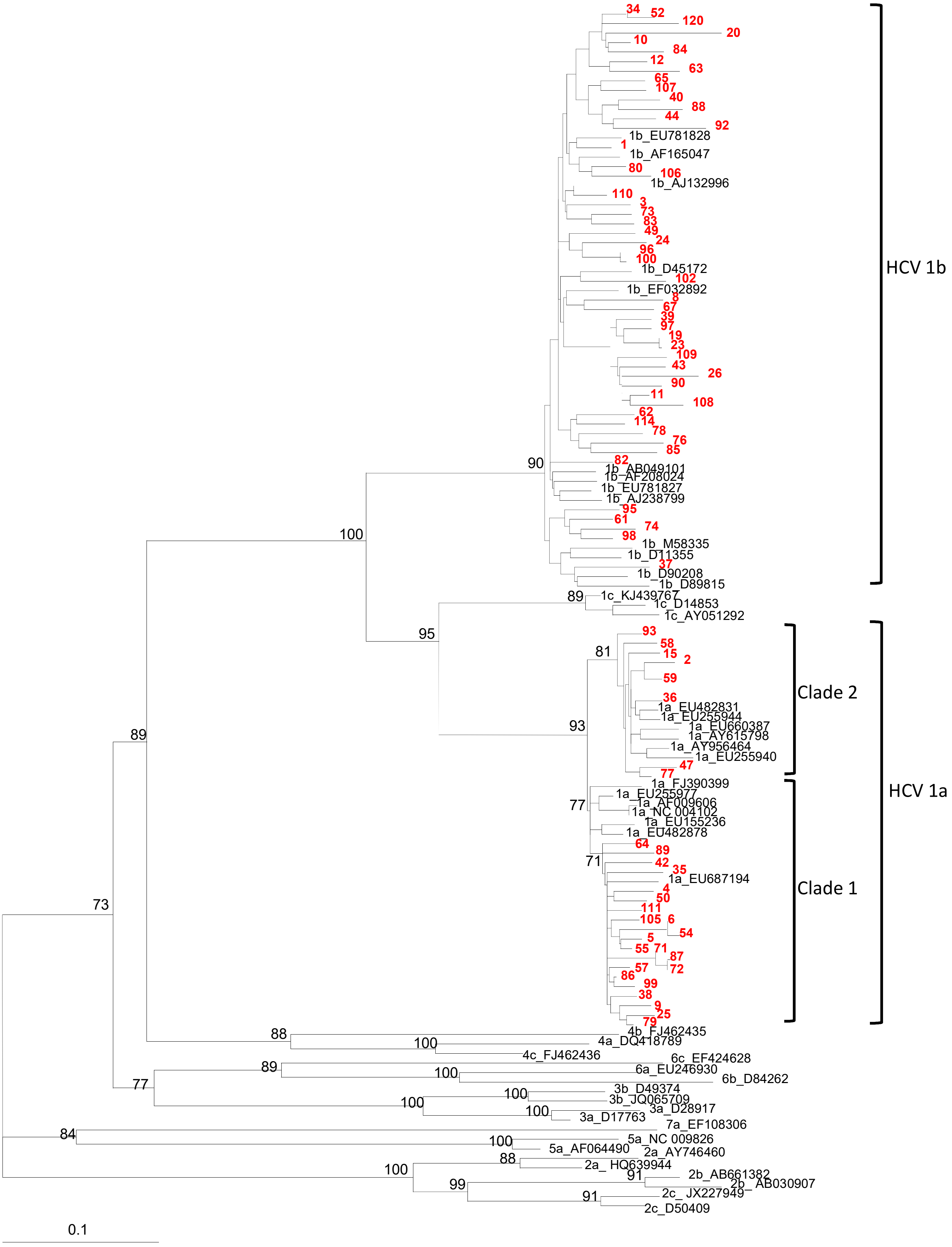
89
2b_AB030907
2b_AB661382
0.1
HCV 1b
Clade 2
Clade 1
HCV 1a

Supplementary Figure S1. Maximum-likelihood phylogenetic tree (GTR+Γ+I model for nucleotide substitutions) including 48 references sequences (in black) and the 84 HCV-*NS5A* samples of this study (in red). The numbers at each node correspond to bootstrap values obtained with 100 replicates (values lower than 70 are not shown).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1b_D11355
37
1b_D90208
1b_D89815
HCV 1b
100
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1c_KJ439767
1c_D14853
1c_AY051292
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81
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1a_EU482831
1a_EU255944
93
1a_EU660387
1a_AY615798
1a_AY956464
1a_EU255940
47
77
Clade 2
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77
1a_NC 004102
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1a_EU482878
64
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1a_EU687194
4
50
111
105
6
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72
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38
9
25
79
Clade 1
HCV 1a
89
73
88
4b_FJ462435
4a_DQ418789
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6c_EF424628
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6a_EU246930
6b_D84262
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100
3b_D49374
3b_JQ065709
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3a_D28917
100
3a_D17763
84
7a_EF108306
100
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5a_AF064490
2a_AY746460
88
2a_HQ639944
100
91
2b_AB661382
2b_AB030907
99
2c_JX227949
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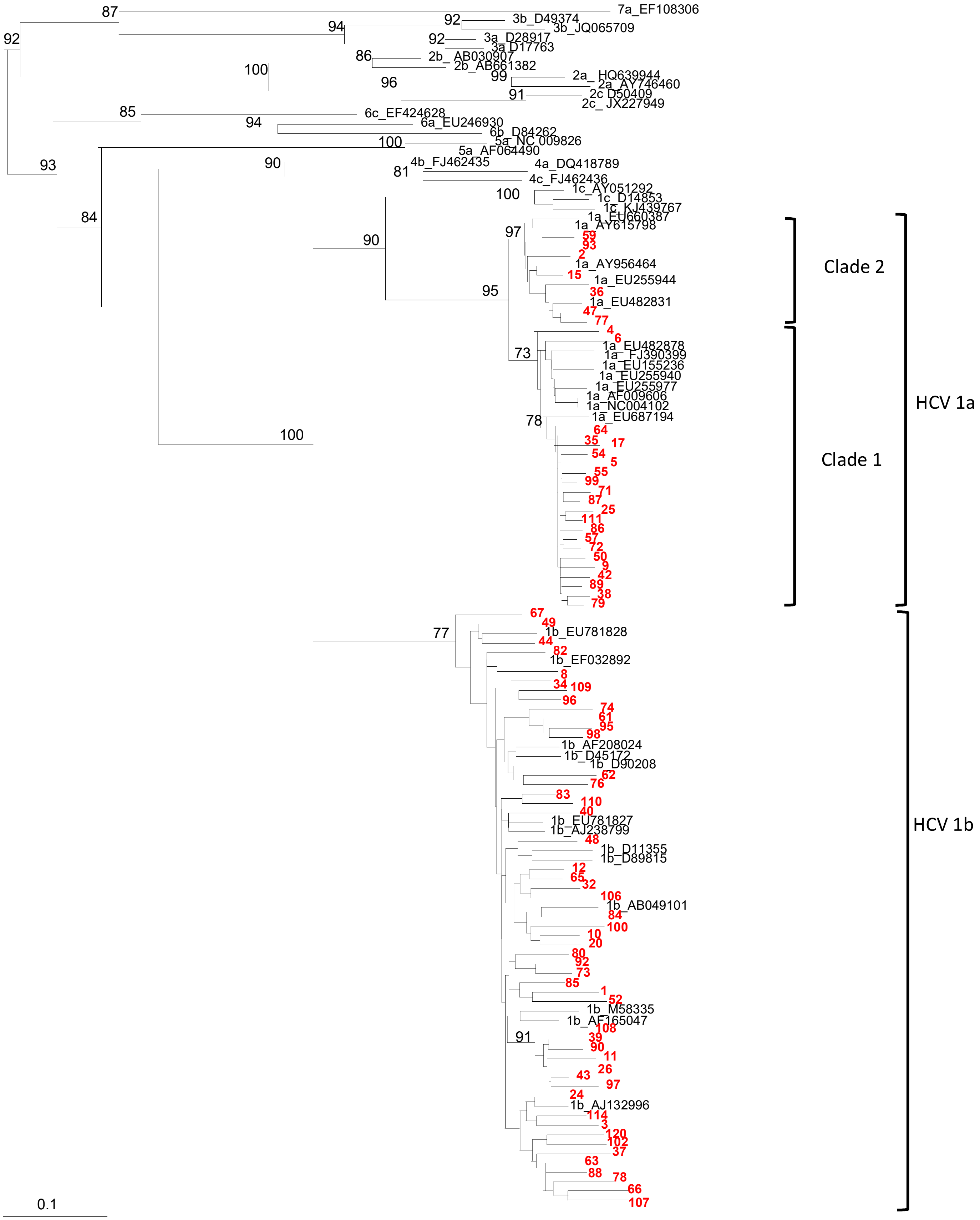
2c_D50409
0.1

Supplementary Figure S2. Maximum-likelihood phylogenetic tree (GTR+Γ+I model for nucleotide substitutions) including 48 references sequences (in black) and the 79 HCV-*NS5B* samples of this study (in red). The numbers at each node correspond to bootstrap values obtained with 100 replicates (values lower than 70 are not shown).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3b_D49374
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2b_AB661382
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2c_ JX227949
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6c_EF424628
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1b_M58335
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91
39
90
11
26
43
97
24
1b_AJ132996
114
3
120
102
37
63
88
78
66
107
0.1
Clade 2
Clade 1
HCV 1a
HCV 1b

Supplementary Figure S3. Maximum-likelihood phylogenetic tree (GTR+Γ+I model for nucleotide substitutions) including 48 references sequences (in black) and the 79 HCV-*NS3* samples of this study (in red). The numbers at each node correspond to bootstrap values obtained with 100 replicates (values lower than 70 are not shown).