**Legend**

**Supplement table 1**

Clinical characteristics and genotype of HCV infected patients in Thailand. In total, 187 patients have complete clinical data.

**Supplement table 2**

Genotype distribution classified according to geographical region**.**

**Supplement table 3**

Historic risk factors of patients classified according to genotype. Only 130 patients could identify suspected risk factors.

**Supplement fig. 1** Phylogenetic trees are constructed using neighbor-joining method based on partial (a) Core and (b) NS5B sequences of all samples isolated in this study. Reference sequences are indicated in black circle and italic letters.

**Supplement fig. 2** Maximum likelihood trees constructed from Core sequences using MEGA v.5. A) Phylogenetic tree of Core sequences isolated in this study. Black triangles represent a group of subtype 3a, 1a and 6f. B) Strains of HCV subtype 1a, C) subtype 6f and D) subtype 3a. Black circles represent reference strains. Bootstrap values more than 70% are shown.

**Supplement fig. 3** Maximum likelihood trees constructed from NS5B sequences using MEGA v.5. A) Phylogenetic tree of NS5B sequences isolated in this study. Black triangles represent a group of subtype 1a, 1b and 3a. B) Strains of HCV subtype 1a, C) subtype 1b and D) subtype 3a. Black circles represent reference strains. Bootstrap values more than 70% are shown.

**Supplement table 1**

Clinical characteristics and genotype of HCV infected patients in Thailand. In total, 187 patients have complete clinical data.

 **Clinical Feature**

 **Chronic hepatitis Cirrhosis HCC Total**

 **(N=172) (N=10) (N=5) (N=187)**

**Age (Mean±SD)** 43.7±10.7 46.3±7.5 57±11.7 44.2±10.8

**Sex (M/F)** 115/56 5/5 3/2 123/63

**Genotype (%)**a

 **HCV-1** 47(85.5) 5(9.1) 3(5.1) 55(29.4) b

 **HCV-2** 1(100) 0(0.0) 0(0.0) 1(0.5) b

 **HCV-3** 72(93.5) 3(3.9) 2(2.6) 77(41.2) b

 **HCV-6** 52(96.3) 2(3.7) 0(0.0) 54(28.9) b

a Percentage calculated with respected to each genotype

b Percentage calculated with respected to a total of 187 samples with clinical data

**Supplement table 2**

Genotype distribution classified according to geographical region**.**

 **Genotype(%)**

**Region(%)** **HCV-1 HCV-2 HCV-3 HCV-6 Total(%)a**

**Central** 99(34.6) 2(0.7) 122(42.7) 63(22.0) 286(92.0)

**Eastern**  4(66.6) 0(0.0) 1(16.7) 1(16.7) 6(1.9)

**Northern** 1(20.0) 0(0.0) 3(60.0) 1(20.0) 5(1.6)

**Northeastern**  3(33.3) 0(0.0) 3(33.3) 3(33.3) 9(2.3)

**Southern** 0(0.0) 0(0.0) 2(1.5) 1(1.4) 3(1.0)

**Western** 1(50.0) 0(0.0) 1(50.0) 0(0.0) 2(0.6)

**Total** 108(34.7) 2(0.6) 132(42.4) 69(22.2) 311(87.4)b

a Percentage calculated with respect to the total of 311 samples with regional data

b Percentage calculated with respect to the total of 356 samples in the study

**Supplement table 3**

Historic risk factors of patients classified according to genotype. Only 130 patients could identify suspected risk factors.

  **Genotype(%)**

**Risk factor (n=130)**  **HCV-1 HCV-2 HCV-3 HCV-6 Total(%)a**

**IVDUb** 8(22.9) 1(2.9) 12(34.3) 14(40.0) 35(26.9)

**Tatoo** 8(22.2) 0(0.0) 16(44.4) 12(33.3) 36(27.7)

**Commercial sex** 4(23.5) 0(0.0) 6(35.3) 7(41.2) 17(13.1)

**Shaving barber** 10(33.3) 0(0.0) 9(30.0) 11(36.7) 30(23.1)

**Medical injection**  9(29.0) 0(0.0) 9(29.0) 13(42.0) 31(23.8)

**Blood transfusion** 15(34.8) 0(0.0) 14(32.6) 14(32.6) 43(33.1)

**Needle stick** 1(6.7) 0(0.0) 13(86.7) 1(6.7) 15(11.5)

**HIV co-infection**  0(0.0) 0(0.0) 2(100) 0(0.0) 2(1.5)

**HIV/HCV husband** 0(0.0) 0(0.0) 1(50.0) 1(50.0) 2(1.5)

a Percentage calculated with respect to each of risk factor

b Intravenous drug use