

Supplemental Table 1. Information of primers and probes for TaqMan allelic discrimination

Polymorphism		Sequence(5'-3')
<i>DMA</i> rs1050391	Primer	F: AGGTCTTCTTCCAGGCAAGGA R: GAGCTATAGACAGGAAGTGCTGAA
	Probe	FAM-CTAGACGTAGAAGCAG-MGB HEX-AGCTAGACATAGAAGCAGA-MGB
<i>DMA</i> rs1063478	Primer	F: CCACCCATGCTGACAGTGA R: AGTCCATCGACAGCTGAGACA
	Probe	FAM-ATCATTCCGTCCCTGTG-MGB HEX-CATCATTCCATCCCTGT-MGB
<i>DMA</i> rs3135029	Primer	F: TCGCTTGGGTGTTCCCTGTATAA R: CAGGGCCCACGTGATCTG
	Probe	FAM-TAAGCTACAAATTCTGGCA-MGB HEX-ATAAGCTACAAATTCGGGCAA-MGB
<i>DMB</i> rs23544	Primer	F: CCACTGTATTAGAGAGGACCTGGAA R: ACCACCCACTCCCAAGAAAAT
	Probe	FAM-AGATGGATTCCCC-MGB HEX-AGATGGGTTCCCC-MGB
<i>DMB</i> rs2071556	Primer	F: GTTGAAATCTAAGGAGGCTAGAATAGTGTA R: GGAGCGTGCTTGCTTTGAA
	Probe	FAM-ATTGCCAAATTTACAGCC-MGB HEX-TGCCAAATTTACATCCT-MGB
<i>DOA</i> rs408036	Primer	F: CCAGGCCTTGGCCAGTT R: GTAACACACAATGGGCCAAATG
	Probe	FAM-TTGGCAGCCGTCCT-MGB HEX-ATTGGCAGCCATC-MGB
<i>DOA</i> rs3128935	Primer	F: TGTCGGGTGGACATGTTTAC R: GGATCCACATGGTCTGTGTTCTC
	Probe	FAM-AGAACACCGCTAACA-MGB HEX-AGAACACCGCCAACA-MGB
<i>DOA</i> rs3129304	Primer	F: AAAACATACAAAGAGATAAATCACCATACC R: TGAAAACCGTAATCTGTATTGCTCAT
	Probe	FAM-CATAGTTTATGTCAGGACC-MGB HEX-CATAGTTTATGTCAAGACC-MGB
<i>DOA</i> rs376892	Primer	F: CTTGGCTGTGGTCTGGTAACTG R: CCTTCCTAGTCCACCTCAGACCTT
	Probe	FAM-TAATCAGGTGCCATTGG-MGB HEX-TAATCAGGTGCCATCGG-MGB
<i>DOA</i> rs369150	Primer	F: GAAAGAAAGGAACAGGGCATGAC R: GGCGGGAAGGTCCAGAGA
	Probe	FAM-TGATGGGAACCTAGG-MGB HEX-TGATGGGAGCCTAGG-MGB
<i>DOA</i> rs86567	Primer	F: GGTGCGGGTCTACAGATGGTT R: GAGCAACAGTTATTGAGGAACTAGCAT
	Probe	FAM-TGGCCCCCATTG-MGB HEX-TGGCCCACCATTG-MGB
<i>DOA</i> rs2284191	Primer	F: TCCTCCATCTCAGAGCATTATGAC R: TGTTGCTCAAACAACCTTCATAGAGTTC
	Probe	FAM-CTTCCATAACTGTTGTCTAG-MGB HEX-TAACTGTTATCTAGTTTTCTGG-MGB
<i>DOA</i> rs6913008	Primer	F: GTCCTGTTTCAGAGTCATCCACTTT R: TCCTCATCATCATGGGCACAT

Polymorphism		Sequence(5'-3')
<i>DOA</i> rs6913008	Probe	FAM-CCCAGACTCCCGG-MGB HEX-CCCAGACTCCTGG-MGB
<i>DOA</i> rs2582	Primer	F: TGATCCTTCTGAGAGAAATGACTTGT R: CACAGCGGGATGCACTTAAA
	Probe	FAM-TGTGACAGACCCTGC-MGB HEX-TGTGACAGCCCCTG-MGB
<i>DOA</i> rs416622	Primer	F: CAGCCTGGTGACAGAGTGAGA R: TCACCCAGACCTACTGAATTAGAATCT
	Probe	FAM-AGACAGCCCCCTGT-MGB HEX-AGACAGCCTCCCTGTT-MGB
<i>DOA</i> rs453779	Primer	F: GTCACCCGTGGAGGCACTA R: AACGTCCCTTAATCCCAGTCCTA
	Probe	FAM-AGGAACAGGCCCTG-MGB HEX-AGGAACGGGCCCTG-MGB
<i>DOA</i> rs1044429	Primer	F: TCACACAAAGAGGGTTTCTGTTACTG R: GAATAAGTTGAAATCAATGACCAGAAGA
	Probe	FAM-TGAGATGATTCTCCTCCAC-MGB HEX-TGAGATGATTTTCTCCTCCAC-MGB
<i>DOB</i> rs2857111	Primer	F: TCTCTTGCCTCCGTTCTCATT R: TGCTACATATTTCTAAAAGCCACTCTCATA
	Probe	FAM-TCCCCTCCCTGGAGA-MGB HEX-CTCCCCTCCCTAGAG-MGB
<i>DOB</i> rs11244	Primer	F: CAAGGGCATTGTCCAGAAACTC R: GCTGGACCACAGAAAAGTAAATGA
	Probe	FAM-ACTCCTTCCAGTCCCA-MGB HEX-CTCCTTCCAGCCCCA-MGB
<i>DOB</i> rs1383258	Primer	F: TTACCAGACACGTTTAGAATGGATTC R: GAGTTCACAGCACATTGTAATTATTGG
	Probe	FAM-AGAAGAGATGAGAGAGTC-MGB HEX-CAAGAGAAGAGACGAGAG-MGB
<i>DOB</i> rs2071469	Primer	F: GAAGCCAGAAAAACAGCGATTTAT R: AGGGGACCCACCCAGAAC
	Probe	FAM-TGAATTTTATGAACTCATTC-MGB HEX-TGAATTTTATGAGCTCATTC-MGB
<i>DOB</i> rs2071472	Primer	F: GACTGGATTCTCCATGACTCAA R: CATGCCAATTCTTGCATACACA
	Probe	FAM-AACAGAGCAATTGTT-MGB HEX-AACAGAGCAATTATT-MGB
<i>DOB</i> rs7383287	Primer	F: CGTAATTTACCAGGCATGGGTTT R: CAGTCAGCCTTTGCCTGAATC
	Probe	FAM-TTCCAGAAGATTTTG-MGB HEX-TTTCCAGAAGACTTTG-MGB
<i>DOB</i> rs2856997	Primer	F: CCAAATCCAATGCTAGCTAGAGAAA R: ATGGGCTGTGAGAATCTGTAACC
	Probe	FAM-CATGGAGTTACCCCC-MGB HEX-CCATGGAGTTACCACC-MGB
<i>DOB</i> rs2071471	Primer	F: CATGCCAATTCTTGCATACACACT R: GGTGGCTCTGCTAGTGAATCTGA
	Probe	FAM-CTGGAGAATCTGTGC-MGB HEX-CTGGAGAGTCTGTGC-MGB
<i>DOB</i> rs2071475	Primer	F: GGTCTCTCTGGGTACACTGTCA R: GGTTTTCTTTACGGTGTCTCAT
	Probe	FAM-CTAGGAAGGGAGGAAA-MGB HEX-ACTAGGAAGAGAGGAAA-MGB

Polymorphism		Sequence(5'-3')
<i>DOB</i> rs2856995	Primer	F: CTCCCCTCCCTAGAGAATCCA R: AAGAAACAGAATGGGATTCAACAGA
	Probe	FAM-TGTCTGGTATGTCTCTAA-MGB HEX-TGTCTGGTAAGTCTC-MGB
<i>TAP1</i> rs1135216	Primer	F: CACACATGTGGCTATACCGTTCTC R: TCGCTGACCCCCTGACA
	Probe	FAM-TGCAGAGGTAGGCG-MGB HEX-TCTGCAGAGGTAGACG-MGB
<i>TAP2</i> rs1800454	Primer	F: CCTGGAACGCGCCTTGTA R: CCTTTCACAACCACTCTGGTATCTT
	Probe	FAM-TGCTCGTAAGGAGG-MGB HEX-CTGCTCATAAGGAGG-MGB
<i>LMP2</i> rs17587	Primer	F: TGAACCGAGTGTGTTGACAAGCT R: GCTGAACCAGAGAGTGCACAGT
	Probe	FAM- CTGCACGAGCGCA-MGB HEX- CTGCACGAGCACAT-MGB
<i>LMP7</i> rs2071543	Primer	F: GCGACCCTCCACTCCTCA R: GGACACTACAGTTTCTCTATGCGATCT
	Probe	FAM- CCGACCTTCATTCC-MGB HEX- CCGACCTGCATTC-MGB
<i>tapasin</i> rs9277972	Primer	F: GTCTAGGTCCCTTCAGGTAGAAGTAATCTTT R: CTAAGTGAAATTGCATACTGTTTTACTCTAC
	Probe	FAM-CCTATAAGGTTAAACTGTTCT-MGB HEX-CCTATAAGGTTTAACTGTTCT-MGB
<i>tapasin</i> rs1059288	Primer	F: TGGGCCTTAGGTCCCTATGC R: AAGTGATCGTGTGAGTCGTCGTT
	Probe	FAM-CAGACAGGCCGGTC-MGB HEX-ACAGACAGGCCAGTC-MGB
<i>tapasin</i> rs2282851	Primer	F: CCTCATTCTTGAATTATCTGCACAGT R: GCCCAGGAGTCAGAAGCTTTT
	Probe	FAM-CCACGTCTCAGCCTA-MGB HEX-CCACGTCCCAGCCT-MGB

Supplemental Table 2. Comparison results of SNPs distribution in dominant, recessive, and additive models

SNPs	Location	Dominant		Recessive		Additive		Dominant		Recessive		Additive	
		<i>P</i> Value*	FDR*	<i>P</i> Value*	FDR*	<i>P</i> Value*	FDR*	<i>P</i> Value†	FDR†	<i>P</i> Value†	FDR†	<i>P</i> Value†	FDR†
<i>DMA</i> rs1050391	intron(C>T)	1.25×10 ⁻¹	0.64	7.70×10 ⁻¹	0.85	1.60×10 ⁻¹	0.68	4.66×10 ⁻¹	0.79	3.54×10 ⁻¹	0.75	3.47×10 ⁻¹	0.84
<i>DMA</i> rs1063478	Missense(C>T)	3.50×10 ⁻²	0.64	4.44×10 ⁻¹	0.82	4.90×10 ⁻²	0.68	8.47×10 ⁻¹	0.96	6.81×10 ⁻¹	0.88	7.44×10 ⁻¹	0.90
<i>DMA</i> rs3135029	5'near gene(C>A)	1.66×10 ⁻¹	0.64	7.43×10 ⁻²	0.82	1.95×10 ⁻¹	0.71	3.43×10 ⁻¹	0.73	6.95×10 ⁻¹	0.88	3.44×10 ⁻¹	0.84
<i>DMB</i> rs23544	intron(G>A)	7.50×10 ⁻²	0.64	2.88×10 ⁻¹	0.82	6.60×10 ⁻²	0.68	1.83×10 ⁻¹	0.72	3.56×10 ⁻¹	0.75	5.71×10 ⁻¹	0.87
<i>DMB</i> rs2071556	intron(C>A)	3.32×10 ⁻¹	0.74	2.66×10 ⁻¹	0.82	2.08×10 ⁻¹	0.71	6.95×10 ⁻¹	0.91	3.49×10 ⁻¹	0.75	4.48×10 ⁻¹	0.87
<i>DOA</i> rs408036	3'UTR(G>A)	3.14×10 ⁻¹	0.74	7.18×10 ⁻¹	0.85	6.64×10 ⁻¹	0.88	7.21×10 ⁻¹	0.91	1.90×10 ⁻¹	0.75	5.92×10 ⁻¹	0.87
<i>DOA</i> rs3128935	3'UTR(T>C)	3.11×10 ⁻¹	0.74	5.05×10 ⁻¹	0.82	2.98×10 ⁻¹	0.72	2.18×10 ⁻¹	0.72	3.76×10 ⁻¹	0.75	1.75×10 ⁻¹	0.82
<i>DOA</i> rs3129304	3'UTR(A>G)	5.12×10 ⁻¹	0.83	2.16×10 ⁻¹	0.82	3.85×10 ⁻¹	0.86	6.50×10 ⁻¹	0.91	9.90×10 ⁻¹	0.99	6.66×10 ⁻¹	0.87
<i>DOA</i> rs376892	3'UTR(C>T)	5.43×10 ⁻¹	0.83	8.30×10 ⁻²	0.82	2.55×10 ⁻¹	0.72	3.17×10 ⁻¹	0.72	4.20×10 ⁻²	0.42	9.18×10 ⁻¹	0.92
<i>DOA</i> rs369150	intron(G>A)	5.64×10 ⁻¹	0.83	9.98×10 ⁻¹	1.00	6.85×10 ⁻¹	0.88	3.00×10 ⁻¹	0.72	3.29×10 ⁻¹	0.75	2.17×10 ⁻¹	0.82
<i>DOA</i> rs86567	intron(A>C)	8.94×10 ⁻¹	0.96	2.42×10 ⁻¹	0.82	4.59×10 ⁻¹	0.86	8.30×10 ⁻²	0.71	4.98×10 ⁻¹	0.85	1.28×10 ⁻¹	0.82
<i>DOA</i> rs2284191	intron(G>A)	4.10×10 ⁻²	0.64	7.72×10 ⁻¹	0.85	5.00×10 ⁻²	0.68	1.40×10 ⁻²	0.24	6.83×10 ⁻¹	0.88	2.40×10 ⁻²	0.41
<i>DOA</i> rs6913008	intron(C>T)	1.21×10 ⁻¹	0.64	2.28×10 ⁻¹	0.82	8.7×10 ⁻¹	0.90	3.99×10 ⁻¹	0.79	4.36×10 ⁻¹	0.78	6.43×10 ⁻¹	0.87
<i>DOA</i> rs2582	3'UTR(C>A)	7.87×10 ⁻¹	0.89	9.33×10 ⁻¹	0.96	8.38×10 ⁻¹	0.90	5.26×10 ⁻¹	0.81	7.76×10 ⁻¹	0.94	6.51×10 ⁻¹	0.87
<i>DOA</i> rs416622	3'UTR(G>A)	9.49×10 ⁻¹	0.96	3.75×10 ⁻¹	0.82	6.94×10 ⁻¹	0.88	3.00×10 ⁻³	0.10	3.00×10 ⁻¹	0.75	1.02×10 ⁻¹	0.82
<i>DOA</i> rs453779	intron(C>T)	6.39×10 ⁻¹	0.86	7.03×10 ⁻¹	0.85	8.57×10 ⁻¹	0.90	4.32×10 ⁻¹	0.79	9.00×10 ⁻¹	0.99	5.19×10 ⁻¹	0.87
<i>DOA</i> rs1044429	3'UTR(G>A)	7.45×10 ⁻¹	0.89	6.73×10 ⁻¹	0.85	6.64×10 ⁻¹	0.88	9.18×10 ⁻¹	0.96	8.12×10 ⁻¹	0.94	8.57×10 ⁻¹	0.92
<i>DOB</i> rs2857111	intron(A>G)	6.54×10 ⁻¹	0.86	4.69×10 ⁻¹	0.82	8.96×10 ⁻¹	0.90	2.73×10 ⁻¹	0.72	3.45×10 ⁻¹	0.75	2.18×10 ⁻¹	0.82
<i>DOB</i> rs11244	3'UTR(C>T)	4.26×10 ⁻¹	0.80	7.30×10 ⁻¹	0.85	5.30×10 ⁻¹	0.86	5.19×10 ⁻¹	0.81	8.26×10 ⁻¹	0.94	5.43×10 ⁻¹	0.87
<i>DOB</i> rs1383258	intron(G>A)	1.36×10 ⁻¹	0.64	4.36×10 ⁻¹	0.82	2.63×10 ⁻¹	0.72	4.52×10 ⁻¹	0.79	6.30×10 ⁻²	0.43	8.24×10 ⁻¹	0.92
<i>DOB</i> rs2071469	5'UTR(A>G)	1.92×10 ⁻¹	0.64	1.66×10 ⁻¹	0.82	1.21×10 ⁻¹	0.68	2.73×10 ⁻¹	0.72	3.75×10 ⁻¹	0.75	2.45×10 ⁻¹	0.83
<i>DOB</i> rs2071472	intron(G>A)	5.31×10 ⁻¹	0.83	4.81×10 ⁻¹	0.82	4.21×10 ⁻¹	0.86	8.61×10 ⁻¹	0.96	4.38×10 ⁻¹	0.78	5.98×10 ⁻¹	0.87
<i>DOB</i> rs7383287	synonymous(A>G)	9.61×10 ⁻¹	0.96	5.58×10 ⁻¹	0.82	8.00×10 ⁻¹	0.90	2.50×10 ⁻²	0.28	1.00×10 ⁻²	0.15	9.00×10 ⁻³	0.31
<i>DOB</i> rs2856997	intron(T>G)	7.21×10 ⁻¹	0.89	4.42×10 ⁻¹	0.82	8.22×10 ⁻¹	0.90	2.44×10 ⁻¹	0.72	2.43×10 ⁻¹	0.75	1.50×10 ⁻¹	0.82
<i>DOB</i> rs2071471	synonymous(C>T)	7.87×10 ⁻¹	0.89	5.36×10 ⁻¹	0.82	6.96×10 ⁻¹	0.88	7.10×10 ⁻¹	0.91	6.62×10 ⁻¹	0.88	8.00×10 ⁻¹	0.92
<i>DOB</i> rs2071475	intron(C>T)	3.70×10 ⁻¹	0.74	8.50×10 ⁻¹	0.90	5.26×10 ⁻¹	0.86	2.16×10 ⁻¹	0.72	6.27×10 ⁻¹	0.88	4.45×10 ⁻¹	0.87
<i>DOB</i> rs2856995	intron(T>A)	3.11×10 ⁻¹	0.74	5.05×10 ⁻¹	0.82	2.98×10 ⁻¹	0.72	2.64×10 ⁻¹	0.72	9.81×10 ⁻¹	0.99	4.30×10 ⁻¹	0.87
<i>TAP1</i> rs1135216	Missense(A>G)	3.53×10 ⁻¹	0.74	7.07×10 ⁻¹	0.85	5.00×10 ⁻¹	0.86	6.73×10 ⁻¹	0.91	3.18×10 ⁻¹	0.75	4.78×10 ⁻¹	0.87

SNPs	Location	Dominant		Recessive		Additive		Dominant		Recessive		Additive	
		<i>P</i> Value*	FDR*	<i>P</i> Value*	FDR*	<i>P</i> Value*	FDR*	<i>P</i> Value†	FDR†	<i>P</i> Value†	FDR†	<i>P</i> Value†	FDR†
<i>TAP2</i> rs1800454	Missense(G>A)	5.52×10 ⁻¹	0.83	3.18×10 ⁻¹	0.82	8.30×10 ⁻¹	0.90	1.58×10 ⁻¹	0.72	5.59×10 ⁻¹	0.88	3.05×10 ⁻¹	0.84
<i>LMP2</i> rs17587	Missense(G>A)	1.70×10 ⁻¹	0.64	2.55×10 ⁻¹	0.82	1.32×10 ⁻¹	0.68	3.03×10 ⁻¹	0.72	9.00×10 ⁻³	0.15	7.70×10 ⁻²	0.82
<i>LMP7</i> rs2071543	Missense(C>A)	6.02×10 ⁻¹	0.85	4.75×10 ⁻¹	0.82	4.89×10 ⁻¹	0.86	7.49×10 ⁻¹	0.91	4.90×10 ⁻²	0.42	3.18×10 ⁻¹	0.84
<i>tapasin</i> rs9277972	intron(A>T)	1.29×10 ⁻¹	0.64	7.48×10 ⁻¹	0.85	1.55×10 ⁻¹	0.68	9.79×10 ⁻¹	0.98	2.35×10 ⁻¹	0.75	6.97×10 ⁻¹	0.88
<i>tapasin</i> rs1059288	5'near gene(T>C)	2.07×10 ⁻¹	0.64	1.00×10 ⁻¹	0.82	8.2×10 ⁻²	0.68	9.29×10 ⁻¹	0.96	6.84×10 ⁻¹	0.88	8.77×10 ⁻¹	0.92
<i>tapasin</i> rs2282851	intron(C>T)	9.03×10 ⁻¹	0.96	3.13×10 ⁻¹	0.82	6.10×10 ⁻¹	0.88	9.02×10 ⁻¹	0.96	9.51×10 ⁻¹	0.99	9.01×10 ⁻¹	0.92

Logistic regression analyses adjusted for age, gender, experience of blood/plasma donation, and numbers of blood/plasma donation.

* HCV infected cases (including both resolvers and chronic cases) versus uninfected subjects.

† HCV chronic cases versus HCV resolvers.

Supplemental Table 3. Conditional analyses of selected SNPs in additive genetic model

a) SNPs associated with anti-HCV status						
SNPs	OR (95%CI) ^a	OR(95%CI) ^b	OR (95%CI) ^c			
rs1063478	0.77(0.62,0.97) ^d	0.79(0.64,0.98)	0.78(0.63-0.98)			
rs2284191	1.42(1.02,1.97)	1.45(1.03,2.03) ^d	1.41(1.00-1.97)			
rs11244	1.23(0.97,1.56)	1.27(1.01,1.62)	1.24(0.98-1.57) ^d			
b) SNPs associated with HCV chronicity						
SNPs	OR (95%CI) ^e	OR(95%CI) ^f	OR (95%CI) ^g	OR (95%CI) ^h	OR (95%CI) ⁱ	OR (95%CI) ^j
rs17587	0.71(0.52,0.97) ^k	0.72(0.53,0.99)	0.77(0.57,1.04)	0.75(0.55,1.01)	0.77(0.57,1.05)	0.78(0.58,1.06)
rs2071543	0.77(0.58,1.04)	0.80(0.59,1.08) ^k	0.84(0.63,1.12)	0.86(0.64,1.15)	0.83(0.62,1.11)	0.83(0.62,1.10)
rs2284191	0.65(0.45,0.95)	0.66(0.45,0.96)	0.71(0.46,1.10) ^k	0.66(0.45,0.97)	0.65(0.45,0.95)	0.70(0.46,1.07)
rs7383287	0.72(0.58,0.92)	0.74(0.59,0.92)	0.73(0.59,0.92)	0.74(0.59,0.92) ^k	0.73(0.58,0.91)	0.74(0.59,0.92)
rs376892	0.97(0.73,1.30)	0.96(0.72,1.29)	0.98(0.73,1.32)	0.96(0.72,1.29)	1.08(0.74,1.57) ^k	1.17(0.82,1.67)
rs416622	0.83(0.65,1.06)	0.81(0.64,1.04)	0.90(0.69,1.18)	0.83(0.65,1.07)	0.76(0.56,1.02)	0.89(0.63,1.27) ^k

Logistic regression analyses adjusted for age, gender, experience of blood/plasma donation, and numbers of blood/plasma donation.

^a Logistic regression analyses conditioned on rs1063478

^b Logistic regression analyses conditioned on rs2284191

^c Logistic regression analyses conditioned on rs11244

^d Logistic regression analyses conditioned on the other two polymorphisms

^e Logistic regression analyses conditioned on rs17587

^f Logistic regression analyses conditioned on rs2071543

^g Logistic regression analyses conditioned on rs2284191

^h Logistic regression analyses conditioned on rs7383287

ⁱ Logistic regression analyses conditioned on rs376892

^j Logistic regression analyses conditioned on rs416622

^k Logistic regression analyses conditioned on the other five polymorphisms

Supplemental Table 4. Stratified analyses of combined favorable alleles and HCV infection outcomes

a) SNPs associated with anti-HCV status (rs1063478-T and rs2284191-G, 0-2 vs.3-4)				
Variables	Uninfected	Infected	OR (95%CI)	P
Age				0.123
<60	152/142	250/159	0.62 (0.43-0.88)	
≥60	112/76	189/127	0.84 (0.53-1.34)	
Gender				0.023
Male	77/57	99/60	0.75 (0.41-1.38)	
Female	187/161	340/226	0.68 (0.49-0.94)	
Blood donation				0.971
Never	33/24	50/29	0.55 (0.24-1.28)	
Ever	231/194	389/257	0.69 (0.51-0.94)	
Numbers of blood donation				0.691
<30	137/113	234/159	0.79 (0.54-1.15)	
≥30	127/105	205/127	0.61 (0.40-0.93)	
Plasma donation				0.024
Never	80/64	18/25	1.14 (0.51-2.57)	
Ever	184/154	421/261	0.66 (0.49-0.90)	
Numbers of plasma donation				0.706
<50	199/164	251/156	0.67 (0.47-0.95)	
≥50	65/54	188/130	0.72 (0.45-1.16)	
b) SNPs associated with HCV chronicity (rs17587-A and rs7383287-G, 0 vs.1-4)				
Variables	Resolver	Chronic	OR (95%CI)	P
Age				0.105
<60	38/73	154/144	0.49 (0.31-0.78)	
≥60	33/49	103/131	0.90 (0.53-1.51)	
Gender				0.923
Male	15/24	61/59	0.51 (0.23-1.13)	
Female	56/98	196/216	0.63 (0.43-0.93)	
Blood donation				0.332
Never	6/17	27/29	0.41 (0.13-1.36)	
Ever	65/105	230/246	0.67 (0.47-0.97)	
Numbers of blood donation				0.144
<30	33/78	127/155	0.50 (0.31-0.81)	
≥30	38/44	130/120	0.80 (0.48-1.33)	
Plasma donation				0.403

Variables	Resolver	Chronic	OR (95%CI)	P
Never	6/8	12/17	0.70 (0.09-5.35)	
Ever	65/114	245/258	0.61 (0.43-0.87)	
Numbers of plasma donation				0.167
<50	44/61	146/156	0.91 (0.57-1.46)	
≥50	27/6	111/119	0.46 (0.27-0.78)	

Logistic regression analyses adjusted for age, gender, experience of blood/plasma donation, and numbers of blood/plasma donation (excluded the stratified factor in each stratum).

^aP value for the heterogeneity test.

Supplemental Table 5. Linkage disequilibrium (LD) information in uninfected subjects

a) LD of rs1063478, rs2284191, and rs11244						
	rs1063478	rs2284191	rs11244			
rs1063478	--	0.10 ^a	0.21 ^a			
rs2284191	0 ^b	--	0.04 ^a			
rs11244	0.01 ^b	0 ^b	--			

b) LD of rs17587, rs2071543, rs2284191, rs7383287, rs376892, and rs416622						
	rs17587	rs2071543	rs2284191	rs7383287	rs376892	rs416622
rs17587	--	0.87 ^a	0.04 ^a	0.24 ^a	0.05 ^a	0.34 ^a
rs2071543	0.04 ^b	--	0.02 ^a	0.08 ^a	0.01 ^a	0.08 ^a
rs2284191	0 ^b	0 ^b	--	0.03 ^a	0.10 ^a	0.94 ^a
rs7383287	0 ^b	0.01 ^b	0 ^b	--	0.01 ^a	0.08 ^a
rs376892	0 ^b	0 ^b	0 ^b	0 ^b	--	0.82 ^a
rs416622	0 ^b	0 ^b	0.19 ^b	0 ^b	0.34 ^b	--

^a D', ^b R