

mg/velpatasvir
100 mg qd) with
or without
Ribavirin

mg/velpatasvir
100 mg qd) with
or without
Ribavirin

mg/velpatasvir
100 mg qd) with or
without Ribavirin

mg/velpatasvir
100 mg qd) with or
without Ribavirin

mg/velpatasvir
100 mg qd) with
or without
Ribavirin

mg/velpatasvir
100 mg qd)
with or without
Ribavirin

DAA: direct-acting antiviral agent; D: duration; W: weeks

Supplementary Table 2. The 13 single-nucleotide polymorphisms evaluated in the study.

Gene	SNP ID	ID number of TaqMan assays	Chromosome	Location	Risk allele	MAF	Allele 2
IFNL3	rs12979860	C__7820464_10	19q13.2	39248147	T	0.07532	C
ABCB1	rs1045642	C__7586657_20	7q21.12	87138645	A	0.3571	G
HLA II	rs9461776	C__30460277_20	6p21.32	32575735	G	0.07171	A
NOTCH4	rs2071286	C__15861180_10	6p21.32	32179896	T	0.1226	C
ACHE	rs6976053	C__32067460_10	7q22.1	100512119	C	0.4056	T
ARNTL	rs6486122	C__2160490_10	11p15.2	13361524	T	0.3909	C
PPARG	rs11128603	NA	3p25.2	12385828	G	0.03038	A
NAMPT	rs61330082	NA	7q22.3	105926865	T	0.4892	C
NAMPT	rs2302559	C__2673293_10	7q22.3	105903904	T	0.1097	C
NAMPT	rs10953502	C__31761492_10	7q22.3	105892431	C	0.1454	T
NAMPT	rs2058539	C__11613113_10	7q22.3	105916637	C	0.1097	A
RETN	rs1423096	C__1394117_20	19p13.2	7674290	C	0.28332	T
RETN	rs1477341	C__8351534_10	19p13.2	7671912	A	0.47552	T

IFNL3: interferon λ 3; ABCB1: ATP-binding cassette sub-family B member 1; HLA II: human leukocyte antigen class II; NOTCH4: neurogenic locus notch homolog protein 4; SERPINE1: Serpin family E member 1; ARNTL: aryl hydrocarbon receptor nuclear translocator-like protein 1; PPARG: peroxisome proliferator-activated receptor gamma; NAMPT: Nicotinamide phosphoribosyltransferase; RETN: resistin; NA: not assessable; MAF: minor allele frequency.

Supplementary Table 3. Primer sequences used in the single-nucleotide polymorphisms of NAMPT-rs61330082.

Genes	Primers	Sequences (5'->3')
NAMPT	NAMPT-F	5'- TGTTTCAAACCTCGTT GCTG -3'
	NAMPT-R	5'- GAGGCATGGCTGAGACTTCTA -3'

ScrFI for rs61330082—Allele C is cuttable, yielding two fragments of 65 and 138 bp; allele T is uncuttable, and the fragment is still 203 bp.

Supplementary Table 4. Genetic analyses for various single-nucleotide polymorphisms with HCV RNA and mixed cryoglobulinemia.

SNPs	A1	A2	Y	allele1	allele2	geno11	geno12	geno22	Geno <i>p</i>	Trend <i>p</i>	Allelic <i>p</i>	Dom <i>p</i>	Rec <i>p</i>	Add <i>p</i>	OR	95% CI OR	Permu <i>p</i>
rs11128603	G	A	RNA	0.03038	0.96962	0	0.060757	0.939243	0.8255	0.671	0.8283	0.8255	1	0.6715	1.225	0.4789-3.135	0.6712
rs11128603	G	A	MC	0.03038	0.96962	0	0.060757	0.939243	0.7901	0.6913	0.7933	0.7901	1	0.6914	1.112	0.6573-1.883	0.6998
rs2071286	T	C	RNA	0.1226	0.8774	0.013903	0.217478	0.76862	0.01202	0.02822	0.03317	0.139	0.0096	0.02956	0.6448	0.4343-0.957	0.02862
rs2071286	T	C	MC	0.1226	0.8774	0.013903	0.217478	0.76862	0.7903	0.5518	0.5839	0.6513	0.7873	0.5519	0.9216	0.7041-1.206	0.5525
rs9461776	G	A	RNA	0.07171	0.92829	0.010956	0.121514	0.86753	0.007141	0.006055	0.006726	0.003383	1	0.007159	0.5492	0.3548-0.85	0.00623
rs9461776	G	A	MC	0.07171	0.92829	0.010956	0.121514	0.86753	0.6394	0.448	0.4853	0.3987	1	0.4484	1.137	0.816-1.584	0.4481
rs1045642	A	G	RNA	0.3571	0.6429	0.128684	0.456778	0.414538	0.4185	0.3394	0.36	0.7528	0.2161	0.3399	1.16	0.8554-1.573	0.3401
rs1045642	A	G	MC	0.3571	0.6429	0.128684	0.456778	0.414538	0.631	0.7451	0.744	0.898	0.3968	0.7451	0.9702	0.8083-1.164	0.7454
rs6976053	C	T	RNA	0.4056	0.5944	0.287119	0.236971	0.47591	1.04X10 ⁻¹²	9.44x10 ⁻¹¹	4.79x10 ⁻¹⁷	3.97x10 ⁻⁸	1.73x10 ⁻¹²	2.64x10 ⁻⁰⁹	2.767	1.979-3.868	0.00001
rs6976053	C	T	MC	0.4056	0.5944	0.287119	0.236971	0.47591	0.3214	0.3836	0.2948	0.8002	0.1846	0.3837	1.067	0.9222-1.234	0.3833
rs10953502	C	T	RNA	0.1454	0.8546	0.061776	0.16731	0.770914	0.1107	0.06614	0.03219	0.179	0.068	0.07314	1.832	0.9448-3.551	0.06896
rs10953502	C	T	MC	0.1454	0.8546	0.061776	0.16731	0.770914	0.283	0.1125	0.06938	0.1214	0.3663	0.1136	1.227	0.9523-1.582	0.1126
rs2302559	T	C	RNA	0.1131	0.8869	0.015171	0.195954	0.788875	0.1058	0.1044	0.1152	0.08215	0.5746	0.1102	1.885	0.8659-4.104	0.1059
rs2302559	T	C	MC	0.1131	0.8869	0.015171	0.195954	0.788875	0.9351	0.7442	0.749	0.7252	1	0.7442	0.9497	0.6967-1.295	0.7481
rs2058539	C	A	RNA	0.1097	0.8903	0.003871	0.211613	0.784516	0.3249	0.1197	0.1495	0.165	1	0.1253	1.877	0.8392-4.198	0.122
rs2058539	C	A	MC	0.1097	0.8903	0.003871	0.211613	0.784516	0.4868	0.2046	0.2499	0.2173	1	0.2052	1.247	0.8862-1.754	0.2048
rs61330082	T	C	RNA	0.4892	0.5108	0.192641	0.593074	0.214286	0.4819	0.4915	0.5827	0.2723	1	0.4917	0.8695	0.5836-1.295	0.4996
rs61330082	T	C	MC	0.4892	0.5108	0.192641	0.593074	0.214286	0.4608	0.8664	0.888	0.5713	0.3998	0.8664	0.9826	0.8011-1.205	0.8678
rs6486122	T	C	RNA	0.3909	0.6091	0.219178	0.343444	0.437378	0.009836	0.7211	0.708	0.0948	0.1692	0.7211	0.954	0.7367-1.235	0.7158
rs6486122	T	C	MC	0.3909	0.6091	0.219178	0.343444	0.437378	0.1045	0.03313	0.01738	0.05637	0.09375	0.03337	1.189	1.014-1.395	0.03284
rs12979860	T	C	RNA	0.07532	0.92468	0.016521	0.11759	0.865889	0.005611	0.00264	0.000428	0.001238	0.4033	0.005809	3.98	1.492-10.62	0.00428
rs12979860	T	C	MC	0.07532	0.92468	0.016521	0.11759	0.865889	0.06041	0.0215	0.01452	0.0428	0.08676	0.0226	0.6996	0.5146-0.951	0.0203
rs1423096	C	T	RNA	0.28332	0.71668	0.087195	0.272885	0.639920	0.889963	0.7188	0.83269	0.71832	0.99321	0.70869	1.180	0.478-2.908	0.8956
rs1423096	C	T	MC	0.28332	0.71668	0.087195	0.272885	0.639920	0.1932	0.1953	0.1023	0.3852	0.22365	0.198	0.829	0.625-1.099	0.2369
rs1477341	A	T	RNA	0.47552	0.52448	0.257660	0.412359	0.329981	0.632123	0.63889	0.77236	0.2358	0.8236520	0.56321	0.7269	0.192-2.751	0.4463
rs1477341	A	T	MC	0.47552	0.52448	0.257660	0.412359	0.329981	0.7472	0.8659	0.7236	0.5689	0.7963	0.4332	0.9552	0.7222-1.2638	0.7896

A1: allele 1 frequency; A2: allele 2 frequency; Y: dependent factor; RNA: HCV RNA; MC: mixed cryoglobulinemia; geno11: genotype 11 frequency; geno12: genotype 12 frequency; geno 22: genotype 22 frequency; Geno *p*: *p* values of genotypic test; Trend *p*: *p* values of trend test; Allelic *p*: *p* values of allelic test; Dom *p*: *p* values of associated test (genetic model=dominant); Rec *p*: *p* values of associated test (genetic model=recessive); Add *p*: *p* values of logistic regression(genetic model=additive) for qualitative trait; OR: odds ration; CI: confidence interval; Permu *p*: *p* values of permutation test (N=100000).

Supplementary Table 5. IFNL3-rs12978960 variant distributions among various status.

	CHC (n=934)			Spontaneous HCV clearance (n=109)		
	MC (0) (n=384)	MC (1) (n=550)	<i>p</i> values	MC (0) (n=70)	MC (1) (n=39)	<i>p</i> values
IFNL3-rs12979860 CC genotype, n (%)	314 (81.8)	477 (86.7)	0.011	67 (95.7)	38 (97.4)	0.518
ARNTL-rs6486122 TT genotype, n (%)	75 (19.5)	132 (24)	0.059	11 (15.7)	6 (15.4)	0.191

CHC: chronic hepatitis C virus infection; MC: mixed cryoglobulinemia

Supplementary Table 6. Genetic associations with pre-therapy cyoglobulinemic vasculitis.

	Univariate analyses		
	OR	95% CI OR	<i>p</i> values
HCV RNA positivity	3.53X10 ⁷	0.00-	0.996
IFNL3-rs12979860 TT, TC, CC genotype (0, 1, 2)	0.762	0.292-1.993	0.58
ABCB1-rs1045642 GG, GA, AA genotype (0, 1, 2)	1.337	0.71-2.516	0.368
HLA II-rs9461776 GG, GA, AA genotype (0, 1, 2)	1.437	0.359-5.757	0.608
NOTCH4-rs2071286 CC, CT, TT genotype (0, 1, 2)	0.368	0.088-1.544	0.172
SERPINE1-rs6976053 TT, TC, CC genotype (0, 1, 2)	1.091	0.644-1.848	0.746
ARNTL-rs6486122 CC, CT, TT genotype (0, 1, 2)	0.948	0.535-1.679	0.854
PPARG-rs11128603 GG, GA, AA genotype (0, 1, 2)	0.574	0.13-2.533	0.464
NAMPT-rs61330082 CC, CT, TT genotype (0, 1, 2)	0.821	0.409-1.648	0.579
NAMPT-rs2302559 CC, CT, TT genotype (0, 1, 2)	0.922	0.327-2.599	0.878
NAMPT-rs10953502 CC, CT, TT genotype (0, 1, 2)	1.242	0.608-2.538	0.553
NAMPT-rs2058539 CC, CT, TT genotype (0, 1, 2)	0.495	0.2-1.222	0.127
RETN-rs1423096 CC, CT, TT genotype (0, 1, 2)	1.322	0.708-2.468	0.381
RETN-rs1477341 AA, AT, AT genotype (0, 1, 2)	3.574	0.842-15.178	0.084

IFNL3: interferon λ 3; ABCB1: ATP binding cassette subfamily B member 1; HLA II: Human leucocyte antigen class II; NOTCH4: neurogenic locus notch homolog protein 4; SERPINE1: Serpin Family E Member 1; ARNTL: aryl hydrocarbon receptor nuclear translocator like; PPARG: peroxisome proliferator-activated receptor gamma; NAMPT: Nicotinamide phosphoribosyltransferase; OR: odds ratio.