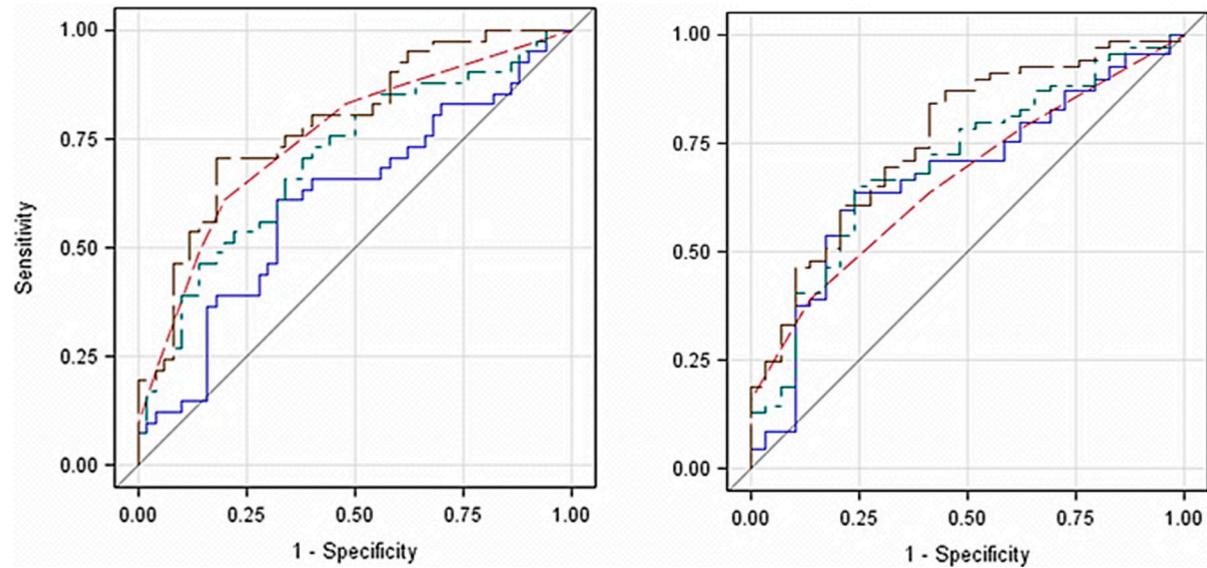


Supplementary Information



	HCV Genotype 1 (Left)	HCV Genotype 3 (Right)
	AUC (95% CI)	AUC (95% CI)
Non-gene classifier (blue line)	0.60 (0.48, 0.73)	0.71 (0.59, 0.83)
Two-gene classifier (red line)	0.74 (0.64, 0.85)	0.68 (0.57, 0.78)
Combined: <i>IL28B</i>*non-gene classifier (green line)	0.73 (0.62, 0.84)	0.75 (0.64, 0.86)
Combined: Two gene*non-gene classifier (brown line)	0.79 (0.69, 0.89)	0.79 (0.69, 0.88)

Figure S1. Operating characteristic (ROC) curves for factors associated with SVR.

Table S1. Allele frequencies for 30 single nucleotide polymorphisms studied in the intrinsic apoptosis pathway.

Candidate Gene Symbol	RS No.	Gene Function	Call Rate, %	Amino Acid Change	Base Change	Overall MAF, %	MAF, %		Allelic p-Value	FDR Corrected p-Value
							SVR	No-Response/Relapse		
GITRL	rs2235577	Intron	98		A/G	26	29	21	0.053	0.031
	rs2236876	Intron	98		C/T	47	30	21	0.073	0.034
	rs975074	Intron	98		T/G	47	44	52	0.080	0.038
	rs9286880	Intron	97		T/G	26	25	28	0.871	0.041
CD27BP	rs1132975	Coding synonymous	98		C/T	22	35	36	0.822	0.044
BCL2L1	rs6119652	Intron	99		C/G	29	34	21	0.011	0.006
	rs6060627	Intron	98		C/T	30	35	23	0.023	0.028
	rs6121172	Intron	99		A/C	29	34	22	0.015	0.013
	rs6087771 **	Intron	-		T/C					
	rs6088997	Intron	97		T/C	29	35	23	0.016	0.016
	rs6060857	Intron	98		A/G	29	35	22	0.010	0.003
	rs6060621	Intron	98		G/C	29	34	22	0.019	0.025
	rs12479491	Intron	97		T/C	29	34	22	0.012	0.009
	rs6060599	Intron	99		T/G	29	34	22	0.015	0.013
	rs6121038	Intron	98		T/G	25	30	18		
	rs6060652	Intron	99		A/G	30	35	23	0.019	0.022
	rs1484994	Intron	98		T/C	29	34	22	0.016	0.019
	rs11550472 *	Exon	94	Leu163/226Pro	C/T	0				
	rs7362890 *	Exon	96	Val163/223Gly	A/C	0				
	rs139457299 **	Exon	-	Leu108Arg	A/C					
	rs138364013 *	Exon	99	Asp76Asn	C/T	0				
	rs11550473 *	Exon	98	Ala64Thr	A/G	0				
	rs145910874 *	Exon	99	Ser43Leu	A/G	0				
	rs148274815 *	Exon	98	Arg6Gln	C/T	0				

Table S2. *Cont.*

Candidate Gene Symbol	RS No.	Gene Function	Call Rate, %	Amino Acid Change	Base Change	Overall MAF, %	MAF, %		Allelic p-Value	FDR Corrected p-Value
							SVR	No-Response/Relapse		
BCL-2	rs148811059 *	Exon	97	Gly203Ser	C/T	0				
	rs138465313 *	Exon	100	Gly237Ser	C/T	0				
	rs113163226 *	Exon	98	Ser222Gly	C/T	0				
	rs61733415 *	Exon	97	Phe124Leu	A/G	0				
	rs1801018	Coding synonymous	100		G/A	46	45	46	1	0.047
	rs1800477 **	Exon	-	Ala43Thr	A/G					

MAF, minor allele frequency; SVR, sustained virological response; FDR, false discovery rate; GITRL, glucocorticoid induced tumor necrosis factor receptor ligand; CD27BP, CD27 binding protein; BCL2L1, B-cell lymphoma2-like1; BCL-2, B-cell lymphoma-2. * Monomorphic SNPs; ** Failed genotyping. SNPs in bold are significant when corrected for multiple testing.

Table S2. Distribution and association to treatment response of four single nucleotide polymorphisms in the *BCL2L1* gene.

SNPs in <i>BCL2L1</i>	SVR <i>n</i> = 117	No-Response/Relapse <i>n</i> = 84	Total	Genotypic <i>p</i> -Value, χ^2 Test	Allelic <i>p</i> -Value, Fisher's Exact Test
rs1484994					
CC	15 (88)	2 (12)	17		
TC	46 (58)	33 (42)	79	0.018	0.016
TT	52 (51)	49 (49)	101		
rs6060652					
AA	52 (52)	48 (48)	100		
GA	45 (62)	33 (38)	78	0.024	0.019
GG	17 (85)	3 (15)	20		
rs6060621					
CC	16 (89)	2 (11)	18		
GC	44 (57)	33 (43)	77	0.016	0.019
GG	53 (52)	48 (48)	101		
rs6060627					
CC	52 (53)	33 (42)	99		
TC	45 (58)	47 (47)	78	0.027	0.023
TT	17 (85)	3 (15)	20		

SNP, single nucleotide polymorphism; BCL2L1, B-cell lymphoma2-like1; SVR, sustained virological response.

Table S3. Univariate logistic regressions of sustained virological response in 201 chronic hepatitis C virus infected individuals.

Characteristic	HCV Genotype 1		HCV Genotype 3	
	Odds Ratio (95% CI)	p-Value	Odds Ratio (95% CI)	p-Value
Sex				1.00
Male	1	0.60	1	
Female	1.3 (0.5, 2.9)		1.0 (0.4, 2.4)	
Age at treatment initiation				
<40 years	1.9 (0.8, 4.9)	0.20	2.8 (1.1, 7.2)	0.03
≥40 years	1		1	
HCV viral load at treatment initiation		0.20		0.05
≥5.8 log IU/mL	1		1	
<5.8 log IU/mL	2.0 (0.8, 5.0)		2.6 (1.0, 7.0)	
IL28B rs12979860				
TT	1		1	
TC	1.6 (0.4, 6.6)	0.50	0.3 (0.0, 1.7)	0.30
CC	6.3 (1.3, 30.2)	0.02	0.3 (0.0, 1.5)	0.20
IL28B group				
TC + TT	1		1	
CC	4.3 (1.6, 11.2)	0.003	0.7 (0.3, 1.7)	0.40
BCL2L1, rs1484994				
TT	1		1	
TC	1.2 (0.5, 2.9)	0.7	1.5 (0.6, 4.1)	0.47
CC	8.8 (1.7, 45.1)	0.01	3.5 (0.6, infinite)	0.30

HCV, hepatitis C virus; CI, confidence interval; IL28B, interleukin 28B, rs12979860; BCL2L1, B-cell lymphoma2-like1.