SUPPLEMENTAL MATERIAL

Bibert et al., http://www.jem.org/cgi/content/full/jem.20130012/DC1

Table S1. Patient characteristics

Proportion	Response to treatment *n* = 540	Spontaneous clearance *n* = 93
Male sex	0.64	0.55
White ethnicity	1.00	1.00
Median age (IQR)[a]	45 (14)	38 (10)
HCV genotype[b]		
1	0.44	NA
2	0.13	NA
3	0.34	NA
4	0.09	NA
HCV RNA ≥6 log10 copies/ml[c]	0.52	NA
Median ALT (IU/L, IQR)[d]	79 (81)	NA
HCV reported risks		
Drug use	0.38	NA
Invasive procedures / needle stick	0.22	NA
Transfusion	0.17	NA
Other/Unknown	0.21	NA
Alcohol consumption[e]		
>40 g/d for ≥5 yr	0.20	NA
Diabetes	0.09	NA
Median BMI (kg/m^2, IQR)[f]	24 (5)	NA
HIV+[g]	0.05	NA
Chronic HBV infection[h]	0.03	NA
Biopsy		
Histological activity[i]		
0 (none or minimal)	0.34	NA
1 (mild, moderate or severe)	0.66	NA
Fibrosis stage (Metavir)[j]		
0–1	0.28	NA
2–4	0.72	NA
Steatosis[k]	0.67	NA

Numbers are the proportion of patients with indicated characteristics.
[a]Age at treatment start for patients with chronic infection, at cohort entry for those with spontaneous clearance.
[b]HCV genotypes are missing in most patients with spontaneous clearance.
[c]Median RNA before treatment was 6 log10 copies/ml; data were missing in 63 patients.
[d]ALT value before treatment was missing in 168 patients.
[e]Alcohol consumption data before treatment was missing in 8 patients.
[f]BMI before/during treatment was missing in 75 patients.
[g]HIV serology was missing in 95 patients.
[h]HBV serology was missing in 106 patients
[i]Histological activity before treatment was missing in 165 patients.
[j]Fibrosis stage before treatment was missing in 164 patients.
[k]Steatosis data before treatment were missing in 113 patients

Table S2. Genotypic association of *IL28B* polymorphisms with response to pegylated IFN-α and ribavirin in chronically infected HCV patients

Polymorphisms	Genotype	*n*	Prop. SVR[a]	Univariate models[b] (*n* = 540)		Multivariate models[b,c] (*n* = 360)	
				OR (95% CI)	P	OR (95% CI)	P
TT/-G	TT/TT	189	0.80				
	TT/-G	292	0.55	0.30 (0.20–0.46)	3.03^{-8}	0.18 (0.09-0.36)	6.95^{-7}
	-G/-G	59	0.41	0.17 (0.09–0.31)	2.77^{-8}	0.11 (0.04-0.33)	7.17^{-5}
rs12979860	CC	189	0.77				
	CT	289	0.56	0.38 (0.25–0.58)	4.41^{-6}	0.24 (0.13-0.46)	1.82^{-5}
	TT	62	0.45	0.24 (0.13–0.44)	4.42^{-6}	0.20 (0.07-0.53)	1.34^{-3}

OR stands for odds ratio and CI for confidence interval.
[a]Data indicate the proportion of patients with SVR for indicated host genotypes.
[b]Odd ratios and p-values for heterozygous and homozygous mutant patients versus WT patients.
[c]Multivariate models are adjusted for age, sex, HCV RNA level, fibrosis stage, and viral genotype. Multivariate models included a smaller number of patients, due to missing covariates in some patients.

Table S3. Primers

	Forward	Reverse	Vic probe	Fam probe
RTPCR amplification				
IL28B	5′-CAGCTGCAGGTGAGGGAGCGCCCCG-3′	5′-GGTGGCCTCCAGAACCTT-3′		
IP-10	5′-CTGCTTTGGGGTTTATCAGA-3′	5′-CCACTGAAAGAATTTGGGC-3′		
TNF	5′-CAGAGGGCCTGTACCTCATC-3′	5′-GGAAGACCCCTCCCAGATAG-3′		
HPRT	5′-GAACGTCTTGCTCGAGATGTG-3′	5′-CCAGCAGGTCAGCAAAGAATT-3′		
PCR amplification				
PAun	5′-TCAGCCTCGCCTGGTCCTCC-3′	5′-TGCTGTGCCTTCACGCTCCG-3′		
BSPA	5′-GTTTTAGGGGGTATAGGGGTTG-3′	5′-AAACCCTCTCTTTAACTTCCCTAAC-3′		
SNP genotyping				
NCBI dbSNP ID				
rs12979860	5′-TGTACTGAACCAGGGAGCTC-3′	5′-GCGCGGAGTGCAATTCAAC-3′	TGGTTCGCGCCTTC	CTGGTTCACGCCTTC
TT/-G	5′-CTCCAGCGAGCGGTAGTG-3′	5′-GATGCGGCCGAGTGTCT-3′	TCGCAGAAGGCCC	ATCGCAGCGGCCC

Fragments containing the TT/-G were amplified from unmethylated DNA with PAun primers and from bisulfite-modified DNA, with bisulfite sequencing primers (BSPA) designed using MethPrimer