

**Additional File 7.** Comparison of senescence-associated secretory phenotype (SASP) proteins between females who spontaneously cleared HCV (SC group) versus controls (C group).

Marker	Un-adjusted			Adjusted		
	AMR (95%CI)	p-value	q-value	aAMR (95%CI)	p-value	q-value
EGF	1.32 (0.97–1.80)	0.092	0.356	1.35 (0.98–1.85)	0.076	0.271
Eotaxin	1.40 (0.88–2.22)	0.172	0.356	1.56 (0.96–2.54)	0.083	0.271
Gro-alpha/KC	1.18 (0.95–1.46)	0.147	0.356	1.18 (0.95–1.48)	0.155	0.354
GM-CSF	1.06 (0.79–1.41)	0.702	0.903	1.00 (0.75–1.32)	0.975	0.975
IFN-gamma	1.02 (0.82–1.26)	0.878	0.913	0.97 (0.79–1.19)	0.784	0.886
IL-1beta	1.03 (0.81–1.32)	0.790	0.903	1.05 (0.82–1.34)	0.710	0.879
IL-1alpha	1.24 (0.96–1.59)	0.107	0.356	1.27 (0.99–1.63)	0.067	0.271
IL-1RA	1.32 (1.03–1.69)	<b>0.035</b>	0.356	1.27 (0.99–1.62)	0.067	0.271
IL-2	1.01 (0.69–1.47)	0.957	0.957	1.04 (0.71–1.52)	0.860	0.894
IL-6	0.98 (0.74–1.29)	0.865	0.913	1.08 (0.83–1.41)	0.571	0.798
IL-7	1.04 (0.79–1.38)	0.765	0.903	1.07 (0.82–1.41)	0.614	0.798
IL-8	1.19 (0.96–1.49)	0.130	0.356	1.18 (0.94–1.49)	0.163	0.354
IL-13	1.15 (0.89–1.49)	0.296	0.494	1.12 (0.85–1.46)	0.429	0.710
IL-15	0.96 (0.73–1.27)	0.798	0.903	0.92 (0.71–1.18)	0.513	0.785
IL-18	1.25 (0.84–1.86)	0.288	0.494	1.23 (0.82–1.87)	0.329	0.611
IP-10	1.32 (0.78–2.22)	0.304	0.494	1.21 (0.75–1.95)	0.437	0.710
MCP-1	1.40 (0.88–2.21)	0.159	0.356	1.32 (0.83–2.11)	0.257	0.513
RANTES	1.07 (0.78–1.45)	0.691	0.903	0.97 (0.69–1.35)	0.841	0.894
SDF-1alpha	1.47 (1.18–1.83)	<b>0.002</b>	<b>0.055</b>	1.44 (1.15–1.80)	<b>0.004</b>	0.105
FGF-2	1.18 (0.95–1.46)	0.153	0.356	1.19 (0.95–1.48)	0.142	0.354
HGF	1.19 (0.93–1.52)	0.178	0.356	1.22 (0.96–1.56)	0.109	0.315
BNGF	1.18 (0.99–1.39)	0.072	0.356	1.20 (1.00–1.42)	<b>0.048</b>	0.271
PLGF-1	1.43 (1.01–2.02)	0.053	0.356	1.48 (1.04–2.08)	<b>0.037</b>	0.271
SCF	1.29 (1.00–1.65)	0.062	0.356	1.31 (1.02–1.68)	<b>0.048</b>	0.271
TNF-alpha	1.04 (0.81–1.34)	0.749	0.903	1.04 (0.80–1.34)	0.774	0.886
TNF-beta	1.05 (0.75–1.46)	0.780	0.903	1.09 (0.79–1.51)	0.591	0.798

**Statistics:** Data were calculated by Generalized Linear Models (GLM) with a gamma distribution (log-link). Multivariable models were adjusted by age, IL28 genotype, and AST, previously selected by a stepwise method (forward) (see **Results Section**). The q-values represent p-values corrected for multiple testing using the False Discovery Rate (FDR). Significant differences are shown in bold.

**Abbreviations:** AMR, arithmetic mean ratio; aAMR, adjusted AMR; 95%CI, 95% of confidence interval; p, level of significance; q, corrected level of significance; EGF, epidermal growth factor; GRO-alpha/KC, chemokine growth-regulated protein alpha; GM-CSF, granulocyte macrophage colony-stimulating factor; IFN, interferon; IL, interleukin; MCP-1, C-C motif chemokine ligand 2; RANTES, C-C motif chemokine ligand 5; SDF-1alpha, stromal cell-derived factor 1alpha; FGF-2, fibroblast growth factor 2; HGF, hepatocyte growth factor; Beta-NGF, nerve growth factor  $\beta$ ; PLGF-1, placental growth factor; SCF, skp, cullin, F-box containing complex; TNF, tumoral necrosis factor.