

Table S3. Experimental samples and sequencing platforms used throughout this study.

Viral sample	Sequencing platform	Number of samples	Number of amplicons	Aim
HCV double mutant DNA	454 GS-Junior	3	3	Control of basal nucleotide sequencing error
	MiSeq	3	3	
Standard HCV DNA +HCV double mutant DNA at proportion of 10%	454 GS-Junior	8	8	Control of PCR recombination
	MiSeq	4	4	
Viral RNA from G1a, G1b, G3a, and G4d HCV-infected patients at DAA treatment failure	MiSeq	4	16	Validation of subtype-specific deep-sequencing procedure
Viral RNA from G1a HCV-infected patient subjected to sequential DAA treatments	MiSeq	4	16	Validation of subtype-specific deep-sequencing procedure
Viral RNA from G1b HCV-infected patient at DAA treatment failure	454 GS-Junior	1	4	Comparative analysis using inter-sequencing platforms
	MiSeq	1	4	
Viral RNA from G1b HCV-infected patient at DAA treatment failure	MiSeq	1	4	Comparative analysis using intra-sequencing platforms