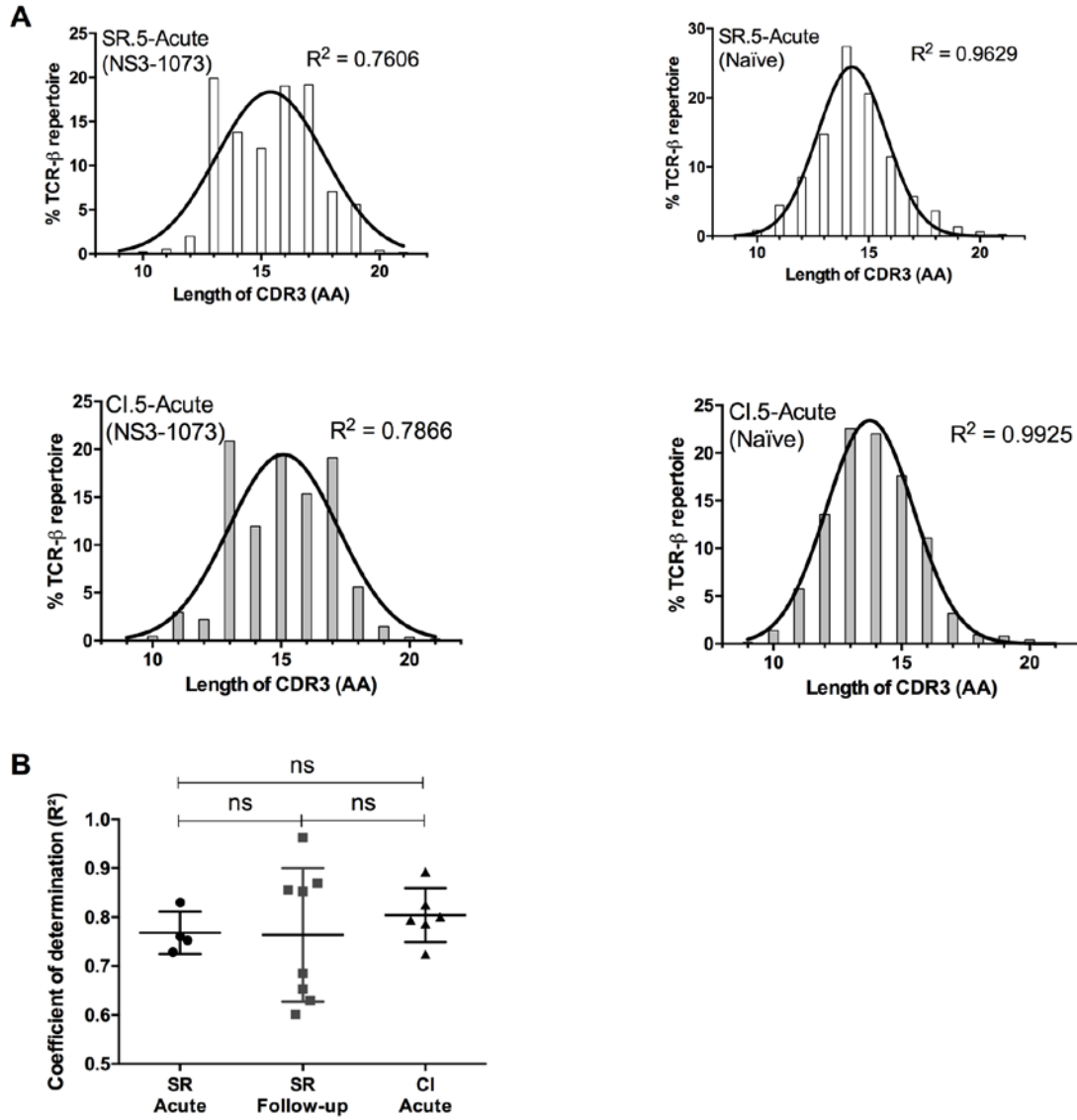


Supplementary Table S1: TCR deep-sequencing summary information

Sample Name	HCV NS3-1073 Tet+ Frequency (% of CD8 ⁺ T cells)	Sorted Cells (Number)	Productive Sequences (Total)	Productive Sequences (Unique) ^a	Clonality ^b
SR.1-Acute	2.55	25 815	8 422	783	0.3935
SR.1-Follow-up	2.16	5 459	766	244	0.1941
SR.2-Follow-up	0.83	27 279	9 834	3 399	0.1525
SR.3-Follow-up	0.63	1 505	777	461	0.0590
SR.4-Follow-up	0.89	14 051	4 691	1 475	0.1240
SR.5-Acute	5.74	49 531	15 141	2 093	0.2043
SR.5-Follow-up	0.73	3 041	362	241	0.0445
SR.6-Follow-up	0.51	910	595	299	0.0759
SR.7-Acute	2.30	10 888	2 900	1 306	0.0875
SR.7-Follow-up	0.70	3 871	496	299	0.0742
SR.8-Acute	0.77	2 753	521	339	0.0405
SR.8-Follow-up	0.27	756	113	103	0.0101
CI.1-Acute	2.33	15 485	8 699	653	0.3935
CI.2-Acute	5.42	35 471	9 739	1 805	0.1476
CI.3-Acute	11.03	27 433	8 421	650	0.2568
CI.4-Acute	0.95	2 714	675	302	0.0980
CI.5-Acute	39.08	285 445	61 180	5 103	0.18
CI.6-Acute	0.19	2 092	718	402	0.0617

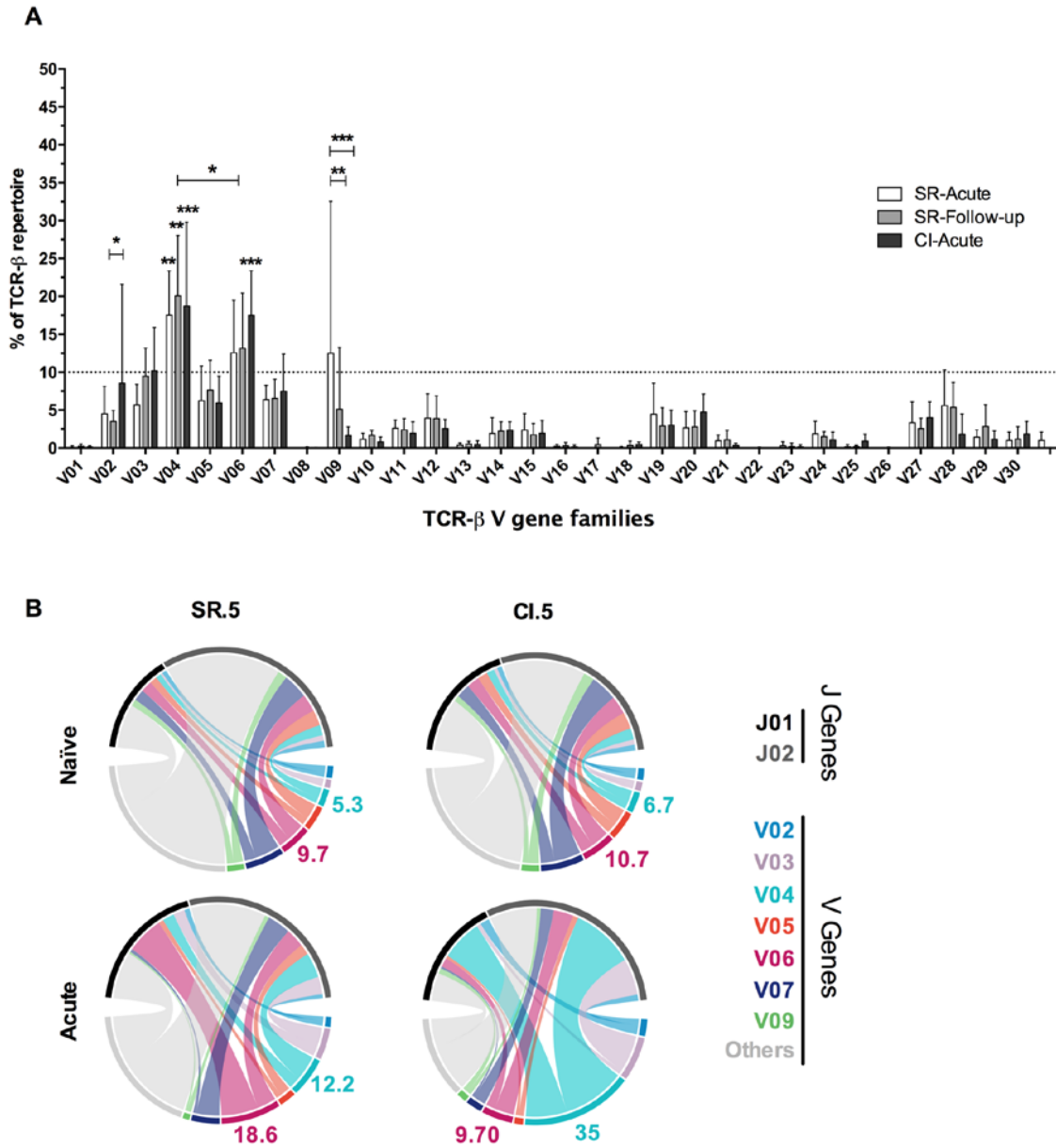
^aThe number of sequences in the sample that are in-frame and do not contain a STOP codon.

^bClonality measures the TCR repertoire distribution. It ranges from 0 (all clonotypes are equally abundant) to 1 (all clonotypes originated from a unique progenitor cell).



Supplementary Figure S1. Comparable NS3-1073 specific CD8⁺ T cell repertoire (TCR) CDR3 length between SR-Acute, SR-Follow-up and CI-Acute.

(A) Representative CDR3 amino acid (AA) length distribution analysis of the HCV-specific (left) and naïve (right) repertoire of SR.5 (Top) and CI.5 (Bottom) subjects. (B) Pooled data of the coefficient of determination (R^2) to compare CDR3 length distribution in all SR and CI subjects. One-way ANOVA; ns: not significant.



Supplementary Figure S2. V gene family usage of HCV NS3-1073 specific and naïve CD8⁺ T cells.

(A) Frequency of all TCRBV families among dominant ($\geq 1\%$), sub-dominant ($\geq 0.5\%$) and low abundance clonotypes ($\geq 0.1\%$) in SR subjects during acute (n=4) and follow-up (n=8) as well as CI-acute (n=6). Two-way ANOVA; *: $p \leq 0.05$; **: $p \leq 0.01$; ***: $p \leq 0.0001$. The dotted line indicates the 10% threshold used to select highly utilized V gene families. For simplicity, only key V gene families and those significant compared to at least three other families are highlighted. (B) V and corresponding J gene usage of HCV naïve (top) and HCV NS3-1073 specific CD8⁺ T cells (bottom) from SR.5-Follow-up and CI.5-Acute samples shown as chord diagrams representing frequencies of the dominant ($\geq 1\%$), sub-dominant ($\geq 0.5\%$), low frequency ($\geq 0.1\%$) and lowest abundance ($< 0.1\%$) clonotypes. The size of the colored arcs is proportional to V genes frequencies and the corresponding V-J pair