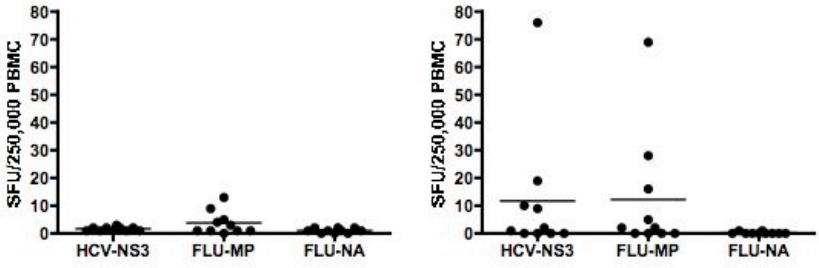
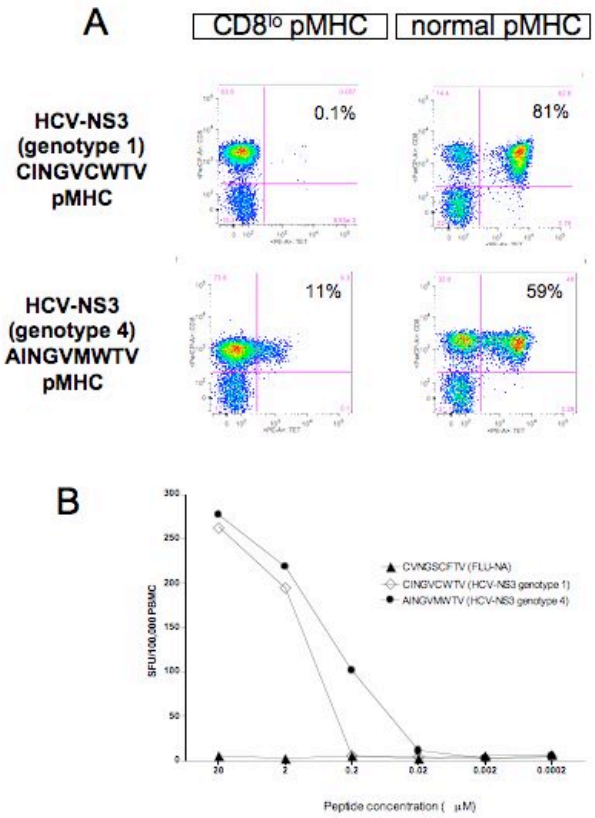
Sup.figure 1



HCV- individuals HCV+ individuals


A
CD8lo pMHC
normal pMHC
HCV-NS3 (genotype 1) CINGVCWTV pMHC
0.1%
81%
HCV-NS3 (genotype 4) AINGVMWTV pMHC
11%
59%
B
SFU/100,000 PBMC
CVNGSCFTV (FLU-NA)
CINGVCWTV (HCV-NS3 genotype 1)
AINGVMWTV (HCV-NS3 genotype 4)
Peptide concentration (μM)

N1 strains

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#EF382360_A/Egypt/0636-NAMRU3/2007_H5N1     IL RTQESECACV NGSCFTVMTD GPSSGQASYK
#ISDN257551_A/California/05/2007_H1N1       .. .......V.M ......I... ...NRA....
#CY025773_A/Florida/UR06-0280/2007_H1N1     .. .......V.. ......I... ...N.A....
#AB289338_A/Japan/305/1957-Bellamy/42_H2N1  .. .......V.. ......I... ...D.P....
#CY021703_A/Albany/4836/1950_H1N1           .. .......V.. ......I... ...D.P...R
#CY019973_A/Roma/1949_H1N1                  .. .......V.. ......I... ...D.P...R
#CY009614_A/FortMonmouth/1/1947_H1N1        .. .......V.. ......I... ...G.P....
#AY122327_A/Rhodes/1947_H1N1                .. .......V.. ......I... ...G.P....
#CY009598_A/Cam/1946_H1N1                   .. .......V.. ......I... ...G.P....
#EF467823_A/Puerto_Rico/8/1934_H1N1         .. .......... ......I... ...D.L....
#AF494252_A/Weiss/1943_H1N1                 .. .......V.. ......I... ...D.P....
#CY020463_A/Iowa/1943_H1N1                  .. .......... ......I... ...G.P....
#CY009278_A/Bellamy/1942_H1N1               .. .......V.. ......I... ...D.P....
#CY009326_A/Melbourne/1935_H1N1             .. .......... ......I... ...D.P....
#CY020471_A/Phila/1935_H1N1                 .. .......... ......I... ...D.L....
#EF190976_A/hvPR8/1934_(MA)_H1N1            .. .......... ......I... ...D.L....
#DQ508907_A/Wilson-Smith/1933_H1N1          .. .......T.. ......I... ...D.L....
#L25815_A/NWS/1933_H1N1                     .. .......T.. ......I... ...D.L....
#AF250356_A/Brevig_Mission/1/1918_H1N1      .. .......... ......I... ...N......
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N2 strains

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#ISDN257715_A/Colorado/15/2007_H3N2         LR TQESECVCIN GTCTVVMTDG SASGKADTKI
#CY007797_A/Canterbury/01/2005_H3N2         .. .......... .......... ..........
#CY009102_A/Canterbury/3/2000_H3N2          .. .......... .......... ..........
#CY000699_A/New_York/174/2000_H3N2          .. .......... .......... ..........
#AY377552_A/Finland/133/1990_H3N2           .. .......... .......... ...ER.....
#CY003066_A/Memphis/1/1990_H3N2             .. .......... .......... ...ER.....
#CY006893_A/Memphis/9/1980_H3N              .. .......... .......... ...ER.....
#CY006205_A/Nanjing/13/1980_H3N2            .. .......... .......... ...ER.....
#CY022948_A/Albany/3/1970_H3N2              .. .......... .......... ....R...R.
#AY210125_A/Queensland/7/1970_H3N2          .. .......... .......... ....R...R.
#AY209904_A/England/1/1961_H2N2             .. .......... .I........ ....R...R.
#CY021935_A/Albany/1/1960_H2N2              .. .......... .......... N...R...R.
#AB124655_A/Ann_Arbor/6/1960_H2N2           .. .......... .......... ....R...R.
#AY209898_A/ElSalvador/2/1957_H2N2          .. .......... .I........ ....R...R.
#L37330_A/Leningrad/134/17/1957_H2N2        .. .......... .......... ....R...R.
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Supplementary Figure Legends

Supplementary Fig 1: Ex vivo ELISpot responses from healthy donors and HCV+ donors

PBMC from a set of healthy donors (right hand panel) and the cohort of HCV+ donors (left hand panel) were stimulated in parallel in *ex vivo* IFNγ ELIspots using Flu matrix peptide, HCV-NS3 and Flu-NA peptide. HCV-NS3 responses were only identified in the HCV+ group, Flu Matrix responses were detectable in a proportion of both groups and Flu-NA responses were not detectable in either cohort. The HCV donor cells in this experiment were taken from a later timepoint than in Table 2. A new set of HLA-A2+ healthy donors was taken in parallel.

Supplementary Figure 2: pMHC staining and functional data using a peptide variant of HCV-NS3

Data are as for Figure 6A, using HCV-NS3 stimulated cell lines. A An enhanced staining pattern with the $CD8^{lo}$ tetramer refolded with the genotype 4 variant compared to the genotype 1 variant is illustrated in a further HCV+ donor (07-39). B A similar ELISpot response is illustrated from a further donor (554), indicating a functional response at lower peptide concentrations using the genotype 4 peptide.

Supplementary Figure 3: Variation in the Flu-NA epitope in circulating influenza strains

A series of global influenza strains were randomly downloaded from the Los Alamos influenza database on the basis of date at roughly 10 yearly intervals and the sequence of the major neuraminidase types N1 and N2 analyzed. There is variability at position 9 amongst N1 strains. The consensus sequence of N2 strains is divergent from that of N1 strains in this region but there is additional variability outside the epitope. For comparison the typical sequence of (avian) strains including N3, N4, N5, N6, N7 and N8 in this region are CIDGTCVVA, CQDEFCYTL, CIKGECYWV, CHNGICPVV and CIQGECYWV.