SUPPLEMENTARY FIGURES

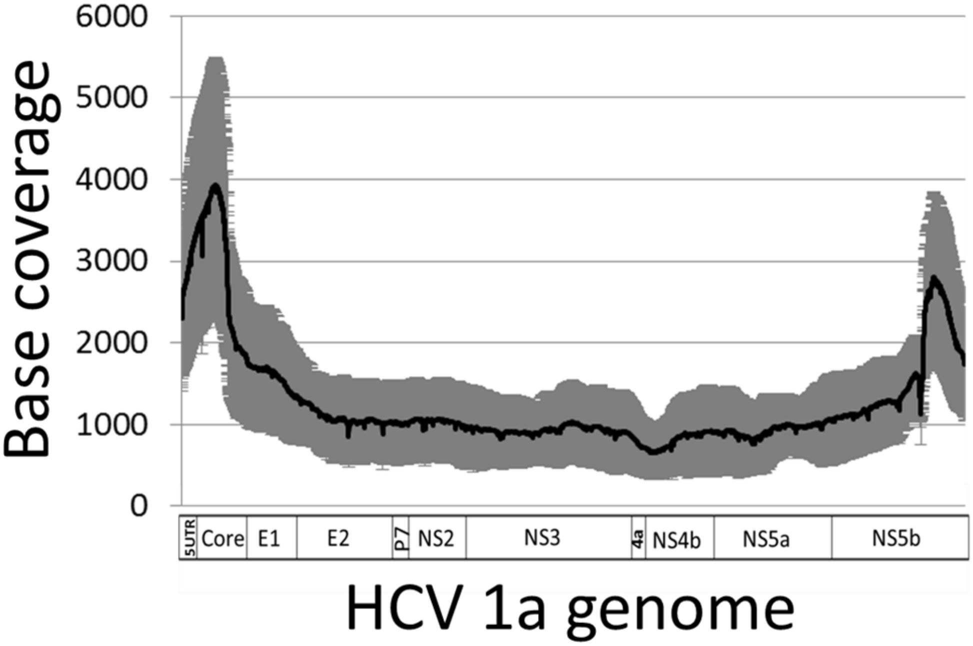

Fig. S1. Average base coverage over 9022-bp amplicon after read quality control. The amplicon covers 96% HCV genome from 5’UTR to NS5b as indicated at the bottom. Grey area represented standard derivation at each HCV genomic position.

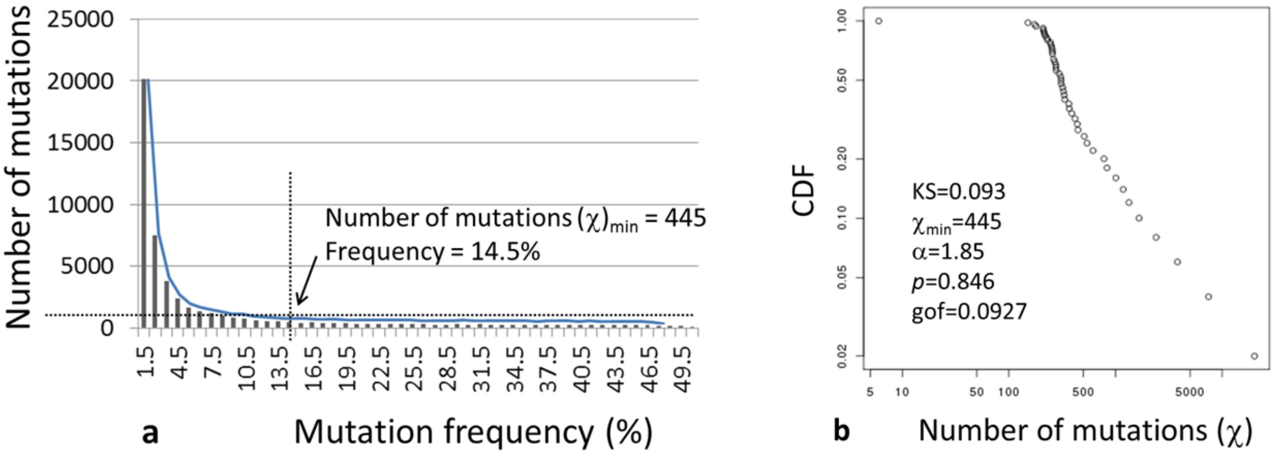

Fig. S2. The mutation frequency-based histogram of a total of 64,221 mutations identified in 104 samples (a), which fitted in with a power law distribution (b) with the low-bound point (χ_{min}) at 445, corresponding with a mutation frequency at 14.5% (a). CDF, cumulative distribution function.

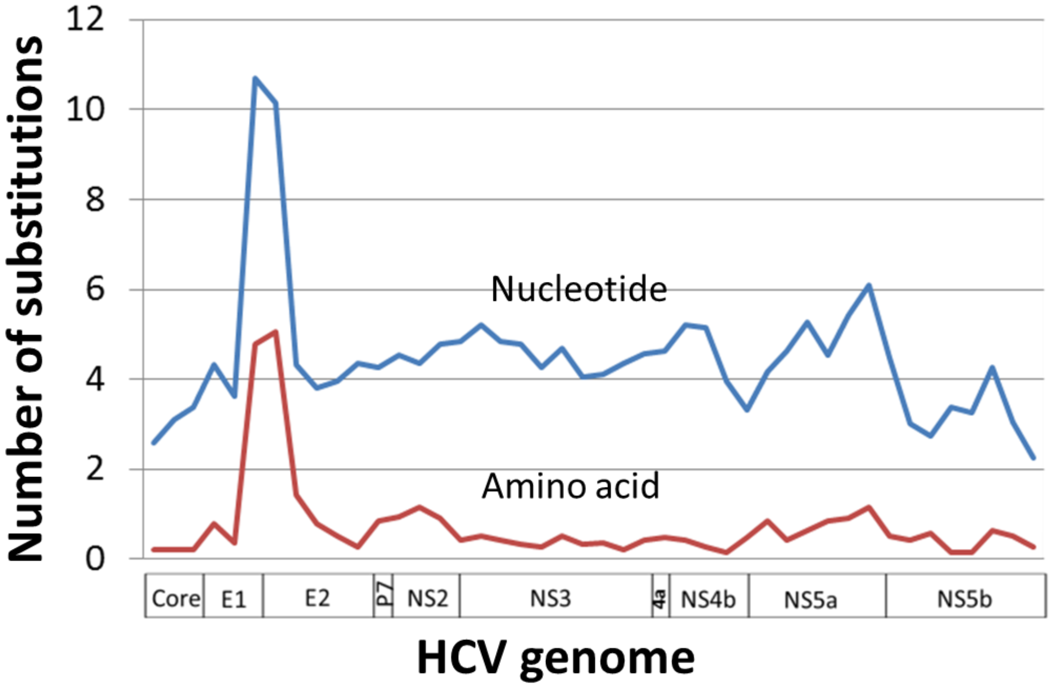

Fig. S3. Sliding window analysis (window=300 bp, step=99 bp) of amino acid (red) and nucleotide (blue) substitutions over the HCV genome in patients relapsed from the antiviral therapy. Peaks appeared on both curves correspond to the HCV HVR1 region.