Figure S7. Control of PCR-based recombination. A full-length reference (wt) viral HCV DNA was mixed with HCV DNA with mutations A7010C and G7073A (corresponding to amino acid substitutions N248K and E269K in NS5A) at a 90:10 ratio (depicted on the left of the top box). The total number of DNA molecules was 100,000. The mixture was used as a template to determine the degree of recombination after the amplification and sequencing process, following four different protocols (termed 1 to 4), and two next-generation sequencing platforms (454 GS-Junior and Illumina MiSeq). Protocol conditions are described in Materials and Methods. Top box depicts the four types of expected molecules; wt clone, mutant N248K/E269K, and recombinant molecules N248K/wt and wt/E269K. Each experiment was performed in duplicate (replicates 1 and 2), and the average frequency (%) of both replicates is shown on the right of each molecule; n.d. means not detected. The percentage of reads that include the indicated substitutions is represented for each haplotype and protocol in the three panels at the bottom.