Figure S4

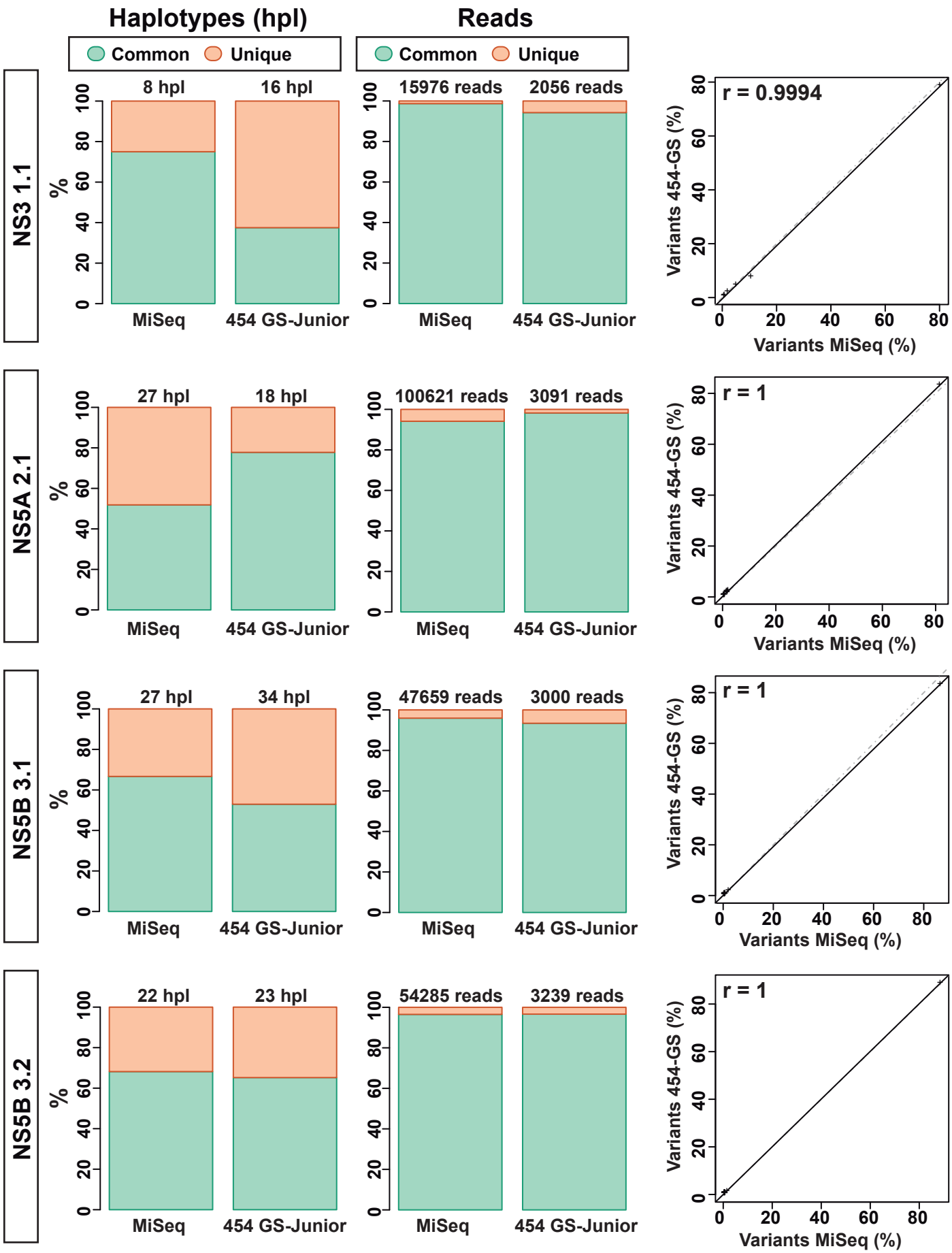
Haplotypes (hpl)
Reads
Common
Unique
NS3 1.1
8 hpl
16 hpl
15976 reads
2056 reads
NS5A 2.1
27 hpl
18 hpl
100621 reads
3091 reads
NS5B 3.1
27 hpl
34 hpl
47659 reads
3000 reads
NS5B 3.2
22 hpl
23 hpl
54285 reads
3239 reads
%
MiSeq
454 GS-Junior
r = 0.9994
r = 1
Variants 454-GS (%)
Variants MiSeq (%)

Figure S4 *(continued)*

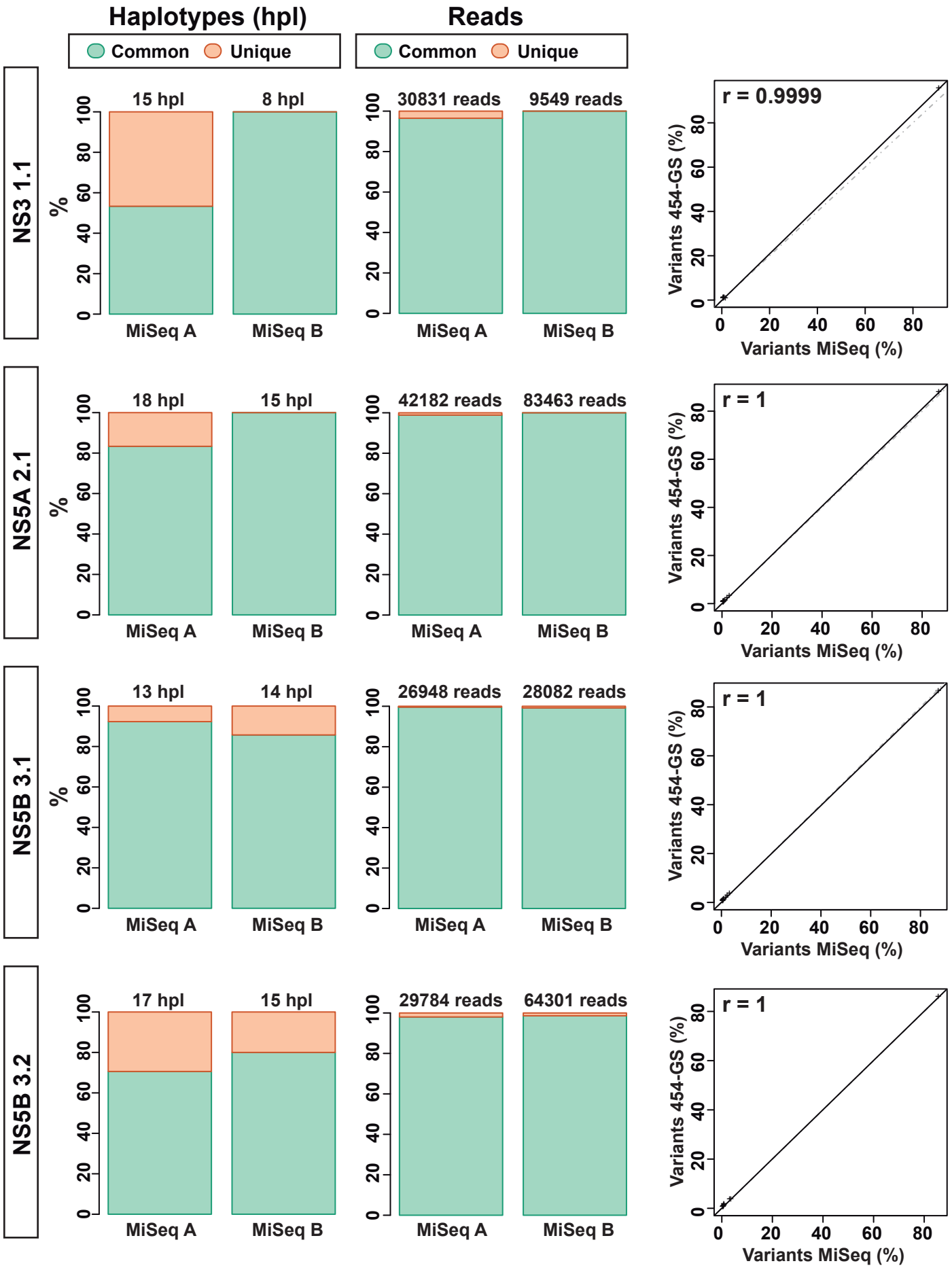

Figure S4. Comparative analysis using inter- and intra- sequencing platforms. Viral RNAs of two G1b HCV-infected patients (termed 8101 and JRR) at treatment (simeprevir/sofosbuvir/ribavirin) failure were used to amplify NS3- (PCR 1.1 in Figure 2), NS5A- (PCR 2.1 in Figure 2), and NS5B-coding regions (PCRs 3.1 and 3.2 in Figure 2), following the procedure described in Materials ans Methods. Amplicons derived from 8101 viral RNA amplifications were sequenced in parallel using MiSeq and 454 GS-Junior platforms (inter-sequencing platforms comparison). Amplicons derived from JRR viral RNA amplifications were sequenced twice in two different runs using MiSeq platform (MiSeq A and B) (intra-sequencing platform comparison). Percentage of common and unique haplotypes and reads between both runs at each comparison are represented. Scatter plots comparing the percentage of variants obtained according to the two runs of each amplicon are shown on the right.