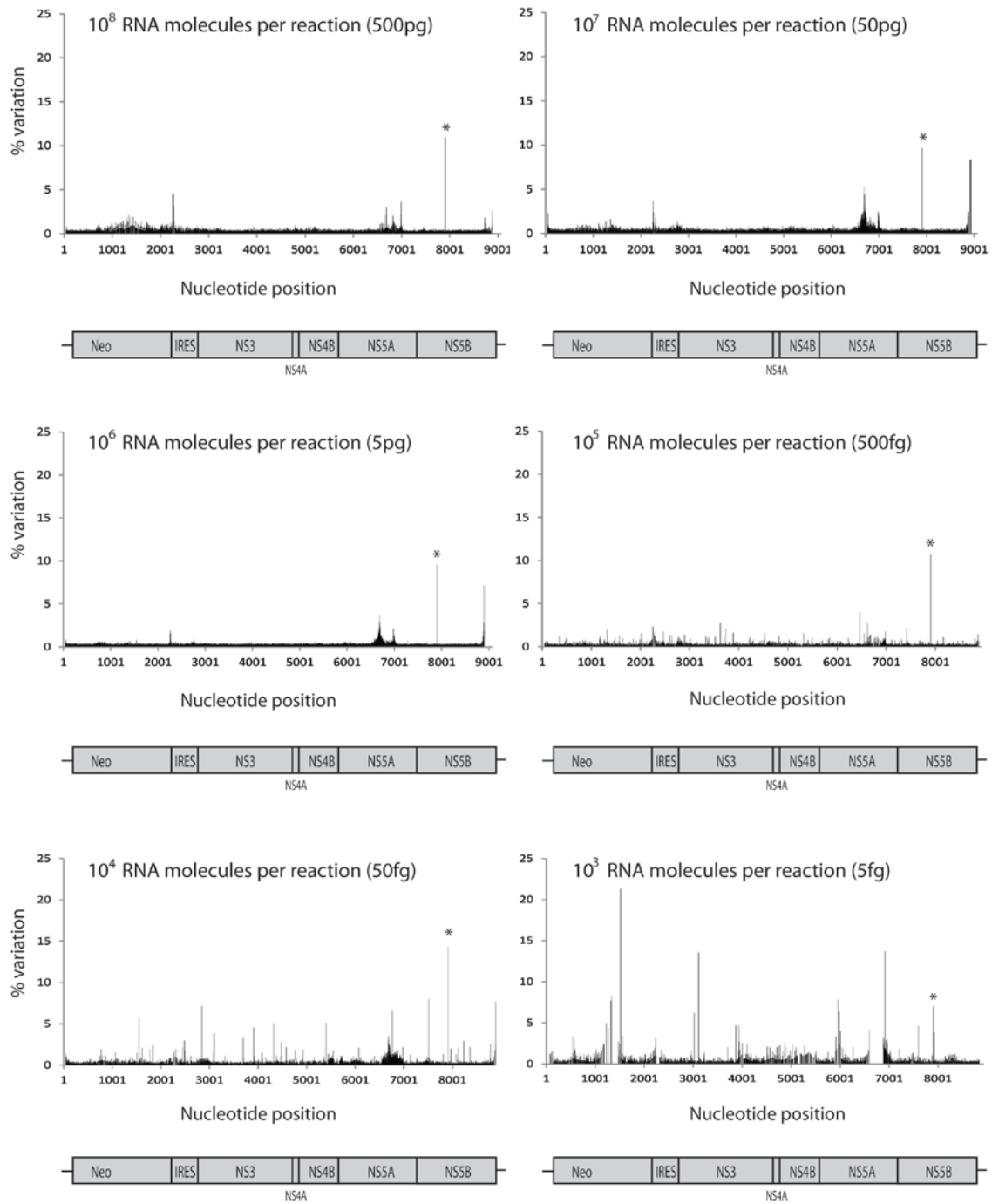


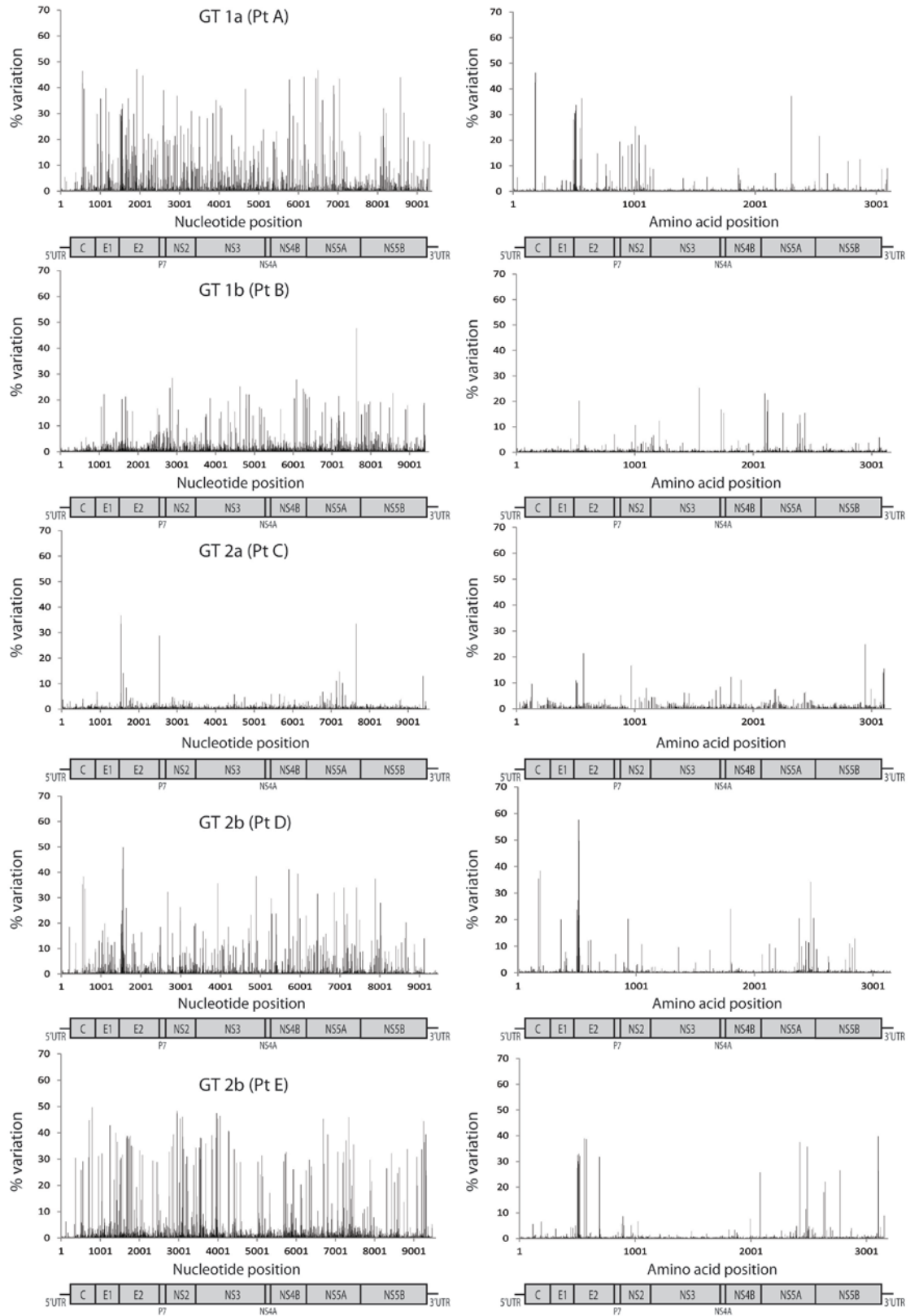
Suppl. Figure 1.



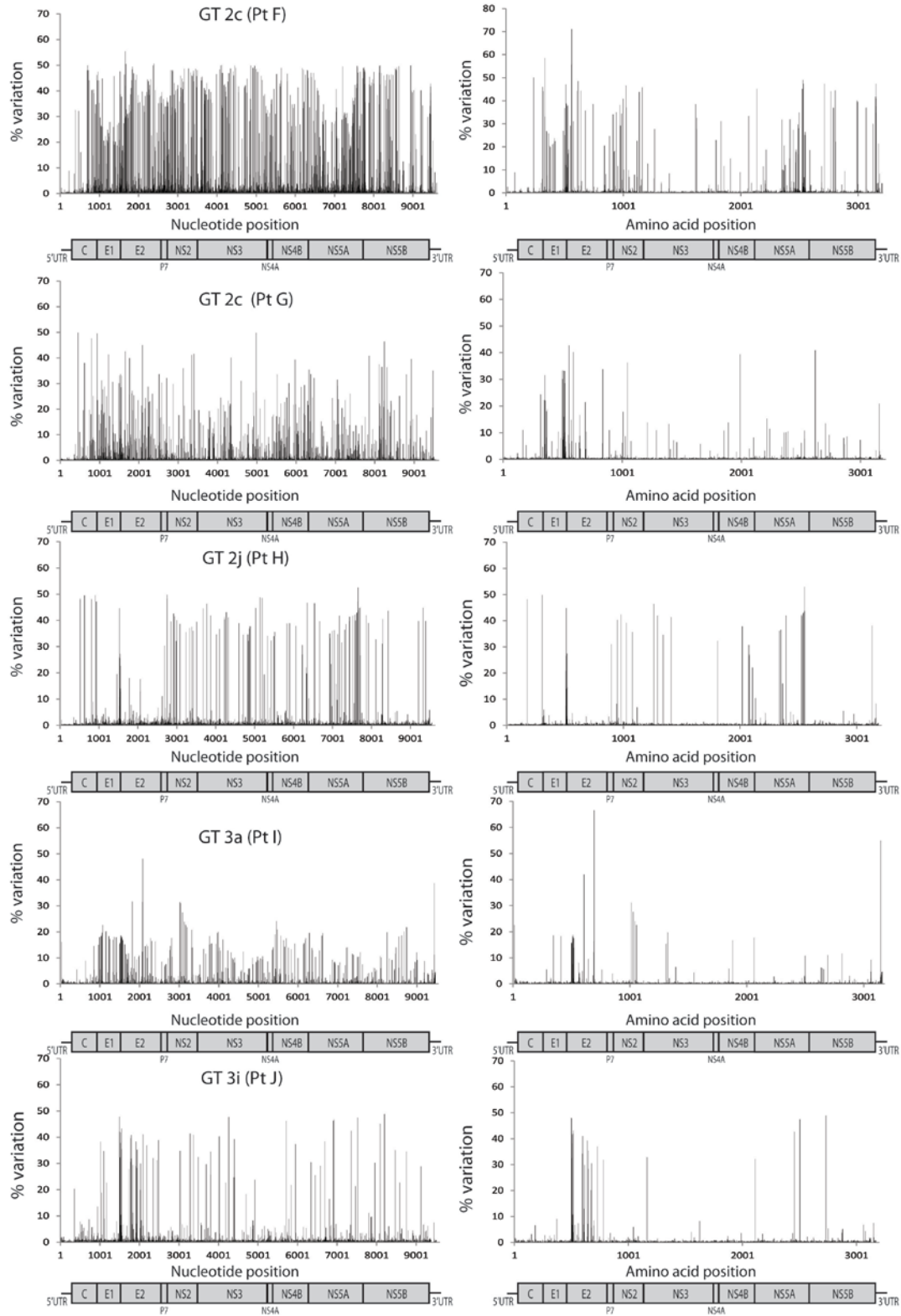
Suppl. Figure 1. Nucleotide variation for the *in vitro* transcribed RNA samples

Nucleotide differences compared to the 2aRlucNeo reference sequence is plotted for each position and sample. The S282T position is marked with a (\*) and the frequency was consistent with the 10% S282T addition in all *in vitro* RNA samples.

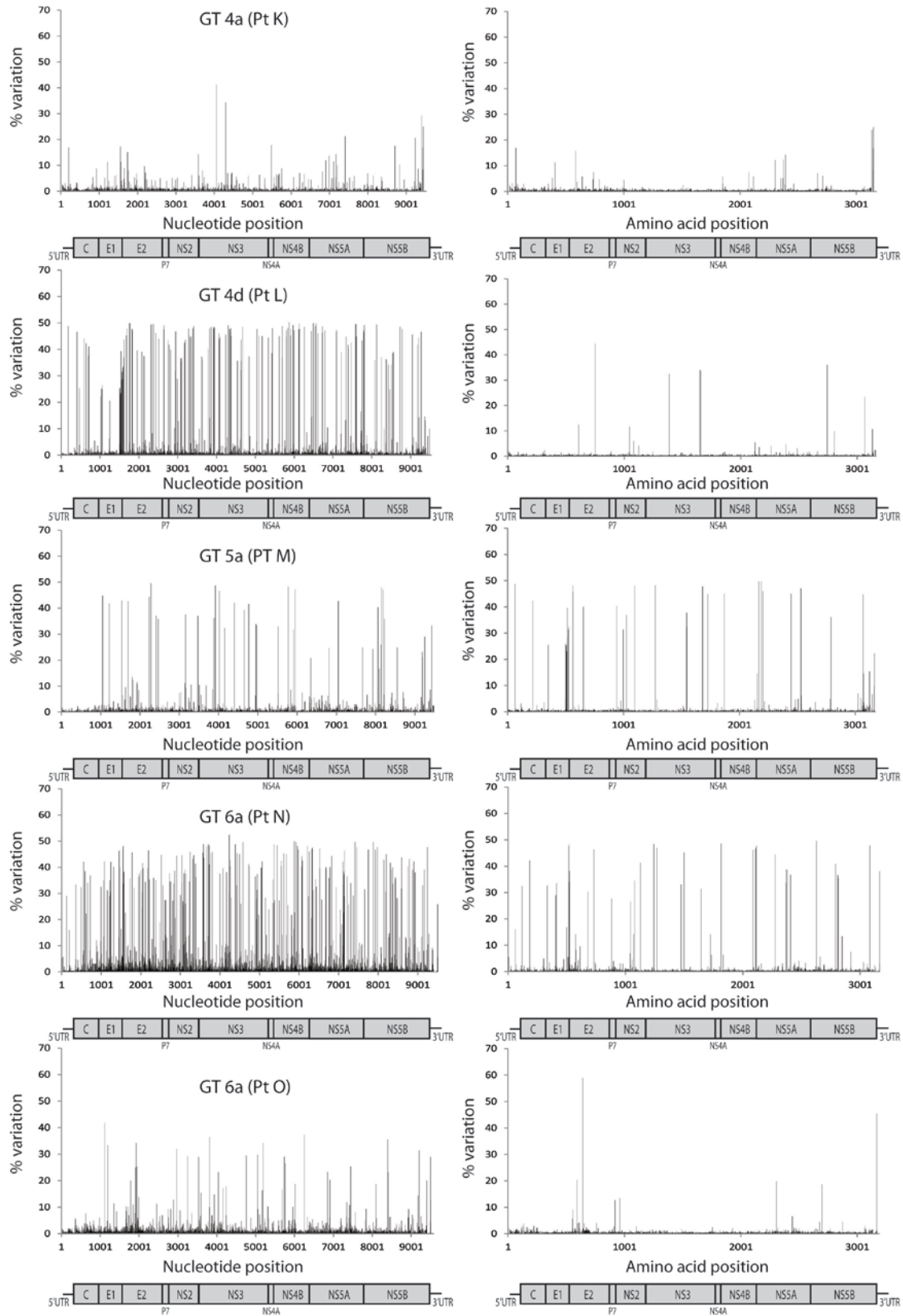
## Suppl. Figure 2.



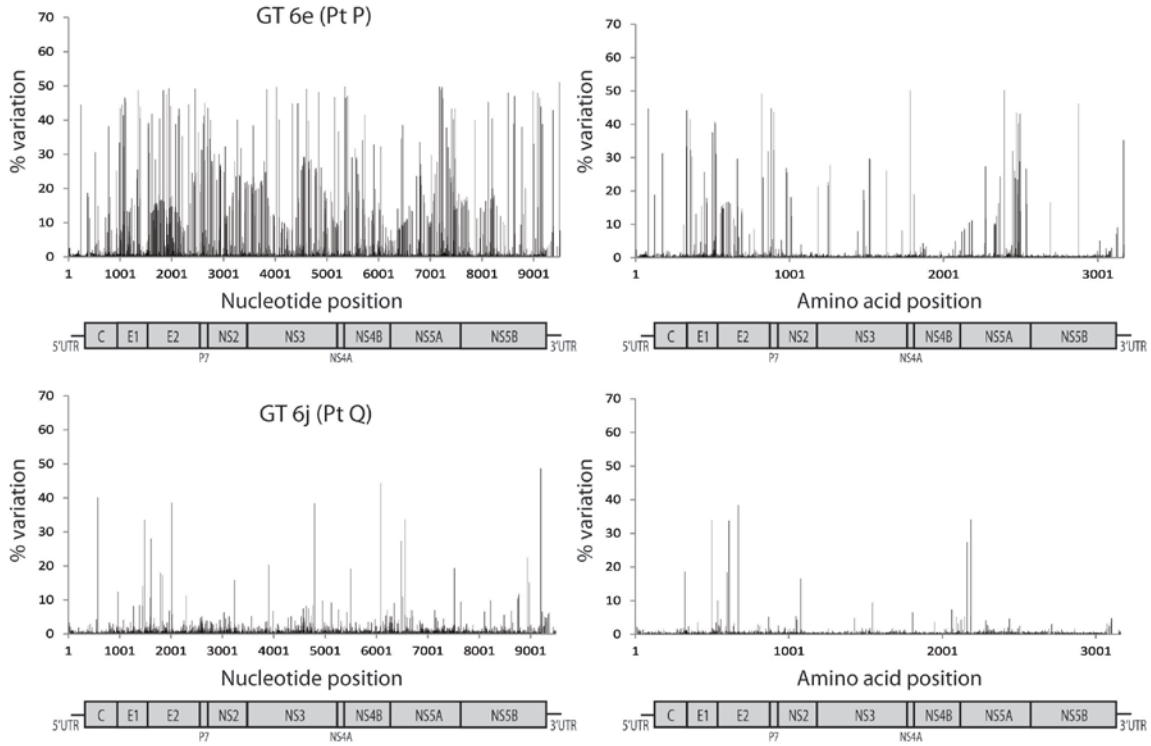
Suppl. Figure 2. continued



Suppl. Figure 2. continued



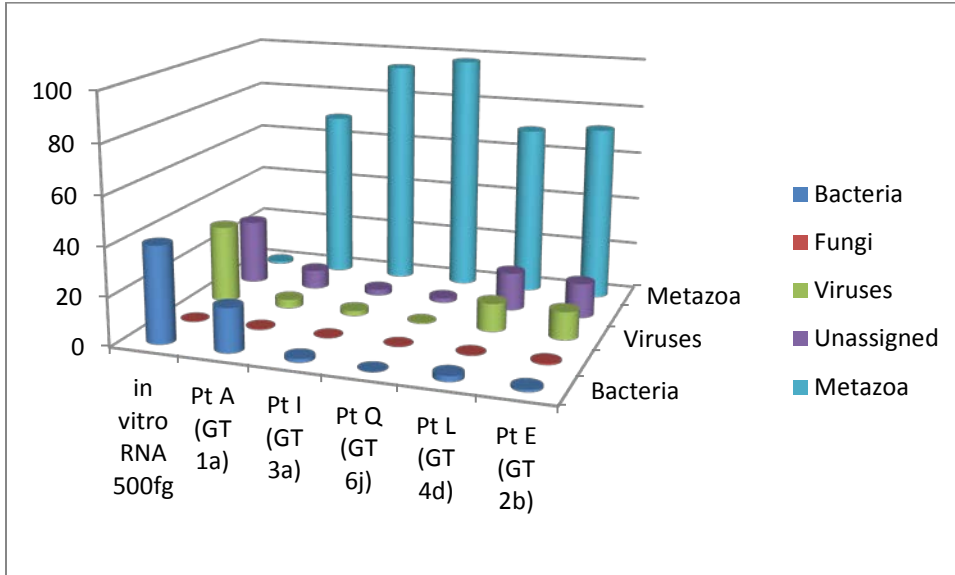
**Suppl. Figure 2. continued**



**Suppl. Figure 2. Nucleotide and amino acid variation in the patient samples**

Within patient genetic variation is plotted for each position in the HCV genome for each sample. The nucleotide variation is shown on the left panel and the amino acid variation in the right panel.

Suppl. Figure 3.



**Suppl. Figure 3.** Taxonomic groups of unaligned reads. Y-axis show frequency in percent.