

Figure S1: Number of TTV species detected by mNGS for each patient. Median is reported (black bar).

Figure S2: Linear regression analysis of the number of TTV reads and the age of the patients (month). Each black dot represents one TTV positive patient.

Figure S3: Maximum likelihood phylogenetic tree of TTV using the ORF1 nucleotide sequences. Each phylogenetic group is shown individually. Non-human primate TTV genotypes/species are specifically notified.

Figure S4: Distribution of the number of reads for each TTV genotype. Median is reported (black bar).

Figure S5: Age distribution of TTV genotypes. Median is reported (black bar).

Figure S6: Relative abundances of TTV genotypes. Median is reported (black bar).

Table S1: patient's dataset

Table S2: Database complete Alphatorquevirus genotypes. For each TTV genotype in our database the corresponding GenBank accession number is provided.

Table S3: Number of reads detected for each TTV genotype per sample.