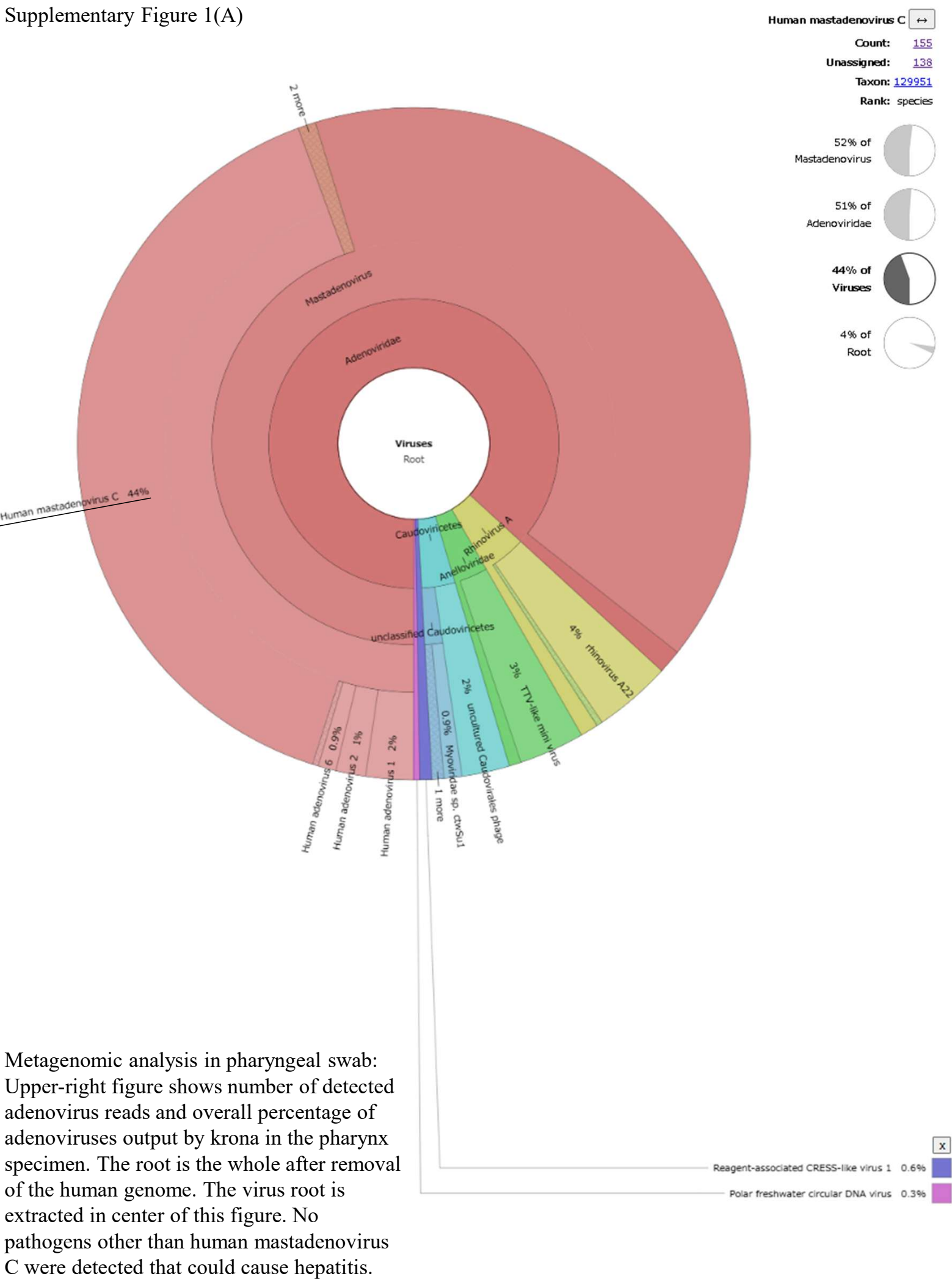



Supplementary Figure 1(A)



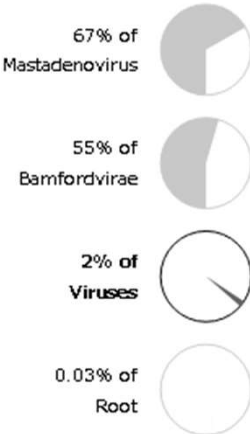
Metagenomic analysis in pharyngeal swab:  
Upper-right figure shows number of detected  
adenovirus reads and overall percentage of  
adenoviruses output by krona in the pharynx  
specimen. The root is the whole after removal  
of the human genome. The virus root is  
extracted in center of this figure. No  
pathogens other than human mastadenovirus  
C were detected that could cause hepatitis.

Human mastadenovirus C 

Count: 6

Taxon: [129951](#)

Rank: species

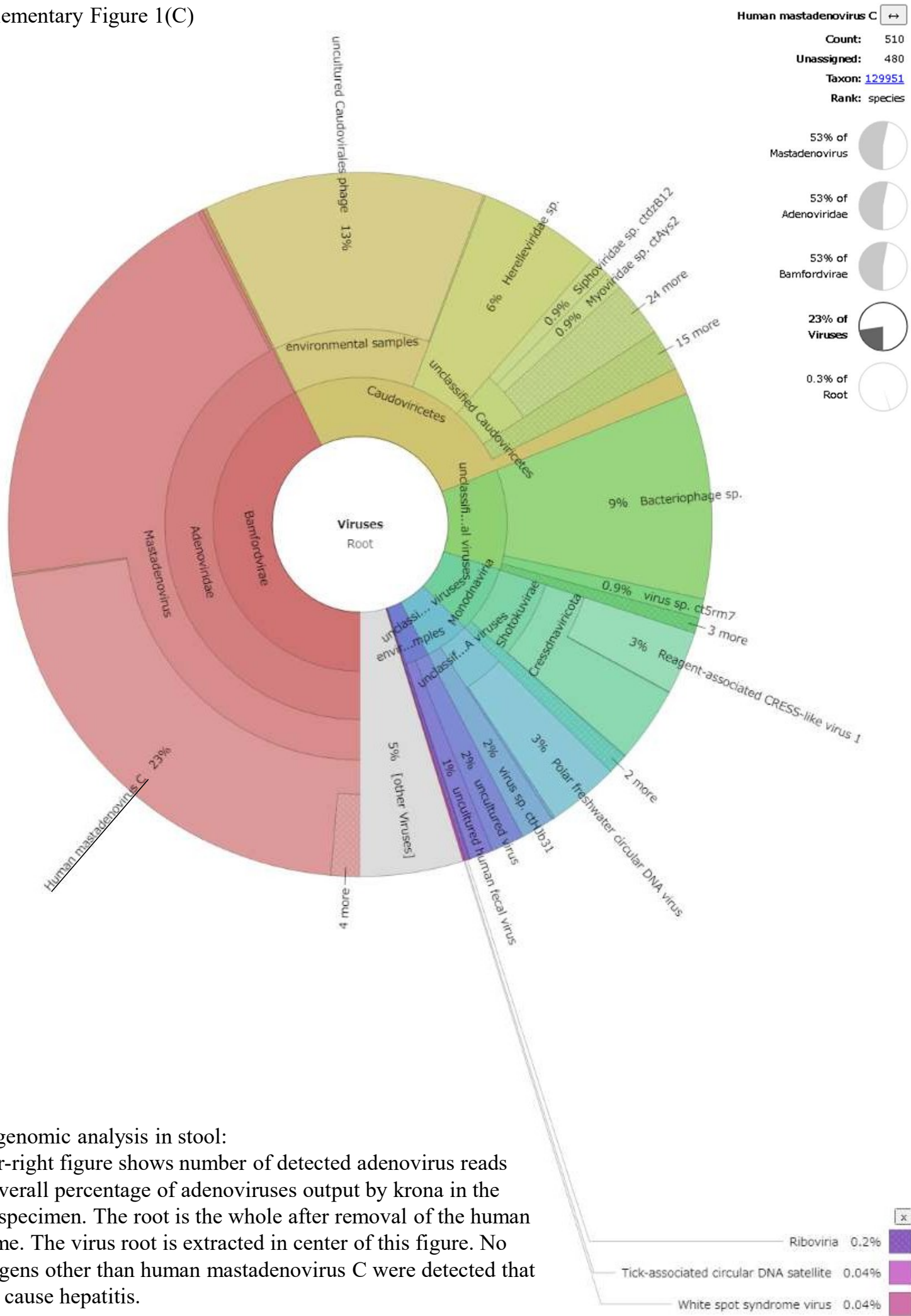


Orthornavirae 0.7%

Alphasatellitidae sp. 0.4%

[other Viruses] 0.7%

Supplementary Figure 1(C)



Metagenomic analysis in stool:  
Upper-right figure shows number of detected adenovirus reads and overall percentage of adenoviruses output by krona in the stool specimen. The root is the whole after removal of the human genome. The virus root is extracted in center of this figure. No pathogens other than human mastadenovirus C were detected that could cause hepatitis.

Supplementary Figure 1(D)

