



Supplementary Result Figure 6: ZeptoMetrix RP 2.1 sequencing and classification comparison between inStrain and Kraken2/Bracken

inStrain with option 2 parameters (no database mode, min genome coverage 0, min read ani of 0.9) compared with Kraken2/Bracken analysis using HQ paired end short read sequences from the ZeptoMetrix Respiratory Virus Control 1 and 2. The relative abundances of the identified viral signals are shown in a heat map generated in GraphPad Prism (v 10.0.3). The ZeptoMetrix taxa are shown in boxes and single lines under the heading 'ZeptoMetrix taxa'. The Zepto Metrix control was sequenced using the same viral bait capture methods used in the Pilot 2 experiment.