

Supplementary Figure 2. %G+C range of virus communities, as seen using various amplification (linker amplification, phi29 multiple displacement amplification, and linker amplified shotgun libraries) and sequencing platforms (454 pyrosequencing, Sanger sequencing). (a) in-house sequence data, (b) and (c) are identifiable by name and available on the CAMERA web portal, including all metadata and publication references.

