



Supplemental Figure 4. Graphical representation showing the ratio of viral reads to assembled cellular contigs. The boxes showing expected bias were calculated using 30kb as the average size of thermophilic Archaeal viral genomes and an average thermophilic Archaeal genome size of 1.5-2Mbp. On all graphs different read cutoff levels from 1-10 150bp are shown. **A.** The number of infected SAGs, **B.** the percentage of infected SAGs with two or more viral types present, and **C.** the average number of viral partitions present per infected SAG.