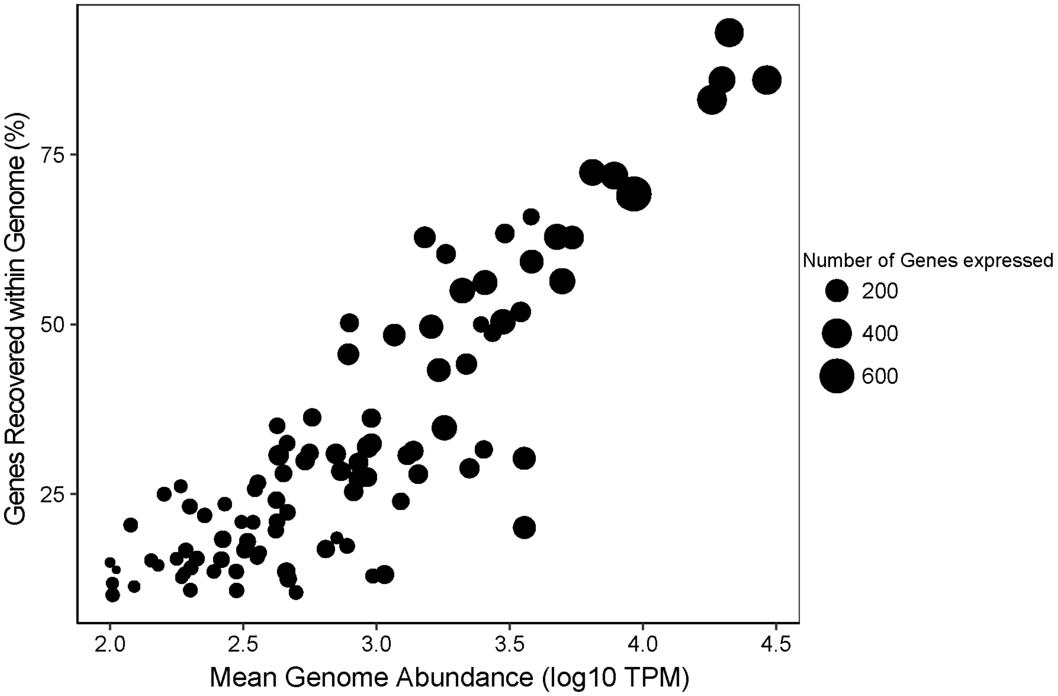

**Supplementary Figure 4.** Results of read recruitments to candidate Nucleocytoviricota isolate and metagenome-assembled genomes detected at SOTS. Each dot represents a candidate Nucleocytoviricota genome with transcripts detected. Genes recovered indicate the percentage of genes within each candidate genome that had reads mapped, where the mean genome abundance indicates the total normalized read count (log10 TPM) recruited to that genome. The total number of genes within each candidate genome is represented by dot size.