



**Figure 1– Supplement 2. Ribosome profiling libraries show a strong bias in size distribution.**

The fraction of total reads with a size of 26-34 nucleotides was plotted for each ribosome profiling library used in this study. These graphs clearly show that the ribosome profiling libraries used in this study have a strong bias for 27-28 nucleotide fragments, consistent with the size of the footprint of the ribosome. Columns indicate infection condition. Rows indicate BMM genotype and/or drug treatment.