

**Supplemental figure 3** . Venn diagram representing the intersection of the sRNA differential abundance across each transcript based on the three different library sizes for normalization (i.e. 1- the total number of sRNA reads that mapped on the reference genome, 2- the total number of reads analysed in edgeR (i.e. following size-filtering and counts), 3- the fraction of miRNA sized molecules that mapped onto a set of validated miRNAs). A) siRNA abundance across in infected vs blood-fed ovaries. B) siRNA abundance across in infected vs blood-fed carcasses. C) piRNA abundance across in infected vs blood-fed ovaries. D) piRNA abundance across in infected vs blood-fed carcasses.

