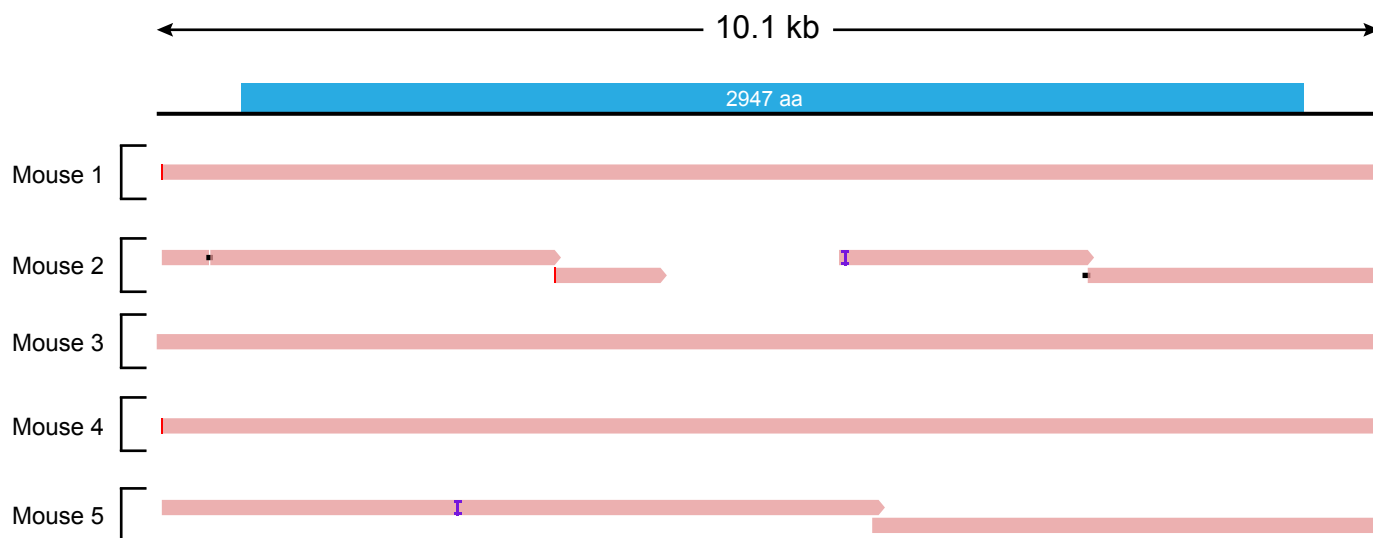


A.



B.

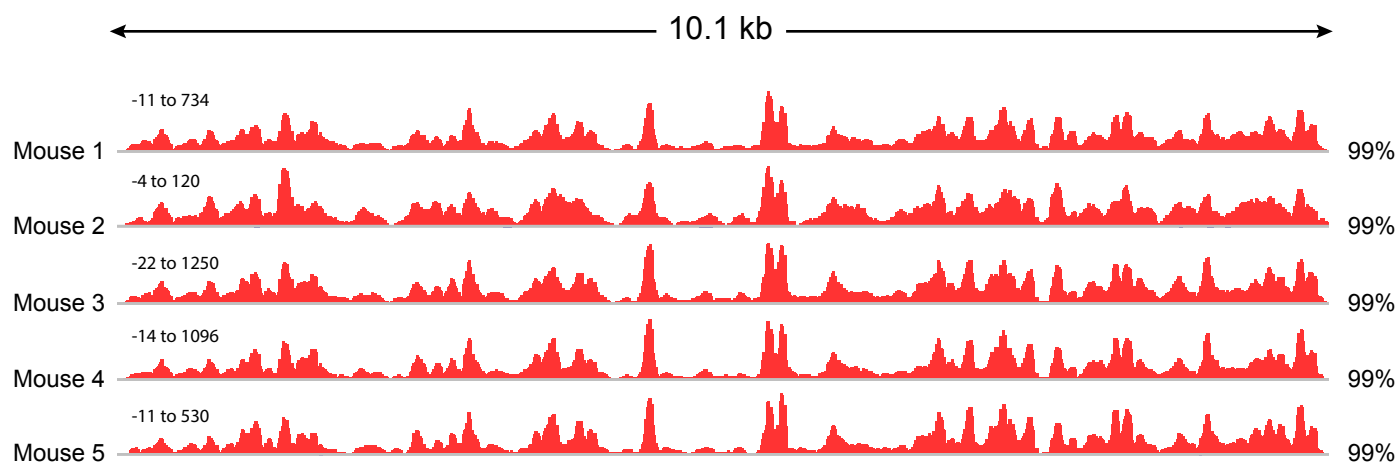


Figure S3

**Figure S3. Picorna-like viral contigs assembled from mouse dsRNA-Seq libraries are derived from single-stranded RNA.** (a) Alignment of contigs representing novel picorna-like virus. The longest contig with similarity to Sanxia picorna-like virus 7 (MM3\_TRINITY\_DN634\_c0\_g1\_i5) was selected as a representative. Contigs assembled from each mouse dsRNA-Seq library were aligned to the representative contig using bwa-mem. The location of the long open reading frame present in the representative contig is illustrated at the top. (b) Bedgraphs indicating the base count of reads from dsRNA-Seq libraries that aligned to each position of the representative picorna-like virus contig. Red indicates counts on positive strand. Blue indicates counts on negative strand. The percentage of total reads that mapped to the representative picorna-like virus contig that aligned to the positive strand are indicated on the right. The bedgraphs were not scaled relative to total number of dsRNA-Seq reads in each sample. Each read set was scaled individually, scale is indicated at top left for each set.