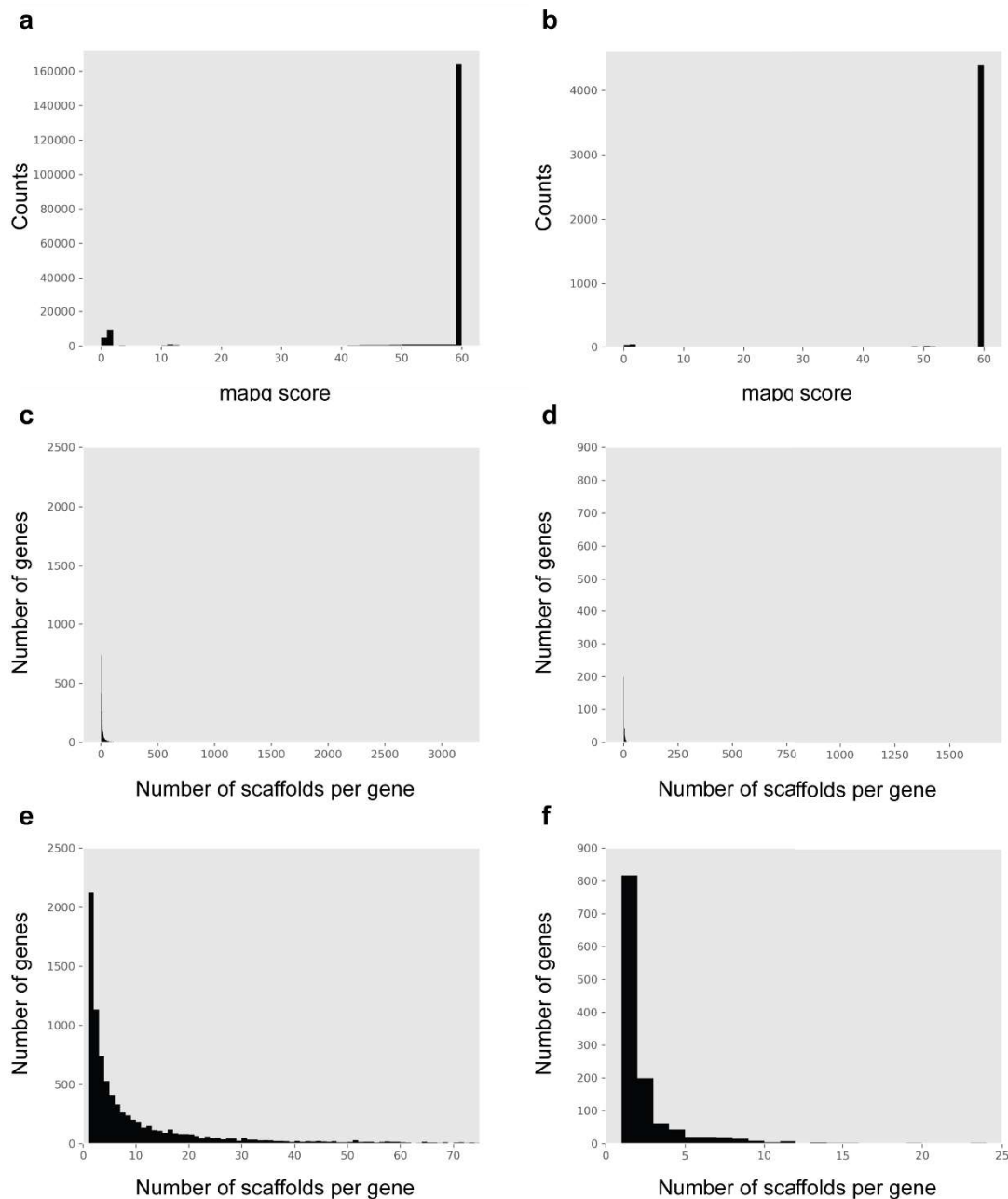




Supplementary Figure 5 RNA isoform scaffold summary. **(a)** A histogram of map quality (mapq) scores for all the full-length RNA scaffolds. Mapq scores can range from 0-to-60. The x-axis is the mapq score for each read, and the y-axis is the number of reads with the corresponding mapq score. **(b)** A histogram of mapq scores for the unannotated RNA isoform scaffolds. The axes are the same as in panel **a**. **(c)** A histogram of the number of scaffolds per gene for the full-length RNA scaffolds. The x-axis is the number of scaffolds that aligned to each gene and the y-axis is the number of genes that had the corresponding number of scaffolds. **(d)** A histogram of the number of scaffolds per gene for the unannotated full-length RNA scaffolds. The axes are the same as in panel **c**. **(e)** The same plot as in panel **c**, except the x-axis has been narrowed to view most of the data. **(f)** The same plot as in panel **d**, except the x-axis has been narrowed to view most of the data.