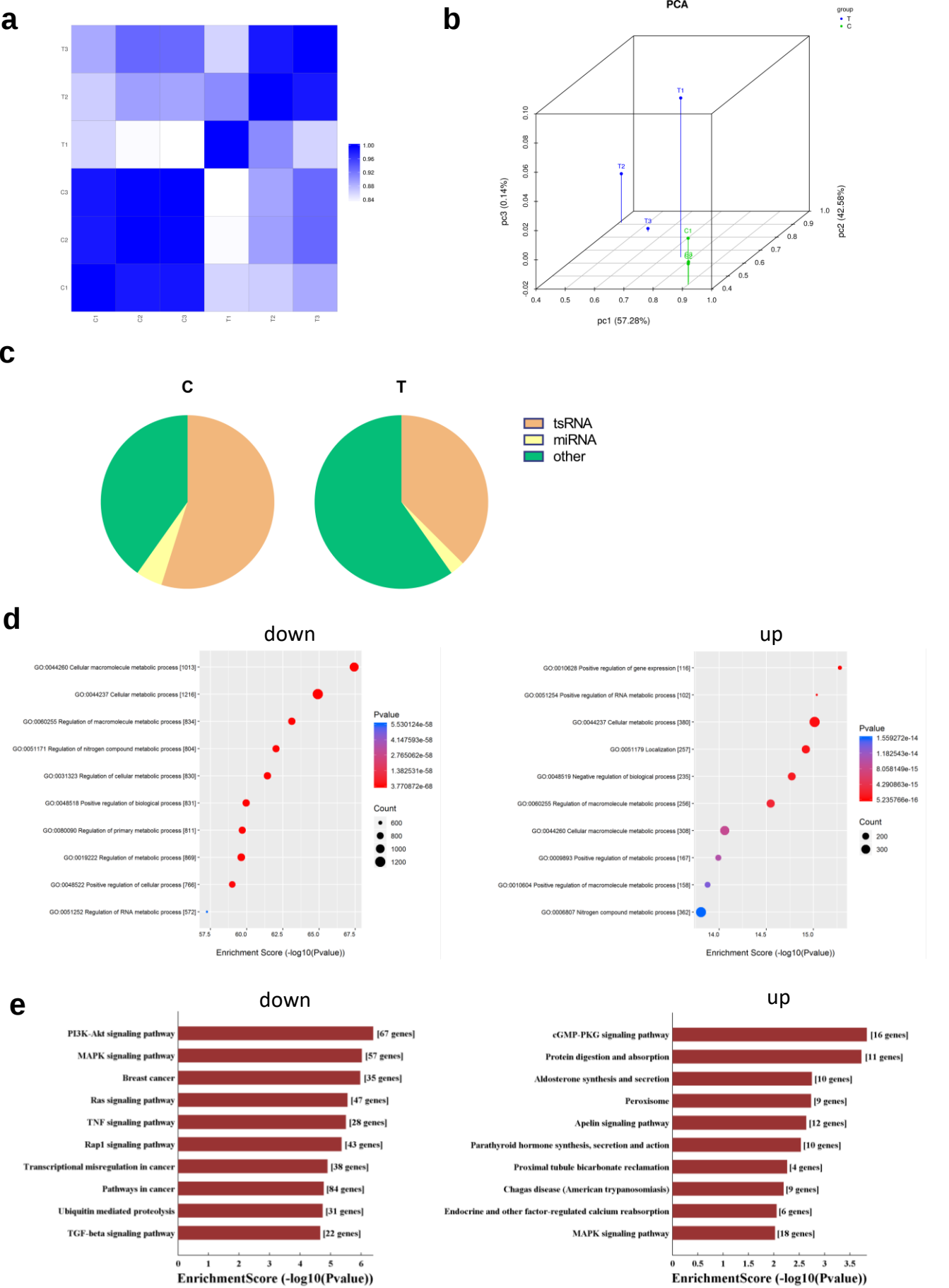
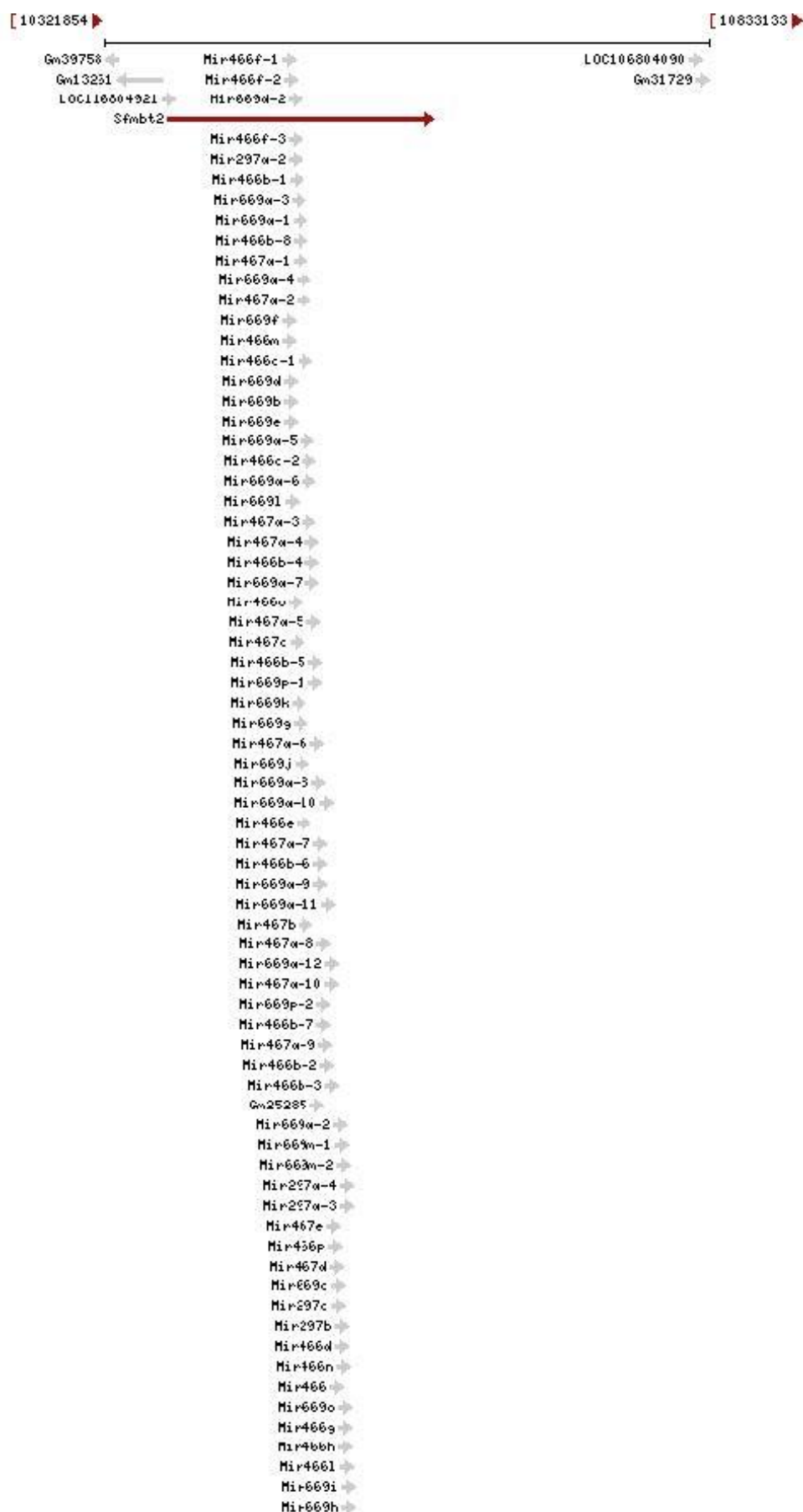
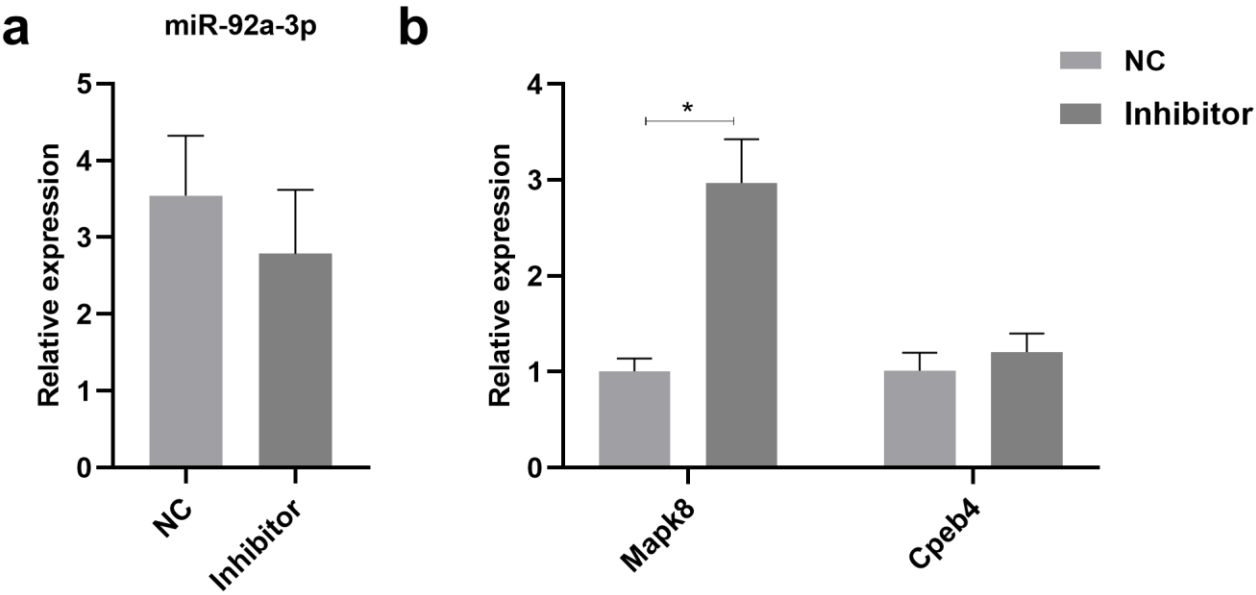




Supplementary figure 1. The bioinformatics analysis of sperm sRNA sequencing. **a** Heatmap of correlation coefficient of sperm sRNAs from the CON and OEE group. **b** Principal component (PC) analysis of sperm sRNAs from the CON and OEE group. **c** Comparison of the proportion of sperm miRNAs and tsRNAs from the CON and OEE group. **d** The GO enrichment analysis of differentially expressed miRNAs that were down-regulated or up-regulated in the OEE group. **e** KEGG pathway analysis of differentially expressed miRNAs that were down-regulated or up-regulated in the OEE group. C refers to CON group, T refers to OEE group.



Supplementary figure 2. The overview of the Sfmbt2 miRNA cluster profile (Sfmbt2 miRNA cluster profile can be browsed using NCBI database, <https://www.ncbi.nlm.nih.gov/gene>).



Supplementary figure 3. The validation of the function of the anti-sense oligos **a**. The expression of miR-92a-3p in HIN3T3 cells transfected with miR-92a-3p inhibitor or negative control inhibitor. (N=3 samples/group). **b**. The expression of target genes mRNA of miR-92a-3p in HIN3T3 cells transfected with miR-92a-3p inhibitor or negative control inhibitor. (N=3 samples/group). The relative expression of genes was normalized to the level of Gapdh, **p*-value <0.05, NC refers to the negative control inhibitor and inhibitor refers to miR-92a-3p inhibitor