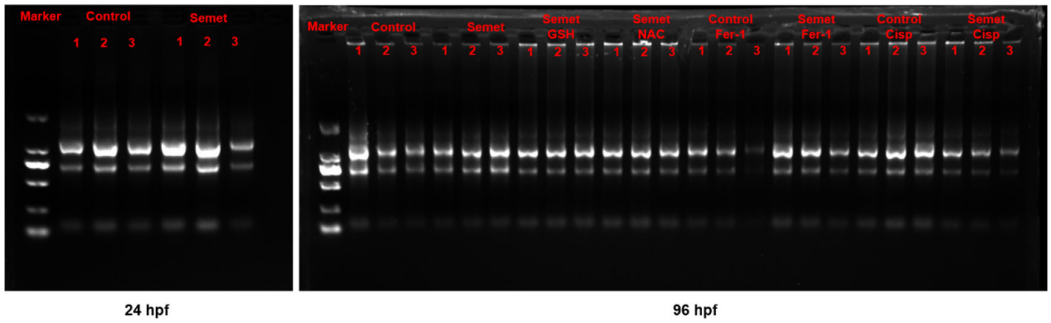


**Figure S1.** Agarose gel electrophoresis of RNA used in this study.

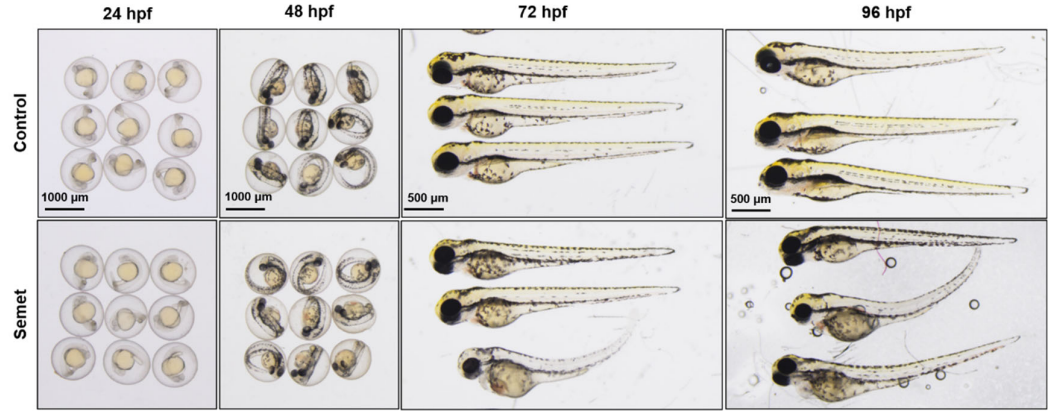


**Figure S2.** Phenotypes of representative selenium-stressed embryos at 24, 48, 72 and 96 hpf.

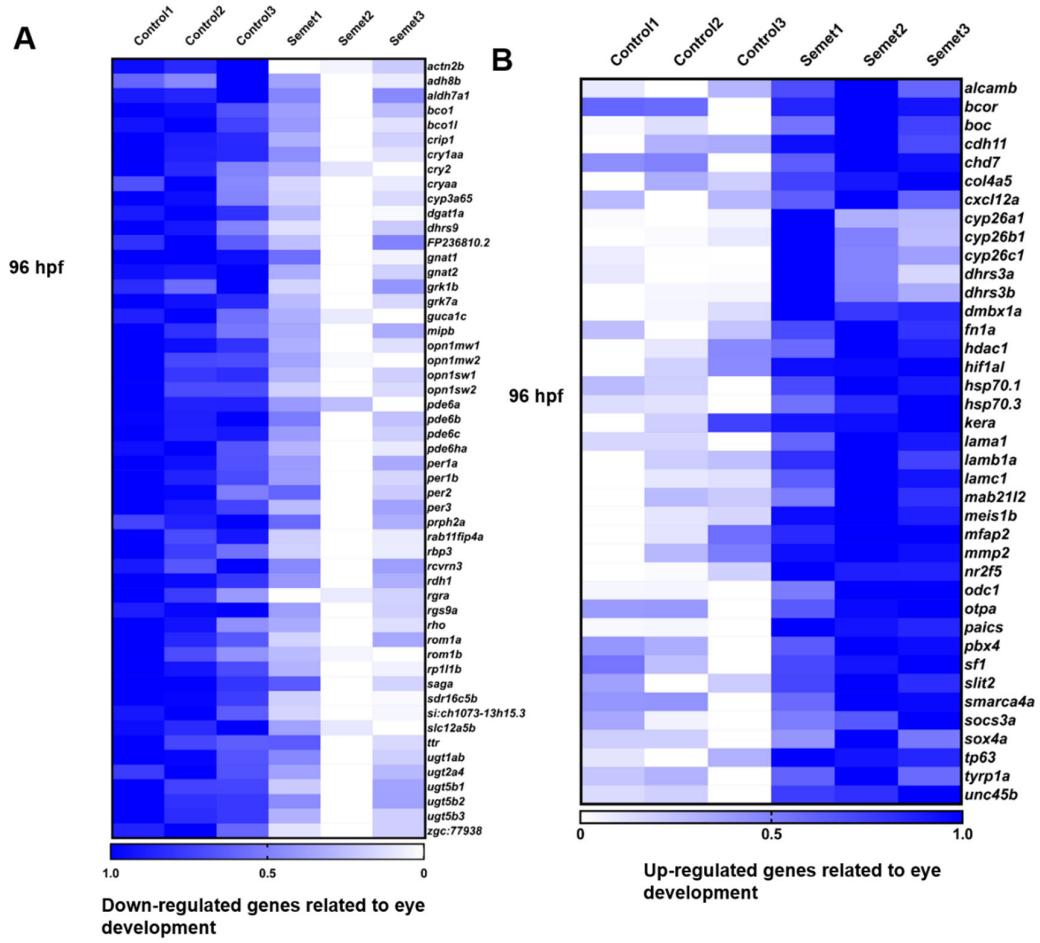


**Figure S3.** Heatmaps of genes related to eye development (A, down-regulation; B, upregulation) based on RNA-seq data at 96 hpf.

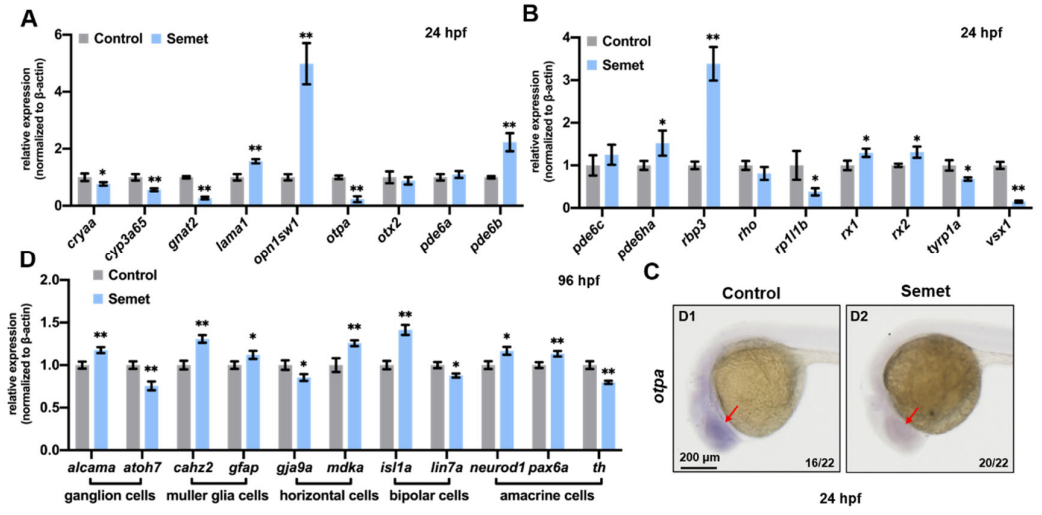


**Figure S4.** Expression of ocular marker genes in selenium-treated embryos. (A, B) The expression of ocular marker genes in selenium-treated embryos at 24 hpf detected by qRT-PCR. (C) The expression of

ganglion, muller glia, horizontal, bipolar and amacrine cell marker genes at 96 hpf. (D) WISH data of *otpa* (D3-D4) in control and selenium-treated embryos at 24 hpf.

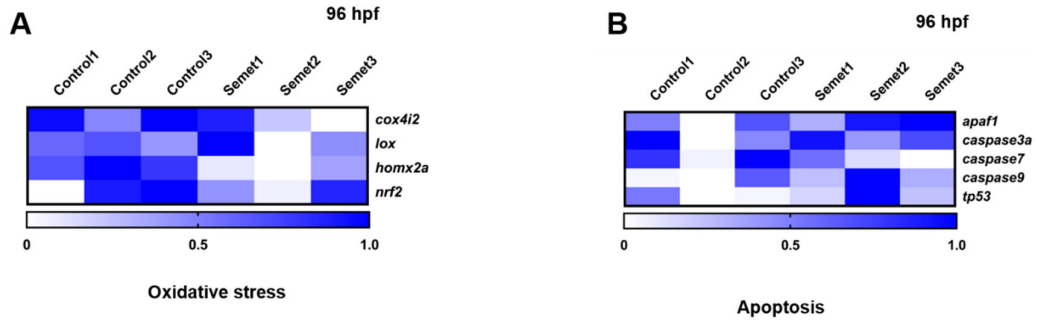


**Figure S5.** Heatmaps of genes related to oxidative stress (A) and apoptosis (B) based on RNA-seq data at 96 hpf.

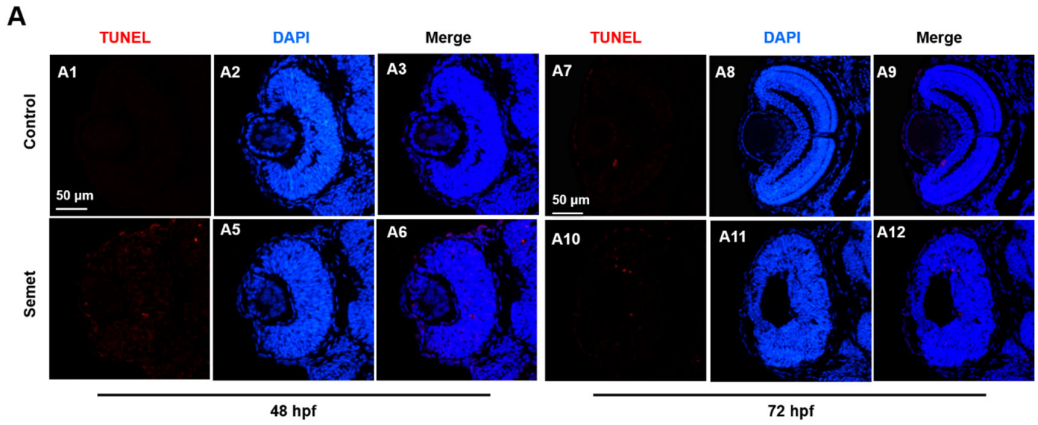


**Figure S6.** Cell apoptosis detected by TUNEL assay in control and selenium-treated embryos at 48 hpf and 72 hpf.

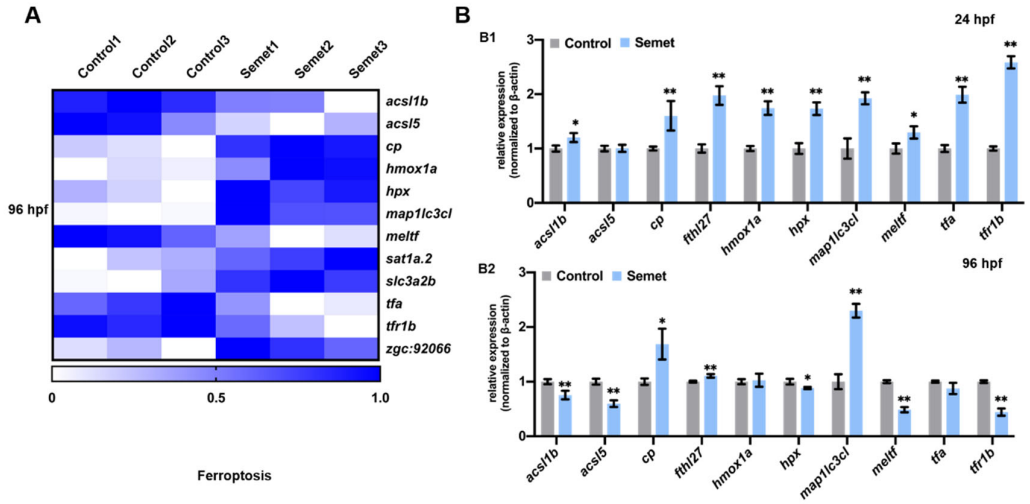

**Figure S7.** Expression of ferroptosis marker genes in selenium-treated embryos. (**A**) DEGs of ferroptosis detected by RNA-seq in selenium-treated embryos at 96 hpf. (**B**) The expression of ferroptosis marker genes in selenium-treated embryos at 24 hpf (**B1**) and 96 hpf (**B2**) detected by qRT-PCR.