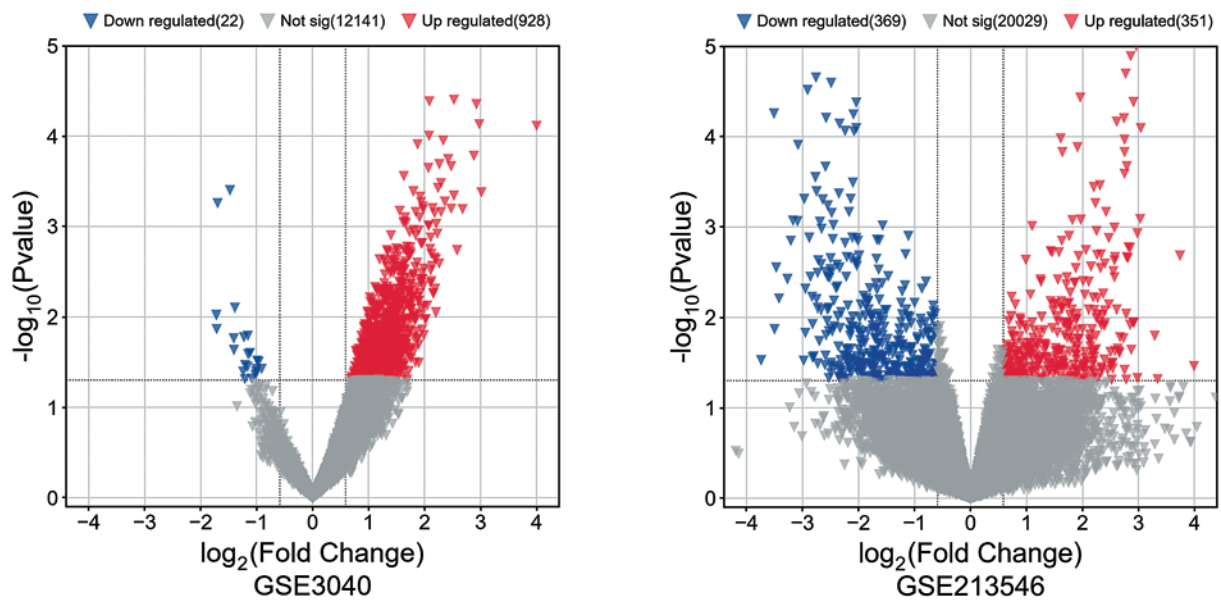
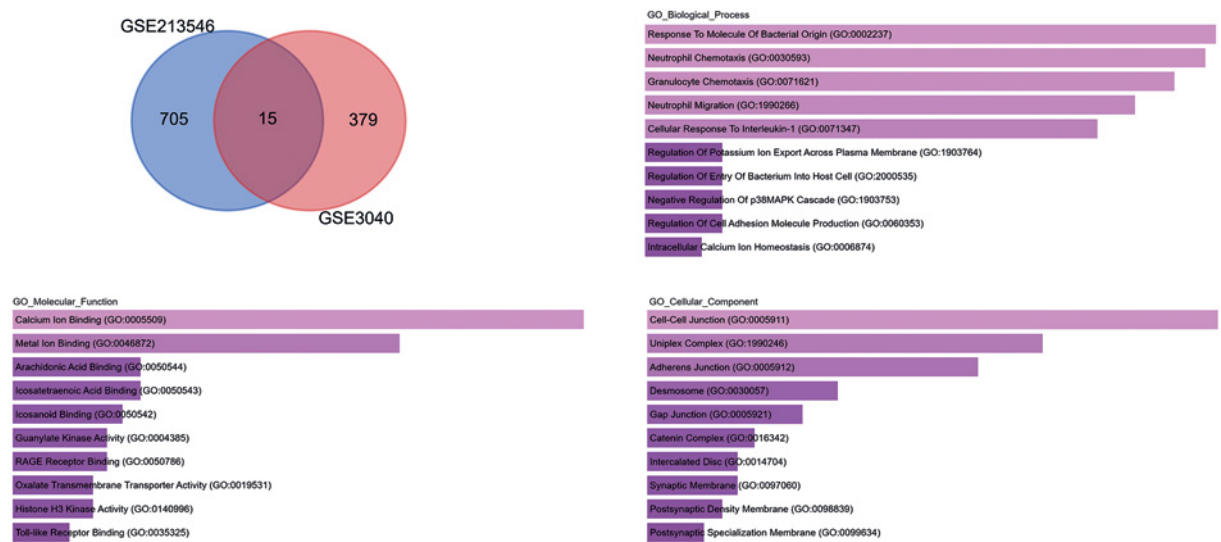




Supplementary Fig. 1. Identification of differentially expressed genes (DEGs) in age-related cataract (ARC) datasets. **A, B** Volcano plot of DEGs in the GSE3040 (**A**) and GSE213546 (**B**) datasets, showing significantly upregulated genes (red), downregulated genes (blue), and non-significant genes (gray)



Supplementary Fig. 2. Screening and enrichment analysis of overlapping genes in the GSE213546 and GSE3040 datasets. **A**) Venn diagram showing the overlap of differentially expressed genes (DEGs) between GSE213546 and GSE3040 datasets, with a total of 15 genes. **B-D**) Bar charts showing the results of Gene Ontology (GO) enrichment analysis for biological processes (**B**), molecular function (**C**), and cellular component (**D**). The length of each bar represents the enrichment level