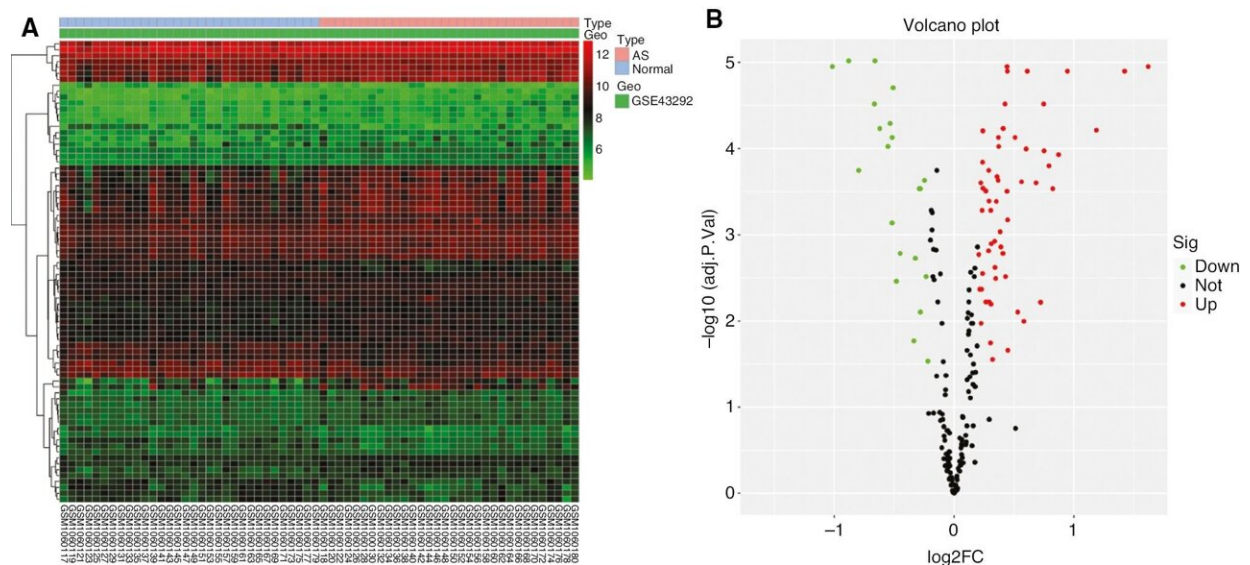


Immune infiltration in atherosclerosis is mediated by cuproptosis-associated ferroptosis genes

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Differentially Expressed Genes in a Heatmap and Volcano Plot. (A) Heatmap of differentially expressed genes between the atherosclerosis group and the control group. Each column represents a tissue sample and each row represents a differentially expressed gene. (B) Volcano plot of differentially expressed genes between the atherosclerosis group and the control group. Red indicates upregulated genes, whereas green indicates downregulated genes. Credit: *Cardiovascular Innovations and Applications* (2023). DOI: 10.15212/CVIA.2023.0003

In a new study published in the journal *Cardiovascular Innovations and Applications*, the authors identified cuproptosis-associated ferroptosis genes in the atherosclerosis microarray of the Gene Expression Omnibus (GEO) database and explored hub gene-mediated immune infiltration in atherosclerosis. Immune infiltration plays a crucial role in atherosclerosis development.

Ferroptosis is a mode of [cell death](#) caused by the iron-dependent accumulation of lipid peroxides. Cuproptosis is a recently discovered type of programmed cell death. No previous studies have examined the mechanism of cuproptosis-associated ferroptosis gene regulation in immune infiltration in atherosclerosis.

The qualified atherosclerosis gene microarray was researched in the GEO [database](#), integrated with ferroptosis and cuproptosis genes, and calculated with the correlation coefficients. The authors then obtained the cuproptosis-associated ferroptosis gene matrix and screened differentially expressed genes. Subsequently, they performed Gene Ontology and Kyoto Encyclopedia of Genes and Genomes enrichment analyses and [protein](#)–protein interaction network analysis of differentially expressed genes.

The authors also screened hub genes according to the Matthews correlation coefficient (MCC) algorithm. The authors conducted enrichment analysis of hub genes to explore their functions and predict related microRNAs (P

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