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Cuproptosis-related gene ATOX1 promotes MAPK signaling and diffuse large B-cell lymphoma proliferation via modulating copper transport

Supplementary content

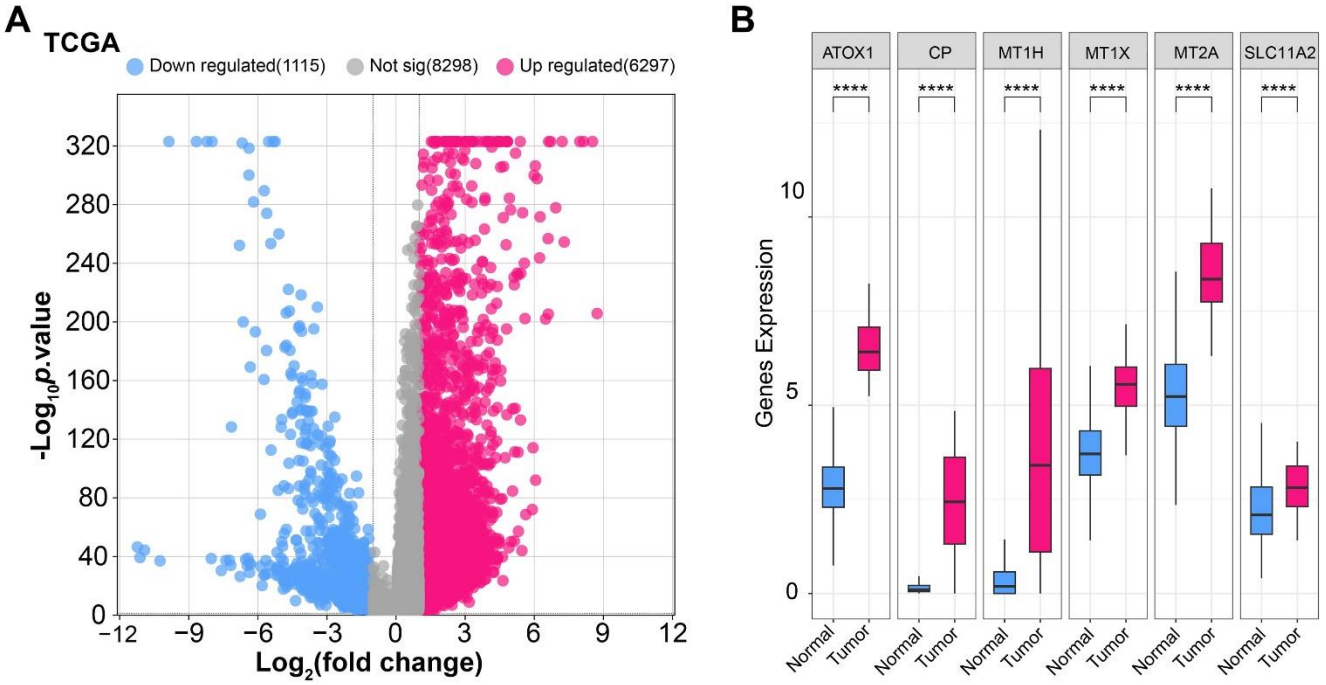

Figure S1. (A) Volcano plot showing differential gene expression in TCGA data:

The plot illustrates the log2 fold change of gene expression against the -log10 p-value for each gene. Blue dots represent 1,115 downregulated genes, red dots represent 6,297 upregulated genes, and gray dots represent 8,298 genes with no significant change in expression. The x-axis indicates the log2 fold change, while the y-axis shows the -log10 p-value. Genes with significant changes in expression are plotted on either side, with downregulated genes on the left and upregulated genes on the right.

(B) Box plots of gene expression levels in normal and tumor samples:

The plots compare the expression levels of ATOX1, CP, MT1H, MT1X, MT2A, and SLC11A2 genes between normal and tumor tissues. Each box plot displays the median gene expression (line within the box), interquartile range (box), and range (whiskers). Pink boxes represent tumor samples, and blue boxes represent normal samples. Asterisks above the boxes indicate significant differences in expression levels between normal and tumor tissues (**** $p < 0.0001$).

Supplementary Table 1. Sequences of primers.

Gene Name	Sequences of Primer	Annealing temperature	Product length
ATOX1	Forward: 5'-TCTGAGCACAGCATGGACACTC-3' Reverse: 5'-TCTGGAAGCCAGCGGGAGGAT-3'	53℃	22 bp
GAPDH	Forward: 5'-CAGTCAGCCGCATCTTCTTTTGCGTCG-3' Reverse: 5'-CAGAGTTAAAAGCAGCCCTGGTGACCAGG-3'	55℃	27 bp

Supplementary Table 1. lists the sequences of primers used for PCR amplification of the ATOX1 and GAPDH genes. For each gene, the forward and reverse primer sequences are provided. The table also includes the annealing temperatures used during PCR and the length of the PCR product in base pairs (bp). The annealing temperatures for ATOX1 and GAPDH primers are 53℃ and 55℃, respectively, with product lengths of 22 bp for ATOX1 and 27 bp for GAPDH.