

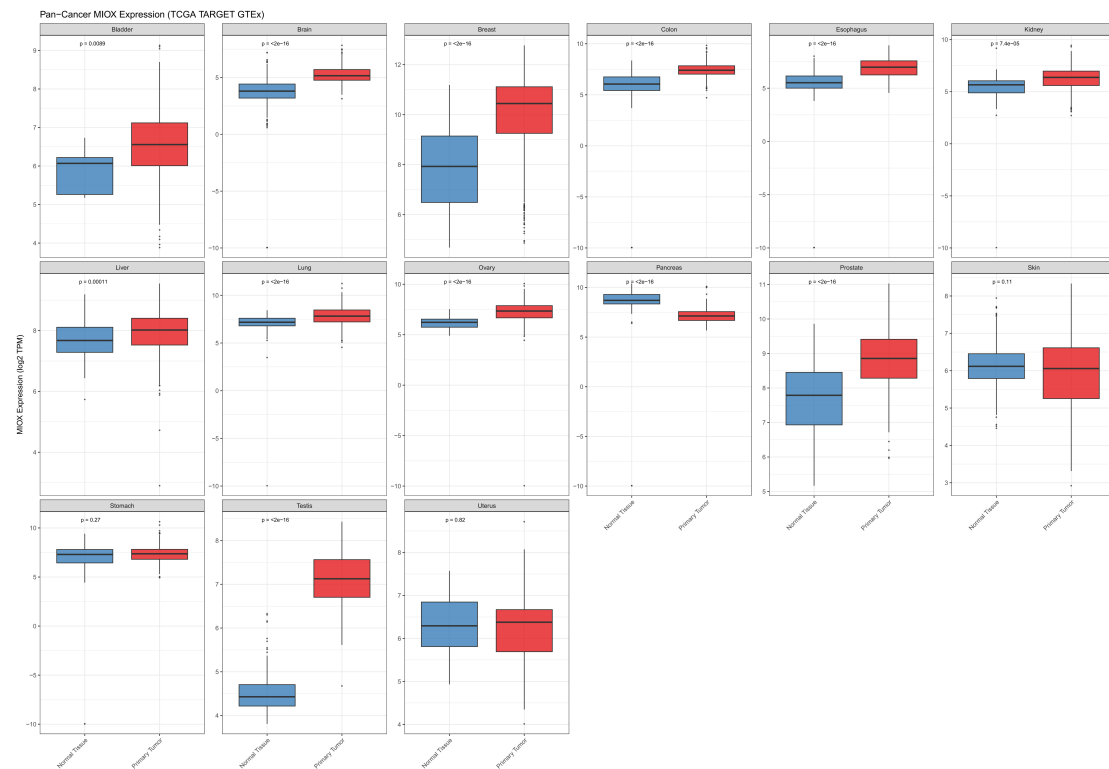


Figure S1. Pan-cancer expression profile of MIOX.

Boxplots showing MIOX expression across multiple cancer types and corresponding normal tissues based on TCGA, TARGET, and GTEx data. Statistical significance was evaluated by Wilcoxon test. **** $P < 0.0001$.

Abbreviations: TCGA, The Cancer Genome Atlas; TARGET, Therapeutically Applicable Research to Generate Effective Treatments; GTEx, Genotype-Tissue Expression.

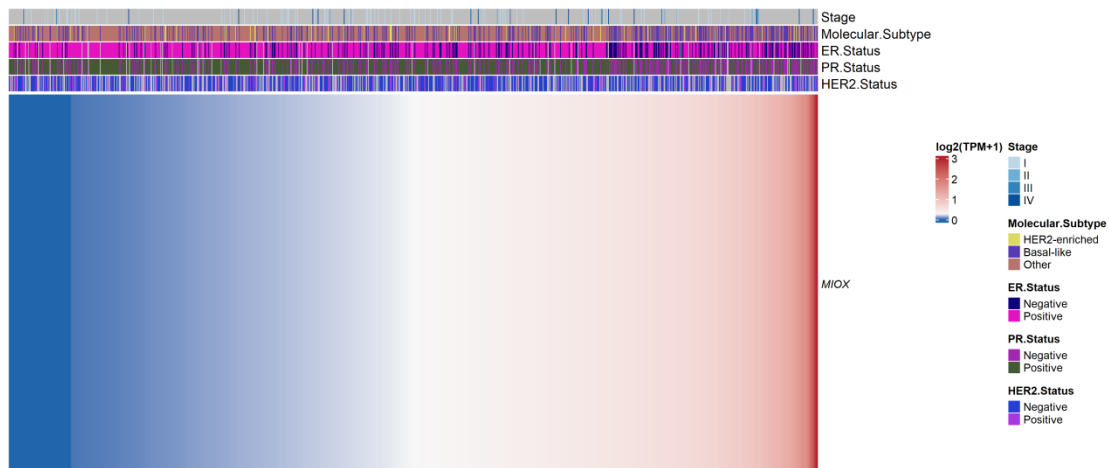


Figure S2. Heatmap of MIOX expression and clinical annotations in TCGA-BRCA.

Rows represent MIOX expression (log₂(TPM+1)) and columns represent individual breast cancer samples, sorted by increasing MIOX expression. Top annotations indicate ER status, PR status, HER2 status, PAM50 subtype, and tumor stage. Abbreviations: ER, estrogen receptor; PR, progesterone receptor; HER2, human epidermal growth factor receptor 2; TPM, transcripts per million.

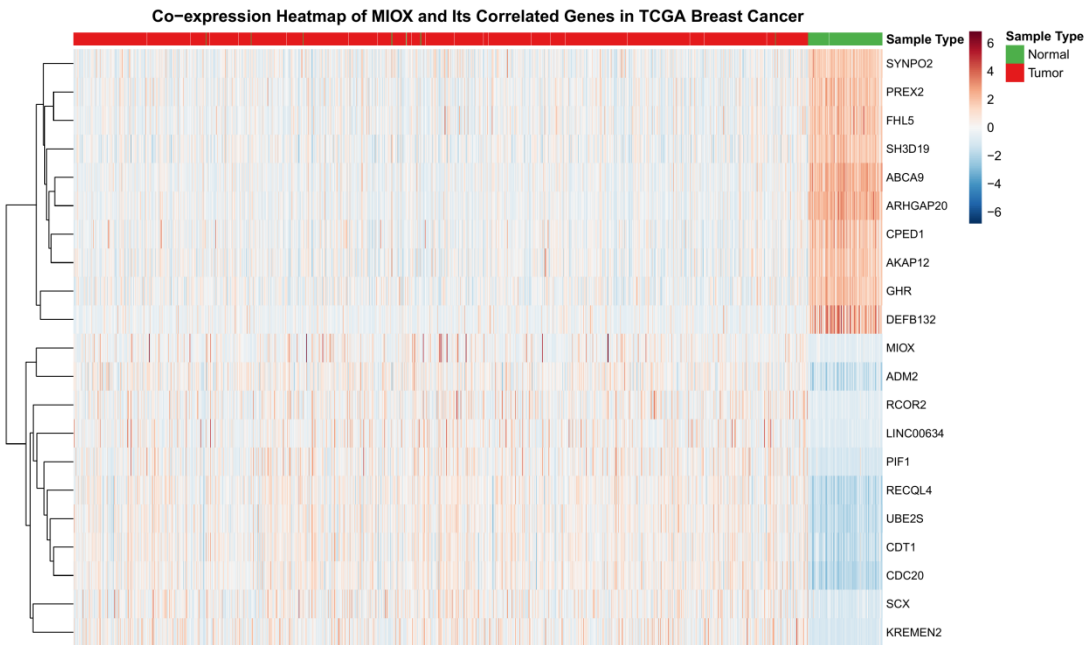


Figure S3. Co-expression heatmap of MIOX and its correlated genes in TCGA-BRCA.

Heatmap showing the top 10 positively and top 10 negatively correlated genes with MIOX (Spearman correlation). Columns represent tumor (red) and normal (green) samples. Row names are gene symbols (italicized). Color scale indicates row Z-score.

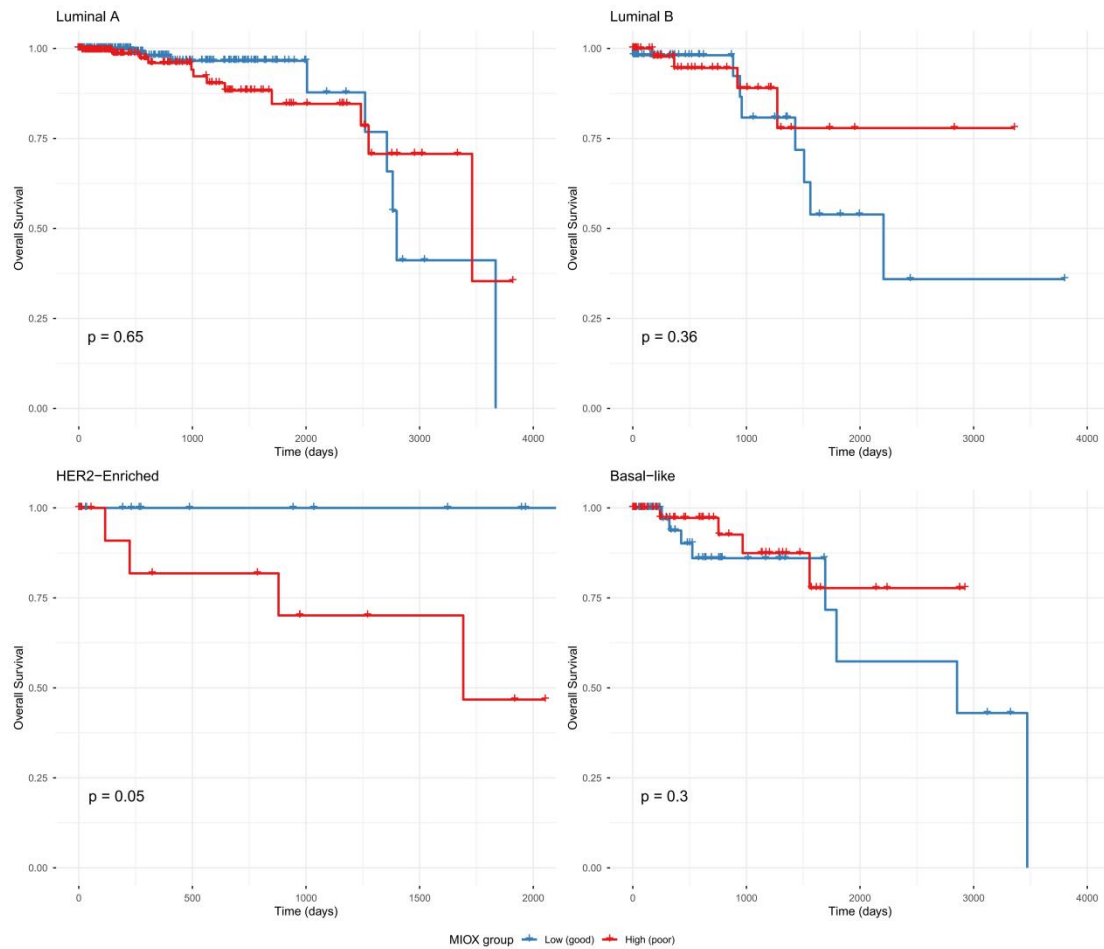


Figure S4. Subgroup survival analysis of MIOX by molecular subtype.

Kaplan-Meier curves for overall survival (OS) in Luminal A, Luminal B, HER2-enriched, and Basal-like subtypes, stratified by MIOX expression (optimal cut-off). P values from log-rank test.

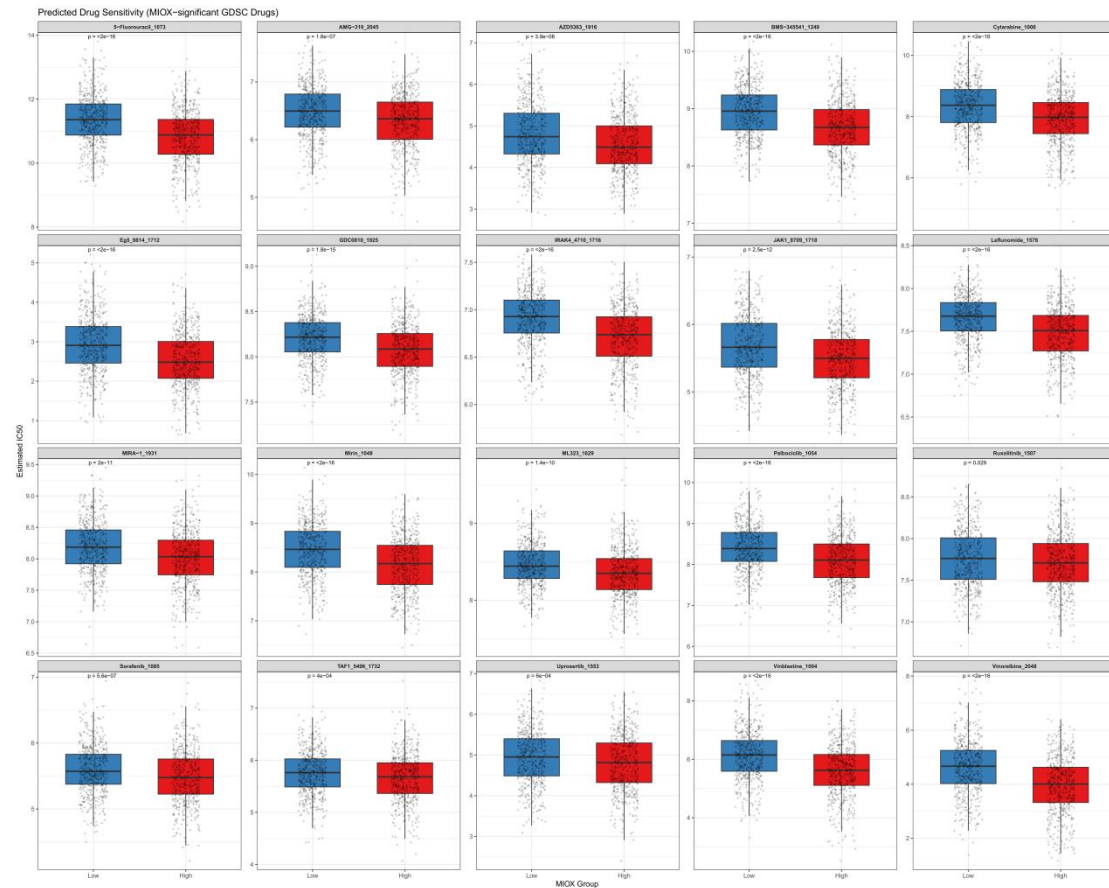


Figure S5. Predicted drug sensitivity for 18 drugs significantly associated with MIOX.

Boxplots comparing estimated IC50 values between MIOX-high and MIOX-low groups for all drugs with FDR < 0.05 in GDSC2 analysis. Wilcoxon test, all $P < 0.05$. Abbreviations: IC50, half-maximal inhibitory concentration; FDR, false discovery rate; GDSC2, Genomics of Drug Sensitivity in Cancer 2.

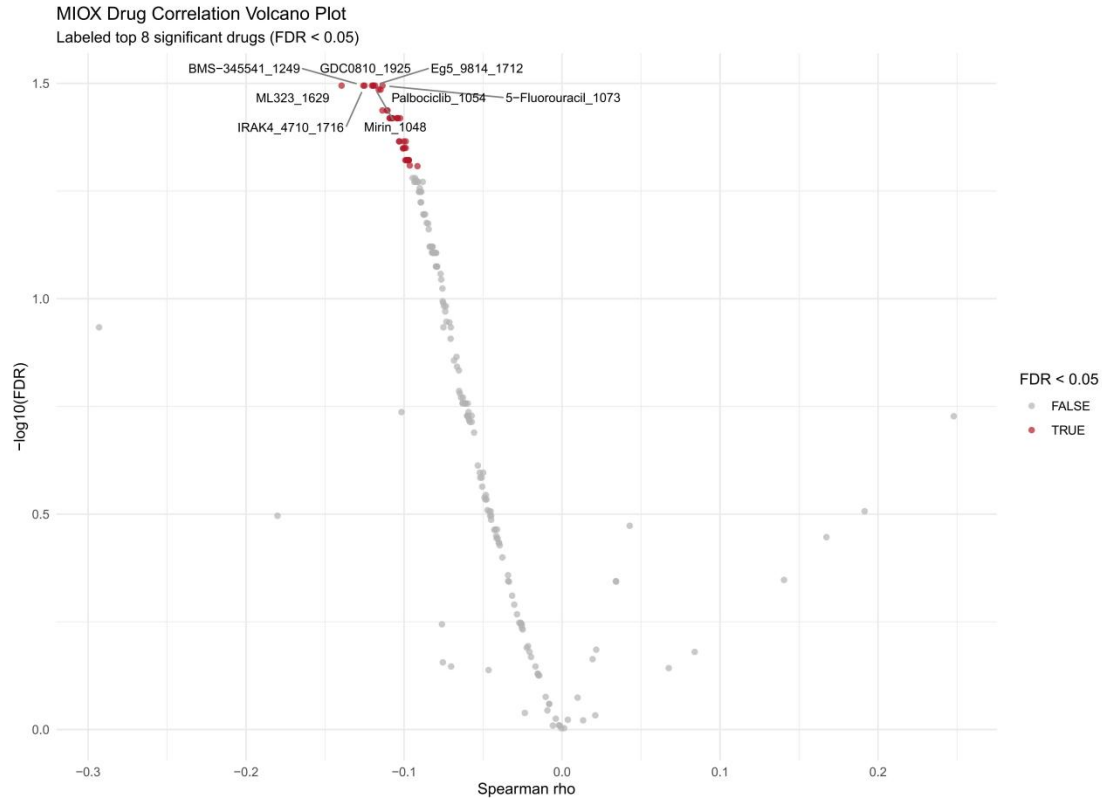


Figure S6. Volcano plot of drug sensitivity associations with MIOX.

Global view of Spearman correlations between MIOX expression and GDSC2 drug IC50 values. Red dots indicate drugs with FDR < 0.05. Top eight drugs are labeled. Abbreviations: IC50, half-maximal inhibitory concentration; FDR, false discovery rate.

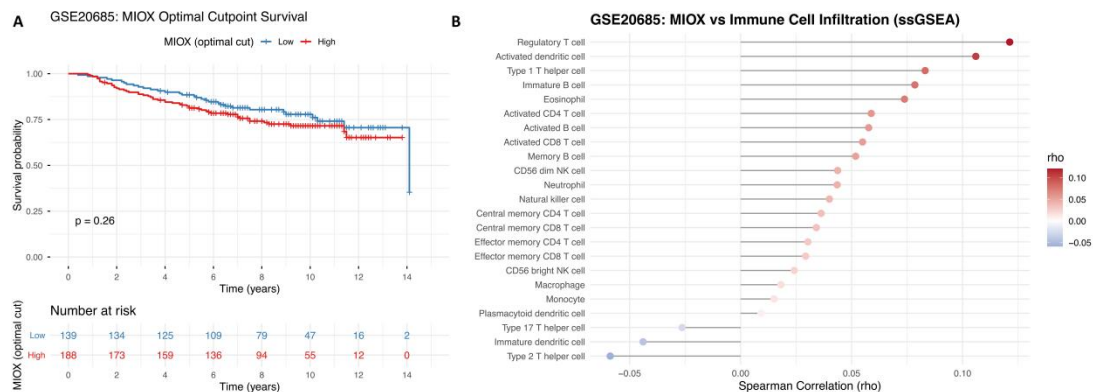


Figure S7. Survival and immune correlation analysis in GSE20685 cohort.

(A) Kaplan-Meier OS curves stratified by MIOX expression (optimal cut-off). Log-rank P = 0.26.

(B) Heatmap of Spearman correlations between MIOX and immune cell types (rho values). No P-value markers are shown due to lack of statistical significance. This cohort is included as exploratory data.

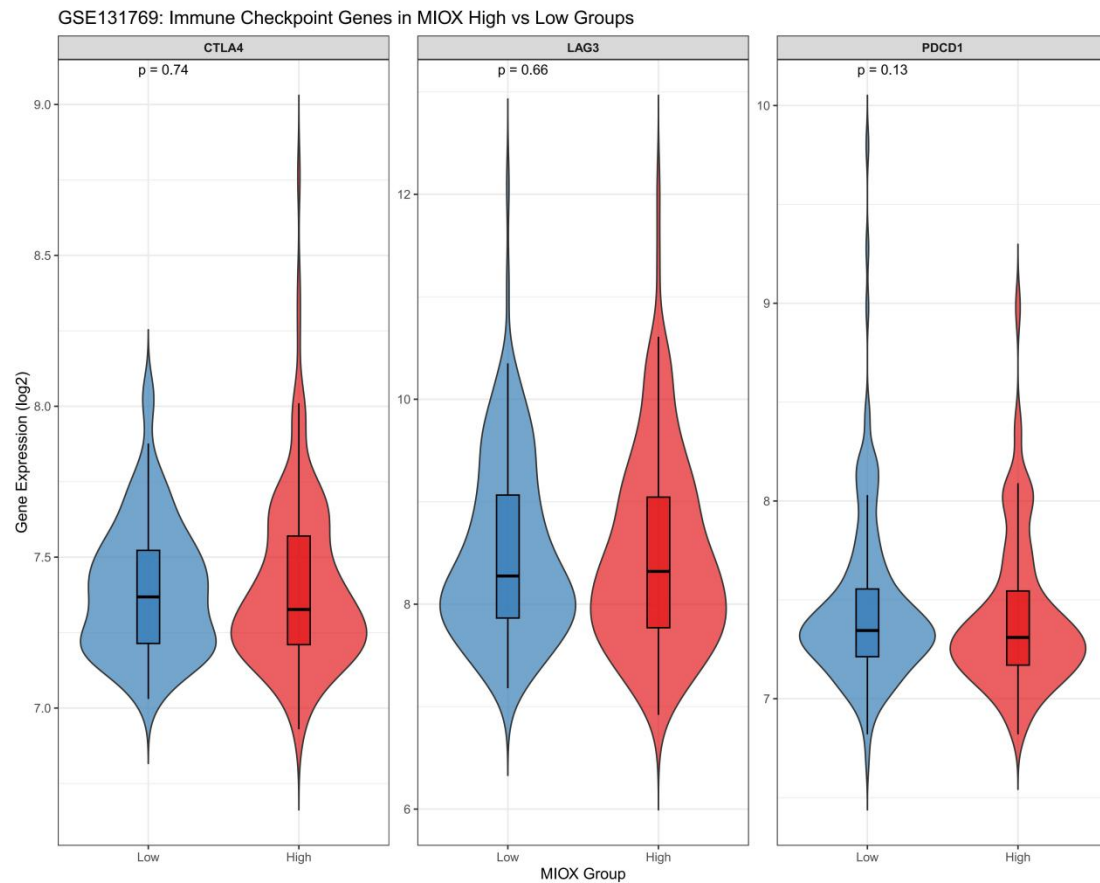


Figure S8. Immune checkpoint gene comparison in GSE131769 cohort.

Boxplots comparing expression levels of CTLA4, LAG3, and PDCD1 between MIOX-high and MIOX-low groups in the GSE131769 cohort. Wilcoxon test, all $P > 0.05$.

Abbreviations: CTLA4, cytotoxic T-lymphocyte-associated protein 4; LAG3, lymphocyte activation gene 3; PDCD1, programmed cell death 1 (PD-1).

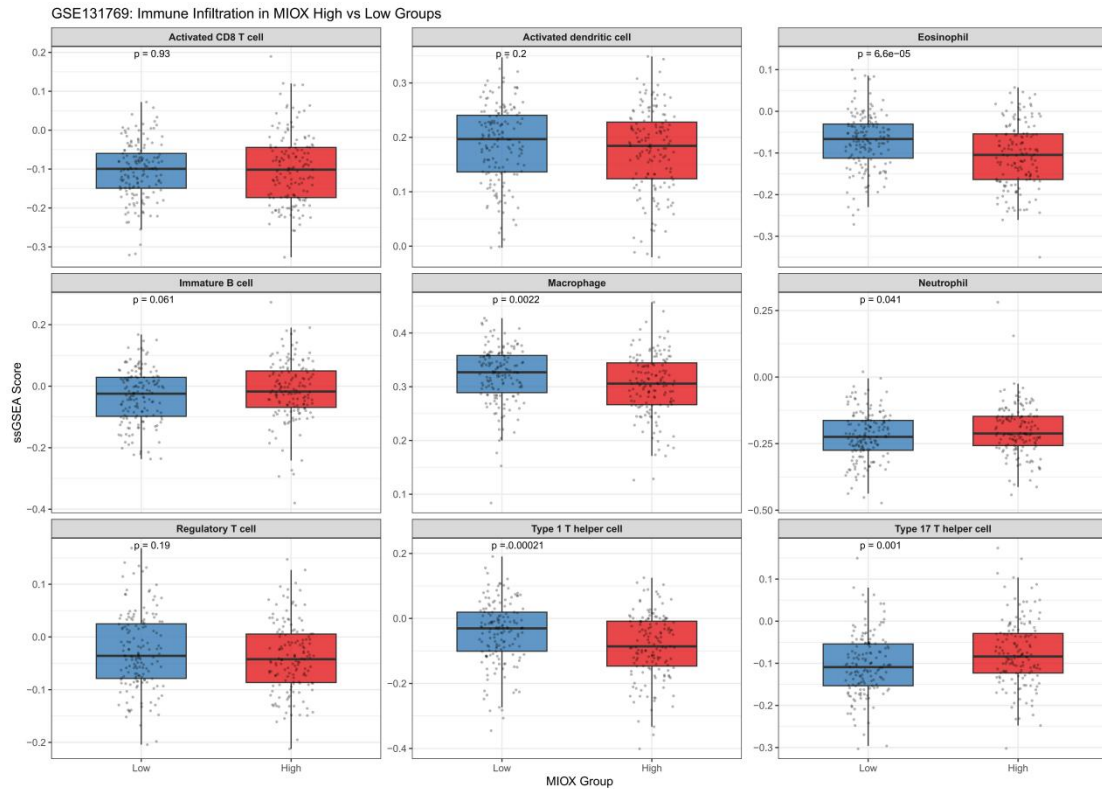


Figure S9. Immune cell infiltration comparison in GSE131769 cohort.

Boxplots showing ssGSEA scores of key immune cell types (activated CD8⁺ T cell, activated dendritic cell, regulatory T cell, etc.) between MIOX-high and MIOX-low groups in GSE131769. Wilcoxon test, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Abbreviations: ssGSEA, single-sample gene set enrichment analysis.

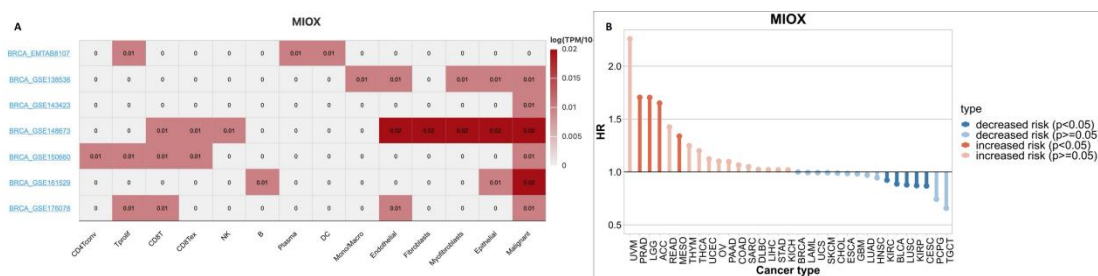


Figure S10. Single-cell expression and pan-cancer prognosis of MIOX.

(A) Single-cell expression heatmap showing MIOX expression in malignant cells, T cells, B cells, and myeloid cells from breast cancer scRNA-seq data (GSE176078).

(B) Forest plot of pan-cancer univariate Cox regression analysis for MIOX across multiple cancer types in TCGA. HR, hazard ratio; CI, confidence interval.

Abbreviations: HR, hazard ratio; CI, confidence interval; scRNA-seq, single-cell RNA sequencing.