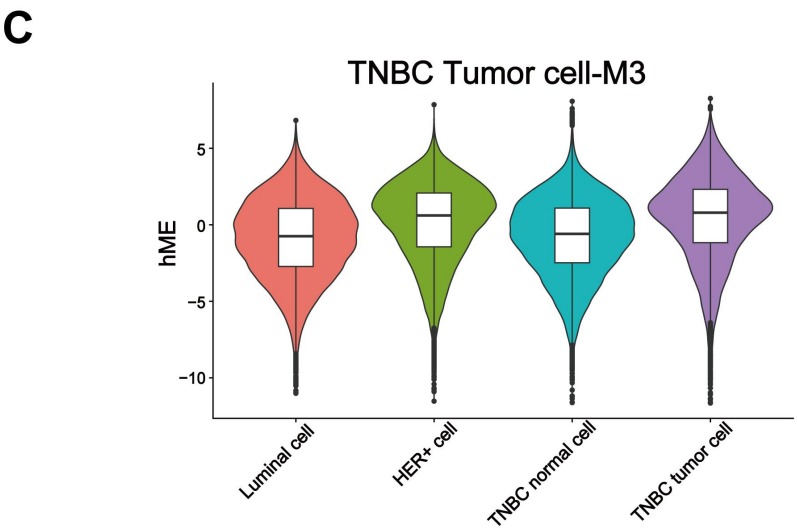
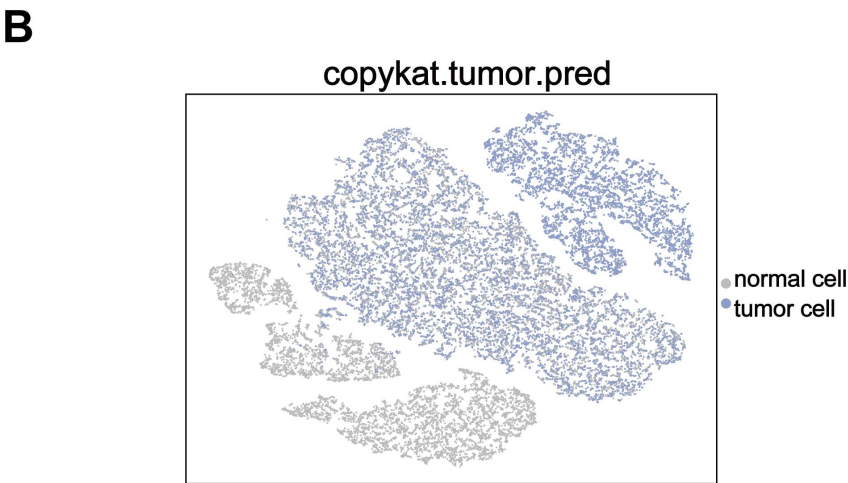
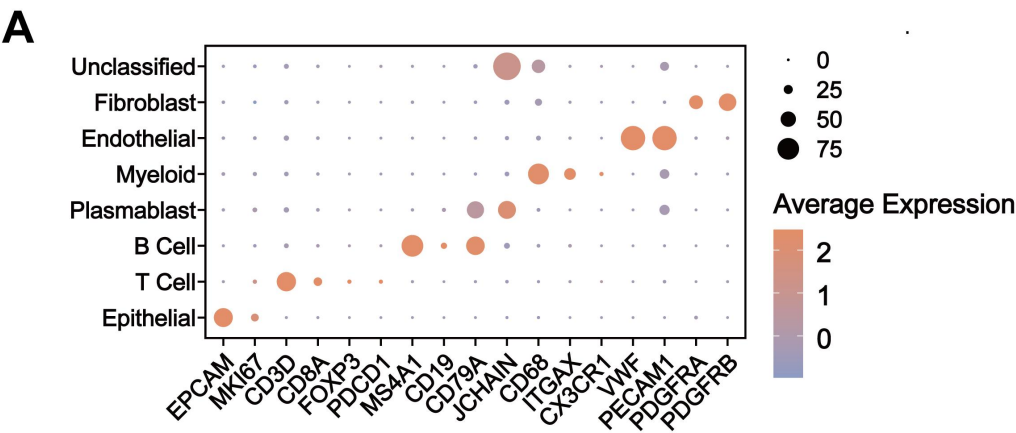


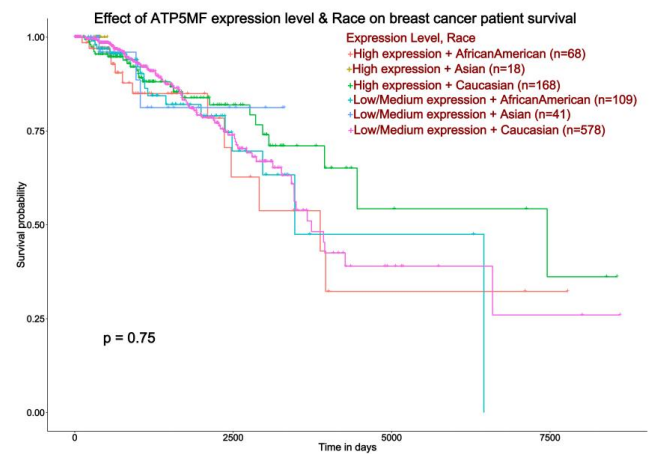
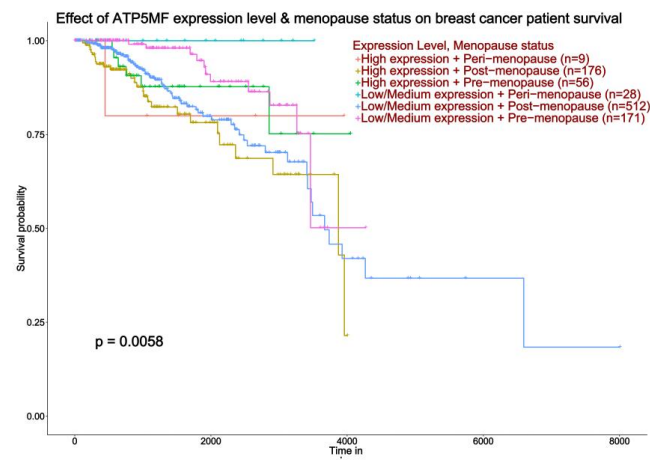
Supplementary material

Supplementary Figure1

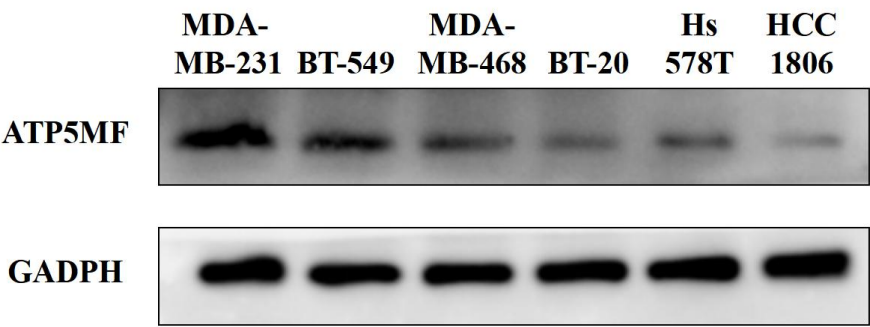


Supplementar Figure2

A



B



Supplementary Figure1. (A) Dot plot showing the average expression of marker genes across different types in tumor samples. Color indicates average expression levels and dot size represents the proportion of cells. (B) t-SNE plot depicting the distribution of tumor cells (blue) and normal cells (grey) using CopyKAT analysis. (C) Violin plot displaying the hME values of different cell types in the M3 module for TNBC.

Supplementary Figure2. (A) Kaplan-Meier survival curves showing the effect of ATP5MF expression level on breast cancer patient survival. The top graph examines the interaction between ATP5MF expression and menopause status. Patients were stratified by high and low/medium expression levels, with further subdivisions based on peri-, post-, and pre-menopausal status. The statistical significance was determined using the log-rank test ($p = 0.0058$). The bottom graph investigates the interaction between ATP5MF expression and race. Patients were divided into high and low/medium expression groups and further classified by race (African American, Asian, Caucasian). The statistical significance was assessed by the log-rank test ($p = 0.75$). (B) Western blot analysis of ATP5MF protein expression in various breast cancer cell lines. The cell lines include MDA-MB-231, BT-549, MDA-MB-468, BT-20, Hs 578T, and HCC 1806. GADPH was used as a loading control.