

Figure S1 For univariate cox regression analysis of mCAFs marker genes from single cell analysis, all had p value <0.05 and HR> 1.

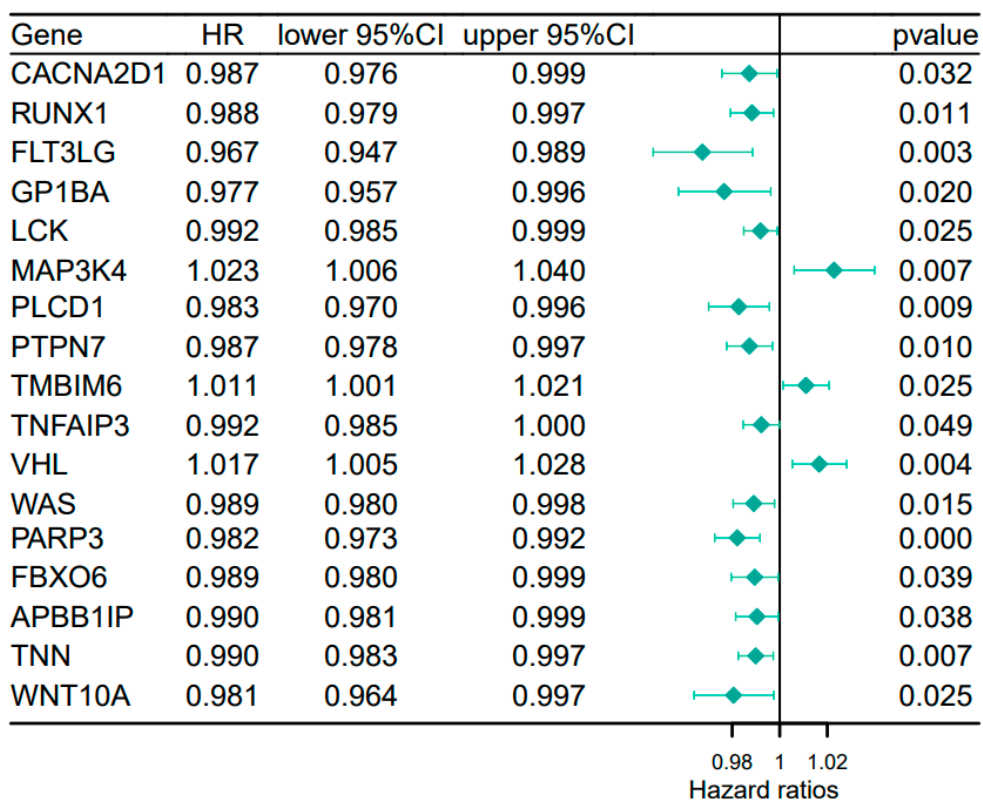


Figure S2 Univariate Cox regression analysis was performed on 17 mCAFs feature genes, and all p-values were found to be less than 0.05.

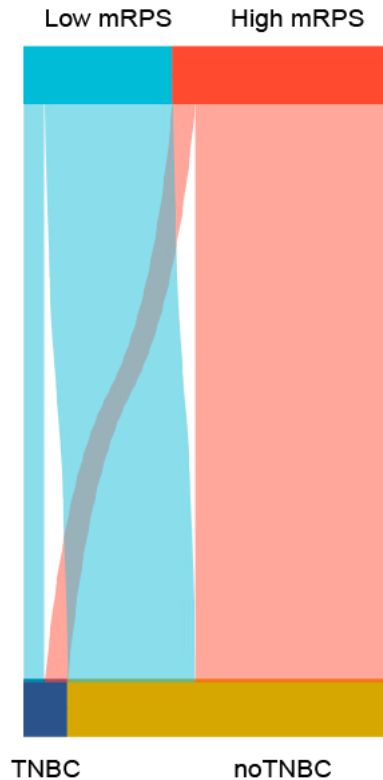


Figure S3 The distribution of triple-negative breast cancer (TNBC) within breast cancer subtypes in high mRPS and low mRPS groups. The high mRPS group shows a slightly higher proportion of

TNBC patients compared to the low mRPS group, indicating an important indicator of malignancy in BRCA.

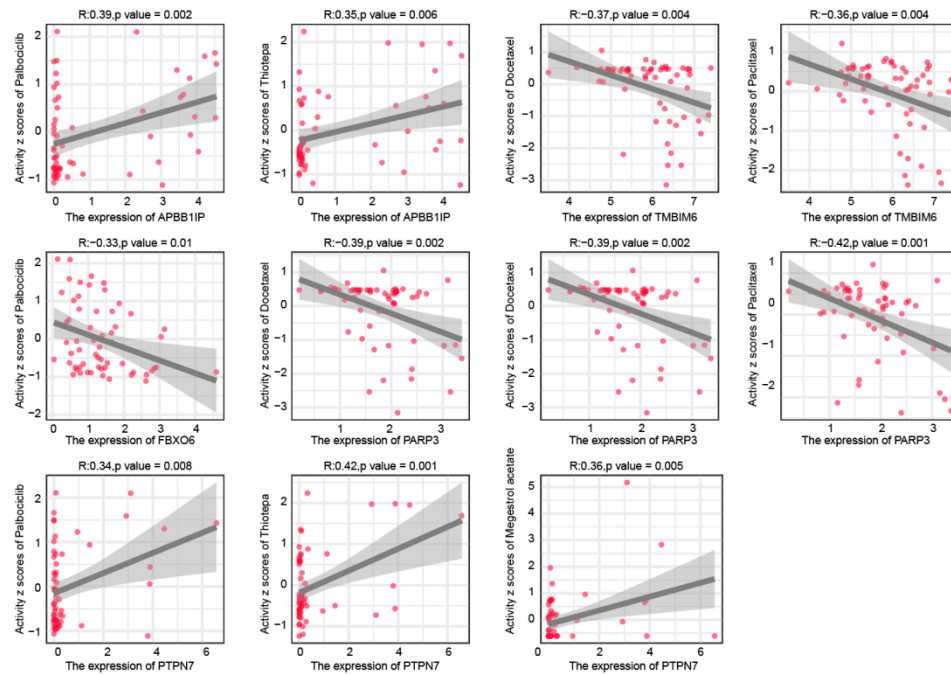


Figure S4 Clinical drug characteristics of mRPS. Pearson correlation analysis was performed between 11 prognostic genes and their potential therapeutic targets. Positive correlation indicates that as the gene expression levels increase, the IC values of the drugs also increase, and vice versa. Lower IC values suggest a higher tolerance of the cells to the drug.

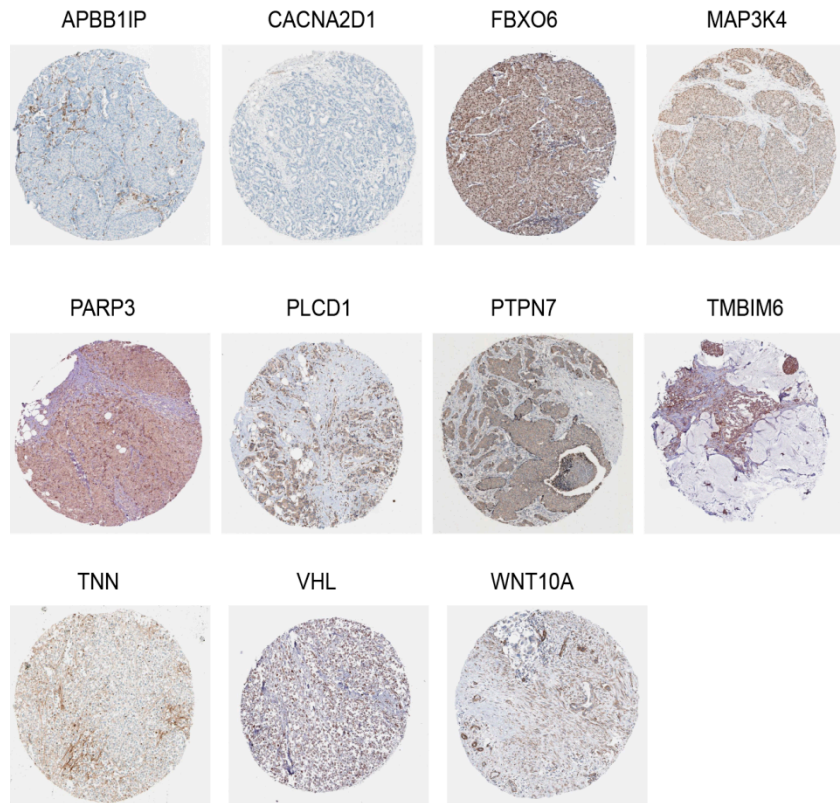


Figure S5 The immunohistochemistry results of 11 genes containing mRPS features were collected from the HPA database. The proteins were expressed in the cytoplasm of BRCA malignant tumor cells. High expression of these 11 genes was found to be associated with the malignancy level of BRCA, with moderately or strongly stained intensity observed in poorly differentiated BRCA samples.