Supplementary Figure 1. Screening for CAF-related genes by WGCNA in breast cancer. (A) Samples were clustered and outlier samples were not found. (B, C) According to the instructions of the WGCNA package, 5 was selected as the soft threshold power. (D) Correlation plot of infiltration of CAFs by XCELL and MCPCOUNTER. (E) Correlation plot of infiltration of CAFs by EPIC and XCELL. (F) Scatter plot between the yellow module and EPIC. (G) Scatter plot between the yellow module and XCELL.
Supplementary Figure 2. Validation of the CAF-related prognostic signature. (A) Kaplan-Meier survival analysis was performed on the relationship between the risk score and OS using the GSE37751 validation cohort. (B) The rank of risk score in the GSE37751 validation cohort. (C) Survival status in the GSE37751 validation cohort. (D) Time-dependent ROC curve analysis of the prognostic model (2, 3, and 5 years) in the GSE37751 validation cohort. (E) Kaplan-Meier survival analysis was performed on the relationship between the risk score and OS using the GSE58812 validation cohort. (F) The rank of risk score in the GSE58812 validation cohort. (G) Survival status in the GSE58812 validation cohort. (H) Time-dependent ROC curve analysis of the prognostic model (2, 3, and 5 years) in the GSE58812 validation cohort.
Supplementary Figure 3. Correlation between clinical characteristics and the risk score in breast cancer. (A–D) Kaplan-Meier survival analyses were performed on the relationship between the risk score and OS in the STAGE I, II, III and IV of breast cancer. (E–I) Kaplan-Meier survival analyses were performed on the relationship between the risk score and OS in the luminal A/B, HER2-enriched, basal-like and normal-like subtypes of breast cancer.
Supplementary Figure 4. Correlation between the risk score and pathway activities. (A–C) GSEA analysis showing the up-regulated pathways in the high-risk group. (D–F) GSEA analysis showing the up-regulated pathways in the low-risk group.
**Supplementary Figure 5.** Dissection of tumor immune microenvironment features based on the CAF-related prognostic signature. (A) Boxplots showing the proportion of 22 immune cells in high/low-risk groups of breast cancer estimated by CIBERSORT.ABS. Paired two-sided Wilcoxon test. (B–E) Scatter plots showing the correlation between the risk score and the proportion of M2-like macrophages, CD8+ T cells, M1-like macrophages and activated NK cells. (F) Boxplots showing the proportion of 22 immune cells in high/low-risk groups of breast cancer estimated by MCPCOUNTER. Paired two-sided Wilcoxon test. The asterisks represent the statistical P-value (*p < 0.05; **p < 0.01; ***p < .001; ****p < 0.0001; n.s.*p > 0.05).
Supplementary Figure 6. High/low-risk group patients differ in drug sensitivity. (A) Scatter plots showing the correlation between the expression of PRKG1 and the IC50 of Leflunomide. (B) Scatter plots showing the correlation between the expression of TNN and the IC50 of Nutlin.3a. (C) Boxplot showing the levels of risk score between CR/PR and SD/PD patients in I-SPY2. Paired two-sided Wilcoxon test. (D) Boxplot showing the levels of risk score between CR/PR and SD/PD patients in GSE123845. Paired two-sided Wilcoxon test.