Supplementary Figures



Supplementary Figure 1. Validation of the IRLP in TCGA cohort. (A) Distribution of riskscore in TCGA training cohort. (B) Survival status of breast cancer patients in TCGA training cohort. (C) Heatmap of the lncRNAs expression profiles of the lncRNAs in TCGA training cohort. (D) Distribution of riskscore in TCGA internal validation cohort. (E) Survival status of breast cancer patients in TCGA internal validation cohort. (F) Heatmap of the lncRNAs expression profiles of the lncRNAs in TCGA internal validation cohort. (F) Heatmap of the lncRNAs expression profiles of the lncRNAs in TCGA internal validation cohort. (G) Distribution of riskscore in the entire TCGA cohort. (H) Survival status of breast cancer patients in the entire TCGA cohort. (I) Heatmap of the lncRNAs expression profiles of the lncRNAs in the entire TCGA cohort. (J-L) The correlation between riskscore and different breast cancer subtypes in TCGA training cohort (J), TCGA internal validation cohort (K) and the entire TCGA cohort (L). (M-P) Four immune-related prognostic lncRNAs associated with OS in breast cancer patients using Kaplan–Meier curves and log-rank tests in the entire TCGA cohort. **p* < 0.05; ***p* < 0.01.



Supplementary Figure 2. Gain-of-function assay of selected immune-related lncRNAs in MDA-MB-468 cells. (A) The overexpression efficiencies of selected lncRNAs. (B) Effects of selected lncRNAs on cell proliferation were evaluated using the MTT assay. (C) Effects of selected lncRNAs on cell proliferation were tested using the EdU assay. Scale bars: 100 μ m. (D) Effects of selected lncRNAs on cell migration were verified by performing a scratch assay. Scale bars: 200 μ m. *p < 0.05; **p < 0.01.



Supplementary Figure 3. PURPL upregulation in MDA-MB-468 promotes the recruitment and M2 polarization of macrophages. (A) qRT–PCR detection of ARG1 and iNOS in macrophages cocultured with MDA-MB-468 cells. (B-C) PURPL-overexpressing MDA-MB-468 cells promoted the migration of macrophages. Five random fields per chamber were observed to count cells at a magnification of 100×. Each assay was performed in triplicate. Scale bars: 200 μ m. (D) A group of cytokines related to macrophage recruitment and polarization as evaluated using qRT–PCR after coculture with PURPL-overexpressing MDA-MB-468 cells. *p < 0.05; **p < 0.01.

Supplementary Tables

1	1 0	1
Primer set	Primers	Sequence (5'-3')
AC022196.1	Forward	ACAACATCTGTTTCCTGCTGGG
	Reverse	TTCTGCCTCTCTCAATGCTTCC
ARHGAP26- AS1	Forward	CAAAGCCCAACACTCTACTGCTT
	Reverse	GTTGGGAGGTTCACCTCTGATG
DPYD-AS1	Forward	AATCCCTGCTTCCTGTCTGCT
	Reverse	CTGGGTTAGGCAAGCTGTTCA
PURPL	Forward	CGTGTGAAAAGAACCCAGGTA
	Reverse	CGCCTGGTAAAACAACCAGT
CCL4	Forward	CTGTGCTGATCCCAGTGAATC
	Reverse	TCAGTTCAGTTCCAGGTCATACA
CX3CL1	Forward	ACCACGGTGTGACGAAATG
	Reverse	TGTTGATAGTGGATGAGCAAAGC
IL6	Forward	ACTCACCTCTTCAGAACGAATTG
	Reverse	CCATCTTTGGAAGGTTCAGGTTG
IL10	Forward	GACTTTAAGGGTTACCTGGGTTG
	Reverse	TCACATGCGCCTTGATGTCTG
IFN-γ	Forward	TCGGTAACTGACTTGAATGTCCA
	Reverse	TCGCTTCCCTGTTTTAGCTGC

Supplementary Table 1. Primer sets used for qRT–PCR

TNF-α	Forward	CCTCTCTCTAATCAGCCCTCTG
	Reverse	GAGGACCTGGGAGTAGATGAG
iNOS	Forward	AGCATGAGCCCCTTCATCAAT
	Reverse	CTGTTTCAACGACCTCCGGG
ARG1	Forward	TGGACAGACTAGGAATTGGCA
	Reverse	CCAGTCCGTCAACATCAAAACT
β-Actin	Forward	CATGTACGTTGCTATCCAGGC
	Reverse	CTCCTTAATGTCACGCACGAT
CCL2	Forward	TCATAGCAGCCACCTTCATTC
	Reverse	CATGGAATCCTGAACCCACTT
CCL5	Forward	GCAAGCTTTGTCACCCGAAA
	Reverse	AAGTTCAGGTTCAAGGACTCTCCA
TGF-β	Forward	CTAATGGTGGAAACCCACAACG
	Reverse	TATCGCCAGGAATTGTTGCTG
CSF-1	Forward	AGACCTCGTGCCAAATTACATT
	Reverse	AGGTGTCTCATAGAAAGTTCGGA