

Resource Summary Report

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GSE1456

RRID:SCR_003642

Type: Tool

Proper Citation

GSE1456 (RRID:SCR_003642)

Resource Information

URL: <http://ranchobiosciences.com/gse1456/>

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Description: Curated series of expression data for 159 tumors from which RNA could be collected in sufficient amounts and quality for analysis from breast cancer patients. Tissue material was collected from all breast cancer patients receiving surgery at Karolinska Hospital from 1994-1996.

Abbreviations: GSE1456

Resource Type: data or information resource, data set

Keywords: adult human, breast

Related Condition: Breast cancer, Tumor

Availability: Free, Public

Resource Name: GSE1456

Resource ID: SCR_003642

Alternate IDs: nlx_157793

Record Creation Time: 20220129T080220+0000

Record Last Update: 20260728T043149+0000

Ratings and Alerts

No rating or validation information has been found for GSE1456.

No alerts have been found for GSE1456.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 184 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Yang XY, et al. (2025) The microenvironment cell index is a novel indicator for the prognosis and therapeutic regimen selection of cancers. *Journal of translational medicine*, 23(1), 61.

Fujita Y, et al. (2025) Exploration of genes related to the development of cancer of unknown primary. *Oncology reports*, 53(6).

Hu C, et al. (2025) Human papillomavirus-related syntaxin 11 reprograms tumor-associated macrophages to induce breast cancer cell apoptosis via PI3K/AKT signaling. *Molecular medicine (Cambridge, Mass.)*, 31(1), 285.

Lee JH, et al. (2025) Nidogen-1 suppresses cell proliferation, migration, and glycolysis via integrin α 1-mediated HIF-1 α downregulation in triple-negative breast cancer. *Scientific reports*, 15(1), 10633.

Yu H, et al. (2025) TCF19 expression and significance analysis in breast cancer: integrated bioinformatics analysis and histological validation. *Discover oncology*, 16(1), 1047.

Xu J, et al. (2025) FRMD8 inhibits tumor metastasis in BRCA1-associated TNBC by negatively regulating tmTNF- α . *Cellular & molecular biology letters*, 30(1), 76.

Chen Y, et al. (2025) Integrative transcriptomic and single-cell analysis reveals IL27RA as a key immune regulator and therapeutic indicator in breast cancer. *Discover oncology*, 16(1), 977.

Yuan Z, et al. (2024) Comprehensive pan-cancer analysis of YBX family reveals YBX2 as a potential biomarker in liver cancer. *Frontiers in immunology*, 15, 1382520.

Feng K, et al. (2024) Construction and validation of a ubiquitination-related prognostic risk score signature in breast cancer. *Heliyon*, 10(15), e35553.

Islam SS, et al. (2024) Long noncoding RNA DLEU2 and ROR1 pathway induces epithelial-to-mesenchymal transition and cancer stem cells in breast cancer. *Cell death discovery*, 10(1), 61.

Mendiburu-Eliçabe M, et al. (2024) NCAPH drives breast cancer progression and identifies a gene signature that predicts luminal a tumour recurrence. *Clinical and translational medicine*, 14(2), e1554.

Jeong Y, et al. (2024) Induction of SUSD2 by STAT3 Activation Is Associated with Tumor Recurrence in HER2-Positive Breast Cancer. *Cells*, 14(1).

Bong AHL, et al. (2024) TMCO1 is upregulated in breast cancer and regulates the response to pro-apoptotic agents in breast cancer cells. *Cell death discovery*, 10(1), 421.

Liao M, et al. (2024) BCAR4 Expression as a Predictive Biomarker for Endocrine Therapy Resistance in Breast Cancer. *Clinical breast cancer*, 24(4), 368.

Mao J, et al. (2024) Integrating single-cell transcriptomics and machine learning to predict breast cancer prognosis: A study based on natural killer cell-related genes. *Journal of cellular and molecular medicine*, 28(15), e18549.

Wang T, et al. (2024) Machine learning-informed liquid-liquid phase separation for personalized breast cancer treatment assessment. *Frontiers in immunology*, 15, 1485123.

Chen Y, et al. (2023) Performance of a PLK1-based immune risk model for prognosis and treatment response prediction in breast cancer. *Cancer medicine*, 12(9), 11020.

Lin C, et al. (2023) Copper homeostasis-associated gene PRNP regulates ferroptosis and immune infiltration in breast cancer. *PloS one*, 18(8), e0288091.

Ditz JC, et al. (2023) COmic: convolutional kernel networks for interpretable end-to-end learning on (multi-)omics data. *Bioinformatics (Oxford, England)*, 39(39 Suppl 1), i76.

Mendiburu-Eliçabe M, et al. (2023) NCAPH Drives Breast Cancer Progression and Identifies a Gene Signature that Predicts Luminal A Tumor Recurrence. *Research square*.