Resource Summary Report

Generated by <u>NIF</u> on May 5, 2025

GSE1456

RRID:SCR_003642 Type: Tool

Proper Citation

GSE1456 (RRID:SCR_003642)

Resource Information

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

Proper Citation: GSE1456 (RRID:SCR_003642)

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

Funding:

Availability: Free, Public

Resource Name: GSE1456

Resource ID: SCR_003642

Alternate IDs: nlx_157793

Record Creation Time: 20220129T080220+0000

Record Last Update: 20250429T054837+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 177 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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.

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 epithelialto-mesenchymal transition and cancer stem cells in breast cancer. Cell death discovery, 10(1), 61.

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.

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.

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.

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.

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

Wang M, et al. (2023) IGJ suppresses breast cancer growth and metastasis by inhibiting

EMT via the NF??B signaling pathway. International journal of oncology, 63(3).

Shen HY, et al. (2023) Integration of bioinformatics and machine learning strategies identifies APM-related gene signatures to predict clinical outcomes and therapeutic responses for breast cancer patients. Neoplasia (New York, N.Y.), 45, 100942.

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.

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.

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

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

Huang N, et al. (2023) TRIM21 mediates the synergistic effect of Olaparib and Sorafenib by degrading BRCA1 through ubiquitination in TNBC. NPJ breast cancer, 9(1), 85.

Liao H, et al. (2023) Expression of the prognostic marker IL-8 correlates with the immune signature and epithelial-mesenchymal transition in breast cancer. Journal of clinical laboratory analysis, 37(3), e24797.

Jiang K, et al. (2023) Deleterious Mechanical Deformation Selects Mechanoresilient Cancer Cells with Enhanced Proliferation and Chemoresistance. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 10(22), e2201663.

Kim HS, et al. (2023) Low CDKN1B Expression Associated with Reduced CD8+ T Lymphocytes Predicts Poor Outcome in Breast Cancer in a Machine Learning Analysis. Journal of personalized medicine, 14(1).

Zhang S, et al. (2022) Adaptor SH3BGRL drives autophagy-mediated chemoresistance through promoting PIK3C3 translation and ATG12 stability in breast cancers. Autophagy, 18(8), 1822.