

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 2026

GSE20194

RRID:SCR_003645

Type: Tool

Proper Citation

GSE20194 (RRID:SCR_003645)

Resource Information

URL: <http://ranchobiosciences.com/gse20194/>

Proper Citation: GSE20194 (RRID:SCR_003645)

Description: Curated data set of gene expression data from 230 stage I-III breast cancers that were generated from fine needle aspiration specimens of newly diagnosed breast cancers before any therapy. The biopsy specimens were collected sequentially during a prospective pharmacogenomic marker discovery study between 2000 and 2008. These specimens represent 70-90% pure neoplastic cells with minimal stromal contamination. In the study, patients received 6 months of preoperative (neoadjuvant) chemotherapy including paclitaxel, 5-fluorouracil, cyclophosphamide and doxorubicin followed by surgical resection of the cancer.

Abbreviations: GSE20194

Resource Type: data or information resource, data set

Keywords: gene expression, chemotherapy, paclitaxel, 5-fluorouracil, cyclophosphamide, doxorubicin, adult human

Related Condition: Cancer, Breast cancer

Availability: Free, Public

Resource Name: GSE20194

Resource ID: SCR_003645

Alternate IDs: nlx_157797

Record Creation Time: 20220129T080220+0000

Record Last Update: 20260912T200314+0000

Ratings and Alerts

No rating or validation information has been found for GSE20194.

No alerts have been found for GSE20194.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 70 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Banerjee S, et al. (2026) Tumor-infiltrating lymphocytes display prognostic signatures associated with chemotherapy response in TNBC patients. *iScience*, 29(6), 116295.

Chen X, et al. (2026) USADAE: a deep learning approach to disentangle hidden covariates in RNA-seq data. *Briefings in bioinformatics*, 27(3).

Chida K, et al. (2026) Ki67 Gene Expression is Associated with Immune Cell Infiltration and Neoadjuvant Chemotherapy Response in ER+/HER2- Breast Cancer. *Annals of surgical oncology*, 33(7), 6422.

Amniouel S, et al. (2026) Development and validation of a highly accurate multigene gene expression biomarker to predict chemotherapy response in primary triple-negative breast cancer. *Breast cancer research and treatment*, 217(1).

Chida K, et al. (2025) DEPTH2 score was associated with cell proliferation and immune cell infiltrations but not with systemic treatment response in breast cancer. *Scientific reports*, 15(1), 42225.

Alamukii NA, et al. (2025) Immune-stromal heterogeneity in breast cancer across diverse ancestries: impact on prognosis and treatment response. *NPJ breast cancer*, 11(1), 142.

Hu M, et al. (2025) Ensemble model for neoadjuvant chemotherapy response prediction and treatment sensitivity in TNBC based on DNA replication stress signatures. *Scientific reports*, 15(1), 38079.

Lusby R, et al. (2024) Decoding gene regulatory circuitry underlying TNBC chemoresistance reveals biomarkers for therapy response and therapeutic targets. *NPJ precision oncology*, 8(1), 64.

Fu C, et al. (2024) GSDME-mediated pyroptosis promotes anti-tumor immunity of neoadjuvant chemotherapy in breast cancer. *Cancer immunology, immunotherapy : CII*, 73(9), 177.

Kwon YJ, et al. (2024) Cysteine protease I29 propeptide from *Calotropis procera* R. Br. As a potent cathepsin L inhibitor and its suppressive activity in breast cancer metastasis. *Scientific reports*, 14(1), 23218.

Sato T, et al. (2024) CD133 expression is associated with less DNA repair, better response to chemotherapy and survival in ER-positive/HER2-negative breast cancer. Research square.

Ning L, et al. (2024) scRNA-seq characterizing the heterogeneity of fibroblasts in breast cancer reveals a novel subtype SFRP4+ CAF that inhibits migration and predicts prognosis. *Frontiers in oncology*, 14, 1348299.

Ning L, et al. (2024) SIRT3 Expression Predicts Overall Survival and Neoadjuvant Chemosensitivity in Triple-Negative Breast Cancer. *Cancer management and research*, 16, 137.

Inayatullah M, et al. (2024) Basal-epithelial subpopulations underlie and predict chemotherapy resistance in triple-negative breast cancer. *EMBO molecular medicine*, 16(4), 823.

Li P, et al. (2024) Improving drug response prediction via integrating gene relationships with deep learning. *Briefings in bioinformatics*, 25(3).

Shen M, et al. (2024) DNAJC12 causes breast cancer chemotherapy resistance by repressing doxorubicin-induced ferroptosis and apoptosis via activation of AKT. *Redox biology*, 70, 103035.

Ozcan G, et al. (2023) PTCH1 and CTNNB1 emerge as pivotal predictors of resistance to neoadjuvant chemotherapy in ER+/HER2- breast cancer. *Frontiers in oncology*, 13, 1216438.

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.

Masroni MSB, et al. (2023) Dynamic altruistic cooperation within breast tumors. *Molecular cancer*, 22(1), 206.

Son S, et al. (2023) CCN3/NOV promotes metastasis and tumor progression via GPNMB-induced EGFR activation in triple-negative breast cancer. *Cell death & disease*, 14(2), 81.