Resource Summary Report

Generated by kravitz2 on Sep 5, 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: 20260904T000553+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 kravitz2 .

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.

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.

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.

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.