Resource Summary Report

Generated by NIF on Apr 9, 2025

GeneChip Operating Software

RRID:SCR_003408
Type: Tool

Proper Citation

GeneChip Operating Software (RRID:SCR_003408)

Resource Information

URL: http://www.scripps.edu/researchservices/dna_array/pages/Data_Analysis_GCOS.htm

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Description: Affymetrix has recently released a new software for the acquisition, management, and analysis of gene expression data. The new GeneChip Operating Software (GCOS) platform enables researchers to perform gene expression, SNP mapping and resequencing analysis with integrated data management and scalable client server configurations. * Compatible with additional Affymetrix analysis software such as Data Mining Tool (DMT) and GeneChip DNA Analysis Software (GDAS) * Supports Gene Expression, Resequencing and Genotyping Applications * Baseline Comparison Analysis Input: Affymetrix .DAT file Output: Affymetrix files (.CEL, .CHP, .RPT, .EXP, .TXT) Availability: The Core Facility has a copy of GCOS, as well as an older version of the Affymetrix software, Microarray Suite (MAS), available for use upon request.

Abbreviations: GCOS

Synonyms: GeneChip Operating Software (GCOS), DNA Array Core Facility GeneChip Operating Software, DNA Array Core Facility GeneChip Operating Software (GCOS)

Resource Type: software application, sequence analysis software, data analysis software, data processing software, software resource

Keywords: gene expression, snp mapping, resequencing, analysis, genotyping, platform, software, comparison, analysis

Funding:

Resource Name: GeneChip Operating Software

Resource ID: SCR_003408

Alternate IDs: nif-0000-33019

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250407T215350+0000

Ratings and Alerts

No rating or validation information has been found for GeneChip Operating Software.

No alerts have been found for GeneChip Operating Software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 649 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Gómez-Pascual A, et al. (2023) Polyglucosan body density in the aged mouse hippocampus is controlled by a novel modifier locus on chromosome 1. bioRxiv : the preprint server for biology.

Chen M, et al. (2020) CTNNB1/?-catenin dysfunction contributes to adiposity by regulating the cross-talk of mature adipocytes and preadipocytes. Science advances, 6(2), eaax9605.

Mao C, et al. (2020) OsNAC2 integrates auxin and cytokinin pathways to modulate rice root development. Plant biotechnology journal, 18(2), 429.

Gai X, et al. (2020) Hyperactivation of IL-6/STAT3 pathway leaded to the poor prognosis of post-TACE HCCs by HIF-1?/SNAI1 axis-induced epithelial to mesenchymal transition. Journal of Cancer, 11(3), 570.

Yu C, et al. (2020) Down-regulation of MTHFD2 inhibits NSCLC progression by suppressing cycle-related genes. Journal of cellular and molecular medicine, 24(2), 1568.

Xu Q, et al. (2020) Association of iRhom1 and iRhom2 expression with prognosis in patients with cervical cancer and possible signaling pathways. Oncology reports, 43(1), 41.

Diedrichs F, et al. (2019) Enhanced Immunomodulation in Inflammatory Environments Favors Human Cardiac Mesenchymal Stromal-Like Cells for Allogeneic Cell Therapies.

Frontiers in immunology, 10, 1716.

Liu JY, et al. (2019) NETO2 promotes invasion and metastasis of gastric cancer cells via activation of PI3K/Akt/NF-?B/Snail axis and predicts outcome of the patients. Cell death & disease, 10(3), 162.

Cao D, et al. (2019) Metallopanstimulin-1 (MPS-1) mediates the promotion effect of leptin on colorectal cancer through activation of JNK/c-Jun signaling pathway. Cell death & disease, 10(9), 655.

Fu Y, et al. (2019) Downregulation of CPA4 inhibits non small-cell lung cancer growth by suppressing the AKT/c-MYC pathway. Molecular carcinogenesis, 58(11), 2026.

Gao Q, et al. (2019) Heterotypic CAF-tumor spheroids promote early peritoneal metastatis of ovarian cancer. The Journal of experimental medicine, 216(3), 688.

Yang S, et al. (2019) Promoting Osteogenic Differentiation of Human Adipose-Derived Stem Cells by Altering the Expression of Exosomal miRNA. Stem cells international, 2019, 1351860.

Taškova K, et al. (2019) Literature optimized integration of gene expression for organ-specific evaluation of toxicogenomics datasets. PloS one, 14(1), e0210467.

Gladilin E, et al. (2019) TGF?-induced cytoskeletal remodeling mediates elevation of cell stiffness and invasiveness in NSCLC. Scientific reports, 9(1), 7667.

Zeng J, et al. (2019) Down-regulated HSDL2 expression suppresses cell proliferation and promotes apoptosis in papillary thyroid carcinoma. Bioscience reports, 39(6).

Yamashita S, et al. (2019) Distinct DNA methylation targets by aging and chronic inflammation: a pilot study using gastric mucosa infected with Helicobacter pylori. Clinical epigenetics, 11(1), 191.

Lage P, et al. (2019) Transcriptomic and chemogenomic analyses unveil the essential role of Com2-regulon in response and tolerance of Saccharomyces cerevisiae to stress induced by sulfur dioxide. Microbial cell (Graz, Austria), 6(11), 509.

Silkenstedt E, et al. (2019) Notch1 signaling in NOTCH1-mutated mantle cell lymphoma depends on Delta-Like ligand 4 and is a potential target for specific antibody therapy. Journal of experimental & clinical cancer research : CR, 38(1), 446.

Ganbold M, et al. (2019) Isorhamnetin Alleviates Steatosis and Fibrosis in Mice with Nonalcoholic Steatohepatitis. Scientific reports, 9(1), 16210.

Nuthikattu S, et al. (2019) The Western Diet Regulates Hippocampal Microvascular Gene Expression: An Integrated Genomic Analyses in Female Mice. Scientific reports, 9(1), 19058.