Resource Summary Report

Generated by T1D on Aug 1, 2026

OncoSNP

RRID:SCR_012985
Type: Tool

Proper Citation

OncoSNP (RRID:SCR_012985)

Resource Information

URL: https://sites.google.com/site/oncosnp/

Proper Citation: OncoSNP (RRID:SCR_012985)

Description: An analytical software tool for characterizing copy number alterations and loss-of-heterozygosity (LOH) events in cancer samples from SNP genotyping data.

Abbreviations: OncoSNP

Resource Type: software resource

Related Condition: Cancer

Availability: Freely available for academic use, Non-commercial, Commercial with permission

Resource Name: OncoSNP

Resource ID: SCR_012985

Alternate IDs: OMICS_00728

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260725T190742+0000

Ratings and Alerts

No rating or validation information has been found for OncoSNP.

No alerts have been found for OncoSNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Li MY, et al. (2024) TRAF3 loss-of-function reveals the noncanonical NF-??B pathway as a therapeutic target in diffuse large B cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 121(18), e2320421121.

Takata K, et al. (2022) Tumor-associated antigen PRAME exhibits dualistic functions that are targetable in diffuse large B cell lymphoma. The Journal of clinical investigation, 132(10).

Athans S, et al. (2022) STAG2 expression is associated with adverse survival outcomes and regulates cell phenotype in muscle-invasive bladder cancer. Cancer research communications, 2(10), 1129.

Haider S, et al. (2020) Systematic Assessment of Tumor Purity and Its Clinical Implications. JCO precision oncology, 4.

Luo F, et al. (2019) A systematic evaluation of copy number alterations detection methods on real SNP array and deep sequencing data. BMC bioinformatics, 20(Suppl 25), 692.

Schuster EF, et al. (2019) Genomic Instability and TP53 Genomic Alterations Associate With Poor Antiproliferative Response and Intrinsic Resistance to Aromatase Inhibitor Treatment. JCO precision oncology, 3.

Veeramachaneni R, et al. (2019) Analysis of head and neck carcinoma progression reveals novel and relevant stage-specific changes associated with immortalisation and malignancy. Scientific reports, 9(1), 11992.

Cross W, et al. (2018) The evolutionary landscape of colorectal tumorigenesis. Nature ecology & evolution, 2(10), 1661.

Arthur SE, et al. (2018) Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature communications, 9(1), 4001.

Heits N, et al. (2018) Evolutionary Distance Predicts Recurrence After Liver Transplantation in Multifocal Hepatocellular Carcinoma. Transplantation, 102(10), e424.

Wang J, et al. (2016) Collecting duct carcinoma of the kidney is associated with CDKN2A deletion and SLC family gene up-regulation. Oncotarget, 7(21), 29901.

Findlay JM, et al. (2016) Differential clonal evolution in oesophageal cancers in response to neo-adjuvant chemotherapy. Nature communications, 7, 11111.

Suraweera N, et al. (2016) Relative telomere lengths in tumor and normal mucosa are related to disease progression and chromosome instability profiles in colorectal cancer.

Oncotarget, 7(24), 36474.

Savas P, et al. (2016) The Subclonal Architecture of Metastatic Breast Cancer: Results from a Prospective Community-Based Rapid Autopsy Program "CASCADE". PLoS medicine, 13(12), e1002204.

Jorissen RN, et al. (2015) Wild-type APC predicts poor prognosis in microsatellite-stable proximal colon cancer. British journal of cancer, 113(6), 979.

Williams RD, et al. (2015) Multiple mechanisms of MYCN dysregulation in Wilms tumour. Oncotarget, 6(9), 7232.

Ross-Adams H, et al. (2015) Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study. EBioMedicine, 2(9), 1133.

Xie T, et al. (2014) Patterns of somatic alterations between matched primary and metastatic colorectal tumors characterized by whole-genome sequencing. Genomics, 104(4), 234.

Yau C, et al. (2010) A statistical approach for detecting genomic aberrations in heterogeneous tumor samples from single nucleotide polymorphism genotyping data. Genome biology, 11(9), R92.