Resource Summary Report

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Virmid

RRID:SCR_006780
Type: Tool

Proper Citation

Virmid (RRID:SCR_006780)

Resource Information

URL: http://sourceforge.net/projects/virmid/

Proper Citation: Virmid (RRID:SCR_006780)

Description: A Java based variant caller designed for disease-control matched samples. Virmid is also specialized for identifying potential within individual contamination where the disease sample cannot be purified enough. While the SNP calling rate is severely compromised with this heterogeneity, Virmid can uncover SNPs with low allele frequency by considering the level of contamination (alpha). The important features of Virmid are: * Estimation of accurate proporation of control sample in a (mixed) disease sample * Improved SNP and somatic mutation calling with regard to the estimated proportion

Abbreviations: Virmid

Synonyms: Virtual Microdissection for SNP calling

Resource Type: software resource

Defining Citation: PMID:23987214

Keywords: somatic mutation, sample impurity, java, snp, variant, disease, control

Funding:

Resource Name: Virmid

Resource ID: SCR_006780

Alternate IDs: OMICS_00095

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250410T065453+0000

Ratings and Alerts

No rating or validation information has been found for Virmid.

No alerts have been found for Virmid.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Suzuki H, et al. (2019) Recurrent noncoding U1 snRNA mutations drive cryptic splicing in SHH medulloblastoma. Nature, 574(7780), 707.

Lu IL, et al. (2018) Identification of genes associated with cortical malformation using a transposon-mediated somatic mutagenesis screen in mice. Nature communications, 9(1), 2498.

Krøigård AB, et al. (2016) Evaluation of Nine Somatic Variant Callers for Detection of Somatic Mutations in Exome and Targeted Deep Sequencing Data. PloS one, 11(3), e0151664.

Hatlen MA, et al. (2016) Integrative genetic analysis of mouse and human AML identifies cooperating disease alleles. The Journal of experimental medicine, 213(1), 25.

Kim S, et al. (2013) Virmid: accurate detection of somatic mutations with sample impurity inference. Genome biology, 14(8), R90.