

Resource Summary Report

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MAQC

RRID:SCR_002351

Type: Tool

Proper Citation

MAQC (RRID:SCR_002351)

Resource Information

URL:

<http://www.fda.gov/ScienceResearch/BioinformaticsTools/MicroarrayQualityControlProject/default.htm>

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Description: Project to improve the microarray and next-generation sequencing technologies and foster their proper applications in discovery, development and review of FDA regulated products by developing standards and quality measures. Microarrays and next-generation sequencing represent core technologies in pharmacogenomics and toxicogenomics; however, before these technologies can successfully and reliably be used in clinical practice and regulatory decision-making, standards and quality measures need to be developed. Everyone is invited to participate in the MAQC project.

Abbreviations: MAQC

Synonyms: MicroArray Quality Control

Resource Type: data or information resource, knowledge environment, narrative resource, standard specification

Keywords: microarray, next-generation sequencing, pharmacogenomics, toxicogenomics, quality control

Resource Name: MAQC

Resource ID: SCR_002351

Alternate IDs: OMICS_01784

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260829T182731+0000

Ratings and Alerts

No rating or validation information has been found for MAQC.

No alerts have been found for MAQC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Apostolides M, et al. (2024) Accurate isoform quantification by joint short- and long-read RNA-sequencing. bioRxiv : the preprint server for biology.

Wang D, et al. (2024) A real-world multi-center RNA-seq benchmarking study using the Quartet and MAQC reference materials. Nature communications, 15(1), 6167.

Zheng Y, et al. (2024) Multi-omics data integration using ratio-based quantitative profiling with Quartet reference materials. Nature biotechnology, 42(7), 1133.

Yu Y, et al. (2024) Quartet RNA reference materials improve the quality of transcriptomic data through ratio-based profiling. Nature biotechnology, 42(7), 1118.

Tang K, et al. (2021) Rank-in: enabling integrative analysis across microarray and RNA-seq for cancer. Nucleic acids research, 49(17), e99.

Hamaguchi Y, et al. (2021) Impact of human gene annotations on RNA-seq differential expression analysis. BMC genomics, 22(1), 730.

Morlion A, et al. (2021) Custom long non-coding RNA capture enhances detection sensitivity in different human sample types. RNA biology, 18(sup1), 215.

Sun Z, et al. (2021) Immune-related gene expression signatures in colorectal cancer. Oncology letters, 22(1), 543.

Hu Y, et al. (2021) LIQA: long-read isoform quantification and analysis. Genome biology, 22(1), 182.

Li X, et al. (2020) Choice of library size normalization and statistical methods for differential gene expression analysis in balanced two-group comparisons for RNA-seq studies. BMC genomics, 21(1), 75.

Lataretu M, et al. (2020) RNAflow: An Effective and Simple RNA-Seq Differential Gene Expression Pipeline Using Nextflow. Genes, 11(12).

Liao Y, et al. (2020) Read trimming is not required for mapping and quantification of RNA-seq reads at the gene level. NAR genomics and bioinformatics, 2(3), lqaa068.

Zahoor J, et al. (2020) Classification of Microarray Gene Expression Data Using an Infiltration Tactics Optimization (ITO) Algorithm. *Genes*, 11(7).

Li S, et al. (2020) The Important Role of Perituberal Tissue in Epileptic Patients with Tuberous Sclerosis Complex by the Transcriptome Analysis. *BioMed research international*, 2020, 4980609.

Zou C, et al. (2020) Use of peripheral blood transcriptomic biomarkers to distinguish high-grade cervical squamous intraepithelial lesions from low-grade lesions. *Oncology letters*, 20(3), 2280.

Baik B, et al. (2020) Benchmarking RNA-seq differential expression analysis methods using spike-in and simulation data. *PloS one*, 15(4), e0232271.

Kallarackal J, et al. (2020) A 3-gene biomarker signature to predict response to taxane-based neoadjuvant chemotherapy in breast cancer. *PloS one*, 15(3), e0230313.

Abrams ZB, et al. (2019) A protocol to evaluate RNA sequencing normalization methods. *BMC bioinformatics*, 20(Suppl 24), 679.

Kusko R, et al. (2018) Large-scale transcriptomic analysis reveals that pridopidine reverses aberrant gene expression and activates neuroprotective pathways in the YAC128 HD mouse. *Molecular neurodegeneration*, 13(1), 25.

Zhou W, et al. (2017) Imputing gene expression to maximize platform compatibility. *Bioinformatics (Oxford, England)*, 33(4), 522.