

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

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: 20260728T043131+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 [nidm-terms](#) .

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

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.

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.

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

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

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

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.

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

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.

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.

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

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.

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.

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.