

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

NGS QC Toolkit

RRID:SCR_005461

Type: Tool

Proper Citation

NGS QC Toolkit (RRID:SCR_005461)

Resource Information

URL: <http://www.nipgr.res.in/ngsqctoolkit.html>

Proper Citation: NGS QC Toolkit (RRID:SCR_005461)

Description: A software toolkit for the quality control (QC) of next generation sequencing (NGS) data. The toolkit comprises of user-friendly stand alone tools for quality control of the sequence data generated using Illumina and Roche 454 platforms with detailed results in the form of tables and graphs, and filtering of high-quality sequence data. It also includes few other tools, which are helpful in NGS data quality control and analysis., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: NGS QC Toolkit

Resource Type: software resource

Defining Citation: [PMID:22312429](#)

Keywords: next generation sequencing

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: NGS QC Toolkit

Resource ID: SCR_005461

Alternate IDs: OMICS_01062

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260912T195626+0000

Ratings and Alerts

No rating or validation information has been found for NGS QC Toolkit.

No alerts have been found for NGS QC Toolkit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 284 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hu Y, et al. (2026) Invasive patterns of *Biomphalaria straminea* revealed by genetic mapping in the Greater Bay Area, China. *Infectious diseases of poverty*, 15(1), 9.

Liu X, et al. (2025) Functional validation to explore the protective role of miR-223 in *Staphylococcus aureus*-induced bovine mastitis. *Journal of animal science and biotechnology*, 16(1), 34.

Yang J, et al. (2025) The development of ideal insertion and deletion (InDel) markers and initial indel map variation in cucumber using re-sequenced data. *BMC genomics*, 26(1), 391.

Zhu C, et al. (2025) Global diversity and distribution of antibiotic resistance genes in human wastewater treatment systems. *Nature communications*, 16(1), 4006.

Mengist MF, et al. (2025) Identification and functional characterization of BAHD acyltransferases associated with anthocyanin acylation in blueberry. *Horticulture research*, 12(5), uhaf041.

Huang M, et al. (2025) Goose multi-omics database: A comprehensive multi-omics database for goose genomics. *Poultry science*, 104(3), 104842.

Liu X, et al. (2025) Multi-omics investigation of spontaneous T2DM macaque emphasizes gut microbiota could up-regulate the absorption of excess palmitic acid in the T2DM progression. *eLife*, 14.

Tong L, et al. (2025) Functional characterization in *Chimonobambusa utilis* reveals the role of bHLH gene family in bamboo sheath color variation. *Frontiers in plant science*, 16, 1514703.

Shi J, et al. (2025) Dynamic epigenomic landscape and gene regulatory networks during embryonic development in Pacific white shrimp (*Litopenaeus vannamei*) as revealed by histone modification profiling using CUT&Tag. *Epigenetics & chromatin*, 18(1), 50.

White K, et al. (2025) Lactococcal phage-host profiling through binding studies between cell wall polysaccharide types and Skunavirus receptor-binding proteins. *Microbial genomics*, 11(4).

Luo P, et al. (2025) The first complete chloroplast genome sequence of *Sterculia foetida* Linnaeus (Malvaceae) and a comparative phylogenetic analysis. *Mitochondrial DNA. Part B, Resources*, 10(8), 731.

Tang B, et al. (2025) METTL3 and METTL14 drive pancreatic adenocarcinoma progression via m6A-dependent alternative splicing in PANC-1 cells. *Discover oncology*, 16(1), 1590.

Huang Y, et al. (2025) The first complete mitochondrial genome assembly and comparative analysis of the fern *Blechnaceae* family: *Blechnopsis orientalis*. *Frontiers in plant science*, 16, 1534171.

Cui H, et al. (2025) Branched-chain amino acid metabolism supports *Roseobacteraceae* positive interactions in marine biofilms. *Applied and environmental microbiology*, 91(3), e0241124.

He S, et al. (2024) Genome-wide identification, characterization and expression analysis of the bZIP transcription factors in garlic (*Allium sativum* L.). *Frontiers in plant science*, 15, 1391248.

Xia L, et al. (2024) Spatio-temporal expression patterns of glycine-rich beta proteins and cysteine-rich beta proteins in setae development of *Gekko japonicus*. *BMC genomics*, 25(1), 535.

Lin Y, et al. (2024) Molecular evidence provides new insights into the evolutionary origin of an ancient traditional Chinese medicine, the domesticated "Baizhi". *Frontiers in plant science*, 15, 1388586.

Guo N, et al. (2024) A graph-based pan-genome of *Brassica oleracea* provides new insights into its domestication and morphotype diversification. *Plant communications*, 5(2), 100791.

Cao S, et al. (2024) Cytoplasmic genome contributions to domestication and improvement of modern maize. *BMC biology*, 22(1), 64.

Pires GP, et al. (2024) Effects of trimer repeats on *Psidium guajava* L. gene expression and prospection of functional microsatellite markers. *Scientific reports*, 14(1), 9811.