

Resource Summary Report

Generated by T1D on Jul 30, 2026

phantompeakqualtools

RRID:SCR_005331

Type: Tool

Proper Citation

phantompeakqualtools (RRID:SCR_005331)

Resource Information

URL: <https://code.google.com/p/phantompeakqualtools/>

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Description: Software package that computes quick but highly informative enrichment and quality measures for ChIP-seq/DNase-seq/FAIRE-seq/MNase-seq data. It can also be used to obtain robust estimates of the predominant fragment length or characteristic tag shift values in these assays.

Abbreviations: phantompeakqualtools

Synonyms: phantompeakqualtools - Computes quick but highly informative enrichment and quality measures and fragment lengths for ChIP-seq/DNase-seq/FAIRE-seq/MNase-seq data

Resource Type: software resource

Keywords: chip-seq, dnase-seq, faire-seq, mnase-seq, dataquality, enrichment, phantompeak, cross-correlation, spppeakcaller, chipseq, dnaseseq, fairseq, mnaseseq, bio.tools

Availability: MIT License

Resource Name: phantompeakqualtools

Resource ID: SCR_005331

Alternate IDs: biotools:phantompeakqualtools, OMICS_00431

Alternate URLs: <https://bio.tools/phantompeakqualtools>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260725T190602+0000

Ratings and Alerts

No rating or validation information has been found for phantompeakqualtools.

No alerts have been found for phantompeakqualtools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 86 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Kanduri M, et al. (2025) IER3: exploring its dual function as an oncogene and tumor suppressor. *Cancer gene therapy*, 32(4), 450.

Bresnahan ST, et al. (2025) Intragenomic conflict associated with extreme phenotypic plasticity in queen-worker caste determination in honey bees (*Apis mellifera*). *Genome biology*, 26(1), 171.

Palma LG, et al. (2025) Chromatin activity of I?B? mediates the exit from naïve pluripotency. *eLife*, 14.

Mukherjee S, et al. (2025) Tumor-associated neutrophil precursors impair homologous DNA repair and promote sensitivity to PARP inhibition. *Nature communications*, 16(1), 6999.

Severson TM, et al. (2025) Epigenetic profiling identifies markers of endocrine resistance and therapeutic options for metastatic castration-resistant prostate cancer. *Cell reports. Medicine*, 6(7), 102215.

Cheng CCY, et al. (2025) Multi-omic analysis of hepatocellular carcinoma reveals aberrant cis-regulatory changes and dysregulated retrotransposons with prognostic potential. *Communications biology*, 8(1), 1792.

Budkina A, et al. (2025) Functional characterization of DNAAF3-AS1 in chromatin remodeling and H3K36me3 distribution. *bioRxiv : the preprint server for biology*.

Zhu T, et al. (2024) Comprehensive mapping and modelling of the rice regulome landscape unveils the regulatory architecture underlying complex traits. *Nature communications*, 15(1), 6562.

Hu G, et al. (2024) Evolutionary Dynamics of Chromatin Structure and Duplicate Gene Expression in Diploid and Allopolyploid Cotton. *Molecular biology and evolution*, 41(5).

Silveira AB, et al. (2024) Base-excision repair pathway shapes 5-methylcytosine deamination signatures in pan-cancer genomes. *Nature communications*, 15(1), 9864.

Gao L, et al. (2024) Selective gene expression maintains human tRNA anticodon pools during differentiation. *Nature cell biology*, 26(1), 100.

Pham VC, et al. (2024) Epigenetic regulation by polycomb repressive complex 1 promotes cerebral cavernous malformations. *EMBO molecular medicine*, 16(11), 2827.

Lyu P, et al. (2024) Chromatin profiling reveals TFAP4 as a critical transcriptional regulator of bovine satellite cell differentiation. *BMC genomics*, 25(1), 272.

Puri D, et al. (2023) CTCF deletion alters the pluripotency and DNA methylation profile of human iPSCs. *Frontiers in cell and developmental biology*, 11, 1302448.

Yin L, et al. (2023) Transcription Factor Dynamics in Cross-Regulation of Plant Hormone Signaling Pathways. *bioRxiv : the preprint server for biology*.

Yazar V, et al. (2023) Impaired ATF3 signaling involves SNAP25 in SOD1 mutant ALS patients. *Scientific reports*, 13(1), 12019.

Quintela M, et al. (2023) In silico enhancer mining reveals SNS-032 and EHMT2 inhibitors as therapeutic candidates in high-grade serous ovarian cancer. *British journal of cancer*, 129(1), 163.

Spracklin G, et al. (2023) Diverse silent chromatin states modulate genome compartmentalization and loop extrusion barriers. *Nature structural & molecular biology*, 30(1), 38.

Alexandari AM, et al. (2023) De novo distillation of thermodynamic affinity from deep learning regulatory sequence models of in vivo protein-DNA binding. *bioRxiv : the preprint server for biology*.

Diego-Martin B, et al. (2022) The TRIPLE PHD FINGERS proteins are required for SWI/SNF complex-mediated +1 nucleosome positioning and transcription start site determination in Arabidopsis. *Nucleic acids research*, 50(18), 10399.