

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

BMIQ

RRID:SCR_003446

Type: Tool

Proper Citation

BMIQ (RRID:SCR_003446)

Resource Information

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

Proper Citation: BMIQ (RRID:SCR_003446)

Description: Software using a beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data.

Abbreviations: BMIQ

Synonyms: bmiq - Beta Mixture Quantile Model, Beta Mixture Quantile dilation

Resource Type: software resource

Defining Citation: [PMID:23175756](#)

Keywords: illumina infinium 450k, dna methylation, probe design, normalization

Availability: Free, Available for download, Freely available

Resource Name: BMIQ

Resource ID: SCR_003446

Alternate IDs: OMICS_02304

Alternate URLs: <https://aeteschendorff-lab.github.io/software/BMIQ/>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260725T190540+0000

Ratings and Alerts

No rating or validation information has been found for BMIQ.

No alerts have been found for BMIQ.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 125 mentions in open access literature.

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

Kashiwagi T, et al. (2025) Variation of Gene Expression and Methylation Profiling in Gingival and Tongue Cancers. *Cancer science*, 116(12), 3459.

Bozack A, et al. (2025) Dietary Fatty Acids and Epigenetic Aging in US Adults: Results from the National Health and Nutrition Examination Survey. *medRxiv : the preprint server for health sciences*.

Jiang X, et al. (2025) Identification of blood-derived DNA methylation biomarkers of glaucoma and intraocular pressure measurements in three European ancestry cohorts including the Canadian longitudinal study on aging. *Epigenetics*, 20(1), 2566496.

Li P, et al. (2025) Peripheral blood mononuclear cell DNA methylation biomarkers for prognostic stratification in Chinese lung adenocarcinoma: a genome-wide epigenetic profiling study. *Clinical epigenetics*, 17(1), 177.

Jiang T, et al. (2025) Associations of Epigenetic Age Acceleration with Motor Impairment: Evidence from the PPMI Cohort. *medRxiv : the preprint server for health sciences*.

Qin M, et al. (2025) DNA methylation predicts adverse outcomes of coronary artery disease. *Nature communications*, 16(1), 11396.

Tang X, et al. (2025) Causality-driven candidate identification for reliable DNA methylation biomarker discovery. *Nature communications*, 16(1), 680.

Chernoff M, et al. (2025) Differential DNA Methylation in the Benign and Cancerous Prostate Tissue of African American and European American Men. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 34(3), 428.

Guo X, et al. (2025) Variations in Innate Immune Cell Subtypes Correlate with Epigenetic Clocks, Inflammaging and Health Outcomes. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(43), e05922.

Kuznetsov DV, et al. (2025) Genetic and environmental contributions to epigenetic aging across adolescence and young adulthood. *Clinical epigenetics*, 17(1), 78.

Wallén E, et al. (2025) Effects of alcohol on the transcriptome, methylome and metabolome of in vitro gastrulating human embryonic cells. *Disease models & mechanisms*, 18(6).

Zelenova E, et al. (2025) Multi-omics study of molecular and genetic bases of orthostatic hypotension. *Clinical epigenetics*, 17(1), 202.

Chen JQ, et al. (2024) Matched analysis of detailed peripheral blood and tumor immune microenvironment profiles in bladder cancer. *Epigenomics*, 16(1), 41.

Wen B, et al. (2024) Causal impact of DNA methylation on refracture in elderly individuals with osteoporosis - a prospective cohort study. *BMC musculoskeletal disorders*, 25(1), 432.

Lee HS, et al. (2024) Genome- and epigenome-wide association studies identify susceptibility of CpG sites and regions for metabolic syndrome in a Korean population. *Clinical epigenetics*, 16(1), 60.

Martínez-Montoro JI, et al. (2024) Interactions between the gut microbiome and DNA methylation patterns in blood and visceral adipose tissue in subjects with different metabolic characteristics. *Journal of translational medicine*, 22(1), 1089.

Juran BD, et al. (2024) Epigenetic disease markers in primary sclerosing cholangitis and primary biliary cholangitis-methylomics of cholestatic liver disease. *Hepatology communications*, 8(8).

Tong H, et al. (2024) Quantifying the stochastic component of epigenetic aging. *Nature aging*, 4(6), 886.

Zhu T, et al. (2024) An improved epigenetic counter to track mitotic age in normal and precancerous tissues. *Nature communications*, 15(1), 4211.

Halama A, et al. (2024) A roadmap to the molecular human linking multiomics with population traits and diabetes subtypes. *Nature communications*, 15(1), 7111.