Resource Summary Report

Generated by dkNET on May 19, 2025

swDMR

RRID:SCR_007316
Type: Tool

Proper Citation

swDMR (RRID:SCR_007316)

Resource Information

URL: https://code.google.com/p/swdmr/

Proper Citation: swDMR (RRID:SCR_007316)

Description: A free software using a sliding-window approach to identify differentially methylated regions (DMR) from whole-genome bisulfite sequencing.

Abbreviations: swDMR

Resource Type: software resource

Funding:

Availability: Apache License

Resource Name: swDMR

Resource ID: SCR_007316

Alternate IDs: OMICS_00625

Record Creation Time: 20220129T080241+0000

Record Last Update: 20250420T014356+0000

Ratings and Alerts

No rating or validation information has been found for swDMR.

No alerts have been found for swDMR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Lu X, et al. (2022) A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. GigaScience, 11.

Chen LJ, et al. (2022) Gm364 coordinates MIB2/DLL3/Notch2 to regulate female fertility through AKT activation. Cell death and differentiation, 29(2), 366.

Lin JQ, et al. (2020) Multi-omics analysis reveals that natural hibernation is crucial for oocyte maturation in the female Chinese alligator. BMC genomics, 21(1), 774.

Xuan A, et al. (2020) Changes in DNA Methylation in Response to 6-Benzylaminopurine Affect Allele-Specific Gene Expression in Populus Tomentosa. International journal of molecular sciences, 21(6).

Li R, et al. (2020) Whole genome bisulfite sequencing methylome analysis of mulberry (Morus alba) reveals epigenome modifications in response to drought stress. Scientific reports, 10(1), 8013.

Yu X, et al. (2020) Genome-Wide DNA Methylation Pattern of Cancer Stem Cells in Esophageal Cancer. Technology in cancer research & treatment, 19, 1533033820983793.

Zhang M, et al. (2019) Integrated Methylome and Transcriptome Analysis between the CMS-D2 Line ZBA and Its Maintainer Line ZB in Upland Cotton. International journal of molecular sciences, 20(23).

Guan DL, et al. (2019) Cadmium-induced genome-wide DNA methylation changes in growth and oxidative metabolism in Drosophila melanogaster. BMC genomics, 20(1), 356.

Chen LJ, et al. (2019) Single xenotransplant of rat brown adipose tissue prolonged the ovarian lifespan of aging mice by improving follicle survival. Aging cell, 18(6), e13024.

Lin Z, et al. (2019) Genome-Wide DNA Methylation Profiling in the Lotus (Nelumbo nucifera) Flower Showing its Contribution to the Stamen Petaloid. Plants (Basel, Switzerland), 8(5).

Chen X, et al. (2018) Suppression of SUN2 by DNA methylation is associated with HSCs activation and hepatic fibrosis. Cell death & disease, 9(10), 1021.

Xu P, et al. (2018) Single-base resolution methylome analysis shows epigenetic changes in

Arabidopsis seedlings exposed to microgravity spaceflight conditions on board the SJ-10 recoverable satellite. NPJ microgravity, 4, 12.

Xu J, et al. (2018) Single-base methylome analysis reveals dynamic epigenomic differences associated with water deficit in apple. Plant biotechnology journal, 16(2), 672.

Li R, et al. (2018) Comparative Methylome Analysis Reveals Perturbation of Host Epigenome in Chestnut Blight Fungus by a Hypovirus. Frontiers in microbiology, 9, 1026.

Wang Z, et al. (2018) Genome-Wide DNA Methylation Comparison between Brassica napus Genic Male Sterile Line and Restorer Line. International journal of molecular sciences, 19(9).

Zhang M, et al. (2017) Genome-wide DNA methylation profiles reveal novel candidate genes associated with meat quality at different age stages in hens. Scientific reports, 7, 45564.

Li Y, et al. (2017) Genome-wide DNA methylation changes associated with olfactory learning and memory in Apis mellifera. Scientific reports, 7(1), 17017.

Fang X, et al. (2017) Comparative genome-wide methylation analysis of longissimus dorsi muscles between Japanese black (Wagyu) and Chinese Red Steppes cattle. PloS one, 12(8), e0182492.

Li Y, et al. (2017) Genome-wide comparative analysis of DNA methylation between soybean cytoplasmic male-sterile line NJCMS5A and its maintainer NJCMS5B. BMC genomics, 18(1), 596.

Lu X, et al. (2017) Single-base resolution methylomes of upland cotton (Gossypium hirsutum L.) reveal epigenome modifications in response to drought stress. BMC genomics, 18(1), 297.