

Resource Summary Report

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[swDMR](#)

RRID:SCR_007316

Type: Tool

Proper Citation

swDMR (RRID:SCR_007316)

Resource Information

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

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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

Availability: Apache License

Resource Name: swDMR

Resource ID: SCR_007316

Alternate IDs: OMICS_00625

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260801T190332+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 [PRECISE-TBI](#) .

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.

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.

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).

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 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.

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

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.

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.