

The DMRcatedata package user's guide

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Package Contents

DMRcatedata accompanies the DMRcate package, providing data for examples, probe filtering and transcript annotation.

```
library(DMRcatedata)
data(crosshyb)
data(snpsall)
data(hg19.grt)
data(hg19.generanges)
```

Nine objects are contained in DMRcatedata. `crosshyb` is a factor listing probe IDs potentially confounded by cross-hybridisation to other parts of the genome[1][2]. It is used internally by `rmSNPandCH()`.

`snpsall` is a data.frame containing probes that are potentially confounded by a SNP or indel variant[1]. It lists the ID, distance (in nucleotides) to the CpG in question, and minor allele frequency for each associated variant.

`XY.probes` is a vector of Illumina probes whose targets are on human sex chromosomes.

Objects named `.*(grt|generanges)` are annotation objects that are needed by `extractRanges()` and `DMR.plot()` respectively. `hg38` and `mm10` objects have been parsed from Release 96 of Ensembl, and `hg19` from Release 75. These are accessed within the environment of the aforementioned functions.

Sources

- `snpsall` sourced from https://static-content.springer.com/esm/art\%3A10.1186\%2F13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM4_ESM.csv, https://static-content.springer.com/esm/art\%3A10.1186\%2F13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM5_ESM.csv, https://static-content.springer.com/esm/art\%3A10.1186\%2F13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM6_ESM.csv, <http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48640-polymorphic-CpGs-Illumina450k.xlsx> (accessed October 2016)

- crosshyb sourced from https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM2_ESM.csv, https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM3_ESM.csv (accessed October 2016) and <http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48639-non-specific-probes-Illumina450k.xlsx>, (accessed February 2014).

References

- [1] Pidsley R, Zotenko E, Peters TJ, Lawrence MG, Risbridger GP, Molloy P, Van Dijk S, Muhlhausler B, Stirzaker C, Clark SJ. Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. *Genome Biology*. 2016 17(1), 208.
- [2] Chen YA, Lemire M, Choufani S, Butcher DT, Grafodatskaya D, Zanke BW, Gallinger S, Hudson TJ, Weksberg R. Discovery of cross-reactive probes and polymorphic CpGs in the Illumina Infinium HumanMethylation450 microarray. *Epigenetics*. 2013 Jan 11;8(2).