

Package: muscData (via r-universe)

October 10, 2026

Version 1.27.1

Title Multi-sample multi-group scRNA-seq data

Description Data package containing a collection of multi-sample multi-group scRNA-seq datasets in SingleCellExperiment Bioconductor object format.

URL <https://github.com/HelenaLC/muscData>

BugReports <https://github.com/HelenaLC/muscData/issues>

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Depends R (>= 3.6), ExperimentHub, SingleCellExperiment

Imports utils

Suggests BiocStyle, dplyr, DropletUtils, knitr, GEOquery, Matrix, matrixStats, methods, muscat, rmarkdown, R.utils, readxl, scater, scds, Seurat

biocViews ExperimentHub, ExperimentData, ExpressionData, GEO, Homo_sapiens_Data, ImmunoOncologyData, SingleCellData

VignetteBuilder knitr

RoxygenNote 6.1.1

Config/Bioconductor/UnsupportedPlatforms windows

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository <https://bioc.r-universe.dev>

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RemoteUrl <https://github.com/bioc/muscData>

RemoteRef HEAD

RemoteSha d208f34f69c596f0e1e6ddc198709f3762881c42

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Kang18_8vs8	Kang18_8vs8 <i>dataset</i>
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Description

- 10x droplet-based scRNA-seq PBMC data from 8 Lupus patients before and after 6h-treatment with INF-beta.
- The dataset contains 35635 features across 29065 cells, and no filtering or preprocessing has been applied.
- The original data is deposited in the Gene Expression Omnibus (GEO) under accession number GSE96583.

Usage

```
Kang18_8vs8(metadata = FALSE)
```

Arguments

metadata	logical value indicating whether ExperimentHub metadata (describing the overall dataset) should be returned only, or if the whole dataset should be loaded. Defaults to FALSE.
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Details

link to reference: <https://www.ncbi.nlm.nih.gov/pubmed/29227470>

link to raw data: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE96583>

Value

an object of class `SingleCellExperiment`.

Author(s)

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References

Kang et al. (2019). "Multiplexed droplet single-cell RNA-sequencing using natural genetic variation", *Nature Biotechnology* **36**, 89-94.

Examples

```
# load metadata only
Kang18_8vs8(metadata = TRUE)

# load SingleCellExperiment
Kang18_8vs8(metadata = FALSE)
```

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