Package ‘macrophage’

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Title Human macrophage immune response

Version 1.20.0

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Description This package provides the output of running Salmon on a set of 24 RNA-seq samples from Alasoo, et al. ‘Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response’, published in Nature Genetics, January 2018. For details on version numbers and how the samples were processed see the package vignette.

biocViews ExperimentData, SequencingData, RNASeqData

License GPL (>= 2)

Depends R (>= 3.5.0)

Suggests knitr, markdown

VignetteBuilder knitr

NeedsCompilation no

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**Description**

This package provides the output of running Salmon on a set of 24 RNA-seq samples from Alasoo, et al. (2018). For more details on the data and steps used to generate the quantification files, please refer to the package vignette.

**References**


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**gse**

*Macrophage dataset - Salmon quantification*

**Description**

Estimated counts, abundance and effective length per gene for macrophage RNA-Seq experiment

**Usage**

data("gse")

**Format**

RangedSummarizedExperiment

**Details**

This package provides the output of running Salmon on a set of 24 RNA-seq samples from Alasoo, et al. (2018). For more details on the data and steps used to generate the quantification files, please refer to the package vignette. For the script used to build the gse object, see the gse_create.R script in the scripts directory.

**Source**

FASTQ files from ENA

**References**

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