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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macrophage-package  Salmon quantifications for human macrophage immune response

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

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

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