Package ‘macrophage’

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Title Human macrophage immune response

Version 1.25.0

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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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Contents

`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

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

`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

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

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