# Package 'macrophage'

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Title Human macrophage immune response

**Version** 1.23.0

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<b>Description</b> 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)
<b>Depends</b> 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

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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