

# Package ‘macrophage’

October 17, 2019

**Title** Human macrophage immune response

**Version** 1.0.0

**Author** Michael Love

**Maintainer** Michael Love <michaelisaiahlove@gmail.com>

**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)

**Suggests** knitr

**VignetteBuilder** knitr

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/macrophage>

**git\_branch** RELEASE\_3\_9

**git\_last\_commit** 1fb3e6d

**git\_last\_commit\_date** 2019-05-02

**Date/Publication** 2019-10-17

## R topics documented:

macrophage-package . . . . . 1

**Index** 3

---

macrophage-package	<i>Salmon quantifications for human macrophage immune response</i>
--------------------	--

---

## 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.

# Index

\*Topic **package**

macrophage-package, [1](#)

macrophage-package, [1](#)