

# Package: macrophage (via r-universe)

October 10, 2026

**Title** Human macrophage immune response

**Version** 1.29.1

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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, SummarizedExperiment, S4Vectors

**VignetteBuilder** knitr

**NeedsCompilation** no

**Encoding** UTF-8

**Config/roxygen2/version** 8.1.0

**Repository** <https://bioc.r-universe.dev>

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**RemoteUrl** <https://github.com/bioc/macrophage>

**RemoteRef** HEAD

**RemoteSha** 2ba828bcd733ad3c3c463c6829711cf3893a49dd

## Contents

|                              |   |
|------------------------------|---|
| macrophage-package . . . . . | 2 |
| gse . . . . .                | 2 |
| macro_tx2gene . . . . .      | 3 |
| macro_txp_se . . . . .       | 3 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>5</b> |
|--------------|----------|

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

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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|-----|---------------------------------------------------|
| gse | <i>Macrophage dataset - Salmon quantification</i> |
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**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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|               |                                                      |
|---------------|------------------------------------------------------|
| macro_tx2gene | <i>Macrophage dataset - transcript-to-gene table</i> |
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**Description**

A table mapping all transcripts of the Gencode v29 human reference (as indexed by Salmon for the macrophage dataset) to genes. It can be used to summarize [macro\\_txp\\_se](#) to the gene level with `tximeta::summarizeToGene(se, skipRanges=TRUE, tx2gene=macro_tx2gene)`, which does not require the GTF file. For the script used to build this object, see `makeSumExp.R` in the `scripts` directory of the installed package.

**Usage**

```
data("macro_tx2gene")
```

**Format**

A `DataFrame` with 205870 rows and columns `tx_name` and `gene_id`.

**Source**

Gencode v29 human reference transcripts

**See Also**

[macro\\_txp\\_se](#)

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|              |                                                                                         |
|--------------|-----------------------------------------------------------------------------------------|
| macro_txp_se | <i>Macrophage dataset - transcript-level quantification with inferential replicates</i> |
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**Description**

Salmon quantification of 24 RNA-seq samples from Alasoo, et al. (2018), imported with `tximeta`, including the 20 inferential replicates from Salmon's Gibbs sampler (assays `infRep1`, ..., `infRep20`). It is used in the `swish` vignette of the `fishpond` package.

**Usage**

```
data("macro_txp_se")
```

**Format**

A `RangedSummarizedExperiment` with 15294 transcripts and 24 samples. Assays: `counts`, `abundance`, `length`, and `infRep1`, ..., `infRep20`. `colData` columns: `names`, `id`, `line`, `condition`.

**Details**

To reduce size, the object contains all transcripts of a random subset of 2000 expressed genes (at least one transcript with a count of 10 or more in 3 or more samples) plus the GBP gene family (GBP1-GBP7), and the counts and infRep assays are rounded to 1 decimal. The full Salmon output for all transcripts, including the inferential replicates, is archived on Zenodo: [doi:10.5281/zenodo.22982581](https://doi.org/10.5281/zenodo.22982581). For the script used to build this object, see makeSumExp.R in the scripts directory of the installed package.

**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/s4158801800467](https://doi.org/10.1038/s4158801800467).

**See Also**

[macro\\_tx2gene](#)

# Index

- \* **datasets**

- [gse](#), [2](#)

- [macro\\_tx2gene](#), [3](#)

- [macro\\_txp\\_se](#), [3](#)

- \* **package**

- [macrophage-package](#), [2](#)

[gse](#), [2](#)

[macro\\_tx2gene](#), [3](#), [4](#)

[macro\\_txp\\_se](#), [3](#), [3](#)

[macrophage-package](#), [2](#)