

# Package ‘zebrafishRNASeq’

November 19, 2024

**Title** Zebrafish RNA-Seq Experimental Data from Ferreira et al. (2014)

**Version** 1.27.0

**Author** Davide Risso

**Description** Gene-level read counts from RNA-Seq for gallein-treated and control zebrafish.

**biocViews** ExperimentData, Danio\_rerio\_Data, RNASeqData

**Maintainer** Davide Risso <risso.davide@gmail.com>

**License** GPL

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr

**Depends** R (>= 2.10)

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

**git\_branch** devel

**git\_last\_commit** 2504652

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-11-19

## Contents

|                   |          |
|-------------------|----------|
| zfGenes . . . . . | 2        |
| <b>Index</b>      | <b>3</b> |

---

zfGenes

*Zebrafish RNA-Seq Experimental Data from Ferreira et al. (2014)*

---

**Description**

Gene-level read counts from the RNA-Seq experiment of Ferreira et al. (2014). The data correspond to RNA libraries for three pairs of gallein-treated and control embryonic zebrafish cell pools. Please see the vignette for details on pre-processing.

**Usage**

```
data(zfGenes)
```

**Source**

A citation for the dataset can be generated using `citation("zebrafishRNASeq")`.

# Index

\* **datasets**

zfGenes, [2](#)

zebrafishRNASeq (zfGenes), [2](#)

zfGenes, [2](#)