

# Package ‘zebrafishRNASeq’

October 16, 2021

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

**Version** 1.12.0

**Author** Davide Risso

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

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

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**License** GPL

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr

**Depends** R (>= 2.10)

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

**git\_branch** RELEASE\_3\_13

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**Date/Publication** 2021-10-16

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zfGenes	<i>Zebrafish RNA-Seq Experimental Data from Ferreira et al. (2014)</i>
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### 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")`.

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## \* datasets

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