

# Package ‘HumanRetinaLRSData’

June 4, 2026

**Type** Package

**Title** Long-read RNA-seq gene count data from human retinal organoids

**Version** 1.1.0

**Description** Dataset package containing gene and isoform count matrices, and sample metadata for long-read direct cDNA sequencing of human retinal organoids, 2D retinal ganglion cell (RGC) cultures, and flowthrough fractions from H9 and EP1 iPSC cell lines. Data were generated using Oxford Nanopore Technology (ONT) direct cDNA sequencing and mapped to the GRCh38 reference genome (GENCODE v46 annotation). The package provides accessor functions returning SummarizedExperiment objects for gene-level counts, isoform-level counts, and a matrix of allele-specific expression (ASE) gene counts. Data files are stored in flat CSV format in an Open Science Framework (OSF) repository and cached locally via BiocFileCache.

**License** MIT + file LICENSE

**Encoding** UTF-8

**URL** <https://github.com/sparthib/HumanRetinaLrsData>

**BugReports** <https://github.com/sparthib/HumanRetinaLrsData/issues>

**biocViews** ExperimentData, RNASeqData, ExpressionData,  
Homo\_sapiens\_Data, CellCulture

**RoxygenNote** 7.3.2

**Depends** R (>= 4.6.0), SummarizedExperiment

**Imports** osfr, BiocFileCache

**Suggests** testthat, knitr, rmarkdown, ggplot2, ggrepel

**VignetteBuilder** knitr

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

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ASEGeneCounts	<i>Allele-specific expression (ASE) gene counts</i>
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### Description

Allele-specific expression (ASE) gene counts

### Usage

```
ASEGeneCounts()
```

### Value

A numeric matrix

### Examples

```
ase_counts <- ASEGeneCounts()
head(ase_counts)
```

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clear_osf_cache	<i>Clear OSF cache</i>
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### Description

Clear OSF cache

### Usage

```
clear_osf_cache(
  bfc = BiocFileCache::BiocFileCache(tools::R_user_dir("HumanRetinalLRSDData", which =
    "cache"), ask = FALSE)
)
```

### Arguments

bfc                      BiocFileCache object

**Value**

NULL (invisibly). Called for side effect of clearing cache.

**Examples**

```
clear_osf_cache()
```

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FTRGCGeneLevelData	<i>Gene-level counts for flow through (FT) and retinal ganglion cell (RGC) samples</i>
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**Description**

Gene-level counts for flow through (FT) and retinal ganglion cell (RGC) samples

**Usage**

```
FTRGCGeneLevelData()
```

**Value**

A SummarizedExperiment object

**Examples**

```
ftrgc_data <- FTRGCGeneLevelData()
ftrgc_data
```

---

FTRGCIsoformLevelData	<i>Isoform-level counts for flow through (FT) and retinal ganglion cell (RGC) samples</i>
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**Description**

Isoform-level counts for flow through (FT) and retinal ganglion cell (RGC) samples

**Usage**

```
FTRGCIsoformLevelData()
```

**Value**

A SummarizedExperiment object

**Examples**

```
ftrgc_iso_data <- FTRGCIsoformLevelData()
ftrgc_iso_data
```

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list_osf_files	<i>List available files on OSF</i>
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**Description**

List available files on OSF

**Usage**

```
list_osf_files()
```

**Value**

Character vector of file names

**Examples**

```
list_osf_files()
```

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load_object	<i>Load a dataset from OSF with BiocFileCache</i>
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**Description**

Validates `osf_file_name` against the bundled `inst/extdata/metadata.csv` (no internet connection required for validation). On first use the data files are downloaded from OSF and cached via **BiocFileCache**; subsequent calls load from the local cache.

**Usage**

```
load_object(  
  osf_file_name,  
  bfc = BiocFileCache::BiocFileCache(tools::R_user_dir("HumanRetinalLRSData", which =  
    "cache"), ask = FALSE)  
)
```

**Arguments**

`osf_file_name` Character scalar. Dataset base name; see [list\\_osf\\_files](#).  
`bfc` A [BiocFileCache](#) object. Defaults to a per-user package cache.

**Value**

A [SummarizedExperiment](#) or a matrix, depending on the dataset.

**Examples**

```
## Not run:  
se <- load_object("ROGeneLevelData")  
se  
  
## End(Not run)
```

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ROGeneLevelData	<i>Gene-level counts for retinal organoid (RO) samples</i>
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**Description**

Gene-level counts for retinal organoid (RO) samples

**Usage**

```
ROGeneLevelData()
```

**Value**

A SummarizedExperiment object

**Examples**

```
ro_data <- ROGeneLevelData()  
ro_data
```

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ROIsoformLevelData	<i>Isoform-level counts for retinal organoid (RO) samples</i>
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**Description**

Isoform-level counts for retinal organoid (RO) samples

**Usage**

```
ROIsoformLevelData()
```

**Value**

A SummarizedExperiment object

**Examples**

```
ro_iso_data <- ROIsoformLevelData()  
ro_iso_data
```

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