

# Package ‘GeuvadisTranscriptExpr’

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**Type** Package

**Title** Data package with transcript expression and bi-allelic genotypes from the GEUVADIS project

**Version** 1.32.0

**Date** 2021-11-21

**Description** Provides transcript expression and bi-allelic genotypes corresponding to the chromosome 19 for CEU individuals from the GEUVADIS project, Lappalainen et al.

**Depends** R (>= 3.3.0)

**License** GPL (>= 3)

**LazyData** true

**biocViews** Homo\_sapiens\_Data, SNPData, Genome, RNASeqData, SequencingData, ExpressionData

**VignetteBuilder** knitr

**Suggests** limma, rtracklayer, GenomicRanges, Rsamtools, VariantAnnotation, tools, BiocStyle, knitr, testthat

**NeedsCompilation** no

**Author** Malgorzata Nowicka [aut, cre]

**Maintainer** Malgorzata Nowicka <gosia.nowicka@uzh.ch>

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

**git\_branch** RELEASE\_3\_19

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## Contents

counts . . . . .	2
<b>Index</b>	<b>4</b>

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counts

*Sample data for sQTL analysis*

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## Description

Subsets of raw data available in this package and saved as Rdata objects for faster loading.

## Usage

counts

gene\_ranges

genotypes

snp\_ranges

## Format

counts is a data frame with subset of counts from TrQuantCount\_CEU\_chr19.tsv

gene\_ranges is a GRanges object containing subset of gene coordinates from genes\_chr19.bed

genotypes is a data frame with subset of genotypes from genotypes\_CEU\_chr19.tsv

snp\_ranges is a Granges object containing subset of SNP coordinates from genotypes\_CEU\_chr19.tsv

For all the details on how these data sets were produced, see examples.

## Value

counts, gene\_ranges, genotypes, snp\_ranges

## Source

Lappalainen T, Sammeth M, Friedlander MR, et al. Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*. 2013;501(7468):506-11

## Examples

```
library(rtracklayer)
data_dir <- system.file("extdata", package = "GeuvadisTranscriptExpr")

gene_id_subset <- readLines(file.path(data_dir, "gene_id_subset.txt"))
snp_id_subset <- readLines(file.path(data_dir, "snp_id_subset.txt"))

# Load gene ranges with names!
gene_ranges <- import(file.path(data_dir, "genes_chr19.bed"))
names(gene_ranges) <- mcols(gene_ranges)$name

gene_ranges <- gene_ranges[gene_id_subset, ]
```

```
# Load transcript counts
counts <- read.table(file.path(data_dir, "TrQuantCount_CEU_chr19.tsv"),
                    header = TRUE, sep = "\t", as.is = TRUE)

counts <- counts[counts$Gene_Symbol %in% gene_id_subset, ]

# Load genotypes
genotypes <- read.table(file.path(data_dir, "genotypes_CEU_chr19.tsv"),
                      header = TRUE, sep = "\t", as.is = TRUE)

genotypes <- genotypes[genotypes$snpId %in% snp_id_subset, ]

# Create SNP ranges with names!
snp_ranges <- GRanges(Rle(genotypes$chr), IRanges(genotypes$start,
                                                  genotypes$end))
names(snp_ranges) <- genotypes$snpId
```

# Index

\* **datasets**

counts, [2](#)

counts, [2](#)

gene\_ranges (counts), [2](#)

genotypes (counts), [2](#)

snp\_ranges (counts), [2](#)