# Package 'GeuvadisTranscriptExpr'

October 17, 2024

**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

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**git_url** https://git.bioconductor.org/packages/GeuvadisTranscriptExpr

**git_branch** RELEASE_3_19

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**Repository** Bioconductor 3.19

**Date/Publication** 2024-10-17

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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
```

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