Package ‘vermeulen’

April 23, 2024

Type Package

Title Biomarker Data Set by Vermeulen et al. (2009)

Description The biomarker data set by Vermeulen et al. (2009) <doi:10.1016/S1470-2045(09)70154-8> is provided. The data source, however, is by Ruijter et al. (2013) <doi:10.1016/j.ymeth.2012.08.011>. The original data set may be downloaded from <https://medischebiologie.nl/wp-content/uploads/2019/02/qpcrdatamethods.zip>. This data set is for a real-time quantitative polymerase chain reaction (PCR) experiment that comprises the raw fluorescence data of 24,576 amplification curves. This data set comprises 59 genes of interest and 5 reference genes. Each gene was assessed on 366 neuroblastoma complementary DNA (cDNA) samples and on 18 standard dilution series samples (10-fold 5-point dilution series x 3 replicates + no template controls (NTC) x 3 replicates).

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Encoding UTF-8

RoxygenNote 7.3.1

Depends R (>= 2.10)

Imports memoise

Suggests dplyr, ggplot2, rmarkdown, spelling, testthat (>= 3.0.0), tibble

Language en-US

URL https://github.com/ramiromagno/vermeulen,

https://rmagno.eu/vermeulen/

BugReports https://github.com/ramiromagno/vermeulen/issues

Config/testthat/edition 3

NeedsCompilation no

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**get_biomarker_dataset**

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**Repository** CRAN

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### Description

This function retrieves the Biomarker data set, a data set containing raw fluorescence amplification data: 24,576 amplification curves, of 50 cycles each.

### Usage

```r
get_biomarker_dataset()
```

### Details

Data was gathered from Ruijter et al. (2013), doi:10.1016/j.ymeth.2012.08.011 but original source is by Vermeulen et al. (2009), doi:10.1016/S14702045(09)701548. The tidy version of the data is kept at the repository of the source of `{vermeulen}` package. This function fetches such data and thus requires internet connection. It takes a few seconds to run.

The Biomarker data set comprises a set of 59 targets previously identified as a 59-mRNA gene expression signature, that has been developed and validated for improved outcome prediction of children with neuroblastoma. In short, 59 biomarkers and 5 reference genes were measured in 8 μl reactions in a 384-well plate using the LightCycler480 SYBR Green Master (Roche) in a sample maximization experiment design. The 59 genes were carefully selected as being previously reported as prognostic genes in neuroblastoma in at least two independent studies. Each plate contained 366 cDNA samples (n = 1) from primary tumor biopsies, a 5-point 10-fold serial dilution series based on an external oligonucleotide standard (n = 3, from 150,000 to 15 copies), and a no template control (NTC, n = 3). Raw (baseline uncorrected) fluorescent data were exported from the LightCycler480 instrument software.

### Value

A data frame with 24,576 amplification curves, of 50 cycles each:

- **plate** Plate identifier. Because one plate was used per gene, the name of the plate is the same as the values in `target`.
- **well** Well identifier.
dye  In all reactions the SYBR Green I master mix (Roche) was used, so the value is always “SYBR”.
target  Target identifier, in almost all cases the name of a gene.
target_type  Target type: either target of interest (“toi”) or reference target (“ref”).
sample  Sample identifier.
sample_type  Sample type.
copies  Standard copy number.
dilution  Dilution factor. Higher number means greater dilution.
cycle  PCR cycle.
fluor  Raw fluorescence values.

Source


Examples

# Takes ~ 10-30 sec
head(get_biomarker_dataset())
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