

Package: batsch (via r-universe)

September 19, 2024

Type Package

Title Real-Time PCR Data Sets by Batsch et al. (2008)

Version 0.1.1

Description Real-time quantitative polymerase chain reaction (qPCR) data sets by Batsch et al. (2008) <[doi:10.1186/1471-2105-9-95](https://doi.org/10.1186/1471-2105-9-95)>.

This package provides five data sets, one for each PCR target: (i) rat SLC6A14, (ii) human SLC22A13, (iii) pig EMT, (iv) chicken ETT, and (v) human GAPDH. Each data set comprises a five-point, four-fold dilution series. For each concentration there are three replicates. Each amplification curve is 45 cycles long. Original raw data file:

<https://static-content.springer.com/esm/art%3A10.1186%2F1471-2105-9-95/MediaObjects/12859_2007_2080_MOESM5_ESM.xls>.

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Roxygen list(markdown = TRUE)

Depends R (>= 2.10)

Imports tibble

URL <https://github.com/ramiromagno/batsch>, <https://rmagno.eu/batsch/>

BugReports <https://github.com/ramiromagno/batsch/issues>

Repository <https://patterninstitute.r-universe.dev>

RemoteUrl <https://github.com/ramiromagno/batsch>

RemoteRef HEAD

RemoteSha 50129eacdf3168682049f9c50574351424c7fb4f

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batsch

*qPCR data sets by Batsch et al. (2008)***Description**

Each data set comprises a five-point, four-fold dilution series. For each concentration there are three replicates. Each amplification curve is 45 cycles long.

A single reaction (total volume 10 μ l) contained 1 μ l master mix (LightCycler TaqMan Master; Roche 04735536001), 1 μ mol/l each of forward and reverse primer, SYBR Green I at 1:30 dilution (Invitrogen S7563) or 50 nmol/l probe, and various amounts of cDNA or plasmid DNA. Contamination controls contained water instead of DNA. After enzyme activation (10 min, 95°C), thermocycling consisted of 45 cycles of 10 s at 95°C, 30 s at 55°C, and 1 s at 72°C; velocity of temperature change was 1.1°C/s. Please read the Methods section of Batsch et al. (2008) for more details.

Usage

SLC6A14r

SLC22A13h

EMTp

ETTch

GAPDHh

Format

Each data set is provided as a [tibble](#) with 675 rows and 9 variables:

`plate` Plate identifier. Because one plate was used per target, the name of the plate is the same as the values in `target`.

`well` Well identifier. Values are always NA (not available) for these data sets. This variable is kept nevertheless to be coherent with other data sets from other similar R data packages.

`dye` Either SYBR Green I master mix (Roche) ("SYBR") or TaqMan probe ("TaqMan").

`target` Target identifier: rat SLC6A14 ("SLC6A14r"), human SLC22A13 ("SLC22A13h"), pig EMT ("EMTp"), chicken ETT ("ETTch") or human GAPDH ("GAPDHh").

`sample_type` Sample type (all curves are standards, i.e. "std").

`replicate` Replicate identifier: 1 thru 3.

`dilution` Dilution factor. Higher number means greater dilution.

`cycle` PCR cycle.

`fluor` Raw fluorescence values.

Source

[doi:10.1186/14712105995](https://doi.org/10.1186/14712105995)

Examples

SLC6A14r

SLC22A13h

EMTp

ETTch

GAPDHh

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