Package 'TENxVisiumData'

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Version 1.20.0

Title Visium spatial gene expression data by 10X Genomics

Description Collection of Visium spatial gene expression datasets by 10X Genomics, formatted into objects of class SpatialExperiment.
Data cover various organisms and tissues, and include:
single- and multi-section experiments, as well as single sections
subjected to both whole transcriptome and targeted panel analysis.
Datasets may be used for testing of and as examples in packages,
for tutorials and workflow demonstrations, or similar purposes.

URL https://github.com/helenalc/TENxVisiumData

BugReports https://github.com/helenalc/TENxVisiumData/issues

biocViews ExperimentHub, ExpressionData, ExperimentData, Homo_sapiens_Data, Mus_musculus_Data, ReproducibleResearch

Depends ExperimentHub, SpatialExperiment

Imports utils

Suggests BiocStyle, knitr, rmarkdown

VignetteBuilder knitr

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Encoding UTF-8

RoxygenNote 7.1.1

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`TENxVisiumData` *TENxVisiumData*

Description

Collection of Visium spatial gene expression datasets by 10X Genomics, formatted into objects of class SpatialExperiment. Data cover various organisms and tissues, and include: single- and multi-section experiments, as well as single sections subjected to both whole transcriptome and targeted panel analysis. Datasets may be used for testing of and as examples in packages, for tutorials and workflow demonstrations, or similar purposes.

Details

The following Visium Spatial Transcriptomics datasets by 10X Genomics are currently available (see the package vignette for links to details):

- HumanBreastCancerIDC
- HumanBreastCancerILC
- HumanCerebellum
- HumanColorectalCancer
- HumanGlioblastoma
- HumanHeart
- HumanLymphNode
- HumanOvarianCancer
- HumanSpinalCord
- MouseBrainCoronal
- MouseBrainSagittalPosterior
- MouseBrainSagittalAnterior
- MouseKidneyCoronal

Value

a `SpatialExperiment` with rows corresponding to samples (spots) and columns to features (transcripts). If, in addition to whole transcriptome analysis, the specified dataset contains measurements from targeted panel analysis/es, these will be stored as `altExps`.

Author(s)

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Examples

```
# initialize hub instance
eh <- ExperimentHub()

# query for TENxVisium datasets
(q <- query(eh, "TENxVisium"))

# retrieve dataset of interest
pat <- "HumanCerebellum$"
idx <- grep(pat, q$title)
id <- q$ah_id[idx]
(spe <- eh[[id]])

# access targeted panel
altExpNames(spe)
altExp(spe, "TargetedNeuroscience")
```

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