

# Package ‘Qindex.data’

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**Type** Package

**Title** Data for Package 'Qindex'

**Version** 0.1.1

**Date** 2024-04-24

**Description** Example data used in package 'Qindex'.

**LazyData** true

**LazyDataCompression** xz

**RoxygenNote** 7.3.1

**Encoding** UTF-8

**License** GPL-2

**Depends** R (>= 4.3),

**Language** en-US

**Suggests** knitr

**NeedsCompilation** no

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**Repository** CRAN

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Qindex.data-package     *Data for Package 'Qindex'*

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### Description

Example data used in package 'Qindex'.

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### References

Selection of optimal quantile protein biomarkers based on cell-level immunohistochemistry data. Misung Yi, Tingting Zhan, Amy P. Peck, Jeffrey A. Hooke, Albert J. Kovatich, Craig D. Shriver, Hai Hu, Yunguang Sun, Hallgeir Rui and Inna Chervoneva. BMC Bioinformatics, 2023. [doi:10.1186/s12859023054088](#)

Quantile index biomarkers based on single-cell expression data. Misung Yi, Tingting Zhan, Amy P. Peck, Jeffrey A. Hooke, Albert J. Kovatich, Craig D. Shriver, Hai Hu, Yunguang Sun, Hallgeir Rui and Inna Chervoneva. Laboratory Investigation, 2023. [doi:10.1016/j.labinv.2023.100158](#)

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celldata                     *Ki67 Data*

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### Description

Ki67 cell data containing 622 patients

### Usage

Ki67

### Format

PATIENT\_ID [factor](#), unique patient identifier

tissueID [factor](#), TMA core identifier

RECURRENCE [integer](#), recurrence indicator, 1 = Recurred, 0 = not Recurred

RECFREESURV\_MO [integer](#), recurrence-free survival time in months

Marker [double](#), cell signal intensity of the protein immunofloerscence signal

inner\_x [integer](#),  $x$ -coordinate in the cell centroid in the TMA core

inner\_y **integer**, *y*-coordinate in the cell centroid in the TMA core  
AGE\_AT\_DX **integer**, age at diagnosis  
Tstage **integer**, tumor stage  
NodeSt **integer**, node stage, -1 = unknown, 0 = Node Negative, 1 = Node Positive  
HRpos **integer**, indicator of hormone positive status (ER+ or PR+), 1 = positive, 0 = negative  
HistologicalGrade **integer**, histology grade  
Her2\_path\_qIF **integer**, Her2 status, 1 = positive, 0 = negative  
RACE **character**, race, White, Black, Asian, Native Hawaiian or Other Pacific Islander, American Indian or Alaska Native, Unknown  
RadjCHEMO **integer**, adjuvant chemo treatment, 0 = unknown, 1 = done, 2 = NOT done  
RadjRAD **integer**, adjuvant radiation treatment, 0 = unknown, 1 = done, 2 = NOT done  
HORM\_4cat **integer**, hormone treatment, 0 = unknown, 1 = not indicated, 2 = done, 3 = recommended, but not done  
MSI **double**, mean signal intensity (mean over all cells in the TMA core)

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