

R documentation

of ‘TCGA.breast.small.Rd’

September 3, 2020

TCGA.breast.small *Breast cancer bulk RNA-Seq samples from TCGA Research Network.*

Description

Subset of Breast cancer bulk RNA-Seq samples from TCGA Research Network. FPKMs were transformed in TPMs and aggregated based on SYMBOL genes.

Usage

```
TCGA.breast.small
```

Format

An object of class `matrix` with 44831 rows and 15 columns.

Source

<https://www.cancer.gov/tcga>

References

- Koboldt, D. C., Fulton, R. S., McLellan, M. D., Schmidt, H., Kalicki-Veizer, J., McMichael, J. F., et al. (2012). Comprehensive molecular portraits of human breast tumours. *Nature* 490 (7418), 61–70. doi: 10.1038/nature11412
- Ciriello, G., Gatza, M. L., Beck, A. H., Wilkerson, M. D., Rhie, S. K., Pastore, A., et al. (2015). Comprehensive molecular portraits of invasive lobular breast cancer. *Cell*. 163 (2), 506–519. doi: 10.1016/j.cell.2015.09.033
- Torroja, C. y Sánchez-Cabo, F. (2019). digitalDLSorter: A Deep Learning algorithm to quantify immune cell populations based on scRNA-Seq data. *Frontiers in Genetics* 10, 978. doi: [10.3389/fgene.2019.00978](https://doi.org/10.3389/fgene.2019.00978)

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*Topic **datasets**

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