

ivygapSE – Bioconductor container for Ivy-GAP expression and metadata

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1 Introduction

CSV files from the Ivy-GAP project have been assembled into a SummarizedExperiment instance.

```
## Warning: replacing previous import 'ggplot2::last_plot' by
## 'plotly::last_plot' when loading 'ivygapSE'
## Warning: replacing previous import 'ggplot2::%+%' by 'survminer::%+%' when
## loading 'ivygapSE'
```

```
library(ivygapSE)
data(ivySE)
ivySE
## class: SummarizedExperiment
## dim: 25873 270
## metadata(5): README URL builder tumorDetails subBlockDetails
## assays(1): fpkm
## rownames(25873): A1BG A2M ... PP12719 LOC100653024
## rowData names(5): gene_id chromosome gene_entrez_id gene_symbol
##   gene_name
## colnames(270): 305273026 305405294 ... 305273038 306124458
## colData names(28): tumor_id tumor_name ... bam_download_link
##   bai_download_link
```

There are several types of metadata collected with the object, including the README.txt (use `cat(metadata(ivySE)$README, sep="\n")` to see this in R), the URL where data were retrieved, a character vector (builder) with the R code for creating (much of) the SummarizedExperiment, and two tables of tumor-specific and block-specific information.

2 Summary information

The number of RNA-seq samples is 270. The FPKM matrix has dimensions

```
dim(ivySE)
## [1] 25873 270
```

There are 42 different donors.

```
length(unique(metadata(ivySE)$tumorDetails$donor_id))
## [1] 42
```

However, only 37 donors contributed tumor RNA:

```
sum(metadata(ivySE)$tumorDetails$tumor_name %in% ivySE$tumor_name)
## [1] 37
```

The subBlockDetails metadata (946 × 26) includes feature quantifications. The names of the quantification fields and their interpretation are

```
## normalized_area_le
## "Leading Edge (LE)"
## normalized_area_lehbv
## "Hyperplastic blood vessels in leading edge (LEhbv)"
## normalized_area_it
## "Infiltrating Tumor (IT)"
## normalized_area_ithbv
## "Hyperplastic blood vessels in infiltrating tumor (IThbv)"
## normalized_area_ct
## "Cellular Tumor (CT)"
## normalized_area_ctpnz
## "Perinecrotic zone (CTpnz)"
## normalized_area_cthbv
## "Hyperplastic blood vessels in cellular tumor (CThbv)"
## normalized_area_ctpnn
## "Pseudopalisading cells but no visible necrosis (CTpnn)"
## normalized_area_ctpan
## "Pseudopalisading cells around necrosis (CTpan)"
## normalized_area_ctmvp
## "Microvascular proliferation (CTmvp)"
## normalized_area_ctne
## "Necrosis (CTne)"
```

3 Exploring with the app

The ivyGlimpse function starts a shiny app. Use the mouse to select image features to scatterplot, and then select a region of the scatterplot to stratify the blocks into two groups. Once the selection is made, the survival profiles of the groups are plotted, and expression patterns for genes in selected pathways can be compared.