Package ‘curatedTCGAData’

April 11, 2019

Type Package

Title Curated Data From The Cancer Genome Atlas (TCGA) as MultiAssayExperiment Objects

Version 1.4.3

Description This package provides publicly available data from The Cancer Genome Atlas (TCGA) Bioconductor MultiAssayExperiment class objects. These objects integrate multiple assays (e.g. RNA-seq, copy number, mutation, microRNA, protein, and others) with clinical / pathological data. The MultiAssayExperiment class links assay barcodes with patient IDs, enabling harmonized subsetting of rows (features) and columns (patients / samples) across the entire experiment.

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Depends R (>= 3.5.0), MultiAssayExperiment

Imports AnnotationHub, ExperimentHub, S4Vectors, utils

Suggests BiocStyle, knitr, readr, rmarkdown, testthat

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, CancerData

RoxygenNote 6.1.1

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R topics documented:

`curatedTCGAData-package` *curatedTCGAData-package*

Description

The following are the TCGA cancer codes and full names.

```
   Study Abbreviation                                                Study Name
----------------------------------------------------------------------------
1     ACC                                          Adrenocortical Carcinoma
2    BLCA                                      Bladder Urothelial Carcinoma
3    BRCA                                         Breast Invasive Carcinoma
4    CESC   Cervical Squamous Cell Carcinoma And Endocervical Adenocarcinoma
```

```
5    CHOL                                                Cholangiocarcinoma
6    CNTL                                                          Controls
7    COAD                                              Colon Adenocarcinoma
8    DLBC                   Lymphoid Neoplasm Diffuse Large B-cell Lymphoma
9    ESCA                                              Esophageal Carcinoma
10    GBM                                           Glioblastoma Multiforme
11   HNSC                             Head And Neck Squamous Cell Carcinoma
12   KICH                                                Kidney Chromophobe
13   KIRC                                 Kidney Renal Clear Cell Carcinoma
14   KIRP                             Kidney Renal Papillary Cell Carcinoma
15   LAML                                            Acute Myeloid Leukemia
16    LGG                                          Brain Lower Grade Glioma
17   LIHC                                    Liver Hepatocellular Carcinoma
18   LUAD                                               Lung Adenocarcinoma
19   LUSC                                      Lung Squamous Cell Carcinoma
20   MESO                                                      Mesothelioma
21     OV                                 Ovarian Serous Cystadenocarcinoma
22   PAAD                                         Pancreatic Adenocarcinoma
23   PCPG                                Pheochromocytoma And Paraganglioma
24   PRAD                                           Prostate Adenocarcinoma
25   READ                                             Rectum Adenocarcinoma
26   SARC                                                           Sarcoma
27   SKCM                                           Skin Cutaneous Melanoma
28   STAD                                            Stomach Adenocarcinoma
29   TGCT                                       Testicular Germ Cell Tumors
30   THCA                                                 Thyroid Carcinoma
31   THYM                                                           Thymoma
32   UCEC                              Uterine Corpus Endometrial Carcinoma
33    UCS                                            Uterine Carcinosarcoma
34    UVM                                                    Uveal Melanoma
```

Author(s)

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Examples

```
help(package = "curatedTCGAData")
```

`ACC` *Adrenocortical carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( ACC )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [7] Mutation-20160128: RaggedExperiment with 20166 rows and 90 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns

> rownames( ACC )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( ACC )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["CNVSNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["Methylation-20160128"]] TCGA-OR-A5J1-01A-11D-A29J-05 ...
[["miRNASeqGene-20160128"]] TCGA-OR-A5J1-01A-11R-A29W-13 ...
[["Mutation-20160128"]] TCGA-OR-A5J1-01A-11D-A29I-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-OR-A5J1-01A-11R-A29S-07 ...
[["RPPAArray-20160128"]] TCGA-OR-A5J2-01A-21-A39K-20 ...

Sizes of each ExperimentList element:

                        assay size.Mb
1                 CNASNP-20160128  2.2 Mb
2                 CNVSNP-20160128  0.6 Mb
3       GISTIC_AllByGene-20160128  4.9 Mb
```

```
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5             Methylation-20160128   75 Mb
6            miRNASeqGene-20160128  0.1 Mb
7                Mutation-20160128 12.6 Mb
8          RNASeq2GeneNorm-20160128  1.3 Mb
9               RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   58 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  34.00   34.00    1.51    1.34    3.03


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  14.00   35.50   48.50   47.16   60.00   83.00

vital_status:
 0  1
58 34

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   399.0   551.5   854.6  1202.2  2405.0      58

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  383.0   917.8  1453.5  1781.6  2339.2  4673.0      34

tumor_tissue_site:
adrenal
     92

pathologic_stage:
  stage i  stage ii stage iii  stage iv      NA's
        9        44        19        18         2

pathology_T_stage:
  t1   t2   t3   t4 NA's
   9   49   11   21    2

pathology_N_stage:
```

```
  n0   n1 NA's
  80   10    2

gender:
female   male
    60     32

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1997    2005    2008    2007    2011    2012

radiation_therapy:
  no  yes NA's
  71   18    3

histological_type:
   adrenocortical carcinoma- myxoid type
                                       1
adrenocortical carcinoma- oncocytic type
                                       4
    adrenocortical carcinoma- usual type
                                      87

residual_tumor:
  r0   r1   r2   rx NA's
  64    7   12    6    3

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   2.548   0.500  52.000      61

race:
                    asian black or african american                     white
                        2                         1                        78
                     NA's
                       11

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                     8                     40                    44

Including an additional 806 columns
```

`BLCA` *Bladder Urothelial Carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( BLCA )
ExperimentList class object of length 11:
 [1] CNASeq-20160128: RaggedExperiment with 35692 rows and 232 columns
 [2] CNASNP-20160128: RaggedExperiment with 479978 rows and 806 columns
 [3] CNVSNP-20160128: RaggedExperiment with 104349 rows and 797 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 434 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 429 columns
 [8] Mutation-20160128: RaggedExperiment with 39312 rows and 130 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 427 columns
 [10] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 67 columns
 [11] RPPAArray-20160128: SummarizedExperiment with 208 rows and 344 columns

> rownames( BLCA )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22 tAKR
...
<1 more element>

> colnames( BLCA )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-BL-A0C8-01A-11D-A10R-02 ...
[["CNASNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["CNVSNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["Methylation-20160128"]] TCGA-2F-A9KO-01A-11D-A38H-05 ...
[["miRNASeqGene-20160128"]] TCGA-2F-A9KO-01A-11R-A38M-13 ...
[["Mutation-20160128"]] TCGA-BL-A0C8-01A-11D-A10S-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2F-A9KO-01A-11R-A38B-07 ...
[["RNASeqGene-20160128"]] TCGA-BL-A0C8-01A-11R-A10U-07 ...
...
<1 more element>

Sizes of each ExperimentList element:

                          assay size.Mb
1                CNASeq-20160128    1 Mb
2                CNASNP-20160128 13.1 Mb
3                CNVSNP-20160128    3 Mb
4      GISTIC_AllByGene-20160128  4.9 Mb
```

```
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6              Methylation-20160128 75.1 Mb
7             miRNASeqGene-20160128  0.1 Mb
8                 Mutation-20160128 56.1 Mb
9           RNASeq2GeneNorm-20160128  1.3 Mb
10              RNASeqGene-20160128  1.3 Mb
11               RPPAArray-20160128    0 Mb

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Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   232 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
180.000 180.000   1.125   0.992   1.332


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  34.00   60.00   69.00   68.08   76.00   90.00       1

vital_status:
  0   1
230 182

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   19.0   235.8   410.5   552.8   654.5  3183.0     232

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  -64.0   398.2   639.0  1016.7  1458.8  5050.0     182

tumor_tissue_site:
bladder
    412

pathologic_stage:
  stage i  stage ii stage iii  stage iv      NA's
        2       131       141       136         2



pathology_M_stage:
  m0   m1   mx NA's
```

```
 196   11  202    3

gender:
female   male 
   108    304 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1999    2009    2011    2010    2012    2013      18 

radiation_therapy:
  no  yes NA's 
 366   20   26 

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  30.00   80.00   90.00   83.09   90.00  100.00     276 

histological_type:
muscle invasive urothelial carcinoma (pt2 or above) 
                                               409 
                                              NA's 
                                                 3 

number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   0.15   20.00   30.00   39.04   50.00  730.00     188 

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  0.000   0.000   0.000   2.088   2.000  97.000     115 

race:
                    asian black or african american                     white 
                       44                        23                       327 
                     NA's 
                       18 

ethnicity:
    hispanic or latino not hispanic or latino                  NA's 
                     9                    371                    32 

Including an additional 1695 columns
```

`BRCA` *Breast invasive carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( BRCA )
ExperimentList class object of length 13:
 [1] CNASeq-20160128: RaggedExperiment with 5298 rows and 38 columns
 [2] CNASNP-20160128: RaggedExperiment with 1132786 rows and 2209 columns
 [3] CNVSNP-20160128: RaggedExperiment with 284458 rows and 2199 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 343 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 885 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 849 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 590 columns
 [10] Mutation-20160128: RaggedExperiment with 90490 rows and 993 columns
 [11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 1212 columns
 [12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 878 columns
 [13] RPPAArray-20160128: SummarizedExperiment with 226 rows and 937 columns

> rownames( BRCA )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

> colnames( BRCA )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-A2-A0EU-01A-22D-A060-02 ...
[["CNASNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["CNVSNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A1-A0SD-01A-11D-A112-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3C-AAAU-01A-11D-A41Q-05 ...
[["miRNASeqGene-20160128"]] TCGA-3C-AAAU-01A-11R-A41G-13 ...
[["mRNAArray-20160128"]] TCGA-A1-A0SD-01A-11R-A115-07 ...
[["Mutation-20160128"]] TCGA-A1-A0SB-01A-11D-A142-09 ...
...
<3 more elements>

Sizes of each ExperimentList element:

                        assay size.Mb
1                 CNASeq-20160128  0.2 Mb
2                 CNASNP-20160128 30.9 Mb
```

```
3                    CNVSNP-20160128  8.2 Mb
4          GISTIC_AllByGene-20160128    5 Mb
5  GISTIC_ThresholdedByGene-20160128    5 Mb
6      Methylation_methyl27-20160128  4.9 Mb
7     Methylation_methyl450-20160128 75.1 Mb
8              miRNASeqGene-20160128  0.1 Mb
9                 mRNAArray-20160128  1.2 Mb
10                 Mutation-20160128 67.4 Mb
11         RNASeq2GeneNorm-20160128  1.4 Mb
12              RNASeqGene-20160128  1.4 Mb
13               RPPAArray-20160128  0.1 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   947 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 151.00  151.00    3.48    2.83    4.50



---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   26.0    49.0    59.0    58.6    68.0    90.0      16

vital_status:
   0    1 NA's
 945  152    1

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  116.0   700.5  1272.0  1644.7  2367.0  7455.0     947

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     -7     440     761    1183    1572    8605     153

tumor_tissue_site:
breast   NA's
  1097      1




pathology_M_stage:
```

```
cm0 (i+)       m0       m1       mx     NA's
       6      906       22      163        1

gender:
female   male   NA's
  1085     12      1

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1988    2007    2009    2008    2010    2013       3

days_to_last_known_alive:
 735 2576 NA's
   1    1 1096

radiation_therapy:
  no  yes NA's
 446  556   96


number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   1.000   2.363   2.000  35.000     169

race:
american indian or alaska native                           asian
                               1                              61
       black or african american                           white
                             183                             757
                            NA's
                              96

ethnicity:
    hispanic or latino not hispanic or latino                   NA's
                    39                    884                    175

Including an additional 2667 columns
```

`CESC` *Cervical squamous cell carcinoma and endocervical adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( CESC )
ExperimentList class object of length 10:
 [1] CNASeq-20160128: RaggedExperiment with 7834 rows and 100 columns
 [2] CNASNP-20160128: RaggedExperiment with 267855 rows and 586 columns
```

```
 [3] CNVSNP-20160128: RaggedExperiment with 59450 rows and 586 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 312 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 312 columns
 [8] Mutation-20160128: RaggedExperiment with 46547 rows and 194 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 309 columns
 [10] RPPAArray-20160128: SummarizedExperiment with 192 rows and 173 columns

> rownames( CESC )
CharacterList of length 10
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( CESC )
CharacterList of length 10
[["CNASeq-20160128"]] TCGA-C5-A1BQ-01C-11D-A20X-26 ...
[["CNASNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CNVSNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["Methylation-20160128"]] TCGA-2W-A8YY-01A-11D-A37Q-05 ...
[["miRNASeqGene-20160128"]] TCGA-2W-A8YY-01A-11R-A37P-13 ...
[["Mutation-20160128"]] TCGA-BI-A0VR-01A-11D-A10S-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2W-A8YY-01A-11R-A37O-07 ...
[["RPPAArray-20160128"]] TCGA-2W-A8YY-01A-21-A40H-20 ...

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASeq-20160128  0.3 Mb
2                    CNASNP-20160128  7.3 Mb
3                    CNVSNP-20160128  1.8 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6               Methylation-20160128   75 Mb
7              miRNASeqGene-20160128  0.1 Mb
8                  Mutation-20160128 29.8 Mb
9           RNASeq2GeneNorm-20160128  1.3 Mb
10                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------
```

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   235 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  72.00   72.00    1.70    1.39    2.29


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   20.0    38.0    46.0    48.2    56.0    88.0       2

vital_status:
  0   1
235  72

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   14.0   349.5   620.0   881.3  1069.5  4086.0     235

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
      0     374     688    1071    1362    6408      72

tumor_tissue_site:
cervical
     307


pathology_N_stage:
  n0   n1   nx NA's
 135   60   67   45

pathology_M_stage:
  m0   m1   mx NA's
 116   10  131   50

gender:
female
   307

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1994    2006    2010    2008    2012    2013       2

radiation_therapy:
  no  yes NA's
```

```
  55  129  123


number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.20    6.50   15.00   17.38   25.00   57.00     214

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   1.044   1.000  16.000     148


ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                    24                    171                   112

weight_kg_at_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  31.00   58.25   70.50   73.04   83.75  210.00      29

tumor_status:
tumor free with tumor       NA's
       201         80         26


tobacco_smoking_year_stopped:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1949    1995    2003    2000    2010    2013     264

tobacco_smoking_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.20    6.50   15.00   17.38   25.00   57.00     214

tobacco_smoking_history:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  1.000   1.000   1.000   1.829   2.000   5.000      44

agebegansmokinginyears:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  11.00   16.00   18.00   21.14   24.00   44.00     222

radiation_therapy_status:
   completed as planned treatment not completed                    NA's
                     29                      3                      275

pregnancies_count_total:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    2.00    3.00    3.61    5.00   15.00      40

pregnancies_count_stillbirth:
   0    1    3 NA's
 106    5    1  195
```

```
pregnancy_spontaneous_abortion_count:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
 0.0000  0.0000  0.0000  0.5442  1.0000  6.0000     160

pregnancies_count_live_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   1.250   2.000   2.844   4.000  11.000      45

pregnancy_therapeutic_abortion_count:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
 0.0000  0.0000  0.0000  0.8525  1.0000 13.0000     185

pregnancies_count_ectopic:
   0    1    2 NA's
 104   11    1  191


lymph_node_location:
lymph_node_location_positive_pathology_name|lymph_node_location_positive_pathology_text
                                                                            307


menopause_status:
                                      indeterminate (neither pre or postmenopausal)
                                                                              3
                                     peri (6-12 months since last menstrual period)
                                                                             25
         post (prior bilateral ovariectomy or >12 mo since lmp with no prior hysterectomy)
                                                                             84
pre (<6 months since lmp and no prior bilateral ovariectomy and not on estrogen replacement)
                                                                            125
                                                                           NA's
                                                                             70

lymphovascular_involvement:
 absent present    NA's
     72      80     155

lymph_nodes_examined_he_count:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   1.044   1.000  16.000     148

lymph_nodes_examined:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   2.00   13.00   21.00   22.28   29.00   63.00     127

keratinization_squamous_cell:
    keratinizing squamous cell carcinoma
                                      55
non-keratinizing squamous cell carcinoma
                                     120
```

```
                                    NA's
                                     132

initial_pathologic_dx_year:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1994    2006    2010    2008    2012    2013       2

hysterectomy_type:
hysterectomy_performed_type|hysterectomy_performed_text
                                                    307

history_hormonal_contraceptives_use:
current user  former user   never used         NA's
          15           54           90          148

height_cm_at_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    132     157     160     161     165     183      43

corpus_involvement:
 absent present    NA's
     99      19     189

chemo_concurrent_type:
carboplatin   cisplatin       other        NA's
          7         104           2         194

cervix_suv_results:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    8.70   12.00   13.22   16.92   28.80     290

cause_of_death:
cardiopulmonary arrest            lung cancer          renal failure
                     1                      1                      1
                  NA's
                   304

age_at_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  20.00   38.00   46.00   48.27   56.50   88.00


Including an additional 1330 columns
```

`CHOL` *Cholangiocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( CHOL )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 39698 rows and 85 columns
 [2] CNVSNP-20160128: RaggedExperiment with 7570 rows and 85 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 45 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 45 columns
 [7] Mutation-20160128: RaggedExperiment with 6755 rows and 35 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 45 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 30 columns

> rownames( CHOL )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( CHOL )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CNVSNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["Methylation-20160128"]] TCGA-3X-AAV9-01A-72D-A418-05 ...
[["miRNASeqGene-20160128"]] TCGA-3X-AAV9-01A-72R-A41D-13 ...
[["Mutation-20160128"]] TCGA-3X-AAV9-01A-72D-A417-09 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3X-AAV9-01A-72R-A41I-07 ...
[["RPPAArray-20160128"]] TCGA-3X-AAV9-01A-81-A45N-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                   CNASNP-20160128  1.1 Mb
2                   CNVSNP-20160128  0.2 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5              Methylation-20160128   75 Mb
6             miRNASeqGene-20160128  0.1 Mb
7                 Mutation-20160128  4.6 Mb
8          RNASeq2GeneNorm-20160128  1.3 Mb
9                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
```

```
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   18 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 18.000  18.000   1.370   0.742   2.532


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  29.00   56.50   66.50   63.03   72.00   82.00

vital_status:
 0  1
18 18

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   21.0   195.2   500.0   592.9   731.0  1939.0      18

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   10.0   539.8   942.5   936.6  1394.0  1976.0      18

tumor_tissue_site:
bile duct
       36


pathology_T_stage:
 t1  t2 t2a t2b  t3
 19   6   2   4   5

pathology_N_stage:
n0 n1 nx
26  5  5

pathology_M_stage:
m0 m1 mx
28  5  3

gender:
female   male
    20     16

date_of_initial_pathologic_diagnosis:
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   2005    2010    2011    2010    2012    2013 

radiation_therapy: 
  no NA's 
  35    1 

histological_type: 
         cholangiocarcinoma; distal cholangiocarcinoma; hilar/perihilar 
                                  2                                    4 
   cholangiocarcinoma; intrahepatic 
                                 30 

residual_tumor: 
r0 r1 rx 
28  5  3 

race: 
                    asian black or african american                      white 
                        3                         2                         31 

ethnicity: 
    hispanic or latino not hispanic or latino                   NA's 
                     2                     33                      1 

Including an additional 622 columns
```

COAD *Colon adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( COAD )
ExperimentList class object of length 13:
 [1] CNASeq-20160128: RaggedExperiment with 40530 rows and 136 columns
 [2] CNASNP-20160128: RaggedExperiment with 459490 rows and 914 columns
 [3] CNVSNP-20160128: RaggedExperiment with 90534 rows and 914 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 202 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 333 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 221 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 172 columns
 [10] Mutation-20160128: RaggedExperiment with 62530 rows and 154 columns
 [11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 191 columns
 [12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 10 columns
 [13] RPPAArray-20160128: SummarizedExperiment with 208 rows and 360 columns
```

```
> rownames( COAD )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

> colnames( COAD )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-A6-2671-01A-01D-1405-02 ...
[["CNASNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["CNVSNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A6-2672-11A-01D-1551-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3L-AA1B-01A-11D-A36Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-A6-2675-01A-02T-1722-13 ...
[["mRNAArray-20160128"]] TCGA-A6-2671-11A-01R-1758-07 ...
[["Mutation-20160128"]] TCGA-A6-2672-01A-01W-0833-10 ...
...
<3 more elements>

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASeq-20160128  1.1 Mb
2                    CNASNP-20160128 12.5 Mb
3                    CNVSNP-20160128  2.7 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6      Methylation_methyl27-20160128  4.9 Mb
7     Methylation_methyl450-20160128   75 Mb
8              miRNASeqGene-20160128  0.1 Mb
9                 mRNAArray-20160128  1.1 Mb
10                 Mutation-20160128 23.6 Mb
11          RNASeq2GeneNorm-20160128  1.3 Mb
12               RNASeqGene-20160128  1.3 Mb
13                RPPAArray-20160128    0 Mb


---------------------------
Available sample meta-data:
---------------------------
```

```
years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  31.00   58.00   68.00   66.95   77.00   90.00       2 

tumor_tissue_site:
colon  NA's 
  456     1 



date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   1998    2007    2009    2008    2010    2013 

radiation_therapy:
  no  yes NA's 
 378    9   70 

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  0.000   0.000   0.000   2.058   2.000  50.000      25 

race:
american indian or alaska native                            asian 
                               1                               11 
       black or african american                            white 
                              59                              213 
                            NA's 
                             173 

ethnicity:
    hispanic or latino not hispanic or latino                  NA's 
                     4                    270                   183 

Including an additional 2604 columns
```

`curatedTCGAData` *Create a MultiAssayExperiment from specific assays and cohorts*

Description

Create a MultiAssayExperiment from specific assays and cohorts

Usage

```
curatedTCGAData(diseaseCode = "*", assays = "*", dry.run = TRUE, ...)
```

Arguments

`diseaseCode`	a character vector containing the name(s) of TCGA cohorts
`assays`	a character vector containing the name(s) of TCGA assays
`dry.run`	logical (default TRUE) whether to return the dataset names before actual download
`...`	Additional arguments passed on to the ExperimentHub constructor

Details

This function will check against available resources in ExperimentHub. Currently, only the latest runDate ("2016-01-28") is supported. Use the `dry.run = FALSE` to download remote datasets and build an integrative MultiAssayExperiment object.

Value

a MultiAssayExperiment of the specified assays and cancer codes

Examples

```
curatedTCGAData(diseaseCode = c("GBM", "ACC"), assays = "CNASNP")
```

`DLBC` *Lymphoid Neoplasm Diffuse Large B-cell Lymphoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( DLBC )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 44725 rows and 94 columns
 [2] CNVSNP-20160128: RaggedExperiment with 9343 rows and 94 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 48 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 47 columns
 [7] Mutation-20160128: RaggedExperiment with 16918 rows and 48 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 48 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 33 columns

> rownames( DLBC )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( DLBC )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["CNVSNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["Methylation-20160128"]] TCGA-FA-8693-01A-11D-2399-05 ...
[["miRNASeqGene-20160128"]] TCGA-FA-8693-01A-11R-2401-13 ...
[["Mutation-20160128"]] TCGA-FA-8693-01A-11D-2397-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-FA-8693-01A-11R-2404-07 ...
[["RPPAArray-20160128"]] TCGA-FA-8693-01A-21-A45K-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                   CNASNP-20160128  1.2 Mb
2                   CNVSNP-20160128  0.3 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5              Methylation-20160128   75 Mb
6             miRNASeqGene-20160128  0.1 Mb
7                 Mutation-20160128 12.6 Mb
8          RNASeq2GeneNorm-20160128  1.3 Mb
9                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   39 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  9.000   9.000   1.630   0.858      NA


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  23.00   46.00   57.50   56.27   67.00   82.00

vital_status:
 0  1
```

```
39  9

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
     58     313     595    1505    1252    6425      39 

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
      0     616     946    1328    1581    5980       9 


gender:
female   male 
    26     22 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   1987    2009    2011    2009    2012    2013 

radiation_therapy:
  no  yes NA's 
  40    7    1 

histological_type:
diffuse large b-cell lymphoma (dlbcl) nos (any anatomic site nodal or extranodal) 
                                                                               41 
                                                        primary dlbcl of the cns 
                                                                                3 
                                              primary mediastinal (thymic) dlbcl 
                                                                                4 

race:
                    asian black or african american                      white 
                       18                         1                         29 

ethnicity:
    hispanic or latino not hispanic or latino 
                    12                     36 

Including an additional 607 columns
```

`ESCA` *Esophageal carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( ESCA )
```

```
ExperimentList class object of length 11:
 [1] CNASeq-20160128: RaggedExperiment with 17059 rows and 104 columns
 [2] CNASNP-20160128: RaggedExperiment with 203186 rows and 373 columns
 [3] CNVSNP-20160128: RaggedExperiment with 60803 rows and 373 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 202 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 198 columns
 [8] Mutation-20160128: RaggedExperiment with 58602 rows and 185 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 196 columns
 [10] RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 198 columns
 [11] RPPAArray-20160128: SummarizedExperiment with 192 rows and 126 columns

> rownames( ESCA )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 AB074166 ... VCY XKRY ZFY
...
<1 more element>

> colnames( ESCA )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-IG-A3I8-01A-11D-A248-26 ...
[["CNASNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["CNVSNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["Methylation-20160128"]] TCGA-2H-A9GF-01A-11D-A37D-05 ...
[["miRNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37J-13 ...
[["Mutation-20160128"]] TCGA-2H-A9GF-01A-11D-A37C-09 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
[["RNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
...
<1 more element>

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASeq-20160128  0.5 Mb
2                    CNASNP-20160128  5.5 Mb
3                    CNVSNP-20160128  1.7 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6               Methylation-20160128   75 Mb
```

```
7             miRNASeqGene-20160128  0.1 Mb
8                 Mutation-20160128 41.2 Mb
9          RNASeq2GeneNorm-20160128  1.3 Mb
10              RNASeqGene-20160128  1.7 Mb
11               RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   108 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 77.000  77.000   0.962   0.677   1.353


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  27.00   54.00   61.00   62.46   72.00   90.00

vital_status:
  0   1
108  77

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    9.0   180.0   351.0   495.2   650.0  2532.0     108

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    4.0   336.5   402.5   570.1   696.8  3714.0      77

tumor_tissue_site:
esophagus
      185




pathology_M_stage:
  m0   m1  m1a   mx NA's
 136    4    5   18   22

gender:
female   male
    27    158
```

```
date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1998    2007    2011    2009    2012    2013       7

radiation_therapy:
  no  yes NA's
 124   43   18

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  20.00   60.00   80.00   73.82   90.00  100.00     117

histological_type:
    esophagus adenocarcinoma, nos esophagus squamous cell carcinoma
                             89                               96

number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1.00   17.62   30.00   34.48   47.25  102.00      87

residual_tumor:
  r0   r1   r2   rx NA's
 137   13    2    7   26

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   1.000   2.526   4.000  21.000      50

race:
                    asian black or african american                     white
                       46                         5                       114
                     NA's
                       20

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                     6                     88                    91

Including an additional 940 columns
```

`GBM` *Glioblastoma multiforme*

Description

A document describing the TCGA cancer code

Details

```
> experiments( GBM )
```

```
ExperimentList class object of length 16:
 [1] CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 81512 rows and 438 columns
 [2] CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 57975 rows and 338 columns
 [3] CNASNP-20160128: RaggedExperiment with 602338 rows and 1104 columns
 [4] CNVSNP-20160128: RaggedExperiment with 146852 rows and 1104 columns
 [5] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [6] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [7] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 285 columns
 [8] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 154 columns
 [9] miRNAArray-20160128: SummarizedExperiment with 534 rows and 565 columns
 [10] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 0 columns
 [11] mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 431 columns
 [12] mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 502 columns
 [13] mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 528 columns
 [14] Mutation-20160128: RaggedExperiment with 22073 rows and 290 columns
 [15] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 166 columns
 [16] RPPAArray-20160128: SummarizedExperiment with 208 rows and 244 columns

> rownames( GBM )
CharacterList of length 16
[["CNACGH_CGH_hg_244a-20160128"]] character(0)
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNAArray-20160128"]] ebv-miR-BART1-3p ebv-miR-BART1-5p ... kshv-miR-K12-9*
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<6 more elements>

> colnames( GBM )
CharacterList of length 16
[["CNACGH_CGH_hg_244a-20160128"]] TCGA-02-0001-01C-01D-0185-02 ...
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-02-2466-01A-01D-0787-02 ...
[["CNASNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["CNVSNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["Methylation_methyl27-20160128"]] TCGA-02-0001-01C-01D-0186-05 ...
[["Methylation_methyl450-20160128"]] TCGA-06-0125-01A-01D-A45W-05 ...
[["miRNAArray-20160128"]] TCGA-02-0001-01C-01T-0179-07 ...
[["miRNASeqGene-20160128"]] character(0)
...
<6 more elements>

Sizes of each ExperimentList element:

                               assay size.Mb
1         CNACGH_CGH_hg_244a-20160128  2.3 Mb
```

```
2  CNACGH_CGH_hg_415k_g4124a-20160128  1.7 Mb
3                    CNASNP-20160128 16.4 Mb
4                    CNVSNP-20160128  4.2 Mb
5           GISTIC_AllByGene-20160128  4.9 Mb
6   GISTIC_ThresholdedByGene-20160128  4.9 Mb
7       Methylation_methyl27-20160128  4.9 Mb
8      Methylation_methyl450-20160128   75 Mb
9                 miRNAArray-20160128  0.1 Mb
10              miRNASeqGene-20160128  0.1 Mb
11            mRNAArray_huex-20160128  1.2 Mb
12       mRNAArray_TX_g4502a-20160128  1.2 Mb
13  mRNAArray_TX_ht_hg_u133a-20160128  0.8 Mb
14                  Mutation-20160128   31 Mb
15           RNASeq2GeneNorm-20160128  1.3 Mb
16                 RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   109 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
490.000 490.000   1.047   0.981   1.156


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  10.00   50.00   59.00   57.82   68.00   89.00       4

vital_status:
   0    1 NA's
 104  491    4

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    3.0   170.5   382.0   504.5   609.2  3881.0     109

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   156.2   261.0   479.4   628.0  2818.0     497

tumor_tissue_site:
brain  NA's
  595     4
```

```
gender:
female   male   NA's
   230    365      4

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1989    2002    2006    2005    2009    2013       4

radiation_therapy:
  no  yes NA's
  78  489   32

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   70.00   80.00   77.04   80.00  100.00     157

histological_type:
  glioblastoma multiforme (gbm)             treated primary gbm
                             31                              20
untreated primary (de novo) gbm                            NA's
                            544                               4

race:
                    asian black or african american                     white
                       13                        51                       506
                     NA's
                       29

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                    13                    489                    97

Including an additional 4368 columns
```

HNSC *Head and Neck squamous cell carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( HNSC )
ExperimentList class object of length 11:
 [1] CNASeq-20160128: RaggedExperiment with 32905 rows and 225 columns
 [2] CNASNP-20160128: RaggedExperiment with 499142 rows and 1090 columns
 [3] CNVSNP-20160128: RaggedExperiment with 110289 rows and 1089 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 580 columns
```

```
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 532 columns
 [8] Mutation-20160128: RaggedExperiment with 51799 rows and 279 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 566 columns
 [10] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 294 columns
 [11] RPPAArray-20160128: SummarizedExperiment with 160 rows and 212 columns

> rownames( HNSC )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22 tAKR
...
<1 more element>

> colnames( HNSC )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-BA-4074-01A-01D-1431-02 ...
[["CNASNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["CNVSNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["Methylation-20160128"]] TCGA-4P-AA8J-01A-11D-A392-05 ...
[["miRNASeqGene-20160128"]] TCGA-4P-AA8J-01A-11R-A39B-13 ...
[["Mutation-20160128"]] TCGA-BA-4074-01A-01D-1434-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-4P-AA8J-01A-11R-A39I-07 ...
[["RNASeqGene-20160128"]] TCGA-BA-4074-01A-01R-1436-07 ...
...
<1 more element>

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASeq-20160128    1 Mb
2                    CNASNP-20160128 13.6 Mb
3                    CNVSNP-20160128  3.3 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6               Methylation-20160128 75.1 Mb
7              miRNASeqGene-20160128  0.1 Mb
8                  Mutation-20160128 68.9 Mb
9           RNASeq2GeneNorm-20160128  1.3 Mb
10               RNASeqGene-20160128  1.3 Mb
11                RPPAArray-20160128    0 Mb

---------------------------
```

```
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   305 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 223.00  223.00    1.18    1.06    1.35


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  19.00   53.00   61.00   60.91   69.00   89.00       1

vital_status:
  0   1
304 224

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    2.0   260.0   430.0   740.0   814.5  6417.0     305

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   11.0   529.5   851.0  1042.9  1404.0  5480.0     225

tumor_tissue_site:
head and neck
          528




pathology_M_stage:
  m0   m1   mx NA's
 191    1   65  271

gender:
female   male
   142    386

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1992    2007    2010    2008    2011    2013       1

days_to_last_known_alive:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
```

```
   98.0   483.0   848.5  1226.9  1647.5  3930.0     506

radiation_therapy:
  no  yes NA's
 163  303   62

histological_type:
                      head & neck squamous cell carcinoma
                                                      517
        head & neck squamous cell carcinoma basaloid type
                                                       10
head & neck squamous cell carcinoma, spindle cell variant
                                                        1

number_pack_years_smoked:
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.      NA's
  0.01685  25.00000  40.00000  45.75496  60.00000 300.00000       230

year_of_tobacco_smoking_onset:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1936    1959    1968    1967    1975    2001     246

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   1.000   2.186   3.000  44.000     115

race:
american indian or alaska native                            asian
                               2                               11
       black or african american                            white
                              48                              452
                            NA's
                              15

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                    26                    465                    37

Including an additional 1426 columns
```

`KICH` *Kidney Chromophobe*

Description

A document describing the TCGA cancer code

Details

```
> experiments( KICH )
ExperimentList class object of length 9:
```

```
 [1] CNASNP-20160128: RaggedExperiment with 57729 rows and 132 columns
 [2] CNVSNP-20160128: RaggedExperiment with 10164 rows and 132 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 66 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 91 columns
 [7] Mutation-20160128: RaggedExperiment with 7559 rows and 66 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 91 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns

> rownames( KICH )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( KICH )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["CNVSNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["Methylation-20160128"]] TCGA-KL-8323-01A-21D-2312-05 ...
[["miRNASeqGene-20160128"]] TCGA-KL-8323-01A-21R-2314-13 ...
[["Mutation-20160128"]] TCGA-KL-8323-01A-21D-2310-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["RPPAArray-20160128"]] TCGA-KL-8324-01A-21-A421-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                   CNASNP-20160128  1.6 Mb
2                   CNVSNP-20160128  0.3 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5              Methylation-20160128   75 Mb
6             miRNASeqGene-20160128  0.1 Mb
7                 Mutation-20160128  2.6 Mb
8          RNASeq2GeneNorm-20160128  1.3 Mb
9                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
```

```
    -1)

   57 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
   9.00    9.00    2.34    1.99      NA


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  17.00   42.00   50.00   51.52   61.75   86.00

vital_status:
 0  1
56 10

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    325     725     855    1001    1158    2172      57

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     30    1366    2713    2320    3138    4676      10

tumor_tissue_site:
kidney
    66

pathologic_stage:
  stage i  stage ii stage iii  stage iv
       21        25        14         6


pathology_N_stage:
n0 n1 n2 nx
40  3  2 21

pathology_M_stage:
  m0   m1   mx NA's
  34    2    9   21

gender:
female   male
    27     39

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   2000    2004    2005    2005    2007    2011
```

```
radiation_therapy:
no
66

karnofsky_performance_score:
  90  100 NA's
   3   10   53

histological_type:
kidney chromophobe
                66

number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1.00    8.00   24.00   25.09   31.00   75.00      55

year_of_tobacco_smoking_onset:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1949    1964    1974    1974    1984    1997      58

race:
                    asian black or african american                     white
                        2                         4                        58
                     NA's
                        2

ethnicity:
    hispanic or latino not hispanic or latino                   NA's
                     4                     32                     30

Including an additional 718 columns
```

KIRC *Kidney renal clear cell carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( KIRC )
ExperimentList class object of length 12:
 [1] CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
 [2] CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
 [5] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 418 columns
 [6] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 480 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
```

```
 [9] Mutation-20160128: RaggedExperiment with 26369 rows and 437 columns
 [10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 606 columns
 [11] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 537 columns
 [12] RPPAArray-20160128: SummarizedExperiment with 217 rows and 478 columns

> rownames( KIRC )
CharacterList of length 12
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( KIRC )
CharacterList of length 12
[["CNASNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["CNVSNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A3-3306-11A-01D-0859-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3Z-A93Z-01A-11D-A36Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-3Z-A93Z-01A-11R-A37P-13 ...
[["mRNAArray-20160128"]] TCGA-A3-3306-01A-01R-0864-07 ...
[["Mutation-20160128"]] TCGA-A3-3308-01A-01D-0966-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3Z-A93Z-01A-11R-A37O-07 ...
...
<2 more elements>

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASNP-20160128 13.4 Mb
2                    CNVSNP-20160128  2.6 Mb
3          GISTIC_AllByGene-20160128  4.9 Mb
4  GISTIC_ThresholdedByGene-20160128  4.9 Mb
5      Methylation_methyl27-20160128  4.9 Mb
6     Methylation_methyl450-20160128 75.1 Mb
7              miRNASeqGene-20160128  0.1 Mb
8                mRNAArray-20160128  1.1 Mb
9                 Mutation-20160128  8.2 Mb
10         RNASeq2GeneNorm-20160128  1.3 Mb
11              RNASeqGene-20160128  1.3 Mb
12               RPPAArray-20160128  0.1 Mb

---------------------------
```

```
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   360 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 177.00  177.00    2.24    1.77    2.61


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  26.00   52.00   61.00   60.57   70.00   90.00       1

vital_status:
  0   1
360 177

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    2.0   333.0   819.0   961.2  1432.0  3615.0     360

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   710.5  1454.5  1536.9  2172.0  4537.0     177

tumor_tissue_site:
kidney
   537

pathologic_stage:
  stage i  stage ii stage iii  stage iv      NA's
      269        57       125        84         2


pathology_N_stage:
 n0  n1  nx
240  17 280

pathology_M_stage:
  m0   m1   mx NA's
 426   79   30    2

gender:
female   male
   191    346
```

```
date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   1998    2004    2006    2006    2007    2013 

days_to_last_known_alive:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
      0     191    1172    1117    1887    2799     510 

radiation_therapy:
  no  yes NA's 
 142    2  393 

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   0.00   90.00   90.00   85.56  100.00  100.00     483 

histological_type:
kidney clear cell renal carcinoma 
                              537 

number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   7.00   14.00   30.00   28.33   40.00   65.00     516 

year_of_tobacco_smoking_onset:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1946    1966    1978    1979    1996    2001     525 

race:
                    asian black or african american                     white 
                        8                        56                       466 
                     NA's 
                        7 

ethnicity:
    hispanic or latino not hispanic or latino                   NA's 
                    26                    359                    152 

Including an additional 2250 columns
```

`KIRP` *Kidney renal papillary cell carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( KIRP )
ExperimentList class object of length 12:
```

```
 [1] CNASNP-20160128: RaggedExperiment with 300681 rows and 593 columns
 [2] CNVSNP-20160128: RaggedExperiment with 46914 rows and 590 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [5] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 21 columns
 [6] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 321 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 16 columns
 [9] Mutation-20160128: RaggedExperiment with 15585 rows and 161 columns
 [10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 323 columns
 [11] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 14 columns
 [12] RPPAArray-20160128: SummarizedExperiment with 195 rows and 216 columns

> rownames( KIRP )
CharacterList of length 12
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( KIRP )
CharacterList of length 12
[["CNASNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["CNVSNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["Methylation_methyl27-20160128"]] TCGA-AL-3466-01A-01D-1191-05 ...
[["Methylation_methyl450-20160128"]] TCGA-2K-A9WE-01A-11D-A383-05 ...
[["miRNASeqGene-20160128"]] TCGA-2K-A9WE-01A-11R-A38N-13 ...
[["mRNAArray-20160128"]] TCGA-AL-3466-01A-01R-1193-07 ...
[["Mutation-20160128"]] TCGA-A4-7286-01A-11D-2136-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2K-A9WE-01A-11R-A38C-07 ...
...
<2 more elements>

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASNP-20160128  8.2 Mb
2                    CNVSNP-20160128  1.4 Mb
3          GISTIC_AllByGene-20160128  4.9 Mb
4  GISTIC_ThresholdedByGene-20160128  4.9 Mb
5      Methylation_methyl27-20160128  4.9 Mb
6     Methylation_methyl450-20160128   75 Mb
```

```
7              miRNASeqGene-20160128  0.1 Mb
8                 mRNAArray-20160128  1.1 Mb
9                  Mutation-20160128 10.6 Mb
10          RNASeq2GeneNorm-20160128  1.3 Mb
11               RNASeqGene-20160128  1.3 Mb
12                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   247 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  44.00   44.00    1.76    1.35    3.60


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  28.00   53.25   61.50   61.52   71.00   88.00       5

vital_status:
  0   1
247  44

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  122.0   341.2   641.0   989.8  1498.5  2941.0     247

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   438.2   774.5  1070.2  1513.0  5925.0      45

tumor_tissue_site:
kidney
   291

pathologic_stage:
  stage i  stage ii stage iii  stage iv      NA's
      173        21        52        15        30


pathology_N_stage:
  n0   n1   n2   nx NA's
  50   24    4  212    1
```

```
pathology_M_stage:
  m0   m1   mx NA's 
  95    9  172   15 

gender:
female   male 
    77    214 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1996    2008    2011    2010    2012    2013      25 

days_to_last_known_alive:
  34 NA's 
   1  290 

radiation_therapy:
  no  yes NA's 
 209    1   81 

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   0.00   90.00   90.00   87.66  100.00  100.00     214 

histological_type:
kidney papillary renal cell carcinoma 
                                  291 

number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   3.00   15.00   24.50   31.73   41.25  185.00     215 

year_of_tobacco_smoking_onset:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1941    1961    1970    1972    1984    2010     235 

race:
american indian or alaska native                            asian 
                               2                                6 
       black or african american                            white 
                              61                              207 
                            NA's 
                              15 

ethnicity:
    hispanic or latino not hispanic or latino                   NA's 
                    12                    243                     36 

Including an additional 1686 columns
```

`LAML` *Acute Myeloid Leukemia*

Description

A document describing the TCGA cancer code

Details

```
> experiments( LAML )
ExperimentList class object of length 7:
 [1] CNASNP-20160128: RaggedExperiment with 874897 rows and 392 columns
 [2] CNVSNP-20160128: RaggedExperiment with 28324 rows and 380 columns
 [3] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 194 columns
 [4] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 194 columns
 [5] Mutation-20160128: RaggedExperiment with 2585 rows and 197 columns
 [6] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 173 columns
 [7] RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 179 columns

> rownames( LAML )
CharacterList of length 7
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] AADACL3 AADACL4 ABCA4 ABCB10 ... VCY XGPY2 XKRY2 ZFY

> colnames( LAML )
CharacterList of length 7
[["CNASNP-20160128"]] TCGA-AB-2802-03A-01D-0756-21 ...
[["CNVSNP-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["Methylation_methyl27-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...
[["Methylation_methyl450-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...
[["Mutation-20160128"]] TCGA-AB-2802-03B-01W-0728-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["RNASeqGene-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...

Sizes of each ExperimentList element:

                           assay size.Mb
1                CNASNP-20160128 23.5 Mb
2                CNVSNP-20160128  0.9 Mb
3  Methylation_methyl27-20160128  4.9 Mb
4 Methylation_methyl450-20160128   75 Mb
5              Mutation-20160128  2.6 Mb
6       RNASeq2GeneNorm-20160128  1.3 Mb
7            RNASeqGene-20160128  1.3 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)
```

```
   80 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
120.000 120.000   0.748   0.586   0.918


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  18.00   44.75   57.00   55.02   67.00   88.00

vital_status:
  0   1
 67 133

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0    91.5   273.0   355.7   489.0  1706.0      80

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   296.2   699.0   913.5  1506.8  2861.0     132

tumor_tissue_site:
bone marrow        NA's
        199           1

gender:
female   male
    91    109

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   2001    2004    2006    2006    2008    2010

race:
                    asian black or african american                     white
                        2                        15                       181
                     NA's
                        2

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                     3                    194                     3

Including an additional 478 columns
```

LGG *Brain Lower Grade Glioma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( LGG )
ExperimentList class object of length 11:
 [1] CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
 [2] CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns
 [3] CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 530 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 526 columns
 [8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 27 columns
 [9] Mutation-20160128: RaggedExperiment with 9885 rows and 286 columns
 [10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 530 columns
 [11] RPPAArray-20160128: SummarizedExperiment with 201 rows and 435 columns

> rownames( LGG )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<1 more element>

> colnames( LGG )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-CS-4938-01B-11D-1891-02 ...
[["CNASNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["CNVSNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["Methylation-20160128"]] TCGA-CS-4938-01B-11D-1894-05 ...
[["miRNASeqGene-20160128"]] TCGA-CS-4938-01B-11R-1895-13 ...
[["mRNAArray-20160128"]] TCGA-CS-4942-01A-01R-1470-07 ...
[["Mutation-20160128"]] TCGA-CS-4938-01B-11D-1893-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-CS-4938-01B-11R-1896-07 ...
...
<1 more element>

Sizes of each ExperimentList element:

                              assay size.Mb
```

```
1                   CNASeq-20160128  0.2 Mb
2                   CNASNP-20160128 11.3 Mb
3                   CNVSNP-20160128  2.4 Mb
4         GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6              Methylation-20160128 75.1 Mb
7             miRNASeqGene-20160128  0.1 Mb
8                mRNAArray-20160128  1.1 Mb
9                 Mutation-20160128  4.2 Mb
10         RNASeq2GeneNorm-20160128  1.3 Mb
11               RPPAArray-20160128  0.1 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   391 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 125.00  125.00    2.23    1.87    2.83


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  14.00   32.00   41.00   42.93   53.00   86.00       2

vital_status:
   0    1 NA's
 389  126    1

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
      7     438     814    1219    1547    5166     391

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   -1.0   384.0   629.0   880.1  1147.0  6423.0     127

tumor_tissue_site:
central nervous system                   NA's
                   515                      1

gender:
female   male   NA's
   230    285      1
```

```
date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1992    2008    2011    2009    2012    2013       1 

radiation_therapy:
  no  yes NA's 
 186  296   34 

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  40.00   80.00   90.00   86.64  100.00  100.00     209 

histological_type:
      astrocytoma  oligoastrocytoma oligodendroglioma              NA's 
              194               130               191                 1 

race:
american indian or alaska native                            asian 
                               1                                8 
       black or african american                            white 
                              21                              475 
                            NA's 
                              11 

ethnicity:
    hispanic or latino not hispanic or latino                  NA's 
                    32                    449                    35 

Including an additional 1764 columns
```

LIHC *Liver hepatocellular carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( LIHC )
ExperimentList class object of length 10:
 [1] CNASNP-20160128: RaggedExperiment with 363628 rows and 760 columns
 [2] CNVSNP-20160128: RaggedExperiment with 93328 rows and 760 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 429 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 424 columns
 [7] Mutation-20160128: RaggedExperiment with 27892 rows and 198 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 423 columns
 [9] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 26 columns
 [10] RPPAArray-20160128: SummarizedExperiment with 219 rows and 184 columns
```

```
> rownames( LIHC )
CharacterList of length 10
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( LIHC )
CharacterList of length 10
[["CNASNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["CNVSNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["Methylation-20160128"]] TCGA-2V-A95S-01A-11D-A36Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-2V-A95S-01A-11R-A37G-13 ...
[["Mutation-20160128"]] TCGA-BC-4073-01B-02D-A12Z-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2V-A95S-01A-11R-A37K-07 ...
[["RNASeqGene-20160128"]] TCGA-BC-4073-01B-02R-A131-07 ...
[["RPPAArray-20160128"]] TCGA-BC-4072-01B-21-A40L-20 ...

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASNP-20160128  9.9 Mb
2                    CNVSNP-20160128  2.7 Mb
3          GISTIC_AllByGene-20160128  4.9 Mb
4  GISTIC_ThresholdedByGene-20160128  4.9 Mb
5               Methylation-20160128 75.1 Mb
6              miRNASeqGene-20160128  0.1 Mb
7                  Mutation-20160128 16.8 Mb
8           RNASeq2GeneNorm-20160128  1.3 Mb
9                RNASeqGene-20160128  1.3 Mb
10                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   245 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
132.000 132.000   1.144   0.956   1.633
```

```
--------------------------
Available sample meta-data:
--------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  16.00   51.00   61.00   59.27   69.00   87.00       4 

vital_status:
  0   1 
245 132 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    9.0   194.8   417.5   672.1   837.0  3258.0     245 

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    0.0   395.8   649.5   885.8  1222.0  3675.0     133 

tumor_tissue_site:
liver 
  377 



pathology_N_stage:
  n0   n1   nx NA's 
 257    4  115    1 

pathology_M_stage:
 m0  m1  mx 
272   4 101 

gender:
female   male 
   122    255 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1995    2008    2011    2010    2012    2013       3 

radiation_therapy:
  no  yes NA's 
 345    9   23 

histological_type:
         fibrolamellar carcinoma         hepatocellular carcinoma 
                               3                              367 
hepatocholangiocarcinoma (mixed) 
                               7 
```

```
residual_tumor:
  r0   r1   r2   rx NA's 
 330   17    1   22    7 

race:
american indian or alaska native                            asian 
                               2                              161 
       black or african american                            white 
                              17                              187 
                            NA's 
                              10 

ethnicity:
    hispanic or latino not hispanic or latino                  NA's 
                    18                    340                    19 

Including an additional 1218 columns
```

`LUAD` *Lung adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( LUAD )
ExperimentList class object of length 13:
 [1] CNASeq-20160128: RaggedExperiment with 399592 rows and 249 columns
 [2] CNASNP-20160128: RaggedExperiment with 501475 rows and 1095 columns
 [3] CNVSNP-20160128: RaggedExperiment with 115836 rows and 1095 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 89 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 492 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 498 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 32 columns
 [10] Mutation-20160128: RaggedExperiment with 72541 rows and 230 columns
 [11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 576 columns
 [12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 162 columns
 [13] RPPAArray-20160128: SummarizedExperiment with 223 rows and 365 columns

> rownames( LUAD )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
```

```
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

> colnames( LUAD )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-05-4249-01A-01D-1103-02 ...
[["CNASNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["CNVSNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["Methylation_methyl27-20160128"]] TCGA-05-4244-01A-01D-1104-05 ...
[["Methylation_methyl450-20160128"]] TCGA-05-4384-01A-01D-1756-05 ...
[["miRNASeqGene-20160128"]] TCGA-05-4384-01A-01T-1754-13 ...
[["mRNAArray-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["Mutation-20160128"]] TCGA-05-4249-01A-01D-1105-08 ...
...
<3 more elements>

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASeq-20160128 10.8 Mb
2                    CNASNP-20160128 13.7 Mb
3                    CNVSNP-20160128  3.4 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6      Methylation_methyl27-20160128  4.9 Mb
7     Methylation_methyl450-20160128 75.1 Mb
8              miRNASeqGene-20160128  0.1 Mb
9                 mRNAArray-20160128  1.1 Mb
10                 Mutation-20160128 92.9 Mb
11         RNASeq2GeneNorm-20160128  1.3 Mb
12              RNASeqGene-20160128  1.3 Mb
13               RPPAArray-20160128  0.1 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   336 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 184.00  184.00    1.70    1.37    2.00
```

```
---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  33.00   59.00   66.00   65.22   72.00   88.00      31

vital_status:
  0   1
332 188

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   297.8   619.0   791.4  1120.0  4961.0     336

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   459.5   670.0   968.7  1139.0  7248.0     193

tumor_tissue_site:
lung
 520




gender:
female   male
   279    241

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1991    2007    2010    2008    2011    2013      19

days_to_last_known_alive:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    9.0    96.5   141.0   327.6   386.0  1178.0     513

radiation_therapy:
  no  yes NA's
 413   61   46

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   80.00   90.00   78.55  100.00  100.00     382


number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.15   20.50   40.00   41.79   50.00  154.00     165
```

```
year_of_tobacco_smoking_onset:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1930    1956    1965    1965    1972    1999     241 

residual_tumor:
  r0   r1   r2   rx NA's 
 347   13    4   26  130 

race:
american indian or alaska native                            asian 
                               1                                8 
       black or african american                            white 
                              53                              392 
                            NA's 
                              66 

ethnicity:
    hispanic or latino not hispanic or latino                   NA's 
                     7                    388                    125 

Including an additional 2607 columns
```

LUSC *Lung squamous cell carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( LUSC )
ExperimentList class object of length 15:
 [1] CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [9] mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
 [10] mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
 [11] mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
 [12] Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
 [13] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 552 columns
 [14] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns
 [15] RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns

> rownames( LUSC )
```

```
CharacterList of length 15
[["CNACGH-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray_huex-20160128"]] C9orf152 ELMO2 RPS11 ... SLC39A6 CTSC AQP7
[["mRNAArray_TX_g4502a-20160128"]] ELMO2 CREB3L1 RPS11 ... SNRPD2 AQP7 CTSC
...
<5 more elements>

> colnames( LUSC )
CharacterList of length 15
[["CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["Methylation_methyl27-20160128"]] TCGA-18-3406-11A-01D-0979-05 ...
[["Methylation_methyl450-20160128"]] TCGA-18-3417-11A-01D-1440-05 ...
[["miRNASeqGene-20160128"]] TCGA-18-5592-01A-01T-1634-13 ...
[["mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
...
<5 more elements>

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNACGH-20160128  2.5 Mb
2                    CNASNP-20160128 14.8 Mb
3                    CNVSNP-20160128  3.9 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6      Methylation_methyl27-20160128  4.9 Mb
7     Methylation_methyl450-20160128   75 Mb
8              miRNASeqGene-20160128  0.1 Mb
9            mRNAArray_huex-20160128  1.2 Mb
10      mRNAArray_TX_g4502a-20160128  1.1 Mb
11 mRNAArray_TX_ht_hg_u133a-20160128  0.8 Mb
12                 Mutation-20160128   81 Mb
13         RNASeq2GeneNorm-20160128  1.3 Mb
14              RNASeqGene-20160128  1.3 Mb
15               RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------
```

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   289 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 215.00  215.00    1.51    1.25    1.88


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  39.00   62.00   68.00   67.26   73.00   90.00      10

vital_status:
  0   1
284 220

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    1.0   280.0   550.0   872.3  1110.5  5287.0     289

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
      0     394     757    1049    1374    4765     221

tumor_tissue_site:
lung
 504



pathology_N_stage:
 n0  n1  n2  n3  nx
320 133  40   5   6


gender:
female   male
   131    373

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1992    2005    2009    2008    2011    2013      25

days_to_last_known_alive:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    4.0   298.8   706.0   904.8  1051.8  3724.0     436

radiation_therapy:
```

```
  no  yes NA's
 387   53   64

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0     0.0    80.0    60.3    90.0   100.0     338

histological_type:
                      lung basaloid squamous cell carcinoma
                                                         15
                     lung papillary squamous cell caricnoma
                                                          6
                    lung small cell squamous cell carcinoma
                                                          1
lung squamous cell carcinoma- not otherwise specified (nos)
                                                        482

number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1.00   31.12   50.00   52.91   64.50  240.00      77

year_of_tobacco_smoking_onset:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1933    1952    1960    1960    1968    1997     183

residual_tumor:
  r0   r1   r2   rx NA's
 401   12    4   23   64

race:
                    asian black or african american                     white
                        9                        31                       351
                     NA's
                      113

ethnicity:
    hispanic or latino not hispanic or latino                   NA's
                     8                    319                    177

Including an additional 2238 columns
```

MESO *Mesothelioma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( MESO )
```

```
ExperimentList class object of length 8:
 [1] CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
 [2] CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns
 [7] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 87 columns
 [8] RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns

> rownames( MESO )
CharacterList of length 8
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( MESO )
CharacterList of length 8
[["CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...
[["miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A45O-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                   CNASNP-20160128  2.5 Mb
2                   CNVSNP-20160128  0.6 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5              Methylation-20160128   75 Mb
6             miRNASeqGene-20160128  0.1 Mb
7          RNASeq2GeneNorm-20160128  1.3 Mb
8               RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   14 observations deleted due to missingness
```

```
      n  events  median 0.95LCL 0.95UCL
  73.00   73.00    1.25    1.11    1.67


--------------------------
Available sample meta-data:
--------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  28.00   57.00   64.00   62.99   69.00   81.00

vital_status:
 0  1
13 74

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   20.0   253.0   457.0   584.1   789.0  2790.0      14

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     -8     499    1168    1091    1490    2359      74

tumor_tissue_site:
pleura
    87



pathology_N_stage:
n0 n1 n2 n3 nx
44 10 26  3  4

pathology_M_stage:
m0 m1 mx
57  3 27

gender:
female   male
    16     71

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1999    2008    2010    2009    2012    2013

radiation_therapy:
  no  yes NA's
  62   24    1

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
```

```
    0.00   80.00   90.00   77.65   90.00  100.00      70

histological_type:
              biphasic mesothelioma diffuse malignant mesothelioma - nos
                                 23                                    5
           epithelioid mesothelioma            sarcomatoid mesothelioma
                                 57                                    2

residual_tumor:
  r0   r1   r2   rx NA's
  17    3   15   11   41

race:
                    asian black or african american                     white
                        1                         1                        85

ethnicity:
not hispanic or latino                  NA's
                    73                    14

Including an additional 636 columns
```

OV *Ovarian serous cystadenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( OV )
ExperimentList class object of length 17:
 [1] CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
 [2] CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
 [3] CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
 [4] CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns
 [5] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [6] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [7] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
 [8] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns
 [9] miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
 [10] miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
 [11] mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
 [12] mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 577 columns
 [13] mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
 [14] Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
 [15] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 307 columns
 [16] RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
 [17] RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns
```

```
> rownames( OV )
CharacterList of length 17
[["CNACGH_CGH_hg_244a-20160128"]] character(0)
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNAArray-20160128"]] DarkCorner dmr_285 dmr_3 ... NegativeControl SCorner3
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<7 more elements>

> colnames( OV )
CharacterList of length 17
[["CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["Methylation_methyl27-20160128"]] TCGA-04-1331-01A-01D-0432-05 ...
[["Methylation_methyl450-20160128"]] TCGA-13-A5FT-01A-11D-A409-05 ...
[["miRNAArray-20160128"]] TCGA-04-1331-01A-01T-0438-07 ...
[["miRNASeqGene-20160128"]] TCGA-04-1331-01A-01R-1569-13 ...
...
<7 more elements>

Sizes of each ExperimentList element:

                                assay size.Mb
1         CNACGH_CGH_hg_244a-20160128  3.6 Mb
2  CNACGH_CGH_hg_415k_g4124a-20160128  6.8 Mb
3                     CNASNP-20160128 24.6 Mb
4                     CNVSNP-20160128  7.3 Mb
5           GISTIC_AllByGene-20160128  4.9 Mb
6    GISTIC_ThresholdedByGene-20160128  4.9 Mb
7       Methylation_methyl27-20160128  4.9 Mb
8      Methylation_methyl450-20160128   75 Mb
9                 miRNAArray-20160128  0.1 Mb
10              miRNASeqGene-20160128  0.1 Mb
11            mRNAArray_huex-20160128  1.2 Mb
12       mRNAArray_TX_g4502a-20160128  1.2 Mb
13   mRNAArray_TX_ht_hg_u133a-20160128  0.8 Mb
14                  Mutation-20160128  7.6 Mb
15          RNASeq2GeneNorm-20160128  1.3 Mb
16               RNASeqGene-20160128  1.3 Mb
17                RPPAArray-20160128  0.1 Mb

---------------------------
```

```
Overall survival time-to-event summary (in years):
--------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   247 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 343.00  343.00    2.94    2.76    3.17


--------------------------
Available sample meta-data:
--------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  26.00   51.00   59.00   59.78   69.00   89.00      21

vital_status:
  0   1
246 344

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    8.0   567.5  1073.0  1147.4  1557.0  4624.0     247

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     16     266     842    1216    1931    5481     358

tumor_tissue_site:
         omentum            ovary peritoneum ovary             NA's
               3              575                2               10

gender:
female   NA's
   580     10

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1992    2001    2004    2004    2007    2013      10

radiation_therapy:
  no  yes NA's
 556    5   29

karnofsky_performance_score:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  40.00   60.00   80.00   75.83   80.00  100.00     506

histological_type:
```

```
serous cystadenocarcinoma                      NA's
                      580                        10

residual_tumor:
  r0   r1   r2   rx NA's
  15   31    5    3  536

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                    11                    338                   241

Including an additional 2869 columns
```

PAAD *Pancreatic adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( PAAD )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
 [2] CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
 [7] Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns

> rownames( PAAD )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( PAAD )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
```

```
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["Methylation-20160128"]] TCGA-2J-AAB1-01A-11D-A40Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                  CNASNP-20160128  5.6 Mb
2                  CNVSNP-20160128    1 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5             Methylation-20160128   75 Mb
6            miRNASeqGene-20160128  0.1 Mb
7                Mutation-20160128  111 Mb
8         RNASeq2GeneNorm-20160128  1.3 Mb
9               RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   85 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
100.000 100.000   1.079   0.967   1.315


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  35.00   57.00   65.00   64.86   73.00   88.00

vital_status:
  0   1
 85 100

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   12.0   228.5   394.0   459.5   596.5  2182.0      85

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   338.0   517.0   692.4   951.0  2741.0     100
```

```
tumor_tissue_site:
pancreas
     185



pathology_N_stage:
  n0   n1  n1b   nx NA's
  50  126    4    4    1

pathology_M_stage:
m0 m1 mx
85  5 95

gender:
female   male
    83    102

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   2001    2010    2012    2011    2012    2013       1

radiation_therapy:
  no  yes NA's
 125   45   15

histological_type:
             pancreas-adenocarcinoma ductal type
                                             154
           pancreas-adenocarcinoma-other subtype
                                              25
pancreas-colloid (mucinous non-cystic) carcinoma
                                               4
             pancreas-undifferentiated carcinoma
                                               1
                                            NA's
                                               1

number_pack_years_smoked:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.30   15.00   25.00   26.84   40.00   75.00     128

year_of_tobacco_smoking_onset:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1948    1960    1971    1971    1982    1993     138

residual_tumor:
  r0   r1   r2   rx NA's
 111   53    5    4   12

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
```

```
  0.000   0.000   2.000   2.989   4.000  16.000       4

race:
                    asian black or african american                      white
                       11                         7                        162
                     NA's
                        5

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                     5                    137                    43

Including an additional 960 columns
```

PCPG *Pheochromocytoma and Paraganglioma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( PCPG )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns
 [7] Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns

> rownames( PCPG )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( PCPG )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
```

```
[["GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["Methylation-20160128"]] TCGA-P7-A5NX-01A-11D-A35E-05 ...
[["miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                 CNASNP-20160128  8.1 Mb
2                 CNVSNP-20160128  0.9 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5             Methylation-20160128   75 Mb
6            miRNASeqGene-20160128  0.1 Mb
7                Mutation-20160128  8.4 Mb
8         RNASeq2GeneNorm-20160128  1.3 Mb
9               RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   173 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
   6.00    6.00    1.24    0.26      NA


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  19.00   35.00   46.00   47.33   58.50   83.00

vital_status:
  0   1
173   6

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   88.0   148.5   452.5   901.0   715.2  3563.0     173

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
      2     352     766    1071    1301    9634       6
```

```
tumor_tissue_site:
     adrenal gland extra-adrenal site
              147                 32

gender:
female   male
   101     78

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1988    2009    2011    2010    2012    2013

radiation_therapy:
  no  yes NA's
 172    5    2

karnofsky_performance_score:
  70   80   90  100 NA's
   1    2   13   46  117

histological_type:
                                paraganglioma
                                           18
paraganglioma; extra-adrenal pheochromocytoma
                                           13
                             pheochromocytoma
                                          148

number_of_lymph_nodes:
   0    1    2   13 NA's
  16    3    1    1  158

race:
american indian or alaska native                            asian
                               1                                6
       black or african american                            white
                              20                              148
                            NA's
                               4

ethnicity:
    hispanic or latino not hispanic or latino                   NA's
                     5                    138                     36

Including an additional 894 columns
```

PRAD *Prostate adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( PRAD )
ExperimentList class object of length 10:
 [1] CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
 [2] CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
 [3] CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
 [8] Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 550 columns
 [10] RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns

> rownames( PRAD )
CharacterList of length 10
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( PRAD )
CharacterList of length 10
[["CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["Methylation-20160128"]] TCGA-2A-A8VL-01A-21D-A378-05 ...
[["miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
[["Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["RPPAArray-20160128"]] TCGA-2A-A8VL-01A-11-A43M-20 ...

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASeq-20160128  0.7 Mb
2                    CNASNP-20160128 15.6 Mb
3                    CNVSNP-20160128  3.4 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
```

```
6               Methylation-20160128 75.1 Mb
7              miRNASeqGene-20160128  0.1 Mb
8                  Mutation-20160128 21.5 Mb
9           RNASeq2GeneNorm-20160128  1.3 Mb
10                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   488 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  10.00   10.00    3.02    1.99      NA


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  41.00   56.00   61.00   61.02   66.00   78.00      11

vital_status:
  0   1
488  10

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  146.0   743.8  1102.0  1579.0  2315.5  3502.0     488

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   23.0   523.5   926.0  1076.5  1458.0  5024.0      10

tumor_tissue_site:
prostate
     498


pathology_N_stage:
  n0   n1 NA's
 346   79   73

gender:
male
 498

date_of_initial_pathologic_diagnosis:
```

```
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
      2000    2009    2011    2010    2012    2013      31 

radiation_therapy:
  no  yes NA's 
 395   59   44 

histological_type:
   prostate adenocarcinoma acinar type prostate adenocarcinoma, other subtype 
                                   483                                     15 

residual_tumor:
  r0   r1   r2   rx NA's 
 316  147    5   15   15 

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
 0.0000  0.0000  0.0000  0.4447  0.0000 15.0000      91 

gleason_score:
  6   7   8   9  10 
 45 248  64 137   4 

psa_value:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  0.000   0.030   0.100   1.742   0.110 323.000      57 

days_to_psa:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
 -164.0   191.0   512.0   685.6   926.0  3447.0      53 

race:
                    asian black or african american                     white 
                        2                         7                       147 
                     NA's 
                      342 

ethnicity:
not hispanic or latino                   NA's 
                   152                    346 

Including an additional 1126 columns
```

READ *Rectum adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( READ )
ExperimentList class object of length 13:
 [1] CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
 [2] CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
 [3] CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [10] Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
 [11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 72 columns
 [12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
 [13] RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns

> rownames( READ )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

> colnames( READ )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["Methylation_methyl27-20160128"]] TCGA-AF-2689-11A-01D-1552-05 ...
[["Methylation_methyl450-20160128"]] TCGA-AF-2687-01A-02D-1734-05 ...
[["miRNASeqGene-20160128"]] TCGA-AF-2687-01A-02T-1735-13 ...
[["mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
...
<3 more elements>

Sizes of each ExperimentList element:

                         assay size.Mb
1                  CNASeq-20160128  1.5 Mb
2                  CNASNP-20160128  4.3 Mb
```

```
3                    CNVSNP-20160128  1.1 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6      Methylation_methyl27-20160128  4.9 Mb
7     Methylation_methyl450-20160128   75 Mb
8              miRNASeqGene-20160128  0.1 Mb
9                 mRNAArray-20160128  1.1 Mb
10                 Mutation-20160128  9.6 Mb
11         RNASeq2GeneNorm-20160128  1.3 Mb
12               RNASeqGene-20160128  1.3 Mb
13                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   142 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  27.00   27.00    2.00    1.44    3.25


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  31.00   57.00   66.00   64.37   72.00   90.00

vital_status:
  0   1
141  28

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   59.0   347.5   730.0   786.1  1193.0  1741.0     142

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   366.0   625.0   779.5  1096.0  3932.0      28

tumor_tissue_site:
rectum   NA's
   166      3




pathology_M_stage:
```

```
  m0   m1  m1a   mx NA's 
 128   22    2   14    3 

gender:
female   male 
    77     92 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   1999    2007    2009    2008    2010    2012 

days_to_last_known_alive:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   31.0   292.2   863.0  1420.1  2214.5  3667.0     161 

radiation_therapy:
  no  yes NA's 
 114   22   33 

histological_type:
         rectal adenocarcinoma rectal mucinous adenocarcinoma 
                           150                             13 
                          NA's 
                             6 

tumor_stage:
stage iia      NA's 
        1       168 

residual_tumor:
  r0   r1   r2   rx NA's 
 126    2   12    5   24 

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  0.000   0.000   0.000   2.692   3.000  31.000      10 

ethnicity:
    hispanic or latino not hispanic or latino                   NA's 
                     1                     84                     84 

Including an additional 2242 columns
```

SARC *Sarcoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( SARC )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns
 [7] Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 265 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns

> rownames( SARC )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( SARC )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["Methylation-20160128"]] TCGA-3B-A9HI-01A-11D-A388-05 ...
[["miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                   CNASNP-20160128  9.2 Mb
2                   CNVSNP-20160128    3 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5              Methylation-20160128   75 Mb
6             miRNASeqGene-20160128  0.1 Mb
7                 Mutation-20160128 18.1 Mb
8          RNASeq2GeneNorm-20160128  1.3 Mb
9                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
```

```
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   162 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  99.00   99.00    1.78    1.51    2.46


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  20.00   53.00   61.00   60.88   71.00   90.00       1

vital_status:
  0   1
162  99

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   17.0   322.5   648.0   863.6  1169.5  2694.0     162

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   15.0   585.8  1092.0  1391.1  1891.8  5723.0      99


gender:
female   male
   142    119

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1994    2007    2010    2009    2012    2013       4

radiation_therapy:
  no  yes NA's
 181   74    6


residual_tumor:
  r0   r1   r2   rx NA's
 155   70    9   26    1

race:
                    asian black or african american                     white
                        6                        18                       228
                     NA's
```

```
                         9

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                     5                   223                     33

Including an additional 1413 columns
```

SKCM *Skin Cutaneous Melanoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( SKCM )
ExperimentList class object of length 8:
 [1] CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns
 [5] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [6] Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [7] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [8] RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns

> rownames( SKCM )
CharacterList of length 8
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( SKCM )
CharacterList of length 8
[["CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["Methylation-20160128"]] TCGA-3N-A9WB-06A-11D-A38H-05 ...
[["miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
[["Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["RPPAArray-20160128"]] TCGA-3N-A9WC-06A-21-A444-20 ...

Sizes of each ExperimentList element:
```

```
                    assay  size.Mb
1          CNASeq-20160128   0.9 Mb
2          CNASNP-20160128  12.3 Mb
3          CNVSNP-20160128   3.2 Mb
4     Methylation-20160128  75.1 Mb
5    miRNASeqGene-20160128   0.1 Mb
6        Mutation-20160128 299.6 Mb
7 RNASeq2GeneNorm-20160128   1.3 Mb
8       RPPAArray-20160128     0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   249 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 221.00  221.00    2.99    2.40    3.90


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  15.00   48.00   58.00   58.24   71.00   90.00       8

vital_status:
  0   1
247 223

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     79     518    1093    1789    2073   10870     249

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   -2.0   477.5  1146.0  1885.3  2658.8 11252.0     230

days_to_submitted_specimen_dx:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     -2       0     344    1017    1372   10847      14




melanoma_ulceration:
```

```
  no  yes NA's 
 146  167  157 

melanoma_primary_known:
 no yes 
 47 423 

Breslow_thickness:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  0.000   1.300   3.000   5.585   6.950  75.000     111 

gender:
female   male 
   180    290 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1978    2003    2008    2006    2011    2013      11 

radiation_therapy:
  no  yes NA's 
 420   49    1 

race:
                    asian black or african american                     white 
                       12                         1                       447 
                     NA's 
                       10 

ethnicity:
    hispanic or latino not hispanic or latino                   NA's 
                    11                    446                     13 

Including an additional 1517 columns
```

`STAD` *Stomach adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( STAD )
ExperimentList class object of length 12:
 [1] CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
 [2] CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
 [3] CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
```

```
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
 [9] Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
 [10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [11] RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 36 columns
 [12] RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns

> rownames( STAD )
CharacterList of length 12
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( STAD )
CharacterList of length 12
[["CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["Methylation_methyl27-20160128"]] TCGA-BR-4183-11A-01D-1129-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3M-AB46-01A-11D-A411-05 ...
[["miRNASeqGene-20160128"]] TCGA-3M-AB46-01A-11R-A415-13 ...
[["Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
...
<2 more elements>

Sizes of each ExperimentList element:

                               assay  size.Mb
1                    CNASeq-20160128   0.9 Mb
2                    CNASNP-20160128  12.1 Mb
3                    CNVSNP-20160128   3.4 Mb
4          GISTIC_AllByGene-20160128   4.9 Mb
5  GISTIC_ThresholdedByGene-20160128   4.9 Mb
6      Methylation_methyl27-20160128   4.9 Mb
7     Methylation_methyl450-20160128    75 Mb
8              miRNASeqGene-20160128   0.1 Mb
9                  Mutation-20160128 161.5 Mb
10           RNASeq2GeneNorm-20160128   1.3 Mb
11                RNASeqGene-20160128   1.7 Mb
```

```
12                RPPAArray-20160128     0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   273 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
170.000 170.000   0.948   0.792   1.085


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  30.00   58.00   67.00   65.73   73.00   90.00       9

vital_status:
  0   1
268 175

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   194.0   346.0   423.7   553.5  2197.0     273

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    0.0   335.5   547.5   673.7   912.0  3720.0     177

tumor_tissue_site:
stomach
    443




pathology_M_stage:
 m0  m1  mx
391  30  22

gender:
female   male
   158    285

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   1996    2010    2011    2010    2012    2013       6
```

```
radiation_therapy:
  no  yes NA's 
 323   77   43 


residual_tumor:
  r0   r1   r2   rx NA's 
 350   18   19   25   31 

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  0.000   0.000   3.000   5.635   8.000  57.000      51 

race:
                                    asian 
                                       89 
                black or african american 
                                       13 
native hawaiian or other pacific islander 
                                        1 
                                    white 
                                      278 
                                     NA's 
                                       62 

ethnicity:
    hispanic or latino not hispanic or latino                   NA's 
                     5                    318                    120 

Including an additional 1390 columns
```

TGCT *Testicular Germ Cell Tumors*

Description

A document describing the TCGA cancer code

Details

```
> experiments( TGCT )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [7] Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 139 columns
```

```
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns

> rownames( TGCT )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( TGCT )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["Methylation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Z-05 ...
[["miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...
[["Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                   CNASNP-20160128  3.8 Mb
2                   CNVSNP-20160128  0.8 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5              Methylation-20160128   75 Mb
6             miRNASeqGene-20160128  0.1 Mb
7                 Mutation-20160128   10 Mb
8          RNASeq2GeneNorm-20160128  1.3 Mb
9                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   130 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 4.0000  4.0000  1.5493  0.0466      NA


---------------------------
```

```
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  14.00   26.00   31.00   31.99   37.00   67.00

vital_status:
  0   1
130   4

days_to_death:
  17  513  618 6972 NA's
   1    1    1    1  130

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    3.0   688.2  1265.5  2092.7  2826.2  7437.0       4

tumor_tissue_site:
testes
   134


pathology_T_stage:
t1 t2 t3 tx
76 51  6  1

pathology_N_stage:
  n0   n1   n2   nx NA's
  46   11    2   65   10

pathology_M_stage:
  m0   m1  m1a  m1b NA's
 115    2    1    1   15

gender:
male
 134

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1992    2006    2009    2008    2012    2013

radiation_therapy:
  no  yes NA's
 111   21    2

karnofsky_performance_score:
  80   90  100 NA's
   5   41   56   32
```

```
race:
                    asian black or african american                     white
                        4                         6                       119
                     NA's
                        5

ethnicity:
    hispanic or latino not hispanic or latino                   NA's
                    12                    111                     11

Including an additional 762 columns
```

`THCA` *Thyroid carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( THCA )
ExperimentList class object of length 11:
 [1] CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
 [2] CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
 [3] CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
 [8] Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 568 columns
 [10] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
 [11] RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns

> rownames( THCA )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22 tAKR
...
<1 more element>

> colnames( THCA )
```

```
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["Methylation-20160128"]] TCGA-4C-A93U-01A-11D-A398-05 ...
[["miRNASeqGene-20160128"]] TCGA-4C-A93U-01A-11R-A39B-13 ...
[["Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["RNASeqGene-20160128"]] TCGA-DJ-A1QE-01A-21R-A14Y-07 ...
...
<1 more element>

Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASeq-20160128  0.2 Mb
2                    CNASNP-20160128 10.7 Mb
3                    CNVSNP-20160128  1.8 Mb
4          GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6               Methylation-20160128 75.1 Mb
7              miRNASeqGene-20160128  0.1 Mb
8                  Mutation-20160128   14 Mb
9           RNASeq2GeneNorm-20160128  1.3 Mb
10               RNASeqGene-20160128  1.3 Mb
11                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   487 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  16.00   16.00    2.80    2.23    4.80


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  15.00   35.00   46.00   47.26   58.00   89.00

vital_status:
  0   1
487  16
```

```
days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    174     743    1021    1176    1631    2973     487 

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
      0     535     943    1220    1513    5423      16 

tumor_tissue_site:
thyroid 
    503 



pathology_N_stage:
 n0  n1 n1a n1b  nx 
227  58  93  75  50 

pathology_M_stage:
  m0   m1   mx NA's 
 280    9  213    1 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   1993    2008    2010    2009    2011    2013 

radiation_therapy:
  no  yes NA's 
 181  306   16 

radiation_exposure:
  no  yes NA's 
 423   17   63 

extrathyroidal_extension:
           minimal (t3) moderate/advanced (t4a)                    none 
                    133                      18                     333 
    very advanced (t4b)                    NA's 
                      1                      18 

residual_tumor:
  r0   r1   r2   rx NA's 
 385   52    4   30   32 

number_of_lymph_nodes:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  0.000   0.000   1.000   3.658   5.000  41.000     114 

multifocality:
multifocal   unifocal       NA's 
       227        266         10 
```

```
tumor_size:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.300   1.700   2.600   2.975   4.000   8.200     100

Including an additional 1481 columns
```

`THYM` *Thymoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( THYM )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
 [7] Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns

> rownames( THYM )
CharacterList of length 9
[[”CNASNP-20160128”]] character(0)
[[”CNVSNP-20160128”]] character(0)
[[”GISTIC_AllByGene-20160128”]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[[”GISTIC_ThresholdedByGene-20160128”]] ACAP3 ... WASIR1|ENSG00000185203.7
[[”Methylation-20160128”]] cg00000029 cg00000108 ... rs966367 rs9839873
[[”miRNASeqGene-20160128”]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[[”Mutation-20160128”]] character(0)
[[”RNASeq2GeneNorm-20160128”]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[[”RPPAArray-20160128”]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( THYM )
CharacterList of length 9
[[”CNASNP-20160128”]] TCGA-3G-AB0O-01A-22D-A422-01 ...
[[”CNVSNP-20160128”]] TCGA-3G-AB0O-01A-22D-A422-01 ...
[[”GISTIC_AllByGene-20160128”]] TCGA-3G-AB0O-01A-22D-A422-01 ...
[[”GISTIC_ThresholdedByGene-20160128”]] TCGA-3G-AB0O-01A-22D-A422-01 ...
[[”Methylation-20160128”]] TCGA-3G-AB0O-01A-22D-A424-05 ...
[[”miRNASeqGene-20160128”]] TCGA-3G-AB0O-01A-22R-A42W-13 ...
[[”Mutation-20160128”]] TCGA-3G-AB0O-01A-22D-A423-09 ...
[[”RNASeq2GeneNorm-20160128”]] TCGA-3G-AB0O-01A-22R-A42C-07 ...
[[”RPPAArray-20160128”]] TCGA-3G-AB0O-01A-11-A45R-20 ...
```

```
Sizes of each ExperimentList element:

                              assay size.Mb
1                   CNASNP-20160128  2.9 Mb
2                   CNVSNP-20160128  0.5 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5              Methylation-20160128   75 Mb
6             miRNASeqGene-20160128  0.1 Mb
7                 Mutation-20160128  3.1 Mb
8          RNASeq2GeneNorm-20160128  1.3 Mb
9                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   115 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
   9.00    9.00    2.34    1.04      NA


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  17.00   49.50   60.00   58.15   68.50   84.00       1

vital_status:
  0   1
115   9

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    124     379     853    1423    2488    3488     115

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   14.0   725.2  1267.5  1486.3  1947.0  4575.0      10

tumor_tissue_site:
anterior mediastinum               thymus
                  27                   97

gender:
female   male
```

```
    60     64

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   2000    2008    2010    2010    2012    2013       1

radiation_therapy:
 no yes
 81  43


race:
                    asian black or african american                     white
                       13                         6                       103
                     NA's
                        2

ethnicity:
    hispanic or latino not hispanic or latino                  NA's
                    10                    100                    14

Including an additional 685 columns
```

UCEC *Uterine Corpus Endometrial Carcinoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( UCEC )
ExperimentList class object of length 13:
 [1] CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
 [7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns
 [8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [10] Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
 [11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 380 columns
 [12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
 [13] RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns

> rownames( UCEC )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
```

```
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

> colnames( UCEC )
CharacterList of length 13
[["CNASeq-20160128"]] TCGA-A5-A0G5-01A-11D-A043-02 ...
[["CNASNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["CNVSNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A5-A0G2-01A-11D-A039-05 ...
[["Methylation_methyl450-20160128"]] TCGA-2E-A9G8-01A-11D-A409-05 ...
[["miRNASeqGene-20160128"]] TCGA-2E-A9G8-01A-11R-A404-13 ...
[["mRNAArray-20160128"]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[["Mutation-20160128"]] TCGA-A5-A0G3-01A-11W-A062-09 ...
...
<3 more elements>

Sizes of each ExperimentList element:

                               assay size.Mb
1                  CNASeq-20160128    1 Mb
2                  CNASNP-20160128 16.9 Mb
3                  CNVSNP-20160128  3.7 Mb
4        GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6     Methylation_methyl27-20160128  4.9 Mb
7    Methylation_methyl450-20160128 75.1 Mb
8            miRNASeqGene-20160128  0.1 Mb
9               mRNAArray-20160128  1.1 Mb
10               Mutation-20160128 73.1 Mb
11        RNASeq2GeneNorm-20160128  1.3 Mb
12             RNASeqGene-20160128  1.3 Mb
13              RPPAArray-20160128  0.1 Mb


---------------------------
Available sample meta-data:
---------------------------

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   50.0   367.0   709.0   881.8  1063.0  3423.0     457
```

```
days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   -6.0   543.0   948.5  1195.1  1753.2  6859.0      92 

tumor_tissue_site:
   endometrial other  specify 
           547             1 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   1995    2007    2009    2009    2010    2013       9 

days_to_last_known_alive:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    145     404     729    1405    2096    4144     535 

radiation_therapy:
  no  yes NA's 
 295  228   25 

histological_type:
endometrioid endometrial adenocarcinoma           mixed serous and endometrioid 
                                    411                                      22 
      serous endometrial adenocarcinoma 
                                    115 

residual_tumor:
  r0   r1   r2   rx NA's 
 376   22   16   41   93 

Including an additional 1779 columns
```

UCS *Uterine Carcinosarcoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( UCS )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
 [7] Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
```

```
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns

> rownames( UCS )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( UCS )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["Methylation-20160128"]] TCGA-N5-A4R8-01A-11D-A28S-05 ...
[["miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...

Sizes of each ExperimentList element:

                              assay size.Mb
1                   CNASNP-20160128  1.5 Mb
2                   CNVSNP-20160128  0.6 Mb
3         GISTIC_AllByGene-20160128  4.9 Mb
4 GISTIC_ThresholdedByGene-20160128  4.9 Mb
5              Methylation-20160128   75 Mb
6             miRNASeqGene-20160128  0.1 Mb
7                 Mutation-20160128 19.7 Mb
8          RNASeq2GeneNorm-20160128  1.3 Mb
9                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   22 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  35.00   35.00    1.43    1.04    1.96
```

```
---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
  51.00   62.00   68.00   69.72   76.00   90.00 

vital_status:
 0  1 
22 35 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    8.0   304.0   522.0   705.4   790.5  3115.0      22 

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    0.0   591.2   828.0  1183.4  1647.5  4269.0      35 

tumor_tissue_site:
uterus 
    57 

gender:
female 
    57 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   2002    2007    2009    2009    2011    2012 

radiation_therapy:
  no  yes NA's 
  29   25    3 

histological_type:
uterine carcinosarcoma/ malignant mixed mullerian tumor (mmmt): nos 
                                                                 24 
                    uterine carcinosarcoma/ mmmt: heterologous type 
                                                                 20 
                       uterine carcinosarcoma/mmmt: homologous type 
                                                                 13 

race:
                    asian black or african american                      white 
                        3                         9                         44 
                     NA's 
                        1 

ethnicity:
    hispanic or latino not hispanic or latino                   NA's 
```

```
                    1                     43                    13

Including an additional 632 columns
```

`UVM` *Uveal Melanoma*

Description

A document describing the TCGA cancer code

Details

```
> experiments( UVM )
ExperimentList class object of length 10:
 [1] CNASeq-20160128: RaggedExperiment with 6496 rows and 102 columns
 [2] CNASNP-20160128: RaggedExperiment with 69487 rows and 160 columns
 [3] CNVSNP-20160128: RaggedExperiment with 12973 rows and 160 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [8] Mutation-20160128: RaggedExperiment with 2174 rows and 80 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [10] RPPAArray-20160128: SummarizedExperiment with 192 rows and 12 columns

> rownames( UVM )
CharacterList of length 10
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

> colnames( UVM )
CharacterList of length 10
[["CNASeq-20160128"]] TCGA-RZ-AB0B-01A-11D-A40D-26 ...
[["CNASNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["CNVSNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["Methylation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39X-05 ...
[["miRNASeqGene-20160128"]] TCGA-RZ-AB0B-01A-11R-A40B-13 ...
[["Mutation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39W-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
[["RPPAArray-20160128"]] TCGA-V3-A9ZX-01A-21-A41Z-20 ...
```

```
Sizes of each ExperimentList element:

                               assay size.Mb
1                    CNASeq-20160128  0.2 Mb
2                    CNASNP-20160128  1.9 Mb
3                    CNVSNP-20160128  0.4 Mb
4           GISTIC_AllByGene-20160128  4.9 Mb
5  GISTIC_ThresholdedByGene-20160128  4.9 Mb
6               Methylation-20160128   75 Mb
7              miRNASeqGene-20160128  0.1 Mb
8                  Mutation-20160128 12.3 Mb
9           RNASeq2GeneNorm-20160128  1.3 Mb
10                RPPAArray-20160128    0 Mb

---------------------------
Overall survival time-to-event summary (in years):
---------------------------

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
    -1)

   57 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  23.00   23.00    1.66    1.14    3.05


---------------------------
Available sample meta-data:
---------------------------

years_to_birth:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  22.00   51.00   61.50   61.65   74.25   86.00

vital_status:
 0  1
57 23

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   40.0   393.5   606.0   693.9  1029.0  1581.0      57

days_to_last_followup:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    4.0   495.0   821.0   861.9  1184.0  2600.0      23

tumor_tissue_site:
choroid
     80
```

```
pathology_N_stage:
  n0   nx NA's 
  52   27    1 

pathology_M_stage:
  m0   m1  m1b   mx NA's 
  51    2    2   23    2 

gender:
female   male 
    35     45 

date_of_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   2007    2011    2012    2012    2013    2013 

radiation_therapy:
  no  yes NA's 
  76    3    1 

race:
white  NA's 
   55    25 

ethnicity:
    hispanic or latino not hispanic or latino                     NA's 
                     1                     52                       27 

Including an additional 448 columns
```

Index